KEY: Z is charge state. XCorr, DeltCn, SpR (for Sp Rank), SpScore are SEQUEST results. M+H+ is the measured parent ion mass and the CalcM+H+ is the calculated parent ion mass. IonProportion is the percent of matched ions. In Sequence, a number after every letter indicates a 15N peptide.

0	ionProportio	n is the percent of matched ions. In Sequence, a number after every letter indicates a	15N peptide							
Caution 344 printed pages LocusID	Y Name	Description ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport: member of heat shock protein 70 (HSP70) family. forms a	Z	XCorr	DeltCN	M+H+	CalcM+H+ SpR	S	pScore Io	nProportion Sequence
gi 6319314 ref NP_009396.1	YAL005C	chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	:	2 3.991	5 0.3211	1991.35	1991.102	4	445.9	50 L.V1T1D1Y1F1N2G1K2E1P1N2R4S1I1N2P1D1.E
gi 6319314 ref NP_009396.1	YAL005C	chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	:	2 3.349	7 0.3254	2671.49	2671.882	1	338.3	33.333336 N.D1A1V1V1T1V1P1A1Y1F1N2D1S1Q2R4Q2A1T1K2D1A1G1T11A1.G
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed		1 2.281	2 0.1939	1159.47	1160.188	1	232.8	61.11111 T.HLGGEDFDNR.L
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed		1 2.415	5 0.1761	1175.36	1176.188	1	270.5	66.66667 T.H3L1G1G1E1D1F1D1N2R4.L
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed		1 3.2904	4 0.2992	1533.7	1531.795	1	484.2	53.571426 T.GIPPAPRGVPQIEVT.F
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	:	2 4.5170	6 0.354	1937.45	1938.101	1	1077.3	66.66667 E.AEKFKEEDEKESQRIA.S
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed		1 3.281	7 0.3412	1353.69	1354.59	1	714.8	72.72727 F.KLIDVDGKPQIQ.V
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NI S)-directed	:	2 4.41:	3 0.3052	2 1354.01	1354.59	1	1864.4	86.36364 F.KLIDVDGKPQIQ.V
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Sa1p ATPase involved in protein folding and nuclear localization signal (NI S)-directed		1 3.613	8 0.2801	1370.51	1370.59	1	807.7	72.72727 F.K2L111D1V1D1G1K2P1Q2I1Q2.V
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Sa1p.	:	2 3.775	3 0.3391	1403.79	1404.522	1	435.4	68.181816 A.H3F1A1N2D1R4V1D11111A1N2.D
gi 6319314 ref NP_009396.1	YAL005C	A rease involved in protein rotung and notein localization signal (NLS)-chienced nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Sas1p	:	2 3.262	1 0.152	2 1461.33	1460.686	8	321.8	68.181816 L.D1K2K2G1K2E1E1H3V1L11F1.D
gi 6319314 ref NP_009396.1	YAL005C	A I Pase involved in protein tolding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p		1 2.935	9 0.2362	2 1442.74	1443.686	1	432.3	59.090908 L.DKKGKEEHVLIF.D
gi 6319314 ref NP_009396.1	YAL005C	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	:	2 3.316	8 0.3578	3 1443.01	1443.686	8	230.9	63.636364 L.DKKGKEEHVLIF.D
ail6319314 refINP 009396.1	YAL005C	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa10	:	2 3.194	2 0.3995	5 1631.77	1632.897	1	283.5	57.692307 Y.G1L1D1K2K2G1K2E1E1H3V1L111F1.D
ail6310314/rafINP_000306.11	XAL 005C	ATP ase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Seate		2 3 230	4 0.2603	1606.20	1605 618	1	521.8	
-:::::::::::::::::::::::::::::::::::::	VALOOSC	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall;		2 3.230	0.2030	0000.23	2020.002		521.0	
gij6319314 ref NP_009396.1	YAL005C	Sarip ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall;		2 3.49	9 0.2675	2028.13	2029.092	1	523	47.22222 K.ATTTATGTUTTTH3LTGTGTETUTFTUTN2K4LTVTN2.H
gi 6319314 ref NP_009396.1	YAL005C	Saa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall;	:	2 3.233	8 0.2465	5 2003.43	2003.092	1	407.8	44.444447 K.ATAGDTHLGGEDFDNRLVN.H
gi 6319314 ref NP_009396.1	YAL005C	Sa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall;	:	2 3.166	4 0.2432	2 1352.11	1354.59	1	699.3	77.27273 F.KLIDVDGKPQIQ.V
gi 6319314 ref NP_009396.1	YAL005C	Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydi fp; localized to the nucleus, cytoplasm, and cell wall	:	2 3.641	5 0.269	2532.11	2529.684	1	436	40.476192 L.V1T1D1Y1F1N2G1K2E1P1N2R4S1I1N2P1D1E1A1V1A1Y1.G
gi 6319314 ref NP_009396.1	YAL005C	Satip ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a	:	2 3.539	9 0.163	2019.61	2020.305	3	606.9	46.875 E.EFDDKLKELQDIANPIM.S
gi 6319314 ref NP_009396.1	YAL005C	Ssa1p	:	2 3.559	8 0.1511	2041.83	2041.305	5	683.5	50 E.E1F1D1D1K2L1K2E1L1Q2D1I1A1N2P1I1M1.S

		ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall;								
gi 6319314 ref NP_009396.1	YAL005C	Saa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chanerone complex with Virito localized to the nucleus; cutoplasm; and cell wall:	2	4.4116	0.1919	1372.31	1370.59	1	1475	81.818184 F.K2L111D1V1D1G1K2P1Q2I1Q2.V
gi 6319314 ref NP_009396.1	YAL005C	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a	1	3.3319	0.341	1353.73	1354.59	1	805.8	72.72727 F.KLIDVDGKPQIQ.V
gi 6319314 ref NP_009396.1	YAL005C	chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a	2	3.5609	0.2739	2500.89	2500.684	1	597.6	40.476192 L.VTDYFNGKEPNRSINPDEAVAY.G
gi 6319314 ref NP_009396.1	YAL005C	chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	2	3.1143	0.3749	2020.49	2022.181	1	374.7	41.17647 Y.FNGKEPNRSINPDEAVAY.G
gi 6319314 ref NP_009396.1	YAL005C	Autoreal transport, memoer of near shock protein 70 (HSP70) family, forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	2	3.8942	0.3645	2212.49	2211.357	4	290.7	38.88889 D.Y1F1N2G1K2E1P1N2R4S1I1N2P1D1E1A1V1A1Y1.G
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	2	3.9763	0.4749	1622.85	1623.725	1	456.5	65.38461 T.HLGGEDFDNRLVNH.F
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	3.1629	0.2045	1461.71	1460.686	1	451.3	63.636364 L.D1K2K2G1K2E1E1H3V1L111F1.D
gi 6319314 ref NP_009396.1	YAL005C	A I Pase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	2.9325	0.2937	1442.68	1443.686	1	507.8	63.636364 L.DKKGKEEHVLIF.D
	V/41 0050	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall;		0.4045	0.070.4	1000 57	1000.0		504.4	
gi 6319314 ret NP_009396.1	YAL005C	Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall;	2	3.1015	0.2784	1882.57	1883.2	1	564.1	50 K.HEPERLIDVDGKPQIQ.V
gi 6319314 ref NP_009396.1	YAL005C	Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a changroup complex with vitro localized to the nucleus cutoplagment and call wall:	1	2.4512	0.1775	1247.54	1248.381	2	131.9	60.000004 H.FANDRVDIIAN.D
gi 6319314 ref NP_009396.1	YAL005C	Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a	2	3.221	0.1753	1371.39	1370.59	1	702	72.72727 F.K2L111D1V1D1G1K2P1Q2I1Q2.V
gi 6319314 ref NP_009396.1	YAL005C	chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a	1	3.6795	0.3253	1370.57	1370.59	1	842.4	72.72727 F.K2L111D1V1D1G1K2P1Q211Q2.V
gi 6319314 ref NP_009396.1	YAL005C	chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport: member of heat shock protein 70 (HSP70) family: forms a	2	4.4942	0.3686	2326.43	2327.446	1	482.3	42.105263 T.D1Y1F1N2G1K2E1P1N2R4S1I1N2P1D1E1A1V1A1Y1.G
gi 6319314 ref NP_009396.1	YAL005C	chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	2	4.1382	0.3494	2298.75	2300.446	2	481.6	39.473686 T.DYFNGKEPNRSINPDEAVAY.G
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; memoer of neat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	2	3.1681	0.1549	1396.27	1397.481	3	351.7	70 E.KFKEEDEKESQ.R
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed	2	5.026	0.2624	1756.47	1758.907	1	1455.9	76.92308 E.K2F1K2E1E1D1E1K2E1S1Q2R4I1A1.S
gi 6319314 ref NP_009396.1	YAL005C	nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p ATPracting involved in protein folding and nuclear localization signal (NILS) directed	2	4.8959	0.3685	1737.35	1737.907	1	1472.4	76.92308 E.KFKEEDEKESQRIA.S
gi 6319314 ref NP_009396.1	YAL005C	Arr as involved in protein localing and localization localization (RLS) related to nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	3.2424	0.3812	1549.7	1550.795	2	302.9	46.42857 T.G111P1P1A1P1R4G1V1P1Q211E1V1T1.F
gi 6319314 ref NP_009396.1	YAL005C	A I Pase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	2.4917	0.1594	1598.68	1599.828	1	489.4	57.692307 F.RSTLDPVEKVLRDA.K
nil6319314/refINP_009396-11	XAL005C	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssatn	2	2 9663	0 1828	1600 39	1599 828	1	589.2	
910313314[relini _003330.1]	TALOUSC	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall;	2	2.3003	0.1020	1000.33	1399.020		303.2	
gi 6319314 ref NP_009396.1	YAL005C	Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Vd11p; localized to the nucleus: cytoplasm and cell wall:	2	3.0745	0.3087	1444.73	1443.686	1	297.1	68.181816 L.DKKGKEEHVLIF.D
gi 6319314 ref NP_009396.1	YAL005C	Ssa1p ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a	1	2.8026	0.3393	1442.64	1443.686	1	438	59.090908 L.DKKGKEEHVLIF.D
gi 6319314 ref NP_009396.1	YAL005C	cnaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	3.0099	0.1769	1459.65	1460.686	3	336.3	54.545456 L.D1K2K2G1K2E1E1H3V1L1I1F1.D

gi 6319312 ref NP_009395.1	YAL007C	Protein that forms a heterotrimeric complex with Erp1p, Emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi transport and localized to COPII-coated vesicles; Erp2p Protein that forms a heterotrimeric complex with Ero1p. Emp24p, and Erv25p;	2	4.2975	0.3776	1873.37	1871.996	1	713.9	63.333332 T.LEKEKTLTDEHEADVN.N
gi 6319312 ref NP_009395.1	YAL007C	member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi transport and localized to COPII-coated vesicles; Erp2p	2	3.0344	0.2332	1783.21	1780.985	3	198.9	50 N.N2A1V1E1E111D1R4N2L1N2K2I1T1K2.T
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	4.109	0.3968	2420.33	2419.691	1	873.8	58.333332 S.W2D1F1P1S1G1E1I1Y1P1D1Y1L1D1Y1V1K2M1R4.L
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	1	2.2721	0.2071	1312.6	1311.399	1	225	55 N.NHVVWDEAHFG.K
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	1	3.9454	0.3475	1585.72	1586.75	1	752.6	75 N.NHVVWDEAHFGKF.G
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	1	3.0074	0.4212	1244.65	1245.424	1	551	68.181816 L.HTHPVAAPVSKT.Q
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	1	3.2972	0.4176	1262.55	1262.424	1	672.1	72.72727 L.H3T1H3P1V1A1A1P1V1S1K2T1.Q
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	3.4194	0.3826	1391.77	1392.555	1	645.1	79.16667 L.H3T1H3P1V1A1A1P1V1S1K2T1Q2.W
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	1	3.8861	0.4159	1458.52	1458.69	1	1163.5	77.27273 E.F1Y1H3D1V1H3P1P1L1G1K2M1.L
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	1	3.3582	0.3811	1440.49	1441.69	1	1176.3	77.27273 E.FYHDVHPPLGKM.L
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	3.6536	0.2486	1836.81	1836.91	1	548.8	53.333336 A.DERDAEDFSKEKPAAQ.S
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	3.4434	0.3225	2395.41	2395.691	1	558	47.22222 S.WDFPSGEIYPDYLDYVKMR.L
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	2.9069	0.2042	2468.83	2469.676	1	280.1	44.736843 E.THENERLPPRPEDFQYPKTN.F
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	3.6092	0.3548	1585.81	1586.75	1	2000.5	83.33333 N.NHVVWDEAHFGKF.G
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	4.0658	0.1762	1940.31	1941.116	9	352.2	46.875 Y.G1D1N2V1V1G1D1N2K2D1N2W2V111E111M1.D
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	3.6604	0.2884	1920.35	1919.116	3	308.4	46.875 Y.GDNVVGDNKDNWVIEIM.D
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	3.6645	0.2843	1674.45	1674.746	1	427.4	61.538464 M.D1Q2R4G1D1E1D1P1E1K2L1H3T1L1.T
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	3.7838	0.3785	1457.45	1458.69	1	1429.3	86.36364 E.F1Y1H3D1V1H3P1P1L1G1K2M1.L
gi 27469358 ref NP_009379.2	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	2	2.9489	0.2039	1443.45	1441.69	1	1116.9	77.27273 E.FYHDVHPPLGKM.L
gi 6319293 ref NP_009376.1	YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 18S rRNA; Drs2p	3	4.6938	0.371	3469.04	3470.62	1	532.9	29.310345 Y.Y111P1P1S1H3V1L1P1E1E1T111D1L1D1A1D1D1D1D1N2I1E1N2D1V1H3E1N2L1.F
gi 6319293 ref NP_009376.1	YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 18S rRNA; Drs2p	2	4.081	0.2536	1798.35	1797.083	3	405	53.571426 L.NDRQIPLSPDQMILR.G
gi 6319293 ref NP_009376.1	YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 18S rRNA; Drs2p	2	3.8775	0.4432	1879.61	1880.105	1	922.6	62.5 T.AIEDKLQDGVPETIHTL.Q
gi 6319293 ref NP_009376.1	YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 18S rRNA; Drs2p	2	3.5151	0.2911	1980.39	1981.21	1	789.4	52.941177 A.TAIEDKLQDGVPETIHTL.Q

gi 6319293 ref NP_009376.1	YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 18S rRNA; Drs2p	3	3.8146	0.2467	3432.14	3433.62	1	592.9	25.862068 Y.YIPPSHVLPEETIDLDADDDNIENDVHENL.F
gi 6319293 ref NP_009376.1	YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 18S rRNA; Drs2p	3	4.0538	0.3233	3749.18	3750.989	1	1071	Y.Y1I1P1P1S1H3V1L1P1E1E1T111D1L1D1A1D1D1D1N2I1E1N2D1V1H3E1N2L1F1 28.225807 M1.S
gi 6319293 ref NP_009376.1	YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 18S rRNA; Drs2p	2	3.0312	0.219	1857.19	1857.052	1	366.2	56.666668 Y.Y111P1P1S1H3V1L1P1E1E1T111D1L1D1.A
gi 6319293 ref NP_009376.1	YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 185 rRNA; Drs2p One of two two V movies; required for mother-specific HO expression for the bud	2	2.9958	0.1529	1259.39	1258.372	4	702	60.000004 A.E1K2L1D1E1A1A1N2L111E1.K
gi 6319290 ref NP_009373.1	YAL029C	tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p; Myodp One of two two V movies: required for mather specific HO expression, for the bud	2	3.8897	0.3524	2606.59	2607.836	1	756.8	45.454548 N.SFENDDDHPTLPVLRNPPILEST.D
gi 6319290 ref NP_009373.1	YAL029C	tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p; Myodp One of two two V sweapper required for matter specifie HO suprantian for the bud	2	4.244	0.4104	2637.55	2637.836	1	820.7	45.454548 N.S1F1E1N2D1D1D1H3P1T1L1P1V1L1R4N2P1P1I1L1E1S1T1.D
gi 6319290 ref NP_009373.1	YAL029C	tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p; Myo4p	2	3.0431	0.1574	1957.73	1955.215	1	483.9	53.333336 Y.LNDLENETLKVFDKIY.S
gi 6319290 ref NP_009373.1	YAL029C	tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p; Myo4p	2	3.3544	0.3548	2445.81	2447.653	1	313.8	35 N.S1F1E1N2D1D1D1H3P1T1L1P1V1L1R4N2P1P1I1L1E1.S
gi 6319290 ref NP_009373.1	YAL029C	One of two type v myosins; required for mother-specific HO expression, for the bud tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p; Myo4p	2	3.6015	0.3217	2316.85	2317.538	1	796.7	47.368423 N.S1F1E1N2D1D1D1H3P1T1L1P1V1L1R4N2P1P1I1L1.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	5.6262	0.4529	3536.6	3536.355	1	697.1	27.67857 S.HENEDQNQGEEEEEGEEEEEEERAHVH.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	4.818	0.3854	2833.7	2834.083	1	1711.1	35.416664 S.R4L1L1V1V1G1P1E1D1D1E1D1E1L1M1D1D1V1M1D1D1L1T1G1L1.L
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	4.5574	0.3137	2808.47	2806.083	1	2162.2	52.083332 S.RLLVVGPEDDEDELMDDVMDDLTGL.L
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	4.7499	0.4341	2836.45	2834.083	1	2072.8	52.083332 S.R4L1L1V1V1G1P1E1D1D1E1D1E1L1M1D1D1V1M1D1D1L1T1G1L1.L
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	4.2338	0.3409	4205.84	4205.647	1	619	19.736843 S.RLLVVGPEDDEDELMDDVMDDLTGLLDSVDTTGKGVVVQ.A
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.8444	0.1888	1515.43	1514.819	1	1029.4	83.33333 K.V111E1E1K2K2D1G1K2P111L1K2.S
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	1	2.4108	0.1943	926.53	927.075	1	311.5	78.57143 T.L1R4V1G1T1P1I1C1.A
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	5.8402	0.4674	3269.09	3270.098	1	704.6	27.884615 E.NEDQNQGEEEEEGEEEEEEERAHVH.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	5.7112	0.4053	3306.08	3308.098	1	979.6	26.923079 E.N2E1D1Q2N2Q2G1E1E1E1E1E1G1E1E1E1E1E1E1E1E1E1E1E1R4A1H3V1H3.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	4.4668	0.3192	2961.95	2962.106	1	857.9	33.333336 K.K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L111D1D1W2E1N2L1.A
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	7.0203	0.5072	3579.65	3578.355	1	1380.9	32.142857 S.H3E1N2E1D1Q2N2Q2G1E1E1E1E1E1G1E1E1E1E1E1E1E1E1E1E1E1E1R4A1H3V1H3.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	4.7213	0.4456	3692.18	3694.512	1	903.5	30.833334 T.ASHENEDQNQGEEEEEGEEEEEEERAHVH.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.5286	0.2083	3147.13	3148.358	2	366.2	30.769232 D.SKKDSEVVPDDELKESEDVLIDDWENLA
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	5.8958	0.2754	3266.15	3263.447	1	1418.7	31.48148 S.DSKKDSEVVPDDELKESEDVLIDDWENLA
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	6.4723	0.4089	3481.85	3482.685	1	2030.7	S.D1S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L1I1D1D1W2E1N2L1A1L1. 35.344826 G
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	4.8	0.273	3448.97	3447.685	1	1350.8	30.172413 S.DSKKDSEVVPDDELKESEDVLIDDWENLAL.G
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	4.0158	0.4218	2833.05	2834.083	1	912.4	39.583336 S.R4L1L1V1V1G1P1E1D1D1E1D1E1L1M1D1D1V1M1D1D1L1T1G1L1.L
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.4309	0.1891	1352.21	1352.533	1	858.1	83.33333 A.L1N2K2I1D1R4L1Y1D1W2.K
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.0796	0.2284	1464.33	1464.707	1	599	80 A.LNKIDRLYDWK.A
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.031	0.2023	1593.45	1593.756	1	409.9	65.38461 S.S1A1S1P1N2K2K2D1L1R4S1P111C1.C

gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.5318	0.2976	1881.81	1883.282	1	569.7	63.333332 Q.EKKVIEEKKDGKPILK.S
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	5.6824	0.5081	3739.07	3738.512	1	1334.4	T.A1S1H3E1N2E1D1Q2N2Q2G1E1E1E1E1G1E1E1E1E1E1E1E1E1E1E1E1E1E1E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	4.1775	0.3589	2514.23	2515.678	1	1014.8	50 D.S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L1I1D1.D
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.8231	0.2969	2490.19	2490.678	1	660.5	50 D.SKKDSEVVPDDELKESEDVLID.D
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.894	0.1829	2630.49	2631.766	1	444.7	40.909092 S.D1S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L111D1.D
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.2668	0.198	2605.11	2605.766	1	514.6	43.18182 S.DSKKDSEVVPDDELKESEDVLID.D
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	4.1431	0.1987	2935.16	2936.068	3	578.3	26.041666 S.D1S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L1I1D1D1W2.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	7.4007	0.4634	3295.64	3296.447	1	1750.7	34.25926 S.D1S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L111D1D1W2E1N2L1.A
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	5.6161	0.2529	2347.65	2347.416	1	199.4	58.823532 LE1R4E1E1E1E1R4L1E1K2E1E1E1E1R4L1A1N2.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	3.6759	0.2699	1762.37	1762.944	1	486.8	64.28571 A.V1R4L1E1D1P1S1G1Q2Q2P111W2G1R4.H
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	3.8117	0.192	3223.49	3226.386	2	675.3	27.083334 Q.L1E1E1Q2E1K2L1E1R4E1E1E1E1R4L1E1K2E1E1E1E1R4L1A1N2.E
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	5.1949	0.1932	3484.97	3486.617	2	640	23.076923 Q.L1E1E1Q2E1K2L1E1R4E1E1E1E1R4L1E1K2E1E1E1E1R4L1A1N2E1E1.K
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	3	5.0418	0.3348	3180.59	3180.358	1	1337.5	34.615387 D.S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L1I1D1D1W2E1N2L1.A
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-IRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	2	2.9639	0.2025	1104.47	1104.311	1	689.2	83.33333 M.S111G1L1G1P1V1Y1K2R4.D
gi 6319282 ref NP_009365.1	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	4.1127	0.3007	1905.61	1905.282	1	700.8	66.66667 Q.E1K2K2V111E1E1K2K2D1G1K2P111L1K2.S
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	1	2.9592	0.2231	1184.44	1184.335	1	358.7	65 T.IGPKTNNPETL.V
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	1	2.6177	0.2194	1508.61	1509.743	1	559.3	53.571426 H.KGVNLPGTDVDLPAL.S
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	4.8673	0.3985	1797.47	1796.854	1	862.3	67.85714 F.E1K2E1P1V1S1D1W2T1D1D1V1E1A1R4.I
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	1	4.0387	0.375	1495.64	1496.717	1	490.1	65.38461 A.R4G1D1L1G111E111P1A1P1E1V1L1.A
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	1	3.618	0.212	1481.79	1479.717	2	582.3	69.230774 A.RGDLGIEIPAPEVLA
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.0839	0.2968	2007.37	2008.173	1	369.2	46.666668 A.Y1L1P1N2Y1D1D1M1R4N2C1T1P1K2P1T1.S
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.8629	0.3544	2251.73	2250.427	1	628	52.77778 F.VFEKEPVSDWTDDVEARIN.F
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.2248	0.1971	2273.65	2275.427	3	340.8	44.444447 F.V1F1E1K2E1P1V1S1D1W2T1D1D1V1E1A1R4I1N2.F
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	4.7569	0.4649	2659.15	2659.927	1	820.3	50 K.G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	4.2204	0.2792	1827.67	1829.103	1	890.6	63.333332 N.N2F1D1E111L1K2V1T1D1G1V1M1V1A1R4.G
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.3537	0.4645	1549.11	1548.736	1	924.1	79.16667 L.PALSEKDKEDLRF.G
gi 6319279 ref NP_009362.1	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	5.1414	0.5418	2755.91	2758.101	1	1167.3	54.166668 H.KGVNLPGTDVDLPALSEKDKEDLRF.G
gi 6319279 ref NP_009362.1	YAL038W	pnospnoenoipyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	5.2992	0.4832	2787.67	2790.101	1	1138.1	54.166668 H.K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi 6319279 ref NP_009362.1	YAL038W	pnospnoenoipyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	4.2782	0.3084	2816.09	2815.153	2	501.1	36 H.KGVNLPGTDVDLPALSEKDKEDLRFG.V
gi 6319279 ref NP_009362.1	YAL038W	glucose fermentation) respiration; Cdc19p	3	4.608	0.288	2815.91	2815.153	1	804.1	31 H.KGVNLPGTDVDLPALSEKDKEDLRFG.V

		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
-: 102402701 END 000202 41	VAL 020W/	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic	2	0.7000	0.0000	4404.07	4404 000	0	C00	
gil6319279[ret]NP_009362.1]	YALU38W	(glucose termentation) respiration; CdC19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.7632	0.3623	1464.37	1464.662	2	689	77.27273 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	4.9192	0.3104	2709.31	2709.956	1	714.8	50 C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1.R
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	4.157	0.4292	2354.73	2355.701	1	340.8	42.5 S.V111D1N2A1R4K2S1E1E1L1Y1P1G1R4P1L1A111A1L1.D
		phosphoenolpvruvate to pvruvate, the input for aerobic (TCA cvcle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	2.9249	0.2972	2079.21	2078.33	6	251.9	34.210526 C.SHKGVNLPGTDVDLPALSEK.D
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	1	3.2777	0.1917	1463.65	1464.662	2	263	63.636364 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.5442	0.37	1447.25	1445.662	1	652.8	72.72727 A.RKSEELYPGRPL.A
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.7149	0.2868	3038.81	3039.372	1	758.7	38.88889 C.SHKGVNLPGTDVDLPALSEKDKEDLRFG.V
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP 009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	4.6499	0.3731	3017.73	3018.32	1	853.9	46.153847 C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
ail6319279/refINP 009362.11	YAL038W	(alucose fermentation) respiration: Cdc19p	2	4.267	0.4026	2980.83	2982.32	1	1023.4	50 C.SHKGVNLPGTDVDLPALSEKDKEDLRF.G
51		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
ail6319279/refINP_009362.11	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (ICA cycle) or anaerobic (glucose fermentation) respiration: Cdc19p	1	2.9832	0.2955	1526.6	1526,743	2	487	53.571426 H.K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1.S
3.1		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
ail6319279/refINP_009362_11	YAI 038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (alucose fermentation) respiration: Cdc19p	2	5 6553	0 4536	2044 37	2045 163	1	1564 5	81 25 F V1F1F1K2F1P1V1S1D1W2T1D1D1V1F1A1R4 I
giloo rozi olioilui _000002.11		Pyruvate kinase, functions as a homotetramer in glycolysis to convert	-	0.0000	0.1000	2011.01	2010.100	·	1001.0	
ail6319270/refINP_009362.11	YAL 038W/	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (alucose fermentation) respiration: Cdc19n	2	3 5315	0.2602	2003 71	2004 117	1	434.2	
gilos 1321 sitelini _003002.11	INECCON	Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	0.0010	0.2002	2000.71	2004.111		404.2	
gil6310270/rofIND_000362.11	VAL 038/M	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic	3	5 2682	0.2622	2024 18	2023 163	1	2560	
gilos 1321 sitelini _003002.11	INECCON	Pyruvate kinase, functions as a homotetramer in glycolysis to convert	0	0.2002	0.2022	2024.10	2020.100		2000	00.1201.W EREI VODWIDDVERU.I
ail6310270/rofIND_000362_11	VAL 038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic	3	5 2134	0 3127	2044.67	2045 163	1	1647.1	45 3125 E V/E1E1K2E1P1V/1S1D1W2T1D1D1V/1E1A1P4 I
gilo313273[rei]NF_003502.1]	TALUSOW	Pyruvate kinase, functions as a homotetramer in glycolysis to convert	5	3.2134	0.5127	2044.07	2043.103	'	1047.1	43.31231.011121122111010101011211010101121111141
ail62102701rofIND_000262.11	VAL 029/M	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic	2	2 2450	0.2700	1094 77	1096 173	1	426.2	
gilo313273[rei]NF_003502.1]	TALUSOW	Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.2433	0.2735	1304.77	1300.173	'	420.2	33.535550 A. TELINT DOMINING IT NET.5
ail6210270/rofIND_000262_11	VAL 029W/	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic	2	2 057	0 2205	2472 11	2472 742	1	000 5	
gilo319279/rei/NP_009362.1/	TALUSOVV	Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.957	0.3395	2473.11	24/3./42	1	900.5	47.61905 V.NEPGTDVDEPALSEKDKEDERF.G
- 100400701 - (IND - 000000 4)	V/41 00 014/	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic		4 4570	0.45	0000 75	0000 007		005.0	
gilo319279[rei]NP_009362.1]	TALUSOV	Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	4.4578	0.45	2028.75	2029.927	1	865.9	50 K.GVNLPGTDVDLPALSEKDKEDLRF.G
-100400701(INID: 000000-41		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic		0.0505	0.0700	4 4 4 9 5 7			774.0	
gi 6319279 ret NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.3585	0.3703	1413.57	1412.614	1	774.6	72.72727 G.R4I111Y1V1D1D1G1V1L1S1F1.Q
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	3	6.7234	0.45	2787.14	2790.101	1	1132.9	40.625 H.K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	3	3.9263	0.3402	2757.2	2758.101	1	632.4	30.208334 H.KGVNLPGTDVDLPALSEKDKEDLRF.G
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	3.1795	0.2855	1820.73	1821.04	1	387.7	47.058823 C.SHKGVNLPGTDVDLPALS.E
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	3	5.26	0.3201	2680.76	2678.956	1	1448.3	34.375 C.SHKGVNLPGTDVDLPALSEKDKEDL.R
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	2.9265	0.2214	1666.53	1666.884	1	408.1	46.666668 S.H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1.S
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.6133	0.3004	1463.71	1464.662	2	685.3	72.72727 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	1	3.0193	0.1526	1464.73	1464.662	1	220.1	59.090908 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.6166	0.3832	1445.49	1445.662	1	953.5	77.27273 A.RKSEELYPGRPL.A
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	1	3.0563	0.311	1444.73	1445.662	1	272.2	63.636364 A.RKSEELYPGRPL.A
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	3	5.0551	0.3342	2981.24	2982.32	1	1166.8	35.576923 C.SHKGVNLPGTDVDLPALSEKDKEDLRF.G
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	3	5.3145	0.325	3018.11	3018.32	1	1104.9	33.653847 C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	2.918	0.192	1236.63	1238.42	3	570.5	72.22222 F.S1H3L1Y1R4G1V1F1P1F1.V

		Pyruvate kinase functions as a homotetramer in alvcolvsis to convert								
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	1	2.9137	0.1839	1323.48	1323.529	1	702.6	62.5 R.GDLGIEIPAPEVL.A
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.4481	0.2392	1237.19	1236.367	1	1400	88.88889 F.VFEKEPVSDW.T
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoepolovruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	4.5071	0.3813	1682.47	1682.781	1	999.9	61.538464 F.V1F1E1K2E1P1V1S1D1W2T1D1D1V1.E
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.9518	0.2489	1668.35	1666.781	1	1162.2	69.230774 F.VFEKEPVSDWTDDV.E
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
ail6319279/refINP_009362.11	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (alucose fermentation) respiration: Cdc19p	1	2,8892	0.3036	1197.42	1198.335	1	347.3	60.000004 T.I1G1P1K2T1N2N2P1E1T1L1.V
3.1		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
ail6210270/rofIND_000262_11	VAL 029/M	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic	1	2 4417	0 2252	1001 41	1000 001	2	276.0	61 11111 S1E4KOD1KOE1D1 104E1 C
gilo313273[rei]14r_003302.1]	TALUSOW	Pyruvate kinase, functions as a homotetramer in glycolysis to convert		2.4417	0.2200	1201.41	1202.301	2	570.5	
- 100400701 - (IND, 000000 4)	V/41 00014/	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic		0.0450	0.0004	1000 55	1007.001		400.0	
gil6319279/ret/NP_009362.1/	YAL038W	(glucose termentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	1	2.3456	0.2861	1266.55	1267.381	1	403.3	61.11111 L.SEKDKEDLRF.G
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.3426	0.2944	1776.33	1776.854	1	534.4	57.14286 F.EKEPVSDWTDDVEAR.I
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	5.0172	0.47	2022.01	2023.163	1	1672.9	84.375 F.VFEKEPVSDWTDDVEAR.I
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.8297	0.2773	2500.57	2501.742	1	1216.7	54.761906 V.N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoepolovruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	4.2227	0.3923	1970.63	1973.156	1	1012.7	52.77778 C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1.K
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	4.1884	0.4936	1948.49	1950.156	1	839.7	52.77778 C.SHKGVNLPGTDVDLPALSE.K
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP 009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	3	5.3844	0.4036	2759.84	2758.101	1	853	35.416664 H.KGVNLPGTDVDLPALSEKDKEDLRF.G
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
ail6319279/refINP_009362.11	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration: Cdc19p	2	4.2017	0.2595	1757.65	1754.962	1	1615	71.875 C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1.S
3.1		Pyruvate kinase, functions as a homotetramer in glycolysis to convert	_							
gil6310270/rofIND_000362.11	VAL 038/M	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (ducose fermentation) respiration: Cdc19p	3	6.0313	0 377	2710 10	2700 056	1	1/10 1	35 416664 C S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1 P
gilo313273[rei]14r_003302.1]	TALUSOW	Pyruvate kinase, functions as a homotetramer in glycolysis to convert	5	0.0313	0.577	2710.13	2103.330	'	1413.1	33.410004 C.3113A2GTV 112ETF 1GTT 1DTV 1DTETF TATE 13TE 112D1A2ETDTET.K
-:::::::::::::::::::::::::::::::::::::	VAL 020W/	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic	2	0.0447	0.0000	4700 44	4700.000	0	C4C 0	
gilo319279/rei/ivP_009362.1/	TAL036VV	Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	2.9447	0.2839	1732.41	1733.962	2	646.2	53.125 S.HKGVNLPGIDVDLPALS.E
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p Pyruvate kinase, functions as a homotetramer in glycolysis to convert	2	4.2081	0.3378	1733.41	1733.962	1	1077.6	65.625 C.SHKGVNLPGTDVDLPAL.S
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.0162	0.2311	1646.13	1646.884	1	621.7	56.666668 S.HKGVNLPGTDVDLPAL.S
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	2	3.7436	0.3511	1463.63	1464.662	1	1178.4	86.36364 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
		phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	1	2.6179	0.2387	1273.48	1274.515	2	304.5	66.66667 S.KYRPNCPIIL.V
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	1	3.1672	0.169	1463.61	1464.662	1	297.8	68.181816 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP_009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	1	3.0602	0.2939	1445.7	1445.662	1	252.4	63.636364 A.RKSEELYPGRPL.A
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
gi 6319279 ref NP 009362.1	YAL038W	(glucose fermentation) respiration; Cdc19p	3	5.1481	0.3258	2982.41	2982.32	1	1383.9	35.576923 C.SHKGVNLPGTDVDLPALSEKDKEDLRF.G
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
ail6319279/refINP_009362.11	YAL038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (alucose fermentation) respiration: Cdc19p	2	2.9605	0.3262	1225.75	1223.42	1	612.4	72,22222 E.SHLYRGVEPE.V
51		Pyruvate kinase, functions as a homotetramer in glycolysis to convert								
ail6319279/refINP_009362.11	YAI 038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (alucose fermentation) respiration: Cdc19p	2	4 0306	0.3728	2983.07	2982.32	1	635.7	42 307693 C. SHKGVNI PGTDVDI PALSEKDKEDI RE G
		Pyruvate kinase, functions as a homotetramer in glycolysis to convert	-		0.0720	2000.01	2002.02	·	000.1	
ail6319279/refINP_009362.11	YAI 038W	phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration: Cdc19p	3	5 9739	0 4052	3015 41	3018.32	1	1135.8	33 653847 C S1H3K2G1V1N2I 1P1G1T1D1V1D1I 1P1A1I 1S1E1K2D1K2E1D1I 1R4E1 G
		Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-	0	0.0700	0.1002	0010.11	0010.02	·	1100.0	
gil6310278/rofIND_000361_1	VAL 030C	Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role	2	3 0557	0.304	2100.01	2100 256	1	344.4	
	INLOSSO	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-	2	0.0007	0.004	2100.01	2103.200		044.4	
ail6310278/rofIND_000264_41	VAL 0200	Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role	2	3 1610	0 1617	2369 47	2268 570	4	333 5	
9103132101101P_00301.1	1 ALU390	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-	2	3.1312	0.1017	2300.47	2300.579	1	333.5	
	VAL 0000	Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role		0.0700	0.0507	4553.03	4550 700		400.0	
9103132101101P_00301.1	1 ALU390	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-	1	2.0729	0.2581	1007.07	1000./02	1	0.601	
	VAL 0000	Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role		0.0510	0.0776	4540.00	45 40 700		400.0	
gilo319276[rei]NP_009361.1]	TALU39C	in microphinaimia with linear skin delects (MLS); CyC3p	1	2.0012	0.2776	1040.69	1540.762	1	100.0	34.343430 Q.ELPFUKIDWIVL.K

		Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-								
gi 6319278 ref NP_009361.1	YAL039C	Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role in microphthalmia with linear skin defects (MLS); Cyc3p	3	4.0513	0.2166	1476.02	1474.674	1	1185.9	52.499996 L.P1F1D1R4H3D1W2I1V1L1R4.G
		Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-								
gi 6319278 ref NP_009361.1	YAL039C	in microphthalmia with linear skin defects (MLS); Cyc3p	2	3.9829	0.3612	1847.41	1847.982	1	549.1	64.28571 L.EWEKPHTDESHVQPK.L
		Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-								
gi 6319278 ref NP_009361.1	YAL039C	in microphthalmia with linear skin defects (MLS); Cyc3p	2	2.9877	0.1607	1870.19	1870.982	2	268.1	46.42857 L.E1W2E1K2P1H3T1D1E1S1H3V1Q2P1K2.L
		Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo- Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role								
gi 6319278 ref NP_009361.1	YAL039C	in microphthalmia with linear skin defects (MLS); Cyc3p	2	3.1476	0.2385	2130.39	2131.256	1	325.5	44.11765 S.S1I1P1K2S1P1D1S1N2E1F1W2E1Y1P1S1P1Q2.Q
		chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during								
ail6319258/refINP 009341.11	YAL060W	fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth: Bdh1p	2	4.3647	0.4088	1840.49	1839.07	1	1216.4	63.333332 C.G1S1D1L1H3E1Y1L1D1G1P1I1F1M1P1K2.D
3.1		NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-								
		fermentation and allows using 2,3-butanediol as a carbon source during aerobic								
gi 6319258 ref NP_009341.1	YAL060W	growth; Bdh1p NAD-dependent (2R-3R)-2 3-butanedial dehydrogenase, a zinc-containing medium-	2	4.7226	0.3627	1695.05	1692.94	1	1901.4	76.92308 S.D1L1H3E1Y1L1D1G1P1I1F1M1P1K2.D
		chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during								
qi 6319258 ref NP 009341.1	YAL060W	fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth; Bdh1p	1	3.3832	0.3447	1398.53	1398.694	1	722.9	63.636364 A.V1W2G1P1K2P1V1P1F1Q2P1M1.D
		NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-								
		fermentation and allows using 2,3-butanediol as a carbon source during aerobic								
gi 6319258 ref NP_009341.1	YAL060W	growth; Bdh1p NAD-dependent (2R-3R)-2 3-butanedial dehydrogenase, a zinc-containing medium-	2	3.4174	0.2507	1945.43	1945.12	5	502.1	50 T.G1K2Q2R4I1E1D1G1W2E1K2G1F1Q2E1L1.M
		chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during								
ail6319258/refINP 009341.11	YAL060W	fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth: Bdh1p	3	4.0282	0.2134	2688.26	2688.939	1	721.4	29.545454 C.G1S1D1L1H3E1Y1L1D1G1P1I1F1M1P1K2D1G1E1C1H3K2L1.S
51		NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-								
		fermentation and allows using 2,3-butanediol as a carbon source during aerobic								
gi 6319258 ref NP_009341.1	YAL060W	growth; Bdh1p NAD-dependent (2R-3R)-2 3-butanedial debydrogenase, a zinc-containing medium-	2	3.0049	0.2009	2691.07	2688.939	3	403.4	36.363636 C.G1S1D1L1H3E1Y1L1D1G1P1I1F1M1P1K2D1G1E1C1H3K2L1.S
		chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during								
qi 6319258 ref NP 009341.1	YAL060W	fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth; Bdh1p	2	3.6634	0.1852	1700.51	1699.015	3	752.3	53.571426 Q.H3H3I1I1P1V1P1K2E1I1P1L1D1V1A1.A
		Protein that forms a heterotrimeric complex with Erp2p, Emp24p, and Erv25p;								
gi 6319319 ref NP_009402.1	YAR002C-A	transport and localized to COPII-coated vesicles; Erp1p	2	5.2172	0.36	1816.25	1816.931	1	1347.7	71.42857 L.I1D1I1E1E1T1F1D1D1N2H3L1V1V1H3.Q
		Protein that forms a heterotrimeric complex with Erp2p, Emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi								
gi 6319319 ref NP_009402.1	YAR002C-A	transport and localized to COPII-coated vesicles; Erp1p	2	4.9266	0.4012	1797.03	1796.931	1	1842	82.14286 L.IDIEETFDDNHLVVH.Q
		Protein that forms a heterotrimeric complex with Erp2p, Emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi								
gi 6319319 ref NP_009402.1	YAR002C-A	transport and localized to COPII-coated vesicles; Erp1p	2	3.2835	0.3879	2088.29	2089.275	1	917.6	55.88235 F.G1V1L111D111E1E1T1F1D1D1N2H3L1V1V1H3.Q
		member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi								
gi 6319319 ref NP_009402.1	YAR002C-A	transport and localized to COPII-coated vesicles; Erp1p Protein that forms a beterotrimeric complex with Erp2p, Emp24p, and Ep/25p;	2	4.7111	0.3651	2065.55	2066.275	1	1055.8	64.70589 F.GVLIDIEETFDDNHLVVH.Q
		member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi								
gi 6319319 ref NP_009402.1	YAR002C-A	transport and localized to COPII-coated vesicles; Erp1p Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats;	2	3.2288	0.1884	1761.27	1761.01	8	272.7	50 D.E1K2L1D1S1K2G1K2A1T111D111L1H3A1.K
gi 37362612 ref NP_009421.2	YAR042W	localizes to the Golgi and the nucleus-vacuole junction; Swh1p	2	3.3345	0.2255	2523.23	2523.731	1	373	38.636364 N.K2E1T1P1A1N2A1K2P1Q2E1E1A1P1E1D1E1S1L1I1V1I1S1.S
gi 37362612 ref NP_009421.2	YAR042W	localizes to the Golgi and the nucleus-vacuole junction; Swh1p	2	3.3972	0.2456	1942.67	1945.191	1	806.7	53.125 S.T1T1N2R4V1S1K2P1F1N2P1L1L1G1E1T1F1.E
ail37362612[refINP_009421.2]	YAR042W	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats;	2	3 7986	0.39	1822 15	1821 086	1	710 1	70 T TNR\/SKPENDI I GETE E
gijo/302012 tei titr_003421.2	171104211	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats;	2	3.7900	0.55	1022.15	1021.000	'	710.1	10 T. HNRVORT HYPELGETT.E
gi 37362612 ref NP_009421.2	YAR042W	localizes to the Golgi and the nucleus-vacuole junction; Swh1p Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats;	2	4.2299	0.4213	1966.17	1967.111	1	475.8	56.666668 T.I1R4P1D1H3N2I1S1V1P1E1E1T1Y1S1W2.K
gi 37362612 ref NP_009421.2	YAR042W	localizes to the Golgi and the nucleus-vacuole junction; Swh1p	2	3.6296	0.4143	1945.41	1944.111	1	692	63.333332 T.IRPDHNISVPEETYSW.K
gi 37362612 ref NP_009421.2	YAR042W	localizes to the Golgi and the nucleus-vacuole junction; Swh1p	2	3.1185	0.2105	1561.89	1560.648	1	708.5	63.636364 T.W2T1E1S1P1K2W2D1F1Y1G1E1.C
gil37362612[refINP_009421.2]	YAR042W	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; localizes to the Golgi and the nucleus-vacuole junction; Swh1n	2	3 1041	0 2807	1921 73	1922 191	4	376.3	40.625 S TTNRVSKPENPLI GETE E
		Component of the small-suburit (SSU) processome, which is involved in the	-		0.2007					
gi 14270688 ret NP_009551.2	YBL004W	Component of the small-subunit (SSU) processome, which is involved in the	2	3.3247	0.3107	1885.65	1886.028	1	513.5	53.333336 A.DSIIRNPVNDDHYVDL.V
gi 14270688 ref NP_009551.2	YBL004W	biogenesis of the 18S rRNA; Utp20p	2	3.1503	0.1987	1963.47	1964.182	1	445	50 F.IKLPDENQNLDYYQPL.L
gi 14270688 ref NP_009551.2	YBL004W	biogenesis of the 18S rRNA; Utp20p	2	3.0962	0.2956	1686.97	1687.933	1	644.3	61.538464 N.FHDEFSLQPLLDLL.A
gi 14270688 ref NP_009551.2	YBL004W	biogenesis of the 18S rRNA; Utp20p	2	3.2699	0.2556	1859.77	1858.148	2	525.9	53.333336 F.SESGRKIPDWNKITIL.I
ail14270688/rofIND_000551.21	VBI 004W	Component of the small-subunit (SSU) processome, which is involved in the	2	4 0113	0 2175	1083.07	1095 192	3	401.5	53 333336 E 11K2I 101D1E1N2O2N2I 1D1V1V1O2D1I 1 I
gi[14270000]tei[14F_003351.2]	I DL004W	Component of the small-subunit (SSU) processome, which is involved in the	2	4.0115	0.2175	1303.37	1905.102	5	491.5	33.3333001.1112E111D1E1112Q2112E1D11111Q211E1.E
gi 14270688 ref NP_009551.2	YBL004W	biogenesis of the 18S rRNA; Utp20p Component of the small-subunit (SSU) processome, which is involved in the	2	2.9791	0.2704	1495.95	1496.724	1	750.1	85 S.R4M1H3E1Y1D1F1P1R4I1L1.S
gi 14270688 ref NP_009551.2	YBL004W	biogenesis of the 18S rRNA; Utp20p	2	4.1143	0.3082	2221.97	2221.437	1	642	50 L.S1F1I1K2L1P1D1E1N2Q2N2L1D1Y1Y1Q2P1L1.L
gi 14270688 ref NP_009551.2	YBL004W	biogenesis of the 18S rRNA; Utp20p	2	4.2988	0.3324	2199.37	2198.437	1	914.1	61.764706 L.SFIKLPDENQNLDYYQPL.L
ail14270688/refINP_009551.2	YBL004W	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of the 18S rRNA: Utp20p	2	3.2679	0.3452	1881 07	1881.148	1	534.2	53.333336 F.S1E1S1G1R4K2I1P1D1W2N2K2I1T1111 1 I
5-1 · 121 0000[-04141 _000001.2]		Cytoskeletal protein binding protein required for assembly of the cortical actin	2	0.2010	0.0402				001.2	
gi 6319464 ref NP_009546.1	YBL007C	cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin dynamics and with proteins required for endocytosis; Sla1p	3	4.3438	0.2285	3943.37	3944.428	1	485.1	19.23077 A.STPEPNLKDLEPVKTGGTTVPAAPVSSAPVSSAPAPLDPF.K
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		Cytoskeletal protein binding protein required for assembly of the cortical actin								
ail6319464/refINP_009546.11	VBL007C	cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin	2	4 3095	0 3589	2054.85	2056 226	1	983.6	
gilo319404[rei]in=_009540.1]	TBLUUTC	Cytoskeletal protein binding protein required for assembly of the cortical actin	2	4.3093	0.5569	2004.00	2030.220		903.0	00.75 N.FDREQLIEDMMFDINNS.M
-100404041(INID-00054041	VDI 0070	cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin	•	0.0400	0.0500	107115	4075 044		500.4	
gi 6319464 ret NP_009546.1	YBL007C	cynamics and with proteins required for endocytosis; Sia1p Cytoskeletal protein binding protein required for assembly of the cortical actin	2	3.6493	0.2508	1874.15	1875.044	1	526.1	60.714287 N.F1D1R4E1Q2L111E1D1M1M1P1D111N2.N
		cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin								
gi 6319464 ret NP_009546.1	YBL007C	dynamics and with proteins required for endocytosis; Sla1p Cytoskeletal protein binding protein required for assembly of the cortical actin	2	3.4607	0.3042	1853.77	1855.044	1	618.2	67.85/14 N.FDREQLIEDMMPDIN.N
		cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin								
gi 6319464 ref NP_009546.1	YBL007C	dynamics and with proteins required for endocytosis; Sla1p	3	4.9784	0.4651	2593.43	2593.738	1	1355.9	33.695652 M.QSKEDQAPDEDEEGPPPAMPARPT.A
		cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin								
gi 6319464 ref NP_009546.1	YBL007C	dynamics and with proteins required for endocytosis; Sla1p	3	5.8774	0.4743	2623.13	2623.738	1	1989.3	42.391304 M.Q2S1K2E1D1Q2A1P1D1E1D1E1E1G1P1P1P1A1M1P1A1R4P1T1.A
gi 6319456 ref NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p	2	3.7259	0.4223	2258.51	2257.546	1	575.3	54.545456 T.AIKEDGSIVPGPSVGGSPEFITV.S
		Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate								
gi 6319456 ret NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate	2	3.5209	0.2179	2532.51	2533.907	1	464.5	40 S.FEGIHDIDMPVNPPFRKPYPY.L
gi 6319456 ref NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p	3	5.4148	0.3435	2673.74	2676.066	4	614.9	29.761904 S.F1E1G1I1H3D1I1D1M1P1V1N2P1P1F1R4K2P1Y1P1Y1L1.K
ail6319456 refINP 009538.1	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	2	4.4302	0.3264	2678.71	2676.066	4	477.8	40.476192 S.F1E1G1I1H3D1I1D1M1P1V1N2P1P1F1R4K2P1Y1P1Y1L1.K
2.1111		Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate								
gi 6319456 ref NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p Acetyl-coA hydrolase, primarily localized to mitochondria: required for acetate	3	3.8414	0.1658	3138.26	3138.55	1	477.4	25.961538 N.T1A1T1P1S1F1E1G1I1H3D1I1D1M1P1V1N2P1P1F1R4K2P1Y1P1Y1L1.K
gi 6319456 ref NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p	3	5.028	0.217	2647.34	2647.066	1	1391.4	41.666664 S.FEGIHDIDMPVNPPFRKPYPYL.K
ail63104561rofIND_000538_1	VBI 015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate	2	4 7663	0.4268	2645.01	2647.066	1	079	
gilos 19450/rei/14r _009550.1/	IDEOIGW	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate	2	4.7003	0.4200	2043.01	2047.000	'	570	34.701300 3.1 EGHIDIDIME VIETERKETTELK
gi 6319456 ref NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p	3	4.8696	0.2971	2931.59	2932.366	2	519.9	28.125 A.TPSFEGIHDIDMPVNPPFRKPYPYL.K
gi 6319456 ref NP 009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p	3	4.1999	0.2968	3106.19	3104.55	1	483.5	26.923079 N.TATPSFEGIHDIDMPVNPPFRKPYPYL.K
		Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate								
gi 6319456 ret NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p Acetyl-coA hydrolase, primarily localized to mitochondria: required for acetate	2	4.0538	0.2361	2064.29	2063.422	1	405.1	50 H.DIDMPVNPPERKPYPYL.K
gi 6319456 ref NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p	2	3.8648	0.2185	2532.65	2533.907	1	714.3	47.5 S.FEGIHDIDMPVNPPFRKPYPY.L
gil6319456 refINP_009538.1	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth: Ach1p	3	5.1609	0.3414	2534.24	2533.907	1	1461.4	40 S.FEGIHDIDMPVNPPERKPYPY L
2.1		Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate	-					-		
gi 6319456 ref NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p Acetyl-coA bydrolase, primarily localized to mitochondria; required for acetate	2	4.3462	0.3111	2646.87	2647.066	1	973.2	52.380955 S.FEGIHDIDMPVNPPFRKPYPYL.K
gi 6319456 ref NP_009538.1	YBL015W	utilization and for diploid pseudohyphal growth; Ach1p	3	4.0895	0.1841	2674.91	2676.066	1	552.3	29.761904 S.F1E1G1I1H3D1I1D1M1P1V1N2P1P1F1R4K2P1Y1P1Y1L1.K
ail63104561rofIND_000538_1	VBI 015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate	3	4 05 35	0 3210	2648.24	2647.066	1	663.3	
gilos 19450/rei/14r _009550.1/	IDEOIGW	dilization and for diploid pseudonyphal growth, Achtp	5	4.3333	0.5215	2040.24	2047.000	'	005.5	
-102404541{IND_00052041		Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles	2	5.0400	0.0004	2240.00	0040.004		005.0	
gilo319454[rei]in=_009556.1]	IDLUITC	between the late-Goigi and prevacuolar endosome-like compartments, reptp	2	5.0190	0.2021	2340.09	2340.334		905.0	03.00009 F.NZDTKZTICTETETNZDTFTETDTWZNZLTATETOTKZ.C
	VDI 0470	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles		4 5700	0.0400	001170	0045 004		007.0	
gi 6319454 ret NP_009536.1	YBL017C	between the late-Golgi and prevacuolar endosome-like compartments; Pep1p	2	4.5739	0.3489	2314.73	2315.334	1	667.9	58.333332 F.NDKTCEENDFEDWNLAEGK.C
		Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles								
gi 6319454 ret NP_009536.1	YBL017C	between the late-Golgi and prevacuolar endosome-like compartments; Pep1p	2	3.5457	0.3242	2461.97	2462.511	1	329.4	47.368423 A.FNDKTCEENDFEDWNLAEGK.C
		Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles								
gi 6319454 ref NP_009536.1	YBL017C	between the late-Golgi and prevacuolar endosome-like compartments; Pep1p	3	4.007	0.2141	2488.22	2488.511	1	1140.1	34.210526 A.F1N2D1K2T1C1E1E1N2D1F1E1D1W2N2L1A1E1G1K2.C
		Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles								
gi 6319454 ref NP_009536.1	YBL017C	between the late-Golgi and prevacuolar endosome-like compartments; Pep1p	2	3.9515	0.2439	1616.41	1615.737	1	618.1	69.230774 L.IHDQFLDEADDLLA.G
		involved in degradation of misfolded proteins in mitochondria; required for bigenesis								
gi 6319449 ref NP_009531.1	YBL022C	and maintenance of mitochondria; Pim1p	1	2.9277	0.3507	1362.59	1363.615	2	169.6	59.090908 D.RLYETTPPGVVM.G
		involved in degradation of misfolded proteins in mitochondria; required for bigenesis								
gi 6319449 ref NP_009531.1	YBL022C	and maintenance of mitochondria; Pim1p	3	5.109	0.2922	3890.63	3890.068	1	1114.6	27.142859 Q.AKDTDTETTVVEDANNPEDQESTSPATPKLEDIVVE.R
		Mitochondrial A I P-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria: required for bigenesis								
gi 6319449 ref NP_009531.1	YBL022C	and maintenance of mitochondria; Pim1p	1	2.4778	0.1841	1421.59	1422.566	1	183.4	54.166668 L.I1D1E1I1D1K2I1G1H3G1G1I1H3.G
		Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis;								
gi 6319449 ref NP_009531.1	YBL022C	and maintenance of mitochondria; Pim1p	2	3.7682	0.4234	2132.57	2132.304	1	463.7	40 A.SIHLHCPEGATPKDGPSAGVT.M
		Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis;								
gi 6319449 ref NP_009531.1	YBL022C	and maintenance of mitochondria; Pim1p	1	3.0989	0.2631	1388.3	1386.593	1	549.8	65 S.HIIKSPTWQEF.Q
		Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis;								
gi 6319449 ref NP_009531.1	YBL022C	and maintenance of mitochondria; Pim1p	3	4.6674	0.1831	3075.38	3072.397	1	531.8	32 K.T1I1I1F1P1K2D1N2L1N2D1W2E1E1L1P1D1N2V1K2E1G1L1E1P1L1.A
		Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis;								
gil6319449/refINP_009531.11	YBL022C	involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	2	3.5072	0.2381	3071.75	3072.397	1	456.9	32 K.T1I1I1F1P1K2D1N2L1N2D1W2E1E1L1P1D1N2V1K2E1G1L1E1P1L1.A
2.1		Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis;	_							
ail6319449/refINP 009531 1	YBL022C	involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	2	2,9809	0.2338	3038 47	3040.397	1	626.5	
9-1-2-10 1 (a)	. 520220	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis;	-	2.0000	0.2000	5000.47	50 10.001		020.0	
ail6319449/refIND 000534 41	VBI 022C	involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1n	2	4 51 95	0 3450	236/ 31	2365 505	1	507 9	44 736843 K D1N2I 1N2D1W2E1E1I 1D1D1N2V4K2E1C1I 1E1D1I 1 A
9-100-10-10-10-10-10-10-10-10-10-10-10-10	. 020220	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis;	2	4.0100	0.0408	2004.01	2000.000		301.3	
ail6319449/refIND 000534 41	VBI 022C	involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1n	2	4 4075	0 2880	2338 03	2340 505	1	1050	
Siloo i saaslieiline "00802111	IDLUZZO	and maintenance of mitochonuna, rimitp	2	4.4970	0.2009	2000.90	2040.000		1000	STOSTOT RUNLINDWELEF DIVIREGELF LA

gi 6319439 ref NP_009521.1	YBL032W	RNA binding protein with similarity to hnRNP-K that localizes to the cytoplasm and to subtelomeric DNA; required for the proper localization of ASH1 mRNA; involved in the regulation of telomere position effect and telomere length; Hek2p	2	3.4917	0.3202	1830.77	1832.11	1	718.1	60.000004 F.LNHILPAPSKDEIRDL.Q
gi 6319439 ref NP_009521.1	YBL032W	RNA binding protein with similarity to hnRNP-K that localizes to the cytoplasm and to subtelomeric DNA; required for the proper localization of ASH1 mRNA; involved in the regulation of telomere position effect and telomere length; Hek2p	2	3.9558	0.2024	1830.69	1828.936	3	455.6	57.692307 E.RKDDDDKDENFRKF.I
gi 6319432 ref NP_009514.1	YBL039C	Major CTP synthase isozyme (see also URA8), catalyzes the ATP-dependent transfer of the amide nitrogen from glutamine to UTP, forming CTP, the final step in de novo biosynthesis of pyrimidines; involved in phospholipid biosynthesis; Ura7p	2	5.1614	0.3697	2047.21	2045.319	1	1213.2	64.70589 A.KIPVDDTGMEPDVCIIEL.G
gi 6319432 ref NP_009514.1	YBL039C	Major CTP synthase isozyme (see also URA8), catalyzes the ATP-dependent transfer of the amide nitrogen from glutamine to UTP, forming CTP, the final step in de novo biosynthesis of pyrimidines; involved in phospholipid biosynthesis; Ura7p	2	4.3543	0.3525	2062.89	2064.319	1	1003.8	58.823532 A.K2I1P1V1D1D1T1G1M1E1P1D1V1C1111E1L1.G
gi 6319432 ref NP_009514.1	YBL039C	Major CTP synthase isozyme (see also URA8), catalyzes the ATP-dependent transfer of the amide nitrogen from glutamine to UTP, forming CTP, the final step in de novo biosynthesis of pyrimidines; involved in phospholipid biosynthesis; Ura7p	2	3.213	0.2539	1870.63	1871.053	1	443.7	53.571426 A.E1F1Y1P1D1I1D1E1K2N2H3V1V1V1F1.M
gi 6319432 ref NP_009514.1	YBL039C	Major CTP synthase isozyme (see also URA8), catalyzes the ATP-dependent transfer of the amide nitrogen from glutamine to UTP, forming CTP, the final step in de novo biosynthesis of pyrimidines; involved in phospholipid biosynthesis; Ura7p	2	3.39	0.2015	1804.29	1803.044	1	1217.4	66.66667 A.KIPVDDTGMEPDVCII.E
gi 6319432 ref NP_009514.1	YBL039C	Major CTP synthase isozyme (see also URA8), catalyzes the ATP-dependent transfer of the amide nitrogen from glutamine to UTP, forming CTP, the final step in de novo biosynthesis of pyrimidines; involved in phospholipid biosynthesis; Ura7p Key endcoytic protein involved in a network of interactions with other endcoytic	2	4.5357	0.3834	2115.89	2116.397	1	813.9	52.77778 V.AKIPVDDTGMEPDVCIIEL.G
gi 6319424 ref NP_009506.1	YBL047C	proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p Key endocytic protein involved in a network of interactions with other endocytic	2	2.9102	0.2704	1794.49	1795.984	1	340.8	43.333332 N.SILPVKDEFDDEFAGLE
gi 6319424 ref NP_009506.1	YBL047C	proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p Key endocytic protein involved in a network of interactions with other endocytic	2	3.8869	0.296	2244.33	2245.357	1	414.6	47.058823 M.E1Q2F1E1T111D1H3K2D1L1D1D1E1L1Q2M1N2.A
gi 6319424 ref NP_009506.1	YBL047C	proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Edelp Key endocytic protein involved in a network of interactions with other endocytic creation beinde another more loa ubiquitie dependent ensered memory bind	2	3.8156	0.3102	2447.65	2446.587	1	666.7	47.5 Q.SVRDDVELPETLEERDTINNT.A
gi 6319424 ref NP_009506.1	YBL047C	proteins, britas memoranes in a dougland-optimetric manner, may also brind ubiquitinated membrane-associated proteins; Edelp Key endocytic protein involved in a network of interactions with other endocytic moteins brinds membranes in a ubiquitin-dependent manner, may also brind	1	2.8232	0.1522	1511.62	1512.731	9	286.1	53.846157 Q.K2K2N2A1G1V1E1L1P1D1V111P1N2.E
gi 6319424 ref NP_009506.1	YBL047C	proteins, which embrances in a backgrown deproteins; Edel proteins in a state of the ubiquitinated membranes in a ubiquitin deproteins; Edel proteins; Edel proteins with other endocytic proteins. binds membranes in a ubiquitin-dependent manner, may also bind	2	3.0926	0.2336	2431.09	2429.819	1	381.3	38.636364 T.KVATPSIPQQPIPLKNDPIVDAS.L
gi 6319424 ref NP_009506.1	YBL047C	ubiquitinated membrane-associated proteins; Ede1p Key endocytic protein involved in a network of interactions with other endocytic proteins bide prombranes in a ubiquitie dependent manager manager bid	2	3.6007	0.2415	2459.11	2457.819	2	355.9	36.363636 T.K2V1A1T1P1S1I1P1Q2Q2P1I1P1L1K2N2D1P1I1V1D1A1S1.L
gi 6319424 ref NP_009506.1	YBL047C	proteins, brinds membranes in a doughum regeneration mainter, may also brind ubiquitinated membrane-sociated proteins; Edelp Key endocytic protein involved in a network of interactions with other endocytic motions brinds membranes in a ubiquitin-dependent manner, may also brind	2	3.483	0.3701	1616.41	1616.829	2	415.5	57.692307 S.R4A1S1K2P1S1L1Q2D1M1P1H3Q2V1.S
gi 6319424 ref NP_009506.1	YBL047C	proteins, binto motivolario a dialeguni populationi maniferi, may also binto ubiquitinated membrane-associated proteins; Edel p Key endocytic protein involved in a network of interactions with other endocytic proteins bind proteinsce is a ubiquiti dependent emperer more data bind	2	3.3506	0.256	1835.81	1836.934	3	206.5	53.571426 F.E1T111D1H3K2D1L1D1D1E1L1Q2M1N2.A
gi 6319424 ref NP_009506.1	YBL047C	proteins, ondo methodanes and outquint-operatorin manner, may also bind ubiquitinated methodanes associated proteins; Edel p Key endocytic protein involved in a network of interactions with other endocytic proteins bind proteinsce is a ubinuitia dependent appear and up to bind	2	4.3314	0.2416	1945.33	1945.091	1	919.9	66.66667 Q.SIIKEEPEEQEQLRES.S
gi 6319424 ref NP_009506.1	YBL047C	proteins, binds memoranes in a dougland-operative manner, may also bind ubiquitinated membrane-associated proteins; Edelp Key endocytic protein involved in a network of interactions with other endocytic rotation. Eviden proteinsce is a ubiquiti dependent energies, may also bind	2	3.2408	0.3165	1490.83	1489.798	1	862.2	65.38461 T.KVATPSIPQQPIPL.K
gi 6319424 ref NP_009506.1	YBL047C	proteins, billos memorares in a dolquin-cepterent manner, may also billo ubiquitinated membrane-associated proteins; Edel p Key endocytic protein involved in a network of interactions with other endocytic protein and the second secon	3	4.3947	0.359	3680.03	3680.239	1	923.4	28.030304 Q.KKNAGVELPDVIPNELLQSPALGLYPPNPLPQQQ.S
gi 6319424 ref NP_009506.1	YBL047C	proteins, binds memoranes in a ubiquin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Edelp Key endocytic protein involved in a network of interactions with other endocytic roteins higher membranes in a ubiquitin-dependent manner, may also bind also bind	3	4.0336	0.2742	3721.1	3723.239	1	487.5	22.727274 1020202.S
gi 6319424 ref NP_009506.1	YBL047C	ubiquitinated membrana easociated proteins; Edelphated interactions with other endocytic protein interaction and a set of the set o	2	4.3505	0.4321	1924.09	1925.099	1	629.4	56.25 N.SILPVKDEFDDEFAGLE.Q
gi 6319424 ref NP_009506.1	YBL047C	proteins, bilds memoranes in a douquin-operaterit manner, may also bild ubiquinated memorane-associated proteins; Edel p Key endocytic protein involved in a network of interactions with other endocytic protein and a second	2	3.7984	0.3392	1812.91	1812.984	2	634.1	53.333336 N.S1I1L1P1V1K2D1E1F1D1D1E1F1A1G1L1.E
gi 6319424 ref NP_009506.1	YBL047C	proteins, onde memoranes in a doiquint-oppendent manner, may also bind ubiquitinated memorane-associated proteins; Edel p Key endocytic protein involved in a network of interactions with other endocytic	3	4.2784	0.2292	3762.11	3760.97	1	460.8	24.13793 L.SNKDTDLTDREKQLEERNRQIEEQENLYHQ.H
gi 6319424 ref NP_009506.1	YBL047C	proteins, binds membrane-associated proteins; Ede1p Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and	3	3.9906	0.3783	2429.57	2429.819	1	492.3	32.954548 T.KVATPSIPQQPIPLKNDPIVDAS.L
gi 6319420 ref NP_009502.1	YBL051C	several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and	3	3.811	0.3039	2060.75	2060.41	1	791.5	40.625 K.KEQLLDIIEEMDLPLPY.A
gi 6319420 ref NP_009502.1	YBL051C	several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad50; contains an RNA recognition motif, a nuclear localization signal and	2	5.8258	0.4532	2076.59	2079.41	1	1201.1	68.75 K.K2E1Q2L1L1D1I1I1E1E1M1D1L1P1L1P1Y1.A
gi 6319420 ref NP_009502.1	YBL051C	several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p Protein involved in G2/M phase progression and response to DNA damage, interacts	2	5.1115	0.3485	2059.11	2060.41	1	1192	68.75 K.KEQLLDIIEEMDLPLPY.A
gi 6319420 ref NP_009502.1	YBL051C	when reactory, contents an river recognition mout, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p	3	4.1099	0.3488	2078.12	2079.41	2	801.1	37.5 K.K2E1Q2L1L1D1111E1E1M1D1L1P1L1P1Y1.A

ail63194201refINP 009502.11	YBL051C	Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4o	2	4.0062	0.3092	2075.97	2076.41	1	805.4	56.25 K KEQLLDIIEEM@DLPLPY.A
9-1		Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SO/TC cluster domains: breathosthordized in response to DNA damage.	-					-		
gi 6319420 ref NP_009502.1	YBL051C	Pin4p Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and	2	3.8341	0.3316	2316.87	2315.666	1	619.9	47.22222 K.K2E1Q2L1L1D1111E1E1M\$D1L1P1L1P1Y1A1F1.N
gi 6319420 ref NP_009502.1	YBL051C	several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p Protein involved in G2/M phase progression and response to DNA damage, interacts	2	5.6005	0.4819	2058.79	2060.41	1	1237.6	68.75 K.KEQLLDIIEEMDLPLPY.A
gi 6319420 ref NP_009502.1	YBL051C	with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p Protein involved in G2/M phase progression and response to DNA damage, interacts	2	5.3703	0.3795	2078.41	2079.41	1	1179.3	65.625 K.K2E1Q2L1L1D1111E1E1M1D1L1P1L1P1Y1.A
gi 6319420 ref NP_009502.1	YBL051C	with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p Protein involved in G2/M phase progression and response to DNA damage, interacts	2	3.8885	0.3151	2277.47	2278.666	1	889.6	52.77778 K.KEQLLDIIEEMDLPLPYAF.N
gi 6319420 ref NP_009502.1	YBL051C	with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p	2	3.6819	0.2904	2299.15	2299.666	1	423.6	38.88889 K.K2E1Q2L1L1D1111E1E1M1D1L1P1L1P1Y1A1F1.N
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.3433	0.2221	1776.45	1777.025	2	532	53.333336 E.S111K2F1P1P1S1S1V1T1P1E1V111Q2Q2.E
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.535	0.2258	2050.55	2053.257	1	710.9	56.25 Y.R4T1P1D1E1I1F1E1D1L1I1D1N2P1L1P1F1.V
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.537	0.2113	2218.01	2217.433	2	331.3	38.235294 K.Y1R4T1P1D1E111F1E1D1L111D1N2P1L1P1F1.V
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.8003	0.2521	2193.91	2195.433	1	762.5	55.88235 K.YRTPDEIFEDLIDNPLPF.V
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.945	0.1574	2266.47	2267.549	1	696.8	50 Y.R4T1P1D1E1I1F1E1D1L1I1D1N2P1L1P1F1V1L1.N
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	4.3708	0.2535	2246.83	2244.549	1	831.8	58.333332 Y.RTPDEIFEDLIDNPLPFVL.N
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	6.148	0.4425	2370.39	2371.583	1	1741.8	62.5 F.S1K2P1S1P1A1N2K2E1D1F1D1L1D1D1V1I1L1S1P1R4.F
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	4.7295	0.3751	2114.27	2113.412	1	986.2	62.5 Q.N2R4E1E1K2L1L1D111E1T1P1F111L1P1Y1.L
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	4.6422	0.365	2089.89	2091.412	1	1250.2	62.5 Q.NREEKLLDIETPFILPY.L
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	3	4.8493	0.1775	3134.33	3136.674	1	1345	32.692307 Q.NREEKLLDIETPFILPYLMEKAGSSLK.I
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.6847	0.2434	2226.27	2227.571	1	689.2	47.058823 Q.N2R4E1E1K2L1L1D111E1T1P1F111L1P1Y1L1.M
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	4.8257	0.4177	2654.39	2654.936	1	1657.6	54.545456 F.SKPSPANKEDFDLDDVILSPRFY.G
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	4.6529	0.4138	2683.49	2683.936	1	1187.2	47.727272 F.S1K2P1S1P1A1N2K2E1D1F1D1L1D1D1V1I1L1S1P1R4F1Y1.G
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.1008	0.1801	2204.51	2204.571	1	752.7	50 Q.NREEKLLDIETPFILPYL.M
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.6107	0.2213	2325.57	2323.607	3	356.3	44.444447 Y.KYRTPDEIFEDLIDNPLPF.V
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.5543	0.2352	2464.41	2466.811	1	742.4	44.736843 G.K2N2V1Q2D1S1E1F111F1P111F1E1L1F1P111V1C1.N
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	4.1895	0.2437	2446.37	2443.811	1	841.3	50 G.KNVQDSEFIFPIFELFPIVC.N

gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.6045	0.2351	2639.29	2639.022	1	392.9	38.095238 K.I1G1K2N2V1Q2D1S1E1F1I1F1P1I1F1E1L1F1P1I1V1C1.N
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.8589	0.3142	2346.31	2347.607	1	483.3	50 Y.K2Y1R4T1P1D1E1I1F1E1D1L1I1D1N2P1L1P1F1.V
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.7762	0.2745	2613.59	2614.022	1	675.8	45.238094 K.IGKNVQDSEFIFPIFELFPIVC.N
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.5785	0.3341	2181.31	2181.487	1	982.7	58.333332 L.R4L1E1S111K2F1P1P1S1S1V1T1P1E1V111Q2Q2.E
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.2707	0.2701	1757.57	1758.025	1	497.9	50 E.SIKFPPSSVTPEVIQQ.E
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	3.2919	0.1645	2245.61	2243.543	1	311.6	44.11765 S.Q2N2R4E1E1K2L1L1D111E1T1P1F111L1P1Y1.L
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	4.0801	0.2033	2220.41	2219.543	1	531.8	52.941177 S.QNREEKLLDIETPFILPY.L
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	3	4.3106	0.1752	2344.43	2344.583	1	1123.3	45 F.SKPSPANKEDFDLDDVILSPR.F
gi 6319392 ref NP_009474.1	YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	2	5.6242	0.4393	2344.59	2344.583	1	1776.3	62.5 F.SKPSPANKEDFDLDDVILSPR.F
		Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporties within the NPC, involved in nuclear envelope permeability								
gi 6319392 ref NP_009474.1	YBL079W	and in chromosome segregation, has similarity to Nup157p; Nup170p Protein required for mitochondrial translation; mutation is functionally complemented	2	3.851	0.3848	2158.65	2156.487	1	632.8	52.77778 L.RLESIKFPPSSVTPEVIQQ.E
gi 6319391 ref NP_009473.1	YBL080C	by a Bacillus subtilis ortholog; Pet112p Partia required for mitochoodrial translation; mutation is functionally complemented	2	3.2041	0.3811	1922.69	1925.358	1	625.8	50 S.GVRGLMPQLPDDIMRIL.M
gi 6319391 ref NP_009473.1	YBL080C	by a Bacillus subtilis ortholog; Pet112p	2	3.3182	0.2477	1991.87	1989.227	1	877.4	58.823532 N.LSKELDDIDESAKEIGIL.Q
gi 6319391 ref NP_009473.1	YBL080C	by a Bacillus subtilis ortholog; Pet112p	2	3.0159	0.1806	1613.97	1612.986	1	532.7	65.38461 R.GLMPQLPDDIMRIL.M
gi 6319391 ref NP_009473.1	YBL080C	Protein required for mitochondrial translation; mutation is functionally complemented by a Bacillus subtilis ortholog; Pet112p	2	3.6314	0.3019	1442.13	1442.775	1	822	81.818184 L.MPQLPDDIMRIL.M
gi 6319378 ref NP_009460.1	YBL092W	Protein component of the large (60S) ribosomal subunit, has similarity to rat L32 ribosomal protein; overexpression disrupts telomeric silencing; Rpl32p	1	3.0267	0.2616	1366.8	1367.678	3	230.7	58.333332 L.GIKVTNPKGRLAL.E
gi 6319378 ref NP_009460.1	YBL092W	Protein component of the large (60S) ribosomal subunit, has similarity to rat L32 ribosomal protein; overexpression disrupts telomeric silencing; Rpl32p	1	2.6918	0.2066	1385.56	1386.678	8	196.4	54.166668 L.G1I1K2V1T1N2P1K2G1R4L1A1L1.E
gi 6319378 ref NP 009460.1	YBL092W	Protein component of the large (60S) ribosomal subunit, has similarity to rat L32 ribosomal protein; overexpression disrupts telomeric silencing; Rpl32p	1	2.3732	0.2251	1182.73	1183.44	7	204.4	60.000004 L.GIKVTNPKGRLA
gil6319378lrefINP_009460.11	YBL092W	Protein component of the large (60S) ribosomal subunit, has similarity to rat L32 ribosomal protein; overexpression disrupts telomeric silencing; Rpl32p	1	2.2375	0.1723	1103.54	1104.354	1	378.8	66.66667 M.A1S1L1P1H3P1K2I1V1K2.K
gil6319367/refINP_009449.1	VBI 101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding	3	4 1100	0.2786	2930	2032 243	1	961.4	30 000002 K N2E1E1S1G1E1E1D11E1A1E1Y1P111K2V111R4T1P1P1P1V1A1V1 S
gil0313307 [ref[NP_009443.1]	VPL 101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding	2	4.1133	0.1552	2350	2352.245	2	959.6	
cilc2402c7lrefINP_009449.1	VELAGAC	Non-essential protein of unknown function; promoter contains several Gcn4p binding	3	4.7079	0.1555	3149.54	3150.495	3	570.0	
gil6319367[rei]NP_009449.1]	TBLIUIC	Non-essential protein of unknown function; promoter contains several Gcn4p binding	3	5.1647	0.3878	3305.87	3306.707		579.9	22.32.1426 M. Q2LIK2NZETETSTGTETETUTTETATETTTPTTK2VTTK4TTPTPTVTATVT.S
gi 6319367 ref NP_009449.1	YBL101C	elements; Ecm21p Non-essential protein of unknown function; promoter contains several Gcn4p binding	2	4.3796	0.3905	1659.29	1659.887	1	501.6	69.230774 M.L1R41151K2P1D1P1E1C1P151K2L1.R S.S1H3Q2L1K2N2E1E1S1G1E1E1D111F1A1E1Y1P111K2V111R4T1P1P1P1V1A1V1
gi 6319367 ref NP_009449.1	YBL101C	elements; Ecm21p Non-essential protein of unknown function; promoter contains several Gcn4p binding	3	5.034	0.3999	3620.96	3623.004	5	361.1	20.967741 S1.T
gi 6319367 ref NP_009449.1	YBL101C	elements; Ecm21p Non-essential protein of unknown function; promoter contains several Gcn4p binding	2	4.1219	0.4134	2686.59	2686.023	1	519.8	36.95652 E.E1S1G1E1E1D111F1A1E1Y1P111K2V111R4T1P1P1P1V1A1V1.S
gi 6319367 ref NP_009449.1	YBL101C	elements; Ecm21p One of two identical histone H4 proteins (see also HHF2); core histone required for	3	5.6996	0.518	3059.99	3062.417	1	1259.3	33.653847 L.K2N2E1E1S1G1E1E1D111F1A1E1Y1P111K2V111R4T1P1P1P1V1A1V1.S
gi 6319481 ref NP_009563.1	YBR009C	chromatin assembly and chromosome function; contracting the dement silencing; N- terminal domain involved in maintaining genomic integrity; Hhf1p One of two identical histone H4 proteins (see also HHF2); core histone required for the dement histone H4 proteins (see also HHF2); core histone required for	1	2.5228	0.3078	1503.61	1504.726	1	211.1	58.333332 L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi 6319481 ref NP_009563.1	YBR009C	terminal domain involved in maintaining genomic integrity; Hhftp	2	4.6301	0.3826	1502.59	1504.726	1	816.2	79.16667 L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi 6319481 ref NP_009563.1	YBR009C	chromatin assembly and chromosome function; contracting regulator for terminal domain involved in maintaining genomic integrity; Hhf1p One of two identical histone H4 proteins (see also HHF2); core histone required for	3	4.1497	0.175	1503.29	1504.726	2	1435.8	58.333332 L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi 6319481 ref NP_009563.1	YBR009C	cnromatin assembly and chromosome function; contributes to telomeric silencing; N- terminal domain involved in maintaining genomic integrity; Hhf1p One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function: contributes to telomeric silencing: N-	3	4.0401	0.1596	1502.6	1504.726	1	985.3	50 L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi 6319481 ref NP_009563.1	YBR009C	terminal domain involved in maintaining genomic integrity; Hhf1p One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function: contribute to telemetic ellevices. N	3	4.2628	0.1755	1483.31	1482.726	4	1006.3	50 L.RDNIQGITKPAIR.R
gi 6319481 ref NP_009563.1	YBR009C	terminal domain involves in maintaining genomic integrity; HHTp One of two identical histone H4 proteins (see also HHF2); core histone required for	2	4.1063	0.2973	1503.71	1504.726	1	482.6	70.83333 L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi 6319481 ref NP_009563.1	YBR009C	cnromatin assembly and chromosome function; contributes to telomeric silencing; N- terminal domain involved in maintaining genomic integrity; Hhf1p	2	4.9104	0.3626	1482.05	1482.726	1	765.6	79.16667 L.RDNIQGITKPAIR.R

		One of two identical histone H4 proteins (see also HHF2); core histone required for								
gi 6319481 ref NP_009563.1	YBR009C	chromatin assembly and chromosome function; contributes to telomeric silencing; N- terminal domain involved in maintaining genomic integrity; Hhtfp Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.7896	0.3267	1504.31	1504.726	1	339.4	66.66667 L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.2598	0.1975	1712.15	1712.925	1	865.1	61.538464 N.D111E1D1V1E1K2Y1F1P1G1L1L1R4.A
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.4767	0.2994	1711.77	1708.865	1	814.6	65.38461 F.H3D111P1L1Y1A1D1K2E1N2N2I1F1.N
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; lpp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.2843	0.2681	2639.99	2641.998	3	202.6	36.363636 D.I1N2D1P1L1A1P1K2L1N2D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; lpp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.6715	0.2317	2871.39	2872.246	1	287.8	35.416664 A.IID1I1N2D1P1L1A1P1K2L1N2D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; lpp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	3	4.8575	0.2962	2871.8	2872.246	1	877.2	37.5 A.IID1I1N2D1P1L1A1P1K2L1N2D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; [pp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	4.1195	0.2566	2846.05	2843.246	1	360.9	37.5 A.IDINDPLAPKLNDIEDVEKYFPGLL.R
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; [pp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.6715	0.3056	1558.21	1558.629	1	1080.5	79.16667 Q.T1W2E1D1P1N2V1S1H3P1E1T1K2.A
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli Pase; [pp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.1169	0.1884	2613.79	2614.998	2	287.7	38.636364 D.INDPLAPKLNDIEDVEKYFPGLL.R
gi 6319483 ref NP_009565.1	YBR011C	oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; [pp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.0011	0.1587	1508.37	1508.687	1	983.6	75 Y.K2I1P1D1G1K2P1E1N2Q2F1A1F1.S
gi 6319483 ref NP_009565.1	YBR011C	oxygens from PI with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	3.2777	0.2139	1552.25	1552.737	1	477.4	66.66667 N.D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi 6319483 ref NP_009565.1	YBR011C	oxygens from PI with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of	2	4.0891	0.3462	1694.39	1694.925	1	1569.5	73.07692 N.DIEDVEKYFPGLLR.A
gi 6319483 ref NP_009565.1	YBR011C	oxygens non er win water, nigny expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p Alpha-1,2-manosyltransferase, responsible for addition of the first alpha-1,2-linked expressed to from the knowbear or the measure headthone of alignmendbridge	3	4.1402	0.1879	2871.11	2872.246	6	540.1	27.083334 A.IID1I1N2D1P1L1A1P1K2L1N2D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi 6319489 ref NP_009571.1	YBR015C	harinose to one any Goigi compartment in Innan backbone or oligosaccharloss, localizes to an early Goigi compartment; Inn2p Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked approach to form the knowboa or the measure headthane of alignmendbridge	2	4.157	0.3778	2905.75	2905.215	1	459.7	44 L.RNMGTTLPVEVLIPPGDEGETEFCNK.I
gi 6319489 ref NP_009571.1	YBR015C	harinose to one the transmission are maintain backbone or bigosaccharides, localizes to one antly Goig compartment; Inn2p Alpha-1,2-manosyltransferase, responsible for addition of the first alpha-1,2-linked manages to form the branches on the manage has/thome of allorescabaride	2	4.8183	0.3847	2268.27	2268.541	1	1901	76.47059 F.KYLDDLLGQDKTEWKRVC.G
gi 6319489 ref NP_009571.1	YBR015C	Inalities to one after Statutes on the mathem backbone or bigosacchances, localizes to one afty Golgi compartment; Inn2p Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked mannae to form the branches on the mannae hardhone of bigosaccharides	2	5.4895	0.3938	2293.15	2294.541	1	1524.3	67.64706 F.K2Y1L1D1D1L1L1G1Q2D1K2T1E1W2K2R4V1C1.G
gi 6319489 ref NP_009571.1	YBR015C	Incalizes to an early Goldstormartmant, Mnn2p Alpha-1,2-manosyltransferase, responsible for addition of the first alpha-1,2-linked manonse to form the branches on the manona backhone of alionsaccharides	2	4.9359	0.2522	1685.41	1684.871	1	1544.8	80.769226 N.K2N2P1F1K2Y1L1D1D1L1L1G1Q2D1.K
gi 6319489 ref NP_009571.1	YBR015C	Incalizes to an early Goldsmorths InAlman Ministry and State and S	2	4.6546	0.2025	1570.23	1568.783	1	1542.3	79.16667 N.K2N2P1F1K2Y1L1D1D1L1L1G1Q2.D
gi 6319489 ref NP_009571.1	YBR015C	Incalizes to an early Goldsmorths InAlman Ministry and State and S	2	5.2535	0.4439	2032.73	2034.279	1	978.3	65.625 L.KGDIGDRPDHYKDLYKLS
gi 6319489 ref NP_009571.1	YBR015C	localizes to an early Golgi compartment; Mnn2p Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked mannose to form the branches on the mannan backhone of olicoascharides.	2	2.9895	0.2049	2017.11	2018.101	1	531.5	52.941177 A.DDSTPLRDNDEAGNEKLK.S
gi 6319489 ref NP_009571.1	YBR015C	localizes to an early Golgi compartment; Mnn2p Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked mannose to form the branches on the mannan backbone of oligosaccharides,	2	4.9573	0.4237	1864.55	1863.975	1	2267.7	82.14286 E.KYTEEFFDNEDLNAK.N
gi 6319489 ref NP_009571.1	YBR015C	localizes to an early Golgi compartment; Mnn2p Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked mannose to form the branches on the mannan backbone of oligosaccharides,	2	3.6165	0.2928	1792.35	1792.946	1	910.1	60.714287 L.KGDIGDRPDHYKDLY.K
gi 6319489 ref NP_009571.1	YBR015C	localizes to an early Golgi compartment; Mnn2p Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked mannose to form the branches on the mannan backbone of oligosaccharides,	2	3.6617	0.1749	1551.47	1551.783	2	923.5	66.66667 N.KNPFKYLDDLLGQ.D
gi 6319489 ref NP_009571.1	YBR015C	localizes to an early Golgi compartment; Mnn2p Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous	2	4.1516	0.352	2059.85	2059.279	1	563.1	56.25 L.K2G1D111G1D1R4P1D1H3Y1K2D1L1Y1K2L1.S
gi 6319491 ref NP_009573.1	YBR017C	nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	2	4.1169	0.2729	1900.11	1899.163	1	554.8	56.666668 L.Q2D1H3T1E1F1L11P1V1L1E1P1I111N2.T
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	2	3.2398	0.1889	1958.51	1961.204	1	378.1	46.875 K.S1H3Q2D1P1T1I1V1V1P1E1K2D1F1I1I1T1.S
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	3	4.3663	0.3487	2849.81	2848.036	1	653	30.208334 L.E1A1S1N2D1D1D1A1F1L1E1D1K2D1E1D111K2P1I1A1P1R4I1V1.K
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	2	3.7991	0.2541	2847.79	2848.036	1	451.9	39.583336 L.E1A1S1N2D1D1D1A1F1L1E1D1K2D1E1D111K2P111A1P1R4I1V1.K
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	2	3.8132	0.3862	2816.57	2817.036	1	397.5	39.583336 L.EASNDDDAFLEDKDEDIKPIAPRIV.K

gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	3	4.9083	0.3309	2527.79	2529.763	1	734.1	34.523808 S.NDDDAFLEDKDEDIKPIAPRIV.K
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	2	2.9452	0.1655	1811.57	1809.067	4	355.4	46.666668 H.S1Q2D1L1L1F1P1Q2G1T1K2D1L1T111L1.K
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	2	3.8374	0.2204	1769.23	1769.032	1	596.6	60.714287 Q.D1H3T1E1F1L11P1V1L1E1P11111N2.T
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	3	5.1734	0.3066	2341.13	2343.471	1	824	34.210526 S.N2D1D1D1A1F1L1E1D1K2D1E1D111K2P1I1A1P1R4.I
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	3	5.3581	0.4689	2846.75	2848.036	1	849.2	32.291664 L.E1A1S1N2D1D1D1A1F1L1E1D1K2D1E1D1I1K2P111A1P1R4I1V1.K
gi 6319491 ref NP_009573.1	YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p Chitin synthase III, catalyzes the transfer of N-acetylglucosamine (GicNAc) to chitin;	2	3.7559	0.2459	1877.77	1879.163	1	522.3	53.333336 L.QDHTEFLIPVLEPIIN.T
gi 6319497 ref NP_009579.1	YBR023C	required to synthesis of the hispony of cell wall childrin, the childrin ming during bud emergence, and spore wall childsan; (ChS3) Chiltri synthase III, catalyzes the transfer of N-acetylglucosamine (G(cNAc) to chiltin; required for synthesis of the maiority to cell wall childrin. the chiltri na durina durina bud	2	3.7828	0.3468	2045.11	2045.385	1	766.4	59.375 T.I111H3P1D1I1V1Q2Q2P1P1L1D1F1M1P1Y1.G
gil6319497/refINP_009579_1	YBR023C	emergence, and spore wall chitosan. Chs3p	2	4 1359	0.3993	2023 39	2024 385	1	843.6	62.5 T JIHPDIVOOPPI DEMPY G
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	1	3.3293	0.1841	1515.46	1516.645	3	633.8	58.333332 M.SPEDAEEELKKLQ.T
gil6319499/refINP_009581_1	YBR025C	hypothetical protein; Ybr025cp	1	4 3594	0.1833	1531.51	1532 645	3	817.2	66 66667 M S1P1E1D1A1E1E1E11 1K2K2I 1Q2 T
gil6319499/refINP_009581_1	YBR025C	hypothetical protein; Ybr025cp	2	3 6686	0.1754	1388 41	1388 514	3	1478.8	81 818184 M SPEDAEEEI KKL Q
gil6319499/refINP_009581.1	YBR025C	hypothetical protein; Ybr025cp	3	4.0454	0.2706	1388.63	1388.514	1	1809.5	70.454544 M.SPEDAEEELKKL.Q
gil6319499/refINP_009581_1	YBR025C	hypothetical protein: Ybr025cp	2	4 3441	0 2421	1646 91	1647 838	1	1015.3	73 07692 H MSPEDAEEEI KKI O T
gil6319499/refINP_009581_1	YBR025C	hypothetical protein; Ybr025cp	2	2 9662	0.2041	1300.51	1301 436	1	702.8	75 S PEDAEEEI KKI O
gil6319499/refINP_009581_1	YBR025C	hypothetical protein; Ybr025cp	2	3 9661	0.3755	1635.27	1633 795	1	815.2	69 230774 K GKDYVVEDGDIIYE R
gil6319499/refINP_009581.1	YBR025C	hypothetical protein: Ybr025cp	2	3.584	0.2835	2179.37	2179.326	1	760	50 C.F1D1D1A1E1I1I1H3V1E1G1D1V1D1P1V1R4D1L1.E
gil6319499/refINP_009581.1	YBR025C	hypothetical protein: Ybr025cp	2	3.8646	0.3836	2605.43	2605.818	1	432.9	38.636364 F.DDAEIIHVEGDVDPVRDLEIINQ.E
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.3478	0.2375	1524.29	1521.606	1	741.3	72.72727 V.R4C1F1D1D1A1E1I1I1H3V1E1.G
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	1	3.0764	0.3949	1503.51	1504.606	1	362.9	59.090908 V.RCFDDAEIIHVE.G
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	1	3.1199	0.3667	1520.49	1521.606	1	368.9	59.090908 V.R4C1F1D1D1A1E1I1I1H3V1E1.G
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.8982	0.2046	1535.51	1534.707	1	689.1	79.16667 H.M1S1P1E1D1A1E1E1E1L1K2K2L1.Q
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.8174	0.3159	1947.99	1949.128	1	590.7	50 I.HVEGDVDPVRDLEIINQ.E
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.0213	0.239	1304.51	1304.461	6	463.8	65 F.S1V1S1L1E1E1R4L1S1H3M1.S
gi 6319499 ret NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.6626	0.4578	2020.57	2021.292	1	1102.3	62.5 L.MQKGKDYVVEDGDIIYF.R
gi 6319499 ret NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.7613	0.3683	2040.87	2041.292	1	810.2	56.25 L.M1Q2K2G1K2D1Y1V1V1E1D1G1D11111Y1F1.R
gi 6319499 ret NP_009581.1	YBR025C	nypotnetical protein; Ybr025cp	3	4.7335	0.1708	2211.77	2209.513	1	698.6	38.88889 A. TITIDIPTETETATR4V111V1PTSTPTR4F1D1K2L1.C
gi[6319499]rei[NP_009581.1]	VBP025C	hypothetical protein; Ybr025cp	2	3.9371	0.2232	2471.51	2471.742	1	407.1	30 V.SLEERLSHWSPEDAEEELKKL.Q 41 304348 E S11/1S11 15151841 S1B3M1S1D151D14151515111482831 103 T
gi[6319499][6][NP_009581.1]	VBP025C	hypothetical protein, 10/025cp	2	3,4393	0.2797	2010.29	2786.083	1	376.7	41.304340 F.STVTSTETETETR4ETSTH3WTSTFTETDTATETETETETR2R2ETQ2.T
gil6319499/refINP_009581_1	YBR025C	hypothetical protein; Ybr025cp	2	3 771	0.3762	2687 25	2687 953	1	867	50 F S1V1S1I 1E1E1R4I 1S1H3M1S1P1E1D1A1E1E1E1I 1K2K2I 1 C
gil6319499lrefINP 009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.6315	0.3766	2656.51	2657.953	1	730.7	47.727272 F.SVSLEERLSHMSPEDAEEELKKL.Q
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	3	3.8747	0.3067	1854.74	1854.159	3	1263	46.666668 D.PEEARVIVPSPRFDKL.C
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	1	3.0868	0.1948	1387.51	1388.514	2	724.3	68.181816 M.SPEDAEEELKKL.Q
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.6863	0.3576	1647.55	1648.795	1	580.1	57.692307 K.G1K2D1Y1V1V1E1D1G1D1I1I1Y1F1.R
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.097	0.2102	1521.31	1519.707	1	822.9	79.16667 H.MSPEDAEEELKKL.Q
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.8225	0.3482	2634.51	2635.818	1	477.4	36.363636 F.D1D1A1E1I1I1H3V1E1G1D1V1D1P1V1R4D1L1E1I1I1N2Q2.E
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	3	4.8163	0.2381	3071.39	3069.321	1	815.2	32 V.RCFDDAEIIHVEGDVDPVRDLEIINQ.E
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	3	5.0265	0.3422	3103.79	3105.321	1	802.5	32 V.R4C1F1D1D1A1E1I1I1H3V1E1G1D1V1D1P1V1R4D1L1E1I1I1N2Q2.E
gi 6319499 ret NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	3	3.9273	0.2947	2252.96	2254.591	3	650.3	35.526314 F.ATIDPEEARVIVPSPRFDKLC
gi[6319499]rei[NP_009581.1]	YPR025C	hypothetical protein; Ybr025cp	3	4.0405	0.2020	2000.77	2007.903	1	1401	30.303030 F.STVISILIEIEIR4LISITI3WISIPIEIDIAIEIEIEILIKZKZLI.G
gi[6319499][6][NP_009581.1] gi[6319499]ref[NP_009581.1]	VBR025C	hypothetical protein; Ybr025cp	2	2.339	0.3098	1504.27	1504 606	1	564.2	63 636364 V RCEDDAEIHVE G
gil6319499/refINP_009581_1	YBR025C	hypothetical protein; Ybr025cp	2	4 2475	0 1814	1663.59	1664 838	1	940.4	73 07692 H M1S1P1E1D1A1E1E1E1I 1K2K2I 102 T
gil6319499/refINP_009581.1	YBR025C	hypothetical protein; Ybr025cp	3	4.3315	0.2154	2182.34	2183.513	1	655.2	40.27778 A TIDPEEARVIVPSPREDKLC
gil6319499lrefINP 009581.1	YBR025C	hypothetical protein; Ybr025cp	3	3.8711	0.212	2280.98	2281.591	1	728.4	34.210526 F.A1T111D1P1E1E1A1R4V111V1P1S1P1R4F1D1K2L1.C
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp	2	3.6901	0.2374	1666.59	1666.961	1	1056.8	64.28571 Q.VEEKKVLLGRPGNNL.K
gi 6319499 ref NP_009581.1	YBR025C	hypothetical protein; Ybr025cp 2-encyl thicester reductase, member of the medium chain dehydrogenase/reductase family: locatized to in microchondria, where it has a probable role in fatty acid	2	4.2936	0.3273	1688.39	1688.961	1	1045.6	60.714287 Q.V1E1E1K2K2V1L1L1G1R4P1G1N2N2L1.K
gi 6319500 ref NP_009582.1	YBR026C	synthesis; Err1p 2-encyl thioester reductase, member of the medium chain dehydrogenase/reductase	1	2.3524	0.1869	1295.61	1296.553	3	242.1	54.545456 K.GDLKLGDRVIPL.Q
gi 6319500 ref NP_009582.1	YBR026C	ramity; localized to in milochondria, where it has a probable role in fatty acid synthesis; Etr1p 2-encyl thicester reductase, member of the medium chain dehydrogenase/reductase	2	3.1417	0.151	1921.67	1921.117	2	408.6	46.666668 M.YNYGHIISPRDEIETL.T
gi 6319500 ref NP_009582.1	YBR026C	family; localized to in mitochondria, where it has a probable role in fatty acid synthesis; Etr1p 2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase	2	3.8464	0.1994	1876.61	1877.108	1	489.4	53.333336 L.SVIRDRDNFDEVAKVLE
gi 6319500 ref NP_009582.1	YBR026C	family; localized to in mitochondria, where it has a probable role in fatty acid synthesis; Etr1p	1	3.3959	0.2721	1510.87	1511.805	1	433.7	57.692307 S.SKGDLKLGDRVIPL.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diadglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	1	2.7053	0.1527	1267.65	1267.513	2	504.4	72.22222 Q.VYRLPPIFFD.K
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	3.4268	0.2503	1354.29	1354.662	1	463.8	75 K.Q21111E1L111D111L111R4.F

gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	3.6979	0.2944	1513.35	1510.82	1	813.7	72.72727 Q.V1Y1R4L1P1P1I1F1F1D1K2V1.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	3.4261	0.3562	1393.71	1395.687	1	1205.1	75 Q.VYRLPPIFFDK.V
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	3	3.9465	0.2633	1511.15	1510.82	1	1514.1	61.363636 Q.V1Y1R4L1P1P111F1F1D1K2V1.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	1	2.9052	0.2135	1509.92	1510.82	2	282	59.090908 Q.V1Y1R4L1P1P1I1F1F1D1K2V1.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	1	2.6654	0.198	1493.7	1494.82	4	285.2	59.090908 Q.VYRLPPIFFDKV.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	2.9013	0.186	1232.49	1232.511	4	810.4	83.33333 Y.RLPPIFFDKV.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	3.3758	0.2096	1412.77	1410.687	1	1438.7	80 Q.V1Y1R4L1P1P1I1F1F1D1K2.V
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	3	3.9071	0.2031	1410.02	1410.687	1	1390.9	60.000004 Q.V1Y1R4L1P1P1I1F1F1D1K2.V
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	3.5943	0.2493	1496.53	1494.82	1	707.6	68.181816 Q.VYRLPPIFFDKV.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	3	3.9875	0.324	1511	1510.82	1	1654.5	63.636364 Q.V1Y1R4L1P1P1I1F1F1D1K2V1.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	3.9265	0.2978	1509.65	1510.82	1	849.1	72.72727 Q.V1Y1R4L1P1P1I1F1F1D1K2V1.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	3	4.3266	0.2899	1494.77	1494.82	1	1572.7	63.636364 Q.VYRLPPIFFDKV.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	2.9198	0.167	1281.09	1280.513	1	538.5	72.22222 Q.V1Y1R4L1P1P1I1F1F1D1.K
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	3	3.9845	0.2223	1495.19	1494.82	1	1136.6	54.545456 Q.VYRLPPIFFDKV.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	3.2136	0.2537	1508.81	1510.82	1	1039.7	77.27273 Q.V1Y1R4L1P1P1I1F1F1D1K2V1.Q
gi 6319503 ref NP_009585.1	YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	2	3.2381	0.2288	1494.35	1494.82	1	914.6	72.72727 Q.VYRLPPIFFDKV.Q
gi 6319505 ref NP_009587.1	YBR031W	N-terminally acetylated protein component or the large (60S) indosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap N-terminally acetylated protein component of the large (60S) ribosomal subunit,	1	2.3631	0.184	1197.63	1196.473	5	470.2	55 E.KIPEIPLVVST.D
gi 6319505 ref NP_009587.1	YBR031W	nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap N-terminally acetylated protein component of the large (60S) ribosomal subunit,	1	3.1445	0.2072	1478.68	1479.803	1	390.3	58.333332 H.RVEKIPEIPLVVS.T
gi 6319505 ref NP_009587.1	YBR031W	nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap N-terminally acetylated protein component of the large (60S) ribosomal subunit.	1	2.7687	0.18	1597.9	1598.908	2	352.3	57.692307 H.R4V1E1K2I1P1E1I1P1L1V1V1S1T1.D
gi 6319505 ref NP_009587.1	YBR031W	nearly identical to RpI4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; RpI4ap N-terminally acetvlated protein component of the Jarce (60S) ribosomal subunit.	1	2.8167	0.1834	1391.78	1392.725	3	312.8	59.090908 H.RVEKIPEIPLVV.S
gi 6319505 ref NP_009587.1	YBR031W	nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap N-terminally acetvlated protein component of the large (60S) ribosomal subunit.	2	2.9906	0.3225	2041.13	2039.406	1	296.6	38.88889 N.A1L1P1L1P1A1V1F1S1A1P111R4P1D111V1H3T1.V
gi 6319505 ref NP_009587.1	YBR031W	nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap N-terminally acetvlated protein component of the large (60S) ribosomal subunit.	2	2.928	0.2551	2287.57	2287.715	1	285.8	35 N.A1L1P1L1P1A1V1F1S1A1P111R4P1D111V1H3T1V1F1.T
gi 6319505 ref NP_009587.1	YBR031W	nearly identical to RpI4Bp and has similarity to E. coil L4 and rat L4 ribosomal proteins; RpI4ap N-terminally acetVlated protein component of the large (60S) ribosomal subunit	1	2.4115	0.3017	1106.65	1106.368	3	369.5	55.555557 E.K2I1P1E1I1P1L1V1V1S1.T
gi 6319505 ref NP_009587.1	YBR031W	nearly identical to RpI4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; RpI4ap N-terminally acetylated protein component of the large (60S) ribosomal subunit.	1	2.9851	0.2846	1208.75	1208.473	1	536	60.000004 E.K2I1P1E1I1P1L1V1V1S1T1.D
gi 6319505 ref NP_009587.1	YBR031W	nearly identical to RpI4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; RpI4ap	2	2.9059	0.2134	1198.17	1196.473	1	495.3	75 E.KIPEIPLVVST.D

		N-terminally acetylated protein component of the large (60S) ribosomal subunit,								
gi 6319505 ref NP 009587.1	YBR031W	nearly identical to RpI4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; RpI4ap	1	3.19	0.3688	1495.69	1496.803	1	452	58.333332 H.R4V1E1K2I1P1E1I1P1L1V1V1S1.T
51		Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a								
ail/16206761rofIND_000507.21		complex with Faa1p or Faa4p that imports and activates exogenous fatty acids;	2	2 06/5	0 2197	1606.05	1604 846	1	1276 1	
gil41023070[rei]i4r_003337.2]	10104111	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a	2	2.3043	0.2107	1000.05	1004.040		12/0.1	0.705220 Q.NEF KOLDOND III W.L
		complex with Faa1p or Faa4p that imports and activates exogenous fatty acids;		0.4000	0.0000	1001 71	4000 040		057.0	
gil41629676[rei]NP_009597.2]	TBR041W	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a	2	3.1606	0.2906	1021.71	1622.640	1	857.2	69.230/74 Q.KZETPTKZGTETDTGTNZDTTTTFTWZ.E
		complex with Faa1p or Faa4p that imports and activates exogenous fatty acids;								
gi 41629676 ret NP_009597.2	YBR041W	Fat1p Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a	1	2.4954	0.156	1468.6	1469.723	3	400.7	54.545456 R.IFFPKKPETSFQ.G
		complex with Faa1p or Faa4p that imports and activates exogenous fatty acids;								
gi 41629676 ref NP_009597.2	YBR041W	Fat1p Eatty acid transporter and year long-chain fatty acyl-CoA synthetace, may form a	3	4.9633	0.2555	3154.67	3154.501	1	726.1	27.777779 Q.VFIDPDASNPIRESEEEIKNALPDVKLN.Y
		complex with Faa1p or Faa4p that imports and activates exogenous fatty acids;								
gi 41629676 ref NP_009597.2	YBR041W	Fat1p	2	2.9179	0.1595	1470.59	1469.723	3	445.8	63.636364 R.IFFPKKPETSFQ.G
gilos 195 tolterini -009590. 1	1010420		2	3.0343	0.3023	1701.13	1700.000		032.4	S.L1A1G1K2S1P1E1R4I1T1E1E1G1E1S1I1W2N2P1E1V1I1D1P1K2Q2I1H3W2P1Y
gi 6319516 ref NP_009598.1	YBR042C	hypothetical protein; Ybr042cp	3	4.712	0.3469	3663.08	3663.043	1	513.1	
gilos 195 tolterini -009590. 1	1010420		5	5.0577	0.2234	3300.34	3307.004	2	557.1	23.273002 E.KOKOF EKT LEGESIWAR EVIDE KQITWETTIN
gi 6319516 ref NP_009598.1	YBR042C	hypothetical protein; Ybr042cp	3	5.2293	0.3648	3548.27	3548.884	1	709.9	28.448275 L.A1G1K2S1P1E1R4I1T1E1E1G1E1S1I1W2N2P1E1V1I1D1P1K2Q2I1H3W2P1Y1.N
gi 6319516 ref NP_009598.1	YBR042C	hypothetical protein; Ybr042cp	3	4.8928	0.3268	3476.39	3476.805	1	935.1	31.25 A.G1K2S1P1E1R4I1T1E1E1G1E1S1I1W2N2P1E1V1I1D1P1K2Q2I1H3W2P1Y1.N
gi 6319516 ref NP_009598.1	YBR042C	hypothetical protein; Ybr042cp	2	3.2141	0.3612	1967.57	1966.065	1	779.6	56.666668 F.DVKDIPLEDENEFSEW.L
gi 6319522 ref NP 009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	2	3.1952	0.2925	1341.73	1342.544	4	722.8	70 S.YIDKKCPFTGL.V
		Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and		0.0545	0.0400	1011.00	1010 511			
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp Protein component of the small (40S) ribosomal subunit: identical to Rps11Ap and	1	3.2515	0.3198	1341.66	1342.544	1	612.4	65 S.YIDKKCPFTGL.V
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	1	2.6984	0.376	1201.57	1202.371	1	421.7	60.000004 R.H3K2N2V1P1V1H3V1S1P1A1.F
ail63195221refINP_009604_11	YBR048W	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and has similarity to E_coli S17 and rat S11 ribosomal proteins; Rps11bp	2	3 1845	0.3593	1185 39	1185 371	1	1297 8	80 R HKNVPVHVSPA F
gilos reszzirolitit _00000 itit	121101011	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and	-	0.1010	0.0000	1100.00	1100.071		120110	
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp Protein component of the small (40S) ribosomal subunit: identical to Rps114p and	1	2.4666	0.3671	1184.6	1185.371	1	463.4	60.000004 R.HKNVPVHVSPA.F
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	2	3.3618	0.3764	1202.97	1202.371	1	1279.2	80 R.H3K2N2V1P1V1H3V1S1P1A1.F
ail62105221rofIND_000604_1	VPD049W	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and	2	2 5225	0 4225	1221.05	1000 540	1	806.2	
gilo319322[rei]14r_003004.1]	10104010	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and	2	3.3333	0.4200	1331.33	1332.340		000.2	
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	2	3.1764	0.3641	1469.77	1470.683	1	580.7	62.5 K.N2V1P1V1H3V1S1P1A1F1R4V1Q2.V
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	2	3.105	0.3196	1202.57	1202.371	1	467.1	65 R.H3K2N2V1P1V1H3V1S1P1A1.F
		Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and		0 7704	0.0704	4004 50	4000 074	4	444.0	
gilo319522[rei]NP_009604.1]	TDR046W	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and		2.7734	0.3704	1201.52	1202.371	I	441.3	00.000004 R.H3K2N2V IPTV IH3V ISTPTAT.F
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	1	2.3308	0.2944	1184.54	1185.371	1	380.3	55 R.HKNVPVHVSPA.F
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	1	3.2481	0.2448	1354.34	1355.544	7	549.6	60.000004 S.Y1I1D1K2K2C1P1F1T1G1L1.V
		Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and		0.750	0 0007	4507.0	4500 000	7	007.0	
gilo319522[rei]NP_009604.1]	TDR046W	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and		2.752	0.2327	1507.6	1008.009	'	227.8	50 Q.STETR4ATFTQ2K2Q2PTH3TFT.N
gi 6319522 ref NP_009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	2	3.0962	0.3575	1185.79	1185.371	1	885.6	75 R.HKNVPVHVSPA.F
gi 6319522 ref NP 009604.1	YBR048W	has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	1	2.4031	0.3867	1184.61	1185.371	1	503.5	65 R.HKNVPVHVSPA.F
		RNA polymerase I enhancer binding protein; DNA binding protein which binds to								
ail63195231refINP 009605.11	YBR049C	genes transcribed by both RNA polymerase I and RNA polymerase II; required for termination of RNA polymerase I transcription; Reb1p	2	4.4213	0.3104	2328.75	2329.577	1	1247.7	52.499996 L.G1I1T1E1D1S1Q2V1D1W2D1E1L1A1A1L1K2P1G1M1K2.L
9.1 · · · · · · · · · · · · · · · ·		RNA polymerase I enhancer binding protein; DNA binding protein which binds to								
ail6319523/refINP_009605.11	YBR049C	genes transcribed by both RNA polymerase I and RNA polymerase II; required for termination of RNA polymerase I transcription; Reb1p	2	4,151	0.2547	2304.23	2304.577	1	791.8	50 L.GITEDSQVDWDELAALKPGMK L
gilos reszejreinti _eccessini	12110100	RNA polymerase I enhancer binding protein; DNA binding protein which binds to	-		0.2011	200 1.20	2001.011		101.0	
ail6319523/refINP_009605_1	VBR049C	genes transcribed by both RNA polymerase I and RNA polymerase II; required for termination of RNA polymerase I transcription; Reh1p	2	3 0079	0 1759	2055 85	2055.26	5	200.2	41 17647 T E1D1S102V1D1W2D1E1I 1A1A1I 1K2D1G1M1K2 I
gilos reszejreinti _eccessini	12110100	RNA polymerase I enhancer binding protein; DNA binding protein which binds to	-	0.0010	0.1100	2000.00	2000.20	0	200.2	
ail63105231rofIND_000605_11	VBR040C	genes transcribed by both RNA polymerase I and RNA polymerase II; required for termination of RNA polymerase I transcription; Reh1p.	2	3 2504	0 2238	1252 25	1252 /1	1	610.8	83 23233 N LI EEEOHLI O D
gi 6319529 ref NP_009611.1	YBR055C	Splicing factor, component of the U4/U6-U5 snRNP complex; Prp6p	1	2.3175	0.1624	1268.72	1268.511	1	162.6	66.66667 T.RLVPNCPLLW.V
gi 6319529 ref NP_009611.1	YBR055C	Splicing factor, component of the U4/U6-U5 snRNP complex; Prp6p	1	2.3812	0.2285	1282.64	1283.511	6	137.2	61.11111 T.R4L1V1P1N2C1P1L1L1W2.V
gi 6319529 ref NP_009611.1	YBR055C	Splicing factor, component of the U4/U6-U5 snRNP complex; Prp6p	2	2.9088	0.2055	1891.77	1893.187	1	347.9	46.666668 S.L1S1K2I1D1E1I1D1L1K2N2P1V1R4A1R4.S
gil6319529[refINP_009611.1]	YBR055C	Splicing factor, component of the U4/U6-U5 snRNP complex; Pro6p	2	3.5972	0.2169	2000 43	2001 283	1	808.9	53 125 R S111 1D1R4G11 11 1K2N2P1D1D1V11 1F1Y1 1
gi 6319530 ref NP_009612.1	YBR056W	hypothetical protein; Ybr056wp	2	3.3881	0.3154	2473.47	2473.676	1	667.3	42.857143 N.S11111K2D1L1P1N2T1V1N2F1P1H3E1D1A1D1Y1T1V1G1.E
gi 6319530 ref NP_009612.1	YBR056W	hypothetical protein; Ybr056wp	2	3.8696	0.4158	2446.39	2446.676	1	710.4	47.61905 N.SIIKDLPNTVNFPHEDADYTVG.E
gi 6319530 ref NP_009612.1	YBR056W	hypothetical protein; Ybr056wp	2	3.4212	0.3745	1778.33	1776.002	1	471.9	56.666668 W.HVEDGKHLDSLPFAPL.R
gi 6319530 ref NP_009612.1	YBR056W	hypothetical protein; Ybr056wp	2	4.8027	0.4496	1982.27	1985.215	1	1160.4	75 Y.W2H3V1E1D1G1K2H3L1D1S1L1P1F1A1P1L1.R
gil6319530/ref/NP_009612.1	YBR056W	hypothetical protein; Ybr056wp	2	3.0899	0.2372	15/7.45	15/6./49	2	655.9	59.090908 Y.IDRIDWEWLSKD.A
gil6319530/refINP_009612.1	YBR056W	hypothetical protein; Ybr056wp	2	4.1793	0.4443	1961.85	1962.215	1	867.6	59.375 Y.WHVEDGKHLDSLPFAPL.R
gi 6319530 ref NP_009612.1	YBR056W	hypothetical protein; Ybr056wp	2	3.0359	0.2037	2140.65	2141.45	1	357.7	44.444447 L.S1T1T1L1P1K2L1P1P1A1K2D1L1D1R4S1T1I1Y1.K
gi 6319530 ref NP_009612.1	YBR056W	hypothetical protein; Ybr056wp	2	3.5328	0.2975	1761.29	1761.01	1	467.6	53.333336 L.S1T1T1L1P1K2L1P1P1A1K2D1L1D1R4S1.T
		Small heat shock protein with chaperone activity that is regulated by a heat induced								
		transition from an inactive oligomeric (24-mer) complex to an active dimer; induced								
gi 6319546 ref NP_009628.1	YBR072W	by heat, upon entry into stationary phase, and during sporulation; Hsp26p	2	3.1531	0.2	1548.37	1548.706	1	560.8	53.846157 K.R4V1I1T1L1P1D1Y1P1G1V1D1A1D1.N
		Small heat shock protein with chaperone activity that is regulated by a heat induced								
		transition from an inactive oligomeric (24-mer) complex to an active dimer; induced								
gi 6319546 ref NP_009628.1	YBR072W	by heat, upon entry into stationary phase, and during sporulation; Hsp26p	2	3.6775	0.3448	1805.91	1807.056	1	934.3	63.333332 K.FKRVITLPDYPGVDAD.N

gil6319546/refINP_009628_1	VBR072W	Small heat shock protein with chaperone activity that is regulated by a heat induced transition from an inactive oligometric (24-mer) complex to an active dimer; induced by heat upon entry into stationary chapse, and during sponulation; Hep26n	1	2 4617	0 1616	1530 73	1531 706	3	281.9	
gilos 13040/16/14/ _000020.1/	1DR0721	Small heat shock protein with chaperone activity that is regulated by a heat induced		2.4017	0.1010	1000.70	1001.700	0	201.5	
gi 6319546 ref NP_009628.1	YBR072W	binai neat stock potent wint ridgebole activity that is regulated by a neat induced transition from an inactive oligomeric (24-mer) complex to an active dimer; induced by heat, upon entry into stationary phase, and during sporulation; Hsp26p	2	3.5606	0.2986	2043.95	2042.253	1	1252	61.764706 R.SVAVPVDILDHDNNYELK.V
	VDD0700	Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Pr1p-Rpg1p-Nip1p) that stimulates binding of		4 470	0.0404	0010 70	0011 001		500 7	
gi 6319553 ref NP_009635.1	YBR079C	mRNA and tRNA(I)Met to ribosomes; Kpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Pt1p.Pro1p.bin1p) that stimulates binding of	3	4.476	0.3404	3010.79	3011.901	1	599.7	30.000002 Q.E1E1K2E1E111D1E1A1L1G1P1Q2E111E1D1G1E1E1K2E1E1E1S1D1.P
gi 6319553 ref NP_009635.1	YBR079C	mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	3.8501	0.3245	3189.75	3191.251	2	286.7	29.62963 A.SKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	3	6.2343	0.3395	3295.64	3296.33	1	837.2	33.035713 T.A1S1K2E1V1S1E1E1E1N2T1E1P1E1V1Q2E1E1K2E1E1T1D1E1A1L1G1P1Q2.E
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the core complex of translation initiation factor 3(eIF3), essential for	3	6.1462	0.406	3192.14	3191.251	1	1044	37.037037 A.SKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p.	3	6.2074	0.3814	3398.51	3398.435	1	1183.8	S.T1A1S1K2E1V1S1E1E1E1N2T1E1P1E1V1Q2E1E1K2E1E1T1D1E1A1L1G1P1Q2 35.344826 E
gi 6319553 ref NP_009635.1	YBR079C	Subunit of the core complex of translation initiation factor 3(eir/3), essential for translation; part of a subcomplex (Pr11p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p	3	5.9175	0.4516	3363.35	3363.435	1	1319.8	34.482758 S.TASKEVSEEENTEPEVQEEKEETDEALGPQ.E
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6319553 ref NP_009635.1	YBR079C	mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Pr1p-Rpg1p-Nip1p) that stimulates binding of	3	5.3326	0.3787	3675.98	3675.76	1	685.9	26.612906 Q.EEKEETDEALGPQETEDGEEKEEESDPVIIRN.S
gi 6319553 ref NP_009635.1	YBR079C	mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	3	5.5203	0.3573	3562.19	3561.656	1	1169.5	31.666666 Q.EEKEETDEALGPQETEDGEEKEEESDPVIIR.N
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	3	5.9334	0.4118	3599.99	3598.656	1	1108.8	Q.E1E1K2E1E1T1D1E1A1L1G1P1Q2E1T1E1D1G1E1E1K2E1E1E1S1D1P1V1I11R 30.833334 4.N
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	3.3197	0.3042	1169.79	1170.299	1	910.9	83.33333 I.P1S1I1G1Y1D1P1H3L1R4.M
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Pr11p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	3.6465	0.3368	1938.65	1941.19	1	774.5	60.000004 Q.L1D1E1I1P1S1I1G1Y1D1P1H3L1R4M1Y1.R
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	1	2.7048	0.1905	1130.56	1130.262	2	455.3	75 Y.R4S1I1E1D1V1F1H3L1.M
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the core complex of translation initiation factor 3(eIF3), essential for	1	3.0702	0.2969	1261.51	1262.455	5	369.3	72.22222 Y.R4S111E1D1V1F1H3L1M1.K
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the core complex of translation binding forter 2(cIE3) accential for	1	2.8335	0.2762	1246.5	1247.455	1	445.1	77.77778 Y.RSIEDVFHLM.K
gi 6319553 ref NP_009635.1	YBR079C	translation is part of a subcomplex of national initiation fraction open 5, essential for translation and tRNA(i)Met to ribosomes; Rpg1p.	2	3.1941	0.4329	2525.21	2525.795	5	155.8	23.076923 A.G1G1S1S1P1A1T1P1A1T1P1A1T1P1A1T1P1S1S1G1P1K2K2M1T1.M
gi 6319553 ref NP_009635.1	YBR079C	translation: part of a subcomplex (Pr11p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p	2	3.5854	0.3688	2566.41	2567.874	1	158	24.074074 R.TAGGSSPATPATPATPATPTPSSGPKKM.T
gi 6319553 ref NP_009635.1	YBR079C	Subunit of the core complex of translation initiation factor 3(eIF-3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p	2	3.4978	0.1733	1908.61	1909.254	4	384.7	53.571426 K.KREFEAIKEREITKM.I
ail63105531rafIND_000635_11	VBR070C	Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of PRNA and tPNA(filter to ribecome: Prod to the subcomplex of t	2	3 7794	0.386	2422.45	2423 60	1	503	38 A C4C1C4S4D1A1T4D1A1T4D1A1T4D1A1T4D1A1T4D1S4S1C4D1K2K2M1 T
	TEROTO	Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of	2	0.1104	0.000	2422.40	2420.00		000	
gi 6319553 ref NP_009635.1	YBR079C	mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Parta Parta Ninta) that stimulates binding of	2	3.7724	0.4548	2394.25	2395.69	1	477.7	36 A.GGSSPATPATPATPATPTPSSGPKKM.T
gi 6319553 ref NP_009635.1	YBR079C	mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	3	5.6608	0.4527	3190.58	3191.251	1	1021.2	37.962963 A.SKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	3.7137	0.3246	3189.91	3191.251	1	297.1	29.62963 A.SKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the core complex of translation initiation factor 3(eIF3), essential for	3	5.5049	0.3464	3715.04	3714.76	1	886.1	Q.E1E1K2E1E1T1D1E1A1L1G1P1Q2E1T1E1D1G1E1E1K2E1E1E1S1D1P1V1I1I1R 28.225807 4N2.S
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the core complex of translation initiation factor 3(eIF3), essential for	2	4.1894	0.2417	1837.47	1839.019	1	1167.6	67.85714 K.V1D1E1E1L1K2E1L1Y1D1I1I1E1V1N2.F
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that situalizes binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p. Subcut of the core complex of translation for the core complex of translation initiation factor 2(aLE3) accential for	2	3.8722	0.2379	1821.37	1822.019	1	1474	75 K. VDEELKELYDIIEVN. F
gi 6319553 ref NP_009635.1	YBR079C	translation: part of a subcomplex (Pr11p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p	2	3.3902	0.2887	1918.79	1920.19	1	1066.9	63.333332 Q.LDEIPSIGYDPHLRMY.R
ail6319553 ref NP_009635_1	YBR079C	suburne or the core complex or translation initiation factor 3(eI+3), essential for translation; part of a subcomplex (Pr1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes: Rpg1p.	1	3.2415	0.2579	1497 59	1498 709	1	387 7	59.090908 E.A1Y1R4S111E1D1V1E1H3L1M1.K
ail6319553/refINP_000635_1	YBR070C	Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and IBNA/IMME to ribosomes: Rpd1p.	1	3 0610	0.2805	1481.82	1481 700	1	402.8	59 090908 E AYRSIEDVEHI M K
9-100-100001-0114r _000000.1	1010130	Suburit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpo1p-Nip1p) that stimulates binding of		0.0013	0.2033	1401.02	1401.703		702.0	
gi 6319553 ref NP_009635.1	YBR079C	mRNA and tRNA(i)Met to ribosomes; Rpg1p	2	3.258	0.3445	1596.57	1596.781	1	355.2	53.571426 G.NREPPSTPSTLPKAT.V

		Subunit of the core complex of translation initiation factor 3(eIF3), essential for								
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	3	3.9347	0.1895	1498.58	1498.709	1	1512.8	59.090908 E.A1Y1R4S1I1E1D1V1F1H3L1M1.K
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	3.4001	0.2541	2242.15	2243.277	1	362.7	52.77778 Q.E1T1E1D1G1E1E1K2E1E1E1S1D1P1V11111R4N2.S
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Pr11p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	3.2155	0.3678	2218.57	2219.277	1	277.5	50 Q.ETEDGEEKEEESDPVIIRN.S
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the core complex of translation initiation factor 3(eIF3), essential for	2	3.6732	0.3573	2125.91	2127.174	3	350.7	47.058823 Q.E1T1E1D1G1E1E1K2E1E1E1S1D1P1V11111R4.N
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Subunit of the core complex of translation initiation factor 3(eIE3) essential for	2	3.4362	0.1974	1111.25	1110.259	1	797.4	87.5 T.F1A1K2D1P1F1D1I1F1.A
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Pr1p-Rpg1p-Np1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the cross commels of translation initiation factor 3(aE3), essential for	2	3.7806	0.3431	1626.63	1625.822	1	732	69.230774 Q.LDEIPSIGYDPHLR.M
gi 6319553 ref NP_009635.1	YBR079C	translation; part of a subcomplex (Pr1p-Rpg1p-Np1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the cross commels of translation initiation factor 3(aE3), essential for	3	3.8137	0.2963	1777.55	1774.952	1	783	46.42857 T.Q2L1D1E1I1P1S1I1G1Y1D1P1H3L1R4.M
gi 6319553 ref NP_009635.1	YBR079C	Constructions part of a subcomplex (Pr1p-Rpg1p-Np1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p Suburit of the crop commely of translation initiation factor 3(aIE3), essential for	2	4.126	0.2157	1969.45	1969.193	1	726	60.000004 G.K2V1D1E1E1L1K2E1L1Y1D1I1I1E1V1N2.F
gi 6319553 ref NP_009635.1	YBR079C	Construct the concentration of the standard metal the standard metal of the standard metal the standard meta	3	4.2033	0.2153	1366.28	1366.517	2	1626.5	65 E.A1Y1R4S1I1E1D1V1F1H3L1.M
gi 6319553 ref NP_009635.1	YBR079C	Construction is and complexed mathematical matchine matchine and the second matchine in the second matchine and the second matchine is th	2	3.7979	0.2415	2026.29	2027.245	3	369.8	50 Y.G1K2V1D1E1E1L1K2E1L1Y1D1I1I1E1V1N2.F
gi 6319553 ref NP_009635.1	YBR079C	Subunit of the Cole Complex (Pr1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p - Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p	2	3.5848	0.2858	2006.43	2007.245	1	349.6	50 Y.GKVDEELKELYDIIEVN.F
	VEDOGAW	different oxidation states of tetrahydrololate (THF): provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase;	4	0.4405	0.004	1400 50	1400 500	2	224.2	
gilo319556[tei]14P_009640.1]	IBR064W	Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF		2.4405	0.224	1408.58	1409.536	2	324.3	50 L.ALESPVPSDIDIS.K
gi 6319558 ref NP_009640.1	YBR084W	synmetase, metnenyi-i Hir cycionydrolase, and metnylene-i Hir denydrogenase; Mist p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different ouridation school of ktorse ydrofolato (TME) zmiridae odrivitios of formul TME	2	4.3965	0.431	2132.87	2132.332	1	776.2	61.764706 L.DIEKEDPDALTPEEVKRF.A
gi 6319558 ref NP_009640.1	YBR084W	dimensional states on terranyolioolate (intr), provides activities or ionity in the synthetase, methenyi-THF cyclohydrolase, and methylene-THF dehydrogenase; Mistp	3	5.2167	0.3672	2154.44	2155.332	1	1668.1	47.058823 L.D111E1K2E1D1P1D1A1L1T1P1E1E1V1K2R4F1.A
oil6310558/rofIND_000640_1		different oxidation states of tetrahydrolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase;	2	3 0103	0 1059	1007 10	1000 206	1	630	
gilos (9556)(ei)(4F_009040.1)	I BR004W	Miscip Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyI-THF arthotoxe, methosul THE oxidehydratesa, ord methodas DHE dehydrosongor.	2	3.9193	0.1956	1997.19	1999.290		030	59.575 LEINQZEIFIEIFIK4R5EIDTETTTTTTNZ.A
gi 6319558 ref NP_009640.1	YBR084W	synatetase, menenyerne cycloadouase, and menyerier denyodenase, Mist p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different outdation school of Laterburghetable (TEE); anvideo services of twice of the TEE	2	3.4394	0.1581	1884.11	1883.192	1	506.4	63.333332 L.L111Q2L1P1L1P1R4H3L1D1E1T1T111T1.N
gi 6319558 ref NP_009640.1	YBR084W	diretent oxidation states or tetrahydrolate (rhrr), provides activities or romprin his synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mistp Mistpoddial C1.1etrahydrofelate synthase, iaelwd ia iatarsonuarsiae between	2	3.4487	0.1982	1860.51	1861.192	1	555.2	56.666668 L.LIQLPLPRHLDETTIT.N
ail6210559/rafiND_000640.11	VPD084W	different oxidation states of tetrahydrolate (THF) provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase;	2	2 6902	0.2559	2204.95	2202 414	1	542.2	
gilos (9556)(ei)(4F_009040.1)	I BR004W	Nits up Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyI-THF synthetises, methosul-THE cyclohydrafase, and methodes a THE dehydrogongor;	2	3.0092	0.2356	2204.85	2203.411		042.5	32.11116 L.DIEREUFDALIFEEVRRA.R
gi 6319558 ref NP_009640.1	YBR084W	Mist p Mist p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THE): provides activities of formvI-THE	2	3.5226	0.2738	2068.99	2068.294	1	426.1	44.11765 S.EKNPLNDKNIHEPGYVVT.E
gi 6319558 ref NP_009640.1	YBR084W	synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mist p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between	2	3.2097	0.3174	1496.49	1497.738	1	693.4	66.66667 F.ARLNINPDTITIR.R
gi 6319558 ref NP_009640.1	YBR084W	different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p	2	3.4137	0.306	2790.51	2790.102	5	164.2	34 H.GGAPNVKPGQSLPKEYTEENIDFVAK.G
		Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyI-THF synthetase, methenyI-THF cyclohydrolase, and methylene-THF dehydrogenase;								
gi 6319558 ref NP_009640.1	YBR084W	Mis1p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyI-THF	1	3.4068	0.2737	1333.84	1334.685	4	642.5	59.090908 E.SEKLPVIKPLPL.H
gi 6319558 ref NP_009640.1	YBR084W	synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mistp Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between	2	3.0295	0.1544	1863.91	1862.136	1	281.8	53.333336 L.IQLPLPRHLDETTITN.A
gi 6319558 ref NP_009640.1	YBR084W	different oxidation states of tetrahydrotolate (THF); provides activities of formyI-THF synthetase, methenyI-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis 19	2	4.2148	0.3296	2067.59	2068.294	2	567.2	50 E.KNPLNDKNIHEPGYVVTE.A
ail6319558 refINP_009640_41	YBR084W	windownand C - returning contract symmase, involved in interconversion between different oxidation states of tetrahydrolotale (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mistin	2	4 3130	0 3077	2552 55	2553 831	1	854 4	
312			-		2.30.1			•		

		Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase methenyl-THF cyclohydrolase and methylene-THE dehydrogenase:								
gi 6319558 ref NP_009640.1	YBR084W	Mistp Mistp Michondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyI-THF	3	4.1722	0.2887	1812.65	1813.234	1	920	38.333332 F.VESEKLPVIKPLPLHL.E
gi 6319558 ref NP_009640.1	YBR084W	synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between	1	2.4213	0.1526	1129.93	1130.492	1	964.8	77.77778 E.K2L1P1V1I1K2P1L1P1L1.H
gi 6319558 ref NP_009640.1	YBR084W	different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between	1	3.4055	0.2884	1118.67	1118.492	1	989.3	77.77778 E.KLPVIKPLPL.H
gi 6319558 ref NP_009640.1	YBR084W	different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p	3	4.088	0.2955	2132.54	2132.332	2	558.9	36.764706 L.DIEKEDPDALTPEEVKRF.A
		Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase;								
gi 6319558 ref NP_009640.1	YBR084W	Mis1p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyI-THF umbhdtoo, methemid THF exclusive/enclose, and drivelose THE divideo angre	2	3.3893	0.1841	2396.49	2393.699	1	657.3	52.499996 N.VKPGQSLPKEYTEENIDFVAK.G
gi 6319558 ref NP_009640.1	YBR084W	Synihetase, ineuteny-in-royounyuudase, and ineuryene-in-rorounyuudaea, Mistp Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyI-THF	2	4.2675	0.2836	1976.89	1975.296	1	545.4	56.25 LLIQLPLPRHLDETTITN.A
gi 6319558 ref NP_009640.1	YBR084W	synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between	2	4.0758	0.2881	1486.41	1486.724	1	839.4	73.07692 A.N2V1R4Q2P1S1L1G1P1T1L1G1V1K2.G
gi 6319558 ref NP_009640.1	YBR084W	different oxidation states of tetranydrotolate (THP); provides activities of formyi-i HP synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between	2	4.4235	0.4125	1469.63	1466.724	1	969.8	76.92308 A.NVRQPSLGPTLGVK.G
gi 6319558 ref NP_009640.1	YBR084W	different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p	2	3.1742	0.2164	1202.79	1200.513	1	777	88.88889 L.LIQLPLPRHL.D
gi 27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	2	2.9995	0.3189	1423.09	1423.522	1	603.5	72.72727 Y.HDTELSDDLHKL.I
gi 27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	2	3.9187	0.2205	2109.33	2109.352	1	1283.5	55.88235 Y.S1K2P1E1Y1F1P1F1P1I1Y1D1K2P1S1S1V1S1.N
gi 27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	2	3.8858	0.1962	1728.71	1729.93	1	851.8	64.28571 L.ARLPTHDSDFIIDTK.R
gi 27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	3	4.0614	0.3428	2878.94	2879.202	1	630.5	35.416664 K.HVVNVQNPPKQEVFEKIPSPEFNSN.N
gi 27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	3	3.8069	0.2694	2913.38	2914.202	1	1155.4	36.458336 K.H3V1V1N2V1Q2N2P1P1K2Q2E1V1F1E1K2I1P1S1P1E1F1N2S1N2.N
gi 27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	3	4.6468	0.2545	2317.19	2316.487	1	856.2	39.285713 T.GGENNENTQAKDDAATKTPLIK.D
gi]27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	3	4.6033	0.285	1423.55	1423.522	1	1792.6	61.363636 Y.HDTELSDDLHKL.I
gi 27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	2	4.1065	0.368	2088.37	2089.352	1	868.9	52.941177 Y.SKPEYFPFPIYDKPSSVS.N
gi 27808701 ref NP_009643.2	YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	2	4.5002	0.3357	1751.65	1750.93	1	1287.2	78.57143 L.A1R4L1P1T1H3D1S1D1F1I1I1D1T1K2.R
gi 6319582 ref NP_009664.1	YBR106W	Proceable memorane protein, involved in prospinate transport; proces proces double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p Probable membrane protein, involved in phosphate transport; pho88 pho86 double	1	2.2028	0.1838	1254.54	1255.518	1	491.2	72.22222 Y.LKYTNPLFMQ.S
gi 6319582 ref NP_009664.1	YBR106W	null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p Probable membrane protein, involved in phosphate transport; pho88 pho86 double	2	3.3447	0.2801	1267.73	1268.518	1	979.7	77.77778 Y.L1K2Y1T1N2P1L1F1M1Q2.S
gi 6319582 ref NP_009664.1	YBR106W	null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p Probable membrane protein, involved in phosphate transport; pho88 pho86 double null water to exhibit a phosened no wheating of a pamerality and be proved store of biobs	2	3.489	0.2987	1304.37	1304.505	3	375.1	68.181816 F.G1K2P1A1T1G1D1L1K2R4P1F1.K
gi 6319582 ref NP_009664.1	YBR106W	Inormanic exhibits eminance symmetrics or repressible acid prosphatase at high inorganic phosphate concentrations; Pho88p Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high	2	3.4769	0.349	1288.43	1287.505	1	408	68.181816 F.GKPATGDLKRPF.K
gi 6319582 ref NP_009664.1	YBR106W	inorganic phosphate concentrations; Pho8p Probable membrane protein, involved in phosphate transport; pho8b pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high	1	2.3898	0.233	1118.46	1119.266	2	382.1	68.75 A.LEHNEVKIH.L
gi 6319582 ref NP_009664.1	YBR106W	inorganic phosphate concentrations; Pho88p	2	2.9396	0.1784	1135.37	1134.266	4	545.4	75 A.L1E1H3N2E1V1K2I1H3.L

		Probable membrane protein, involved in phosphate transport; pho88 pho86 double								
ail6319582/refINP_009664_1	YBR106W	null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations: Pho88p	3	4 8501	0.3507	2673 38	2672 912	1	768	33 M GOTGPKTDKKSIEFAERAGNAGVKAE -
giloo roooziroiru _ooooo riif	Bittioott	Probable membrane protein, involved in phosphate transport; pho88 pho86 double	U		0.0001	2010.00	2012:012	•	100	
		null mutant exhibits enhanced synthesis of repressible acid phosphatase at high	2	F 0707	0 477	2505 77	2505 740	4	1010 5	
gilo319562[rei]NP_009664.1]	TERIUGW	Probable membrane protein, involved in phosphate transport; pho88 pho86 double	3	5.6/6/	0.477	2505.77	2505.718	I	1040.5	41.304348 M.GTQ2TTGTPTK2TTDTK2K2STTETETATETR4ATGTN2ATGTVTK2.A
		null mutant exhibits enhanced synthesis of repressible acid phosphatase at high								
gi 6319582 ret NP_009664.1	YBR106W	Inorganic phosphate concentrations; Pho88p Probable membrane protein, involved in phosphate transport: pho88 pho86 double	2	4.9333	0.3717	2505.51	2505.718	1	388.8	43.47826 M.G1Q211G1P1K211D1K2K2S1I1E1E1A1E1R4A1G1N2A1G1V1K2.A
		null mutant exhibits enhanced synthesis of repressible acid phosphatase at high								
gi 6319582 ref NP_009664.1	YBR106W	inorganic phosphate concentrations; Pho88p	2	4.1741	0.3492	2472.55	2472.718	1	448	43.47826 M.GQTGPKTDKKSIEEAERAGNAGVK.A
		null mutant exhibits enhanced synthesis of repressible acid phosphatase at high								
gi 6319582 ref NP_009664.1	YBR106W	inorganic phosphate concentrations; Pho88p	1	2.6789	0.2254	1286.6	1287.505	6	309.7	59.090908 F.GKPATGDLKRPF.K
		Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high								
gi 6319582 ref NP_009664.1	YBR106W	inorganic phosphate concentrations; Pho88p	2	3.1322	0.2824	1257.17	1255.518	1	947.4	77.77778 Y.LKYTNPLFMQ.S
		Probable membrane protein, involved in phosphate transport; pho88 pho86 double								
gi 6319582 ref NP_009664.1	YBR106W	inorganic phosphate concentrations; Pho88p	1	2.9543	0.2665	1546.81	1547.841	2	382.2	57.692307 H.LFGKPATGDLKRPF.K
		Probable membrane protein, involved in phosphate transport; pho88 pho86 double								
gil6319582 refINP_009664.1	YBR106W	null mutant exhibits ennanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations: Pho88p	2	4.1486	0.294	1565.79	1566.841	1	717.3	76.92308 H.L1F1G1K2P1A1T1G1D1L1K2R4P1F1.K
2.1		Probable membrane protein, involved in phosphate transport; pho88 pho86 double	_							
ail63105821rofIND_000664_11	VBP106W/	null mutant exhibits enhanced synthesis of repressible acid phosphatase at high	1	2 4715	0 2730	1546.68	1547 941	1	464.6	
gilos 19902 [rei]Nr_009004.1]	IDICIOUV	Probable membrane protein, involved in phosphate transport; pho88 pho86 double		2.4715	0.2755	1340.00	1347.041		404.0	01.550404 H.EF OKEATODERKET.K
		null mutant exhibits enhanced synthesis of repressible acid phosphatase at high								
gi 6319582 ret NP_009664.1	YBR106W	Inorganic phosphate concentrations; Pho88p Probable membrane protein, involved in phosphate transport; pho88 pho86 double	1	3.0949	0.3122	1565.72	1566.841	1	478.5	61.538464 H.L1F1G1K2P1A111G1D1L1K2R4P1F1.K
		null mutant exhibits enhanced synthesis of repressible acid phosphatase at high								
gi 6319582 ref NP_009664.1	YBR106W	inorganic phosphate concentrations; Pho88p General transcriptional co-repressor, acts together with Tup1p; also acts as part of a	2	3.5047	0.2111	1547.55	1547.841	1	541.2	69.230774 H.LFGKPATGDLKRPF.K
		transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes								
gi 6319589 ref NP_009670.1	YBR112C	to promoters; Cyc8p	2	3.6147	0.2884	1786.23	1786.889	1	586.5	66.66667 A.T1V1P1A1E1A1S1P1V1E1D1E1V1R4Q2H3.S
		transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes								
gi 6319589 ref NP_009670.1	YBR112C	to promoters; Cyc8p	2	4.1602	0.3957	2585.31	2586.893	1	456.8	44.736843 L.E1C1F1R4Y1I1L1P1Q2P1P1A1P1L1Q2E1W2D1I1W2.F
		General transcriptional co-repressor, acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes								
gi 6319589 ref NP_009670.1	YBR112C	to promoters; Cyc8p	2	3.096	0.2173	2834.55	2835.2	2	384.4	38.095238 L.ECFRYILPQPPAPLQEWDIWFQ.L
		General transcriptional co-repressor, acts together with Tup1p; also acts as part of a								
gi 6319589 ref NP_009670.1	YBR112C	to promoters; Cyc8p	2	2.9243	0.1898	2862.71	2865.2	2	240.1	33.333336 L.E1C1F1R4Y1I1L1P1Q2P1P1A1P1L1Q2E1W2D1I1W2F1Q2.L
		General transcriptional co-repressor, acts together with Tup1p; also acts as part of a								
gi 6319589 ref NP 009670.1	YBR112C	transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; Cyc8p	2	3.0262	0.1513	1381.75	1380.574	1	644.6	72.72727 L.S1N2P1N2V1P1K2L1W2H3G1I1.G
		General transcriptional co-repressor, acts together with Tup1p; also acts as part of a								
gil6319589/refINP_009670.1	YBR112C	transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters: Cvc8p	1	2.3374	0.1607	1361.59	1362.574	1	681.7	63 636364 L.SNPNVPKLWHGLG
2.1111		General transcriptional co-repressor, acts together with Tup1p; also acts as part of a	-					-		
ail6319589/refINP_009670_1	VBR112C	transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes	1	2 6963	0 2205	1379 59	1380 574	1	708.2	68 181816 L S1N2P1N2V1P1K2I 1W2H3G1I1 G
gilos issosfielini _003070.1]	TDI(1120	General transcriptional co-repressor, acts together with Tup1p; also acts as part of a		2.0303	0.2203	137 9.35	1300.374		100.2	0.101010 E.STN2F HV2V1F HV2ETW2FISOTT.G
-:::::::::::::::::::::::::::::::::::::	VDD4400	transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes	2	4.0740	0.445	0404 54	0000 700		005	
gilo319569[rei]NP_009670.1]	TBRIIZC	General transcriptional co-repressor, acts together with Tup1p; also acts as part of a	2	4.27 10	0.445	2401.51	2396.769	1	805	55.555557 F.R TILPQPPAPLQEWDIWFQ.L
		transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes								
gi 6319589 ret NP_009670.1	YBR112C	to promoters; Cyc8p General transcriptional co-repressor, acts together with Tup1p; also acts as part of a	2	3.695	0.2427	2561.51	2559.893	1	543.6	47.368423 L.ECFRYILPQPPAPLQEWDIW.F
		transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes								
gi 6319589 ref NP_009670.1	YBR112C	to promoters; Cyc8p General transcriptional co-repressor, acts together with Tup1p; also acts as part of a	2	4.1852	0.2256	2148.55	2147.462	4	372	46.875 F.R4Y111L1P1Q2P1P1A1P1L1Q2E1W2D111W2.F
		transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes								
gi 6319589 ref NP_009670.1	YBR112C	to promoters; Cyc8p Concret transprinting of a represent sets together with Tup1p; also gets as part of a	2	3.961	0.4333	2423.27	2425.769	1	574	50 F.R4Y1I1L1P1Q2P1P1A1P1L1Q2E1W2D1I1W2F1Q2.L
		transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes								
gi 6319589 ref NP_009670.1	YBR112C	to promoters; Cyc8p	2	3.6632	0.2183	2125.37	2123.462	2	543	53.125 F.RYILPQPPAPLQEWDIW.F
		Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to								
		alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine;								
gi 6319591 ret NP_009673.1	YBR115C	activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	2	2.966	0.2214	2190.01	2187.544	4	342.9	39.473686 V.GFLPPPTHNDKLPLPSTELT.Q
		Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to								
gil6319591/rofIND_009673_11	VBP115C	alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine;	2	3 4868	0 3072	1713 70	1714 074	1	475.6	57 602307 E M1V/1P1P/E1D1K2P1D1D1I 1S1K2E1 O
gilos 1959 (fielini _009073.1)	TDICTI3C		2	3.4000	0.3072	1715.75	17 14.374		475.0	
		Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to								
gi 6319591 ref NP_009673.1	YBR115C	activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	3	4.2989	0.2612	1847.54	1845.105	1	1117.8	50 F.M1V1P1R4F1D1K2P1D1D1L1S1K2F1Q2.S
		Aleks and an Proton of States and the state of the state of the states o								
		Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine;								
gi 6319591 ref NP_009673.1	YBR115C	activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	2	3.6641	0.2059	1845.43	1845.105	1	631.9	57.14286 F.M1V1P1R4F1D1K2P1D1D1L1S1K2F1Q2.S
		Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to								
		alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine;	~	0.0047	0.4000	0450.11	0450 100		045.0	
gilos (359 (frei[NP_009673.1]	IBR 1150	Translational elongation factor EF-1 alpha; also encoded by TEF1: functions in the	2	2.9917	0.1896	2153.41	2153.492	1	210.2	44.444447 O.FILIPIPIPIPIPININ3N2DIK2LIPILIPISIIIEILIII.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.5476	0.2977	1257.54	1258.418	1	237	50 G.G1I1G1T1V1P1V1G1R4V1E1T1G1.V

gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.0868	0.2479	1177.33	1177.344	1	812.2	77.77778 V.P1S1K2P1M1C1V1E1A1F1.S
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.3276	0.3156	2739.57	2738.061	1	882.9	41.6666664 K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.T
gil6319594/refINP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2o	2	3.7529	0.2738	1560.13	1560.643	1	1021.3	73.07692 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1.K
gil6319594/refINP_009676.1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacy/JRN4 (AAJRN4) to riposomes: Tef2p	1	3 0031	0 3027	1559 51	1560 643	1	243 5	61 538464 L E14111D1411E102P1S1R4P1T1D1 K
gile310504[ref[NR_000676.1]	VPD110W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminocoul tPNA (AA tPNA) to hospital Taf2a		3 7337	0.3027	2578.20	2570.976	2	440.0	
gil0319594[ref[NP_009076.1]	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	0.0000	0.2002	2576.59	2379.870	2	449.9	
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.0936	0.3071	2705.89	2708.061	1	583.1	37.5 K.VGYNPKTVPFVPISGWNGDNMIEAT.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.6142	0.1697	2636.69	2635.956	1	583.9	36.95652 K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M111E1A1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1: functions in the	2	3.3216	0.3216	1484.33	1482.682	1	445.2	70.83333 T.VIDAPGHRDFIKN.M
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.9759	0.2141	1413.39	1414.487	1	456	75 M.D1S1V1K2W2D1E1S1R4F1Q2.E
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.2889	0.2899	1101.71	1102.397	2	719.5	72.22222 G.V1I1K2P1G1M1V1V1T1F1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.4313	0.3435	2607.45	2608.928	1	561.6	41.304348 V.GYNPKTVPFVPISGWNGDNMIEAT.T
gi 6319594 ref NP_009676.1	YBR118W	Iranslational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.4251	0.1649	1109.42	1110.188	1	253.2	64.28571 V.K2W2D1E1S1R4F1Q2.E
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	2.9464	0.258	1396.45	1397.487	1	770	75 M.DSVKWDESRFQ.E
ail63195941refINP 009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.7549	0.2122	1397.61	1397.487	1	331.7	65 M.DSVKWDESRFQ.E
gil6319594/rofINP_009676_1	VBP118W/	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacul (PNA) to ribosomes; Tef2n	2	3 1255	0 2227	1991 63	1881 003	5	478 5	
gilos19594[rel[NP_009070.1]	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	5.1200	0.2337	1001.00	1001.095	5	470.5	
gi 6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	5.5963	0.503	1995.59	1993.133	1	1188.1	73.52941 H.H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.6477	0.3074	2227.49	2226.383	1	302.3	44.736843 K.SVEM@HHEQLEQGVPGDNVGF.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.4864	0.3132	2252.33	2253.383	1	327.2	44.736843 K.S1V1E1M\$H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EE-1 alpha: also encoded by TEE1; functions in the	2	4.2164	0.1987	2019.33	2019.184	1	1278.1	66.66667 M.D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.0168	0.3043	2119.61	2121.289	2	656.2	53.125 M.D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1.S
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6517	0.1988	2231.71	2233.517	3	468.1	44.736843 K.T1L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1.R
gi 6319594 ref NP_009676.1	YBR118W	Iranslational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.5285	0.2118	2207.85	2208.517	1	869.9	50 K.TLLEAIDAIEQPSRPTDKPL.R
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.5657	0.2289	1349.49	1348.542	2	721.2	77.27273 K.G1W2E1K2E1T1K2A1G1V1V1K2.G
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	6.2316	0.4384	2394.43	2395.582	1	1431.3	67.5 V.E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.N
gil6319594/refINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	5.4426	0.4888	2364.67	2365.582	1	1418.9	65 V. EMHHEOLEQGVPGDNVGENVK N
gil6310504/rofIND_000676_1		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding roaction of aminocond RNA (AA +RNA) to ribocomory TeF0.	-	2 2552	0.2015	1762.21	1762.964	1	620.7	
gil0319594[ref[NP_009076.1]	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	5.5552	0.3915	0504.40	0500 700		020.7	
gi 6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	5.4909	0.4893	2584.43	2583.793	1	1132	59.090908 K.STV1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.2897	0.3647	2635.94	2635.935	1	1460.1	36.363636 L.E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.4298	0.2617	1213.45	1214.45	9	249.5	61.11111 K.PLRLPLQDVY.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.7781	0.2141	1227.44	1228.45	3	271.7	66.66667 K.P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.885	0.4275	1342.07	1342.597	1	785.9	77.27273 N.P1K2T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.5	0.2669	2094.98	2095.295	1	1064.6	43.75 W.D1E1S1R4F1Q2E1I1V1K2E1T1S1N2F1I1K2.K
gi 6319594 ref NP_009676.1	YBR118W	Iranslational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.9122	0.2463	1088.67	1089.277	1	291.7	72.22222 W.EKETKAGVVK.G
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.9646	0.2117	1113.48	1114.247	1	377.5	75 L.E1D1H3P1K2F1L1K2S1.G
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	2.993	0.2162	1140.37	1140.329	1	886.3	87.5 K.K2L1E1D1H3P1K2F1L1.K
gil6319594/refINP_009676.1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyLtRNA (AA+RNA) to ribosomes; Tef2n	з	4 6606	0 3105	1326.95	1326 552	1	1057	60 416668 \/ P1\/1G1R4\/1E1T1G1\/11K2P1G1 M
sil0210504 ref ND_000070.1	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	9.0000	0.0100	4500.00	4500 700	2	1007	
gilo319594[rel[NP_009676.1]	TERIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the		2.6773	0.3376	1508.66	1509.789	3	108.3	39.2637 13 G. I VEVGRVE IGVIREG.IM
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.858	0.2713	1529.6	1528.789	1	186.7	42.857143 G.T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1.M
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	6.4288	0.4253	2943.11	2944.215	1	707.6	36 T.E1V1K2S1V1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	2	4.3544	0.3232	2943.67	2944.215	1	427	40 T.E1V1K2S1V1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6507	0.3988	1897.49	1895.056	1	778.3	71.875 E.MHHEQLEQGVPGDNVGF.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tet2p	2	3.5759	0.2201	1757.93	1759.053	4	466.7	50 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1.M
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tet2p	1	2.4618	0.2519	1308.68	1309.552	2	159.4	50 V.PVGRVETGVIKPG.M
gi 6319594 ref NP_009676.1	YBR118W	ranslational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	5.0729	0.2689	1712.85	1714.885	1	1024.2	79.16667 V.K2W2D1E1S1R4F1Q2E1I1V1K2E1.T
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.1336	0.2521	1818.31	1816.99	2	456.7	57.692307 V.K2W2D1E1S1R4F1Q2E1I1V1K2E1T1.S
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.6892	0.1998	1456.65	1457.713	1	333.2	63.636364 T.DKPLRLPLQDVY.K

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gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.2236	0.2178	2361.67	2360.716	4	364.4	42.5 L.EAIDAIEQPSRPTDKPLRLPL.Q
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	3.2131	0.338	1358.39	1358.624	1	308.6	60.000004 D.K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.0186	0.1696	2552.89	2552.89	1	335.5	38.095238 I.DAIEQPSRPTDKPLRLPLQDVY.K
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.4848	0.4022	2897.39	2900.244	1	1048.6	31.25 L.E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
ail6319594lrefINP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.0469	0.152	2901.61	2900.244	6	222.8	31.25 L.E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
gil6319594/refINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2n	1	2 3355	0.3624	1327 59	1328 597	1	643.9	63 636364 N PKTVPEVPISGW N
gil6319594[ref[NP_009676.1]	VBP118W/	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl tRNA (A + tRNA) to riposomes; Tef2)		4 4177	0.3407	2552 75	2552.80	6	544.4	
gilo319594 rei NP_009076.1	IDRIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.4177	0.3407	2002.70	2002.09	0	544.4	
gij6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	6.1175	0.3043	3014.54	3014.403	1	797.1	28 L.LTETATITDTATITETQ2PTSTR4P111D1R2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.9356	0.339	2963.6	2966.359	1	711.3	27.000002 K.T1L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	4.5525	0.2553	2716.37	2717.981	1	403.5	42.857143 M.D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1N2F1I1K2.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	2	4.3377	0.3287	2687.37	2686.981	1	415.1	40.476192 M.DSVKWDESRFQEIVKETSNFIK.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.4473	0.3889	1309.7	1309.552	1	948.4	56.25 V.PVGRVETGVIKPG.M
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	6.1794	0.5098	3506.51	3505.884	1	1011.8	28.90625 F.APAGVTTEVKSVEMHHEQLEQGVPGDNVGFNVK.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.9031	0.2911	2470.73	2471.734	1	1095.8	55.263157 N.K2M1D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1.N
gi 6319594 ref NP_009676.1	YBR118W	Iranslational elongation factor EF-1 alpha; also encoded by IEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.234	0.2649	2697.95	2698.05	1	783.7	34.090908 A.I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.5907	0.4749	3695.06	3697.061	1	615.6	T.F1A1P1A1G1V1T1T1E1V1K2S1V1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G 24.242424 1F1N2V1K2.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.7488	0.3849	2770.76	2770.128	1	943.9	30.434782 E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
gil6319594/refINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	2	3.5088	0.408	1328.87	1328.597	1	817.3	77.27273 N. PKTVPFVPISGW N
gil6319594/refINP_009676.1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminaccultRNA (A_tRNA) to ribosomes: Tef2n	-	3 147	0.2216	1140 56	1140 329	1	635.3	75 K K2I 1E1D1H3P1K2E1I 1 K
gile310504[rof[NR_000676.1]	VDD110W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacy it RNA (A the RNA) to incoded by TEF1; functions in the	2	4 1051	0.2210	1706.33	1704.02	1	E46 9	
sil0313534[ref[NP_009070.1]	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	5 7407	0.0304	0500.04	0500.075	1	1440.7	
gil6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5./19/	0.4062	2500.94	2503.875	1	1113.7	39.285/13 L.LTE1A111D1A111E1Q2P1S1R4P111D1R2P1L1R4L1P1L1.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.7276	0.4115	2339.42	2341.792	1	641.6	34.090908 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V111K2P1G1M1V1V1T1F1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	4.0786	0.3577	1907.73	1909.291	1	595.4	52.941177 V.P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1: functions in the	3	4.5956	0.4284	2361.32	2360.716	1	1035.7	37.5 L.EAIDAIEQPSRPTDKPLRLPL.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor FF-1 alpha; also encoded by TFF1; functions in the	1	2.6292	0.2906	1126.54	1127.329	1	565.3	75 K.KLEDHPKFL.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Te2p Translational elongation factor E-1 alpha; also encoded by TE21; functions in the	2	5.6297	0.4635	2265.45	2265.467	1	1534.3	73.68421 E.M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	5.3763	0.4759	2235.35	2236.467	1	1641.7	76.31579 E.MHHEQLEQGVPGDNVGFNVK.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.3817	0.2613	1715.57	1714.98	1	523.2	60.714287 V.TVIDAPGHRDFIKNM.I
gi 6319594 ref NP_009676.1	YBR118W	Iranslational elongation factor EF-1 alpha; also encoded by IEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	2.9821	0.2861	1739.31	1737.053	9	418.9	47.058823 G.GIGTVPVGRVETGVIKPG.M
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	2.962	0.1927	2388.53	2389.731	5	257.1	40 E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	2.9526	0.1853	2502.11	2503.875	6	300.7	40.476192 L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.Q
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.1276	0.3332	3219.59	3221.681	5	427.3	21.428572 L.EAIDAIEQPSRPTDKPLRLPLQDVYKIGG.I
gil6319594/refINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of amingacyl-tRNA (AA-tRNA) to riposomes: Tef2n	2	3 6418	0 2436	2342 45	2341 792	8	289	36 363636 G G11/G1T1V1P1V1G1R4V1F1T1G1V111K2P1G1M1V1V1T1F1 A
gil6319594/refINP_009676.1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminaccultRNA (A_tRNA) to ribosomes: Tef2n	2	3 7033	0.4145	1885.87	1887 291	- 1	701 1	
gil6319594[ref[NP_009676.1]	VBP118W/	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl tRNA (A + tRNA) to riposomes; Tef2)	2	5 2671	0.4165	2817.8	2816 227	1	1300.2	
gilo319594 renine_009076.rl	IDRIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.2071	0.4105	2017.0	2010.227		1399.2	
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.953	0.1726	2616.63	2618.035	1	616.4	45.454548 T.L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.727	0.3245	2615.45	2618.035	1	1762.3	43.18182 T.L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.9983	0.3944	2866.21	2868.235	1	443.7	34 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1: functions in the	3	5.0189	0.3216	2693.66	2694.051	1	1174.4	38.04348 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.4693	0.2936	2692.73	2694.051	1	711.9	43.47826 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tel2p	3	4.9595	0.4573	2865.71	2868.235	1	930.7	31 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2	2	4.4333	0.2893	2384.73	2385.682	1	487	50 V.KWDESRFQEIVKETSNFIK.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.2729	0.4538	2688.65	2688.14	1	1337	34.782608 K.TLLEAIDAIEQPSRPTDKPLRLPL.Q
gi 6319594 ref NP_009676.1	YBR118W	i ransiational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	5.043	0.4873	2068.37	2069.428	1	687.2	57.894737 Q.T1V1A1V1G1V111K2S1V1D1K2T1E1K2A1A1K2V1T1.K
gi 6319594 ref NP_009676.1	YBR118W	I ranslational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.5612	0.3465	2315.84	2317.652	1	859.5	39.473686 A.I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.891	0.3042	3142.88	3144.577	1	648.7	26.923079 L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2.I

		Translational elongation factor EF-1 alpha: also encoded by TEF1: functions in the								
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	6.5846	0.326	2746.19	2748.166	1	2634.7	43.47826 T.L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP 009676.1	YBR118W	I ranslational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.7382	0.2834	2412.41	2413.682	2	519.8	47.22222 V.K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1N2F1I1K2.K
ail6210504/rofIND_000676_1		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminopaul (PNA) (AA tPNA) to it becames: Tof2p	2	E 0509	0 4020	2020 71	2020 402	1	1500 5	
gilos i sosqiterini _003070. 1	IDICTION	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	5	3.0330	0.4033	5050.71	3030.432	'	1333.5	30.33040 N. TELENIDALEQF SKETDIG ENER EQUV.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	3	6.1227	0.3867	2720	2720.14	1	1352.5	35.869564 K.T1L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.0223	0.298	2390.15	2389.731	1	1738.5	43.75 E.A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.0586	0.3072	2465.06	2467.801	2	554.7	33.75 D.A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
cilc210E04lrofIND_000676_1		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding roading of aminocoul tBNA (AA tBNA) to ripageneous Tafan	2	2 5942	0.271	1750 45	1756 009	1	776.0	
gilo319394[rei]iNF_009070.1]	IDKIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.3642	0.271	1736.45	1750.096	1	110.9	01.00114 I.DREREELQUVIRIO.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	3	3.969	0.2683	2394.11	2393.704	1	889.5	35 K.T1L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4.L
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	2.9219	0.2032	1258.11	1255.503	8	345.3	66.66667 K.KLEDHPKFLK.S
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	3.0493	0.2086	1312.76	1312.555	1	587.8	65 S.GKKLEDHPKFL.K
ail6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	5 8545	0 2642	2407 73	2407 736	1	855 1	52 499996 T T1N2A1P1W2Y1K2G1W2F1K2F1T1K2A1G1V1V1K2G1K2 T
		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	-		0.2012	2.07.00	21011100			
gi 6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	4.8675	0.3638	2192.91	2193.51	1	1031.6	61.11111 I.INAPWYKGWEKETKAGVVK.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EE-1 alpha: also encoded by TEE1: functions in the	2	5.8692	0.3191	2219.57	2219.51	1	733.7	55.555557 T.T1N2A1P1W2Y1K2G1W2E1K2E1T1K2A1G1V1V1K2.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	3.919	0.2268	1990.01	1989.326	1	1030.6	43.75 A.IEQPSRPTDKPLRLPLQ.D
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.3988	0.2978	2012.99	2015.326	8	224.5	43.75 A.I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
ail6319594/rofINP_009676_1		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacy/JRNA (AA tRNA) to those mass: Tof2p	2	3 6008	0.2752	1359 63	1358 624	2	334.1	
gilos i sosqiterini _003070. 1	IDICTION	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.0000	0.2752	1550.05	1330.024	2	334.1	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.2147	0.3821	2394.32	2395.723	1	858.1	36.842106 A.I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6533	0.3339	1889.71	1890.235	1	968.1	65.625 K.KVGYNPKTVPFVPISGW.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.5403	0.304	2836.69	2836.235	1	348.4	32 K.KVGYNPKTVPFVPISGWNGDNMIEAT.T
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	3.8472	0.1734	3506.84	3505.052	1	488.8	23.387096 L.LEAIDAIEQPSRPTDKPLRLPLQDVYKIGGIG.T
ail6310504/rofIND_000676_11		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacul tRNA (AA tRNA) to ribosomer; Tatan	2	4 941	0 437	3532 31	3533.053	1	024	K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1
gilos 19394/relini _009070.1	IDICTION	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	5	4.541	0.457	5552.51	5555.055		324	20.00000 0
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.5696	0.2878	3547.4	3549.105	1	611.1	24.193548 K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYKIGG.I
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.9533	0.331	3493.79	3492.053	1	1139.7	29.166666 K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYKIG.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.3049	0.2227	1104.6	1103.306	1	441.2	66.66667 K.TVPFVPISGW.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.1539	0.2807	1626.13	1626.723	1	433.1	64.28571 H.HEQLEQGVPGDNVGF.N
ail631950/licofINP_000676_1		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacul (PNA) (AA (PNA) to it becomes: Tof2p	2	4 1 4	0 4007	17/1 50	17/0 827	1	703.1	
gilos 19394/relini _009070.1	IDICTION	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	4.14	0.4007	1741.55	1740.027		705.1	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	4.1633	0.4494	1761.71	1762.827	1	627.6	66.66667 H.H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.5093	0.3283	1359.61	1360.466	1	213.9	50 E.QLEQGVPGDNVGF.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.476	0.3568	1646.23	1646.723	1	524	67.85714 H.H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1.N
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	3.2026	0.1527	1498.65	1498.602	1	462.9	63.636364 W.D1E1S1R4F1Q2E1I1V1K2E1T1.S
cilc210504lrofIND_000676_1		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2 41 29	0.2147	1595 57	1596 691	1	416	59 222222 W D1E1C1D4E402E114\/4K2E1T1C1 N
gilo319394[rei]iNF_009070.1]	IDKIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the		3.4120	0.2147	1365.57	1300.001	1	410	30.333332 W.DTETSTR4FTQ2ETTTVTR2ETTTST.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	3.3577	0.3461	1567.7	1568.681	1	355.4	58.333332 W.DESRFQEIVKETS.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.2175	0.3561	1680.35	1680.929	1	853.3	67.85714 V.G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.5239	0.3588	1607.63	1605.877	1	569.2	65.38461 G.YNPKTVPFVPISGW.N
ail6319594lrefINP 009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	2	3.3413	0.2178	2320.01	2319.602	1	386.4	37.5 K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1.I
	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	0.0040	0.402.4	4700.40	4704.004	2	740.0	
gilo319594[rei]NP_009676.1]	TERIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	3.8342	0.1834	1780.46	1761.061	3	719.9	41.000004 N. VIGITINZPIKZI IVIPIPIVIPIIISIGIW2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.9075	0.4051	1779.71	1781.061	1	651.3	63.333332 K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.3691	0.2507	1622.29	1622.877	2	528.8	61.538464 G.Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.191	0.2814	1761.57	1762.061	4	371.1	50 K.VGYNPKTVPFVPISGW.N
ail6319594/refINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6003	0.3508	1412.41	1414.487	1	708.1	75 M.D1S1V1K2W2D1E1S1R4F1Q2 E
	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	4	0.4500	0.0400	1000.01	4007 407		400.4	
910319394[rei]NP_009676.1	101411010	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	3.1538	0.3402	1390.64	1397.487	1	406.4	13 MILDOVKWDESKFQ.E
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1: functions in the	2	4.0023	0.3863	2297.67	2299.596	1	769.4	47.5 N.P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elemention factor FE-1 alpha alon encoded by TEF1, functions in the	1	2.6076	0.2628	841.44	841.873	1	519.9	78.57143 G.H3V1D1S1G1K2S1T1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.4437	0.325	830.38	830.873	1	418.4	71.42857 G.HVDSGKST.T
gi 6319594 ref NP 009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.3959	0.2656	1095.53	1096.188	2	292.2	71.42857 V.KWDESRFQ.E
ail631950/lrofIND_000670_1	VBD110\/	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of amingacult ENA (AA tENA) to recomer Taking		3 7703	0.2476	1002 90	1006 194	-	006.9	
8/100/10034/10/10F_0030/0.1	DIVITOW	טוועראן נט ווטטטווופא, דפובף	2	5.1105	0.3470	1333.09	1330.104	1	500.0	

		Translational elemention factor EE-1 alpha: also encoded by TEE1: functions in the								
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2	3	3.8194	0.1795	2210.84	2209.367	4	711.7	35.294117 M.D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1.N
gi 6319594 ref NP_009676.1	YBR118W	Iranslational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.7258	0.314	2210.37	2209.367	1	689.7	50 M.D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.7264	0.1785	1251.45	1252.398	1	274.3	66.66667 S.R4F1Q2E1I1V1K2E1T1S1.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.5079	0.1987	1236.74	1237.398	1	320.2	72.22222 S.RFQEIVKETS.N
ail6319594/refINP 009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	2	3.9591	0.236	1385.51	1386.578	1	665.6	68.181816 T.V1I1D1A1P1G1H3R4D1F1I1K2.N
gil6319594/refINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyL-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4 0811	0.3922	1919 25	1919 056	1	616.7	65 625 F M1H3H3E1Q2I 1E1Q2G1V1P1G1D1N2V1G1E1 N
gil6319594/ref/NP_009676.1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacu/JRNA (AAJRNA) to ribosomes: Taf2n	2	3 4229	0.2312	2387 19	2389 716	3	467.4	47.5 L E14111014111E10201S1R4P1T1D1K2P111R4I 1P11.1 0
sil0310504 ref NP_000070.1	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	-	0.4223	0.4707	4470.07	4474 740	3	205.0	
gilo319594[ref[NP_009070.1]		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	3.1497	0.1707	1473.07	1474.713	1	303.6	
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.4094	0.2163	2583.77	2583.89	1	606.5	32.142857 I.DTATTETQ2PTSTR4PTTTDTK2PTLTK4LTPTLTQ2DTVTYT.K
gi 6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.5709	0.4761	2864.18	2866.244	1	1008.7	29.166666 L.EAIDAIEQPSKPIDKPEREPEQDVY.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	3.002	0.2936	1341.92	1342.597	1	516.7	59.090908 N.P1K2T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.8586	0.3208	1327.77	1328.597	6	420.7	54.5456 N.PKTVPFVPISGW.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.196	0.2028	2020.39	2021.317	6	287.8	46.875 Q.P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.8956	0.2356	1807.57	1808.957	1	479.9	65.38461 V.N2K2M\$D1S1V1K2W2D1E1S1R4F1Q2.E
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.5311	0.2544	1786.13	1786.957	1	688.9	73.07692 V.NKM@DSVKWDESRFQ.E
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.4469	0.3138	1909.65	1909.09	1	474.8	64.28571 A.V1N2K2M\$D1S1V1K2W2D1E1S1R4F1Q2.E
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.4435	0.4175	1885.51	1886.09	1	319.1	53.571426 A.VNKM@DSVKWDESRFQ.E
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6212	0.2734	1676.53	1676.854	1	449.9	66.66667 N.K2M1D1S1V1K2W2D1E1S1R4F1Q2.E
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.8887	0.4401	2035.35	2035.16	1	692.7	67.64706 E.M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2.V
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.3986	0.249	1695.73	1694.885	1	852	75 V.KWDESRFQEIVKE.T
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.0783	0.3775	1903.91	1905.068	1	937.4	60.714287 V.K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.3504	0.3252	2518.13	2519.847	1	1589.5	44.04762 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.728	0.2115	2005.57	2005.2	2	447.3	50 D.S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1.S
ail6319594/refINP 009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	2	4.208	0.3851	2068.47	2069.279	1	1235.6	62.5 D.SVKWDESRFQEIVKETS.N
gil6319594lrefINP_009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	2	4.6701	0.4051	2090.63	2093.279	1	1211.3	62.5 D.S1V1K2W2D1E1S1R4F1Q2E111V1K2E1T1S1.N
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-IRNA (AA-IRNA) to ribosomes: Tef2n	3	6 103	0 4227	2501 51	2503 875	1	1423.2	41 666664 1E1A1IID1A1IIE1Q2P1S1R4P1T1D1K2P1I 1R4I 1P1I 1 Q
gil6319594/ref/NP_009676.1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacu/JRNA (AAJRNA) to ribosomes: Taf2n	2	2 947	0 1573	2503 73	2503 875	2	327.7	42 857143 1E14111D14111E102P1\$1R4P1T1D1K2P1 1R4 1P1 1 O
gil6319594/rof/NP_009676.1	VBP118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacut (PNA (A-PNA) to ribosomos; Tef2	-	3 6217	0 1802	2168 73	2160 348	5	437.1	43 75 V K2W/2D1E1S1D4E102E111V/K2E1T1S1N2E1
sil0319594 rel[NP_009070.1]	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	0.5000	0.1032	2100.75	2109.540	3	437.1	
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	6.5006	0.4503	3126.05	3128.563	1	1786.6	35.576923 1.L1L1E1A11D1A11E1Q2P151R4P111D1R2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.3722	0.2735	2931.17	2931.359	1	949.6	29 K.TLLEAIDAIEQPSRPTDKPLRLPLQD.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.4792	0.4285	3065.54	3066.492	1	1748.9	34.615387 K.T1L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1.Y
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.8969	0.2837	3474.17	3475.001	1	862.6	24.13793 K.T1L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	2	3.1995	0.1871	1138.55	1140.329	1	828.5	87.5 K.K2L1E1D1H3P1K2F1L1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EE-1 alpha: also encoded by TEE1; functions in the	2	4.0495	0.3037	1401.23	1400.646	1	760.3	69.230774 Y.K2I1G1G1I1G1T1V1P1V1G1R4V1E1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to riboacid by TET 1, initiality in the	2	3.9978	0.2253	1561.51	1560.803	2	625.9	56.666668 Y.K2I1G1G1I1G1T1V1P1V1G1R4V1E1T1G1.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.655	0.2843	1541.47	1540.803	1	785.6	63.333332 Y.KIGGIGTVPVGRVETG.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.7517	0.3451	1882.43	1883.068	1	938.9	60.714287 V.KWDESRFQEIVKETS.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.0858	0.2756	2477.36	2474.82	1	1731.1	40.476192 E.AIDAIEQPSRPTDKPLRLPLQD.V
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.1462	0.2131	2572.85	2573.838	1	193.7	40 V.NKM@DSVKWDESRFQEIVKETS.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	2.9272	0.1727	2520.31	2519.847	1	429.6	40.476192 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.7668	0.3649	2443.39	2443.734	1	1048.1	52.63158 N.KMDSVKWDESRFQEIVKETS.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.9471	0.2495	2655.32	2656.97	1	1193.6	38.095238 A.VNKMDSVKWDESRFQEIVKETS.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.1785	0.2127	2685.47	2687.97	2	927.1	30.952381 A.V1N2K2M1D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1.N
gi 6319594 ref NP 009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	3.0971	0.2494	1357.83	1358.624	1	306.3	60.000004 D.K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	3	6.7566	0.4114	2633.57	2634.006	1	2594	45.454548 L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP_009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2o	3	4.1576	0.3129	2330.9	2330.792	1	703.9	36.363636 G.GIGTVPVGRVETGVIKPGM@VVTF.A
	-		-				-			

		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the								
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.4387	0.3749	2358.02	2357.792	1	644.2	36.363636 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M\$V1V1T1F1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.6064	0.2317	3012.92	3014.462	1	796.5	28 E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1.G
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.0123	0.3503	2317.7	2314.792	1	846.8	37.5 G.GIGTVPVGRVETGVIKPGMVVTF.A
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.2311	0.3858	2849.84	2850.227	1	1571.3	35.416664 L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1.Y
ail6319594/refINP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacvI-tRNA (AA-tRNA) to ribosomes: Tef2p	3	4.3698	0.2426	2868.68	2868.235	1	691.2	29 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.T
gil6319594lrefINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	2	4.3146	0.3674	2865.67	2868.235	1	471.8	34 K K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.T
gil6319594/rofINP_009676_1	VBP118W/	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacut-RNA (AA-RNA) to ribosomos: Taf2a	-	4 6730	0.3317	2606.03	2605.08	1	771.9	35 227272 K T1I 1I 1E10.111010.111E10.2015.10.0017110.1K2011 10.11 10.1
	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	5	4.0733	0.3317	2000.33	2003.30		111.0	
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.7165	0.4191	3194.99	3193.668	1	1465.8	30.555555 K. ILLEAIDAIEQPSKP I DKPLKLPLQDVY.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	6.6026	0.4081	3230.45	3230.668	1	1581.7	32.407406 K.T1L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.9501	0.1687	1140.58	1140.329	3	522.1	68.75 K.K2L1E1D1H3P1K2F1L1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	2	3.4753	0.2884	1682.13	1682.92	1	551.1	67.85714 Q.VTVIDAPGHRDFIKN.M
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EE-1 alber also encoded by TEE1; functions in the	3	4.3513	0.3367	2285.81	2288.652	1	1023.3	39.473686 A.IDAIEQPSRPTDKPLRLPLQ.D
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.718	0.4116	2158.88	2160.522	1	1449.7	47.22222 A.IDAIEQPSRPTDKPLRLPL.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.2614	0.2052	2259.65	2259.6	1	1114.7	40.789474 E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.Q
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.3964	0.295	2388.11	2389.716	1	1034.2	37.5 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.Q
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	3.8147	0.2366	3030.05	3030.418	9	304.9	23 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2.I
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-IRNA (AA-IRNA) to ribosomes: Tef2n	2	3 9092	0 4567	2884 75	2884 235	7	185.9	30 000002 K K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M\$I1F1A1T1 T
sil0210504 ref NP_000070.1	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of animology RNA (A-RNA) is reacted by TEF1; functions in the	2	0.0002	0.4307	2004.70	2004.200	,	225.4	
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.4308	0.2472	2339.93	2341.792	1	335.4	38.636364 G.G111G111V1P1V1G1R4V1E111G1V111K2P1G1M1V1V111F1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.0797	0.3443	2344.4	2341.792	1	669.2	34.090908 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V111K2P1G1M1V1V1T1F1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	4.0645	0.3721	2693.79	2694.051	1	653.6	41.304348 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EE-1 alpha; also encoded by TEE1; functions in the	3	5.9365	0.3336	2694.8	2694.051	1	1467.8	40.217392 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	6.187	0.4504	2813.51	2816.271	1	1627.8	36.458336 K.TLLEAIDAIEQPSRPTDKPLRLPLQ.D
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	6.3694	0.3887	2852.09	2850.271	1	1252.3	32.291664 K.T1L1L1E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.7103	0.3343	1503.25	1502.682	1	542.3	70.83333 T.V1I1D1A1P1G1H3R4D1F1I1K2N2.M
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.3337	0.4589	2360.24	2359.731	1	2320.3	47.5 E.AIDAIEQPSRPTDKPLRLPLQ.D
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.3595	0.3128	3202.13	3202.629	9	345.9	20.37037 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.G
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.2571	0.2918	2886.53	2884.235	1	1436.3	38 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M\$I1E1A1T1.T
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to riposomes: Tef2n	2	3 6803	0 2138	1356 47	1358 581	1	1279 2	85 K K2I 1E1D1H3P1K2E1I 1K2S1 G
gil6310504[rof[NR_000676.1]	VPD110W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of a minopage (RNA (A+RNA) to ripogeneous Tef2)	-	2.0004	0.2501	1256.01	1259 624		E74 E	
gil6319594 rei NP_009676.1	TERTION	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.0904	0.3501	1356.91	1358.624	1	574.5	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.0299	0.3082	1774.11	1777.098	2	390.3	50 T.D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.114	0.3692	2367.11	2364.704	1	1589.7	42.5 K.TLLEAIDAIEQPSRPTDKPLR.L
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	2	3.1324	0.1769	2391.87	2393.704	7	204.7	37.5 K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4.L LE1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1G1I1G1
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EE-1 alpha; also encoded by TEE1; functions in the	3	5.2742	0.4204	3431.87	3432.892	1	509.7	22.5 T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.9857	0.4696	3390.29	3391.892	1	793.3	26.666668 L.EAIDAIEQPSRPTDKPLRLPLQDVYKIGGIG.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.2764	0.3745	2448.87	2449.776	1	740.6	47.61905 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1.I
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.1441	0.2367	1826.93	1828.139	1	280.2	43.333332 T.VIDAPGHRDFIKNMIT.G
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	3.8019	0.237	2851.94	2851.275	2	361.3	25 I.DAIEQPSRPTDKPLRLPLQDVYKIG.G
gil6319594lrefINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	3	4.1566	0.3461	2999.18	3000.435	1	489.2	27.000002 A I1D1A1I1E1Q2P1S1R4P1T1D1K2P1I 1R4I 1P1I 1Q2D1V1Y1K2I1G1.G
gil6319594/rofINP_009676_1		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacu/HPNA (AAHPNA) to ribosomes: Tef2	3	4 7605	0.364	2064.02	2064 435	1	800.3	
		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	5	4.7005	0.304	2304.02	2304.433	'	000.5	
gi 6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.2734	0.2309	2998.21	3000.435	6	211.8	32 A.IIDTATITETQ2PTSTR4PTTTDTR2PTLTR4L1PTLTQ2D1V1Y1K2ITG1.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	3.9501	0.1917	3073.85	3072.514	1	523.1	28.846153 E.A111D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	3	4.2366	0.3428	3162.2	3164.629	8	443.9	21.296297 L.EAIDAIEQPSRPTDKPLRLPLQDVYKIG.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1' functions in the	3	4.2346	0.3017	2853.47	2852.235	1	854.6	31 K.KVGYNPKTVPFVPISGWNGDNM@IEAT.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translation alongation factor Ef1 alphas, also associed by TEF1; functions in the	3	5.1786	0.372	3357.95	3360.842	4	432.9	20.535715 K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2.I
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	3.2547	0.1906	1256.72	1255.503	5	337.4	66.66667 K.KLEDHPKFLK.S
gi 6319594 ref NP_009676.1	YBR118W	Inaristational elongation factor EF-1 alpha; also encoded by IEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.2124	0.2324	2668.27	2669.013	1	239.7	38.095238 F.DELLEKNDRRSGKKLEDHPKFL.K

		Translational elongation factor EF-1 alpha: also encoded by TEF1: functions in the								
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	3.9935	0.2832	2062.01	2060.404	1	808.7	44.11765 D.AIEQPSRPTDKPLRLPLQ.D
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.2001	0.2867	1910.63	1911.235	1	739.4	59.375 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	3.8458	0.2439	2574.74	2574.98	1	952.2	31.818182 K.TLLEAIDAIEQPSRPTDKPLRLP.L
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.071	0.1947	3429.44	3430.948	6	387.2	20.689655 T.L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.G
gil6319594[ref]NP_009676.1]	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-IRNA (AA-IRNA) to ribosomes; Tef2p	2	2.9613	0.2782	1116.21	1114.306	1	448.5	83.33333 K.T1V1P1F1V1P111S1G1W2.N
gil6319594/refINP_009676_1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of amingacyLtPNA (AA_tPNA) to riposomes; Tef2p	2	3 2073	0 179	1654 51	1652 847	2	472	53 571426 K T1V1P1E1V1P111S1G1W2N2G1D1N2M1 I
gil6310504[ref[NR_000676.1]	VDD110W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminogoul tBNA (AA tBNA) to ribogomory Tot2p	2	2 244	0.2141	1907.60	1907 100	-	670.2	52.10E K T4/404E4/404484C4W0N2C404N0M44E4 A
gilo319594[rel]NP_009676.1]	TERITOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.341	0.2141	1897.69	1897.122		679.3	53.125 K.117 PTFTVTPTTSTGTW2N2GDTN2MITTET.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.2989	0.2496	1241.64	1242.418	8	228.3	45.833336 G.GIGTVPVGRVETG.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.4328	0.2576	1418.54	1419.663	1	561.9	62.5 V.GYNPKTVPFVPIS.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha: also encoded by TEF1; functions in the	2	3.5468	0.213	1227.23	1226.378	1	515.6	77.77778 A.F1S1E1Y1P1L1G1R4F1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor FE-1 alpha; also encoded by TEF1; functions in the	1	2.6715	0.2625	1115.5	1114.306	1	464.5	66.66667 K.T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tel ² , functions in the	2	3.3383	0.3	2070.53	2071.306	1	461.5	41.6666664 K.T1V1P1F1V1P1I1S1G1W2N2G1D1N2M111E1A1T1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.0872	0.4152	1298.89	1298.457	1	905.1	85 E.A1F1S1E1Y1P1P1L1G1R4F1.A
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6321	0.3768	1284.23	1284.457	1	807.6	85 E.AFSEYPPLGRF.A
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.1492	0.1625	1135.65	1136.256	1	649.9	81.25 T.T1N2A1P1W2Y1K2G1W2.E
gil6319594lrefINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of amingacyl-IRNA (AA-IRNA) to riposomes; Tef2p	2	3 3536	0 1936	1585 91	1586 739	3	1136.9	69 230774 I D1A111E102P1S1R4P1T1D1K2P1I 1 R
gil6319594/rofINE_009676.1	VBP118W/	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacult PNA (A + PNA) to ribecomes; Tef2p	2	3 17/8	0 1541	060.33	968 145	0	660.3	77 77778 C C11/C1T4//1D1//1C1D4//1 E
gilo319594[rel[NF_009676.1]	IDRIIOW	Translational elongation factor EF1 alpha; also encoded by TEF1; functions in the	2	3.1740	0.1541	909.33	900.145	9	009.5	
gi 6319594 ret NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; 1et2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.7715	0.2082	1434.52	1434.663	1	468.4	62.5 V.G1Y1N2P1K211V1P1F1V1P1I1S1.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.1022	0.1738	1421.07	1419.663	1	632.3	75 V.GYNPKTVPFVPIS.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 aloha: also encoded by TEF1; functions in the	1	2.5898	0.2265	1369.49	1370.536	1	443.7	59.090908 E.A1F1S1E1Y1P1P1L1G1R4F1A1.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.4533	0.2659	1517.65	1518.796	1	506.9	57.692307 K.VGYNPKTVPFVPIS.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tel ² , functions in the	2	3.9019	0.3199	1369.67	1370.536	1	679.1	77.27273 E.A1F1S1E1Y1P1P1L1G1R4F1A1.V
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	2.5555	0.2878	1355.25	1355.536	1	555.4	63.636364 E.AFSEYPPLGRFA.V
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.9934	0.3301	2186.59	2187.409	2	472.9	44.736843 K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2.M
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6457	0.2381	2652.49	2653.928	4	334.9	30.434782 V.G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M\$I1E1A1T1.T
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.4417	0.2846	2159.13	2161.417	1	532.5	47.22222 G.Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1.I
gil6319594[ref]NP_009676.1]	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-IRNA (AA-IRNA) to ribosomes; Tef2p	2	4.8478	0.3599	2463.21	2463.744	1	681	45.238094 V.G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1F1.A
gil6319594/rofINE_009676.1	VBP118W/	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacult PNA (A + PNA) to ribecomes; Tef2p	2	3 0805	0.2017	2638.40	2637.028	1	437	26 05652 V C1V1N2D1K2T1V1D1E1V1D11S1C1W2N2C1D1N2M11E1A1T1 T
gilo313534 rel[NF_003070.1]	VERMON	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	0.0000	0.2317	2030.43	2037.320	,	437	
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.4312	0.1739	1025.52	1026.169	4	238.3	64.285/1 L.E1D1H3P1K2F1L1K2.S
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.2113	0.2449	1469.35	1470.651	1	796.2	66.66667 D.A111E1Q2P1S1R4P1T1D1K2P1L1.R
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.8427	0.2281	1771.93	1772.977	3	725	56.666668 E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1.R
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor FF-1 alpha; also encoded by TEF1; functions in the	2	3.8495	0.2105	1903.17	1903.093	6	505.2	53.125 L.E1A111D1A111E1Q2P1S1R4P1T1D1K2P1L1.R
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational alongation factor EF1 alpha; also encoded by TEF1, functions in the	2	4.5781	0.2718	2015.79	2017.252	1	1003.7	58.823532 L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1.R
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; TeF2	2	3.2821	0.2095	1664.19	1662.929	1	760.4	60.714287 V.GYNPKTVPFVPISGW.N
gi 6319594 ref NP_009676.1	YBR118W	Iranslational elongation factor EF-1 alpha; also encoded by IEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.7546	0.3416	2127.69	2125.413	1	1014.5	55.555557 N.P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.2265	0.2936	2404.93	2405.692	1	615.5	50 G.Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	5.3861	0.4559	2564.75	2563.877	1	820.2	47.727272 K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of amingacyl-IRNA (AA-IRNA) to riposomes; Tef2p	2	3 3115	0 2304	2538 31	2535 877	1	790.3	47 727272 K VGYNPKTVPEVPISGWNGDNMIE A
gil6310504[rof]ND_000676.1]	VDD110W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminocond tBNA (AA tBNA) to ribosomory. Tot2n	-	2 494	0.2001	1560.20	1569.916		150.0 150 5	
gilo319594[rel[NF_009070.1]	IDRIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.404	0.2210	1509.59	1506.610	2	436.5	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	2.9101	0.1932	1475.37	1474.713	3	392.6	68.181816 T.D1K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.7091	0.2558	2899.67	2900.244	3	582.9	25 L.E1A1I1D1A111E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	3.1377	0.2537	1458.49	1458.701	1	575.8	62.5 Y.N2P1K2T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.8575	0.4059	1330.53	1328.597	1	904.3	81.818184 N.PKTVPFVPISGW.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6065	0.3432	1445.37	1442.701	1	895.1	79.16667 Y.NPKTVPFVPISGW.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.1459	0.395	1460.13	1458.701	1	1136.9	87.5 Y.N2P1K2T1V1P1F1V1P11S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	ranslational elongation factor Er-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.7279	0.3468	1367.87	1368.578	1	825.9	72.72727 T.VIDAPGHRDFIK.N

		Translational elongation factor EE-1 alpha: also encoded by TEE1: functions in the								
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.4493	0.3442	1853.65	1852.967	1	934	62.5 L.NHPGQISAGYSPVLDCH.T
gi 6319594 ref NP_009676.1	YBR118W	I ranslational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.5133	0.4181	1632.73	1634.875	1	467.6	57.692307 T.V1I1D1A1P1G1H3R4D1F1I1K2N2M1.I
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes. Tef2n	3	4 6875	0 2234	2942 78	2944 215	1	459.5	30 000002 T E1V1K2S1V1E1M1H3H3E1Q2I 1E1Q2G1V1P1G1D1N2V1G1E1N2V1K2 N
		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the				2012.00				
gi 6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	3.9846	0.2794	2908.43	2908.215	3	321.6	25 1.EVKSVEMHHEQLEQGVPGDNVGFNVK.N
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EE-1 alpha; also encoded by TEE1; functions in the	3	4.127	0.3618	2173.79	2175.493	1	862.3	40.27778 I.DAIEQPSRPTDKPLRLPLQ.D
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.2763	0.2971	2073.5	2073.362	2	662.9	41.17647 I.D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.4029	0.2694	2405.36	2403.741	1	1118.7	37.5 A.IDAIEQPSRPTDKPLRLPLQD.V
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.1016	0.2452	2432.75	2433.741	1	803.9	35 A.I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1.V
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes. Tef2n	3	5 4851	0 3742	2519.63	2519 847	1	1532.8	41 666664 E1A1IID1A1I1E102P1S1R4P1T1D1K2P1I 1R4I 1P1I 102 D
	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding register of the second	2	5.4450	0.4077	0007.0	0000 740		4502.5	
gilo319594[rei]NP_009676.1]	TERTION	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.4456	0.4077	2367.3	2369.716	1	1593.5	42.5 LETATIOTATIE 102PTSTR4PTTIDTR2PTLTR4LTPTLT.0
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.2034	0.2222	2358.15	2360.716	4	312.1	40 L.EAIDAIEQPSRPTDKPLRLPL.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor FF-1 alpha: also encoded by TFF1; functions in the	1	3.2506	0.2887	1342.85	1342.624	2	347.7	65 D.KPLRLPLQDVY.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2	3	5.6908	0.3514	2602.55	2602.006	1	1941.1	42.045452 L.LEAIDAIEQPSRPTDKPLRLPLQ.D
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	6.6536	0.4028	2752.79	2750.095	1	1908.9	41.304348 L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1.V
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	6.2799	0.3121	2717.42	2717.095	1	1802.6	41.304348 L.LEAIDAIEQPSRPTDKPLRLPLQD.V
gil6319594/refINP_009676_1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyldRNA (AA-tRNA) to riposomes: Tef2n	3	5 2719	0 3643	2979 56	2070 403	1	989 7	
	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the		0.5744	0.0040	2010.00	1000.075		500.1	
gi 6319594 ret NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.5744	0.3357	1630.25	1629.875	1	571.6	65.38461 T.VIDAPGHRDFIKNM@.I
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.7084	0.3235	1604.37	1604.787	2	322.4	53.846157 V.T1V111D1A1P1G1H3R4D1F1I1K2N2.M
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor FE-1 alpha: also encoded by TEF1; functions in the	2	3.677	0.2888	1616.37	1613.875	1	602.2	65.38461 T.VIDAPGHRDFIKNM.I
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Teff	2	3.7677	0.1897	1852.53	1851.139	1	475.4	56.666668 T.V1I1D1A1P1G1H3R4D1F1I1K2N2M1I1T1.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.626	0.3299	2200.7	2203.493	1	1072.3	44.444447 I.D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.D
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	3.8901	0.3103	2047.82	2047.362	1	616.6	39.705883 I.DAIEQPSRPTDKPLRLPL.Q
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes. Tef2n	2	3 2914	0 2702	2504 27	2505 82	1	534.9	45 238094 E A1I1D1A1I1E102P1S1R4P1T1D1K2P1I 1R4I 1P1I 102D1 V
	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding register of the second	-	0.2011	0.0404	2450.40	0440 705		640.4	
gilb319594[rei]NP_009676.1]	TERTION	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	3.6466	0.2434	2450.48	2449.735	2	640.1	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.9638	0.3461	2491.43	2488.847	1	1287.2	40.476192 L.EAIDAIEQPSRPTDKPLRLPLQ.D
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.0906	0.2294	2552.96	2552.89	1	673.1	30.952381 I.DAIEQPSRPTDKPLRLPLQDVY.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.0403	0.3252	2603.33	2605.952	1	1122.1	32.954548 E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1.Y
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.5184	0.5359	2663.12	2666.05	1	1491.9	39.772728 A.IDAIEQPSRPTDKPLRLPLQDVY.K
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.2677	0.3838	2737.43	2737.128	1	1255	34.782608 E.AIDAIEQPSRPTDKPLRLPLQDVY.K
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes. Tef2n	3	6 3882	0.382	2502.83	2503 875	1	1071 5	38 095238 1E1A1I1D1A1I1E102P1S1R4P1T1D1K2P1 1R4 1P1 1 Q
gil6310504/rofIND_000676_1		Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoand tBNA (A) tBNA to income; Tef2	-	2 1099	0 1926	2502.60	2502.975	1	249.4	
gilo319394 rei i4F_009070.1	IDKIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.1900	0.1030	2505.09	2505.675		340.4	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.5356	0.5025	2471.42	2473.875	1	1176.1	40.476192 L.LEAIDAIEQPSRPTDKPLRLPL.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	4.3309	0.3587	2865.81	2868.235	2	316.8	30.000002 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	6.2317	0.4111	3089.69	3092.563	1	1334.3	35.576923 T.LLEAIDAIEQPSRPTDKPLRLPLQDVY.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	6.0607	0.4711	3317.81	3316.789	1	1029.8	30.357143 L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.G
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.7754	0.2665	1648.35	1650.875	1	877.6	73.07692 T.V1I1D1A1P1G1H3R4D1F1I1K2N2M\$.I
gil6319594/refINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes: Tef2p	2	3.6	0.4678	1736.89	1736.98	1	813	57, 14286 V. T1V1I1D1A1P1G1H3R4D1F1I1K2N2M1.L
gil6310504/rofINP_000676_1	VBP118W/	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoactivit PNA (A + PNA) to riposomes: Tef2	-	5.0318	0.3563	2288 11	2280 731	1	2285.2	
	IDR I IOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	5	5.0510	0.0000	2300.11	2303.731		2303.2	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	5.1032	0.2993	2185.13	2187.522	1	1409.3	45.833336 A.IID1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.8734	0.1953	2194.37	2193.615	3	355.4	38.095238 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1.F
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	3.3912	0.3654	1357.68	1358.624	1	349.3	65 D.K2P1L1R4L1P1L1Q2D1V1Y1.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.0793	0.4266	2111.87	2111.529	2	467.4	44.736843 G.T1V1P1V1G1R4V1E1T1G1V111K2P1G1M1V1V1T1F1.A
gi 6319594 ref NP_009676.1	YBR118W	ransiational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.6202	0.2934	2313.85	2314.792	1	510.7	45.454548 G.GIGTVPVGRVETGVIKPGMVVTF.A
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.7599	0.2005	2339.01	2341.792	6	286	36.363636 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V111K2P1G1M1V1V1T1F1.A
gil6319594/refINP_009676_1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyLtRNA (AA-tRNA) to ribosomes; Tef2p	3	4 804	0.3314	2615.96	2618 035	1	1216 5	37.5 T 1 1E1A111D1A111E102P1S1R4P1T1D1K2P11 1R4I 1P1I 1 0
	VDD440W	Translational elongation factor EF-1 alpha; alos encoded by TEF1; functions in the	5		0.0014	2010.00	2010.000		440	
gilo319594[ref]NP_009676.1]	TBK118W	binding reaction of aminoacyl-tKINA (AA-tKINA) to ribosomes; Tet2p	2	3.826	0.3899	2692.67	2694.051	1	418	34.702000 K.KZV1G1Y1NZP1KZ11V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A

gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.7374	0.3611	2693.93	2694.051	1	1130.2	34.782608 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.A
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.4162	0.407	1835.51	1837.113	1	1004.5	60.000004 Q.V1T1V1I1D1A1P1G1H3R4D1F1I1K2N2M1.I
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.9979	0.4001	1813.49	1814.113	1	1192.8	66.66667 Q.VTVIDAPGHRDFIKNM.I
gil6319594/refINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of amingacyl-IRNA (AA-IRNA) to riposomes: Tef2p	3	4 8495	0 2993	2232 11	2231.6	1	1163.8	42 105263 E AIDAIEOPSRPTDKPI RI PL O
gile310504[rof[NR_000676.1]	VDD110W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reactions of aminoacut tPNA (AA tPNA) to ribocomes; Taf2a	2	2 4592	0.1094	2604.20	2605.09	2	274.0	
	IDRIIOW	Translational elongation factor EF1 alpha; also encoded by TEF1; functions in the	2	3.1302	0.1904	2004.39	2005.98	2	374.9	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.6688	0.2268	3105.44	3107.577	1	653.9	28.846153 L.LEAIDAIEQPSRPTDKPLRLPLQDVYK.I
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	2.9894	0.1816	2438.59	2437.776	9	258	35.714287 K.KVGYNPKTVPFVPISGWNGDNM@.I
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor FE-1 alpha; also encoded by TEF1; functions in the	2	4.2842	0.478	2708.67	2710.051	1	699.8	47.826088 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M\$I1E1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.3868	0.4121	2340.17	2341.792	1	705.3	35.227272 G.G111G1T1V1P1V1G1R4V1E1T1G1V111K2P1G1M1V1V1T1F1.A
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.0067	0.3745	2867.93	2868.235	1	1046.4	33 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.T
gi 6319594 ref NP_009676.1	YBR118W	I ranslational elongation factor EF-1 alpha; also encoded by I EF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.3298	0.3532	2764.79	2766.13	1	729.2	43.75 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1.T
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.9376	0.2135	1662.67	1664.97	1	832.6	71.42857 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1.G
gil6319594lrefINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.4033	0.191	1721.23	1723.022	2	407.8	56.666668 K K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1.W
gil6319594[rof]NP_009676.1]	VBD118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacid (PNA (AA+ENA) to ribosomes; Tef2)	-	3 1/3/	0 102	1357.47	1358 624	-	455.7	75 D K2011 10/1 10/2 D1//1/1 K
		Translational elongation factor EF1 alpha; also encoded by TEF1; functions in the	2	3.1434	0.132	1337.47	1330.024		455.7	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; 1et2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	3.982	0.3582	2367.41	2366.723	1	758.2	36.842106 A.IEQPSRPTDKPLRLPLQDVY.K
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	4.2434	0.3998	2314.73	2317.583	1	461	45 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2.M
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor FE-1 alpha: also encoded by TEF1; functions in the	3	5.3449	0.3343	2884.52	2884.235	1	719.6	31 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M\$I1E1A1T1.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2	3	4.0402	0.3504	2833.82	2836.235	1	1002.5	33 K.KVGYNPKTVPFVPISGWNGDNMIEAT.T
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.1548	0.3839	3279.65	3277.789	1	841.5	28.57143 L.LEAIDAIEQPSRPTDKPLRLPLQDVYKIG.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.1715	0.3454	1311.85	1312.555	1	782	75 S.GKKLEDHPKFL.K
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	1	3.361	0.2522	1328.55	1328.555	1	592.8	65 S.G1K2K2L1E1D1H3P1K2F1L1.K
gil6319594lrefINP_009676.11	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	4.3145	0.1725	2087.03	2087.404	1	1044.4	45 588234 D A111E102P1S1R4P1T1D1K2P1L1R4L1P1L102 D
gil6319594/refINP_009676.1	VBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyLtRNA (AA_tRNA) to riposomes; Tef2n	2	2 9031	0.2846	1704 51	1704 022	2	374.5	
sil0313534[ref[NP_009070.1]	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	2.3031	0.2040	4559.00	4550.000	2	402.0	
gilb319594[rei]NP_009676.1]	TERIIOW	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.0198	0.2118	1558.99	1559.892	1	492.2	61.536464 K.KVG TINPKT VPF VPI.5
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.5329	0.1636	1576.62	1576.892	1	455.9	57.692307 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1.S
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	1	2.3416	0.2468	1558.43	1559.892	1	469	57.692307 K.KVGYNPKTVPFVPI.S
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.8822	0.3135	2464.43	2465.776	2	420.6	35.714287 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M\$.I
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; TET2; functions in the	3	4.0451	0.2939	3002.84	3000.435	1	631.5	29 A.I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.G
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	3.8445	0.27	1913.27	1911.235	1	690.6	37.5 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.N
gi 6319594 ref NP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	2.9866	0.1599	2295.35	2296.544	3	168	47.058823 A.C1R4F1D1E1L1L1E1K2N2D1R4R4S1G1K2K2L1.E
gi 6319594 ref NP 009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	3	5.101	0.2935	2405.96	2407.736	1	1032	38.75 T.T1N2A1P1W2Y1K2G1W2E1K2E1T1K2A1G1V1V1K2G1K2.T
gil6319594lrefINP_009676.1	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-IRNA (AA-IRNA) to ribosomes; Tef2n	2	3 1986	0 2627	1990.65	1989 326	1	302.6	
sil0240504leefIND_0000704l	VDD440W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the hindiag aparties of aminopart 40NA (AA 40NA) to the participant and the second aparts of the	-	0.1000	0.4004	2000.02	2007 404		222.0	
gilo319594[rel[NP_009676.1]	TERIIOW	Translational elongation factor EF1 alpha; also encoded by TEF1; functions in the	2	3.5142	0.1924	2086.63	2087.404	2	333.1	
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	3	4.4679	0.3805	2360.03	2360.716	1	1169.2	37.5 L.EAIDAIEQPSRPTDKPLRLPL.Q
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the	2	3.7718	0.3777	2420.33	2421.776	1	442.3	40.476192 K.KVGYNPKTVPFVPISGWNGDNM.I
gi 6319594 ref NP_009676.1	YBR118W	binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	4.6141	0.3818	1914.15	1911.235	1	1213.3	71.875 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.N
	VED404C	cognate anticological services and the according to a service of the service of t		2 0040	0 2002	4000.00	4002 495		450.0	
gilo319397110114F_009079.11	IBRIZIC	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the	2	3.0910	0.2002	1992.39	1993.165	I	459.0	
gi 6319597 ref NP_009679.1	YBR121C	cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	4.0606	0.3535	1972.47	1973.185	1	1103.4	61.764706 K.VDGVDGEVELDDKLVKIE.Q
		Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA: transcription termination factor that may interact								
gi 6319597 ref NP_009679.1	YBR121C	with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	3.2419	0.238	1314.41	1314.487	1	431.2	75 K.FRKDAPKVESH.L
	VPP4040	cognate anticodon bearing tRNA; transcription termination factor that may interact with the 9' and of an mRNA to promote 2' and formation factor.	0	E 00.40	0.0500	1027.04	1007 450	4	2250.0	
gilo319597 [rei]NP_009679.1]	TBR (210	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the	3	5.9949	0.3533	1927.04	1927.156	1	∠309.8	30.000000 V.KZLIDIDIDIVIVIKZETTIETETITLTATKZ.I
gi 6319597 ref NP_009679.1	YBR121C	cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	4.0636	0.3149	2098.45	2099.367	1	614.9	50 K.A1V1K2L1D1D1D1V1V1K2E1Y1E1E1I1L1A1K2.I
		Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact								
gi 6319597 ref NP_009679.1	YBR121C	with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	3.5304	0.3832	1910.11	1909.145	1	610.2	53.125 E.H3V1R4E1Y1V1P1S1V111E1P1S1F1G111G1.R

		Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact								
gi 6319597 ref NP_009679.1	YBR121C	with the 3-end of pre-mRNA to promote 3'-end formation; Grs1p Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the	2	2.9402	0.2298	1335.29	1332.487	3	431.4	75 K.F1R4K2D1A1P1K2V1E1S1H3.L
gi 6319597 ref NP_009679.1	YBR121C	cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	3.5339	0.3052	1930.11	1927.156	1	544.7	50 V.K2L1D1D1D1V1V1K2E1Y1E1E1I1L1A1K2.I
		Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form;								
gi 6319602 ref NP_009684.1	YBR126C	expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	2	4.1849	0.3548	1621.53	1619.69	1	573.4	66.66667 L.FHYHPGEINFDEN.A
		Synthase subunit of trenaiose-o-prosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form;								
gi 6319602 ref NP_009684.1	YBR126C	pathway; Tps1p	2	5.44	0.4011	2589.27	2589.841	1	936.5	52.499996 F.K2W2F1G1W2P1G1L1E1I1P1D1D1E1K2D1Q2V1R4K2D1.L
		synthesizes the storage carbohydrate trehalose; also found in a monomeric form; avpression is induced by the storage representation and the storage and represend by the Pas-cAMP								
gi 6319602 ref NP_009684.1	YBR126C	pathway; Tps1p Svnthase subunit of trebalose-6-phosphate svnthase/phosphatase complex, which	2	3.4641	0.2911	2084.11	2085.22	3	224.6	50 L.F1H3Y1H3P1G1E1I1N2F1D1E1N2A1W2L1A1.Y
		synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP								
gi 6319602 ref NP_009684.1	YBR126C	pathway; Tps1p Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which	3	5.6977	0.264	2587.61	2589.841	1	1285.8	40 F.K2W2F1G1W2P1G1L1E1I1P1D1D1E1K2D1Q2V1R4K2D1.L
		synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP								
gi 6319602 ref NP_009684.1	YBR126C	pathway; Tps1p Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which	3	4.4479	0.3427	3093.56	3096.452	1	470.1	33.333336 K.W2F1G1W2P1G1L1E1I1P1D1D1E1K2D1Q2V1R4K2D1L1L1E1K2F1.N
		synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP								
gi 6319602 ref NP_009684.1	YBR126C	pathway; Tps1p Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which	2	4.3991	0.3622	1637.89	1638.69	1	544.2	66.66667 L.F1H3Y1H3P1G1E111N2F1D1E1N2.A
	VDD 4000	synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP		0.5000	0.0500	1007.07	1000 000		057.7	
gi 6319602 ret NP_009684.1	YBR126C	pathway; 1ps1p Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which	2	3.5909	0.2589	1897.27	1898.982	1	257.7	50 L.FH3YH3P1G1E111N2F1D1E1N2A1W2.L
ail63196021rofINP_009684_11	VBP126C	expression is induced by the stress response and repressed by the Ras-cAMP	2	3 0248	0 2210	2558 43	2550 841	2	300.8	
gilo313002[tel[ttr _003004.1]	TBI(1200	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose: also found in a monomeric form:	2	3.0240	0.2213	2000.40	2009.041	2	333.0	42.51. KWI GWI GLLII DDENDQVIKU.L
gi 6319602 ref NP 009684.1	YBR126C	expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	2	4.6609	0.2872	2588.95	2589.841	1	797.4	47.5 F.K2W2F1G1W2P1G1L1E1I1P1D1D1E1K2D1Q2V1R4K2D1.L
		Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form;								
gi 6319602 ref NP_009684.1	YBR126C	expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	3	4.5074	0.1555	2589.74	2589.841	1	1121.7	38.75 F.K2W2F1G1W2P1G1L1E1I1P1D1D1E1K2D1Q2V1R4K2D1.L
		Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form;								
gi 6319602 ref NP_009684.1	YBR126C	expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	3	4.5109	0.2949	2559.29	2559.841	2	876.7	37.5 F.KWFGWPGLEIPDDEKDQVRKD.L
		Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form;								
gi 6319602 ref NP_009684.1	YBR126C	pathway; Tps1p	2	4.493	0.3055	2560.37	2559.841	1	763.7	50 F.KWFGWPGLEIPDDEKDQVRKD.L
		synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP								
gi 6319602 ref NP_009684.1	YBR126C	pathway; Tps1p Svnthase subunit of trehalose-6-phosphate svnthase/phosphatase complex, which	1	2.9071	0.2561	1375.53	1376.47	1	648.5	70 L.FHYHPGEINFD.E
		synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP								
gi 6319602 ref NP_009684.1	YBR126C	pathway; Tps1p Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-	1	3.3951	0.3505	1391.49	1392.47	1	567.2	65 L.F1H3Y1H3P1G1E1I1N2F1D1.E
		ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the								
gi 6319603 ref NP_009685.1	YBR127C	cytoplasm; Vma2p Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-	2	4.9263	0.4066	2748.57	2749.645	1	672.7	47.727272 L.DEFYDRARDDADEDEEDPDTRSS.G
aile210602trofIND_000695_1	VPP127C	A I Pase (V-A I Pase), an electrogenic proton pump round throughout the endomembrane system; contains nucleotide binding sites; also detected in the atoplane; Vma2n	2	2 2045	0.0751	1202.10	1200 402	1	706.0	75 04/04/4245404041404041
gilo313003[tel[ttr _003003.1]	TBI(1270	Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (VATPase), an electrogenic proton nump found throughout the	2	3.3043	0.2751	1232.13	1230.433		700.5	
ail6319603lrefINP_009685.11	YBR127C	endomembrane system; contains nucleotide binding sites; also detected in the cytonlasm: Vma2n	2	3 4094	0 2555	1736 75	1734 067	1	695.3	60 714287 E SI RIPVSEDMI GRIE D
3-lee		Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	_							
gi 6319603 ref NP_009685.1	YBR127C	endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; Vma2p	2	4.2312	0.3537	1753.87	1755.067	1	766.9	64.28571 E.S1L1R4I1P1V1S1E1D1M1L1G1R4I1F1.D
		Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the								
gi 6319603 ref NP_009685.1	YBR127C	endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; Vma2p	2	3.7106	0.2086	1853.91	1855.059	1	264.3	60.714287 A.R4E1E1V1P1G1R4R4G1Y1P1G1Y1M1Y1.T
		Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the								
gi 6319603 ref NP_009685.1	YBR127C	enconnernorane system; contains nucleotide binding sites; also detected in the cytoplasm; Vma2p Subusit B of the single-subusit V1 peripheral membrane demain of the vectorial U1.	2	3.4289	0.1815	1830.49	1831.059	1	262.8	57.14286 A.REEVPGRRGYPGYMY.T
		ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system: contains nucleotide binding sites: also detected in the								
gi 6319603 ref NP_009685.1	YBR127C	cytoplasm; Vma2p	3	4.431	0.3003	3229.37	3230.219	1	613.3	29.807693 L.D1E1F1Y1D1R4A1R4D1D1A1D1E1D1E1E1D1P1D1T1R4S1S1G1K2K2K2.D

Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the	
endomembrane system; contains nucleotide binding sites; also detected in the	
gi[6319603]ret]NP_009685.1] YBR127C cytoplasm; Vma2p 2 4.0976 0.3331 1795.35 1794.899 1 324.6 60.714287 T.K2D1V1H3D1G1H3E Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	3E1E1N2F1S1I1V1F1.A
endomembrane system; contains nucleotide binding sites; also detected in the gi[6319603]ref[NP_009685.1] YBR127C cytoplasm; Vma2p Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- A/Them 0 / 4/Them 0 / 4/Them is not domained the unboard the unboard to the text of tex of text of tex of text of t	IVF.A
all rase (v-Ai rase), an electrogenic product binding sites; also detected in the endomembrane system; contains nucleotide binding sites; also detected in the gi[6319603]ref[NP_009685.1] YBR127C cytoplasm; Vma2p 3 4.7983 0.3677 1472.9 1473.731 1 2522.8 62.5 E.SLRIPVSEDMLGR.I Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-	.1
ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the gi[6319603]ref[NP_009685.1] YBR127C cytoplasm; Vma2p 2 4.2679 0.3051 1492.97 1492.731 1 1056.2 75 E.S1L1R4I1P1V1S1E1 Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-	E1D1M1L1G1R4.I
ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the gi[6319603]ref[NP_009685.1] YBR127C cytoplasm; Vma2p 2 3.3509 0.2608 1473.69 1473.731 1 804.1 66.66667 E.SLRIPVSEDMLGR.I	.1
ATPase (V-ATPase), an electogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the elie319603/rdfNP_0066511_VEP120	YM V
Suburit 8 of the eight-suburit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites, also detected in the	
gij6319603[ref]NP_009685.1] YBR127C cytoplasm; Vma2p 2 3.5358 0.1573 1689.65 1690.883 2 252.6 53.846157 A.R4E1E1V1P1G1R4F Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	4R4G1Y1P1G1Y1M1.Y
gi[6319603]ref[NP_009685.1] YBR127C cytoplasm; Vma2p 2 3.5637 0.2302 1749.33 1750.051 3 470 57.692307 L.EKVKFPRYNEIVNL: Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	LT
endomembrane system; contains nucleotide binding sites; also detected in the gi[6319603]ref[NP_009685.1] YBR127C cytoplasm; Vma2p 2 3.0481 0.2769 1923.11 1921.098 1 343.9 53.125 L.T1M1P1N2D1D11171 Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	T1H3P1I1P1D1L1T1G1Y1.I
endomembrane system; contains nucleotide binding sites; also detected in the gi[6319603]ref[NP_009685.1] YBR127C cytoplasm; Vma2p 2 4.1523 0.3467 2491.67 2491.824 1 827.7 50 T.Q211P111L1T1M1P11 Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase). an electrogenic proton pump found throughout the	1N2D1D1I1T1H3P1I1P1D1L1T1G1Y1.I
endomembrane system; contains nucleotide binding sites; also detected in the gij6319603]ref[NP_009685.1] YBR127C cytoplasm; Vma2p 2 3.9539 0.2959 2466.39 2465.824 1 694.7 47.61905 T.QIPILTMPNDDITHPI Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase) (V-ATPase)	PIPDLTGY.I
endomembrane system; contains nucleotide binding sites; also detected in the gi 6319603 ref NP_009685.1 YBR127C cytoplasm; Vma2p 3 4.3959 0.2059 1473.77 1473.731 1 2072.1 52.083332 E.SLRIPVSEDMLGR.I	.1
Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with gi[6319610]ref[NP_009691.1] YBR133C Hsl1p for bud neck recruitment, phosphorylation, and degradation of Swe1p; Hsl7p 2 3.409 0.196 2312.49 2313.593 3 231 36.842106 L.S1E1T1A1K2P1D1H	H3L1D1S111N2K2P1M1F1D1L1K2.S
Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with gi[6319610]ref[NP_009691.1] YBR133C Hsl1p for bud neck recruitment, phosphorylation, and degradation of Swe1p; Hsl7p 3 5.7138 0.1733 3340.97 3342.712 1 681.2 30.357143 V.S1S1H3S1P1E1L1P	P1S1N2Y1D1Y1V1L1L1P1I1T1T1P1R4Y1K2E1I1V1G1Q2.V
Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with gi[6319610]ref[NP_009691.1] YBR133C Hsl1p for bud neck recruitment, phosphorylation, and degradation of Swe1p; Hsl7p 3 4.7907 0.2825 3164.6 3166.555 1 560 26.923079 S.H3S1P1E1L1P1S1N	N2Y1D1Y1V1L1L1P1I1T1T1P1R4Y1K2E1I1V1G1Q2.V
Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation, required along with Bij6319610[ref]NP_009691.1] YBR133C Hsl1p for bud neck recruitment, phosphorylation, and degradation of Swe1p, Hsl7p 2 4.2164 0.3118 2129.59 2129.47 2 467.5 50 Y.D1Y1V1L1L1P1I1T1 Essential nucleolar protein, putative DEAD-box RNA helicase required for	°1T1P1R4Y1K2E1I1V1G1Q2.V
gij6319618]ref[NP_009700.1] YBR142W submits; Mak5p Essential nucleolar protein, putative DEAD-box RNA helicase required for reminientenes of MI de2NU / jews in violand in biogenesis of large (6US) ribosomal	P1D1T1L1D1D1F1G1G1F1Y1.G
glj6319618/ref[NP_009700.1] YBR142W submits, Mak5p 53 of Lage (005) nobsomal so Lage (005)	FDEFEKIIK.H
gij6319618 ref NP_009700.1 YBR142W subunits; Mak5p 37.5 E.S1S1K2L1T1D1P1S Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal	S1E1D1V1D1E1D1V1D1E1D1V1L1K2E1N2.V
gij6319618[ref]NP_009700.1] YBR142W subunits; Mak5p 2 4.6601 0.3044 2604.09 2605.642 1 783.7 50 E.S1S1K2L1T1D1P1S Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal	S1E1D1V1D1E1D1V1D1E1D1V1L1K2E1N2.V
gij6319618[ref]NP_009700.1] YBR142W subunits; Mak5p 2 4.8795 0.3422 2428.35 2429.485 1 790.6 52.499996 S.K2L1T1D1P1S1E1D Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal	D1V1D1E1D1V1D1E1D1V1L1K2E1N2.V
gips is of operative 2 3.7258 0.3114 15/4.57 15/6.731 1 913 70.83333 N.W2K2P1V1D111P1D gips is of operative Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal 2 4.1014 0.312 1958.67 1957.116 1 855.4 56.75 L.N2W2K2P1V1D111PD	P1D1T1L1D1D1F1G1G1F1.Y
Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal gi[6319618]ref[NP_009700.1] YBR142W subunits; Mak5p 2 3.0727 0.2655 1936.59 1937.116 1 763.2 50 L.NWKPVDIPDTLDDF	FGGF.Y

		Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 deBNA virus, involved in biogeneois of large (60S) representation								
gi 6319618 ref NP_009700.1	YBR142W	subunits; Mak5p Essential nucleolar protein, putative DEAD-box RNA helicase required for	2	4.0662	0.348	2102.07	2100.292	1	674.1	50 L.NWKPVDIPDTLDDFGGFY.G
gi 6319618 ref NP_009700.1	YBR142W	maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p Essential nucleolar protein putative DEAD-hox RNA belicase required for	2	3.3595	0.2397	1840.45	1841.012	2	503.2	50 N.W2K2P1V1D111P1D1T1L1D1D1F1G1G1F1.Y
gi 6319618 ref NP_009700.1	YBR142W	maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p Essential nucleolar protein, putative DEAD-box RNA helicase required for	2	4.3637	0.3767	2006.29	2005.188	1	807.5	56.25 N.W2K2P1V1D111P1D1T1L1D1D1F1G1G1F1Y1.G
gi 6319618 ref NP_009700.1	YBR142W	maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	3.4785	0.2748	1989.13	1986.188	1	761.3	53.125 N.WKPVDIPDTLDDFGGFY.G
gi 6319619 ref NP_009701.1	YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor; Sup45p	2	2.9099	0.1524	1667.93	1667.045	1	586	60.714287 M.ISLVIPPKGQIPLYQ.K
gi 6319619 ref NP_009701.1	YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor; Sup45p	2	3.1936	0.2092	1574.29	1572.712	2	271.4	62.5 Y.T1F1K2D1A1E1D1N2E1V1I1K2F1.A
gi 6319619 ref NP_009701.1	YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor; Sup45p	2	3.2415	0.2702	1815.13	1815.219	1	357.7	50 M.I1S1L1V11P1P1K2G1Q2I1P1L1Y1Q2K2.M
gi 6319619 ref NP_009701.1	YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor; Sup45p	2	4.0415	0.3558	1454.75	1455.607	1	993.4	81.818184 T.FKDAEDNEVIKF.A
gi 6319619 ref NP_009701.1	YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor; Sup45p	1	3.0439	0.2557	1469.64	1470.607	1	440.5	54.545456 T.F1K2D1A1E1D1N2E1V111K2F1.A
gi 6319619 ref NP_009701.1	YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor; Sup45p	2	3.8492	0.3275	2003.61	2004.21	1	712.4	56.25 L.YCGDIITEDGKEKKVTF.D
gi 6319619 ref NP_009701.1	YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor; Sup45p	2	3.9547	0.2389	1470.27	1470.607	1	954.4	77.27273 T.F1K2D1A1E1D1N2E1V111K2F1.A
gi 6319619 ref NP_009701.1	YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive complotent suppressor; Sup45p Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence	2	3.3278	0.2486	1686.39	1685.045	1	430	53.571426 M.I1S1L1V1I1P1P1K2G1Q2I1P1L1Y1Q2.K
gi 6319635 ref NP_009717.1	YBR159W	In the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp Microsomal beta-keto-reductase; contains cleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis; accumulate high	2	4.4153	0.3014	1833.55	1833.092	2	697.3	64.28571 V.PFLETEEKELRNIIT.I
gi 6319635 ref NP_009717.1	YBR159W	levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides; Ybr159wp Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutate articlit reduced V/CCA surphasis, exerumulate high	2	4.0706	0.3124	2030.63	2029.341	1	664.7	56.25 I.PVPFLETEEKELRNIIT.I
gi 6319635 ref NP_009717.1	YBR159W	In the promoter region, mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis accumulate high	2	3.7973	0.3529	2228.67	2229.579	1	460.8	50 H.SIPVPFLETEEKELRNIIT.I
gi 6319635 ref NP_009717.1	YBR159W	In the promote region, motants exhibit reduced VLCF A synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the normater region; mutants exhibit reduced VLCFA synthesis; accumulate high	2	4.3989	0.3027	2282.57	2281.604	1	317.4	44.444447 I.P1V1P1F1L1E1T1E1E1K2E1L1R4N2I1I1T1I1N2.N
gi 6319635 ref NP_009717.1	YBR159W	In the promote region, motante exhibit reduced VECF A synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the normater region; mutants exhibit reduced VLCFA synthesis; accumulate high	2	4.2436	0.3089	2257.61	2256.604	1	434.6	47.22222 I.PVPFLETEEKELRNIITIN.N
gi 6319635 ref NP_009717.1	YBR159W	levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides; Ybr159wp Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region: mutants exhibit reduced VLCFA synthesis, accumulate high	2	3.0367	0.3484	1590.39	1589.792	1	171.6	62.5 L.QKELEDQHHVVVK.I
gi 6319635 ref NP_009717.1	YBR159W	levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high	2	2.9947	0.2348	2059.21	2060.355	1	474.3	50 V.PFLETEEKELRNIITIN.N
gi 6319635 ref NP_009717.1	YBR159W	levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately	2	3.387	0.2828	2254.21	2253.579	1	248.8	41.6666664 H.S1I1P1V1P1F1L1E1T1E1E1K2E1L1R4N2I1I1T1.I
gi 6319636 ref NP_009718.1	YBR160W	associates with G1 cyclins (CLNs) and G2/M cyclins (CLBs) which direct the CDK to specific substrates; Cdc28p Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with G1 cycling (CLNs) and G2/M cyclins (CLRs) which direct the CDK to	2	3.7384	0.1958	1407.43	1406.64	7	867.6	72.72727 L.W2Y1R4A1P1E1V1L1L1G1G1K2.Q
gi 6319636 ref NP_009718.1	YBR160W	associates which could be a solution of the so	3	4.9115	0.2243	3001.22	3001.455	1	424.4	25 F.RVLGTPNEAIWPDIVYLPDFKPSFPQ.W
gi 6319636 ref NP_009718.1	YBR160W	catalog marks (CAC) and the set of the set o	2	5.1629	0.4499	3033.61	3034.455	1	887.8	40 F.R4V1L1G1T1P1N2E1A1I1W2P1D111V1Y1L1P1D1F1K2P1S1F1P1Q2.W
gi 6319636 ref NP_009718.1	YBR160W	specific substrates; Cdc28p Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with G1 cyclins (CLNs) and G2/M cyclins (CLBs) which direct the CDK to	2	4.593	0.3163	2999.71	3001.455	1	839.8	42 F.RVLGTPNEAIWPDIVYLPDFKPSFPQ.W
gi 6319636 ref NP_009718.1	YBR160W	specific substrates; Cdc28p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	2	4.1193	0.3319	2658.35	2659.975	1	661.8	38.636364 L.G1T1P1N2E1A1I1W2P1D1I1V1Y1L1P1D1F1K2P1S1F1P1Q2.W
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	2	3.9569	0.4629	1742.75	1744.899	1	989.2	63.333332 N.SRDDPVVGPDQPYSIV.E
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	2	3.7747	0.3453	1716.23	1718.771	1	484.9	57.692307 K.D1N2K2E1Q2V1D1F1D1E1F1A1N2K2.Y
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	1	2.9473	0.2509	1425.47	1426.554	9	209.6	50 T.R4E1F1D1E1V1Y1T1A1P1A1L1.G
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	2	3.2166	0.2937	1826.43	1827.003	1	1132.4	63.333332 T.REFDEVYTAPALGFPN.A
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in linid metabolism, null mutant slightly	3	6.2713	0.2512	2273.39	2271.566	1	1936.5	50 K.D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1H3.G
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase may be involved in linid metabolism, null mutant slightly	3	4.8721	0.2689	2401.88	2401.74	1	736.9	32.894737 L.K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1H3.G
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in linid metabolism, null mutant slightly	2	3.2943	0.1779	2262.17	2261.599	6	295.3	44.444447 L.K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1.H
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p	2	4.3499	0.3027	2541.59	2539.934	1	658	47.5 R.Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1.H

gi 6319655 ref NP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	3	4.6864	0.369	2374.55	2374.74	1	966.4	38.157894 L.KDNELEELREVDLPLVVILH.G
gi 6319655 ref NP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	2	3.6804	0.2702	2649.65	2651.075	1	618.4	42.857143 R.YLKDNELEELREVDLPLVVILH.G
gi 6319655 ref NP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	3	6.511	0.3227	2680.25	2680.075	1	1502.4	39.285713 R.Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V111L1H3.G
gi 6319655 ref NP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	2	3.6695	0.2235	2239.29	2237.599	1	450.4	52.77778 L.KDNELEELREVDLPLVVIL.H
gi 6319655 ref NP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	2	4.8684	0.3405	2192.17	2191.405	1	970.9	67.64706 K.LHLKDNKEQVDFDEFANK.Y
gi 6319655 ref NP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	2	4.5869	0.473	2122.83	2124.36	1	990	55.263157 L.GVPNGSLPDHPPTVKNPSFY.M
gi 6319655 ref NP 009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	2	3.7814	0.2955	1418.77	1420.708	1	1104.4	77.27273 L.R4E1V1D1L1P1L1V1V11L1H3.G
ail6319655/refINP 009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C: Eht1p	2	3.5373	0.353	1402.95	1403.708	1	1142.2	77.27273 L.REVDLPLVVILH.G
gil6319655/refINP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C: Eht1p	3	5.1384	0.305	2653.43	2651.075	1	1477	39.285713 R.YLKDNELEELREVDLPLVVILH.G
gil6319655/refINP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C: Eht1p	2	3.2975	0.3011	2214.41	2217.405	1	329.5	58.823532 K.L1H3L1K2D1N2K2E1Q2V1D1F1D1E1F1A1N2K2.Y
gil6319655/refINP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C: Eht1p	2	3,2594	0.1886	2678.07	2680.075	2	402.1	35.714287 R Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V11L1H3.G
gil6319655/refINP_009736_1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C. Ebt10	2	5 4477	0.4783	1964 63	1967 141	-	2148.4	80 K K2E1D1K2D1E1K2A1T1H3P1E1G1W2P1R4 I
gil6319655/refINP_009736.1	VBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C: Eht1n	3	3 8508	0 3814	1509 14	1508 732	1	1021.9	52 272724 & D1F151K2K2F2F1P1V1F1V1G1R4 F
gil6319655/ref/NP_009736.1	VBP177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 370; Ehtlp	1	3 0921	0.3168	1508.65	1508 732	1	270.5	
gilo319055[iei]NP_009750.1]	VDD4770	Possible series hydrolase, may be involved in lipid metabolism, null mutant slightly	1	3.9021	0.3100	1508.05	1508.732		279.5	
gi 6319655 ret NP_009736.1	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	2	3.4729	0.1903	2512.35	2513.934	1	480.7	
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	3	4.4305	0.2786	1404.14	1403.708	1	2716.8	65.909096 L.REVDLPLVVILH.G
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	2	3.1638	0.1659	2650.87	2651.075	4	356.6	33.333336 R.YLKDNELEELREVDLPLVVILH.G
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	2	4.1512	0.3155	2678.55	2680.075	1	781.3	47.61905 R.Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V111L1H3.G
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	3	4.6	0.301	1420.55	1420.708	1	2632.4	65.909096 L.R4E1V1D1L1P1L1V1V111L1H3.G
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	2	4.5075	0.385	2149.25	2149.36	1	737.4	52.63158 L.G1V1P1N2G1S1L1P1D1H3P1P1T1V1K2N2P1S1F1Y1.M
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	3	3.984	0.231	2679.44	2680.075	1	1132.2	30.952381 R.Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V111L1H3.G
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly	3	4.2571	0.3769	1508.57	1508.732	1	994.8	52.272724 A.D1F1S1K2K2F1P1V1F1Y1G1R4.E
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase may be involved in linid metabolism, null mutant slightly	3	3.982	0.3401	1491.14	1491.732	1	742.7	50 A.DFSKKFPVFYGR.E
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase may be involved in linid metabolism null mutant slightly	2	4.3872	0.2955	1510.29	1508.732	1	711.7	77.27273 A.D1F1S1K2K2F1P1V1F1Y1G1R4.E
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Possible serine hydrolase may be involved in linid metabolism, null mutant slightly	1	2.5983	0.2334	1490.73	1491.732	1	245.7	54.545456 A.DFSKKFPVFYGR.E
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Dessible series hydrolase, may be involved in lipid metabolism, null mutant slightly	2	4.1345	0.3479	1766.63	1764.899	1	979.3	63.333332 N.S1R4D1D1P1V1V1G1P1D1Q2P1Y1S1I1V1.E
gi 6319655 ref NP_009736.1	YBR177C	temperature sensitive at 37C; Eht1p Perateira companyant of the small (40C) rihecomel subusit, packy identical to ResORe	2	3.5968	0.3168	1941.85	1942.141	1	460.8	56.666668 K.KFDKDEKATHPEGWPR.L
gi 6319666 ref NP_009748.1	YBR189W	and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	1	3.0442	0.3386	1260.54	1260.435	1	732	70 E.KHIDFAPTSPF.G
gi 6319666 ref NP_009748.1	YBR189W	and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	2	3.1182	0.2013	2274.63	2274.542	5	168.5	38.88889 A.ARDLLTRDEKDPKRLFEGN.A
gi 6319666 ref NP_009748.1	YBR189W	and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	1	2.2539	0.1996	861.48	860.991	4	120.6	75 M.PRAPRTY.S
gi 6319666 ref NP_009748.1	YBR189W	Protein component of the small (4US) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	2	3.8199	0.3011	2412.87	2413.655	1	455.5	45.454548 L.DSEKHIDFAPTSPFGGARPGRVA.R
gi 6319666 ref NP_009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	2	3.8055	0.24	2444.47	2445.655	2	371.9	45.454548 L.D1S1E1K2H3I1D1F1A1P1T1S1P1F1G1G1A1R4P1G1R4V1A1.R
gi 6319666 ref NP_009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	2	3.1341	0.2845	2525.69	2526.814	4	228.5	36.95652 R.LDSEKHIDFAPTSPFGGARPGRVA.R
gi 6319666 ref NP_009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	1	3.2983	0.3485	1591.9	1591.717	1	499.9	50 L.DSEKHIDFAPTSPF.G
gi 6319666 ref NP_009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	2	3.9508	0.3806	1590.65	1591.717	1	991.8	69.230774 L.DSEKHIDFAPTSPF.G
gi 6319666 ref NP_009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	2	3.0341	0.2091	1704.61	1704.877	1	646.4	57.14286 R.LDSEKHIDFAPTSPF.G
gi 6319666 ref NP_009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	2	3.7751	0.3174	2226.79	2227.415	1	582.1	42.5 R.L1D1S1E1K2H3I1D1F1A1P1T1S1P1F1G1G1A1R4P1G1.R
gi 6319666 ref NP 009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	2	3.4785	0.2873	1261.39	1260.435	1	1230.5	85 E.KHIDFAPTSPF.G
gil6319666lrefINP 009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E, coli S4 and rat S9 ribosomal proteins; Rps9bp	2	4.0695	0.3184	1608.21	1608.717	1	835.2	65.38461 L.D1S1E1K2H3I1D1F1A1P1T1S1P1F1.G
gil6319666/refINP_009748.1	YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and bas similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	1	3 1047	0.3386	1274 62	1274 435	1	618.3	70 E K2H3I1D1E1A1P1T1S1P1E1 G
giles reception in _coor long	Diricon	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of ducose 6 phosphate and fructose 6 phosphate; required for cell cycle progression	•	0.1011	0.0000	121 1102	121 11 100	·	010.0	
gi 6319673 ref NP_009755.1	YBR196C	and completion of the gluconeogenic events of sporulation; Pgi1p	2	3.6034	0.3297	1756.49	1755.021	1	1438.6	64.70589 K.KITDVVNIGIGGSDLGPV.M
	VED1000	glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the adjuccose agence prosts of constraints in the second	0	2 2002	0.2755	1715 47	1714 040	0	E00.4	
9103 1907 Streitine_009755.1	I DR 190C	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of	2	3.3293	u.2755	1/15.1/	17 14.913	3	502.1	07.007 14 N.HOFTTTQ2TTFTETETUNZITFTETETUNZI
gi 6319673 ref NP_009755.1	YBR196C	and completion of the gluconeogenic events of sporulation; Pgi1p	2	3.043	0.2375	1697.39	1695.913	2	506.1	67.85714 N.HFTQTPLEDNIPLLG.G
	VDD	glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression	-			100/ 07	1000			
gilos raor streitine_009755.1	1 DK 1960	and completion of the gluconeogenic events of sporulation; PgPp	2	3.005	0.2896	1301.07	1303.520	1	457.9	03.030304 L.WIVGNDEEQVNAE.G

		Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of								
gi 6319673 ref NP_009755.1	YBR196C	glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation; Pgi1p	2	3.6583	0.3229	1888.97	1887.124	1	445	53.125 N.H3F1T1Q2T1P1L1E1D1N2I1P1L1L1G1G1L1.L
gi 6319673 ref NP_009755.1	YBR196C	Giycovjuc enzyme phosphogiucose isomerase, catalyzes the interconversion or glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation; Pgi1p	2	4.2557	0.2749	2002.57	2001.283	1	583	55.88235 N.H3F1T1Q2T1P1L1E1D1N2I1P1L1L1G1G1L1L1.S
		Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression								
gi 6319673 ref NP_009755.1	YBR196C	and completion of the gluconeogenic events of sporulation; Pgi1p Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II	2	3.8987	0.3371	1552.35	1551.745	1	1197.6	86.36364 F.DQYLHRFPAYLQ.Q
gi 6319675 ref NP_009757.1	YBR198C	transcription initiation and in chromatin modification; Taf5p Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II	2	3.3959	0.3366	2517.09	2518.866	1	350	35.714287 N.SVPVKLGPFPKDEEFVKEIETE.L
gi 6319675 ref NP_009757.1	YBR198C	transcription initiation and in chromatin modification; Taf5p Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II	3	3.8961	0.3168	2355.35	2355.656	1	704.3	39.473686 V.P1V1K2L1G1P1F1P1K2D1E1E1F1V1K2E1I1E1T1E1.L
gi 6319675 ref NP_009757.1	YBR198C	transcription initiation and in chromatin modification; Taf5p Subunit (00 kDa) of TEIID and SAGA complexes, involved in RNA polymorase II	2	3.5983	0.2349	2400.45	2401.74	9	295.5	47.368423 L.G1P1F1P1K2D1E1E1F1V1K2E1I1E1T1E1L1K2I1K2.D
gi 6319675 ref NP_009757.1	YBR198C	transcription initiation and in chromatin modification; Taf5p	3	5.0992	0.2683	2401.07	2401.74	2	843.1	36.842106 L.G1P1F1P1K2D1E1E1F1V1K2E1I1E1T1E1L1K2I1K2.D
gi 6319675 ref NP_009757.1	YBR198C	transcription initiation and in chromatin modification; Taf5p	2	4.7263	0.2814	2376.97	2377.74	1	952.4	55.263157 L.GPFPKDEEFVKEIETELKIK.D
gi 6319675 ref NP_009757.1	YBR198C	Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification; Taf5p	2	3.3494	0.1874	2542.41	2543.866	1	327	35.714287 N.S1V1P1V1K2L1G1P1F1P1K2D1E1E1F1V1K2E1I1E1T1E1.L
gi 6319675 ref NP_009757.1	YBR198C	Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification; Taf5p	2	4.3045	0.3319	1937.37	1937.255	1	748.8	62.5 N.S1V1P1V1K2L1G1P1F1P1K2D1E1E1F1V1K2.E
gi 6319676 ref NP 009758.1	YBR199W	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr4p	2	4.7065	0.4005	2183.85	2185.419	1	1269.9	68.75 N.F1E1I1V1D1L1D1F1L1R4S1E1P1Y1E1K2Y1.M
gil6319676lrefINP_009758_1	YBR199W	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family: Ktr4n	3	4 87	0 2795	3368 24	3368 719	1	708.2	25 Y T1F1I 1N2D1F1F1F1T1D1F1F1K2D1G1I1K2S1I1I 1P1K2D1R4V1V1F1F1 G
aile210676/refIND_000758.1	VPP100W	Putative mannosyltransferase involved in protein glycosylation; member of the	2	2 4054	0.2/100	2165.23	2164 410	1	04E E	
	TBRI99W	Putative mannosyltransferase involved in protein glycosylation; member of the	2	3.4651	0.3418	2165.23	2164.419	, ,	845.5	50.25 N.FEIVULUFLKSEPTEKT.M
gi 6319676 ref NP_009758.1	YBR199W	KRE2/MN11 mannosyltransferase family; Ktr4p Component of the hexameric MCM complex, which is important for priming origins of	2	3.7497	0.3246	2067.35	2069.198	1	847.9	59.375 Y. 11F1L1N2D1E1E1F111D1E1F1K2D1G111K2.S
		DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase;								
gi 6319679 ref NP_009761.1	YBR202W	Cdc47p Component of the bexameric MCM complex, which is important for priming origins of	2	3.9495	0.1828	2457.01	2458.687	1	497.7	47.5 M.NDALREVVEDETELFPPNLTR.R
		DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase;								
gi 6319679 ref NP_009761.1	YBR202W	Cdc47p Component of the hexameric MCM complex, which is important for priming origins of	2	3.8077	0.3192	2486.41	2487.687	1	443.2	45 M.N2D1A1L1R4E1V1V1E1D1E1T1E1L1F1P1P1N2L1T1R4.R
		DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase;								
gi 6319679 ref NP_009761.1	YBR202W	Cdc47p Component of the hexameric MCM complex, which is important for priming origins of DNA replication in C1 and becomes an active ATP-dependent helicase that	2	3.3036	0.3198	2070.45	2073.369	1	720.6	47.058823 L.RLADMVDIDDVEEALRLV.R
	VEDOOOW	promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase;	0	4 0040	0.0507	0464.57	24.02 404	4	700 5	
gil6319679 ret NP_009761.1	YBR202W	Corporent of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that	2	4.0612	0.3597	2164.57	2162.404	1	793.5	52.941177 A.NKELNSVIIDLDDILQYQ.N
gi 6319679 ref NP_009761.1	YBR202W	promotes DNA meiting and elongation when activated by Cdc/p-Dor4p in S-phase; Cdc47p Component of the hexameric MCM complex, which is important for priming origins of	2	3.2989	0.2057	2333.65	2332.714	1	426.3	42.105263 N.NMPLPTKEIDYKDDVLDVIL.N
		DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase;								
gi 6319679 ref NP_009761.1	YBR202W	Cdc47p Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that	2	3.4154	0.1785	2701.17	2702.066	3	297.2	34.090908 A.I1D1N2N2M1P1L1P1T1K2E1I1D1Y1K2D1D1V1L1D1V1I1L1.N
ail63196791refINP 009761.11	YBR202W	promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	3.8296	0.24	2673.31	2675.066	1	429.2	38.636364 A.IDNNMPLPTKEIDYKDDVLDVIL.N
3 10 0 1 1 200 1		Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that								
gi 6319679 ref NP_009761.1	YBR202W	promotes DNA melting and elongation when activated by Cdc/p-Dbt4p in S-phase; Cdc47p	2	3.8348	0.3036	2772.47	2774.145	2	348.6	34.782608 R.A1I1D1N2N2M1P1L1P1T1K2E1I1D1Y1K2D1D1V1L1D1V1I1L1.N
		Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that								
ail6319679/refINP_009761.1	YBR202W	promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	4.0695	0.3426	2744.53	2746.145	4	375.9	32 608696 R AIDNNMPLPTKEIDYKDDVLDVILN
gil6319682/rofINP_009764_1	VBP205W	Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein	-	2 /651	0 3012	1580.61	1591 766	1	270.7	
vil0010002[ref NP_000704.1]	VDDoostw	Putative alpha-1,2-manosyltransferase involved in O- and N-linked protein		2.4031	0.0012	1500.01	1501.700		700.0	
gi 6319682 ref NP_009764.1	YBR205W	giycosylation; member of the KRE2/MN11 mannosyltransferase family; Ktr3p Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein	2	2.9284	0.2064	1545.25	1544.602	1	700.9	68.181816 D.ATYTR4ETYTF1D1Y1L1D1S1S1.G
gi 6319682 ref NP_009764.1	YBR205W	glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein	1	2.8549	0.19	1529.49	1529.602	1	229.3	50 D.AYREYFDYLDSS.G
gi 6319682 ref NP_009764.1	YBR205W	glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein	2	5.9037	0.409	2296.51	2297.578	1	1254.9	62.5 F.T1D1K2S1Q2G1V111H3P1V1D1D1G1K2K2E1K2G1V1M1.V
gi 6319682 ref NP_009764.1	YBR205W	glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p Putative alpha-1.2-mannosyltransferase involved in Q- and N-linked protein	2	3.6567	0.2336	1709.49	1710.001	1	909.4	63.333332 Q.GVIHPVDDGKKEKGVM.V
gi 6319682 ref NP_009764.1	YBR205W	glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p	2	3.3122	0.3453	1799.83	1800.934	1	430.6	53.571426 L.GFHHPDFTSCPIEQK.I
gi 6319682 ref NP_009764.1	YBR205W	glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p	2	3.8325	0.4286	1819.33	1821.934	1	359.9	50 L.G1F1H3H3P1D1F1T1S1C1P1I1E1Q2K2.I
gi 6319682 ref NP_009764.1	YBR205W	glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p	2	3.5455	0.2798	1700.19	1700.935	1	408.9	57.14286 K.AKYGTIPKDHWSIPS.W
gi 6319682 ref NP_009764.1	YBR205W	Putative alpria-1,2-mannosyltransterase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p	3	4.6358	0.3616	2297.06	2297.578	1	1201.6	41.25 F.T1D1K2S1Q2G1V1I1H3P1V1D1D1G1K2K2E1K2G1V1M1.V
gi 6319682 ref NP_009764.1	YBR205W	Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p	2	5.2522	0.4193	2268.71	2269.578	1	1407.2	60.000004 F.TDKSQGVIHPVDDGKKEKGVM.V
gi 6319682 ref NP_009764.1	YBR205W	Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p	2	3.5282	0.2088	1925.73	1925.21	1	679	52.941177 K.SQGVIHPVDDGKKEKGVM.V
gi 6319682 ref NP_009764.1	YBR205W	Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p	2	3.682	0.3191	1830.65	1831.134	1	900.4	56.25 Q.G1V1I1H3P1V1D1D1G1K2K2E1K2G1V1M1V1.T

		E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an								
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.7695	0.2703	1004.48	1004.046	2	314.1	71.42857 Q.HSQDFSPW.Y
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	2.9507	0.3037	2820.49	2822.13	1	333.2	28 T.G1A1D1V1P1T1P1Y1A1K2E1L1E1D1F1A1F1P1D1T1P1T111V1K2A1.V
-102400001fIND 000700 41	VDD004C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	2	2 5700	0.0007	2507.40	2504 024	4	4400	
gilp319698[ret[NP_009780.1]	IBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	2	3.5786	0.2927	2597.49	2594.921	1	1122	47.727272 A.DVPTPYAKELEDFAFPDTPTIVK.A
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	5.2033	0.4488	2191.31	2189.473	1	1503.3	63.88889 A.AIRDPNPVVFLENELLYGE.S
ail6319698/refINP_009780_11	VBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria: Pdh1n	2	3 3472	0 2878	2677 61	2679 004	1	377.2	
gilos recollicitui _coor corri	IBREETO	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	-	0.0112	0.2070	2011.01	2010.001		011.2	
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.5791	0.2341	1214.65	1215.522	1	595.6	60.000004 A.ALKGLKPIVEF.M
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	2.9272	0.2067	1175.15	1174.476	1	1045.7	77.77778 L.K2G1L1K2P1I1V1E1F1M1.S
		E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an								
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	1	2.6009	0.2242	1345.65	1346.714	1	679.9	59.090908 A.ALKGLKPIVEFM.S
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	3.0092	0.2829	1359.62	1360.714	1	522.7	54.545456 A.A1L1K2G1L1K2P1I1V1E1F1M1.S
ail6319698/refINP_009780_1	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria: Pdh1p	2	2 9121	0.3059	1644 65	1645 056	2	511	50 L AVGAALKGI KPIVEEM S
3.1		E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	_					_		
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.1478	0.1966	1348.77	1346.714	1	980.9	72.72727 A.ALKGLKPIVEFM.S
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.343	0.3525	2417.49	2417.731	1	339.8	40 Q.H3S1Q2D1F1S1P1W2Y1G1S1I1P1G1L1K2V1L1V1P1Y1.S
-:::C240C001{IND_000700_4	VDD004C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	2	2 2040	0.0450	4050.05	4000 744		040 5	
gilo319696[rei]NP_009760.1]	TBRZZIC	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	2	3.3910	0.3152	1359.65	1300.714	1	946.5	12.12121 A.AILIKZGILIKZPIIIVIEIFIMI.S
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.6312	0.2729	1173.55	1174.476	1	772.8	66.66667 L.K2G1L1K2P1I1V1E1F1M1.S
ail6319698/refINP_009780_1	VBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria: Pdh1n	1	2 7723	0 2213	1346 71	1346 714	1	760.3	63 636364 A ALKOLKPIVEEM S
gilos reconiciliar _005700.11	TBRZZTO	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an		2.1120	0.2210	1040.71	1040.114		100.0	
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.3135	0.2453	1525.73	1526.702	1	766.4	66.66667 E.A1F1D1Y1L1D1A1P1I1Q2R4V1T1.G
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.484	0.1604	1535.56	1536.635	7	125	50 E.ELDRDDDVFLIGE.E
	VERGOIN	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an		0.0570	0.400	4400 57	1100 010		000 4	
gi 6319698 ret NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	1	2.6576	0.162	1193.57	1193.342	1	228.4	61.11111 R.RVVDIPILEY.G
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	4.842	0.352	2120.85	2118.394	1	1752.6	67.64706 A.IRDPNPVVFLENELLYGE.S
ail6319698/refINP_009780_1	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria: Pdh1p	2	3 9932	0 3222	2213 51	2213 473	1	726.9	47 22222 A A111R4D1P1N2P1V1V1F1L1F1N2F1L1L1Y1G1F1 S
3.1		E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	_					-		
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	4.6056	0.362	2141.45	2141.394	1	1340.4	61.764706 A.I1R4D1P1N2P1V1V1F1L1E1N2E1L1L1Y1G1E1.S
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.0112	0.2105	1292.31	1291.635	1	1374.1	80 A.LKGLKPIVEFM@.S
-:::C240C001{IND_000700_4	VDD004C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an		0.0400	0 4574	4400 50	4400 470		4052.2	
gilo319696[rei]NP_009760.1]	TBRZZIC	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	I	2.6493	0.1571	1162.59	1102.470	1	1053.3	12.22222 L.KGLKPIVEFM.S
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.7354	0.2959	1173.61	1174.476	1	567.1	55.555557 L.K2G1L1K2P1I1V1E1F1M1.S
ail6319698/refINP 009780.11	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria: Pdb1p	1	3.1273	0.3083	1359.56	1360.714	1	784.1	63.636364 A.A1L1K2G1L1K2P1I1V1E1F1M1.S
51	-	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an								
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	2	3.2938	0.288	1346.51	1346.714	1	1067.8	72.72727 A.ALKGLKPIVEFM.S
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.9041	0.1765	1275.62	1275.635	1	1073.8	75 A.LKGLKPIVEFM.S
ail6319698/refINP_009780_11	VBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily conserved multi-protein complex found in mitochondria: Pdh1n	2	3 5558	0 3464	1359 75	1360 714	1	1004.2	72 72727 A A1I 1K2G1I 1K2P1I1V1E1E1M1 S
gilos 19090[rei]NF_009700.1]	TDIX2210	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an	2	3.3330	0.3404	1333.73	1300.714	'	1004.2	
gi 6319698 ref NP_009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.8101	0.2768	1345.64	1346.714	1	873.2	68.181816 A.ALKGLKPIVEFM.S
gi 6319698 ref NP 009780.1	YBR221C	evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.9871	0.2532	1287.72	1288.635	1	662.6	60.000004 A.L1K2G1L1K2P1I1V1E1F1M1.S
		Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral								
ail6319699/refINP_009781_1	YBR222C	membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase: Pcs60n	2	3 6592	0.3783	1571 93	1572 857	2	653.6	60 714287 R GGEKISPIELDGIML S
gilos recollicitui _coor o	IBREED	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral	-	0.0002	0.0700	107 1.00	1012.001	-	000.0	
ail6310600/rofIND_000781_1	VBP222C	membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli	1	2 0423	0.2855	1572 7	1572 957	2	515 7	50 P CCEKISPIEL DCIMI S
gilo319099[rei]NF_009781.1]	I DR2220	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral		2.9423	0.2000	1572.7	1372.037	2	515.7	50 R.OGERISFIELDGINE.S
	VERANO	membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli	~	0 5007	0 4404	0040 70	00.45.000		400 7	
gi 6319699 ret NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral	2	3.5997	0.4161	2043.79	2045.302	1	499.7	46.875 K.IGAPLNPNYKEKEFNFY.L
		membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral	2	3.4347	0.4488	1955.87	1956.308	1	654.2	52.941177 L.INRGGEKISPIELDGIML.S
		membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p Perovisomal AMP-binding protein, localizes to both the perovisomal peripheral	2	3.2569	0.3487	1749.53	1749.045	1	607.8	53.333336 N.R4G1G1E1K2I1S1P1I1E1L1D1G1I1M1L1.S
		membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	3.3924	0.2307	1790.35	1789.041	1	819.2	64.28571 F.HKLEKEFNAPVLEAY.A
		membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	3.6364	0.257	1650.57	1651.002	4	605	73.07692 Y.K2L1T1P1L1D1R4S1Y1V1V1M1P1L1.F
		Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E, coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	4.6768	0.3451	1613.85	1614.856	1	801.3	73.07692 K.F1V1N2T1N2P1V1K2F1P1G1F1A1R4.S
		Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix expression is highly inducible by cleic acid, similar to E, coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	3.8554	0.3362	2224.11	2223.583	1	454.5	44.736843 K.E1L1I1N2R4G1G1E1K2I1S1P1I1E1L1D1G1I1M1L1.S
		Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral								
gi 6319699 ref NP 009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	3.362	0.1703	2197.53	2198.583	1	438.3	44.736843 K.ELINRGGEKISPIELDGIML.S

		Description of AMD big disc protein levelings to both the convincent level parishes								
		membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	4.2473	0.3633	2385.61	2385.643	1	389.6	44.736843 M.D1A1K2I1G1A1P1L1N2P1N2Y1K2E1K2E1F1N2F1Y1.L
		Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	4.8774	0.3849	2358.81	2359.643	1	995.9	57.894737 M.DAKIGAPLNPNYKEKEFNFY.L
		Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral								
ail6319699/refINP_009781_1	VBR222C	membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli	2	3 2079	0 1989	1077 00	1979 308	3	287.9	41 17647 L 11N2R4G1G1E1K2/1S1P1/1E1/ 1D1G1/1M1/1 S
gilos raosalterini _003701.1	TDIAZZZO	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral	2	5.2015	0.1303	1911.99	1979.300	5	207.5	
		membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p Perovisomal AMP-binding protein, localized to both the perovisomal peripheral	2	2.9209	0.2519	1809.55	1809.041	1	489.3	53.571426 F.H3K2L1E1K2E1F1N2A1P1V1L1E1A1Y1.A
		membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	3.4615	0.2235	1701.85	1702.935	1	684.3	64.28571 K.F1V1N2T1N2P1V1K2F1P1G1F1A1R4S1.S
		Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is bighty inducible by oleic acid, similar to E, coli								
gi 6319699 ref NP_009781.1	YBR222C	long chain acyl-CoA synthetase; Pcs60p	2	4.4564	0.3943	1596.77	1594.856	1	1101.5	76.92308 K.FVNTNPVKFPGFAR.S
		Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral								
ail6319699/refINP_009781_1	VBR222C	membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl.CoA synthetase: Pcs60p	2	3 1486	0 2339	2065 49	2067 302	8	285.9	37.5 K I1G141P1I 1N2P1N2Y1K2E1K2E1E1N2E1Y1 I
gi 6319702 ref NP_009784.1	YBR225W	hypothetical protein; Ybr225wp	2	4.3427	0.1611	1800.95	1799.028	4	430.8	60.000004 N.S1P1R4P1V1I1S1D1P1L1D1E1I1D1I1L1.L
gi 6319702 ref NP_009784.1	YBR225W	hypothetical protein; Ybr225wp	2	3.4296	0.2901	1780.69	1780.028	2	435.3	56.666668 N.SPRPVISDPLDEIDIL.L
gi 6319702 ref NP_009784.1	YBR225W	hypothetical protein; Ybr225wp Protein associated with U3 and U14 spoRNAs, required for pre-rRNA processing and	2	4.1816	0.2302	1987.03	1987.211	1	426.9	52.941177 E.A1N2S1P1R4P1V1I1S1D1P1L1D1E1I1D1I1L1.L
		40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the								
gi 6319724 ref NP_009806.1	YBR247C	nucleolus; Enp1p	2	4.0725	0.3165	2566.39	2567.656	1	616.6	52.499996 A.K2E1Q2Q2D1E1I1E1G1E1E1L1A1E1S1E1R4N2K2Q2F1.E
		Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and 40S ribosomal subunit synthesis: localized in the nucleus and concentrated in the								
gi 6319724 ref NP 009806.1	YBR247C	nucleolus; Enp1p	2	4.8358	0.4168	2537.83	2537.656	1	1078.1	52.499996 A.KEQQDEIEGEELAESERNKQF.E
		Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and								
ail62107241rofIND_000906_11	VPP247C	40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the	2	4 3550	0.2406	2609 72	2609 725	1	1250.0	
gilo319724[rei]NP_009806.1]	IBR24/C	Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and	3	4.3008	0.3496	2008.73	2608.735	1	1250.9	40.478192 LAREQUDEIEGEELAESERINKQF.E
		40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the								
gi 6319724 ref NP_009806.1	YBR247C	nucleolus; Enp1p	1	2.7498	0.3398	1261.73	1262.494	1	190	60.000004 L.RLPFSPPTTVF.I
		40S ribosomal subunit synthesis: localized in the nucleus and concentrated in the								
gi 6319724 ref NP_009806.1	YBR247C	nucleolus; Enp1p	1	2.7695	0.3445	1275.49	1276.494	2	156	55 L.R4L1P1F1S1P1P1T1T1V1F1.I
		Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and								
ail6319724/refINP_009806.1	YBR247C	40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the nucleolus; Enp1p	1	2,9938	0.2279	1487.7	1488.813	1	491.7	66.66667 Y.LLRI PESPPTTVE I
3.1		Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and								
- 100407041- (IND, 00000041	VDD0470	40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the		0.0007	0 474 4	4505.00	1501.010		007.0	
gi 6319724 ret NP_009806.1	YBR247C	nucleolus; Enp1p Protein associated with U3 and U14 spoRNAs, required for pre-rRNA processing and	1	2.9607	0.1714	1505.66	1504.813	1	337.8	58.333332 Y.L1L1R4L1P1F1S1P1P11111V1F1.I
		40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the								
gi 6319724 ref NP_009806.1	YBR247C	nucleolus; Enp1p	2	2.9785	0.2841	1502.65	1504.813	1	465.9	66.66667 Y.L1L1R4L1P1F1S1P1P1T1T1V1F1.I
		Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and 40S ribosomal subunit synthesis: localized in the nucleus and concentrated in the								
gi 6319724 ref NP_009806.1	YBR247C	nucleolus; Enp1p	2	4.5997	0.4314	2271.55	2271.453	1	1267.1	58.823532 L.RNWQDVIYVTNPEEWSPH.V
		Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and								
ail6319724/refINP_009806.1	YBR247C	40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the nucleolus; Enp1p	2	3.5931	0.2368	1504.99	1504.813	1	395.4	62.5 Y.L1L1R4L1P1F1S1P1P1T1T1V1F1.
3.1		Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and	_							
- 100407041- (IND, 00000041	VDD0470	40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the		0.0000	0.0014	4500 70	1501.010		005.0	
gilo319724[rei]NP_009606.1]	TBR24/C	Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and	'	2.8989	0.3211	1503.73	1504.813	1	295.6	54.100008 Y.LILIR4LIPIFISIPIPIIIIIVIFI.
		40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the								
gi 6319724 ref NP_009806.1	YBR247C	nucleolus; Enp1p	1	2.8148	0.1546	1487.78	1488.813	1	327.9	54.166668 Y.LLRLPFSPPTTVF.I
		Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and 40S ribosomal subunit synthesis: localized in the nucleus and concentrated in the								
gi 6319724 ref NP_009806.1	YBR247C	nucleolus; Enp1p	2	3.5205	0.3216	1490.31	1488.813	1	571.4	75 Y.LLRLPFSPPTTVF.I
gi 6319728 ref NP_009810.1	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	2	4.1727	0.2819	2306.61	2307.613	1	781.4	58.333332 S.RNVEFAPPYLDDFTKIHPF.W
gi 6319728 ref NP_009810.1 gi 6319728 ref NP_009810.1	YBR251W YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p Mitochondrial ribosomal protein of the small subunit; Mrps5p	2	5.4939 3.2443	0.4017	2306.21	2307.613	1	977.9 469.1	45.833336 S.RNVEFAPPYLDDFTKIHPF.W 41.666664 S.R4N2V1E1E1A1P1P1Y1L1D1D1E1T1K2I1H3P1E1 W
gi 6319728 ref NP_009810.1	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	2	3.9659	0.2825	2306.89	2307.613	1	681	52.77778 S.RNVEFAPPYLDDFTKIHPF.W
gi 6319728 ref NP_009810.1	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	3	5.6578	0.3811	2335.19	2333.613	1	694	41.6666664 S.R4N2V1E1F1A1P1P1Y1L1D1D1F1T1K2I1H3P1F1.W
gi 6319728 ref NP_009810.1 gi 6319728 ref NP_009810.1	YBR251W YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p Mitochondrial ribosomal protein of the small subunit; Mrps5p	3	5.7573 6.0847	0.3948	2306.96	2307.613	1	1179.5	50 S.RNVEFAPPYLDDFTKIHPF.W 31 896553 F.RWDOVOOPI PGEGNII PPGVSI PNDGGRKS K
gilos 19720/10/14 _000010.1/	101/2011		0	0.0047	0.2004	0210.02	0210.00		1000.0	F.R4W2D1Q2V1Q2Q2P1L1P1G1E1G1N2I1L1P1P1G1V1S1L1P1N2D1G1G1R4K2S
gi 6319728 ref NP_009810.1	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	3	5.892	0.3517	3255.44	3256.58	1	1160.4	30.172413 1.K
gi 6319728 ref NP_009810.1	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p Subunit of the Sch1 translocon complex: Sec61p homolog involved in co-	3	4.7056	0.333	3125.9	3126.502	1	907.2	28.57143 F.RWDQVQQPLPGEGNILPPGVSLPNDGGRK.S
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	2	3.1243	0.2431	1641.67	1640.833	2	344	57.692307 K.A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.G
		Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-								
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p Subunit of the Ssh1 translocon complex: Sec61p bornolog involved in co-	2	4.2079	0.4302	2404.59	2403.783	1	1215.1	50 F.AQFPLVGLPKATTPNVNDPIYF.L
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	3	3.822	0.1635	3417.41	3415.048	1	379.1	23.214285 I.D1I1V1K2P1I1L1P1I1L1P1E1V1E1L1P1F1E1K2L1P1F1D1D1K2I1V1Y1T1.I
		Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-								
gi 6319760 ret NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p Subunit of the Ssh1 translocon complex; Sec61p bornolog involved in co-	3	4.9574	0.3166	3310.61	3312.943	1	538.9	27.777791.0111V1K2P111L1P111L1P1E1V1E1L1P1F1E1K2L1P1F10101K2I1V1Y1.1
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	3	5.5991	0.3264	3494.75	3496.208	1	630.1	26.724138 L.IDIVKPILPILPEVELPFEKLPFDDKIVYT.I
ail6310760/rofIND_000942.41	VED2020	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	•	5 9944	0 3144	3527.06	3520 209	4	510.2	25 1D111\/1K2D111 1D111 1D1E1\/1E1 4D4E4E4K2 4D4E4D4D4K2 4\/4\/4\/4
gilo313700[rei]NP_003642.1	1012030	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	3	0.0044	0.3141	3327.00	3329.200	I	010.Z	25 E.10111 VINZETITETETITETETETETETETETETETETETETETETE
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	3	4.7255	0.1793	3424.19	3427.103	1	673.7	25 L.I1D1I1V1K2P1I1L1P1I1L1P1E1V1E1L1P1F1E1K2L1P1F1D1D1K2I1V1Y1.T
ail6319760/refINP_009842_11	YBR283C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co- translational pathway of protein translocation: not essential: Ssh1p	3	5.0218	0.2751	3392 81	3395,103	1	503.5	24.107143 LIDIVKPIL PIL PEVEL PEEKL PEDDKIVY T
91. 9. et et per la 2000 (211)	000	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	Ŭ							
gi 6319760 ref NP 009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	2	3.467	0.3041	2016.39	2017.335	1	669.3	44.11765 V.GLPKATTPNVNDPIYFLR.G

		Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-								
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	2	3.9201	0.4321	2325.03	2326.744	1	824.6	52.499996 F.PLVGLPKATTPNVNDPIYFLR.G
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	2	3.6554	0.367	2630.43	2632.051	1	361.2	38.636364 A.Q2F1P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.G
gi 6319760 ref NP 009842.1	YBR283C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co- translational pathway of protein translocation; not essential; Ssh1p	2	3.4236	0.3592	2601.09	2602.051	1	394.1	38.636364 A.QFPLVGLPKATTPNVNDPIYFLR.G
gil6319760/refINP_009842.1	YBR283C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co- translational pathway of protein translocation; not essential; Ssh1p	3	4,4646	0.3407	2354.33	2353.744	1	1582.2	41.25 F P1I 1V1G1I 1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1I 1R4 G
gil6319760/rofINP_009842.1	VBP283C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co- translational pathway of protein translocation; not essential; Ssh1p	2	3 0555	0 1741	2354.05	2353 744	3	367.5	35 E D11 1/1 C11 1D1K201T1T1D1N2)/(N)2D1D111V1E11 1D4 C
gilos19700/reline_009042.1	VERANO	Subunit of the Ssh1 translocan complex; Sec61p homolog involved in co-	2	0.4040	0.1741	2004.00	2000.744	5	050.0	
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	2	3.4046	0.2856	2502.47	2501.921	1	652.2	45.238094 Q.F1P1L1V1G1L1P1K2A11111P1N2V1N2D1P1I1Y1F1L1R4.G
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	2	4.0349	0.2532	2672.71	2673.13	1	660.2	45.652176 F.AQFPLVGLPKATTPNVNDPIYFLR.G
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	2	4.5397	0.3865	2702.15	2704.13	1	834.3	50 F.A1Q2F1P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.G
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	3	3.9358	0.3624	2602.61	2602.051	1	1356.2	39.772728 A.QFPLVGLPKATTPNVNDPIYFLR.G
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	3	4.5269	0.4344	2672.03	2673.13	1	1520.4	40.217392 F.AQFPLVGLPKATTPNVNDPIYFLR.G
gi 6319760 ref NP_009842.1	YBR283C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co- translational pathway of protein translocation; not essential; Ssh1p	2	3.1748	0.1851	2472.95	2473.921	1	486.2	35.714287 Q.FPLVGLPKATTPNVNDPIYFLR.G
gi 6319760 ref NP_009842.1	YBR283C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co- translational pathway of protein translocation; not essential; Ssh1p	2	4.7737	0.4666	2429.69	2429.783	1	1187	52.380955 F.A1Q2F1P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1.L
gil6319760/refINP_009842.1	YBR283C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co- translational pathway of protein translocation: not essential: Ssh1p	2	4.3211	0.3893	2517.69	2516.943	1	929.6	47.727272 F. AOFPL VGLPKATTPNVNDPIYFL R
gile310760[rofIND_000843.1]	VER2020	Subunit of the Ssh1 translocan complex; Sec61p homolog involved in co- translocan complex; Sec61p homolog involved in co-	-	2 2605	0.2126	2470.90	2471 964		412	
gilo319700[tel]NF_009842.1]	TBR203C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	2	3.3003	0.3120	2470.09	2471.004		412	
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	2	3.0699	0.201	1819.83	1818.293	3	432	50 D.IVKPILPILPEVELPF.E
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-	2	3.7927	0.222	1835.05	1835.293	2	570.5	53.333336 D.I1V1K2P1I1L1P1I1L1P1E1V1E1L1P1F1.E
gi 6319760 ref NP_009842.1	YBR283C	translational pathway of protein translocation; not essential; Ssh1p	3	4.8674	0.4134	2702.09	2704.13	1	896.8	33.695652 F.A1Q2F1P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.G
gi 6319764 ref NP_009846.1	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	3	3.8417	0.1874	3887.87	3889.064	1	304.2	20.967741 L.LERTPNIDNEELVNEEQEEQELLEEENNRMNS.S
gi 6319764 ref NP_009846.1	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	3	6.0288	0.4956	3973.46	3976.142	1	767.2	24.21875 L.LERTPNIDNEELVNEEQEEQELLEEENNRMNSS.F
gi 6319764 ref NP_009846.1	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	3	7.6104	0.5428	4175.03	4176.38	1	2033.4	33.088234 Q.SLLERTPNIDNEELVNEEQEEQELLEEENNRMNSS.F
gi 6319764 ref NP_009846.1	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	2	3.4594	0.196	1500.27	1499.681	1	695.5	68.181816 L.QRELFMEDGFIN.N
gi 6319764 ref NP 009846.1	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	3	7.7258	0.4755	3801.05	3801.986	1	2359.4	33.333336 L.LERTPNIDNEELVNEEQEEQELLEEENNRMN.S
gil6319764 refINP_009846.1	YBR287W	Protein of unknown function: mutation results in a zinc sensitive phenotype: Zsp1p	3	7.0992	0.4261	4023.23	4023.142	1	1622.3	L.L1E1R4T1P1N2I1D1N2E1E1L1V1N2E1E1Q2E1E1Q2E1L1L1E1E1E1N2N2R4M1N 28.90625 2S1S1.F
gil6319764/refINP_009846.1	VBR287W		3	7 4142	0.4261	4003 13	4002 223	1	1969 1	
sil0310704[ref[NI]_000040.1]	VDD007W		2	0.0004	0.5044	4047.00	4040.000		0070	Q.S1L1L1E1RHT1PIN2I1D1N2E1E1L1V1N2E1E1Q2E1E1Q2E1L1L1E1E1E1N2N2F
gilb319764[rei]NP_009846.1]	TDR207W	Protein of unknown function; mutation results in a zinc sensitive phenotype; zsp rp	3	9.0824	0.5641	4047.20	4049.223	1	2872	Q.S1L1L1E1R4T1P1N2I1D1N2E1E1L1V1N2E1E1Q2E1E1Q2E1L1L1E1E1E1N2N2F
gi 6319764 ref NP_009846.1	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous	3	8.1961	0.5575	4222.7	4225.38	1	1660	28.676472 4M1N2S1S1.F
gi 6319771 ref NP_009853.1	YBR294W	activated sulfate intermediates; Sul1p High affinity sulfate permease; sulfate uptake is mediated by specific sulfate	1	3.1464	0.362	1419.48	1420.596	1	892.5	70 F.F1H3I1D1I1P1D1F1S1K2W2.D
gi 6319771 ref NP_009853.1	YBR294W	transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates; Sul1p	2	4.1836	0.2766	1418.67	1420.596	1	1943.5	95 F.F1H3I1D1I1P1D1F1S1K2W2.D
		High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous								
gi 6319771 ref NP_009853.1	YBR294W	activated sulfate intermediates; Sul1p High affinity sulfate permease; sulfate untake is mediated by specific sulfate	1	3.1254	0.3415	1419.54	1420.596	1	870.1	70 F.F1H3I1D1I1P1D1F1S1K2W2.D
-100407741(IND-000050-41	VEDOG	transporters Sul1p and Sul2p, which control the concentration of endogenous		0.0040	0.0054	4 400 00	4 400 500			
gilo319771[rei]NP_009853.1]	1 DR294W	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate	2	3.0948	0.2951	1423.29	1420.596	I	1442	65 F.F.III3IIDIIIPIDIFISIK2W2.D
gi 6319771 ref NP_009853.1	YBR294W	transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates; Sul1p	2	3.7915	0.2754	1420.99	1420.596	1	1583.1	90 F.F1H3I1D1I1P1D1F1S1K2W2.D
		Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the IIv2p catalytic								
gi 6319837 ref NP_009918.1	YCL009C	subunit, localizes to mitochondria; Ilv6p Regulatory subunit of acetolactate synthese, which catalyzes the first step of	2	4.4998	0.4174	1852.55	1852.057	1	989	62.5 H.ATRPPLPTLDTPSWNAN.S
ail6210827irofIND_000018_1		branched-chain amino acid biosynthesis; enhances activity of the IIv2p catalytic	2	2 0020	0 2269	1790.02	1790 079	1	400.8	
gilos 19657 [lei]INF_009916.1]	TCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of	2	3.0930	0.3200	1760.03	1700.970	1	499.0	30 A. IKFEFILDIFSWINAN.S
gi 6319837 ref NP_009918.1	YCL009C	branched-chain amino acid biosynthesis; enhances activity of the IIv2p catalytic subunit, localizes to mitochondria; IIv6p	2	3.8483	0.4244	1804.21	1802.978	1	603.8	53.333336 A.T1R4P1P1L1P1T1L1D1T1P1S1W2N2A1N2.S
		Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic								
gi 6319837 ref NP_009918.1	YCL009C	subunit, localizes to mitochondria; Ilv6p Regulatory subunit of acetolactate synthese, which catalyzes the first step of	1	2.403	0.1635	1549.63	1550.767	7	151	54.166668 Q.A1R4R4Q2I1E1D1L1V1P1V1Y1A1.V
ail6210827irofIND_000018_1		branched-chain amino acid biosynthesis; enhances activity of the IIv2p catalytic	1	0.0675	0 1900	1520 74	1520 767	2	947	
giloo 1909/ [rei]INF_009910.1]	1010090	Regulatory subunit of acetolactate synthase, which catalyzes the first step of	1	2.0070	0.1099	1330.74	1330.707	2	04.7	
gi 6319837 ref NP_009918.1	YCL009C	oranicrieu-criain amino acio biosyntnesis; enhances activity of the IIv2p catalytic subunit, localizes to mitochondria; Ilv6p	1	3.0507	0.2224	1351.48	1352.475	1	372.8	60.000004 L.K2H3E1H3L1N2D1I1T1N2L1.T
		Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the IIv2p catalytic								
gi 6319837 ref NP_009918.1	YCL009C	subunit, localizes to mitochondria; Ilv6p Regulatory subunit of acetolactate synthase, which catalyzes the first step of	2	3.498	0.2048	1351.37	1352.475	1	778	85 L.K2H3E1H3L1N2D1I1T1N2L1.T
ail6319837/refINP_000019_11	YCI 009C	branched-chain amino acid biosynthesis; enhances activity of the IIv2p catalytic subunit localizes to mitochondria: IIv6n	2	4 788	0 4082	1873 69	1875 057	1	830	59 375 H A1T1R4P1P1I 1P1T1I 1D1T1P1S1W2N2A1N2 S
9.1 10001 hollin _000010.11			2		0. 7002				000	
		Regulatory subunit of acetolactate synthase, which catalyzes the first step of								
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ail6319837/refINP_009918_1	YCI 009C	branched-chain amino acid biosynthesis; enhances activity of the IIv2p catalytic	1	2 599	0 2006	1387 47	1388 61	7	116.9	
gil0010001 [Ini](N _000011 2)	VCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine		2.000	0.1627	1222.20	1222 52		749	75 1 0242540404140414W/25414.0
gi10363772 iei NP_009911.2	VOLODOW	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine	2	3.2333	0.1027	1005 50	1332.33	1	740	
gi 10383772 ref NP_009911.2	YCL018W	biosynthesis pathway; Leu2p Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine	2	3.5458	0.1566	1625.59	1624.875	1	651	57.14286 K.K2I1V1V1L1P1G1D1H3V1G1Q2E1I111.A
gi 10383772 ref NP_009911.2	YCL018W	biosynthesis pathway; Leu2p Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine	2	4.1479	0.4695	1781.61	1783.003	1	471.6	46.875 C.H3G1S1A1P1D1L1P1K2N2K2V1N2P1I1A1T1.I
gi 10383772 ref NP_009911.2	YCL018W	biosynthesis pathway; Leu2p Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine	2	4.2238	0.2529	1993.47	1993.235	1	834.7	55.263157 L.G1A1V1G1G1P1K2W2G1T1G1S1V1R4P1E1Q2G1L1L1.K
gi 10383772 ref NP_009911.2	YCL018W	biosynthesis pathway; Leu2p Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine	2	5.0335	0.4096	2335.33	2336.55	1	754.8	50 L.Y1E1P1C1H3G1S1A1P1D1L1P1K2N2K2V1N2P1I1A1T1.I
gi 10383772 ref NP_009911.2	YCL018W	biosynthesis pathway; Leu2p	1	3.0099	0.1776	1223.53	1224.444	1	504.6	65 D.S1L1L1D1L1S1P1I1K2P1Q2.F
gi 10383772 ref NP_009911.2	YCL018W	biosynthesis pathway; Leu2p	1	2.5577	0.2839	1437.75	1438.695	2	491.4	50 L.V1K2N2P1T1H3L1N2G1I1I1IT1.S
gi 10383772 ref NP_009911.2	YCL018W	biosynthesis pathway; Leu2p	2	3.7291	0.38	2308.89	2309.55	1	282.7	37.5 L.YEPCHGSAPDLPKNKVNPIAT.I
gi 10383772 ref NP_009911.2	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway; Leu2p	2	3.8651	0.3748	1680.45	1680.898	1	730.5	56.666668 C.H3G1S1A1P1D1L1P1K2N2K2V1N2P1I1A1.T
		Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase.								
ail103837611refINP_009900.21	YCI 030C	phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	2	4 524	0 2071	2168 41	2165 45	1	1360.3	58 333332 V KI SNPVI NAPEPEEYEEGL T
gi1000070100101 _000000.21	1020000		2	4.024	0.2071	2100.41	2100.40		1000.0	
		phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities;								
gi 10383761 ref NP_009900.2	YCL030C	catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	2	6.6389	0.4157	2188.37	2187.45	1	1919.3	66.66667 V.K2L1S1N2P1V1L1N2A1P1F1P1E1E1Y1F1E1G1L1.T
		Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities:								
gi 10383761 ref NP_009900.2	YCL030C	catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	2	4.91	0.4491	2331.73	2333.652	1	948.1	52.499996 K.F1V1G1Q2P1K2A1E1E1E1K2L1T1G1P111H3L1D1V1V1.K
		Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase,								
gi 10383761 ref NP_009900.2	YCL030C	catalyzes the second, third, ninth and tenth steps in histidino biosynthesis; His4p	2	4.0944	0.332	1902.63	1903.111	1	503.3	53.125 M.H3L1V1N2P1I1I1E1N2V1R4D1K2G1N2S1A1.L
		Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase,								
ail103837611refINP_009900.21	YCL030C	phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis: His4p	2	4.5514	0.4513	2016.51	2017.298	1	950	61.764706 K.F1V1G1Q2P1K2A1E1E1E1K2L1T1G1P1I1H3L1.D
3.1										
		phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities;								
gi 10383761 ref NP_009900.2	YCL030C	catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	2	3.0806	0.281	1937.85	1939.184	1	322.3	44.11765 A.S1P1P1R4K2S1D1G1K2V1S1P1E1V1V1Y1V1A1.E
		Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities;								
gi 10383761 ref NP_009900.2	YCL030C	catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	2	4.6395	0.449	2535.79	2535.905	1	776.9	47.727272 K.F1V1G1Q2P1K2A1E1E1E1K2L1T1G1P1I1H3L1D1V1V1K2A1.S
		Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase,								
gi 10383761 ref NP_009900.2	YCL030C	catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	3	5.6306	0.2237	2186.66	2187.45	1	1487.1	47.22222 V.K2L1S1N2P1V1L1N2A1P1F1P1E1E1Y1F1E1G1L1.T
		Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase,								
gi 10383761 ref NP_009900.2	YCL030C	phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	2	3.5812	0.3384	1644.37	1646.924	1	479.5	60.714287 E.T1I1P1K2V1D1K2I1L1G1P1G1N2Q2F1.V
		Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase.								
ail10383761/rafINP_000000.21	VCI 030C	phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities;	2	3 6468	0 3400	1947.65	1840 162	1	563.8	56 25 E T111D1K2\/4D1K21111C1D1C1N2O2E1\/4T1 A
gi 10363761 1e1 NF_009900.2	TCL030C	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic	2	3.0408	0.3409	1047.05	1649.102	I	505.0	50.25 E.THTETR2VIDTR2HETGTETGTIV2Q2ETVTTT.A
gi 6319806 ref NP_009887.1	YCL043C	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p	2	3.0238	0.2183	1570.13	1570.607	1	697.6	65.38461 D.AELADEEDAIHDEL
		Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-								
gi 6319806 ref NP_009887.1	YCL043C	surface proteins, unscrambles non-native disulfide bonds; Pdi1p Protein disulfide isomerase, multifunctional protein resident in the endoplasmic	2	3.0133	0.1731	1585.95	1586.607	1	524.4	57.692307 D.A1E1L1A1D1E1E1D1A1I1H3D1E1L1
ail63108061rofIND_000887.11	VCI 043C	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-	3	3 0854	0 2555	2730 47	2728 75	1	021.8	
gilos 19000/16/14/ _009007.11	1010430	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic	5	3.3034	0.2000	2130.41	2120.15	'	331.0	33.410004 A.QEINALEADADALEADEEDAIHDEL."
gi 6319806 ref NP_009887.1	YCL043C	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p	3	4.9146	0.4248	3254.81	3254.236	1	752.8	28.57143 L.Y1E1E1A1Q2E1K2A1A1E1E1A1D1A1D1A1E1L1A1D1E1E1D1A111H3D1E1L1
		Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-								
gi 6319806 ref NP_009887.1	YCL043C	surface proteins, unscrambles non-native disulfide bonds; Pdi1p Protein disulfide isomerase, multifunctional protein resident in the endoplasmic	2	3.3507	0.2192	2129.81	2130.346	1	665.9	50 T.ENQDLCMEHNIPGFPSLK.I
-::C24000ClflND_00007_4	VCI 0420	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-	0	2 0500	0.0500	2002 72	2000 474		200 7	
gilo319606/rei/NP_009687.1/	10L0430	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic	2	3.0599	0.2538	2002.73	2880.174	I	380.7	34.782008 Q.IDCTENQDLGMERINIPGPPSLKIF.K
gi 6319806 ref NP_009887.1	YCL043C	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p	2	4.3387	0.4384	2391.67	2390.682	1	751	52.63158 T.ENQDLCMEHNIPGFPSLKIF.K
		Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-								
gi 6319806 ref NP_009887.1	YCL043C	surface proteins, unscrambles non-native disulfide bonds; Pdi1p	2	3.016	0.196	1648.35	1648.945	2	356.4	46.153847 C.M1E1H3N2I1P1G1F1P1S1L1K2I1F1.K
	VOLAZOO	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-	~	0.047	0.0500	4500.00	4400 750		205.0	
gilo319806[ret[NP_009887.1]	TCL043C	surrace proteins, unscramples non-native disulfide bonds; Pdi1p Protein disulfide isomerase, multifunctional protein resident in the endoplasmic	2	3.347	0.2509	1500.89	1499.753	4	365.8	02.3 M.EMNIPGFP3LKIF.K
gi 6319806 ref NP_009887.1	YCL043C	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p	1	2.9162	0.2426	1499.62	1499.753	1	255.8	58.333332 M.EHNIPGFPSLKIF.K

ail63108061rofIND_000887.11	VCI 043C	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins unscrambles processing disulfide bonds. Pdf 10.	2	3 3600	0.2445	1633.40	1630 945	1	833.3	
gilos 19600/18/10F_009667.1	1010430	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen. essential for the formation of disulfide bonds in secretory and cell-	2	3.3009	0.2445	1033.49	1030.945	1	032.3	09.230/ /+ C.IMERINIF GFFSENIF.K
gi 6319806 ref NP_009887.1	YCL043C	surface proteins, unscrambles non-native disulfide bonds; Pdi1p Protein disulfide isomerase, multifunctional protein resident in the endoplasmic	1	2.392	0.2417	1369.63	1370.637	1	478.3	68.181816 E.HNIPGFPSLKIF.K
gi 6319806 ref NP_009887.1	YCL043C	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p Protein disulfide isomerase, multifunctional protein resident in the endoplasmic	2	3.0951	0.2242	1818.59	1818.931	1	660.8	57.692307 L.FYNDEEELEEYKPL.F
gi 6319806 ref NP_009887.1	YCL043C	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p Protein divelifide isomerses, multifunctional protein resident in the androlasmic	1	2.5044	0.1847	1153.56	1154.369	1	617.6	75 L.NMKEQFPLF.A
gi 6319806 ref NP_009887.1	YCL043C	reticulum lumen, essential for the formation of disulfide bonds: near the ordoption of efficiency of the sential for the formation of disulfide bonds; Pdi1p	2	3.9405	0.376	2343.81	2343.33	1	418.3	45.238094 K.AAEEADADAELADEEDAIHDEL
gi 6319806 ref NP_009887.1	YCL043C	reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p	2	3.4155	0.4049	2727.71	2728.75	1	525.6	39.583336 A.QEKAAEEADADAELADEEDAIHDEL
gi 6319806 ref NP_009887.1	YCL043C	receim dustinee isomerase, multiuncional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p	2	3.2914	0.2382	2756.05	2757.75	2	368.3	31.25 A.Q2E1K2A1A1E1E1A1D1A1D1A1E1L1A1D1E1E1D1A1I1H3D1E1L1
gi 6319806 ref NP_009887.1	YCL043C	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell- surface proteins, unscrambles non-native disulfide bonds; Pdi1p	2	3.7346	0.2886	1871.27	1871.094	1	267.6	53.333336 K.N2H3D1E1I1V1N2D1P1K2K2D1V1L1V1L1.Y
ail63108061rofINP_009887.11	YCI 043C	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-	2	3 4620	0 3497	2414.00	2416 692	1	460.9	30 473686 T E1N202011 401141E1H2N2110401E101211 4621E4 K
gilos i soboli elline_003667. 1	1010430	Protein disulfide isomeranes, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-	2	3.4029	0.3497	2414.99	2410.002	1	400.9	33.473000 1.2 INZUZULI CIMIE INSINZI FIGIFIFIGIE INZI FI.K
gi 6319806 ref NP_009887.1	YCL043C	surface proteins, unscrambles non-native disulfide bonds; Pdi1p Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-	2	2.9572	0.2267	2034.03	2034.32	2	460.4	50 V.GKNHDEIVNDPKKDVLVL.Y
gi 6319806 ref NP_009887.1	YCL043C	surface proteins, unscrambles non-native disulfide bonds; Pdi1p Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-	2	3.0044	0.2427	1386.97	1386.637	1	1184.7	77.27273 E.H3N2I1P1G1F1P1S1L1K2I1F1.K
gi 6319806 ref NP 009887.1	YCL043C	surface proteins, unscrambles non-native disulfide bonds; Pdi1p	1	2.4082	0.1573	1253.53	1254.417	1	233	70 M.E1H3N2I1P1G1F1P1S1L1K2.I
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	2	4.1307	0.394	1822.95	1821.024	1	619.8	65.38461 T.E1L1I1P1V1W2Q2R4D1E1W2L1T1N2.V
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	2	3.4138	0.3804	1706.19	1704.92	1	445.6	62.5 T.E1L1I1P1V1W2Q2R4D1E1W2L1T1.N
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	2	3.8217	0.3546	1799.55	1800.024	1	703.8	65.38461 T.ELIPVWQRDEWLTN.V
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	2	3.5946	0.2974	2167.07	2167.4	1	893.3	58.823532 Q.EHKDSPDFRFPMDIVFGE.Y
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	2	3.1378	0.3701	2355.67	2355.576	1	562.5	47.22222 Q.E1H3K2D1S1P1D1F1R4F1P1M1D111V1F1G1E1Y1.W
gil6319804[ref]NP_009884.1]	YCL045C	hypothetical protein; Ycl045cp	2	2 5010	0.3004	2331.31	2330.576	6	432.5	
gil0319804/refINP_009884.1	YCL045C	hypothetical protein; Vcl045cp	2	4 0578	0.2132	2578.47	2580.019	1	714.6	45 238004 K K2K2E1E1M1A1T1P1Y1T1P1Y/11P1I1N2D1N2E1I1I1T1 H
gil6319804/refINP_009884.1	YCL045C	hypothetical protein; Ycl045cp	1	2.5855	0.2112	1370.5	1371.495	1	244.2	59.090908 T.HERNLI PGSDSQ.L
gil6319804lrefINP 009884.11	YCL045C	hypothetical protein; Ycl045cp	2	3.7973	0.2336	1373.59	1371.495	1	620.8	77.27273 T.HFRNLLPGSDSQ.L
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	1	2.7988	0.2471	1389.42	1390.495	1	244.9	59.090908 T.H3F1R4N2L1L1P1G1S1D1S1Q2.L
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	2	3.4668	0.27	2552.91	2554.019	1	570.3	38.095238 K.KKEFMATPYTPVIPINDNFIIT.H
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	2	4.0991	0.4125	2540.47	2540.836	1	370	38.636364 T.HFRNLLPGSDSQLISIPTNLEST.S
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	2	4.0832	0.3033	2252.47	2251.537	1	1680.1	71.05263 T.H3F1R4N2L1L1P1G1S1D1S1Q2L1I1S1I1P1T1N2L1.E
gi 6319804 ref NP_009884.1	YCL045C	hypothetical protein; Ycl045cp	3	3.8613	0.1604	3484.97	3483.018	1	413.3	21.774193 K.AVNSKEKMVAYSKRETTNLNTLGITLGDKSVL.Y
gi 6319804 ref NP_009884.1 gi 6319804 ref NP_009884.1	YCL045C YCL045C	hypothetical protein; YcI045cp hypothetical protein; YcI045cp Diadenosine 5,5"-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase),	2 2	3.5176 3.5535	0.3011 0.2279	1505.79 2570.83	1506.676 2571.836	1	389.4 440.5	68.181816 Q.EHKDSPDFRFPM.D 38.636364 T.H3F1R4N2L1L1P1G1S1D1S1Q2L111S111P1T1N2L1E1S1T1.S
gi 10383757 ref NP_009880.2	YCL050C	involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p; Apa1p Diadenosine 5'.5"-P1 P4-tetraphosphate phosphorylase I (AP4A phosphorylase).	2	3.9999	0.3188	1816.11	1818.053	2	1137.1	67.85714 K.I1T1E1K2P1E1L1I1N2D1I1L1L1E1C1.G
gi 10383757 ref NP_009880.2	YCL050C	involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p; Apa1p	2	3.7998	0.3486	2192.37	2193.411	2	341.5	47.22222 A.H3F1V1L1P1M1P1E1S1E1E1T1V1D1E1D1L1L1A1.M
gi 10383757 ref NP_009880.2	YCL050C	Diadenosine 5',5"-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p; Apa1p	3	4.249	0.2273	4176.65	4177.557	5	283.3	S.H3M1P1S1L111E1K2P1E1R4G1Q2T1P1E1G1E1D1P1L1G1K2P1E1E1E1L1T1V1 19.594595 1P1E1F1G1G1A1D1.N
ail10383757/refINP_009880.21	YCL050C	Diadenosine 5',5"-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5-nucleosidyI) tetraphosphates; has similarity to Apa2p; Apa1n	3	5.0161	0.4158	4060.61	4061.469	1	560.1	S.H3M1P1S1L111E1K2P1E1R4G1Q2T1P1E1G1E1D1P1L1G1K2P1E1E1E1L1T1V1 25.1P1E1E1G1G1A1.D
	VCLOEOC	Diadenosine 5',5"-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p;	1	0.6010	0.0744	1202.6	1204 59	1	601.2	
gi 10363737 Ter INF_009660.2	TCL050C	Apa ip Diadenosine 5',5"-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p;		2.0312	0.2741	1293.0	1294.36		091.5	05 NARF VIETILL.V
gi 10383757 ref NP_009880.2	YCL050C	Apa1p Diadenosine 5',5"-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p;	1	3.3106	0.2577	1537.66	1538.843	1	515.4	58.333332 LL1N2K2F1P1V111P1E1H3T1L1L1.V
gi 10383757 ref NP_009880.2	YCL050C	Apa1p Diadenosine 5',5"-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p;	2	3.2976	0.2728	1520.83	1521.843	7	696.2	62.5 L.LNKFPVIPEHTLL.V
gi 10383757 ref NP_009880.2	YCL050C	Apa1p Diadenosine 5',5"-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidvl) tetraphosphates: has similarity to Apa2p.	3	4.2483	0.2727	3565.43	3563.94	1	488.7	27.34375 S.LIEKPERGQTPEGEDPLGKPEEELTVIPEFGGA.D S.H3M\$P1S1L111E1K2P1E1R4G102T1P1E1G1E1D1P1L1G1K2P1E1E1E1L1T1V1
gi 10383757 ref NP_009880.2	YCL050C	Apa1p Essential nucleolar protein required for the synthesis of 18S rRNA and for the	3	4.591	0.4279	4075.4	4077.469	1	399.7	20.833332 1P1E1F1G1G1A1.D
gijb319791[ret]NP_009872.1	YCL059C	assembly or 40S ribosomal subunit; Krr1p Essential nucleolar protein required for the synthesis of 18S rRNA and for the eccembly of 40S ribosomal subunit; Krr1p	2	3.3464	0.3769	2382.53	2383.712	2	288.8	
ail6319791/refINP_009872.1	YCL059C	Essential nucleolar protein required for the synthesis of 18S rRNA and for the assembly of 40S filosomal subunit Krr1p	2	3.3539	0.2413	1803.95	1804 913	1	484 9	11.22222 N.YTTFFFAUERNYDLEIE.9
gi 6319791 ref NP_009872.1	YCL059C	Essential nucleolar protein required for the synthesis of 18S rRNA and for the assembly of 40S ribosomal subunit; Krr1p	2	2.9342	0.2413	1712.41	1710.809	2	652	62.5 N.R4D1K2P1W2D1T1D1D111D1K2W2.K
gi 6319791 ref NP_009872.1	YCL059C	Essential nucleolar protein required for the synthesis of 18S rRNA and for the assembly of 40S ribosomal subunit; Krr1p	2	3.4894	0.1728	1975.45	1976.172	1	357.5	60.714287 L.NEQKEKQMEREIERQ.E
gi 6319791 ref NP_009872.1	YCL059C	Essential nucleolar protein required for the synthesis of 18S rRNA and for the assembly of 40S ribosomal subunit; Krr1p	2	3.0839	0.2124	1633.01	1632.943	1	730.9	69.230774 K.V1Y1T1P1F1P1P1A1Q2L1P1R4K2V1.D

		Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GEP)-fusion protein localizes to the cytoplasm in a								
gi 6319849 ref NP_009930.1	YCR004C	proctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins;	2	3.3689	0.1658	933.15	933.108	1	1379.8	92.85714 L.PDEVLTKM.N
gi 6319849 ref NP_009930.1	YCR004C	green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins;	1	2.5797	0.2931	1442.6	1443.648	1	288.9	58.333332 F.GVPTRFGNLPAQW.S
gi 6319849 ref NP_009930.1	YCR004C	green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins;	1	2.8827	0.2905	1461.5	1462.648	5	199.2	50 F.G1V1P1T1R4F1G1N2L1P1A1Q2W2.S
gi 6319849 ref NP_009930.1	YCR004C	green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins;	2	3.0667	0.286	2590.35	2590.89	1	527.1	38.636364 M.NAPQKPEDIPVATEKTLLEYDAF.L
gi 6319849 ref NP_009930.1	YCR004C	green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins;	2	3.2018	0.2513	1446.21	1443.648	1	513.9	62.5 F.GVPTRFGNLPAQW.S
gi 6319849 ref NP_009930.1	YCR004C	green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins;	2	3.3707	0.2734	1464.31	1462.648	1	785.1	75 F.G1V1P1T1R4F1G1N2L1P1A1Q2W2.S
gi 6319849 ref NP_009930.1	YCR004C	green fluorescent protein (GPP)-rusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins;	2	4.5162	0.3549	1726.57	1724.984	1	1124.4	78.57143 F.L1F1G1V1P1T1R4F1G1N2L1P1A1Q2W2.S
gi 6319849 ref NP_009930.1	YCR004C	green nuorescent protein (GPP)-rusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins;	2	4.047	0.3713	1703.61	1703.984	1	913.5	71.42857 F.LFGVPTRFGNLPAQW.S
gi 6319849 ref NP_009930.1	YCR004C	green indulescent protein (GPP)-ruision protein localizes to the cytoplasm in a punctate pattern, Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins; cross flurencent tracticul (CED) kurgie creaticul booking to the actigutes to be	2	4.1439	0.386	1637.89	1637.83	1	574.4	64.28571 M.NAPQKPEDIPVATEK.T
gi 6319849 ref NP_009930.1	YCR004C	green induces early protein (GPP) vision protein localizes to the cytoplash in a punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins; areas fluorescent protein (GPD) vision protein localizes to the cytoplasm in a	2	4.0729	0.3056	1680.51	1678.923	1	1217.2	73.07692 Y.R4V1E1E1T1L1P1D1E1V1L1T1K2M1.N
gi 6319849 ref NP_009930.1	YCR004C	green induces definition (GF) / reason potent localizes to the cytoplash ma punctate pattern; Ycp4p Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GPI)-fusion protein localizes to the cytoplasm in a protein constraint of the cytoplasm in a second structural similarity to flavodoxins;	2	4.2212	0.2632	1530.45	1529.731	1	1515.3	79.16667 Y.RVEETLPDEVLTK.M
gi 6319849 ref NP_009930.1	YCR004C	proceeding and the second seco	1	3.1114	0.1743	1545.9	1546.731	7	257.3	54.166668 Y.R4V1E1E1T1L1P1D1E1V1L1T1K2.M
gi 10383781 ref NP_009938.2	YCR012W	in glycolysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acvi phosphate of 1.3-bisphosphoducerate to ADP to produce ATP; key enzyme	2	3.506	0.3026	1302.79	1300.538	7	538.5	72.72727 D.NLLDKVDSIIIG.G
gi 10383781 ref NP_009938.2	YCR012W	in glycolysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	2	3.7309	0.3678	1571.85	1572.888	1	1284.1	75 A.GFLLEKELKYFGK.A
gi 10383781 ref NP_009938.2	YCR012W	in glycolysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	1	2.4091	0.186	1166.56	1166.326	5	290.5	68.75 L.E1H3H3P1R4Y1V1V1L1.A
gi 10383781 ref NP_009938.2	YCR012W	in glycodysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	1	2.8399	0.1648	1385.57	1384.66	2	344.7	50 K.G1V1E1V1V1L1P1V1D1F1I1I1A1.D
gi 10383781 ref NP_009938.2	YCR012W	in glycodysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	1	2.9083	0.2145	1461.62	1462.687	1	638.6	62.5 R.V1D1F1N2V1P1L1D1G1K2K2I1T1.S
gi 10383781 ref NP_009938.2	YCR012W	in glycolysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	2	3.0202	0.2018	1587.47	1586.913	4	698.4	57.14286 K.A1K2G1V1E1V1V1L1P1V1D1F11111A1.D
gi 10383781 ref NP_009938.2	YCR012W	in glycolysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	2	3.4822	0.3234	1683.97	1682.786	1	591.8	69.230774 A.S1H3L1G1R4P1N2G1E1R4N2E1K2Y1.S
gi 10383781 ref NP_009938.2	YCR012W	in glycolysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	2	3.1304	0.2159	1596.09	1594.708	4	360.9	70.83333 S.H3L1G1R4P1N2G1E1R4N2E1K2Y1.S
gi 10383781 ref NP_009938.2	YCR012W	in glycolysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	2	2.9517	0.2919	1727.77	1728.865	1	252.4	50 L.ASHLGRPNGERNEKY.S
gi 10383781 ref NP_009938.2	YCR012W	in glycolysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	2	3.8158	0.2998	1315.43	1314.538	6	663.3	77.27273 D.N2L1L1D1K2V1D1S1111111G1.G
gi 10383781 ref NP_009938.2	YCR012W	in glycodysis and gluconeogenesis; Pgk1p 3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme	1	2.6747	0.2709	1445.63	1446.687	1	460.8	58.333332 R.VDFNVPLDGKKIT.S
gi[10383781]ref]NP_009938.2]	YCR012W	in givcovisis and giuconeogenesis; Poki p 3-phosphogloverate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme is alwaying and an unconcensorie; Poki phosphoglycerate to ADP to produce ATP; key enzyme	1	2.3214	0.255	1183.7	1183.433	1	534.b	/SF.LLERELKYF.G
gi 10363761 1e1 14F_009936.2	TCRUIZW	In groupsis and groupledgenesis, run p Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative divorsivlation and phosphorylation	1	2.4133	0.2342	1149.59	1150.526	3	203.2	00.75 LENDERT VVL.A
gi 10383785 ref NP_009943.2	YCR017C	sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p Putative sensor/transporter protein involved in cell wall biogenesis: contains 14-16	2	3.2181	0.2331	1700.17	1699.816	4	460.3	57.692307 N.AHYTYPDEWFPSVS.A
gi 10383785 ref NP_009943.2	YCR017C	transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	1	2.2345	0.2838	1317.36	1318.52	2	425.1	50 E.SHGPLPWPWGAL.T
gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	2	2.9805	0.1646	1718.03	1716.816	6	347.3	50 N.A1H3Y1T1Y1P1D1E1W2F1P1S1V1S1.A
gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	2	4.1325	0.3101	2064.41	2062.255	1	562.7	53.125 M.SEPEYEDMKFPDKFLGE.G

gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	1	2.7862	0.3367	1437.84	1438.67	1	457	53.846157 T.HHLLPSPVGELAPA.I
gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	1	2.8872	0.3258	1455.75	1456.67	1	344.6	50 T.H3H3L1L1P1S1P1V1G1E1L1A1P1A1.I
gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	2	3.7334	0.333	1437.83	1438.67	1	717.6	76.92308 T.HHLLPSPVGELAPA.I
gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	2	3.313	0.2343	1459.05	1456.67	6	427.4	61.538464 T.H3H3L1L1P1S1P1V1G1E1L1A1P1A1.I
gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	2	3.4297	0.3433	2259.57	2262.356	1	433.6	47.058823 S.G1M1H3D1I1D1P1S1D1D1D1R4W2C1E1Y1I1L1.Y
gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	1	2.4408	0.1726	1090.28	1090.23	1	435.7	68.75 E.S1H3G1P1L1P1W2P1W2.G
gi 10383785 ref NP_009943.2	YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p Protein with a potential role in actin cytoskeletal organization; overexpression	2	3.0681	0.2197	1317.79	1318.52	1	618.1	68.181816 E.SHGPLPWPWGAL.T
gi 10383792 ref NP_009959.2	YCR030C	suppresses a pfy1 (profilin) null mutation; Syp1p	2	3.6987	0.3878	2138.19	2139.322	1	986.8	55.263157 N.N2W2T1P1G1E1A1S1D1T1P1P1L1P1P1H3A1T1P1K2.N
ail10383792/refINP_009959.21	YCR030C	Protein with a potential role in actin cytoskeletal organization; overexpression suppresses a ptv1 (profilin) null mutation: Svp1p	2	2.9757	0.3162	1676.27	1677.04	1	644.5	57,14286 K.YSIKEPIAPIVIHPV.W
		Protein with a potential role in actin cytoskeletal organization; overexpression	-	2.07.07	0.0102					
gi[10383792]ret[NP_009959.2]	YCR030C	Protein with a potential role in actin cytoskeletal organization; overexpression	2	3.5545	0.3209	1515.91	1513.864	1	806	73.07692 Y.SIKEPIAPIVIHPV.W
gi 10383792 ref NP_009959.2	YCR030C	suppresses a pfy1 (profilin) null mutation; Syp1p Protein with a potential role in actin cytoskaletal organization; overexpression	2	4.0647	0.2876	1529.63	1530.864	1	681.5	69.230774 Y.S1I1K2E1P1I1A1P1I1V1I1H3P1V1.W
gi 10383792 ref NP_009959.2	YCR030C	suppresses a pfy1 (profilin) null mutation; Syp1p	1	2.4825	0.2851	1512.82	1513.864	2	232.4	46.153847 Y.SIKEPIAPIVIHPV.W
gi 10383792 ref NP 009959.2	YCR030C	Protein with a potential role in actin cytoskeletal organization; overexpression suppresses a pfy1 (profilin) null mutation; Syp1p	2	3.4489	0.2516	1789.47	1790.023	1	796.6	60.714287 R.NVWDTVIEELKSDLK.S
ail10383702/rofIND_000050.21	VCP030C	Protein with a potential role in actin cytoskeletal organization; overexpression	2	3 035	0 3769	1674 51	1675 020	1	360.5	
gi 10000102/10/141 _000000.2/	10110500	Protein with a potential role in actin cytoskeletal organization; overexpression	-	0.000	0.0700	1074.01	1010.020		000.0	
gi 10383792 ref NP_009959.2	YCR030C	suppresses a pfy1 (profilin) null mutation; Syp1p Protein with a potential role in actin cytoskeletal organization; overexpression	1	2.4521	0.2497	1530.86	1530.864	1	312.5	53.846157 Y.S1I1K2E1P1I1A1P1I1V1I1H3P1V1.W
gi 10383792 ref NP_009959.2	YCR030C	suppresses a pfy1 (profilin) null mutation; Syp1p	2	3.4415	0.31	1513.15	1513.864	1	747.9	69.230774 Y.SIKEPIAPIVIHPV.W
gi 10383792 ref NP_009959.2	YCR030C	suppresses a pfy1 (profilin) null mutation; Syp1p	2	3.0723	0.33	1700.37	1700.077	1	695	60.714287 Y.SIKEPIAPIVIHPVW.R
gi 10383792 ref NP_009959.2	YCR030C	Protein with a potential role in actin cytoskeletal organization; overexpression suppresses a ph/1 (profilm) null mutation; Syp1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	2	4.2402	0.348	1719.33	1719.077	1	1119	71.42857 Y.S111K2E1P111A1P111V111H3P1V1W2.R
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar TPase, and the secretory pathway; Fentj Fatty acid elongase, involved in sphingolipid biosynthesis; acid so fatty acids of up to	3	3.916	0.2964	1417.79	1417.564	1	747.5	52.499996 S.LWEHFDDVVTR.V
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p action of the secretory pathway; Fen1p actions of the secretory path	1	3.245	0.3495	1418.7	1417.564	1	653	65 S.LWEHFDDVVTR.V
gi 6319882 ref NP_009963.1	YCR034W	vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphinoolioid biosynthesis; acts on fatty acids of up to	3	3.8803	0.2313	2376.59	2375.649	1	1084.8	39.473686 S.LWEHFDDVVTRVTNGRFVPS.E
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	2	4.8304	0.4196	2347.65	2349.628	1	544.5	52.941177 L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1.F
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase. involved in sphingolini biosynthesis: acts on fatty acids of up to	2	3.5013	0.3227	2583.27	2583.908	4	171.2	36.842106 L.FERYPQLHDYLPTLERPFFN.I
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	2	3.2421	0.2653	2613.53	2613.908	1	215.5	39.473686 L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1F1N2.I
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	3	4.6717	0.3291	2612.15	2613.908	1	864.5	40.789474 L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1F1N2.I
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar TPase, and the secretory pathway; Fent] Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	3	4.3443	0.276	2586.11	2583.908	2	773.6	36.842106 L.FERYPQLHDYLPTLERPFFN.I
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length, inutations have regulatory entects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; multiations have regulatory effects on 1.3-beta-oliveralized and the secretory pathway.	2	4.5277	0.4325	2814.67	2816.146	1	451.5	45.238094 L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1F1N2l1S1.L
gi 6319882 ref NP_009963.1	YCR034W	vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	3	4.7624	0.3015	2814.2	2816.146	1	1392.2	40.476192 L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1F1N2I1S1.L
gi 6319882 ref NP_009963.1	YCR034W	24 carouns in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1 3-beta-glucan eventage	2	3.8144	0.4101	2782.03	2784.146	1	556.1	47.61905 L.FERYPQLHDYLPTLERPFFNIS.L
gi 6319882 ref NP_009963.1	YCR034W	vacuolar ATPase, and the secretory pathway; Fen p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 ordenes in logethy unditione being englishers.	3	3.8183	0.2041	2782.85	2784.146	5	447.7	26.190477 L.FERYPQLHDYLPTLERPFFNIS.L
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length, invitations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fentj base, and the secretory pathway; F	2	3.0192	0.3018	2031.59	2032.306	1	364.3	50 Y.AAPLFERYPQLHDYLPT.L
gi 6319882 ref NP_009963.1	YCR034W	vacuolar ATPase, and the secretory pathway; Fen1p	2	3.5328	0.3237	1965.69	1963.243	1	723.7	63.333332 Q.LHDYLPTLERPFFNIS.L

gi 6319882 ref NP 009963.1	YCR034W	Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fentjo	2	2.94	0.306	2071.25	2073.288	1	573.9	44.11765 A.VHLYFPILPHCGDCVGST.T
		Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1.3-beta-ducan synthase								
gi 6319882 ref NP_009963.1	YCR034W	Factorial ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 4 prohese in learch; writeriane here explorted wifered as 4.3 bits alured authors.	2	4.6516	0.4055	2322.53	2322.628	1	715.1	58.823532 L.FERYPQLHDYLPTLERPF.F
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length, inutations have regulatory elects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	2	3.5195	0.3097	2174.27	2174.393	1	880.8	55.555557 A.VHLYFPILPHCGDCVGSTT.A
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	2	3.5793	0.2894	2093.97	2095.288	1	513.7	41.17647 A.V1H3L1Y1F1P1I1L1P1H3C1G1D1C1V1G1S1T1.T
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to	2	3.0111	0.2592	1970.65	1972.183	1	282.1	43.75 A.VHLYFPILPHCGDCVGS.T
gi 6319882 ref NP_009963.1	YCR034W	24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p	2	3.3557	0.2748	1984.67	1985.243	1	563.2	53.333336 Q.L1H3D1Y1L1P1T1L1E1R4P1F1F1N2I1S1.L
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.6121	0.1991	1885.17	1885.127	1	716.9	59.375 K.IVRGSDPDTTWLIISPN.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.3564	0.3192	2099.77	2097.245	1	1660.6	64.70589 E.FVDDDWWLGELEKDGSKG.L
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	5.0456	0.2829	2655.29	2655.88	2	665.5	36.363636 E.FVDDDWWLGELEKDGSKGLFPSN.Y
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.2697	0.4237	2541.17	2541.776	1	538.7	36.904762 E.FVDDDWWLGELEKDGSKGLFPS.N
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.937	0.2323	2539.91	2541.776	1	820.4	45.238094 E.FVDDDWWLGELEKDGSKGLFPS.N
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.1745	0.3387	1768.43	1769.008	2	318.5	57.14286 A.EEKAKEDPRLVQKPT.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	3.952	0.2559	3802.64	3802.92	1	365.2	24.193548 S.SRVNDNNDDDDWNEPELKERDFDQAPLKPNQS.S
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	5.1457	0.4474	2281.49	2281.566	1	770.9	57.894737 E.E1A1E1Q2P1K2T1D1Y1K2K2I1G1N2P1L1P1G1M1H3.I
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.0576	0.3274	2526.51	2525.841	1	494.7	42.857143 E.E1A1E1Q2P1K2T1D1Y1K2K2I1G1N2P1L1P1G1M1H3I1E1.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	1	2.8286	0.3752	1305.56	1306.566	1	695.5	68.181816 K.KIGNPLPGMHIE.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.9059	0.248	2289.95	2289.637	1	617.5	50 E.YLKIVRGSDPDTTWLIISPN.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.2581	0.2435	1323.39	1322.566	3	645.2	68.181816 K.K2I1G1N2P1L1P1G1M1H3I1E1.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	5.9054	0.4138	3524.3	3524.947	1	1402.9	LA1A1S1E1K2E1E1E1E1M1E1N2K2F1A1P1P1P1K2K2S1E1P1T11111S1P1K2P1F1 32.5 .S
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.0558	0.3474	1699.89	1700.985	6	263.7	40 A.R4V1S1P1P1G1S1D1V1E1K2l1l1l11G1.W
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	2.9689	0.3259	1680.57	1680.985	6	297.6	43.333332 A.RVSPPGSDVEKIIIIG.W
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	3.8666	0.1601	2392.34	2391.548	1	697.6	29.761904 K.AEAPKPEVPEDEPEGEPDVKDL.K
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.6406	0.4531	2390.61	2391.548	1	741.3	42.857143 K.AEAPKPEVPEDEPEGEPDVKDL.K
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	5.3875	0.3624	2413.53	2415.548	1	888.6	47.61905 K.A1E1A1P1K2P1E1V1P1E1D1E1P1E1G1E1P1D1V1K2D1L1.K
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	5.8036	0.4229	2415.74	2415.548	1	1373.2	36.904762 K.A1E1A1P1K2P1E1V1P1E1D1E1P1E1G1E1P1D1V1K2D1L1.K
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.1229	0.2814	2028.29	2029.177	1	1198.6	59.375 Q.V1T1A1R4D1E1D1D1L1D1E1N2E1L1L1M1K2.I
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.6727	0.3148	2006.49	2007.177	1	1744.6	65.625 Q.VTARDEDDLDENELLMK.I
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.187	0.2801	3345.08	3346.418	1	938.7	28.703705 N.DNNDDDDWNEPELKERDFDQAPLKPNQS.S
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.1901	0.1969	3131.99	3131.209	2	560.8	25 N.DNNDDDDWNEPELKERDFDQAPLKPN.Q
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.2071	0.1856	1908.25	1907.127	1	775.2	59.375 K.IIV1R4G1S1D1P1D1T1T1W2L1I1I1S1P1N2.A

gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.7815	0.2874	2433.59	2435.612	1	307.7	38.095238 S.G1A1P1V1Q2K2E1E1P1E1Q2E1E1I1A1P1S1L1P1S1R4N2.S
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.1013	0.2538	2435.3	2435.612	2	567.3	32.142857 S.G1A1P1V1Q2K2E1E1P1E1Q2E1E111A1P1S1L1P1S1R4N2.S
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.4504	0.2877	3633.26	3632.711	1	546.6	S.S1R4V1N2D1N2N2D1D1D1D1D1W2N2E1P1E1L1K2E1R4D1F1D1Q2A1P1L1K2P1N 25 2.Q
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.1831	0.4062	3803.72	3805.011	1	585.4	23.529411 N.SIPAPKQEEAPEQAPEEEIEEEAEEAAPQLPSRSS.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.2031	0.2689	2281.07	2281.566	1	981.5	36.842106 E.E1A1E1Q2P1K2T1D1Y1K2K2I1G1N2P1L1P1G1M1H3.I
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	5.1729	0.3521	2255.71	2254.566	1	993.6	60.526318 E.EAEQPKTDYKKIGNPLPGMH.I
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.7745	0.3668	2497.85	2496.841	1	716.7	47.61905 E.EAEQPKTDYKKIGNPLPGMHIE.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.8099	0.1515	2318.47	2315.637	1	340.2	39.473686 E.Y1L1K2I1V1R4G1S1D1P1D1T1T1W2L1I1I1S1P1N2.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	5.276	0.447	3486.62	3487.947	1	1165.1	31.666666 L.AASEKEEEEMENKFAPPPKKSEPTIISPKPF.S
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.7212	0.1868	1677.41	1678.765	2	742.1	73.07692 T.ARDEDDLDENELLM.K
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.0795	0.1691	1699.19	1696.765	3	368.2	61.538464 T.A1R4D1E1D1D1L1D1E1N2E1L1L1M1.K
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	3.9372	0.2301	2406.83	2406.612	1	1212.2	44.04762 S.GAPVQKEEPEQEEIAPSLPSRN.S
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	4.4689	0.3723	2405.65	2406.612	1	617	50 S.GAPVQKEEPEQEEIAPSLPSRN.S
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.5081	0.3754	3844.7	3847.011	1	903.3	N.S111P1A1P1K2Q2E1E1A1P1E1Q2A1P1E1E1E111E1E1E1A1E1E1A1A1P1Q2L1P 28.676472 1S1R4S1S1.A
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.7236	0.2329	2567.17	2567.776	3	528.6	40.476192 E.F1V1D1D1D1W2W2L1G1E1L1E1K2D1G1S1K2G1L1F1P1S1.N
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	3.9022	0.175	2540.85	2541.776	1	704.8	42.857143 E.FVDDDWWLGELEKDGSKGLFPS.N
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.5336	0.2378	2540.9	2541.776	2	529.5	35.714287 E.FVDDDWWLGELEKDGSKGLFPS.N
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.6947	0.2745	3586.43	3587.711	1	1177.7	30.172413 S.SRVNDNNDDDDWNEPELKERDFDQAPLKPN.Q
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	2	5.2005	0.4274	2280.39	2281.566	1	713.8	55.263157 E.E1A1E1Q2P1K2T1D1Y1K2K2I1G1N2P1L1P1G1M1H3.I
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	3	4.1496	0.3825	2283.08	2281.566	1	1022.4	38.157894 E.E1A1E1Q2P1K2T1D1Y1K2K2I1G1N2P1L1P1G1M1H3.I
gi 6319931 ref NP_010012.1	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA target in the second sec	2	4.7117	0.4172	2039.67	2041.376	1	406.5	50 S.K2S1P1A1P1V1S1K2K2E1P1V1K2T1P1S1P1A1P1A1.A
gi 10383811 ref NP_010017.2	YCR093W	deadenylation; basal transcription factor; Cdc39p Geadenylation; basal transcription factor; Cdc39p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	1	2.6039	0.4887	1422.5	1423.488	1	290.8	50 L.HDGPVIDEFFSC.D
gi 10383811 ref NP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	1	2.6674	0.2973	1436.54	1437.488	3	290.9	50 L.H3D1G1P1V11D1E1F1F1S1C1.D
gi 10383811 ref NP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	2	3.2814	0.314	1552.29	1551.647	1	719.1	62.5 A.L1H3D1G1P1V1I1D1E1F1F1S1C1.D
gi 10383811 ref NP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	2	4.1602	0.328	2639.41	2640.967	1	430	40.476192 N.M1E1D111P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi 10383811 ref NP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	3	4.9263	0.5003	2614.1	2615.967	1	1311	36.904762 N.MEDIPACKELPEVFFDPVIDLH.S
gi 10383811 ref NP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	3	5.9574	0.3883	2642.93	2640.967	1	1446.4	39.285713 N.M1E1D111P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi 10383811 ref NP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	2	4.1157	0.3138	2147.29	2148.411	1	882.7	52.941177 I.P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi 10383811 ref NP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	3	4.0313	0.225	2872.46	2871.23	1	1075.5	32.608696 D.L1N2M1E1D111P1A1C1K2E1L1P1E1V1F1F1D1P1V111D1L1H3.S
gi 10383811 ref NP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	3	4.0438	0.3442	3844.73	3844.291	1	174.6	21.09375 M.TVPNPYDVDLNMEDIPACKELPEVFFDPVIDLH.S

		Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA								
ai103838111refINP_010017.21	VCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenviation; basal transcription factor; Cdc39n	3	3 9562	0 3384	3880.97	3882 201	1	219.6	M.T1V1P1N2P1Y1D1V1D1L1N2M1E1D1I1P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D 22 65625 1I 1H3 S
gi 10363611 101 14F_010017.2	ICR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	3	3.9502	0.3364	3000.97	3002.291	1	219.0	22.03023 ILTH3.3
		levels including regulation of transcription and destabilizing mRNAs by								
gi 10383811 ref NP_010017.2	YCR093W	deadenylation; basal transcription factor; Cdc39p	2	4.6408	0.3463	1815.67	1817.076	1	1845.9	82.14286 C.K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
		Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA								
gi 10383811 ref NP 010017.2	YCR093W	deadenylation; basal transcription factor; Cdc39p	2	4.3721	0.3395	1801.59	1799.076	1	1374.6	75 C.KELPEVFFDPVIDLH.S
		Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA								
	VODOOON	levels including regulation of transcription and destabilizing mRNAs by		0.4400	0.0040	4044 50	1010 100	0		
gi[10383811]ref[NP_010017.2]	YCR093W	ceadenylation; basal transcription factor; Cocosp Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	1	2.4128	0.2349	1241.58	1242.423	3	154.1	68.75 F.NERPYFRLF.5
		levels including regulation of transcription and destabilizing mRNAs by								
gi 10383811 ref NP_010017.2	YCR093W	deadenylation; basal transcription factor; Cdc39p	1	2.8171	0.2467	1257.5	1258.423	6	145.8	62.5 F.N2E1R4P1Y1F1R4L1F1.S
		Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA								
ail10383811/refINP_010017.2	YCR093W	levels including regulation of transcription and destabilizing mRNAs by deadenylation: basal transcription factor: Cdc39n	з	3 9323	0 2247	2657 69	2656 967	1	1170 5	33 333336 N M\$E1D111P1A1C1K2E1I 1P1E1\/1E1E1D1P1\/1I1D1I 1H3 S
3110000011101111 _010011121	101100011	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	0	0.0020	0.2217	2001.00	2000.001			
		levels including regulation of transcription and destabilizing mRNAs by								
gi 10383811 ref NP_010017.2	YCR093W	deadenylation; basal transcription factor; Cdc39p	2	3.0622	0.2302	1491.41	1490.773	1	467.8	63.636364 T.I1F1V1T1H3P1D1L1K2R4V1F1.Q
		levels including regulation of transcription and destabilizing mRNAs by								
gi 10383811 ref NP_010017.2	YCR093W	deadenylation; basal transcription factor; Cdc39p	2	3.8432	0.1605	1750.89	1750.974	1	774.5	64.28571 Y.E1E1F1G1K2N2I1P1N2L1D1V1I1P1F1.A
		Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA								
cil10383811/rofINP_010017.2		levels including regulation of transcription and destabilizing mRNAs by deadeputation: basal transcription factor: Cdc30p	2	3 1221	0.2818	1969 / 3	1860 128	1	308.2	
gi 10505011[tei]ttr _010017.2]	101(03500	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA	2	5.1221	0.2010	1000.45	1003.120	,	330.2	33.33330 E.S INDERADINI IENVE.A
		levels including regulation of transcription and destabilizing mRNAs by								
gi 10383811 ref NP_010017.2	YCR093W	deadenylation; basal transcription factor; Cdc39p	2	3.0843	0.2529	1472.41	1472.773	1	449.8	59.090908 T.IFVTHPDLKRVF.Q
		One of SIX A I Pases of the 195 regulatory particle of the 265 proteasome involved in the degradation of ubiguitinated substrates; required for normal pentide bydrolysis by								
gi 6320197 ref NP 010277.1	YDL007W	the core 20S particle; Rpt2p	2	5.8568	0.2532	2354.77	2355.612	1	845.3	58.333332 F.E1K2K2Q2E1E1E1K2K2Q2L1E1E1I1R4G1N2P1L1.S
		One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in								
-:::::::::::::::::::::::::::::::::::::		the degradation of ubiquitinated substrates; required for normal peptide hydrolysis by	2	4 5075	0.4004	4000.07	4000 040		4000 7	
gil6320197[rei[NP_010277.1]	TDL007W	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in	2	4.5975	0.4091	1990.27	1990.218	1	1382.7	03.00009 A.GENAPSIVFIDEIDAIGTK.R
		the degradation of ubiquitinated substrates; required for normal peptide hydrolysis by								
gi 6320197 ref NP_010277.1	YDL007W	the core 20S particle; Rpt2p	2	3.5867	0.177	2310.29	2309.587	1	402.8	38.88889 Q.E1I1K2E1S1V1E1L1P1L1T1H3P1E1L1Y1E1E1M1.G
		One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in								
gi 6320197 ref NP 010277.1	YDL007W	the core 20S particle; Rpt2p	2	5.4173	0.2783	2325.67	2326.612	1	677.6	52.77778 F.EKKQEEEKKQLEEIRGNPL.S
		One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in								
		the degradation of ubiquitinated substrates; required for normal peptide hydrolysis by	2	4.00	0.0405	0000 40	0000 010		007.0	
gil6320197 [ref]NP_010277.1]	YDL007W	the core 205 particle; Rpt2p One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in	3	4.06	0.2105	2326.46	2326.612	1	907.8	40.27778 F.EKKQEEEKKQLEEIKGNPL.S
		the degradation of ubiquitinated substrates; required for normal peptide hydrolysis by								
gi 6320197 ref NP_010277.1	YDL007W	the core 20S particle; Rpt2p	2	5.0948	0.2677	2325.79	2326.612	1	794.7	55.555557 F.EKKQEEEKKQLEEIRGNPL.S
		Nucleolar protein, component of the small subunit processome complex, which is required for processing of pro-18S rPNA; has similarity to mammalian fibrillarin;								
gi 6320190 ref NP 010270.1	YDL014W	Nop1p	1	3.1481	0.4106	1356.59	1357.506	1	556.5	62.5 S.HVSDVVGPEGVVY.A
		Nucleolar protein, component of the small subunit processome complex, which is								
ail6220100/rofIND_010270_1		required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;	1	2 5566	0 2057	1071 45	1272 506	1	462.6	50 222222 S H2\/4 C4D4\/4\/4 C1D4E4C4\/4\/4 V4 A
gil0320190/10/10/02/0.1	TDL014W	Nucleolar protein, component of the small subunit processome complex, which is		3.0000	0.3937	1371.43	1372.500		403.0	56.555552 S.H5V151D1V1V161F1E161V1V111.A
		required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;								
gi 6320190 ref NP_010270.1	YDL014W	Nop1p	2	3.4345	0.2221	1331.61	1330.61	1	1346.1	77.27273 L.DELFIAPGKKVL.Y
		Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;								
gi 6320190 ref NP_010270.1	YDL014W	Nop1p	2	3.3134	0.2667	2058.21	2059.249	5	288.3	50 L.EQLTLEPYERDHCIVVG.R
		Nucleolar protein, component of the small subunit processome complex, which is								
		required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;	2	4 2005	0.0074	4000.04	4000 044		000.0	
gilo320190/rei/NP_010270.1/	TDL014W	Nucleolar protein, component of the small subunit processome complex, which is	2	4.3085	0.3971	1900.01	1968.214	1	000.3	55.66235 K.RISVEEPSKEDGVPPTKV.E
		required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;								
gi 6320190 ref NP_010270.1	YDL014W	Nop1p	3	4.3563	0.2858	2285.42	2285.506	5	704.1	36.842106 K.R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1.R
		Nucleolar protein, component of the small subunit processome complex, which is required for processing of pro-18S rPNA; has similarity to mammalian fibrillarin;								
ail6320190/refINP 010270.11	YDL014W	Nop1p	1	2.6533	0.1583	1344.63	1345.582	6	567.1	62.5 M.GGLDELFIAPGKK.V
5111 - 1		Nucleolar protein, component of the small subunit processome complex, which is								
- 100004001- (IND-040070-4)		required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;		1 00 15	0.0404	4575 40	4574 074		000 0	
gi 6320190 ret NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is	2	4.6915	0.2134	1575.43	1574.874	2	982.6	/1.4285/ M.G1G1L1D1E1L1F1I1A1P1G1K2K2V1L1.Y
		required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;								
gi 6320190 ref NP_010270.1	YDL014W	Nop1p	2	3.7973	0.2928	1556.87	1557.874	1	979.8	71.42857 M.GGLDELFIAPGKKVL.Y
		Nucleolar protein, component of the small subunit processome complex, which is								
gil6320190/refINP 010270.11	YDL014W	Nop1p	1	3.5841	0.3017	1556.61	1557.874	1	883.9	60.714287 M.GGLDELFIAPGKKVL.Y
31		Nucleolar protein, component of the small subunit processome complex, which is								
		required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;		0.4000	0.0404	4075 00	1075 077		500.4	
gil6320190/ref/NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is	2	3.1639	0.3421	1875.89	1875.277	1	528.4	50 A.GIM@GGLDELFIAPGKKVL.Y
		required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;								
gi 6320190 ref NP_010270.1	YDL014W	Nop1p	1	2.7299	0.1556	1447.55	1448.591	1	153.4	54.545456 V.E1F1S1H3R4P1G1R4E1L1I1S1.M
		Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA: has similarity to mammalian fibrillarity.								
gi 6320190 ref NP_010270.1	YDL014W	Nop1p	3	4.276	0.2799	2443.64	2445.693	1	709.7	35 K.R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4.V
=		Nucleolar protein, component of the small subunit processome complex, which is								
ail63201001rofIND_010270_11		required tor processing of pre-18S rRNA; has similarity to mammalian fibrillarin;	1	2 5284	0.250	1526.63	1527 722	1	250.3	54 166668 & VEESHROGREUS M
91002010010110F_010270.1	10101411	nohih	'	2.0204	0.209	1020.00	1321.123		200.0	GT. TOUGO A. YET OTHAT ONLEIG.IM

		Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA: has similarity to mammalian fibrillarin:								
gi 6320190 ref NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is	1	2.4023	0.2381	1579.68	1580.783	1	123.8	54.166668 V.E1F1S1H3R4P1G1R4E1L1I1S1M1.A
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-185 rKNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein, component of the small subunit processome complex, which is	1	2.6584	0.3057	1378.51	1379.643	5	210.7	54.545456 K.KRPNIIPIIEDA.R
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein, component of the small subunit processome complex, which is	2	3.1836	0.37	1811.51	1812.027	1	697.5	56.25 R.ISVEEPSKEDGVPPTKV.E
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein, component of the small subunit processome complex, which is	2	4.4235	0.4511	2260.11	2260.506	1	1047	65.789474 R.ISVEEPSKEDGVPPTKVEYR.V
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein. component of the small subunit processome complex, which is	2	4.0209	0.2831	1346.33	1345.582	1	1275.5	70.83333 M.GGLDELFIAPGKK.V
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein, component of the small subunit processome complex, which is	2	2.9435	0.1501	1844.53	1845.031	1	361.9	46.42857 L.TLEPYERDHCIVVGR.Y
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nuclealar protein, component of the small subunit processome complex, which is	1	3.7539	0.3036	1558.96	1557.874	1	882.2	57.14286 M.GGLDELFIAPGKKVL.Y
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Jurdapt rotation component of the email subwit processions complex, which is Jurdapt rotation component of the email subwit processions complex, which is	1	3.8574	0.198	1577.01	1574.874	1	895.3	57.14286 M.G1G1L1D1E1L1F1I1A1P1G1K2K2V1L1.Y
gi 6320190 ref NP_010270.1	YDL014W	required or processing of pre-ISS rRNA; has similarity to mammalian fibrillarin; Nop1p	2	4.3082	0.2863	1559.39	1557.874	1	791.3	67.85714 M.GGLDELFIAPGKKVL.Y
gi 6320190 ref NP_010270.1	YDL014W	Nucleolar protein, component or the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p	2	3.2395	0.1749	1894.15	1895.277	1	335.1	47.058823 A.G1I1M\$G1G1L1D1E1L1F1I1A1P1G1K2K2V1L1.Y
gi 6320190 ref NP_010270.1	YDL014W	Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p	3	4.0793	0.2316	1968.53	1968.214	1	1077.5	47.058823 K.RISVEEPSKEDGVPPTKV.E
ai 6320190 ref NP 010270.1	YDL014W	Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Noo10	2	4.1932	0.3297	2415.77	2416.693	1	443.9	45 K.RISVEEPSKEDGVPPTKVEYR.V
gil6320190/refINP_010270.1	YDL014W	Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Non1n	2	4,9708	0.3094	2445.53	2445.693	1	760	55 K R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4 V
ail6320190/refINP_010270_1		Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Non1o	3	5 7125	0.4133	2444 99	2445 693	1	1081.2	41 25 K R4/151/1E1E1P151K2E1D1G1//1P1P1T1K2//1E1Y1R4 V
	VDL 04 4W	Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;	3	0.0045	0.9400	2444.55	2445.055	1	044.0	
gij6320190[ref]NP_010270.1]	YDL014W	NOP1P Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;	1	2.2845	0.2496	1151.55	1152.299	1	214.2	66.66667 F.SHKPGKELIS.M
gi 6320190 ref NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;	1	2.546	0.2747	1558.85	1559.783	1	173.4	58.333332 V.EFSHRPGRELISM.A
gi 6320190 ref NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin;	2	4.5502	0.4275	2059.59	2060.268	1	1296.9	70.588234 S.VEEPSKEDGVPPTKVEYR.V
gi 6320190 ref NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA: has similarity to mammalian fibrillarin:	2	4.6463	0.4182	2082.55	2083.268	1	798.1	61.764706 S.V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4.V
gi 6320190 ref NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-185 rPNA: bas similarity to mammalian fibrillaring	2	4.1612	0.1711	1358.73	1360.582	9	1005.8	62.5 M.G1G1L1D1E1L1F1I1A1P1G1K2K2.V
gi 6320190 ref NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is required for second on a for a 192 FBMA bac similarity to ensome long file filtering	1	3.6941	0.2131	1575.78	1574.874	1	1018.9	60.714287 M.G1G1L1D1E1L1F1I1A1P1G1K2K2V1L1.Y
gi 6320190 ref NP_010270.1	YDL014W	Nop1p Nucleolar protein, component of the small subunit processome complex, which is	1	3.7963	0.2446	1559.26	1557.874	1	954.7	64.28571 M.GGLDELFIAPGKKVL.Y
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-185 rKNA; has similarity to mammalian fibriliarin; Nop1p Nucleolar protein, component of the small subunit processome complex, which is	1	2.4559	0.2255	1227.58	1228.353	4	179.7	61.11111 V.EFSHRPGRELI
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein, component of the small subunit processome complex, which is	2	3.98	0.2847	2416.61	2416.693	1	493.8	47.5 K.RISVEEPSKEDGVPPTKVEYR.V
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein, component of the small subunit processome complex, which is	2	4.7384	0.241	2447.27	2445.693	1	785.1	57.5 K.R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4.V
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein, component of the small subunit processome complex, which is	3	4.4733	0.3071	2416.52	2416.693	1	765	36.25 K.RISVEEPSKEDGVPPTKVEYR.V
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nucleolar protein. component of the small subunit processome complex, which is	2	3.3084	0.2561	1557.71	1557.874	2	496.1	53.571426 M.GGLDELFIAPGKKVL.Y
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Nuclealar protein, component of the small subunit processome complex, which is	1	2.6744	0.2331	1428.6	1428.591	1	213	63.636364 V.EFSHRPGRELIS.M
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p Jurdapter protein component of the email subwit processors complex which is	1	2.7233	0.2325	1547.65	1548.723	2	186.7	45.833336 A.V1E1F1S1H3R4P1G1R4E1L1I1S1.M
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p	1	2.4528	0.1901	1169.3	1170.299	1	219.1	66.66667 F.S1H3R4P1G1R4E1L1I1S1.M
gi 6320190 ref NP_010270.1	YDL014W	required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p	1	3.7422	0.3557	1597.56	1598.896	1	322.9	61.538464 M.A1K2K2R4P1N2I1I1P1I1I1E1D1A1.R

gi 6320190 ref NP_010270.1	YDL014W	Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p	1	3.1587	0.3432	1578.97	1578.896	1	243.8	53.846157 M.AKKRPNIIPIIEDA.R
gi 6320189 ref NP_010269.1	YDL015C	Enoyl reductase that catalyzes the last step in each cycle of very long chain fatty acid elongation, localizes to the ER, highly enriched in a structure marking nuclear- vacuolar junctions, coimmunoprecipitates with elongases Fen1p and Sur4p; Tsc13p	1	2.9198	0.1924	1285.72	1285.57	1	465.1	65 S.KKPTLDDVLKK.I
gi 6320189 ref NP_010269.1	YDL015C	Enoyl reductase that catalyzes the last step in each cycle of very long chain fatty acid elongation, localizes to the ER, highly enriched in a structure marking nuclear- vacuolar junctions, coimmunoprecipitates with elongases Fen1p and Sur4p; Tsc13p	2	3.8736	0.3933	1533.67	1531.841	1	541.8	70.83333 K.IRVPLNQGIFNLF.V
gi 6320189 ref NP_010269.1	YDL015C	Enoyl reductase that catalyzes the last step in each cycle of very long chain fatty acid elongation, localizes to the ER, highly enriched in a structure marking nuclear- vacuolar junctions, coimmunoprecipitates with elongases Fen1p and Sur4p; Tsc13p	1	2.5171	0.2729	1487.53	1485.808	1	341.7	54.166668 S.KKPTLDDVLKKIS.A
gi 6320189 ref NP_010269.1	YDL015C	Encyl reductase that catalyzes the last step in each cycle of very long chain fatty acid elongation, localizes to the ER, highly enriched in a structure marking nuclear vacuolar junctions, coimmunoprecipitates with elongases Fen1p and Sur4p; Tsc13p Member of an oxysterol-binding protein family with seven members in S. cerevisiae;	1	3.1752	0.1996	1299.66	1300.57	1	621.9	70 S.K2K2P1T1L1D1D1V1L1K2K2.I
gi 6320185 ref NP_010265.1	YDL019C	family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability; Osh2p Member of an oxysterol-binding protein family with seven members in S. cerevisiae:	2	3.3857	0.3227	1609.79	1608.878	1	714.6	61.538464 K.R4V1A1K2P1F1N2P1L1L1G1E1T1F1.E
gi 6320185 ref NP_010265.1	YDL019C	family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability; Osh2p Member of an oxysterol-binding protein family with seven members in S. cerevisiae;	2	2.9827	0.26	1649.33	1647.754	2	324.5	58.333332 K.RRDHDLKDCGDIF
gi 6320185 ref NP_010265.1	YDL019C	family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability; Osh2p Member of an oxysterol-binding protein family with seven members in S. cerevisiae;	2	3.2882	0.2562	1596.99	1596.698	1	842.2	68.181816 T.WTESPRWDFWGE.S
gi 6320185 ref NP_010265.1	YDL019C	family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability; Osh2p	2	3.9648	0.3285	1615.29	1614.698	1	930.2	72.72727 T.W2T1E1S1P1R4W2D1F1W2G1E1.S
gi 6320181 ref NP_010262.1	YDL022W	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high- osmolarity glycerol response pathway; homolog of Gpd2p; Gpd1p	2	5.0606	0.454	2339.37	2341.59	1	1508.4	63.88889 N.N2Y1P1M1K2N2L1P1D1M111E1E1L1D1L1H3E1D1
gi 6320181 ref NP_010262.1	YDL022W	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high- osmolarity glycerol response pathway; homolog of Gpd2p; Gpd1p	2	3.1093	0.1885	3168.83	3170.67	1	284.5	30.357143 K.YLPGITLPDNLVANPDLIDSVKDVDIIVF.N
gi 6320181 ref NP_010262.1	YDL022W	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high- osmolarity glycerol response pathway; homolog of Gpd2p; Gpd1p	3	4.641	0.3613	1420.73	1420.695	1	1303.7	56.81818 A.I1Q2R4V1G1L1G1E1111R4F1.G
gi 6320181 ref NP_010262.1	YDL022W	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high- osmolarity glycerol response pathway; homolog of Gpd2p; Gpd1p	2	3.9131	0.3781	1811.17	1812.001	1	1375.8	71.42857 M.KNLPDMIEELDLHED
gi 6320181 ref NP_010262.1	YDL022W	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high- osmolarity glycerol response pathway; homolog of Gpd2p; Gpd1p	3	4.6795	0.2867	2340.98	2341.591	2	780.5	37.5 N.N2Y1P1M1K2N2L1P1D1M1I1E1E1L1D1L1H3E1D1
gi 6320181 ref NP_010262.1	YDL022W	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high- osmolarity glycerol response pathway; homolog of Gpd2p; Gpd1p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	4.0799	0.2555	2075.73	2077.351	1	959.1	52.77778 Q.N2V1K2Y1L1P1G1I1T1L1P1D1N2L1V1A1N2P1D1.L
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2(3 complex, which is a highly conserved actin	2	4.7787	0.4572	2944.75	2945.221	1	740.3	46 G.QERFEAPECLFQPGLVDVEQPGVGEL.L
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp27 complex, which is a highly conserved actin	2	2.9779	0.2482	1713.31	1713.887	2	417.2	57.14286 G.RAGENFPDYTFPSIV.G
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2(3 complex, which is a highly conserved actin	3	4.2019	0.2875	2978.21	2977.221	1	1304.4	37 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1.L
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp23 complex, which is a highly conserved actin	2	4.7574	0.4585	2977.59	2977.221	1	738.9	44 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1.L
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	4.7593	0.414	2817.81	2817.091	1	607.5	45.833336 Q.ERFEAPECLFQPGLVDVEQPGVGEL.L
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	4.5605	0.4663	2846.29	2847.091	1	449.1	39.583336 Q.E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1.L
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2(3 complex, which is a highly conserved actin	3	5.4247	0.3867	3091.46	3091.381	1	1160.4	36.53846 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp23 complex which is a bibly conserved actin	2	4.6258	0.4388	3090.69	3091.381	1	635.4	38.46154 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Ap2p Essential component of the Ap2/3 complex, which is a highly conserved actin	2	4.0192	0.2423	3056.07	3058.381	1	586	36.53846 G.QERFEAPECLFQPGLVDVEQPGVGELL.F
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp27 complex, which is a highly conserved actin	1	2.7225	0.2521	1523.86	1522.739	1	676.1	53.571426 Q.PGLVDVEQPGVGELL.F
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp23 complex, which is a highly conserved actin	2	5.3952	0.4864	2959.29	2961.25	1	556.4	40 Q.E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	3	4.7011	0.2264	3058.73	3058.381	1	1075.7	34.615387 G.QERFEAPECLFQPGLVDVEQPGVGELL.F

		Example a second state to a second								
gi 6320175 ref NP_010255.1	YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	2	4.6793	0.3989	2687.15	2687.975	1	934.5	54.347824 E.RFEAPECLFQPGLVDVEQPGVGEL.L
gi 6320175 ref NP_010255.1	YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	3	4.9304	0.3135	2930.96	2930.25	1	1131.3	38 Q.ERFEAPECLFQPGLVDVEQPGVGELL.F
		Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in								
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin puckation conter required for the motility and identity of actin patcher; involved in	2	5.5018	0.5628	2927.91	2930.25	1	858.7	46 Q.ERFEAPECLFQPGLVDVEQPGVGELL.F
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity. Arp2n Essential component of the Arp2/3 complex, which is a highly conserved actin	2	3.6517	0.3882	3107.37	3109.427	1	259.1	26.923079 Q.E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1F1.N
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	4.0137	0.4024	3078.63	3077.427	1	488.4	34.615387 Q.ERFEAPECLFQPGLVDVEQPGVGELLF.N
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	4.7175	0.437	2948.49	2948.311	1	634.9	40 E.RFEAPECLFQPGLVDVEQPGVGELLF.N
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	2	3.5253	0.1645	1681.37	1681	3	521.3	61.538464 S.M1Y1P1G1L1P1S1R4L1E1K2E1L1K2.Q
gi 6320175 ref NP_010255.1	YDL029W	essential component or the Arg22 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arg2p	3	4.8235	0.3154	3089.24	3091.381	1	971.7	32.692307 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
ail63201751refINP_010255.11	YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocritosis and membrane growth and polarity: Arp2n	2	3.3954	0.3174	3090.55	3091.381	1	270.7	28.846153 G.02E1R4F1E1A1P1E1C1L1E102P1G1L1V1D1V1E102P1G1V1G1E1L1L1 F
		Essential component of the Arp2/2 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in	-							
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in	2	4.7309	0.4767	2929.63	2930.25	1	596.6	40 Q.ERFEAPECLFQPGLVDVEQPGVGELL.F
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin puckation conter required for the motility and identity of actin patches; involved in	2	4.9136	0.5023	2718.59	2716.975	1	605.8	45.652176 E.R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1.L
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity. Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	4.7449	0.466	2800.81	2801.135	1	1054.1	52.083332 E.RFEAPECLFQPGLVDVEQPGVGELL.F
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/2 complex, which is a highly conserved actin	2	5.2813	0.3732	2831.07	2831.135	1	725.5	45.833336 E.R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	3	4.0367	0.2975	2831.15	2831.135	1	994.1	30.208334 E.R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp/3 complex which is a biply conserved actin	3	4.4436	0.3636	2802.11	2801.135	1	1151.9	35.416664 E.RFEAPECLFQPGLVDVEQPGVGELL.F
gi 6320175 ref NP_010255.1	YDL029W	ucleation conter required for the onlyze complex, which is a highly conserver actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	3	4.5293	0.2511	2981.93	2979.311	1	982.4	33 E.R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1F1.N
gi 6320175 ref NP_010255.1	YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	3	3.8666	0.2111	2947.34	2948.311	1	844.1	30.000002 E.RFEAPECLFQPGLVDVEQPGVGELLF.N
ail6320175 refINP 010255.1	YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocvtosis and membrane growth and polarity: Arp2p	2	5.4073	0.4286	2275.91	2277.562	1	406.3	44.736843 G.R4A1G1E1N2F1P1D1Y1T1F1P1S1I1V1G1R4P1I1L1.R
		Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in concentration and morphysica struttly and calculate and action action and action action and action acti	2	E 2967	0 4711	2606 20	2606 044	1	226.9	
giloszo i / siterine_010255.1	TDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in	3	5.3807	0.4711	2000.39	2000.944	I	330.0	20.40309 G.RAGENEEDTTEESIVGREILKAE.E
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in	2	3.4091	0.3113	1966.37	1966.244	1	714.7	53.125 G.ENFPDYTFPSIVGRPIL.R
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin puckation conter required for the motility and identity of actin patches; involved in	2	3.7485	0.3963	2023.25	2023.296	2	657.3	47.058823 A.GENFPDYTFPSIVGRPIL.R
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity. Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	4.016	0.2509	1987.07	1987.244	1	633.6	53.125 G.E1N2F1P1D1Y1T1F1P1S1I1V1G1R4P1I1L1.R
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	3.0697	0.1595	1734.97	1732.887	1	385.2	50 G.R4A1G1E1N2F1P1D1Y1T1F1P1S1I1V1.G
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	3.1139	0.3004	2701.87	2702.946	1	254.4	34.782608 G.QERFEAPECLFQPGLVDVEQPGVG.E
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	3	3.83	0.1604	3093.35	3091.381	1	729.4	28.846153 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
gi 6320175 ref NP_010255.1	YDL029W	Essential component of the Arp22 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	2	5.1027	0.3947	2830.45	2831.135	1	901.8	50 E.R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
gi 6320175 ref NP_010255.1	YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	3	4.673	0.1718	2830.85	2831.135	1	801.4	32.291664 E.R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.F
ail6320175/refINP 010255 1	YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocvtosis and membrane growth and polarity: Am2n	3	4,2876	0,1575	2799.89	2801.135	1	1124	34.375 E.RFEAPECLFQPGLVDVEQPGVGF11_F
gil6320175/refINP_010255_1	YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocrytosis and membrane growth and polarity: Arp2n	2	4.6846	0.3552	3089 33	3091 381	1	482.8	34 615387 G 0251R45151A19151C111510291G111V1D1V1510291G1V1015111115
		Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in	-					·		
gi 6320175 ref NP_010255.1	YDL029W	endocytosis and membrane growth and polarity; Arp2p	2	4.8475	0.3959	2800.75	2801.135	1	937.5	50 E.RFEAPECLFQPGLVDVEQPGVGELL.F

		Essential component of the Arp2/3 complex, which is a highly conserved actin								
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	4.5942	0.3447	2249.57	2250.562	1	422.2	44.736843 G.RAGENFPDYTFPSIVGRPIL.R
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity: Ap2p Essential component of the Arp2/3 complex, which is a highly conserved actin	2	3.2612	0.2041	1902.71	1903.29	1	608.3	53.333336 S.MYPGLPSRLEKELKQL.W
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Essential component of the Arp2/3 complex, which is a highly conserved actin	3	4.1846	0.3432	2437.22	2437.75	4	387.2	28.75 G.R4A1G1E1N2F1P1D1Y1T1F1P1S1I1V1G1R4P1I1L1R4.A
gi 6320175 ref NP_010255.1	YDL029W	nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p Plasma membrane G protein coupled receptor (GPCR) that interacts with the heterotimeric G protein alpha subunit, Gpa2p, and with Plc1p; sensor that integrates	3	6.1673	0.4947	2640.77	2639.944	1	714.6	35.227272 G.R4A1G1E1N2F1P1D1Y1T1F1P1S1I1V1G1R4P1I1L1R4A1E1.E
gi 6320170 ref NP_010249.1	YDL035C	nutritional signals with the modulation of cell fate via PKA and cAMP synthesis; Gpr1p Plasma membrane G protein coupled receptor (GPCR) that interacts with the heterotrimetic G protein alpha subunit Gpa2p, and with Plc1p; sensor that integrates	2	4.1972	0.354	1910.37	1911.215	1	674.4	55.88235 Y.L1V1K2P1T111P1G1T1T1P1D1P11111E1A1Q2.N
gi 6320170 ref NP_010249.1	YDL035C	nutritional signals with the modulation of cell fate via PKA and cAMP synthesis; Gpr1p Plasma membrane G protein coupled receptor (GPCR) that interacts with the	3	4.6231	0.2974	3465.53	3464.705	1	707.8	24.13793 Y.AMSEQPDLERNNPFDCENDITLNPSELVSK.Q
gi 6320170 ref NP_010249.1	YDL035C	heterotimmeric G protein alpha subunit, Gpa2p, and with PIc1p; sensor that integrates nutritional signals with the modulation of cell fate via PKA and cAMP synthesis; Gpr1p Plasma membrane G protein coupled receptor (GPCR) that interacts with the	2	3.7753	0.3189	1949.51	1951.086	1	681.8	53.333336 N.N2Y1N2F1P1D1S1P1R4Q2G1G1Y1K2P1W2.S
gi 6320170 ref NP_010249.1	YDL035C	heterotrimeric G protein alpha subunit, Gpa2p, and with PIc1p; sensor that integrates nutritional signals with the modulation of cell fate via PKA and cAMP synthesis; Gpr1p	2	3.1893	0.3825	1920.01	1920.277	1	335.6	53.125 H.HIPMLGGIDLDELNRLL.K
ail63201701refINP_010249.11	YDL035C	Plasma membrane G protein coupled receptor (GPCR) that interacts with the heterotrimeric G protein alpha subunit, Gpa2p, and with Plc1p; sensor that integrates nutritional signals with the modulation of cell fate via PKA and cAMP synthesis; Gor1p.	2	3.4913	0.2883	1890.51	1891,215	1	585	52.941177 Y LVKPTIPGTTPDPIIEAQ N
9 (GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), swithesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall								
gi 6320148 ref NP_010228.1	YDL055C	bijnindeze Gerinden och att and and an	2	4.0496	0.3176	2218.93	2219.564	1	703.2	45.238094 T.A1K2I1G1P1D1V1V111G1P1N2V1T111G1D1G1V1R4I1T1.R
gi 6320148 ref NP_010228.1	YDL055C	synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	2	3.0402	0.2405	2191.89	2192.564	3	290	38.095238 T.AKIGPDVVIGPNVTIGDGVRIT.R
gi 6320148 ref NP_010228.1	YDL055C	GUP-mannose pyrophosphorylase (mannose-1-phosphate guanylitransterase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	2	3.0263	0.2748	1179.99	1180.39	1	878.7	72.72727 T.AKIGPDVVIGPN.V
gi 6320148 ref NP_010228.1	YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	2	3.9724	0.4117	2086.59	2087.387	1	666.2	46.875 T.S1I1E1K2E1T1F1P1I1L1V1E1E1K2Q2L1Y1.S
gi 6320148 ref NP_010228.1	YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	3	4.7188	0.2377	3436.25	3437.025	1	623.5	25.892857 G.L1Y111L1N2P1E1V111D1L111E1M\$K2P1T1S111E1K2E1T1F1P111L1V1E1.E
gi 6320148 ref NP_010228.1	YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	1	2.4784	0.1698	1404.31	1405.631	4	417.7	54.545456 T.SIEKETFPILVE.E
gi 6320148 ref NP_010228.1	YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	2	3.6922	0.1654	1408.23	1405.631	2	937	77.27273 T.SIEKETFPILVE.E
gi 6320148 ref NP_010228.1	YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	2	3.0716	0.1568	1535.35	1534.747	1	1149.5	70.83333 T.SIEKETFPILVEE.K
gi 6320148 ref NP_010228.1	YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	1	2.556	0.2534	1422.27	1423.626	1	479.4	59.090908 F.WMDVGQPKDFLS.G
gi 6320148 ref NP_010228.1	YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	1	3.5189	0.2982	1471.49	1472.654	1	472.2	62.5 K.D1E1I1Y1I1N2G1G1K2V1L1P1H3.K
gij6320148 ref NP 010228.1	YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	2	3.0564	0.157	2019.63	2021.417	2	326.7	40.625 G.L1Y111L1N2P1E1V111D1L111E1M1K2P1T1.S
ail6320148/refINP_010228.1	YDI 055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis: ranuired for normal cell wall structure: Psath	2	3 2148	0 2771	1545.03	1545 835	2	516.7	
8-15520 Hoponiai _010220.1	.22000	GDP-mannose prophosphorylase (mannose-1-phosphate guanyltransferase), evaluationse GDP-mannose from GTP and mannose it showshots in coll well	2	0.2140	0.2771		10.000	2	0.0.1	
gi 6320148 ref NP_010228.1	YDL055C	biosynthesis; required for normal cell wall structure; Psa1p	2	3.3495	0.2367	2004.89	2002.417	2	580.1	50 G.LYILNPEVIDLIEMKPT.S
gi 6320143 ref NP_010223.1	YDL060W	rougen required for processing of 205 pre-rKNA in the cytoplasm, associates with pre-40S ribosomal particles; Tsr1p	3	4.1637	0.3182	4221.68	4220.24	1	410.5	21.323528 E.QDNEEVAGDEEYDIEDNEGFEELSPEEEERQLREF.R
gi 6320143 ref NP_010223.1	YDL060W	pre-40S ribosomal particles; Tsr1p Protein required for processing of 20S pre-rRNA in the cytoplasm, associates with	2	3.305	0.3422	1315.49	1316.502	1	746.9	85 N.RLVHIPDFGDF.Q F. 02D1N2F4511/141G1D1F1511/1D11451D1N251G154545454545454545454
gi 6320143 ref NP_010223.1	YDL060W	pre-40S ribosomal particles; Tsr1p Pre-40S ribosomal particles; Tsr1p Pretain reguined for processing of 20S pro-rBNA in the extension processing with	3	4.1251	0.315	4264.31	4265.24	1	463.1	19.117647 Q2L1R4E1F1.R
gi 6320143 ref NP_010223.1	YDL060W	pre-40S ribosomal particles; Tsr1p	2	3.7984	0.3072	1330.79	1332.502	1	751.8	85 N.R4L1V1H3I1P1D1F1G1D1F1.Q

gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; ldp1p	2	3.0848	0.3189	1488.69	1487.662	1	739.6	70.83333 L.LKRGELDNTPALC.K
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; ldp1p	2	3.3915	0.2275	1659.65	1657.874	1	624.9	64.28571 R.GLLKRGELDNTPALC.K
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; ldp1p	2	5.539	0.3703	2399.59	2399.742	1	689	57.894737 K.V1K2Q2P1V1V1E1L1D1G1D1E1M1T1R4I111W2D1K2.I
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p	2	5.197	0.3439	2374.75	2372.742	1	490.8	47.368423 K.VKQPVVELDGDEMTRIIWDK.I
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p	3	4.1369	0.2352	2398.01	2399.742	2	365.3	31.578945 K.V1K2Q2P1V1V1E1L1D1G1D1E1M1T1R4I1I1W2D1K2.I
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p	2	4.6392	0.408	2641.45	2644.075	1	943.4	52.380955 K.V1K2Q2P1V1V1E1L1D1G1D1E1M1T1R4I1I1W2D1K2I1K2.K
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p	2	2.9196	0.1945	2257.83	2258.638	3	253.3	36.11111 Q.PVVELDGDEMTRIIWDKIK.K
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p	2	5.3258	0.3774	2399.49	2399.742	1	619.7	52.63158 K.V1K2Q2P1V1V1E1L1D1G1D1E1M1T1R4I1I1W2D1K2.I
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p	2	5.0891	0.4372	2128.63	2129.479	1	1400.2	70.588234 K.VKQPVVELDGDEMTRIIW.D
gi 6320137 ref NP_010217.1	YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p	2	4.9994	0.3293	2153.49	2153.479	1	905.3	61.764706 K.V1K2Q2P1V1V1E1L1D1G1D1E1M1T1R4I111W2.D
gi 6320128 ref NP_010208.1	YDL075W	Protein component of the large (60S) nbosomal subunit, nearly identical to KpI31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; RpI31ap Protein component of the large (60S) ribosomal subunit, nearly identical to RpI31Bp	2	4.1448	0.1894	1857.55	1858.999	2	937.9	67.85714 S.R4K2R4N2E1E1E1D1A1K2N2P1L1F1S1.Y
gi 6320128 ref NP_010208.1	YDL075W	and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; Rpl31ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin	2	4.817	0.2384	2021.65	2023.175	1	1175.8	66.66667 S.R4K2R4N2E1E1E1D1A1K2N2P1L1F1S1Y1.V
gi 6320128 ref NP_010208.1	YDL075W	Sxm1p; Rpl31ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin	2	4.0034	0.3651	1748.83	1746.921	1	1127.8	80.769226 S.RKRNEEEDAKNPLF.S
gi 6320128 ref NP_010208.1	YDL075W	Sxm1p; Rpl31ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin	2	4.1782	0.2187	1771.65	1770.921	1	1031.7	76.92308 S.R4K2R4N2E1E1E1D1A1K2N2P1L1F1.S
gi 6320128 ref NP_010208.1	YDL075W	Component of the TREX complex required for nuclear mRNA export; DEAD-box RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p	2	4.0244	0.2944	1351.31	1348.466	1	794.1	00.00007 S.KARNEEEDANNPLFST.V 77.27273 F.V1S1S1K2E1D1E1E1V1L1A1K2.I
gi 6320119 ref NP_010199.1	YDL084W	Component of the TREX complex required for nuclear mRNA export; DEAD-box RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP65 Sub2p Component of the TREX complex required for nuclear mRNA export: DEAD-box	2	3.9857	0.2555	1864.41	1865.072	1	1679.8	82.14286 F.VIDECDKVLEELDMR.R
gi 6320119 ref NP_010199.1	YDL084W	RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p Component of the TREX complex required for nuclear mRNA export; DEAD-box	2	4.6613	0.4372	2126.95	2126.352	1	1503.6	68.75 K.NFVIDECDKVLEELDMR.R
gi 6320119 ref NP_010199.1	YDL084W	RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p Component of the TREX complex required for nuclear mRNA export; DEAD-box RNA helicase involved in early and late steps of spliceosome assembly; homolog of	3	4.2848	0.2296	3046.64	3047.343	5	402.2	28.260868 K.N2F1V111D1E1C1D1K2V1L1E1E1L1D1M1R4R4D1V1Q2E11F1.R
gi 6320119 ref NP_010199.1	YDL084W	the human splicing factor hUAP56; Sub2p Component of the TREX complex required for nuclear mRNA export; DEAD-box RNA helicase involved in early and late steps of spliceosome assembly; homolog of	3	4.121	0.2468	3359.27	3359.708	1	602.2	25 H.S1T1G1F1K2D1F1L1L1K2P1E1L1S1R4A11111D1C1G1F1E1H3P1S1E1V1Q2.Q
gi 6320119 ref NP_010199.1 gi 6320119 ref NP_010199.1	YDL084W YDL084W	the human splicing factor hUAP56; Sub2p Component of the TREX complex required for nuclear mRNA export; DEAD-box RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p	3	4.3347	0.2765	3323.3 1883.59	3322.708	1	400.3 1245.6	24.107143 H.STGFKDFLLKPELSRAIIDCGFEHPSEVQ.Q 71.42857 F.V111D1E1C1D1K2V1L1E1E1L1D1M1R4.R
gi 6320119 ref NP_010199.1	YDL084W	Component of the TREX complex required for nuclear mRNA export; DEAD-box RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p	3	4.1929	0.1727	1867.43	1865.072	1	976.2	48.214287 F.VIDECDKVLEELDMR.R
gi 6320119 ref NP_010199.1	YDL084W	Component of the TKEX complex required for nuclear mKNA export; DEAD-box RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p Component of the TKEX complex required for nuclear mRNA export; DEAD-box	2	3.3962	0.1679	1710.63	1708.884	1	735.9	69.230774 F.VIDECDKVLEELDM.R
gi 6320119 ref NP_010199.1	YDL084W	RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p Component of the TREX complex required for nuclear mRNA export; DEAD-box	3	4.1463	0.3267	2783	2783.063	2	791.9	35.714287 F.V1I1D1E1C1D1K2V1L1E1E1L1D1M1R4R4D1V1Q2E1I1F1.R
gi 6320119 ref NP_010199.1	YDL084W	rxvx neucase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-	1	2.3855	0.3645	1122.4	1123.297	1	421.3	66.66667 L.KNKDTAPHIV.V
gi 6320107 ref NP_010188.1	YDL095W	D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt2p in some conditions; target for new antifungals; Pmt1p	2	3.8716	0.3197	2034.31	2037.187	1	601.4	58.823532 E.G1D1G1P1S1Y1E1D1L1M1N2E1D1G1K2K2l1F1.K

gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	4.5112	0.2907	1702.37	1701.871	1	1004.7	78.57143 F.KDTEGNELDPEVVKK.M
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	3.7872	0.3142	1655.45	1653.83	1	1486.4	76.92308 K.RVEQDDPVPELDIK.Q
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	3.6553	0.3137	1780.77	1782.004	4	419.2	57.14286 Y.KRVEQDDPVPELDIK.Q
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	1	3.5598	0.2601	1285.58	1286.461	1	868.2	70 F.S1H3E1V1K2L1P1A1W2G1F1.E
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	1	3.4996	0.4073	1271.59	1271.461	1	880.6	70 F.SHEVKLPAWGF.E
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	3.3068	0.3399	1273.61	1271.461	1	1256	80 F.SHEVKLPAWGF.E
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	4.3647	0.2231	2016.41	2016.187	1	496.9	55.88235 E.GDGPSYEDLMNEDGKKIF.K
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	3.0253	0.222	1285.47	1286.461	1	1171.8	75 F.S1H3E1V1K2L1P1A1W2G1F1.E
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	1	3.1273	0.4242	1270.58	1271.461	1	865.4	70 F.SHEVKLPAWGF.E
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	3.5635	0.1697	1720.57	1719.802	2	627.6	60.714287 F.DGDANDDWVVEIDKK.N
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	1	2.3636	0.1633	1057.56	1058.242	9	274	68.75 H.E1V1K2L1P1A1W2G1F1.E
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	2.9281	0.2842	1341.67	1340.478	1	861	59.090908 D.SVVFDEVHFGGF.A
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	3.62	0.2247	1802.03	1803.004	9	431.1	53.571426 Y.K2R4V1E1Q2D1D1P1V1P1E1L1D111K2.Q
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	2	3.201	0.1686	1952.45	1953.211	1	461.7	53.125 N.S1N2P1L1L1P1E1D1T1K2R4I1S1Y1K2P1A1.S
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	1	3.4513	0.2842	1285.52	1286.461	1	725.3	65 F.S1H3E1V1K2L1P1A1W2G1F1.E
gi 6320107 ref NP_010188.1	YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p ATBece outputs of the CET complex required for the certicized of UDEL proteine	2	3.529	0.2216	1288.27	1286.461	1	1250.5	80 F.S1H3E1V1K2L1P1A1W2G1F1.E
gi 6320103 ref NP_010183.1	YDL100C	Arrase, subunit of the GET complex, required for the retrieval of hDEL proteins from the Gogli to the ER in an ERD2 dependent fashion; involved in resistance to heat and metal stress; Get3p ATPase, subunit of the GET complex; required for the retrieval of HDEL proteins	2	4.5805	0.3423	1708.09	1706.832	1	2075.4	87.5 K.K2Y1L1D1Q2I1D1E1L1Y1E1D1F1.H
gi 6320103 ref NP_010183.1	YDL100C	ATPase, subunit of the EX in an EXD2 dependent fashion; involved in resistance to heat and metal stress; Get3p ATPase, subunit of the GET complex; required for the retrieval of HDEL proteins	2	3.9658	0.3577	1821.47	1820.006	1	735.8	69.230774 Q.KKYLDQIDELYEDF.H
gi 6320103 ref NP_010183.1	YDL100C	from the Golgi to the ER in an ERD2 dependent fashion; involved in resistance to heat and metal stress; Get3p. ATPase, subunit of the GET complex; required for the retrieval of HDEL proteins	2	3.6202	0.2306	2175.99	2177.351	1	403.8	50 K.E1Y1N2P1I1T1D1G1K2V1I1Y1E1L1E1D1K2E1
gi 6320103 ref NP_010183.1	YDL100C	ATPase, subunit of the GET complex; required for the retrieval of HDEL proteins	2	3.7133	0.3177	2155.67	2155.412	1	715.9	56.25 Q.KKYLDQIDELYEDFHVV.K
gi 6320103 ref NP_010183.1	YDL100C	from the Golgi to the ER in an ERD2 dependent fashion; involved in resistance to heat and metal stress; Get3p	2	4.3073	0.3067	1835.55	1837.006	1	1271.1	73.07692 Q.K2K2Y1L1D1Q2I1D1E1L1Y1E1D1F1.H
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	1	2.2238	0.2689	1198.57	1198.402	9	320.3	50 R.KTPLEPGLELT.A
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	4.2387	0.3688	3200.69	3199.269	1	687.3	29.807693 H.WEGEPINREDEENNMNEVGYDDIGGCR.K
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	2.9405	0.3512	1873.85	1871.141	2	598	50 A.TRISVLPIADTIEGITGN.L

gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.7424	0.4533	3454.67	3455.573	1	973.8	29.464287 H.WEGEPINREDEENNMNEVGYDDIGGCRKQ.M
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.5724	0.2711	2306.75	2307.525	2	425.4	44.444447 L.D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.2948	0.4635	1788.69	1791.036	1	1139.8	62.5 T.R4I1S1V1L1P111A1D1T11E1G111T1G1N2.L
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.4835	0.178	1893.63	1893.141	1	980.6	55.88235 A.T1R4I1S1V1L1P1I1A1D1T1I1E1G1I1T1G1N2.L
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	4.379	0.2317	2843.48	2841.098	1	1293.2	34.375 W.DDVGGLDEIKEELKETVEYPVLHPD.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	6.5157	0.4204	3058.22	3058.311	1	1212.8	34 T.W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.1302	0.433	3025.09	3027.311	1	752.4	40 T.WDDVGGLDEIKEELKETVEYPVLHPD.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	4.662	0.3068	3349.85	3352.618	1	915.5	26.85185 T.W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1Q2Y1.T
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.53	0.4401	1814.35	1813.07	1	1416.9	66.66667 R.LGDLVTIHPCPDIKYA.T
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	2.9315	0.2588	1718.49	1717.91	1	596.9	53.571426 L.G1D1L1V1T111H3P1C1P1D111K2Y1A1.T
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.1651	0.2924	2837.6	2837.199	1	1548.7	36.363636 D.EIKEELKETVEYPVLHPDQYTKF.G
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.2635	0.3581	3057.75	3058.311	1	373.9	38 T.W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.7181	0.457	3693.59	3695.074	1	1008.8	26.666668 T.WDDVGGLDEIKEELKETVEYPVLHPDQYTKF.G
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	2.9662	0.2912	2489.49	2491.75	1	295.3	34.210526 K.E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1Q2Y1T1K2F1.G
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	6.633	0.4909	3733.73	3733.074	1	1769.6	T.W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1Q2Y1T1K2 35 F1.G
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.1087	0.2372	4110.62	4109.467	1	609.2	V.N2V1T1W2D1D1V1G1G1L1D1E111K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1Q2 20.588236 Y1T1K2F1G1.L
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	6.7615	0.5027	4052.15	4051.415	1	1487.2	V.N2V1T1W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1Q2 28.787878 Y1T1K2F1.G
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.3807	0.4039	2156.85	2155.477	1	993.4	52.63158 A.T1R411S1V1L1P111A1D1T111E1G111T1G1N2L1F1.D
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.2339	0.4539	2132.63	2131.477	1	1001.9	55.263157 A.TRISVLPIADTIEGITGNLF.D
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	4.5605	0.3177	2330.06	2329.618	1	1508.7	41.25 F.GRFDREVDIGIPDATGRLEVL.R
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.1862	0.2863	2329.79	2329.618	1	353.4	45 F.GRFDREVDIGIPDATGRLEVL.R
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.26	0.1953	2012.37	2015.211	1	365.1	52.941177 F.G1R4F1D1R4E1V1D111G111P1D1A1T1G1R4L1.E
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	3.8129	0.2259	1989.05	1988.211	1	1093.4	44.11765 F.GRFDREVDIGIPDATGRLE

gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.	5088	0.2322	1626.75	1628.927	1	569.6	62.5 R.E1M1V1E1L1P1L1R4H3P1Q2L1F1.K
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3	3.006	0.3049	2358.53	2359.618	1	284.8	37.5 F.G1R4F1D1R4E1V1D111G11P1D1A1T1G1R4L1E1V1L1.R
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	1	3.0	.0143	0.2486	1365.73	1366.619	3	276.5	60.000004 M.V1E1L1P1L1R4H3P1Q2L1F1.K
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	1	2.	5596	0.3146	1348.58	1349.619	2	290.6	60.000004 M.VELPLRHPQLF.K
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	1	2.8	8158	0.2537	1467.71	1467.749	4	303.8	50 Q.LRKTPLEPGLELT.A
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	4.1	1853	0.26	2144.33	2144.479	1	616.6	34.210526 A.RAAAPTVVFLDELDSIAKAR.G
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	7.4	4652	0.2515	2171.39	2171.479	1	2625.9	50 A.R4A1A1A1P1T1V1V1F1L1D1E1L1D1S1I1A1K2A1R4.G
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	1	2.2	2031	0.249	1514.06	1514.635	1	311.5	57.692307 F.DREVDIGIPDATGR.L
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.4	4625	0.2591	1647.57	1648.795	1	838.5	67.85714 F.D1R4E1V1D111G111P1D1A1T1G1R4L1.E
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.9	9146	0.2659	1626.85	1627.795	1	1220.8	78.57143 F.DREVDIGIPDATGRLE
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.5	.5403	0.4895	1768.83	1770.036	1	1078.1	62.5 T.RISVLPIADTIEGITGN.L
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.3	3486	0.2672	1594.53	1595.815	1	646.4	57.692307 R.L1G1D1L1V1T111H3P1C1P1D111K2.Y
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.4	4218	0.2355	1577.81	1578.815	1	774.7	65.38461 R.LGDLVTIHPCPDIK.Y
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.1	2654	0.227	1913.41	1914.175	1	562.2	50 R.LGDLVTIHPCPDIKYAT.R
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.0	6834	0.265	1833.89	1832.07	1	894.6	56.666668 R.L1G1D1L1V1T111H3P1C1P1D111K2Y1A1.T
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.2	2172	0.3766	3056.23	3058.311	1	276.3	34 T.W2D1D1V1G1G1L1D1E111K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.1	1809	0.3489	3340.94	3341.653	1	949	28.57143 V.NVTWDDVGGLDEIKEELKETVEYPVLHPD.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.1	1785	0.2658	2051.99	2053.372	3	324.8	36.11111 T.R4I1S1V1L1P1I1A1D1T111E1G1I1T1G1N2L1F1.D
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.0	6453	0.4045	2946.17	2945.141	1	1090.6	34 H.RQHEAEKEVKVEGEDVEMTDEGAKAE.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	6.2	2993	0.4233	3377.27	3376.653	1	825.2	28.57143 V.N2V1T1W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	6	6.048	0.4062	4009.19	4009.415	1	1287.9	27.272728 V.NVTWDDVGGLDEIKEELKETVEYPVLHPDQYTKF.G
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.9	5128	0.327	2816.71	2816.026	1	930	43.75 H.RQHEAEKEVKVEGEDVEMTDEGAKA.E
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.2	2272	0.3912	2847.89	2850.026	1	1521.1	35.416664 H.R4Q2H3E1A1E1K2E1V1K2V1E1G1E1D1V1E1M1T1D1E1G1A1K2A1.E

gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.1666	0.2446	2328.53	2329.618	1	406.9	45 F.GRFDREVDIGIPDATGRLEVL.R
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	4.1621	0.3176	3058.25	3058.311	6	590.1	24 T.W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	2.9255	0.2679	1466.73	1467.749	1	610.4	66.66667 Q.LRKTPLEPGLELT.A
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.6013	0.2096	2219.51	2219.495	4	434.6	52.77778 T.N2R4P1D1Q2I1D1P1A111L1R4P1G1R4L1D1Q2L1.I
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.1448	0.2844	2283.81	2284.525	2	115.8	38.88889 L.DEIKEELKETVEYPVLHPD.Q
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.1384	0.3041	1610.07	1609.927	1	577.6	62.5 R.EMVELPLRHPQLF.K
gi 6320077 ref NP_010157.1	YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with NpI4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p Homocitrate synthase isozyme, catalyzes the condensation of acetlyI-CoA and alpha-	2	2.9797	0.2467	1481.71	1480.811	1	641.3	63.636364 E.MVELPLRHPQLF.K
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	5.0647	0.4741	2351.93	2351.522	1	1532.8	60.000004 A.R4A1L1D1D1F1G1V1D1Y11E1L1T1S1P1V1A1S1E1Q2.S
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form nomocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	1	2.2954	0.1555	985.47	986.145	1	270.1	62.5 Y.K2T1V1D1K2I1G1V1N2.R
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p, Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	5.0547	0.4076	2593.83	2595.812	1	900	47.826088 E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3.V
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	5.2738	0.345	2782.59	2784.023	1	693.1	42 E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	3	4.6544	0.3617	3125.54	3126.358	1	760.2	29.464287 F.H3A1E1L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	3	4.4739	0.3258	2017.97	2016.264	1	909.8	51.5625 D.T1V1G1C1A1N2P1R4Q2V1Y1E1L111R4T1L1.K
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	4.5969	0.4345	1823.21	1824.821	1	1033.5	65.625 V.N2K2G1T1D1D1D1N2I1D111S1N2G1H3V1S1.K
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isosyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	1	2.9786	0.2398	1315.64	1316.488	7	317.2	65 Y.E1I1L1D1P1H3D1F1G1M1K2.R
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isosyme, Lys20p, Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	1	3.133	0.3891	1581.56	1582.769	1	592.3	62.5 S.T1Y1E1I1L1D1P1H3D1F1G1M1K2.R
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p, Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	4.3809	0.2179	1568.79	1566.769	1	1503.1	83.33333 S.TYEILDPHDFGMK.R
gi 6320071 ref NP_010151.1	YDL131W	ketoglutarate to form nomocitrate, writen is the first step in the lysine biosynthesis pathway; highly similar to the other isosyme, Lys20p, Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	5.7767	0.4359	2267.65	2267.404	1	1171.4	57.5 L.L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi 6320071 ref NP_010151.1	YDL131W	ketoglutatate to form nonocirate, writen is the inits step in the tysine biosynthesis pathway, highly similar to the other isosyme, Lys20p, Lys21p Homocirate synthase isozyme, catalyzes the condensation of a cetyl-CoA and alpha- tertoducteriot of new homogitate, withich is the first trate in the heise bionyethesis	3	5.0593	0.4342	2592.83	2595.812	1	933.4	33.695652 E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D111S1N2G1H3.V
gi 6320071 ref NP_010151.1	YDL131W	Aerogiuratale to onin homourate, which is an inst step in the rysme biosynthesis pathway, highly similar to the other isozyme, Lys20p, Lys21p Homocitrate synthase isozyme, catalyzes the condensation of a cetyl-CoA and alpha- tectorilitation to from borgoritzet, which is the first ten in the histop biosynthesis	2	3.203	0.2252	1396.13	1396.516	1	762.3	75 Q.S1R4K2D1C1E1A111C1K2L1.G
gi 6320071 ref NP_010151.1	YDL131W	Actigurate of the original monochrade, which is an start and intergrate programmes and phatmas; highly similar to the other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha- tectoral tracts to form benegicitate, which is the first tent in the history bioarchase;	3	4.3958	0.1987	1594.4	1594.836	5	915.4	52.083332 C.A1N2P1R4Q2V1Y1E1L111R4T1L1.K
gi 6320071 ref NP_010151.1	YDL131W	Actiguratate to onit homotexit, which is an start explained user provide the system of the provided of the system	1	2.5323	0.2246	1046.34	1047.067	1	430.4	68.75 H.F1H3N2D1T1G1C1A111.A
gi 6320071 ref NP_010151.1	YDL131W	pathway; highly similar to the other isozyme, Lys20p; Lys21p Pathway; highly similar to the other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of a cetyl-CoA and alpha- tertoalutacta b form benegitters, why bit is the first tota in the busing bioarytheseig	2	3.1526	0.2507	2078.35	2079.277	1	322.8	41.666664 S.T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1.N
gi 6320071 ref NP_010151.1	YDL131W	Recognizative to contribution of the other isozyme, Lys20p; Lys21p pathway; highly similar to that other other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of a cetyl-CoA and alpha- tertodutacta b form brongizters, why bit is the first tota in the busine biosynthesis	3	5.4833	0.353	2784.89	2784.023	1	1074.6	32 E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D11IS1N2G1H3V1S1.K
gi 6320071 ref NP_010151.1	YDL131W	Recognizative to contribution of the other isozyme, Lys20p; Lys21p pathway; highly similar to that other other isozyme, Lys20p; Lys21p Homocitrate synthase isozyme, catalyzes the condensation of a cetyl-CoA and alpha- tertodutacta b form brongizters, why bit is the first tota in the busine biosynthesis	2	3.7559	0.3422	2782.09	2784.023	3	349.2	32 E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D111S1N2G1H3V1S1.K
gi 6320071 ref NP_010151.1	YDL131W	pathway; highly similar to the other isozyme, Lys20p Lys21p RNA polymerase II largest subunit B220, part of central core; phosphorylation of C- terminal herateneticide peet domain regulates association with transcription and	2	3.739	0.3326	2278.95	2281.515	1	593.7	45 E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1.N
gi 6320061 ref NP_010141.1	YDL140C	splicing factors; similar to bacterial becapting and prime; possible and prim; possible and prime; possibl	1	2.3484	0.216	1276.56	1277.54	1	488.2	60.000004 R.GVENIERVVMM.K
gi 6320061 ref NP_010141.1	YDL140C	splicing factors; similar to bacterial beta-prime; Rpo21p	2	2.9106	0.2224	1333.45	1332.453	1	650.4	80 W.SEDNDEKLIIR.C

		RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-								
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II largest subunit B220. part of central core: phosphorylation of C-	2	3.7729	0.3301	1719.51	1718.83	1	1454.6	78.57143 K.SLDAETEAEEDHMLK.K
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain egulate association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p BNA polymerses II Jacob submit 2020, part of control costs phosphonidation of C	2	3.669	0.2645	2056.75	2057.484	1	717	52.77778 W.VPDWDGVIPTPAIIKPKPL.W
gi 6320061 ref NP_010141.1	YDL140C	terminal heptimerase in targest subunit bzzu, parts on central robic, prosphoryhaton of or terminal heptipeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p BNA polymerase II transect turbuit 8220, part of control core; obserbondation of C-	2	4.3707	0.4848	2408.81	2406.873	1	1251.2	62.5 L.YWVPDWDGVIPTPAIIKPKPL.W
gi 6320061 ref NP_010141.1	YDL140C	terminal heptimerase in targest subunit bzzu, parts on central robic, prosphoryhaton of or terminal heptipeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p BNA polymerase II transect turbuit 8220, part of control core; obserbondation of C-	3	4.8179	0.2805	1958.93	1958.351	1	1262.6	42.647057 V.PDWDGVIPTPAIIKPKPL.W
gi 6320061 ref NP_010141.1	YDL140C	there is polynomical integers advantiseze polynomical to construct one proceedings of the polynomical of the polynomical terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polynomical largest exhibiting S200 part of central corre: phosphorylation of C-	2	3.0589	0.1857	1980.75	1979.351	1	575.9	50 V.P1D1W2D1G1V11P1T1P1A1I111K2P1K2P1L1.W
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II largest suburit B200, part of central core: phosphorylation of C-	2	3.4446	0.3534	2865.63	2867.185	1	312.2	39.130436 M.KYDRKVPSPTGEYVKEPEWVLETD.G
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II larcest subunit B220, part of central core; phosphorylation of C-	2	2.9142	0.2508	2897.03	2898.185	1	316.2	34.782608 M.K2Y1D1R4K2V1P1S1P1T1G1E1Y1V1K2E1P1E1W2V1L1E1T1D1.G
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-	2	4.108	0.3847	2518.09	2520.032	1	1072.8	54.761906 M.LYWVPDWDGVIPTPAIIKPKPL.W
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-	2	4.4399	0.4303	2543.47	2546.032	1	847.9	52.380955 M.L1Y1W2V1P1D1W2D1G1V1I1P1T1P1A1I1I1K2P1K2P1L1.W
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-	2	2.9673	0.3536	1511.15	1511.677	1	618.6	77.27273 L.RESFEDNVVRFL.N
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-	2	4.6251	0.4253	2267.73	2267.697	1	793	57.894737 Y.W2V1P1D1W2D1G1V1I1P1T1P1A1I1I1K2P1K2P1L1.W
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-	2	3.8178	0.4144	2242.47	2243.697	1	850.6	57.894737 Y.WVPDWDGVIPTPAIIKPKPL.W
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-	2	4.2476	0.4517	2429.83	2431.873	1	903.1	55 L.Y1W2V1P1D1W2D1G1V111P1T1P1A11111K2P1K2P1L1.W
gi 6320061 ref NP_010141.1	YDL140C	terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	3	4.1737	0.2333	2868.89	2867.185	1	990.6	35.869564 M.KYDRKVPSPTGEYVKEPEWVLETD.G
gi 6320058 ref NP_010138.1	YDL143W	the assembly of actin and tubulins in vivo; Cct4p Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	2	3.4403	0.2123	1950.43	1949.164	6	307.4	46.875 Q.F1Q2I1S1P1P1K2P1D1T1E1N2N2I1I1V1N2.D
gi 6320058 ref NP_010138.1	YDL143W	the assembly of actin and tubulins in vivo; Cct4p	2	4.404	0.2899	1876.45	1876.071	1	754	62.5 A.DLVEEIDSDGSKIVRVT.G
gi 6320058 ref NP_010138.1	YDL143W	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct4p	2	5.0883	0.3721	1894.51	1897.071	1	1558.3	65.625 A.D1L1V1E1E1I1D1S1D1G1S1K2I1V1R4V1T1.G
ail6320058/refINP 010138.1/	YDL143W	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo: Cct4p	2	2.9727	0.2469	1634.67	1636.855	3	523.9	54.166668 M.V1V1K2D1I1E1R4E1E1I1E1F1L1.S
ail6220058/rofIND_010128_1	VDI 142W/	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	2	4 1150	0.2927	1760 50	1760.092	4	1661 7	
gilos20056[rei]inF_010136.1]	10114300	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	2	4.1109	0.2637	1760.59	1700.902		1001.7	TO D.LVEEIDSDGSRIVKVI.G
gi 6320058 ref NP_010138.1	YDL143W	the assembly of actin and tubulins in vivo; Cct4p Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	2	4.4433	0.3646	1778.51	1780.982	1	1450.1	70 D.L1V1E1E1I1D1S1D1G1S1K2I1V1R4V1T1.G
gi 6320058 ref NP_010138.1	YDL143W	the assembly of actin and tubulins in vivo; Cct4p Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	2	3.267	0.3915	1441.35	1440.512	1	462.8	70.83333 K.HENGELNDGISVR.R
gi 6320058 ref NP_010138.1	YDL143W	the assembly of actin and tubulins in vivo; Cottap	2	4.0827	0.3626	1837.33	1838.952	1	695.1	63.333332 L.R4S1K2H3E1N2G1E1L1N2D1G1I1S1V1R4.R
gi 6320058 ref NP_010138.1	YDL143W	the assembly of actin and tubulins in vivo; Cct4p	2	3.2911	0.2104	1926.39	1927.164	1	760.7	62.5 Q.FQISPPKPDTENNIIVN.D
gi 6320058 ref NP_010138.1	YDL143W	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct4p	2	4.8552	0.4609	1810.61	1811.952	1	973.3	76.666664 L.RSKHENGELNDGISVR.R
nil6320056/refINP_010136.1	YDI 145C	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early secretory pathway: Con1p.	2	3 3634	0.3522	1988 51	1989 14	1	882.8	58 823532 T Y1K2P1I1Y1F1D1T1P1S1V1S1D1P1I 1T1G1S1 K
	VDI 4450	Alpha subunit of COPI vesicle coarbor complex, which surrounds transport vesicles	-	0.0001	0.0022	1000.01	1070.14		4000.4	
gi 6320056 ref NP_010136.1	YDL145C	In the early secretory pathway; Cop1p Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles	2	3.7948	0.3556	1969.51	1970.14	1	1080.1	64.70589 T.YKPIYEDTPSVSDPLTGS.K
gi 6320056 ref NP_010136.1	YDL145C	in the early secretory pathway; Cop1p Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles	1	2.8085	0.28	1295.61	1296.525	1	501.9	63.636364 W.A1S1F1H3P1T1L1P1L1I1V1S1.G
gi 6320056 ref NP_010136.1	YDL145C	in the early secretory pathway; Cop1p Alpha subunit of COPI vesicle contemps complex, which surrounds transport vesicles	3	3.9031	0.2488	3444.14	3443.977	1	313.4	21.428572 I.FHPHQNLIISVGEDKTLRVWDLDKRTPVK.Q
gi 6320056 ref NP_010136.1	YDL145C	in the early secretory pathway; Cop1p	1	2.3876	0.2075	1253.59	1254.503	6	330.7	50 L.V111H3P1R4E1V111L1Y1.D
gi 6320056 ref NP_010136.1	YDL145C	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early secretory pathway; Cop1p	2	3.1689	0.2367	1447.71	1448.746	8	254.2	53.846157 L.VILPKQPVGAVEPT.S
ail6320056 ref NP 010136.1	YDL145C	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early secretory pathway: Cop1p	2	3.615	0.3495	1464.25	1464.746	1	525.3	57.692307 L.V111L1P1K2Q2P1V1G1A1V1E1P1T1.S
gil6320056lrefINP_010136.1	YDI 145C	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles	2	3 3166	0 3242	1745 79	1746 967	1	838.4	
	1021400	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles	-	0.0100	0.0242				000.4	
gi 6320056 ref NP_010136.1	YDL145C	in the early secretory pathway; Cop1p Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles	2	4.0306	0.3193	2070.73	2071.245	1	1192.2	58.333332 A. LYKPIYED I PSVSDPLIGS.K
gi 6320056 ref NP_010136.1	YDL145C	in the early secretory pathway; Cop1p Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p;	2	3.2995	0.3267	1834.69	1835.166	1	440.1	53.333336 D.Q2I1L1P1Y1V1P1G1L1D1V1V1N2E1K2M1.N
gi 6320054 ref NP_010134.1	YDL147W	Ron5p Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p;	2	3.4561	0.3158	1915.45	1917.033	1	679.5	59.375 Q.K2T1Y1E1P1V1L1N2E1D1D1L1A1F1G1G1E1.A
gi 6320054 ref NP_010134.1	YDL147W	Ron5p Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p;	2	3.1529	0.1857	1291.59	1290.491	1	621.9	70 E.L1L1E1H3I1E1T111G1H3L1.I
gi 6320054 ref NP_010134.1	YDL147W	Rpn5p	2	5.8495	0.4555	1956.57	1957.15	1	2087.1	78.125 W.SHNVDELLEHIETIGHL.I

		Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p;								
gi 6320054 ref NP_010134.1	YDL147W	Rpn5p Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to	2	5.9873	0.3771	1982.99	1981.15	1	1865.9	78.125 W.S1H3N2V1D1E1L1L1E1H3I1E1T1I1G1H3L1.I
gi 6320054 ref NP_010134.1	YDL147W	mammalian pso subunit and to another s. cerevisiae regulatory subunit, kpn/p; Rpn5p Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to	3	4.4944	0.4394	1957.4	1957.15	1	1793.2	51.5625 W.SHNVDELLEHIETIGHL.I
gi 6320054 ref NP_010134.1	YDL147W	mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p; Rpn5p Essential non-ATPase regulatory subunit of the 265 proteesome lid, similar to	3	5.1722	0.3328	1980.2	1981.15	1	1905.6	53.125 W.S1H3N2V1D1E1L1L1E1H3I1E1T1I1G1H3L1.I
gi 6320054 ref NP_010134.1	YDL147W	mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p; Rpn5p	2	2.9159	0.304	1618.53	1618.827	1	692.7	57.692307 N.VDELLEHIETIGHL.I
ail6320054lrefINP 010134.1l	YDL147W	Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p; Rpn5p	3	3.9984	0.3754	1956.98	1957.15	1	1188.8	43.75 W.SHNVDELLEHIETIGHLI
		Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p;	2	5.007	0.4400	1000 15	4004.45		2000.2	
gilo320034[tet]NP_010134.1]	10214710	Rpriop Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p;	2	5.007	0.4190	1960.45	1961.15	1	2099.2	76.123 W.STRONZYTUTETETETETETETETETETTIGTROLLI
gi 6320054 ref NP_010134.1	YDL147W	Rpn5p Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S, cerevisiae regulatory subunit. Rpn7p:	2	3.7958	0.3006	1959.05	1957.15	1	1204.3	65.625 W.SHNVDELLEHIETIGHL.I
gi 6320054 ref NP_010134.1	YDL147W	Rpn5p Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to	2	3.3791	0.3559	1732.85	1732.931	1	759.7	60.714287 H.NVDELLEHIETIGHL.I
gi 6320054 ref NP_010134.1	YDL147W	mammalian ps5 subunit and to another 5, cerevisiae regulatory subunit, kpn/p; Rpn5p	2	4.4752	0.2751	1752.63	1752.931	1	1547.8	75 H.N2V1D1E1L1L1E1H3I1E1T1I1G1H3L1.I
gi 6320053 ref NP_010133.1	YDL148C	Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop14p	2	3.9693	0.2897	2518.77	2519.873	1	775.7	52.499996 M.TQPKKNPMEPKTDLDKEYDIK.V
		Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits; also present in the small subunit processome								
gi 6320053 ref NP_010133.1	YDL148C	complex, which is required for processing of pre-18S rRNA; Nop14p	3	4.4729	0.2523	2651.6	2651.065	1	698.4	32.142857 M.MTQPKKNPMEPKTDLDKEYDIK.V
gi 6320053 ref NP_010133.1	YDL148C	conclude product in some a complex time roomer industrial instantion roomers export of 40S ribosomal subunits, also present in the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop14p	2	3.8506	0.3727	2648.91	2651.065	1	628.6	47.61905 M.MTQPKKNPMEPKTDLDKEYDIK.V
gi 6320053 ref NP_010133.1	YDL148C	Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-185 rRNA; Nop14p	3	5.6297	0.3286	2681	2680.065	1	1598	41.6666664 M.M1T1Q2P1K2K2N2P1M1E1P1K2T1D1L1D1K2E1Y1D1I1K2.V
		Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits: also present in the small subunit processome								
gi 6320053 ref NP_010133.1	YDL148C	complex, which is required for processing of pre-18S rRNA; Nop14p	3	5.9655	0.2918	3144.5	3146.352	1	993.7	32.692307 R.AAPSDRTKTEEEKNAEAEEKKRELEQQ.R
gi 6320053 ref NP_010133.1	YDL148C	Aucceouter proteint joints a complex with rocket that mediates that around an nuclear export of 40S ribosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop14p	3	6.1838	0.229	3185.87	3186.352	1	893.7	32.692307 R.A1A1P1S1D1R4T1K2T1E1E1E1K2N2A1E1A1E1E1K2K2R4E1L1E1Q2Q2.R
gi 6320053 ref NP_010133.1	YDL148C	Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop14p	2	3.8584	0.3668	2649.87	2651.065	1	482.8	42.857143 M.MTQPKKNPMEPKTDLDKEYDIK.V
ail63200531refINP 010133.11	YDL148C	Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA: Nop14p	2	3.4091	0.2186	1989.89	1991.362	4	506.3	53.125 S.T1V1W2K2S1L1P1A1F1N2E1I1I1L1P1I1Q2.Q
3		Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear								
gi 6320053 ref NP_010133.1	YDL148C	export or 4US robosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop14p	3	4.3159	0.3063	2649.35	2651.065	1	1043.1	36.904762 M.MTQPKKNPMEPKTDLDKEYDIK.V
gi 6320053 ref NP_010133.1	YDL148C	export of 406/in, bornis a Complex with rockep tract meturates haddraton and nuclear export of 406 has robusints; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop14p	3	4.7554	0.211	2813.06	2812.258	1	986.9	34.090908 L.M1M1T1Q2P1K2K2N2P1M1E1P1K2T1D1L1D1K2E1Y1D111K2.V
gi 6320041 ref NP_010121.1	YDL160C	Cytoplasmic DExD/H-box helicase, stimulates mRNA decapping, coordinates distinct steps in mRNA function and decay, interacts with both the decapping and deadenylase complexes, may have a role in mRNA export and translation; Dhh1p	2	5.105	0.3507	2110.33	2111.337	1	599.1	55.88235 L.N2I1P1K2K2D1T1R4P1Q2T1D1D1V1L1N2T1K2.G
gi 6320041 ref NP_010121.1	YDL160C	Cytoplasmic DExD/H-box helicase, stimulates mRNA decapping, coordinates distinct steps in mRNA function and decay, interacts with both the decapping and deadenylase complexes, may have a role in mRNA export and translation; Dhh1p	2	4.7611	0.2969	2084.45	2084.337	1	946.6	64.70589 L.NIPKKDTRPQTDDVLNTK.G
gi 6320041 ref NP 010121.1	YDL160C	Cytoplasmic DExD/H-box helicase, stimulates mRNA decapping, coordinates distinct steps in mRNA function and decay, interacts with both the decapping and deadenvlase complexes, may have a role in mRNA export and translation; Dhh1p	2	4.4634	0.3902	2196.25	2197.497	1	728.2	52.77778 A.LNIPKKDTRPQTDDVLNTK.G
		Cytoplasmic DExD/H-box helicase, stimulates mRNA decapping, coordinates distinct								
gi 6320041 ref NP_010121.1	YDL160C	steps in mKNA function and decay, interacts with both the decapping and deaden/size complexes, may have a role in mRNA export and translation; Dh1p NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamica and abba_ketonlutargite: with Gloth forms the secondary nothway for	2	4.5359	0.2534	2225.61	2225.497	1	808.8	52.77778 A.L1N2I1P1K2K2D1T1R4P1Q2T1D1D1V1L1N2T1K2.G
gi 6320030 ref NP_010110.1	YDL171C	glutamate biosynthesis from anmonia; expression regulated by nitrogen source; Git1p NAD(A)denendent dutamate synthesis (GOCAT) evolthesizes dutamate from	2	4.4656	0.3982	2258.27	2257.456	1	663.2	50 A.TFKDELDKLYPIIEEGGSDS.A
	VDI 1740	glutamica and alpha-ketoglutarate; with Gh1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source;	0	4 2007	0 2204	2250 52	2251 525	4	1002.0	
gijo520050[rei]NP_010110.1]	IDEI/IC	σπρ	2	4.3231	0.2301	2000.00	2001.000	1	1093.9	35 A. HEIMZDIEILIDINZLIHFIIIIEIEIGIGISIDISIAI.A

		NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with GIn1p, forms the secondary pathway for electronet bicsphthe is grant and an								
gi 6320030 ref NP_010110.1	YDL171C	glutamate bidsyntresis from animotina, expression regulated by hindgen source, Gittp NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from	2	3.9162	0.4303	2188.45	2191.378	1	639.3	52.77778 A.T1F1K2D1E1L1D1K2L1Y1P1I1IE1E1G1G1S1D1.S
ail6320030/refINP_010110_1	YDI 171C	glutamine and alpha-ketoglutarate, with Gin p, forms the secondary partway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source;	3	4 3488	0 2005	3083.03	3084 504	3	303 5	27 083334 N25151] 1 101510101/1510461K2D1N201W20102W20104//4M1 0
gilos20030[rei]NF_010110.1]	IDEI/IC	NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with GIn1p, forms the secondary pathway for	5	4.0400	0.2003	3003.03	3004.304	5	333.5	
gi 6320030 ref NP_010110.1	YDL171C	Gittp NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from	3	3.8016	0.198	2171.12	2170.378	1	822.8	34.72222 A.TFKDELDKLYPIIEEGGSD.S
ail6320030/refINP_010110.1	YDL171C	glutamine and appra-keuglutarate, with Girr P, forms the secondary patitively for glutamate biosynthesis from ammonia; expression regulated by nitrogen source; Glt1b	2	3.8881	0.2711	2193.69	2191.378	1	534	50 A T1F1K2D1E1L1D1K2L1Y1P1111E1E1G1G1S1D1 S
51		NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with Ginf p, forms the secondary pathway for glutamate biosynthesis from ammonia: expression regulated by unitrogen source:								
gi 6320030 ref NP_010110.1	YDL171C	Glt1p NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with Gln1p, forms the secondary pathway for	3	4.2404	0.3906	2194.22	2191.378	1	872.8	36.11111 A.T1F1K2D1E1L1D1K2L1Y1P1I1I1E1E1G1G1S1D1.S
gi 6320030 ref NP_010110.1	YDL171C	glutamate biosynthesis from ammonia; expression regulated by hitrogen source; Git1p NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with GIn1p, forms the secondary pathway for	2	3.7047	0.3091	2172.57	2170.378	1	461.1	47.22222 A.TFKDELDKLYPIIEEGGSD.S
gi 6320030 ref NP_010110.1	YDL171C	glutamate biosynthesis from ammonia; expression regulated by nitrogen source; Glt1p	2	4.7156	0.2335	1632.99	1632.91	1	992	79.16667 L.L1N2K2D1L1E1I1I1R4E1K2I1Q2.G
		NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with GIn1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source;								
gi 6320030 ref NP_010110.1	YDL171C	Glt1p NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with Gln1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by pitcoge source;	2	3.759	0.228	1575.13	1574.81	1	724.9	68.181816 A.K2D1N2P1W2P1Q2W2P1R4V1M1.R
gi 6320030 ref NP_010110.1	YDL171C	gratamate brogen tools non-annound, explosion regulated by margen bounce, Gittp D-lactate dehydrogenase, existence to pyruvate, transcription is heme-	2	3.0604	0.2789	1425.55	1422.594	1	1288.8	81.818184 L.D1L1D1L1D111P1E1M1G1K2Y1.A
gi 6320027 ref NP_010107.1	YDL174C	be periodent, repressed by guocese, and derepressed in entanto or lactate, located in the mitochondrial inner membrane; DId1p D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-	2	3.0645	0.2036	2069.47	2070.228	2	406.7	46.666668 S.E1S1T1D1R4C1D1W2V1E1K2P1T1M1F1F1.K
gi 6320027 ref NP_010107.1	YDL174C	dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitchondrial inner membrane; DId1p D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-	3	3.8931	0.2622	1792.88	1793.159	1	899.3	44.642857 K.L1A111D1P1K2R4I1M1N2P1D1K2I1F1.K
gi 6320027 ref NP_010107.1	YDL174C	dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitcchondrial inner membrane; DId1p D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-	2	4.1373	0.3879	1763.59	1764.843	3	394.7	57.14286 Q.A1G1L1P1W2E1D1L1N2D1Y1L1S1D1H3.G
gi 6320027 ref NP_010107.1	YDL174C	dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitcchondrial inner membrane; DId1p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	3.8641	0.3234	1733.83	1732.869	1	891.2	67.85714 S.S1L1D1S1P1D1Y1L1H3D1P1V1K2I1D1.K
gi 6320019 ref NP_010099.1	YDL182W	Recognitizate to form nomocritrate, which is the first step in the fysine bioSynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	5.0647	0.4741	2351.93	2351.522	1	1532.8	60.000004 A.R4A1L1D1D1F1G1V1D1Y1I1E1L1T1S1P1V1A1S1E1Q2.S
gi 6320019 ref NP_010099.1	YDL182W	Recognitizate to form nomocritrate, which is the first step in the fysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	1	2.2954	0.1555	985.47	986.145	1	270.1	62.5 Y.K2T1V1D1K2I1G1V1N2.R
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocurate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys2[r, Lys20] Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	3	4.4739	0.3258	2017.97	2016.264	1	909.8	51.5625 D.T1V1G1C1A1N2P1R4Q2V1Y1E1L111R4T1L1.K
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	3	4.5117	0.2585	4103.99	4105.437	2	418.1	M.TTATATK2P1X2P1Y1A1A1K2P1G1D1Y1L1S1N2V1N2N2F1Q2L111D1S1T1L1R4E 19.444445 1G1E1Q2F1A1N2.A
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	3	4.944	0.3827	4175	4177.516	1	513.9	M.T1A1A1K2P1N2P1Y1A1A1K2P1G1D1Y1L1S1N2V1N2N2F1Q2L111D1S1T1L1R4E 22.297297 1G1E1Q2F1A1N2A1.F
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p, Lys20p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	1	2.9786	0.2398	1315.64	1316.488	7	317.2	65 Y.E1I1L1D1P1H3D1F1G1M1K2.R
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p, Lys20p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	1	3.133	0.3891	1581.56	1582.769	1	592.3	62.5 S.T1Y1E1I1L1D1P1H3D1F1G1M1K2.R
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocritrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p Homocritrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	4.3809	0.2179	1568.79	1566.769	1	1503.1	83.33333 S.TYEILDPHDFGMK.R
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	3.7068	0.3006	1899.67	1901.079	1	902.9	55.88235 M.T1A1A1K2P1N2P1Y1A1A1K2P1G1D1Y1L1S1N2.V
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p, Lys20p Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	3.203	0.2252	1396.13	1396.516	1	762.3	75 Q.S1R4K2D1C1E1A111C1K2L1.G
gi 6320019 ref NP_010099.1	YDL182W	ketoglutarate to form homocritrate, which is the trist step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p Homocritrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	3	4.3958	0.1987	1594.4	1594.836	5	915.4	52.083332 C.A1N2P1R4Q2V1Y1E1L11R4T1L1.K
gi 6320019 ref NP_010099.1	YDL182W	Recognicative to form nomocritrate, which is the first step in the fysine biosynthesis pathway, highly similar to the other isosyme, Lys21p, Lys20p Homocritrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-	2	4.3826	0.3172	2063.85	2065.324	1	935.5	61.11111 K.K2N2K2K2N2D1S1D1V1P1E1L1A1T111P1A1A1K2.R
gi 6320019 ref NP_010099.1	YDL182W	xeuguicarate to form nomocritrate, which is the first step in the fysine biosynthesis pathway; highly similar to the other isosyme, Lys21p, Lys20p Homocritrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha- torodultates to form homocritrate, which is the first action is the biology bioarchication.	1	2.5323	0.2246	1046.34	1047.067	1	430.4	68.75 H.F1H3N2D1T1G1C1A1I1.A
gi 6320019 ref NP_010099.1	YDL182W	pathway; highly similar to the other isozyme, Lys21p; Lys20p	1	2.8408	0.2187	1230.62	1230.334	4	442.3	65 N.K2K2N2D1S1D1V1P1E1L1A1.T

gi 6320019 ref NP_010099.1	YDL182W	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha- ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p	2	3.3684	0.2551	1608.43	1606.786	1	689.8	65.38461 A.K2K2N2K2K2N2D1S1D1V1P1E1L1A1.T
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.0537	0.3577	1790.77	1792.973	1	516.2	61.538464 Y.A1P111L1Y1E1N2D1H3F1F1D1Y1M1.Q
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.5756	0.3292	1488.59	1486.711	1	696.6	70.83333 R.GIDTPALDRTIKW.Q
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.619	0.2613	2194.27	2193.353	1	515.7	44.444447 S.K2S1Y1P111S1E1G1P1E1R4A1N2E1L1V1E1S1Y1.R
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.5325	0.4046	1875.27	1874.983	1	324.5	60.000004 K.R4I1S1L1E1D1H3A1E1S1E1Y1G1A1I1Y1.S
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.3035	0.2358	1831.65	1832.989	1	541.3	53.125 V.G1H3D1N2L1V1G1E1V111R4I1D1G1D1K2A1.T
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.2653	0.3512	1456.31	1456.596	1	853.9	70.83333 V.G1H3D1N2L1V1G1E1V111R4I1D1.G
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.349	0.2066	1331.45	1331.598	2	750.1	72.72727 F.LKDGVKNIPSFL.S
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	1	2.8083	0.2674	1330.55	1331.598	1	469.6	59.090908 F.LKDGVKNIPSFL.S
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	1	3.6107	0.405	1534.7	1535.827	1	396.8	53.846157 L.GFLKDGVKNIPSFLS
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	1	3.095	0.2233	1552.59	1552.827	3	385.2	57.692307 L.G1F1L1K2D1G1V1K2N2l1P1S1F1L1.S
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	4.1401	0.4425	2062.33	2063.296	1	531	52.77778 V.K2V1G1H3D1N2L1V1G1E1V1I1R4I1D1G1D1K2A1.T
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	4.6862	0.4284	1688.49	1686.902	1	1505.1	75 V.K2V1G1H3D1N2L1V1G1E1V1I1R4I1D1.G
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.7859	0.3538	1551.81	1552.827	1	879.1	76.92308 L.G1F1L1K2D1G1V1K2N2l1P1S1F1L1.S
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	4.3197	0.3177	1609.79	1610.779	1	338.3	62.5 S.K2F1F1E1P1S1R4G1E1K2E1V1H3.G
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	4.7155	0.2782	2378.87	2380.706	1	1476	59.523808 L.GFLKDGVKNIPSFLSTDNIGTR.E
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.5456	0.306	1446.27	1446.621	1	470	65.38461 S.GRLGEMPADQGFPA.Y
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.922	0.3237	1690.43	1690.85	2	705.8	53.571426 S.KSYPISEGPERANEL V
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.184	0.3032	1710.29	1710.85	1	916.6	60.714287 S.K2S1Y1P111S1E1G1P1E1R4A1N2E1L1.V
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	1	2.5769	0.2324	1330.92	1331.598	7	362.7	54.545456 F.LKDGVKNIPSFL.S
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	3	5.5368	0.3194	2966.21	2966.362	1	657.5	29.166666 A.I1K2E1E1S1Q2S1I1Y1I1P1R4G1I1D1T1P1A1L1D1R4T111K2W2.Q
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	3	4.0929	0.2357	2930.06	2931.362	1	989.5	32.291664 A.IKEESQSIYIPRGIDTPALDRTIKW.Q

gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	3	3.8308	0.1546	2242.58	2243.588	1	584.4	34.72222 Q.S1I1Y1I1P1R4G1I1D1T1P1A1L1D1R4T1I1K2W2.Q
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	3	3.8438	0.3465	2408.51	2409.65	1	989.5	38.157894 S.S1K2F1F1E1P1S1R4G1E1K2E1V1H3G1E1F1E1K2L1.L
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	1	2.3884	0.2347	1230.36	1230.282	2	158.7	56.25 Y.E1N2D1H3F1F1D1Y1M1.Q
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	1	2.6147	0.2596	1297.36	1297.451	1	532.5	66.66667 Y.D1A1F1C1P1I1W2K2T1F1.D
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	1	2.5244	0.238	1284.5	1285.451	1	500.6	66.66667 Y.DAFCPIWKTF.D
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.1494	0.3142	1775.57	1775.973	1	691.3	57.692307 Y.APILYENDHFFDYM.Q
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	4.2483	0.3762	2136.37	2137.377	1	494	50 N.G1I1R4N2N2L1N2T1E1N2P1L1W2D1A1I1V1G1L1.G
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	4.2806	0.4256	1877.09	1877.105	1	1227.6	65.625 L.VKEVSKSYPISEGPERA.N
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	3	6.2789	0.3269	2260.19	2259.483	1	1752.8	46.05263 L.V1K2E1V1S1K2S1Y1P1I1S1E1G1P1E1R4A1N2E1L1.V
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	4.2174	0.3352	1797.53	1798.946	1	491.5	53.571426 S.K2F1F1E1P1S1R4G1E1K2E1V1H3G1E1.F
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.3346	0.327	1777.27	1776.946	1	873.1	64.28571 S.KFFEPSRGEKEVHGE.F
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	2	3.6414	0.3105	1536.53	1535.827	1	836.2	73.07692 L.GFLKDGVKNIPSFL.S
gi 6320016 ref NP_010096.1	YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-Scel), which is a site-specific endonuclease; Tfp1p	3	3.9842	0.2292	2590.61	2591.928	1	841.9	32.142857 E.S1Q2S111Y111P1R4G111D1T1P1A1L1D1R4T111K2W2Q2.F
gi 6320011 ref NP_010091.1	YDL190C	Dorquinn chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3; Ufd2p	2	3.5551	0.2653	1433.73	1435.747	2	710.7	70.83333 Q.IKLPLIPDQIGVE.N
gi 6320011 ref NP_010091.1	YDL190C	Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3; Ufd2p	1	3.3414	0.3704	1450.67	1450.747	1	1141.6	70.83333 Q.I1K2L1P1L111P1D1Q2I1G1V1E1.N
gil63200111refINP_010091_1	YDI 190C	Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to subtrates: a sign functions $a_0 = R^3$. If d_{20}	1	2 7073	0 3147	1434 76	1435 747	3	620.7	
	VDL4000	Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3)		2.7575	0.0147	0000.05	0004 700	3	020.7	
gij6320011 ref NP_010091.1	YDL190C	to conjugate ubiquitin to substrates; also functions as an E-3; Urd2p Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3)	Z	3.5995	0.2823	2620.95	2621.733	1	867	54./61906 Q.R4KZA1D1E1E1E1U1L1E1Y1G1U1V1P1U1E1F1L1D1P1L1.M
gi 6320011 ref NP_010091.1	YDL190C	to conjugate ubiquitin to substrates; also functions as an E3; Ufd2p Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating	3	4.8295	0.3156	3011.69	3012.094	1	629	31.25 A.E1E1Q2R4K2A1D1E1E1E1D1L1E1Y1G1D1V1P1D1E1F1L1D1P1L1.M
gi 6320011 ref NP_010091.1	YDL190C	enzyme (E1), a uoiquitin-conjugating enzyme (E2), and a uoiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3; Ufd2p Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating	2	3.6243	0.2893	1448.29	1450.747	1	873.8	75 Q.I1K2L1P1L11P1D1Q2I1G1V1E1.N
gi 6320011 ref NP_010091.1	YDL190C	enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3, Ufd2p Ubiquitin chain assembly factor (F4) that cooperates with a ubiquitin-activating	2	3.8689	0.3427	1438.71	1435.747	1	969.6	79.16667 Q.IKLPLIPDQIGVE.N
gi 6320011 ref NP_010091.1	YDL190C	enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3; Ufd2p	1	3.2337	0.3331	1449.35	1450.747	1	939.8	62.5 Q.I1K2L1P1L11P1D1Q2I1G1V1E1.N
gi 6320011 ref NP_010091.1	YDL190C	Dorquinn chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3; Ufd2p	2	3.4022	0.2439	2595.51	2595.733	1	623.9	50 Q.RKADEEEDLEYGDVPDEFLDPL.M
gi 6320011 ref NP_010091.1	YDL190C	Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3; Ufd2p	3	4.1492	0.2149	2596.1	2595.733	1	702.8	38.095238 Q.RKADEEEDLEYGDVPDEFLDPL.M
ail6320009/refINP_010089.11	YDI 192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2n; Art1n	1	2 8651	0.3405	1503.66	1504 795	1	418.6	53.848157 K2I 1G1E1V1I1T1T11P1T111G1E1 N
	YDI 192W/	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with 4170; 4110	1	2 7106	0.225	1491 62	1489 795		409.4	53 846157 L KI GEVITTIPTIGE N
91002000910110F_010009.1	10219200	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally		2.1100	0.220	1431.02	1403.780	'	403.4	
gi 6320009 ref NP_010089.1	YDL192W	interchangeable with Arf2p; Arf1p	2	3.3511	0.1608	1488.93	1489.795	1	692.4	73.07692 L.KLGEVITTIPTIGF.N

		ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of								
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	2	3.2282	0.3287	1831.93	1832.147	1	469	53.125 L.KLGEVITTIPTIGFNVE.T
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2p; Art1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	2	3.0312	0.2094	1702.03	1703.022	2	670.3	61.538464 K.L1F1S1N2L1F1G1N2K2E1M1R4I1L1.M
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2p; Art1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	2	3.3342	0.2786	1681.85	1683.022	1	891	69.230774 K.LFSNLFGNKEMRIL.M
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2p; Art1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	2	3.6685	0.504	1601.39	1603.899	1	838.2	67.85714 L.KLGEVITTIPTIGFN.V
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2p; Art1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	2	3.5276	0.3492	1623.05	1620.899	1	878.4	71.42857 L.K2L1G1E1V1I1T1T1I1P1T1I1G1F1N2.V
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2p; Art1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	1	2.3069	0.33	1490.61	1489.795	1	364.6	50 L.KLGEVITTIPTIGF.N
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	2	3.322	0.3493	1503.55	1504.795	1	508.1	65.38461 L.K2L1G1E1V1I1T1T1I1P1T1I1G1F1.N
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2p; Art1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	2	2.9872	0.3124	1849.87	1851.147	1	694.3	59.375 L.K2L1G1E1V1I1T1T1I1P1T1I1G1F1N2V1E1.T
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	2	3.2343	0.2374	1221.05	1221.503	1	735.4	77.77778 N.LFGNKEMRIL.M
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2p; Art1p ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of	1	2.963	0.2345	1235.48	1236.503	1	511.8	72.22222 N.L1F1G1N2K2E1M1R4I1L1.M
gi 6320009 ref NP_010089.1	YDL192W	coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Art2p; Art1p Micochondrial GTP/GDP transporter, essential for mitochondrial genome	1	2.5032	0.2744	1220.6	1221.503	1	447.1	72.22222 N.LFGNKEMRIL.M
gi 6320003 ref NP_010083.1	YDL198C	maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p Mitochondrial GTP/GDP transporter, essential for mitochondrial genome	2	3.583	0.2316	1653.57	1654.789	1	790.6	69.230774 Q.N2R4N2F1D1N2P1E1S1G1L1R4I1V1.K
gi 6320003 ref NP_010083.1	YDL198C	maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p Mitochondrial GTP/GDP transporter, essential for mitochondrial genome	1	3.1217	0.2727	1530.56	1530.649	1	458.2	63.636364 K.H3Y1K2K2D1F1D1N2L1F1G1E1.K
gi 6320003 ref NP_010083.1	YDL198C	maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p Mitochondrial GTP/GDP transporter, essential for mitochondrial genome	2	3.056	0.3115	1514.39	1513.649	1	538.8	68.181816 K.HYKKDFDNLFGE.K
gi 6320003 ref NP_010083.1	YDL198C	maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p Mitochondrial GTP/GDP transporter, essential for mitochondrial genome	1	3.1471	0.3742	1529.5	1530.649	1	330.2	50 K.H3Y1K2K2D1F1D1N2L1F1G1E1.K
gi 6320003 ref NP_010083.1	YDL198C	maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p Mitochondrial GTP/GDP transporter, essential for mitochondrial genome	2	3.6222	0.2816	1531.15	1530.649	1	774.9	77.27273 K.H3Y1K2K2D1F1D1N2L1F1G1E1.K
gi 6320003 ref NP_010083.1	YDL198C	maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family: (putative) mitochondrial carrier protein; Ggc1p Nuclear protein related to mammalian high mobility group (HMG) proteins, essential	2	5.3635	0.3969	1761.71	1762.929	1	1575.5	76.92308 K.H3Y1K2K2D1F1D1N2L1F1G1E1K2T1.G
gi 6319993 ref NP_010073.1	YDL208W	for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing: Nhp2p Nuclear protein related to mammalian high mobility group (HMG) proteins, essential	2	3.9767	0.3335	1982.31	1981.179	1	433.2	56.25 A.DVISHIPVLCEDHSVPY.I
gi 6319993 ref NP_010073.1	YDL208W	for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing: Nhp2p Nuclear protein related to mammalian high mobility group (HMG) proteins, essential	2	4.2772	0.2659	2011.57	2011.205	1	838.4	63.333332 N.K2K2K2D1G1K2N2K2E1E1E1Y1K2E1S1F1.N
gi 6319993 ref NP_010073.1	YDL208W	for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing: Nhp2p Nuclear protein related to mammalian high mobility group (HMG) proteins, essential	2	4.046	0.398	2002.95	2002.179	1	366.8	53.125 A.D1V111S1H311P1V1L1C1E1D1H3S1V1P1Y1.I
gi 6319993 ref NP_010073.1	YDL208W	Tor function of H/ACA-type snoktives, which are involved in 185 rktvA processing: Nhp2p Nuclear protein related to mammalian high mobility group (HMG) proteins, essential	2	3.2499	0.3739	1644.15	1644.782	6	297.2	50 M.GKDNKEHKESKESK.T
gi 6319993 ref NP_010073.1	YDL208W	Tor function of H/ACA-type snoktives, which are involved in 185 rktive processing: Nhp2p Nuclear protein related to mammalian high mobility group (HMG) proteins, essential	2	4.5319	0.3351	1665.53	1666.782	1	751.9	73.07692 M.G1K2D1N2K2E1H3K2E1S1K2E1S1K2.T
gi 6319993 ref NP_010073.1	YDL208W	tor function of mACA-type showers, which are involved in 155 interve processing, Nhp2p Nuclear protein related to mammalian high mobility group (HMG) proteins, essential functionation of U/ACA to an ann NNe which was included in 106 - NNA an essential	1	2.9004	0.1674	1185.72	1186.441	6	165.1	60.000004 L.R4K2G1E1K2G1L1V1V1I1A1.G
gi 6319993 ref NP_010073.1	YDL208W	for function of mAA-type shortys, which are involved in 155 interve processing, Nhp2p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with L estimation partner Zwar back more what is in the what is for the order of the media polymore intervention	2	3.4513	0.2336	1256.41	1256.534	1	488.1	75 K.NVKRGVKEVVK.A
gi 6319972 ref NP_010052.1	YDL229W	Mint - protein particle 200 rp. ritagible information in forming on hermis-indue polypepude chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cutor/section ATDros that is a chapter accessible deployuble subunction	1	3.2281	0.2735	1526.56	1525.742	1	506.6	61.538464 F.KVIDVDGNPVIEVQ.Y
ail6310072/rofIND_010052.1		with J-protein partner Zuoris a mosonine associated interesting of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; setto.	2	4 8645	0 2067	1542.22	1542 742	1	1912.2	84 64530 E K2)/44D1/4D1C4N2D1/444E1/4O2 V
gilos 13372 [ref rir_010032.1]	I DL223W	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with -protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains: member of the HSR2 for privice interacts with begenetrace veluait Pageto;	2	4.0043	0.2307	1040.00	1342.742		1012.2	04.013331.N2V11D1V1D101N2F1V11E1V1Q2.1
gi 6319972 ref NP_010052.1	YDL229W	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with Lorotation partner zurolic may be involved in following of partner partner zurolic and the second partner zurolic may be involved in following of partner zurolic partner zurolic may be involved in following of partner zurolic partner zurolic may be involved in following of partner zurolic partner zurolic may be involved in following of partner zurolic partner zurolic may be involved in following of partner zurolic partner zurolic may be involved in following of partner zurolic partner zurolic may be involved in following of partner zurolic partne	2	3.6844	0.274	1528.29	1525.742	4	776	61.538464 F.KVIDVDGNPVIEVQ.Y
gi 6319972 ref NP_010052.1	YDL229W	chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions	2	3.3776	0.1576	1886.25	1883.34	7	251	46.875 S.A1M1V1L1T1K2M1K2E1I1A1E1A1K2I1G1K2.K
		with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p;								
gijb319972 ret NP_010052.1	YDL229W	SSD1p	1	3.4325	0.3744	1542.68	1542.742	1	470.4	57.692307 F.K2V111D1V1D1G1N2P1V111E1V1Q2.Y

		Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p;								
gi 6319972 ref NP_010052.1	YDL229W	Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains: member of the HSP70 familie interacts with phosphatase subwit Pacific:	2	3.6766	0.2402	2758.99	2758.059	3	617.6	41.304348 Q.K2L1L1S1D1F1F1D1G1K2Q2L1E1K2S111N2P1D1E1A1V1A1Y1.G
gi 6319972 ref NP_010052.1	YDL229W	Soltp Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide	2	3.1598	0.2103	1513.83	1514.806	2	542.8	65.38461 F.G1I1V1V1P1R4N2T1T1V1P1T1I1K2.R
gi 6319972 ref NP_010052.1	YDL229W	chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zup1p; may be involved in folding of newly-made polypeptide	1	2.5025	0.2185	1170.6	1171.385	2	144.1	62.5 S.EKERHVLIF.D
gi 6319972 ref NP_010052.1	YDL229W	chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions	1	2.6113	0.1561	1186.62	1186.385	1	165.1	62.5 S.E1K2E1R4H3V1L111F1.D
gi 6319972 ref NP_010052.1	YDL229W	with -protein partner Zuo1p; may be involved in tolding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions	2	4.4491	0.3621	1959.43	1960.169	1	600.9	66.66667 E.R4V1N2C1K2E1N2T1L1L1G1E1F1D1L1K2.N
gi 6319972 ref NP_010052.1	YDL229W	with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ss1p Cutoplesmic ATPase that is a ribecome associated melacular chaptering functions	2	3.3444	0.3878	1246.55	1247.348	1	1195.1	81.818184 K.TGLDISDDARAL.R
gi 6319972 ref NP_010052.1	YDL229W	with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p	1	3.0524	0.2121	1526.82	1525.742	5	362.3	53.846157 F.KVIDVDGNPVIEVQ.Y
nil63199721refINP_010052.11		Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Seb1n	1	3 3944	0 3766	1541.66	1542 742	1	307 9	53 846157 E K2V/11D1V/1D1C1N2D1V/11E1V/02 V
910010012[[0]]NI _010002.1]	TELEST	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p;		0.0044	0.0700	1041.00	1042.142		001.0	
gi 6319972 ref NP_010052.1	YDL229W	Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains: member of the HSP70 family: interacts with phospbatase subunit Reo1o:	2	4.222	0.2809	1543.55	1542.742	1	1223	73.07692 F.K2V1I1D1V1D1G1N2P1V1I1E1V1Q2.Y
gi 6319972 ref NP_010052.1	YDL229W	Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide	2	3.1407	0.2532	1333.15	1330.466	1	1498.3	72.72727 A.G1E1P1V1L1E1A111F1E1V1D1.A
gi 6319972 ref NP_010052.1	YDL229W	chains; memoer of the HSP7/U family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide	2	3.7255	0.2748	1318.45	1318.466	1	1603.1	77.27273 A.GEPVLEAIFEVD.A
gi 6319972 ref NP_010052.1	YDL229W	chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide	1	3.3288	0.2619	1556.76	1557.784	1	783.8	61.538464 F.KSTLEPVEQVLKDA.K
gi 6319972 ref NP_010052.1	YDL229W	chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with L restrict partner zue to more himshed in folding of partner works and polypopilie	1	2.6019	0.2058	1273.63	1274.463	1	416.2	55.555557 K.S1E1K2E1R4H3V1L111F1.D
gi 6319972 ref NP_010052.1	YDL229W	chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions	3	4.1202	0.2155	2941.37	2943.297	1	731.6	31.25 E.R4V1N2C1K2E1N2T1L1L1G1E1F1D1L1K2N2I1P1M\$M\$P1A1G1E1.P
gi 6319972 ref NP_010052.1	YDL229W	with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions	1	2.6533	0.2733	1416.7	1417.567	1	292.9	65 K.KHEARQRLESY.V
gi 6319972 ref NP_010052.1	YDL229W	with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p Cutrolasmic ATPase that is a ribosome-associated molecular chaperone functions	2	3.8543	0.2181	1528.07	1525.742	4	1111.1	69.230774 F.KVIDVDGNPVIEVQ.Y
gi 6319972 ref NP_010052.1	YDL229W	with J-protein partner Zuotp; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p	2	4.1052	0.256	1543.29	1542.742	1	999.4	73.07692 F.K2V111D1V1D1G1N2P1V111E1V1Q2.Y
gi 6319972 ref NP_010052.1	YDL229W	Syloplasmic Al Pase that is a noisonne-associated molecular chapterine, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p	1	3.0743	0.3191	1526.68	1525.742	1	429.1	57.692307 F.KVIDVDGNPVIEVQ.Y
qi 6319972 ref NP 010052.1	YDL229W	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p	1	3.4488	0.3143	1544.54	1542.742	1	517.7	61.538464 F.K2V111D1V1D1G1N2P1V111E1V1Q2 Y
		Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p;	0	0.0740	0.0000	4707.00	4700 000		700.0	
gilo319972[rei]NP_010052.1]	TDL229W	So ip Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p;	2	3.3718	0.2902	1727.29	1720.898	I	728.3	00.30401 F.UUE3VURUMINI WPF.K
gi 6319972 ref NP_010052.1	YDL229W	Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains: member of the HSPI formit; interacts with beceholtese thunit Beach	2	4.2084	0.3019	1743.75	1744.898	1	669.7	61.538464 F.D1D1E1S1V1Q2K2D1M1K2T1W2P1F1.K
gi 6319972 ref NP_010052.1	YDL229W	Ssb1p Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide	3	5.8157	0.4356	3259.16	3260.588	1	1663.7	30.46875 F.DLGGGTFDVSLLHIAGGVYTVKSTSGNTHLGGQ.D
gi 6319972 ref NP_010052.1	YDL229W	chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p	1	2.6107	0.2113	1257.64	1258.463	7	347.4	55.555557 K.SEKERHVLIF.D

		Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p;		0.0054	0.404	1705 54	1705 175	0	000.0	
gi 6319972 ret NP_010052.1	YDL229W	Sobip Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide	2	2.9254	0.184	1795.51	1795.175	2	398.8	46.666668 D.M1F1G111V1V1P1R4N21111V1P1111K2.R
gi 6319972 ref NP_010052.1	YDL229W	chains; member of the HSP70 tamily; interacts with phosphatase subunit kegip; Ssb1p Neutral trehalase, degrades trehalose; required for thermotolerance and may	1	2.3546	0.1689	1261.2	1262.348	3	335.9	50 K.T1G1L1D1I1S1D1D1A1R4A1L1.R
gi 6320204 ref NP_010284.1	YDR001C	metalate resistance to other cenular stresses, may be prosphorylated by Coccep, Nth1p Neutral trehalase, degrades trehalose; required for thermotolerance and may medicate resistance to ethics enulate strengen; new to becarbendued by Cd20er.	2	4.6244	0.2373	2117.63	2117.375	1	1061.3	62.5 L.Y1N2D1G1K2l1K2E1P1K2L1D1E1F1F1L1H3.D
gi 6320204 ref NP_010284.1	YDR001C	hiediale resistance to other central subsets, may be prosprinty and by Odc20, Nth1p Neutral trehalase, degrades treducer required for thermotolerance and may modiate resistance to other cellular streage: may be percended by Cdc20;	2	3.6026	0.3689	2094.83	2094.375	1	705.3	50 L.YNDGKIKEPKLDEFFLH.D
gi 6320204 ref NP_010284.1	YDR001C	Nexture resistance to other central surgestion may be prospring and of outcop, Nith1p Neutral trehalase, degrades trehalose; required for thermolerance and may mediate resistance to other cellular stresses: may be phosphorulated by Cdc28r;	3	4.8891	0.3904	2116.43	2117.375	1	742.9	42.1875 L.Y1N2D1G1K211K2E1P1K2L1D1E1F1F1L1H3.D
gi 6320204 ref NP_010284.1	YDR001C	Notifue research to the contract concerning of proceeding of the concerning of the c	2	4.8495	0.2464	2118.57	2117.375	1	1046.4	59.375 L.Y1N2D1G1K211K2E1P1K2L1D1E1F1F1L1H3.D
gi 6320205 ref NP_010285.1	YDR002W	ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	3.128	0.1935	1424.41	1424.536	3	284.8	75 M.E1E1D1E1E1V1L1Y1K2V1R4.A
gi 6320205 ref NP_010285.1	YDR002W	Ran GTpase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	3	5.7362	0.4654	4210.88	4211.424	1	552.9	A.E1K2P1E1T1K2K2D1E1E1D1T1K2E1E1T1K2K2E1G1D1D1A1P1E1S1P1D1I1H3F 21.428572 1E1P1V1V1H3.L
gi 6320205 ref NP_010285.1	YDR002W	Ran GTpase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	3	5.7113	0.3396	2455.31	2453.698	1	1281	35.227272 M.S1S1E1D1K2K2P1V1V1D1K2K2E1E1A1A1P1K2P1P1S1S1A1.V
gi 6320205 ref NP_010285.1	YDR002W	Kan GI pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	5.0582	0.419	2454.01	2453.698	1	1035.5	50 M.S1S1E1D1K2K2P1V1V1D1K2K2E1E1A1A1P1K2P1P1S1S1A1.V
gi 6320205 ref NP_010285.1	YDR002W	Kan G pase binding protein; involved in nuclear protein import and KNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	3.0384	0.3009	1825.05	1826.028	1	585.2	57.14286 D.AKEWKERGTGDCKFL.K
gi 6320205 ref NP_010285.1	YDR002W	Ran GI pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	5.284	0.3733	2121.83	2123.351	1	1234.9	63.88889 C.A1N2H3I1I1A1P1E1Y1T1L1K2P1N2V1G1S1D1R4.S
gi 6320205 ref NP_010285.1	YDR002W	Ran GT pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	3.9985	0.3175	2096.11	2096.351	1	627	47.22222 C.ANHIIAPEYTLKPNVGSDR.S
gi 6320205 ref NP_010285.1	YDR002W	Ran GT pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	2.9696	0.287	1910.95	1911.168	1	427.8	53.125 N.HIIAPEYTLKPNVGSDR.S
gi 6320205 ref NP_010285.1	YDR002W	Ran GI pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	4.1405	0.3633	1933.75	1935.168	1	1117.7	62.5 N.H3I1I1A1P1E1Y1T1L1K2P1N2V1G1S1D1R4.S
gi 6320205 ref NP_010285.1	YDR002W	Ran GT pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	5.4172	0.4627	2662.85	2663.951	1	654.4	47.727272 C.A1N2H3I1I1A1P1E1Y1T1L1K2P1N2V1G1S1D1R4S1W2V1Y1.A
gi 6320205 ref NP_010285.1	YDR002W	Ran GT pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	4.527	0.4684	2631.59	2631.951	1	634.3	45.454548 C.ANHIIAPEYTLKPNVGSDRSWVY.A
gi 6320205 ref NP_010285.1	YDR002W	Ran GT pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	3	5.2339	0.3772	3969.32	3971.151	1	535.4	A.E1K2P1E1T1K2K2D1E1E1D1T1K2E1E1T1K2K2E1G1D1D1A1P1E1S1P1D1I1H3F 22.727274 1E1P1V1.V
gi 6320205 ref NP_010285.1	YDR002W	Ran GT pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	3	4.138	0.2705	2426.54	2425.698	2	590.4	32.954548 M.SSEDKKPVVDKKEEAAPKPPSSA.V
gi 6320205 ref NP_010285.1	YDR002W	Ran GTpase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	2	4.1583	0.2151	2146.25	2147.426	1	477.2	44.736843 E.D1K2K2P1V1V1D1K2K2E1E1A1A1P1K2P1P1S1S1A1.V
ail63202051refINP_010285_11		Ran G i pase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and outpolasm; is essential; homolog of human RanBP1; Yho	2	4 2838	0 4292	2122 37	2122 426	1	826 5	
qi 6320214 ref NP_010294.1	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Sng2p	-	2.5997	0.2256	992.56	993.193	1	649.1	78.57143 M.L1H3K2K2P1V1V1C1.K
gi 6320214 ref NP 010294.1	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Sng2p	2	4.8151	0.4633	1768.47	1769.776	1	1201.3	70 A.HADEESPDNVNDIDAK.E
gi 6320214 ref NP 010294.1	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Sng2p	2	5.336	0.3775	1792.07	1790.776	1	1778.9	73.333336 A.H3A1D1E1E1S1P1D1N2V1N2D1I1D1A1K2.E
gi 6320214 ref NP_010294.1	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	2	3.8235	0.379	2016.09	2015.254	1	884.9	56.25 Y.K2A1D1V111Y1N2G1E1L1D1V1H3F1P1Y1L1.T
gi 6320214 ref NP_010294.1	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	2	2.9117	0.2425	1411.15	1409.545	5	316.5	63.636364 F.VRDADEQGIHIR.K
gi 6320214 ref NP_010294.1	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	3	3.8165	0.182	1430.93	1430.545	2	1006.7	47.727272 F.V1R4D1A1D1E1Q2G1I1H3I1R4.K

		ABC transporter protein involved in multidrug resistance and resistance to singlet	2	0 7000	0.0400	4 4 2 2 4 2	4400 545		020.4	
gilo320214/rei/iNP_010294.1/	TDRUTTW	ABC transporter protein involved in multidrug resistance and resistance to singlet	2	3.7289	0.3130	1432.19	1430.545	I	939.1	61.616164 F.VIR4DIAIDTETQ2G11H31R4.K
gi 6320214 ref NP_010294.1	YDR011W	oxygen species; Snq2p ABC transporter protein involved in multidrug resistance and resistance to singlet	2	4.4177	0.2784	1670.61	1670.872	1	968.4	80.769226 W.KDVCFTIPYEGGKR.M
gi 6320214 ref NP_010294.1	YDR011W	oxygen species; Snq2p ABC transporter protein involved in multidrug resistance and resistance to singlet	2	3.0962	0.2708	1493.15	1492.715	6	292.1	62.5 L.11K2P1G1Y1E1N2K2V1P1R4T1A1.E
gi 6320214 ref NP_010294.1	YDR011W	oxygen species; Snq2p	2	3.9197	0.2638	2296.87	2297.519	1	707.7	58.333332 L.I1K2P1G1Y1E1N2K2V1P1R4T1A1E1E1F1E1T1Y1.W
gi 6320214 ref NP_010294.1	YDR011W	oxygen species; Snq2p	1	2.5696	0.2063	982.58	981.193	1	507.1	71.42857 M.LHKKPVVC.K
gi 6320214 ref NP_010294.1	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	1	2.5077	0.1696	1182.64	1182.362	1	881.1	75 T.LFEEFDRLL.L
ail6320214 ref NP 010294.1	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species: Sng2p	2	3.0715	0.2497	1182.29	1182.362	2	1099.7	87.5 T.LFEEFDRLLL
ail6320214/rofINB_010204_1		ABC transporter protein involved in multidrug resistance and resistance to singlet	2	4 1784	0 352	1000 57	1001 005	1	946.6	60 000004 V K2A1D4V414V1N2G1E4L1D1V4H3E4D1V1 L
		ABC transporter protein involved in multidrug resistance and resistance to singlet	2	4.1704	0.332	1900.57	1901.095		340.0	
gij6320214 ref NP_010294.1	YDR011W	oxygen species; snq.p Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which	Z	2.9319	0.1835	1296.15	1295.521	1	/95./	88.88889 F.LFEEFDRLLL.L
gi 6320226 ref NP_010306.1	YDR023W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p	2	3.7674	0.3037	2419.77	2419.644	1	520.8	44.736843 S.EFDEELYKVIDGEDEKYLIA.T
		Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p:								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p Cutacella cond tRNA synthetics, class II emission of tRNA synthetics, that	2	4.1314	0.289	1885.59	1883.123	1	1017.9	64.28571 F.VITEPEKSWEEFEKM.I
		aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p	2	4.2853	0.2383	2621.67	2619.882	1	1273.3	57.14286 Q.LSEFDEELYKVIDGEDEKYLIA.T
		Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
gi 6320226 ref NP_010306.1	YDR023W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p	2	4.8859	0.4694	2142.49	2140.395	1	1164.5	55.88235 A.SVEIVDEIISDYKDWVKT.R
		Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p:								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p Cutacella cond tBNA synthetics, class II emission of tBNA synthetics that	2	4.7799	0.4508	2124.83	2126.335	1	1169.5	62.5 Y.HSGEWFEKPQEQLPIHY.V
		evision services syntheses, class in animodynemic synthese that aminoacytes tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p;								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that	2	3.8962	0.3904	2225.47	2225.468	1	1317	61.764706 Y.HSGEWFEKPQEQLPIHYV.G
		aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p;								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p	2	4.2263	0.3726	2443.93	2445.696	1	720	47.368423 Y.HSGEWFEKPQEQLPIHYVGY.S
		aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
gi 6320226 ref NP_010306.1	YDR023W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p	2	3.1734	0.2159	1594.39	1593.866	1	676.4	70.83333 L.RKYIPGEPEFLPF.V
		Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
ail6320226/refINP_010306.1	VDR023W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Sec1n	1	2 6316	0 1821	1592.64	1593 866	1	379.2	
gilo320220[rei]14r_010300.1]	TDR025W	Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that		2.0310	0.1021	1332.04	1555.000		515.2	30.33332 LINTH OLF LI LITI.V
		enhances discrimination of the serine substrate, interacts with peroxin Pex21p;								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that	2	3.0458	0.3334	1953.21	1952.211	1	406.8	50 S.VEIVDEIISDYKDWVK.T
		aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate interacts with peroxin Pex210:								
gi 6320226 ref NP_010306.1	YDR023W	Sestp Cutacolic cond tBNA supported and all aminocond tBNA supported to the	2	3.1392	0.1786	1814.85	1811.983	1	785.6	57.14286 A.SVEIVDEIISDYKDW.V
		aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
gi 6320226 ref NP_010306.1	YDR023W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p	2	5.0811	0.3723	2062.27	2059.29	1	2444.6	71.875 A.S1V1E1I1V1D1E1I1I1S1D1Y1K2D1W2V1K2.T
		Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
gil6320226lrefINP_010306.1	YDR023W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p	2	4.6321	0.3773	2042.03	2039.29	1	1878	65.625 A SVEIVDEIISDYKDWVK T
51		Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that								
		enhances discrimination of the serine substrate, interacts with peroxin Pex21p;								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that	2	4.553	0.3711	2472.97	2473.696	1	604.3	44./36843 Y.H3S1G1E1W2F1E1K2P1Q2E1Q2L1P111H3Y1V1G1Y1.S
		aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p;								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p Cytosolic servi-tRNA synthetase, class II aminoacyl-tRNA synthetase that	2	3.9944	0.3543	2160.05	2161.395	1	553.1	44.11765 A.S1V1E1I1V1D1E1I1I1S1D1Y1K2D1W2V1K2T1.R
		aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p	3	4.076	0.2463	1902.26	1901.123	1	729.8	50 F.V1I1T1E1P1E1K2S1W2E1E1F1E1K2M1.I
		Cytosolic seryl-tKNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
gi 6320226 ref NP_010306.1	YDR023W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p	2	3.8129	0.2602	2254.17	2255.406	1	817.3	50 S.E1F1D1E1E1L1Y1K2V1I1D1G1E1D1E1K2Y1L1.I
		Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which								
ail6320226/refIND 010206 11	YDR033W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Sec1n	3	3 8130	0 2201	2257 55	2255 /06	1	844	30 705883 S E1E1D1E1E11 1V1K2\/114D1@1E1D1E1K2V1141
3.1002022010114F_010000.1	10102000	0001p	5	0.0100	0.2001	2201.00	2200.400		044	

		Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with perxix in Pex21p;								
gi 6320226 ref NP_010306.1	YDR023W	Ses1p Cytosofic seryl-IRNA synthetase, class II aminoacyl-IRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which	2	4.4875	0.2412	2443.73	2441.644	1	1134.8	52.63158 S.E1F1D1E1E1L1Y1K2V1I1D1G1E1D1E1K2Y1L1I1A1.T
gi 6320226 ref NP_010306.1	YDR023W	enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p Cytosolic seryl-RNA synthetase, class II aminoacyl-tRNA synthetase that	3	3.9518	0.1586	2774.21	2774.012	1	477.5	29.545454 A.Q2L1S1E1F1D1E1E1L1Y1K2V11ID1G1E1D1E1K2Y1L1I1A1.T
gi 6320226 ref NP_010306.1	YDR023W	aminoacytates trivia(Ser), alsplays trivia-dependent amino acto recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that	2	5.5439	0.4171	2151.37	2151.335	1	1355.2	65.625 Y.H3S1G1E1W2F1E1K2P1Q2E1Q2L1P1I1H3Y1.V
gi 6320226 ref NP_010306.1	YDR023W	aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p	2	3.3693	0.1742	1804.71	1806.158	2	643.1	67.85714 E.VLRKYIPGEPEFLPF.V
gi 6320236 ref NP_010316.1	YDR033W	Protein that localizes primarily to the plasma memorane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane. also found at the nuclear	2	4.1029	0.3582	1951.59	1953.162	1	1082	61.11111 R.GGNEAIKINPPTGADFHIT.S
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear	1	2.2551	0.2166	1090.56	1091.299	6	203.1	55 A.PKAPVASPRPA.A
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear	1	2.6369	0.1938	1446.83	1445.702	7	215.8	45.833336 A.ATPNLSKDKKKKS.K
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope. These admitted in the Mor20. availation are induced during beat description.	2	4.1176	0.3679	1620.49	1620.756	1	879.3	66.66667 R.G1G1N2E1A111K2I1N2P1P1T1G1A1D1F1.H
gi 6320236 ref NP_010316.1	YDR033W	envelope, has similarity to respond and trocp, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope: has similarity to Ishs30n and Yro2n, which are induced during heat shock;	1	2.2093	0.2327	1172.65	1173.354	4	327.5	60.000004 A.IKINPPTGADF.H
gi 6320236 ref NP_010316.1	YDR033W	Mintip Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope: has similarity to thesp30p and Yro2p, which are induced during heat shock;	2	4.6555	0.3505	1738.03	1738.897	1	1088.1	65.625 R.GGNEAIKINPPTGADFH.I
gi 6320236 ref NP_010316.1	YDR033W	Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock;	2	5.0976	0.395	1761.33	1760.897	1	797.7	59.375 R.G1G1N2E1A111K211N2P1P1T1G1A1D1F1H3.I
gi 6320236 ref NP_010316.1	YDR033W	Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock;	3	3.9656	0.2273	1978.13	1977.162	1	1026.8	40.27778 R.G1G1N2E1A111K2I1N2P1P1T1G1A1D1F1H3I1T1.S
gi 6320236 ref NP_010316.1	YDR033W	Minhip Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock;	3	4.1434	0.3002	1953.47	1953.162	1	1061.9	40.27778 R.GGNEAIKINPPTGADFHIT.S
gil6320236/ref/NP_010316.1	YDR033W	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p	2	3.0881	0.2573	1227.63	1228.465	2	725.4	70 A.S1N2L1G1W21P1V1K2A1K2.Y
gi 6320236 ref NP_010316.1	YDR033W	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p	2	3.4553	0.24	1215.29	1213.465	1	935.9	80 A.SNLGWIPVKAK.Y
gi 6320236 ref NP_010316.1	YDR033W	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p	1	2.6767	0.1835	1212.7	1213.465	7	480.3	65 A.SNLGWIPVKAK.Y
gi 6320236 ref NP_010316.1	YDR033W	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p	2	3.8719	0.2887	1544.17	1542.76	1	789.9	69.230774 A.I1K211N2P1P1T1G1A1D1F1H311T1.S
gi 6320236 ref NP_010316.1	YDR033W	Protein that localizes primarily to the plasma memorane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p. Protein that localizes primarily to the plasma membrane also found at the nuclear.	2	3.8316	0.2952	1525.23	1524.76	1	721.8	65.38461 A.IKINPPTGADFHIT.S
gi 6320236 ref NP_010316.1	YDR033W	 Protein rush localizes printality to the plasma methodane, also local at use inductant envelope; has similarity to Hsp30p and Yr02p, which are induced uting heat shock; Mrh1p Protein that localizes orimarily to the plasma membrane, also found at the nuclear 	1	2.7707	0.3181	1523.74	1524.76	1	357.2	46.153847 A.IKINPPTGADFHIT.S
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear	1	2.8044	0.3612	1541.58	1542.76	1	440.4	50 A.I1K2I1N2P1P1T1G1A1D1F1H3I1T1.S
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear	2	3.1891	0.2578	1699.45	1698.974	1	397.5	56.25 V.M1A1P1K2A1P1V1A1S1P1R4P1A1A1T1P1N2.L
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp3up and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear envelore: has similarity to Ish300 and Yro2p, which are induced during heat shock;	2	3.2133	0.3435	1675.63	1676.974	1	466.9	50 V.MAPKAPVASPRPAATPN.L
gi 6320236 ref NP_010316.1	YDR033W	Mrhtp Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope: has similarity to the Sh300 and Yro2p, which are induced during heat shock:	2	2.9944	0.3375	1178.07	1178.377	1	540.2	72.72727 M.A1P1K2A1P1V1A1S1P1R4P1A1.A
gi 6320236 ref NP_010316.1	YDR033W	Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock;	1	2.5958	0.327	1292.63	1293.57	1	440.4	66.66667 V.MAPKAPVASPRPA.A
gi 6320236 ref NP_010316.1	YDR033W	Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock;	1	3.5806	0.4443	1177.68	1178.377	1	304.6	63.636364 M.A1P1K2A1P1V1A1S1P1R4P1A1.A
gi 6320236 ref NP_010316.1	YDR033W	Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock;	1	3.0152	0.4264	1162.81	1162.377	1	281.1	63.636364 M.APKAPVASPRA.A
gijb320236 ref NP_010316.1	YDR033W	Mmnip Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock;	2	2.9649	0.2629	1324.41	1326.57	1	789.8	/5 V.M541P1K241P1V14151P1R4P141.A
gilo320230[tet]NP_010316.1]	10003300	MILLIN	1	2.0307	0.3074	1309.00	1310.57		303.9	υ2.5 Υ.ΙΨΙΑΤΕΙΝΖΑΤΕΙΥΤΑΤΟΤΕΙΚ4ΡΊΑΙ.Α

		Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope: bas similarity to Hsn30p and Yro2p, which are induced during beat shock:								
gi 6320236 ref NP_010316.1	YDR033W	Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear	2	3.5845	0.3254	1901.55	1901.212	1	690.9	58.333332 V.M1A1P1K2A1P1V1A1S1P1R4P1A1A1T1P1N2L1S1.K
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear	2	3.2788	0.3658	1879.53	1877.212	1	584.9	55.555557 V.MAPKAPVASPRPAATPNLS.K
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear	2	3.1243	0.1847	2098.59	2099.313	1	300.4	46.875 Q.TSTQKEHPGYRQIFYSR.F
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane. also found at the nuclear	2	4.355	0.4007	1602.45	1601.756	1	828	63.333332 R.GGNEAIKINPPTGADF.H
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear	1	2.5124	0.2169	1213.62	1213.465	9	362.1	60.000004 A.SNLGWIPVKAK.Y
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the puckear.	2	3.1754	0.2316	1213.59	1213.465	3	710.9	75 A.SNLGWIPVKAK.Y
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the puckear.	2	3.0994	0.2929	1312.35	1310.57	1	716.8	79.16667 V.M1A1P1K2A1P1V1A1S1P1R4P1A1.A
gi 6320236 ref NP_010316.1	YDR033W	envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Protein that localizes primarily to the plasma membrane, also found at the nuclear.	1	2.6719	0.3048	1310.54	1310.57	1	310.8	58.333332 V.M1A1P1K2A1P1V1A1S1P1R4P1A1.A
gi 6320236 ref NP_010316.1	YDR033W	envelope; taka similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p Tricep phoenbate iconserved, abundat durable on armor mPNA half life is	2	2.9249	0.1894	1211.15	1210.494	1	1561.9	88.88889 W.F1L1A1L1P1W2P1I1I1Q2.I
gi 6320255 ref NP_010335.1	YDR050C	regulated by iron availability (transcription is controlled by activators Reb1p, Gor1p, regulated by iron availability; (transcription is controlled by activators Reb1p, Gor1p, and Rap1p through binding sites in the 5' non-coding region; Tp11p Trices phenetate isomerge, advander duvelitie agrage; mPIA) ball life is	2	3.2768	0.2027	1520.05	1518.753	1	417.6	66.66667 A.SLKPEFVDIINSR.N
gi 6320255 ref NP_010335.1	YDR050C	regulated by iron availability; transcription is controlled by activators Reb1p, Gcr1p, regulated by iron availability; transcription is controlled by activators Reb1p, Gcr1p, and Rap1p through binding sites in the 5' non-coding region; Tpi1p Triens phenehets ironmerson advanded bland bits argument and Ma betti file in	2	3.2035	0.2476	1502.95	1502.565	1	786.4	72.72727 R.S1Y1F1H3E1D1D1K2F111A1D1.K
gi 6320255 ref NP_010335.1	YDR050C	regulated by iron availability (transcription is controlled by activators Reb1p, Gcr1p, and Rap1p through binding sites in the 5' non-coding region; Tpi1p	1	2.5903	0.2459	1236.39	1237.311	8	468.6	66.66667 Y.FHEDDKFIAD.K
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	2	3.7414	0.2009	1898.61	1899.177	1	452.8	60.714287 Q.MRFPEDFPFSPPQFR.F
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	3	4.1545	0.2356	2302.97	2301.589	1	1119.5	36.764706 A.Q2M1R4F1P1E1D1F1P1F1S1P1P1Q2F1R4F1T1.P
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	3	4.5426	0.2559	2147.99	2147.458	1	2006.2	48.4375 Q.MRFPEDFPFSPPQFRFT.P
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	3	4.5928	0.2684	2168.6	2171.458	1	1803.1	48.4375 Q.M1R4F1P1E1D1F1P1F1S1P1P1Q2F1R4F1T1.P
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	3	4.0735	0.2521	2443.58	2443.785	1	665	38.157894 A.QMRFPEDFPFSPPQFRFTPA.I
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	3	4.9697	0.2938	2473.16	2471.785	1	486.2	39.473686 A.Q2M1R4F1P1E1D1F1P1F1S1P1P1Q2F1R4F1T1P1A1.I
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	2	3.5975	0.2725	2314.03	2315.654	1	461.6	55.555557 Q.MRFPEDFPFSPPQFRFTPA.I
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	2	3.982	0.3555	2172.07	2171.458	1	475.4	59.375 Q.M1R4F1P1E1D1F1P1F1S1P1P1Q2F1R4F1T1.P
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	3	4.2165	0.1645	1922.51	1921.177	1	1632.3	53.571426 Q.M1R4F1P1E1D1F1P1F1S1P1P1Q2F1R4.F
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	2	3.4903	0.2196	1922.47	1921.177	4	370.9	53.571426 Q.M1R4F1P1E1D1F1P1F1S1P1P1Q2F1R4.F
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	3	4.1942	0.2226	2274.92	2275.589	1	2131.8	48.52941 A.QMRFPEDFPFSPPQFRFT.P
gi 6320259 ref NP_010339.1	YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F- box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	3	4.5735	0.1586	1924.07	1921.177	1	1545.4	51.785713 Q.M1R4F1P1E1D1F1P1F1S1P1P1Q2F1R4.F
gi 6320265 ref NP_010345.1	YDR060W	Constituent of 66S pre-ribosomal particles, required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein; Mak21p	3	4.7439	0.4084	2975.03	2976.166	1	710.6	30.208334 Y.D1K2P1W2Y1E1I1P1L1D1P1Q2V1G1Q2N2D1D1V1E1E1L1S1K2E1.Q
gi 6320265 ref NP_010345.1	YDR060W	Constituent of 66S pre-ribosomal particles, required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein; Mak21p	2	3.4829	0.1898	1660.79	1658.848	1	1375.3	79.16667 K.VEDIKPEDKFFYQ.Y

gi 6320265 ref NP_010345.1	YDR060W	Constituent of 66S pre-ribosomal particles, required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein; Mak21p	2	3.8462	0.2226	1673.63	1674.848	1	1295.4	79.16667 K.V1E1D111K2P1E1D1K2F1F1Y1Q2.Y
gi 6320265 ref NP_010345.1	YDR060W	Constituent of 66S pre-ribosomal particles, required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein; Mak21p	2	4.0314	0.3929	1921.19	1921.098	1	536.1	60.000004 Y.D1K2P1W2Y1E1I1P1L1D1P1Q2V1G1Q2N2.D
gi 6320265 ref NP_010345.1	YDR060W	Constituent of 66S pre-ribosomal particles, required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein; Mak21p	2	4.0375	0.3011	1786.51	1785.994	1	794.2	60.714287 Y.DKPWYEIPLDPQVGQ.N
gi 6320265 ref NP_010345.1	YDR060W	Constituent of 66S pre-ribosomal particles, required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein; Mak21p Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family:	2	4.1753	0.2292	2626.33	2627.798	1	503.9	40.476192 Y.D1K2P1W2Y1E1I1P1L1D1P1Q2V1G1Q2N2D1D1V1E1E1L1.S
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp Mitochondral protein, member of the ATP-binding cassette (ABC) transporter family:	2	3.5038	0.3076	1462.69	1463.625	1	704.6	68.181816 L.N2N2K2Y1I1C1E1P1P1L1S1L1.R
gi 6320266 ref NP_010346.1	YDR061W	Interactionally activated by Ymr1p along with genes involved in multiplust resistance; Ydr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	4.0392	0.3563	2295.45	2295.678	1	1308.9	57.5 R.SILKEPDLLLIDDPFLGLDPA.A
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	4.5354	0.3616	2316.93	2317.678	1	1303.2	57.5 R.S1I1L1K2E1P1D1L1L1L1I1D1D1P1F1L1G1L1D1P1A1.A
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	3.917	0.4094	2260.51	2259.598	1	799.4	50 LK2E1P1D1L1L1L11D1D1P1F1L1G1L1D1P1A1A1I1A1.T
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	3.6088	0.2668	2549.33	2550.995	1	610.3	36.95652 R.SILKEPDLLLIDDPFLGLDPAAIA.T
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	5.8423	0.4415	2002.11	2001.281	1	1546.2	67.64706 L.K2E1P1D1L1L1L111D1D1P1F1L1G1L1D1P1A1.A
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	4.2067	0.3899	2237.57	2237.598	1	813.7	50 L.KEPDLLLIDDPFLGLDPAAIA.T
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Vdr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	3.1731	0.3334	1887.91	1888.232	1	1049.1	66.66667 K.EHEIIKMPHLIELDGL.S
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Vdr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	3.0553	0.1808	1736.03	1737.021	8	376.8	50 K.E1H3E1I111K2M1P1H3L11E1L1D1.G
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Vdr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	5.0721	0.4083	1983.15	1982.281	1	1581.7	67.64706 L.KEPDLLLIDDPFLGLDPA.A
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Vdr061wp Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family;	2	3.5605	0.1697	1743.73	1742.895	2	509.8	53.571426 L.R4L111S1P1G1E1Y1E111G1D1M1E1N2
gi 6320266 ref NP_010346.1	YDR061W	transcriptionally activated by Yrm ip along with genes involved in multidrug resistance; Ydr061wp Component of serine palmitoyltransferase, responsible along with Lcb1p for the first	2	3.9558	0.387	1496.63	1496.676	1	1164.5	66.66667 L.R4L111S1P1G1E1Y1E111G1D1M1.E
gi 6320267 ref NP_010347.1	YDR062W	committee step in springouple symmesis, which is the condensation of serine with palmitoyl-CoA to form 3-tetosphinganine; Leb2p Component of serine palmitoyltransferase, responsible along with Lcb1p for the first	2	5.1714	0.3732	2471.15	2472.639	1	795.6	47.368423 A.N2Y1T1R4V1P1L1C1E1P1E1E1L1P1D1D111Q2K2E1.N
gi 6320267 ref NP_010347.1	YDR062W	committed step in sphingolipid synthesis, which is the condensation of senne with palmitoyl-CoA to form 3-tetosphinganine; Leb2p Component of serine palmitoyltransferase, responsible along with Lcb1p for the first	2	5.6323	0.367	2773.41	2774.966	1	930.4	43.18182 T.R4V1P1L1C1E1P1E1E1L1P1D1D111Q2K2E1N2E1Y1G1T1L1.D
gi 6320267 ref NP_010347.1	YDR062W	committee step in springouple symmesis, which is the condensation of serine with palmitoyl-CoA to form 3-tetosphinganine; Leb2p Component of serine palmitoyltransferase, responsible along with Lcb1p for the first	2	5.3743	0.4395	2743.91	2745.966	1	1156.8	47.727272 T.RVPLCEPEELPDDIQKENEYGTL.D
gi 6320267 ref NP_010347.1	YDR062W	committee step in springouple symmesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Leb2p Component of serine palmitoyl/transferase, responsible along with Leb1p for the first	2	4.9743	0.3393	3156.37	3157.351	1	821.5	38 A.N2Y1T1R4V1P1L1C1E1P1E1E1L1P1D1D1I1Q2K2E1N2E1Y1G1T1L1.D
gi 6320267 ref NP_010347.1	YDR062W	committee step in springouple symmesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Leb2p Component of serine palmitoyltransferase, responsible along with Lcb1p for the first	2	4.8043	0.467	3121.99	3124.351	1	913.1	40 A.NYTRVPLCEPEELPDDIQKENEYGTL.D
gi 6320267 ref NP_010347.1	YDR062W	Commuted step in springoupld symmetries, which is the condensation of semite with palmitoyl-CoA to form 3-ketosphinganine; Leb2p Component of serine palmitoyltransferase, responsible along with Lcb1p for the first	2	3.3616	0.233	2089.11	2090.254	2	449.7	46.875 T.R4V1P1L1C1E1P1E1E1L1P1D1D111Q2K2E1.N
gi 6320267 ref NP_010347.1	YDR062W	committee step in springouple symmetries, which is the condensation of semine with painticyl-CoA to form 3-ketosphinganine; Leb2p Component of serine palmitoyl/transferase, responsible along with Lcb1p for the first committed to b is notivismiticial authorized, which is the condensation of participation.	3	4.3798	0.2408	4161.65	4162.481	1	537.8	19.117647 2V1K2S1R4.H
gi 6320267 ref NP_010347.1	YDR062W	Palmited step in spininguipid synthesis, which is the condensation of serine with palmitedyl-CoA to form 3-ketosphinganine; Lcb2p Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15	3	4.733	0.3847	3123.08	3124.351	1	1324.5	33 A.NYTRVPLCEPEELPDDIQKENEYGTL.D
gi 6320269 ref NP_010349.1	YDR064W	and rat S13 ribosomal proteins; Rps13p Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15	2	4.6696	0.3538	2086.59	2085.386	1	1254.9	70.588234 L.K2S1N2G1L1A1P1E11P1E1D1L1Y1Y1L111K2.K
gi 6320269 ref NP_010349.1	YDR064W	and rat S13 ribosomal proteins; Rps13p Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15	2	4.8217	0.1858	2066.87	2064.386	1	1101.2	67.64706 L.KSNGLAPEIPEDLYYLIK.K
gi 6320269 ref NP_010349.1	YDR064W	and rat S13 ribosomal proteins; Rps13p Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15	2	2.9816	0.1814	1543.27	1540.762	1	370.3	62.5 S.A111P1Y1S1R4N2A1P1A1W2F1K2.L
gi 6320269 ref NP_010349.1	YDR064W	and rat S13 ribosomal proteins; Rps13p Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15	1	2.743	0.2982	1409.42	1410.588	1	275.6	54.545456 S.A111P1Y1S1R4N2A1P1A1W2F1.K
gi 6320269 ref NP_010349.1	YDR064W	and rat S13 ribosomal proteins; Rps13p Protein component of the small (40S) ribosomal subunit: has similarity to E. coli S15	2	3.2132	0.2	1838.79	1841.053	1	763	56.666668 L.K2S1N2G1L1A1P1E1I1P1E1D1L1Y1Y1L1.I
gi 6320269 ref NP_010349.1	YDR064W	and rat S13 ribosomal proteins; Rps13p	2	2.9928	0.1797	1822.89	1823.053	1	727	53.333336 L.KSNGLAPEIPEDLYYL.I
gi 6320276 ref NP_010356.1	YDR071C	Polyamine acetyltransferase; acetylates polyamines such as putrescine, spermidine and spermine; may be involved in transcription and/or DNA replication via regulation of levels of polyamines bound to chromosomal DNA; Paa1p	1	2.5317	0.2221	1187.43	1188.303	4	181.5	62.5 F.R4L111N2C1P1E1L1C1.S

gi]6320276 ref NP_010356.1	YDR071C	Polyamine acetyltransferase; acetylates polyamines such as putrescine, spermidine and spermine; may be involved in transcription and/or DNA replication via regulation of levels of polyamines bound to chromosomal DNA; Paa1p	2	3.6983	0.1857	1416.25	1416.602	1	1053.9	81.818184 M.G1T1K2I1P1H3E1Y1I1T1I1E1.S
gi]6320276 ref NP_010356.1	YDR071C	Polyamine acetyltransferase; acetylates polyamines such as putrescine, spermidine and spermine; may be involved in transcription and/or DNA replication via regulation of levels of polyamines bound to chromosomal DNA; Paa1 p Subunit of the Sec61 p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretopy proteins through the androlpasmic reticulum	2	3.5907	0.1661	1403.29	1401.602	1	829.2	77.27273 M.GTKIPHEYITIE.S
gi 6320291 ref NP_010371.1	YDR086C	membrane, and of the Ssh1p complex (Ssh1p-Sbh2p-Sss1p); interacts with Ost4p and Wbp1p; Sss1p Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum	2	4.0526	0.4894	1606.61	1608.791	1	1869.9	80.769226 L.VEAPVEFVREGTQF.L
gi 6320291 ref NP_010371.1	YDR086C	membrane, and of the Ssh1p complex (Ssh1p-Sbh2p-Sss1p); interacts with Ost4p and Wbp1p; Sss1p Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum	2	4.4689	0.3894	1721.51	1721.951	1	1430.5	78.57143 L.VEAPVEFVREGTQFL.A
gi 6320291 ref NP_010371.1	YDR086C	memorane, and or the Sship complex (Sship-Sbn2p-Sssip); interacts with Ost4p and Wbp1p; Sss1p Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum eventsets with the Cetter proteins through the Cetter Strength of the Cetter	2	3.9173	0.3737	1741.99	1740.951	1	772.5	64.28571 L.V1E1A1P1V1E1F1V1R4E1G1T1Q2F1L1.A
gi 6320291 ref NP_010371.1	YDR086C	memorane, and or the Ssnip complex (Ssnip-Son2p-Sssip); interacts with Ost4p and Wbp1p; Sss1p	2	5.1098	0.3939	1627.63	1626.791	1	1592.8	76.92308 L.V1E1A1P1V1E1F1V1R4E1G1T1Q2F1.L
gi 6320298 ref NP_010378.1	YDR093W	Non-essential P-type ATPase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	2	4.1606	0.3233	1965.49	1965.984	2	359.5	56.666668 T.EIHEHENEVDDDLHSF.Q
gi 6320298 ref NP_010378.1	YDR093W	Non-essential P-type AI Pase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	2	3.4558	0.3092	2713.57	2715.073	1	573.9	40.909092 A.SVTNREEELDKVTDVIERELILL.G
gi 6320298 ref NP_010378.1	YDR093W	Idealizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	3	3.8412	0.2653	2715.29	2715.073	2	500.7	31.818182 A.SVTNREEELDKVTDVIERELILL.G
gi 6320298 ref NP_010378.1	YDR093W	Non-essential P-type ATPase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	2	4.9661	0.3457	1888.35	1888.19	1	648	62.5 S.C11111K211P1G1S1T1P1K2D1E1P1K2A1L1.L
gi 6320298 ref NP_010378.1	YDR093W	Idealizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	3	3.9904	0.3176	2744.9	2746.073	2	436.5	30.681818 A.S1V1T1N2R4E1E1E1L1D1K2V1T1D1V111E1R4E1L111L1L1.G
gi 6320298 ref NP_010378.1	YDR093W	Non-essential P-type ATPase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exceptic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	3	3.872	0.3034	3244.79	3245.718	8	244.9	24.074074 Y.YNLPLPEDMLDEDGLPLAVYPRNKIRTT.K
gi 6320298 ref NP_010378.1	YDR093W	Incolaizes to the plasma membrane and late exception or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	3	3.8981	0.2536	3044.87	3043.508	6	311.3	27.000002 Y.YNLPLPEDMLDEDGLPLAVYPRNKIR.T
gi 6320298 ref NP_010378.1	YDR093W	localizes to the plasma membrane and late exception or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	3	6.2271	0.4275	3447.23	3446.894	1	745.9	36.607143 V.Y1Y1N2L1P1L1P1E1D1M1L1D1E1D1G1L1P1L1A1V1Y1P1R4N2K2I1R4T1T1.K
gi 6320298 ref NP_010378.1	YDR093W	Non-essential P-type ATPase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	3	5.9924	0.4656	3240.29	3242.684	1	471.1	33.653847 V.Y1Y1N2L1P1L1P1E1D1M1L1D1E1D1G1L1P1L1A1V1Y1P1R4N2K2I1R4.T
gi 6320298 ref NP_010378.1	YDR093W	Non-essential P-type AI Pase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	3	4.7929	0.4019	3407.42	3408.894	1	288.3	25 V.YYNLPLPEDMLDEDGLPLAVYPRNKIRTT.K
gi 6320298 ref NP_010378.1 gi 6320306 ref NP_010386.1 gi 6320306 ref NP_010386.1 gi 6320306 ref NP_010386.1 gi 6320306 ref NP_010386.1	YDR093W YDR101C YDR101C YDR101C YDR101C YDR101C	Non-essential P-type ATPase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exceptio or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dn2p Protein associated with the ribosomal export complex; Arx1p Protein associated with the ribosomal export complex; Arx1p Protein associated with the ribosomal export complex; Arx1p Protein associated with the ribosomal export complex; Arx1p Brotein associated with the ribosomal export complex; Arx1p Scaffold protein that, in response to pheromone, shuttles from the nucleus to the plasma membrane and assomations from the same f	2 2 2 2 2	4.5035 4.2462 2.9626 3.1815 3.3108	0.2121 0.4427 0.362 0.2133 0.2695	1867.57 2467.75 1672.73 2230.77 1692.59	1868.19 2467.97 1672.021 2231.603 1691.021	1 1 6 1	577.4 776.7 554.9 273.5 673.9	59.375 S.CIIKIPGSTPKDEPKALL 43.18182 T.MVIYPVDETKPILOPTGPLLGGK.A 50 T.LTLPGHELPLPKLGVS.A 32.5 M.VIIY1PIVID1E1T1K2PI1IL1Q2P1T1G1P1L1L1G1G1.K 53.333336 T.L1T1L1P1G1H3E1L1P1L1P1K2L1G1V1S1.A
gi 6320308 ref NP_010388.1	YDR103W	plasmia membrane and assemibles kinases site rip, sterip, and russpirito a specific signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p Scaffold protein that, in response to pheromone, shuttles from the nucleus to the plasma membrane and assembles kinases Ste11p, Ste7p, and Fus3p into a specific	2	3.4183	0.2275	2235.47	2237.602	1	422.7	42.105263 T.LSRTPNQIIELEKPSTLSPL.S
gi 6320308 ref NP_010388.1	YDR103W	signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p Scaffold protein that, in response to pheromone, shuttles from the nucleus to the plasma membrane and assembles kinases Ste11p, Ste7p, and Fus3p into a specific	2	3.2369	0.2566	1778.37	1776.088	9	363	50 Q.SRFPPYSPLLPPFGLS.Y
gi 6320308 ref NP_010388.1	YDR103W	signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p Scaffold protein that, in response to pheromone, shuttles from the nucleus to the plasma membrane and assembles kinases Ste11p, Ste7p, and Fus3p into a specific	2	3.978	0.3195	1796.23	1795.088	1	525.3	56.666668 Q.S1R4F1P1P1Y1S1P1L1L1P1P1F1G1L1S1.Y
gi 6320308 ref NP_010388.1	YDR103W	signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p Scaffold protein that, in response to pheromone, shuttles from the nucleus to the plasma membrane and assembles kinases Ste11p, Ste7p, and Fus3p into a specific	2	3.3918	0.3585	1690.63	1689.01	1	516.4	64.28571 Q.SRFPPYSPLLPPFGL.S
gi 6320308 ref NP_010388.1	YDR103W	signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p	2	3.65	0.3947	1708.53	1707.01	1	400.9	60.714287 Q.S1R4F1P1P1Y1S1P1L1L1P1P1F1G1L1.S

gi 6320327 ref NP_010407.1	YDR122W	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin2p; Kin1p	2	4.7061	0.3226	2025.31	2025.14	1	1095.4	61.764706 N.S1P1S1V1E1K2E1L1T1D1E1E111L1Q2E1A1S1.R
gi 6320327 ref NP_010407.1	YDR122W	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin2p; Kin1p	2	3.5975	0.3778	2004.19	2005.14	1	795.6	55.88235 N.SPSVEKELTDEEILQEAS.R
gi 6320327 ref NP_010407.1	YDR122W	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin2p; Kin1p	2	3.9677	0.252	1920.15	1918.062	3	1327.5	68.75 N.SPSVEKELTDEEILQEA.S
gi 6320327 ref NP_010407.1	YDR122W	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin2p; Kin1p	2	4.2539	0.1813	1938.37	1937.062	1	1580	71.875 N.S1P1S1V1E1K2E1L1T1D1E1E111L1Q2E1A1.S
gi 6320327 ref NP_010407.1	YDR122W	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin2p; Kin1p	2	3.6734	0.3147	1792.71	1790.047	3	351.1	56.25 A.SRAPAGSMPSIDFPRSL.F
gi 6320332 ref NP_010412.1	YDR127W	chorismate, which is a precursor to aromatic amino acids; Aro1p	2	4.3256	0.3857	1663.53	1662.896	1	792.4	73.07692 Y.G1L1P1V1S1P1D1E1K2W2F1K2E1L1.T
ail63203321refINP_010412.11	YDR127W	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids: Aro1p	1	2.8428	0.2368	1555.54	1556.83	1	425.3	57.692307 A.K2V1P111L1G1N2D1111H3V1G1Y1.N
gil63203321rofINP_010412_1		Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a program to acomatic amino acide: Aro1p	2	4 1041	0 3447	1010 /1	1020 13	1	1507 5	
gil0520352[rel]NF_010412.1]	101(12/10)	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of	2	4.1041	0.3447	1313.41	1920.15		1307.5	
gi 6320332 ref NP_010412.1	YDR127W	chorismate, which is a precursor to aromatic amino acids; Aro1p Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of	2	3.0181	0.2227	1816.49	1814.052	2	493.6	56.666668 S.CVPADKPLDDELLSKL.E
gi 6320332 ref NP_010412.1	YDR127W	chorismate, which is a precursor to aromatic amino acids; Aro1p	2	3.333	0.2852	1831.85	1832.052	2	529.2	53.333336 S.C1V1P1A1D1K2P1L1D1D1E1L1L1S1K2L1.E
gi 6320332 ref NP_010412.1	YDR127W	chorismate, which is a precursor to aromatic amino acids; Aro1p	2	4.0115	0.2597	1752.13	1752.762	1	1138.5	75 L.Y1S1W2D1D1A1E1W2E1N2R4F1N2.Q
ail63203321refINP 010412.11	YDR127W	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids; Aro1p	2	4.5508	0.172	1493.59	1492.654	1	1801.2	86.36364 Y.K2L1V1D1L1D1E1L1F1E1Q2Q2.H
		Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of	0	4 5050	0.0005	4000 50	4007.000		2400.4	
gilo320332[rei]NP_010412.1]	TDR127W	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of	2	4.5256	0.2965	1098.59	1097.002	I	2199.4	73.07692 L.GTNLVDLDELFEQQ.H
gi 6320332 ref NP_010412.1	YDR127W	chorismate, which is a precursor to aromatic amino acids; Aro1p Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of	2	4.9965	0.1621	1714.61	1714.882	1	2294.6	76.92308 L.G1Y1K2L1V1D1L1D1E1L1F1E1Q2Q2.H
gi 6320332 ref NP_010412.1	YDR127W	chorismate, which is a precursor to aromatic amino acids; Aro1p	2	3.712	0.3124	1825.55	1827.072	1	609.7	57.14286 A.Y1G1L1P1V1S1P1D1E1K2W2F1K2E1L1.T
gi 6320332 ref NP 010412.1	YDR127W	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids; Aro1p	2	2.9619	0.3935	1294.31	1293.512	1	395.2	75 F.RDTHKNKPLIA.V
ail62202241rofIND_010414_1	VDB120C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	2	2 0275	0 4127	2250.00	2252 561	1	202.2	L.D1V1L1N2G1I1A1P1G1Y1V1D1Y1D1L1V1T1P1G1N2T1E1E1E1R4Y1A1N2A1R4
gil0320334[rei]NF_010414.1]	IDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	3	3.9375	0.4127	3330.99	3332.301	1	292.2	22.413/34 L
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p Fimbrin, actin-bundling protein: cooperates with Scp1p (calponin/transgelin) in the	2	4.7725	0.3583	2388.67	2391.543	1	852.9	50 F.N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	4.4446	0.3365	2364.75	2366.543	1	757.6	50 F.NTHPGLEPIQEEEKPEIEEF.D
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	2.9413	0.1517	2252.43	2252.439	3	399.2	41.666664 N.THPGLEPIQEEEKPEIEEF.D
ail6320334/refINP_010414_1	VDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	2	3 8192	0 2956	2708 27	2709 826	1	397.6	40 909092 E N2T1H3P1G1I 1E1P1I102E1E1E1K2P1E1I1E1E1E1D141E1 G
giloo20004[10][NI _010414.1]	101(1250	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	-	0.0102	0.2000	2100.21	2103.020		001.0	
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	2	5.0035	0.3507	2592.71	2593.722	1	479.6	47.61905 N.T1H3P1G1L1E1P111Q2E1E1E1K2P1E111E1E1F1D1A1E1.G
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	3.8726	0.3208	2567.85	2567.722	1	373.3	42.857143 N.THPGLEPIQEEEKPEIEEFDAE.G
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	3.8726	0.3226	2971.35	2972.162	1	296.2	31.25 H.L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1.G
qi 6320334 ref NP 010414.1	YDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the organization and maintenance of the actin cytoskeleton; Sac6p	2	3.1887	0.2492	2941.67	2942.162	7	238.2	27.083334 H.LFNTHPGLEPIQEEEKPEIEEFDAE.G
ail62202241rofIND_010414_1	VDB120C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	2	4 0011	0.2965	2626 75	2626 972	1	509	
gil0320334[rei]NF_010414.1]	IDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	3	4.0211	0.2805	3020.75	3020.072	1	506	20.000000 F.NI HFOLEFIQEEEKFEIEEFDAEGEKEAKVF.I
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p Fimbrin, actin-bundling protein: cooperates with Scp1p (calponin/transgelin) in the	2	4.7152	0.3609	2652.67	2653.879	1	720.4	45.238094 H.L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	3	4.318	0.3414	2837.21	2838.277	1	1510.9	35.227272 Y.RLLEDDETLEQFLRLPPEQILLR.W
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	4.1296	0.3179	2793.43	2794.02	1	808.1	40.909092 A.H3L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gil6320334/refINP_010414_1	YDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the organization and maintenance of the actin cytoskeleton; Sacon	3	5 4821	0 4106	2792 12	2794 02	1	2054.2	40 909092 A H3I 1F1N2T1H3P1G1I 1F1P1I102F1F1F1K2P1F1I1F1F1F1 D
	10111200	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the					2.0.02		2001.2	
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	2	3.8358	0.3015	2762.79	2764.02	1	634.2	36.36363636 A.HLFNTHPGLEPIQEEEKPEIEEF.D A.H3L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1G1E1R4E1A
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	3	5.5396	0.3949	4070.21	4071.349	1	601.8	25 1R4V1F1.T
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	3.7284	0.3026	1365.87	1366.675	1	1069.9	80 F.L1R4L1P1P1E1Q2I1L1L1R4.W
ail6320334/refINP 010414.1/	YDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the organization and maintenance of the actin cytoskeleton; Sac6p	2	3.3486	0.2799	1418.29	1417.561	1	701.7	68.181816 F.RAIDLDDKGWVE.K
ail6220224/rofIND_010414_1	VDB120C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	2	E 2061	0.292	2020.02	2021 208	1	225	H.L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1G1E1R4E1A1F
gil0320334[tet]NF_010414.1]	IDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	3	5.5001	0.363	3929.93	3931.200	1	335	24.210/34V1F1.1
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p Fimbrin, actin-bundling protein: cooperates with Scp1p (calponin/transgelin) in the	3	5.0139	0.375	3888.02	3887.208	1	420.5	26.5625 H.LFNTHPGLEPIQEEEKPEIEEFDAEGEREARVF.T
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	3	4.6298	0.3823	3110.36	3112.303	1	855.2	29 A.H3L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1.G
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	3	4.8514	0.377	3077.99	3079.303	1	1286.4	34 A.HLFNTHPGLEPIQEEEKPEIEEFDAE.G
gil6320334/refINP_010414_1	YDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the organization and maintenance of the actin cytoskeleton; Sacon	3	4 6725	0.3633	2763.08	2764 02	1	1650	
	VDD4000	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	~	4 0000	0.005		0704.00			
gijo320334[rei]NP_010414.1	TDR 129G	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the	2	4.3203	0.2654	2192.69	2194.02	1	0∠0.3	30.030304 A.H3EIFINZIIH3FIGILIEIFIIIQZEIEIEIKZPIEIIIEIEIFI.D
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p Fimbrin, actin-bundling protein; cooperates with Sco1p (calponin/transgelin) in the	2	3.8053	0.1963	1262.33	1262.489	1	1062.9	85 S.LFDDLKDGLIL.L
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	3.8721	0.2989	2276.55	2275.439	1	484.3	50 N.T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	3	4.8275	0.1793	1366.55	1366.675	4	1648.7	65 F.L1R4L1P1P1E1Q2I1L1L1R4.W

		Finite in acting to addition production and an angle of the Angle of t								
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	3.1545	0.2452	1349.41	1348.675	1	942.9	75 F.LRLPPEQILLR.W
gi 6320334 ref NP_010414.1	YDR129C	organization and maintenance of the actin cytoskeleton; Sac6p	2	3.7279	0.2722	1365.75	1366.675	1	1110.8	80 F.L1R4L1P1P1E1Q2I1L1L1R4.W
		tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell								
gi 6320353 ref NP_010434.1	YDR150W	cortex; Num1p Protein required for nuclear migration, localizes to the mother cell cortex and the bud	1	2.2862	0.1763	1367.61	1365.554	1	461.2	55 K.LTNLSMECRQL.K
gi 6320353 ref NP_010434.1	YDR150W	tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell cortex; Num1p	2	3.2736	0.2866	1671.79	1669.795	1	735.1	66.66667 L.VDQIEYDETIRKC.N
		Protein required for nuclear migration, localizes to the mother cell cortex and the bud tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell								
gi 6320353 ref NP_010434.1	YDR150W	cortex; Num1p Protein required for nuclear migration, localizes to the mother cell cortex and the hud	2	3.7097	0.2807	1713.95	1714.926	2	805.7	60.714287 R.K2E1N2L1P1N2L1E1K2P1I1V1D1N2A1.S
	VDD450W	tip: may mediate interactions of dynein and cytoplasmic microtubules with the cell		0.0400	0.0005	1700.01	1701.010		074.0	
gilb320353[rei]NP_010434.1]	TDR ISUW	Protein required for nuclear migration, localizes to the mother cell cortex and the bud	2	3.0100	0.2305	1730.21	1734.916	1	874.3	61.536464 S.ETETDITIFTDITIVITETTDITISMI.I
gi 6320353 ref NP_010434.1	YDR150W	tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell cortex; Num1p	2	3.5489	0.2438	1907.45	1907.131	1	967.4	63.333332 Q.RKYSELEKEVEQPSLA.Y
		Protein required for nuclear migration, localizes to the mother cell cortex and the bud tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell								
gi 6320353 ref NP_010434.1	YDR150W	cortex; Num1p Protein required for nuclear migration, localizes to the mother cell cortex and the bud	2	3.7354	0.26	1718.97	1718.916	1	864	57.692307 S.EEDIFDIVIEIDHM.I
ail62202521rofIND_010424.41		tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell	2	2 0050	0.2497	1027.25	1020 121	1	208.2	
gilo32033311011NF_010434.11	TDK 150W	Protein required for nuclear migration, localizes to the mother cell cortex and the bud	2	3.0000	0.3407	1927.33	1929.131		396.3	55.555550 Q.R4R21151E1L1E1R2E1V1E1Q2F151L1A1.1
gi 6320353 ref NP_010434.1	YDR150W	tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell cortex; Num1p	2	3.0657	0.212	1697.37	1694.926	1	373	53.571426 R.KENLPNLEKPIVDNA.S
		Protein required for nuclear migration, localizes to the mother cell cortex and the bud tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell								
gi 6320353 ref NP_010434.1	YDR150W	cortex; Num1p Protein required for nuclear migration, localizes to the mother cell cortex and the bud	2	3.634	0.2306	1629.13	1626.977	1	765.6	73.07692 F.NLLKEPTIDFLLPL.T
ail63203531refINP_010434_1	VDR150W	tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell	2	4 0824	0 2433	1605.89	1606 857	1	960.2	70 83333 E I 1E1K2K2I 1E102P1S1I 1E1Y1I 1 V
giloo20000iiciinii _010404.11	IBRIGOW	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the	2	4.0024	0.2400	1000.00	1000.007		500.2	
gi 6320362 ref NP_010442.1	YDR158W	Gcn4p and the general control of amino acid synthesis; Hom2p	2	3.1151	0.2529	1439.89	1440.798	1	792.3	70.83333 A.G1L1V1A1P1L1K2P1L1I1E1K2F1.G
		Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by								
gi 6320362 ref NP_010442.1	YDR158W	Gcn4p and the general control of amino acid synthesis; Hom2p Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the	2	3.7553	0.3147	2949.49	2952.322	1	308.8	35.416664 K.N2Y1R4R4E1Q2D1V1P1L1I1V1P1V1V1N2P1E1H3L1D1I1V1A1Q2.K
ail63203621refINP 010442.11	YDR158W	common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	2	3.5164	0.2563	2914.61	2915.322	1	336.1	33.333336 K.NYRREQDVPLIVPVVNPEHLDIVAQ.K
51		Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and thrennine biosynthesis: expression regulated by								
gi 6320362 ref NP_010442.1	YDR158W	Gcn4p and the general control of amino acid synthesis; Hom2p	2	3.5865	0.1654	2714.85	2716.112	1	246.5	34.090908 K.NYRREQDVPLIVPVVNPEHLDIV.A
		common pathway for methionine and threonine biosynthesis; expression regulated by								
gi 6320362 ref NP_010442.1	YDR158W	Gcn4p and the general control of amino acid synthesis; Hom2p Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the	2	4.1799	0.2542	2750.67	2750.112	3	243.6	36.363636 K.N2Y1R4R4E1Q2D1V1P1L111V1P1V1V1N2P1E1H3L1D111V1.A
gi 6320362 ref NP_010442.1	YDR158W	common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	2	3.0398	0.1648	2636.71	2638.042	1	358.3	38.636364 Y.RREQDVPLIVPVVNPEHLDIVAQ.K
		Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by								
gi 6320362 ref NP_010442.1	YDR158W	Gcn4p and the general control of amino acid synthesis; Hom2p Aspartic beta semi-aldebyde debydrogenase, catalyzes the second step in the	2	3.3715	0.1654	2437.81	2438.833	1	298.6	42.5 Y.RREQDVPLIVPVVNPEHLDIV.A
	VDD450W	common pathway for methionine and threonine biosynthesis; expression regulated by	2	0.070	0.000	2027.00	0000.040		4455 5	
gilo320362[rei]NP_010442.1]	TDRISSW	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the	3	3.873	0.283	2637.89	2038.042	I	1155.5	30.303030 T.RREQUVPLIVPVVNPEHLDIVAQ.R
gi 6320362 ref NP_010442.1	YDR158W	common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	2	3.8171	0.2705	2671.63	2672.042	1	527.5	43.18182 Y.R4R4E1Q2D1V1P1L1I1V1P1V1V1N2P1E1H3L1D1I1V1A1Q2.K
		Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by								
gi 6320362 ref NP_010442.1	YDR158W	Gcn4p and the general control of amino acid synthesis; Hom2p Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the	2	3.5109	0.323	2468.05	2469.833	1	408.3	45 Y.R4R4E1Q2D1V1P1L1I1V1P1V1V1N2P1E1H3L1D1I1V1.A
gil6320362/refINP_010442.1	YDR158W	common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	3	4.9006	0.41	2915.69	2915.322	1	884.9	30.208334 K.NYRREODVPLIVPVVNPEHLDIVAQ.K
<u>9</u> ,1		Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the								
gi 6320362 ref NP_010442.1	YDR158W	Gen4p and the general control of amino acid synthesis; Hom2p	2	3.1689	0.3014	2467.71	2469.833	4	184.2	40 Y.R4R4E1Q2D1V1P1L1I1V1P1V1V1N2P1E1H3L1D1I1V1.A
		common pathway for methionine and threonine biosynthesis; expression regulated by								
gi 6320362 ref NP_010442.1	YDR158W	Gcn4p and the general control of amino acid synthesis; Hom2p	3	4.1395	0.2593	2472.71	2469.833	6	532.5	33.75 Y.R4R4E1Q2D1V1P1L1I1V1P1V1V1N2P1E1H3L1D1I1V1.A
		Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the								
gi 6320374 ref NP_010454.1	YDR170C	cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	3.2349	0.2283	1564.59	1564.664	4	429.4	62.5 M.DKLNDDEERLMDA.Q
		Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the								
gi 6320374 ref NP_010454.1	YDR170C	cytoplasm and on Golgi-associated coated vesicles; Sec7p	3	4.1455	0.1667	2495.33	2495.71	5	1019.5	32.954548 S.N2D1Q2R4Q2D1A1A1D1G1I1T1P1P1P1K2Q2K2I1I1D1A1A1.I
		Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in								
gi 6320374 ref NP_010454.1	YDR170C	cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	4.1417	0.2973	2739.63	2740.969	1	965.7	52.380955 L.N2E1L1F1E1N2E1D1F1A1H3C1I1P1Y1K2E1A1I1R4I1T1.R
		Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in								
gi 6320374 ref NP_010454.1	YDR170C	proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	3.4269	0.2716	2710.31	2710.969	1	417.4	40.476192 L.NELFENEDFAHCIPYKEAIRIT.R

gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	3.1591	0.1938	2096.95	2097.252	1	480.3	59.375 Y.NENKTEEERKHNDALLR.G
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	4.3736	0.3824	2406.45	2407.605	1	456.4	50 C.FYNENKTEEERKHNDALLR.G
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	4.0546	0.3034	2438.51	2439.605	1	411.4	47.22222 C.F1Y1N2E1N2K2T1E1E1E1R4K2H3N2D1A1L1L1R4.G
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	3	3.9184	0.2966	2409.47	2407.605	1	1742.5	43.055553 C.FYNENKTEEERKHNDALLR.G
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	3.499	0.2637	1856.27	1856.079	2	682.8	64.28571 E.D1F1A1H3C111P1Y1K2E1A111R4I1T1.R
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	3.2192	0.3387	1435.69	1436.623	1	478.2	72.72727 F.R4L1P1G1E1G1Q2K2I1D1R4F1.M
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	4.2619	0.3514	2406.79	2407.605	1	574.1	52.77778 C.FYNENKTEEERKHNDALLR.G
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	3	4.421	0.3333	2666.66	2663.86	1	758.9	34.090908 Q.EFLENNEGIDNGRDLPRDFLEGL.F
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	3	3.9327	0.2607	2406.29	2407.605	6	862.5	34.72222 C.FYNENKTEEERKHNDALLR.G
gi 6320374 ref NP_010454.1	YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	2	3.5131	0.3175	2406.47	2407.605	1	286.5	44.444447 C.FYNENKTEEERKHNDALLR.G
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	5.2013	0.378	1943.47	1941.025	1	1647.3	73.333336 L.I1K2E1Q2E1E1E1V1D1D1E1V1V1N2D1M1.F
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.6096	0.4745	2047.83	2050.223	1	857.6	65.625 K.D1H3V1D1P1K2E1C1P1W2Y1T1G1P1T1L1L1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.1788	0.3585	2030.41	2029.223	1	994.5	68.75 K.DHVDPKECPWYTGPTLL.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.8758	0.2501	1898.19	1898.164	3	378.1	50 T.KVEEPVKKEEKPVQTE.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.2501	0.3332	1918.11	1919.164	2	441.9	53.333336 T.K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	6.6778	0.2879	3692.54	3693.103	1	1281.5	T.K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1E1K2T1E1E1K2S1E1L1P1K2V1E1D1L 31.666666 1.K
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	6.2281	0.3964	4024.04	4025.515	1	1500.4	T.K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1E1K2T1E1E1K2S1E1L1P1K2V1E1D1L 33.333336 1K2l1S1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	4.2147	0.2742	2909.3	2910.291	2	396	30.208334 E.TKEPTKEPTKVEEPVKKEEKPVQTE.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.954	0.4015	1897.59	1899.007	1	360.7	60.000004 A.R4K2G1E1Y1E1T1G1F1E1R4G1G1Q2T1R4.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.0366	0.2881	1340.41	1340.453	1	491.7	70 M.N2H3V1D1R4H3I1N2A1P1F1.M
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.5395	0.3981	2384.51	2384.66	1	436.4	50 A.NLKDHVDPKECPWYTGPTLL.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	5.4557	0.4497	2408.59	2410.66	1	510.6	52.63158 A.N2L1K2D1H3V1D1P1K2E1C1P1W2Y1T1G1P1T1L1L1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	1	3.1316	0.2581	1320.53	1320.453	1	161	60.000004 M.NHVDRHINAPF.M

gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	5.261	0.4104	2090.59	2089.201	1	1686.1	65.625 L.I1K2E1Q2E1E1E1V1D1D1E1V1V1N2D1M1F1.G
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.4178	0.3074	1827.07	1828.896	2	363.7	50 M.D1T1N2K2E1E1R4N2D1G1K2T111E1V1G1.K
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	5.123	0.2631	2350.59	2351.479	1	1074.9	55.263157 L.I1K2E1Q2E1E1E1V1D1D1E1V1V1N2D1M\$F1G1G1K2.D
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	5.4222	0.3164	2337.59	2335.479	1	1238.1	39.473686 L.I1K2E1Q2E1E1E1V1D1D1E1V1V1N2D1M1F1G1G1K2.D
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	5.7375	0.3798	2310.71	2311.479	1	2249.5	60.526318 L.IKEQEEEVDDEVVNDMFGGK.D
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.9711	0.2443	2124.51	2125.375	2	402.6	47.058823 E.E1K2T1E1E1K2S1E1L1P1K2V1E1D1L1K2I1S1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	7.2761	0.4719	2334.11	2335.479	1	3275.6	71.05263 L.I1K2E1Q2E1E1E1V1D1D1E1V1V1N2D1M1F1G1G1K2.D
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	4.9615	0.376	3006.02	3008.233	2	513.9	26.923079 K.V1G1T1K2P1A1E1S1D1K2K2E1E1E1K2S1A1E1T1K2E1P1T1K2E1P1T1.K
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	5.6016	0.373	3652.34	3654.103	1	1274.6	33.333336 T.KVEEPVKKEEKPVQTEEKTEEKSELPKVEDL.K
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.6001	0.324	2157.27	2158.341	1	426.8	44.11765 A.NLKDHVDPKECPWYTGPT.L
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.1775	0.3675	2271.27	2270.556	1	476.7	52.77778 N.LKDHVDPKECPWYTGPTLL.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	4.5037	0.153	2410.31	2410.66	4	652.7	36.842106 A.N2L1K2D1H3V1D1P1K2E1C1P1W2Y1T1G1P1T1L1L1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.9312	0.325	1941.55	1943.086	1	566.7	65.625 S.ARKGEYETGFERGGQTR.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	1	3.0255	0.3354	1339.68	1340.453	1	173.5	60.000004 M.N2H3V1D1R4H3l1N2A1P1F1.M
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.9407	0.4063	1872.51	1872.007	1	407.5	63.333332 A.RKGEYETGFERGGQTR.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.5812	0.4724	1969.51	1971.086	1	577.6	65.625 S.A1R4K2G1E1Y1E1T1G1F1E1R4G1G1Q2T1R4.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	4.9794	0.4253	3231.41	3231.582	1	983.7	26.785713 T.KKVGTKPAESDKKEEEKSAETKEPTKEPT.K
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.9364	0.3588	1810.21	1808.832	1	1034.1	64.28571 L.I1K2E1Q2E1E1E1V1D1D1E1V1V1N2D1.M
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.2656	0.2727	1921.51	1922.025	1	1802	76.666664 L.IKEQEEEVDDEVVNDM.F
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	5.3864	0.3962	3071.45	3072.407	1	824.6	33 A.E1T1K2E1P1T1K2E1P1T1K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	5.3305	0.4369	3037.49	3039.407	1	846.3	32 A.ETKEPTKEPTKVEEPVKKEEKPVQTE.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.7361	0.3646	3070.03	3072.407	1	259.9	36 A.E1T1K2E1P1T1K2E1P1T1K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	3.0311	0.2196	3038.75	3039.407	1	229	34 A.ETKEPTKEPTKVEEPVKKEEKPVQTE.E

gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	6.0051	0.2903	3752.06	3753.084	1	1031	K.E1E1E1K2S1A1E1T1K2E1P1T1K2E1P1T1K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T 26.612906 1E1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	1	3.0848	0.2272	1339.52	1340.453	1	164.8	60.000004 M.N2H3V1D1R4H3I1N2A1P1F1.M
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	3	5.1655	0.2838	2940.59	2942.291	1	938.2	32.291664 E.T1K2E1P1T1K2E1P1T1K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	4.3955	0.4314	2293.49	2294.556	1	634.9	58.333332 N.L1K2D1H3V1D1P1K2E1C1P1W2Y1T1G1P1T1L1L1.E
gi 6320377 ref NP_010457.1	YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	2	2.9582	0.2595	1319.87	1320.453	1	557.7	70 M.NHVDRHINAPF.M
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	4.4998	0.3689	2171.33	2169.583	1	438.4	47.058823 F.V1V1D111E1V1P1M1E1Y1P1F1K2P1P1K2M1Q2.F
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	4.0306	0.4253	2146.91	2148.583	1	595	55.88235 F.VVDIEVPMEYPFKPPKMQ.F
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	3.5196	0.1791	1495.59	1493.822	1	1083.6	77.27273 V.PMEYPFKPPKMQ.F
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	3.7025	0.2319	1657.07	1656.998	2	959	66.66667 V.P1M1E1Y1P1F1K2P1P1K2M1Q2F1.D
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	4.2207	0.2734	2298.55	2295.76	1	1061.2	61.11111 F.VVDIEVPMEYPFKPPKMQF.D
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	4.3714	0.3301	2319.85	2317.76	1	1171.7	63.88889 F.V1V1D111E1V1P1M1E1Y1P1F1K2P1P1K2M1Q2F1.D
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	3	4.1582	0.2516	2319.95	2317.76	2	599.6	36.11111 F.V1V1D111E1V1P1M1E1Y1P1F1K2P1P1K2M1Q2F1.D
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	3.1418	0.1898	2639.93	2640.127	5	254.8	30.952381 F.VVDIEVPMEYPFKPPKMQFDTK.V
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	3	3.9736	0.2879	2666.78	2666.127	3	546.9	29.761904 F.V1V1D111E1V1P1M1E1Y1P1F1K2P1P1K2M1Q2F1D1T1K2.V
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	5.2939	0.4918	1773.43	1772.995	1	1650.6	71.875 L.K2G1T1F1L1G1P1P1G1T1P1Y1E1G1G1K2F1.V
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	4.019	0.4085	1467.37	1467.664	1	569.8	69.230774 T.FLGPPGTPYEGGKF.V
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	3.5905	0.4668	1482.09	1482.664	1	681.7	76.92308 T.F1L1G1P1P1G1T1P1Y1E1G1G1K2F1.V
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	3.1933	0.2219	2099.09	2097.495	1	671.6	50 V.DIEVPMEYPFKPPKMQF.D
gi 6320382 ref NP_010462.1	YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	2	4.2243	0.3925	1753.23	1753.995	1	1340.6	71.875 L.KGTFLGPPGTPYEGGKF.V
gi 6320410 ref NP_010490.1	YDR204W	Protein with a role in ubiquinone (Coenzyme Q) biosynthesis, possibly functioning in stabilization of Coq7p; located on the matrix face of the mitochondrial inner membrane; component of a mitochondrial ubiquinone-synthesizing complex; Coq4p	2	2.9446	0.1747	2275.41	2274.556	1	448.8	47.368423 E.NVSPDTRAPVKFIDDPMHAY.I
gi 6320410 ref NP_010490.1	YDR204W	Protein with a role in ubiquinone (Coenzyme Q) biosynthesis, possibly functioning in stabilization of Coq7p; located on the matrix face of the mitochondrial inner membrane; component of a mitochondrial ubiquinone-synthesizing complex; Coq4p	2	3.3421	0.2397	2560.79	2559.859	3	353.6	35.714287 K.RENVSPDTRAPVKFIDDPMHAY.I
gi 6320410 ref NP_010490.1	YDR204W	Protein with a role in ubiquinone (Coenzyme Q) biosynthesis, possibly functioning in stabilization of Coq7p; located on the matrix face of the mitochondrial inner membrane; component of a mitochondrial ubiquinone-synthesizing complex; Coq4p Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine-	2	3.1006	0.1582	1530.31	1530.724	2	402.6	72.72727 A.KEAEERTELRIR.A
gi 6320417 ref NP_010497.1	YDR211W	nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression; Gcd6p	2	4.3079	0.2815	1808.39	1807.007	1	1182.9	71.42857 Q.I1D1P1E1L1L1D1N2V1D1E1F1V1I1R4.N

		Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine- nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorytated eIF2; first identified as a negative regulator of GCN4 expression;								
gi 6320417 ref NP_010497.1	YDR211W	Gcd6p Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine- nucleotide exchange factor for eIF2; activity subsequently regulated by	2	4.3321	0.3593	2014.75	2017.212	1	549.1	50 F.N2V1K2l1D1D1N2M1D1L1D1R4N2T1K2l1S1.A
gi 6320417 ref NP_010497.1	YDR211W	phosphorylated eIF2; first identified as a negative regulator of GCN4 expression; Gcd6p	2	4.0692	0.2007	1987.53	1989.158	4	312.7	53.333336 W.W2D1N2V1S1T1D1P1R4Y1D1E1V1K2K2L1.T
		Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine- nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorytated eIF2; if identified as a negative regulator of GCN4 expression;								
gi 6320417 ref NP_010497.1	YDR211W	Gcd6p Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine- nucleotide exchange factor for eIF2: activity subsequently regulated by	1	2.2181	0.1646	1275.54	1276.453	1	400.1	61.11111 N.S1K2W2N2L1P1W2S1P1F1.K
ail6220417/rofIND_010407_1		phosphorylated eIF2; first identified as a negative regulator of GCN4 expression;	1	2 6505	0.2159	1190 5	1100 275	4	206.4	62 5 5 KOWONOI 404W0540454 K
gij6320417 ret NP_010497.1	YDR211W	Coop Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine- nucleotide exchange factor for eIF2; activity subsequently regulated by	1	2.6595	0.2158	1189.5	1188.375	4	296.4	62.5 S.K2W2N2L1P1W2S1P1F1.K
gi 6320417 ref NP_010497.1	YDR211W	phosphorylated eIF2; first identified as a negative regulator of GCN4 expression; Gcd6p	2	3.318	0.2315	1965.09	1966.158	1	488.9	60.000004 W.WDNVSTDPRYDEVKKL.T
		Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine- nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression;								
gi 6320417 ref NP_010497.1	YDR211W	Gcd6p Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine- nucleotide exchange factor for eIF2; activity subsequently regulated by	1	2.4878	0.1787	1206.45	1206.401	2	436.7	66.66667 Q.S1F1D1K2P1D1L11L1F1.S
ail6320417/refINP_010497_1	VDR211W	phosphorylated eIF2; first identified as a negative regulator of GCN4 expression;	1	2 624	0 1621	1176 52	1175 375	8	278.8	62.5.5. KWNI PWSPE K
giloszo417 [cilital _010457.1]	TDRZTTW	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the		2.024	0.1021	1170.02	1110.010	0	270.0	
gi 6320432 ref NP_010512.1	YDR226W	mitochondria; lacks cleavable signal sequence; Adk1p Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the	2	4.7496	0.4208	2124.93	2125.339	1	897.1	55.88235 Y.H3K2I1F1N2P1P1K2E1D1M1K2D1D1V1T1G1E1.A
gi 6320432 ref NP_010512.1	YDR226W	mitochondria; lacks cleavable signal sequence; Adk1p	3	4.4276	0.3494	2127.86	2125.339	1	926.7	41.17647 Y.H3K2I1F1N2P1P1K2E1D1M1K2D1D1V1T1G1E1.A
gi 6320432 ref NP_010512.1	YDR226W	Adenyiate kinase, required for purine metaoolism; localized to the cytopiasm and the mitochondris; lacks cleavable signal sequence; Adk1p 5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic	2	4.268	0.3544	2102.79	2101.339	1	1126.1	61.764706 Y.HKIFNPPKEDMKDDVTGE.A
gi 6320438 ref NP_010518.1	YDR232W	partway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is required by Hap2P-Hap3P; Hem1p 5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic	1	2.6718	0.1777	1357.49	1357.596	3	285.2	54.166668 I.PNPSHIVPVLIGN.A
gi 6320438 ref NP_010518.1	YDR232W	partway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is required by Hap2P-Hap3p; Hem1p 5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic	2	3.4634	0.3115	1838.75	1837.216	1	692.8	52.941177 L.GIPVIPNPSHIVPVLIGN.A
gi 6320438 ref NP_010518.1	YDR232W	pathway; an N-terminal signal sequence is required to localization to the mitochondrial matrix; expression is requilated by Hap2P-Hap3p; Hem1p 5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic	2	3.8659	0.3806	2218.61	2216.632	1	554.7	45 F.HELGIPVIPNPSHIVPVLIGN.A
gi 6320438 ref NP_010518.1	YDR232W	pathway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is requilated by Hap2P-Hap3p; Hem1p 5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic	2	5.0909	0.4442	2244.53	2243.632	1	549.6	45 F.H3E1L1G111P1V111P1N2P1S1H3I1V1P1V1L111G1N2.A
gi 6320438 ref NP_010518.1	YDR232W	mitochondrial matrix; expression is regulated by Hap2p-Hap3p; Hem1p	2	3.4768	0.3115	1859.55	1859.216	3	584	50 L.G1I1P1V1I1P1N2P1S1H3I1V1P1V1L1I1G1N2.A
gi 6320439 ref NP_010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	3.8092	0.291	1726.29	1725.946	2	340.1	61.538464 A.CEKTKPYLDKVESK.L
ail6320439/refINP 010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily: Rtn1p	3	3.8715	0.1585	4710.14	4712.156	1	455.7	18.75 Q.VMPEVPQHEPSTTQEFNVDELSNELKKSTKNLQNELEKNNA
gil6320439/refINP_010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily: Rtn1n	2	3 5245	0 3111	1742 53	1743 946	1	366.7	65 38461 A C1E1K2T1K2P1Y1I 1D1K2V1E1S1K2 I
gil62201201rofIND_010510.1	VDB333C	Protein of unknown function; has similarity to mammalian reticulon proteins; member	-	E 0000	0.2505	2406 52	2404 604		2215 4	
	IDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member	3	5.2330	0.2595	2400.55	2404.094		2213.4	
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p Protein of unknown function; has similarity to mammalian reticulon proteins; member	2	5.5071	0.4419	2402.25	2404.694	1	766.9	60.000004 M.A1C1E1K211K2P1Y1L1D1K2V1E1S1K2L1G1P111S1N2.L
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p Protein of unknown function; has similarity to mammalian reticulon proteins; member	2	5.6058	0.2782	2025.67	2025.346	1	1489.1	67.64706 K.T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2L1.V
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	5.4115	0.4017	2005.63	2003.346	1	1722.2	64.70589 K.TKPYLDKVESKLGPISNL.V
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	4.9201	0.3377	2490.65	2491.854	1	1220.7	54.761906 M.ACEKTKPYLDKVESKLGPISNL.V
gi 6320439 ref NP_010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	5.6787	0.4227	2517.45	2518.854	1	1483.3	57.14286 M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2L1.V
gi 6320439 ref NP_010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily; Rtn1p	3	5.8833	0.1904	2519	2518.854	2	1284	39.285713 M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2L1.V
gil6320439/refINP_010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily: Rtn1p	2	2,9833	0.2569	1748.37	1749.106	1	716.4	60.714287 F. IKPHIDEALKOLPVE.Q
gi 6320/39/rofINP_010519_1	VDP233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member	2	4 7455	0.3107	1060.83	1071 316	1	1202.4	
	IDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member	2	4.7400	0.3107	1909.83	1971.310		1202.4	
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p Protein of unknown function; has similarity to mammalian reticulon proteins; member	2	3.9983	0.3593	1952.77	1953.335	1	1384.1	68.75 A.GFIKPHIDEALKQLPVF.Q
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p Protein of unknown function; has similarity to mammalian reticulon proteins; member	2	4.2136	0.3085	1797.03	1797.025	1	1134.2	71.42857 M.ACEKTKPYLDKVESK.L
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	4.8135	0.3578	2377.81	2378.694	1	605.4	55 M.ACEKTKPYLDKVESKLGPISN.L
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	3	6.345	0.3351	2521.19	2518.854	1	2595.7	44.04762 M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2L1.V
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	3	5.7839	0.3652	2489.18	2491.854	1	1785.4	39.285713 M.ACEKTKPYLDKVESKLGPISNL.V
gi 6320439 ref NP_010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	5.8941	0.4091	2517.33	2518.854	1	1633.3	59.523808 M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2L1.V
gi 6320439 ref NP_010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	4.2129	0.3299	1877.23	1877.237	1	1079.9	70 F.IKPHIDEALKQLPVFQ.A
gi 6320439 ref NP_010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily; Rtn 1p Protein of unknown function; bas similarity to mammalian reticulon proteins; member	2	3.2386	0.2744	1770.43	1769.106	2	717.4	60.714287 F.I1K2P1H3I1D1E1A1L1K2Q2L1P1V1F1.Q
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	3.8254	0.3264	1947.99	1948.316	1	573.1	50 F.IKPHIDEALKQLPVFQA.H

		Protein of unknown function; has similarity to mammalian reticulon proteins; member								
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p Protein of unknown function; has similarity to mammalian reticulon proteins; member	2	3.5253	0.2274	2081.53	2081.465	1	430.7	44.11765 A.GFIKPHIDEALKQLPVFQ.A
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	3.6194	0.2982	2104.75	2105.466	2	512.4	44.11765 A.G1F1I1K2P1H3I1D1E1A1L1K2Q2L1P1V1F1Q2.A
ail63204391refINP_010519_1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily: Rtn1p	1	3 3043	0 225	1415 43	1416 646	1	863.4	72 72727 H I1D1E1A1I 1K2Q2I 1P1V1E1Q2 A
giloozo400/relini _010010.11	10112000	Protein of unknown function; has similarity to mammalian reticulon proteins; member		0.0040	0.220	1410.40	1410.040		000.4	
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p Protein of unknown function; has similarity to mammalian reticulon proteins; member	1	3.2069	0.3057	1400.61	1401.646	1	873.1	72.72727 H.IDEALKQLPVFQ.A
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	3.6978	0.3113	1399.67	1401.646	1	945.5	81.818184 H.IDEALKQLPVFQ.A
gi 6320439 ref NP 010519.1	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily; Rtn1p	1	3.3889	0.2804	1487.41	1488.725	2	683.6	58.333332 H.I1D1E1A1L1K2Q2L1P1V1F1Q2A1.H
-ilc220.4201fND_040540.41	VDD0000	Protein of unknown function; has similarity to mammalian reticulon proteins; member		2.0502	0.0507	4 474 07	4470 705		704	
gilo320439/rei/NP_010519.1/	TDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member		3.0563	0.2537	1471.37	1472.725	1	701	62.5 H.IDEALKQLPVFQA.H
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p Protein of unknown function: has similarity to mammalian reticulon proteins: member	2	3.0342	0.2444	1472.25	1472.725	2	783.5	70.83333 H.IDEALKQLPVFQA.H
gi 6320439 ref NP_010519.1	YDR233C	of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	4.0292	0.2487	1815.23	1816.025	2	791.2	60.714287 M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2.L
ail63204391refINP 010519.11	YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily: Rtn1p	3	3.9149	0.2916	2517.41	2518.854	3	666.2	32.142857 M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2L1.V
51		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.333	0.3406	1510.27	1510.657	1	421.4	62.5 A.L1E1K2G1S1D1E1Q2K2I1D1T1M1.K
		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.8347	0.2103	1912.49	1913.175	3	498	56.666668 L.LDEVNPEEKKEEVKLL.E
		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.1117	0.1618	1548.47	1548.764	5	726.1	70.83333 C.K2N2I1E1P1I1D1T1P1I1S1F1R4.Q
		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.9265	0.3861	1800.21	1797.981	1	1149.3	71.42857 D.S1C1K2N2I1E1P1I1D1T1P1I1S1F1R4.Q
		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p	3	5.1718	0.2072	2021.63	2021.244	1	1792.9	50 L.KDSCKNIEPIDTPISFR.Q
		trafficking and maintenance of normal ER morphology; shares 43% sequence								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golai protein	2	4.3094	0.3872	2020.39	2021.244	1	1383.8	68.75 L.KDSCKNIEPIDTPISFR.Q
		trafficking and maintenance of normal ER morphology; shares 43% sequence								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p Essential beta-coat protein of the COPI coatomer, involved in ER-to-Goldi protein	2	3.7889	0.3799	2042.33	2044.244	1	725	56.25 L.K2D1S1C1K2N2I1E1P1I1D1T1P1I1S1F1R4.Q
		trafficking and maintenance of normal ER morphology; shares 43% sequence								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein	2	3.2615	0.2775	1965.67	1963.235	2	921	56.25 F.K2V1S1E1H3L1L1P1D1A1K2E1I1I1N2S1F1.I
	VDD0000	trafficking and maintenance of normal ER morphology; shares 43% sequence	2	2 4024	0.0004	4704.05	4700.050		574.0	
gilo320444/rei/inP_010524.1/	TDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein	2	3.4021	0.3284	1/31.00	1730.956	1	574.0	50 T.ARPTGPVILPDGTTATE.S
ail6320444/refINP_010524.1	VDR238C	trafficking and maintenance of normal ER morphology; shares 43% sequence	2	3 486	0 354	1494 25	1494 657	1	551	
giloozo444[ici]i4i _010024.1]	10112000	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein	2	0.400	0.004	1434.20	1404.007		551	00.0000 ALEROODE GRID HILK
ail6320444/refINP_010524.1	YDR238C	trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.7117	0.2419	1932.37	1933.175	2	448.5	56.666668 L.I.1D1E1V1N2P1E1E1K2K2E1E1V1K2L1L1.E
51		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein								
gi 6320444 ref NP_010524.1	YDR238C	trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP); Sec26p	2	4.5784	0.3916	2019.93	2021.244	1	1505.1	71.875 L.KDSCKNIEPIDTPISFR.Q
		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.3495	0.2889	1942.83	1941.235	1	833.4	59.375 F.KVSEHLLPDAKEIINSF.I
		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology: shares 43% sequence								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p	2	4.0403	0.3999	1622.65	1621.794	1	1139.4	76.92308 D.SCKNIEPIDTPISF.R
		Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology: shares 43% sequence								
gi 6320444 ref NP_010524.1	YDR238C	identity with mammalian beta-coat protein (beta-COP); Sec26p	2	4.0234	0.3619	1777.51	1777.981	1	988.5	67.85714 D.SCKNIEPIDTPISFR.Q
gi 6320449 ref NP_010529.1	YDR243C	RNA helicase in the DEAD-box family, involved in RNA isomerization at the 5' splice site; Prp28p	2	3.3729	0.2781	1958.89	1960.281	1	423.5	53.125 Y.ADNDEDKFKKLKPIVAK.Y
ail6220440/rofIND_040520_4	VDD040C	RNA helicase in the DEAD-box family, involved in RNA isomerization at the 5' splice	2	2 2072	0.2720	2260.25	2266 590	1	151.0	
gilo320449/rei/NP_010529.1/	TDR243C	RNA helicase in the DEAD-box family, involved in RNA isomerization at the 5' splice	2	3.3073	0.2739	2208.30	2200.089	1	151.9	47.22222 Q.ETLTR4FTP15TP111P111Q2R4I11111P1N2VTC1.N
gi 6320449 ref NP_010529.1	YDR243C	site; Prp28p RNA balicase in the DEAD box family, involved in RNA isomerization at the 5' splice	2	3.085	0.222	2240.79	2239.589	2	131.5	38.88889 Q.ELRFPSPTPIQRITIPNVC.N
gi 6320449 ref NP_010529.1	YDR243C	site; Prp28p	2	3.5133	0.2703	1983.61	1983.281	4	401.7	43.75 Y.A1D1N2D1E1D1K2F1K2K2L1K2P1I1V1A1K2.Y
gi 6320454 ref NP_010534.1 gi 6320454 ref NP_010534.1	YDR248C	hypothetical protein; Ydr248cp hypothetical protein; Ydr248cp	3	4.0187 4 7583	0.1693	2814.95 3085.04	2816.172 3086.398	2	448.7 1314 1	27.173912 F.K2D1I1Y1P1D1L1K2F1I1E1G1D1D1L1H3P1P1A1N2V1E1K2M1.T 35 L 11H3E1E1K2D111Y1P1D1L1K2E111E1G1D1D1L1H3P1P1A1N2V1E1 k
gi 6320454 ref NP_010534.1	YDR248C	hypothetical protein; Ydr248cp	3	5.3907	0.3343	3346.19	3348.764	1	1245.9	30.555555 LI1H3E1F1K2D1I1Y1P1D1L1K2F1I1E1G1D1D1L1H3P1P1A1N2V1E1K2M1.1
gi 6320454 ref NP_010534.1	YDR248C	hypothetical protein; Ydr248cp	3	4.9115	0.2441	2785.67	2786.172	2	636.8	31.52174 F.KDIYPDLKFIEGDDLHPPANVEKM.T
gi 6320454 ref NP_010534.1	YDR248C	hypothetical protein; Ydr248cp	2	3.3672	0.2972	1925.81	1927.204	1	436.8	53.571426 L.I1H3E1F1K2D1I1Y1P1D1L1K2F1I1E1.G
gi 6320454 ref NP_010534.1	YDR248C	hypothetical protein; Ydr248cp	3	3.8984	0.1826	3094.04	3094.464	1	503.5	24 H.E1F1K2D1I1Y1P1D1L1K2F1I1E1G1D1D1L1H3P1P1A1N2V1E1K2M1.7
gijb320454 ret NP_010534.1	YDR248C	nypotnetical protein; Ydr248cp Oligomeric mitochondrial matrix chanerone that cooperates with Ssc1n in	3	5.029	0.155	3055.16	3053.398	1	1153	32 L.IHEFKDIYPDLKFIEGDDLHPPANVE.K
		mitochondrial thermotolerance after heat shock; prevents the aggregation of								
gil6320464/refINP_010544_1	YDR258C	misfolded matrix proteins; component of the mitochondrial proteolysis system; Hsp78p	2	4.3206	0.4558	1513.33	1514 543	1	1660.2	83.33333 N HEEGEVVEEEAEK -
9-1-0-20 in the line _0 100-41 [Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in	2		0.7000					
		mitochondrial thermotolerance after heat shock; prevents the aggregation of misfolded matrix proteins; component of the mitochondrial protectives system;								
gi 6320464 ref NP_010544.1	YDR258C	Hsp78p	1	2.6786	0.1945	1169.62	1170.414	2	288.2	70 S.R4L1I1G1A1P1P1G1Y1V1L1.S
		Oligometric mitochondrial matrix chaperone that cooperates with Ssc1p in mitochondrial thermotolerance after heat shock prevents the approaching of								
		misfolded matrix proteins; component of the mitochondrial proteolysis system;								
gi 6320464 ref NP_010544.1	YDR258C	Hsp78p	3	3.8244	0.1851	2152.01	2153.405	1	393.2	34.72222 A.R4D1G1K2L1D1P1V111G1R4D1E1E111A1R4A111.Q
		Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in mitochondrial thermotolerance after heat shock; prevents the aggregation of misfolded matrix proteins; component of the mitochondrial proteolysis system;								
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gi 6320464 ref NP_010544.1	YDR258C	Hsp78p Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in mitochondrial thermotolerance after heat shock; prevents the aggregation of	2	3.2853	0.2707	1528.11	1530.543	1	521.7	70.83333 N.H3E1E1G1E1V1V1E1E1E1A1E1K2
gi 6320464 ref NP_010544.1	YDR258C	mistoided matrix proteins; component or the mitochondrial proteolysis system; Hsp78p Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in	2	4.3155	0.2951	2037.93	2037.188	1	1063.2	64.70589 L.VVLPNHEEGEVVEEEAEK
		mitochondrial thermotolerance after heat shock; prevents the aggregation of misfolded matrix proteins: component of the mitochondrial proteolysis system:								
gi 6320464 ref NP_010544.1	YDR258C	Hsp78p Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in	2	3.0015	0.1624	2046.69	2046.337	2	403.8	41.17647 D.RFLPDKAIDLVDEACAVL.R
		mitochondrial thermotolerance after heat shock; prevents the aggregation of misfolded matrix proteins: component of the mitochondrial proteolysis system:								
gi 6320464 ref NP_010544.1	YDR258C	Hsp78p Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in	2	3.2333	0.2565	2067.57	2068.337	1	536	41.17647 D.R4F1L1P1D1K2A1I1D1L1V1D1E1A1C1A1V1L1.R
ail6320464/rofIND_010544_1	VDP258C	misochondrial thermotolerance after heat shock; prevents the aggregation of misfolded matrix proteins; component of the mitochondrial proteolysis system;	2	3 0253	0.2416	1722 50	1720 861	٥	255.3	
giloszo404fielliti _010344.1	TDR256C	Disprop Oligometric mitochondrial matrix chaperone that cooperates with Ssc1p in mitochondrial thermotolerance after heat shock; prevents the aggregation of misfolded matrix proteins; component of the mitochondrial proteolysis system;	2	3.0233	0.2410	1722.55	1720.001	5	200.0	
gi 6320464 ref NP_010544.1	YDR258C	Hsp78p TVB Gag-Pol protein: proteolytically processed to make the Gag, RT, PR, and IN	1	2.3983	0.1806	1156.71	1156.414	1	239.4	65 S.RLIGAPPGYVL.S
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	1	3.1581	0.389	1523.18	1524.671	1	486.8	50 Q.S1Q2F1P1Q2Y1P1S1S1V1G1T1P1L1.S
gi 7839160 ref NP_058148.1	YDR261C-D	ryB Gag-Poi protein; proteolytically processed to make the Gag, R1, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	3.1186	0.2559	1206.53	1204.327	1	757.2	77.77778 T.SPNDFPNWVK.T
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	3.1823	0.1745	2256.31	2257.595	1	267.2	38.88889 W.S1F1Y1G1H3P1S1M1I1P1Y1T1P1Y1Q2M1S1P1M1.Y
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	3.2946	0.2556	1647.49	1648.726	1	424	50 A.S1S1A1V1P1E1N2P1H3H3A1S1P1Q2P1A1.S
ai 7839160 ref NP 058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	3	3.8051	0.2615	3160.94	3159.563	5	415.1	27.777779 A.DLPLPDLPPESPTEFPDPFKELPPINSR.Q
ail7839160/refINP_058148_1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	3 3738	0 2476	1970 73	1969 211	5	292 1	50 T V1N2G1K2P1V1R4O2I1T1D1D1E1I 1T1E1I 1 Y
gil7830160/rofIND_058148_1	VDP261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	-	4 5226	0.2302	3070.43	3078 431	1	977.9	
	VDD2010-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	5	9.0220	0.2002	007 0.40	2250 744	7	500	
gij7839160jreijNP_058148.1	TDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	3	3.8622	0.2008	3356.78	3356.711		529	
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	3	4.5812	0.355	3190.25	3192.563	1	474.4	29.62963 A.D1L1P1L1P1D1L1P1P1E1S1P1T1E1F1P1D1P1F1K2E1L1P1P111N2S1R4.Q Q.N2T1E1E1S1I1I1A1D1L1P1L1P1D1L1P1E1S1P1T1E1F1P1D1P1F1K2E1L1P1
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	3	7.1112	0.4427	4062.05	4059.479	1	641.5	26.428572 P1I1N2S1R4.Q
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TVB Gao-Pol protein: proteolytically processed to make the Gao, RT, PR, and IN	3	5.0154	0.4341	4272.95	4274.725	1	659.8	22.297297 S.EQNTEESIIADLPLPDLPPESPTEFPDPFKELPPINSR.Q S.E102N2T1E1E1S1111A1D1L1P1L1P1D1L1P1P1E1S1P1T1E1E1P1D1P1E1K2E1
gi 7839160 ref NP_058148.1	YDR261C-D	TVB Gag Pol proteins that are required for retrotransposition; Ydr261c-dp	3	5.1094	0.4089	4319.63	4319.725	1	625.4	22.972973 L1P1P1I1N2S1R4.Q
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261rcdp	2	3.6741	0.3421	2394.95	2395.674	2	276.9	37.5 L.PPESPTEFPDPFKELPPINSR.Q
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	3.2696	0.3364	1471.65	1472.569	1	242.5	53.846157 S.A1V1P1E1N2P1H3H3A1S1P1Q2P1A1.S
gi 7839160 ref NP_058148.1	YDR261C-D	ryb Gag-Poi protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	1	2.6064	0.3324	1283.56	1284.374	1	470.5	54.545456 S.AVPENPHHASPQ.P
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	1	2.4737	0.1829	1301.53	1302.374	2	406.6	50 S.A1V1P1E1N2P1H3H3A1S1P1Q2.P
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	2.9387	0.1592	1284.29	1284.374	2	353.3	72.72727 S.AVPENPHHASPQ.P
ail7839160/refINP 058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition: Ydr261c-dp	2	2.9487	0.2671	1114.25	1114.162	1	464.5	77,77778 V.PENPHHASPQ.P
gil7839160/refINP_058148_1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	3 0541	0 3064	1300 19	1300 358	1	562.6	72 72727 V P1E1N2P1H3H3&1S1P1O2P1&1 S
gil7830160/rofIND_058148.1	VDR261C D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	3 3357	0.0004	1619.05	1610 915	1	502.0	
gi//639100 rei NF_036146.1	IDR201C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	3.3357	0.2007	1018.95	1019.015		545.4	
gi/839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	1	3.4098	0.3605	1569.64	1570.832	1	328.5	66.66667 K.E1E1L1Y111K4P1P1P1H3L1G1M1.N
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	1	3.0473	0.3844	1551.58	1552.832	1	311.2	62.5 K.EELYIRPPPHLGM.N
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	4.046	0.3556	1823.55	1821.046	1	610	63.333332 K.VTNIIDRLNNNGIHIN.N
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TVR Gaa-Pol protein: proteolytically processed to make the Gag, RT, PR, and IN	2	3.0524	0.1783	1946.43	1946.211	1	463	50 T.VNGKPVRQITDDELTFL.Y
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	3.6501	0.3226	2131.73	2133.387	4	231.6	41.17647 T.V1N2G1K2P1V1R4Q2I1T1D1D1E1L1T1F1L1Y1.N
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	3.3502	0.2322	2031.45	2032.324	1	552	50 K.YVRPPPMLTSPNDFPNW.V
gi 7839160 ref NP_058148.1	YDR261C-D	ryB Gag-Poi protein; proteolytically processed to make the Gag, R1, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	3.0176	0.2476	1454.15	1452.569	2	292	57.692307 S.AVPENPHHASPQPA.S
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	1	3.5914	0.4133	1471.5	1472.569	1	802.7	61.538464 S.A1V1P1E1N2P1H3H3A1S1P1Q2P1A1.S
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	1	2.7867	0.2601	1299.31	1300.358	1	512.3	59.090908 V.P1E1N2P1H3H3A1S1P1Q2P1A1.S
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	1	2.6313	0.3955	1281.46	1282.358	1	375.7	54.545456 V.PENPHHASPQPA.S
ail7839160/refINP_058148_1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition. Ydr261c-do	1	3,7763	0.4273	1454 55	1452,569	1	684 R	57 692307 S. AVPENPHHASPOPA S
gil7839160/refIND_059149.1	VDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ver261-cdp	, ,	3 6657	0.2507	1630 / 2	1638 915	1	532 /	65 38461 N G1K2P1V1R40211T1D1D1E1L1T1E1
gir 039 rouperine_030 140.1	VDP2010-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	3.0007	0.2097	2010 55	2010.054	1	200.0	
gij/639100[rei]NP_058148.1	TUR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	3.5816	0.3485	2010.55	2010.254	1	200.8	
gij/639160[ret]NP_058148.1]	1DK261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	3.8879	0.3123	1919.39	1917.15	1	418	03.333332 N.G1K2P1V1K4Q2I111U1U1E1L1111111111N

		TVD Cost Del anatoria, anatoria discilla anatoria da mello the Cost DT DD, and IN								
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	4.1199	0.3967	2247.59	2249.491	2	276.5	44.444447 T.V1N2G1K2P1V1R4Q2I1T1D1D1E1L1T1F1L1Y1N2.T
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	3	4.5443	0.1764	3578.96	3579.047	6	518.8	20.161291 K.FLQNSNLGGIIPTVNGKPVRQITDDELTFLYN.T
gil7839160/refINP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition. Ydr/261c-do	2	3.0122	0.228	1932.49	1933.198	5	289.1	50 K E1E1L1Y11R4P1P1P1H3L1G1M1N2D1K2.
	VDD0040 D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	-	4.0244	0.054	0400.45	0140 400	-	005.0	
gi/7839160[rei]NP_058148.1]	TDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	4.0344	0.354	2120.45	2119.430	1	0.000	56.623532 T.ATDTTKZETETETTTTK4PTPTPTBLTGTMTNZ.D
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	1	2.4076	0.2328	1499.7	1500.799	2	102	62.5 K.KYVRPPPMLTSPN.D
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	3.7562	0.2663	2283.77	2285.631	1	439.5	47.22222 K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2.T
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261cdp	2	3.2764	0.1884	2348.25	2347.436	1	183.3	44.444447 N.S1K2P1N2Y1R4R4N2P1S1D1E1K2N2D1S1R4S1Y1.T
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	4.0643	0.2965	1516.93	1518.799	1	1021.6	75 K.K2Y1V1R4P1P1P1M1L1T1S1P1N2.D
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	3.1728	0.255	2274.75	2275.631	1	205.4	41.666664 K.YVRPPPM@LTSPNDFPNWVK.T
ail78391601refINP 058148.11	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-do	2	3.2104	0.1561	2301.41	2301.631	1	318	47.22222 K.Y1V1R4P1P1P1M\$L1T1S1P1N2D1F1P1N2W2V1K2.T
gil7920160/rofIND_059149_1	VDP261C D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	-	4 2462	0.2520	2120.62	2121 455	4	1101.1	
gi/8591001ei/NF_056146.1	10K201C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	4.3403	0.2009	2120.03	2121.400		1101.1	01.704700 1. VIK4F IF IF IMILITISTE IN2DIFTE IN22VZ VIK2.1
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	3	4.7523	0.2835	2285.72	2285.631	1	1523.4	43.055553 K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2.T
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TVB Gag-Pol protein: proteolytically processed to make the Gag, RT, PR, and IN	2	4.1087	0.3232	2385.99	2387.736	1	624.8	52.63158 K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2T1.Y
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	4.0267	0.3202	2550.39	2551.912	1	752.7	50 K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2T1Y1.I
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	1	2.2548	0.172	1262.43	1263.453	2	346	55 Y.GHPSMIPYTPY.Q
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	3	4.4351	0.244	4015.43	4017.479	1	609.7	22.857143 Q.NTEESIIADLPLPDLPPESPTEFPDPFKELPPINSR.Q
ail78391601refINP 058148.11	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-do	2	2.9832	0.2907	1854.39	1855.051	1	527.6	50 T.V1N2G1K2P1V1R4Q2I1T1D1D1E1L1T1F1.L
gil7920160/rofIND_059149_1		TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	4 2505	0.0004	2422.02	2424 074	1	902.2	
	IDR201C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	3	4.2505	0.2004	3433.02	3431.071		802.2	
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	3.3796	0.2321	1832.05	1833.051	1	508.4	50 T.VNGKPVRQITDDELTF.L
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	3.095	0.2077	1734.27	1732.974	1	526.8	60.714287 N.GKPVRQITDDELTFL.Y
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TVB Gag-Pol protein: proteolytically processed to make the Gag, BT, PR, and IN	2	3.5687	0.2097	1750.17	1752.974	1	703.7	67.85714 N.G1K2P1V1R4Q2I1T1D1D1E1L1T1F1L1.Y
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	3.4187	0.3188	1894.71	1896.15	1	277.3	53.333336 N.GKPVRQITDDELTFLY.N
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	3.3421	0.2714	2111.53	2109.387	2	285.8	44.11765 T.VNGKPVRQITDDELTFLY.N
gi 7839160 ref NP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	3.2958	0.2862	1499.91	1500.799	1	828.5	70.83333 K.KYVRPPPMLTSPN.D
ail7839160/refINP_058148.1	YDR261C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-do	2	3.4273	0.2455	2094.63	2094.436	1	514.6	50 Y ADIKEEL YIRPPPHI GMN D
gil7920160/rofIND_059149_1	VDP261C D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	-	4 4656	0.2002	2294.67	2295 624	4	722.0	
gi/8591001ei/NF_056146.1	10K201C-D	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	4.4030	0.2993	2204.07	2203.031		133.2	
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	3	5.031	0.2793	2288.09	2285.631	1	1880.6	47.22222 K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2.T
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN	2	4.113	0.3534	2259.73	2259.631	1	632	55.555557 K.YVRPPPMLTSPNDFPNWVK.T
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	5.3063	0.3193	2010.43	2012.088	1	2492.9	80 Y.IDQDELEIDEDEYKEK.V
gi 7839160 ref NP_058148.1	YDR261C-D	proteins that are required for retrotransposition; Ydr261c-dp	2	3.5386	0.325	1666.29	1666.935	1	655.5	65.38461 K.EELYIRPPPHLGMN.D
		Diacylglycerol pyrophosphate (DGPP) phosphatase, zinc-regulated vacuolar membrane-associated lipid phosphatase, dephosphorylates DGPP to phosphatidate								
gi 6320490 ref NP_010570.1	YDR284C	(PA) and Pi, then PA to diacylglycerol; involved in lipid signaling and cell metabolism; Dpp1p	2	3.3481	0.263	1765.15	1766.136	1	747.1	64.28571 R.RIFPPIDDPLPFKPL.M
		Diacylglycerol pyrophosphate (DGPP) phosphatase, zinc-regulated vacuolar membrane-associated linid phosphatase, dephosphorylates DGPP to phosphatidate								
ail6220400/rofIND_040570.41	VDB204C	(PA) and Pi, then PA to diacylglycerol; involved in lipid signaling and cell	2	2 6600	0.2472	1792.01	1795 196	1	615.6	
gil6320490[rei]NP_010570.1]	TDR284C		2	3.0099	0.2473	1783.91	1765.136	1	015.0	00.714287 R.R4HFTPTPTHDTDTPTLTPTFTR2PTLT.M
		Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases,								
gi 6320500 ref NP_010580.1	YDR294C	prefers C16 dihydrosphingosine-l-phosphate as a substrate; Dpl1p	2	3.2539	0.2206	1496.69	1495.632	1	520.6	61.538464 A.PNFPHGIADDIEGL.G
		Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid								
gi 6320500 ref NP_010580.1	YDR294C	prefers C16 dihydrosphingosine-l-phosphate as a substrate; Dpl1p	2	3.3524	0.3094	1672.55	1672.789	3	276.7	53.333336 G.S1A1P1N2F1P1H3G1I1A1D1D1I1E1G1L1.G
		Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid								
ail63205001refINP 010580.11	YDR294C	long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-l-phosphate as a substrate: Dpl1p	1	2,462	0.2209	1200.49	1200.445	5	347.5	61.11111 N.G1W2Y1G1M1P1I1H3L1L1.R
	VDD0040	long-chain base phosphate (JCBPs), degrades phosphorylated long chain bases,		0.0450	0.0000		1100.000		504.4	
gi 6320500 ref NP_010580.1	YDR294C	prefers C16 dinydrospningosine-i-phosphate as a substrate; Upi1p	1	2.6456	0.2938	1180.48	1180.389	1	531.1	66.66667 A.GYKNLPLEDF.R
		Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases,								
gi 6320500 ref NP_010580.1	YDR294C	prefers C16 dihydrosphingosine-l-phosphate as a substrate; Dpl1p	2	3.0554	0.2345	1182.21	1180.389	2	964.1	83.33333 A.GYKNLPLLDF.R
		Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid								
gi 6320500 ref NP_010580.1	YDR294C	prefers C16 dihydrosphingosine-l-phosphate as a substrate; Dpl1p	2	2.9188	0.2274	1180.39	1180.389	3	921.5	77.77778 A.GYKNLPLLDF.R

gi 6320500 ref NP_010580.1	YDR294C	Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-l-phosphate as a substrate; Dp1p	1	2.6591	0.2025	1191.57	1192.389	1	658	72.22222 A.G1Y1K2N2L1P1L1L1D1F1.R
gi 6320500 ref NP_010580.1	YDR294C	Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-l-phosphate as a substrate; Dp1p	1	2.6111	0.3057	1179.41	1180.389	1	590.8	66.66667 A.GYKNLPLLDF.R
gi 6320500 ref NP_010580.1	YDR294C	Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-l-phosphate as a substrate; Dp1p	1	2.2096	0.2409	1186.84	1187.445	2	445.4	66.66667 N.GWYGMPIHLL.R
gi 6320503 ref NP_010583.1	YDR297W	phytosphingosine in sphingolipid biosyntheis; Sur2p	1	2.3874	0.1704	1583.79	1584.859	1	260.8	53.846157 L.RADLPRIIPDAAIY.Y
ail6320503lrefINP 010583.11	YDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosyntheis: Sur2p	2	3.0478	0.1662	1989.81	1991.347	1	539.9	50 N.L1R4P1K2E1S1L1L1P1E1M1S1D1G1V1L1A1L1.V
ail6220E02irofIND_010E92_1	VDB307W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to	1	2 2740	0 1557	1170.49	1170 050	7	167.1	
gil03203031ei1NF_010363.11	IDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to	1	2.2749	0.1557	1172.40	1172.330	1	107.1	50 L.I INSK4E IQ2IIILIE1.1
gi 6320503 ref NP_010583.1	YDR297W	phytosphingosine in sphingolipid biosyntheis; Sur2p Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to	2	3.515	0.2428	1968.51	1969.347	1	539.4	47.058823 N.LRPKESLLPEMSDGVLAL.V
gi 6320503 ref NP_010583.1	YDR297W	phytosphingosine in sphingolipid biosyntheis; Sur2p Sphinganine C4-bydroxylase, catalyses the conversion of sphinganine to	2	3.4869	0.2931	1856.57	1857.079	1	156.7	57.14286 A.EKYRIHPSEEVAKRN.K
gi 6320503 ref NP_010583.1	YDR297W	phytosphingosine in sphingolipid biosyntheis; Sur2p	2	3.8157	0.2285	1858.55	1856.188	1	643.6	56.25 N.LRPKESLLPEMSDGVLA.L
gi 6320503 ref NP_010583.1	YDR297W	sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosyntheis; Sur2p	2	3.5143	0.3869	1787.27	1785.109	1	664	56.666668 N.LRPKESLLPEMSDGVL.A
ail63205031refINP 010583.11	YDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosyntheis: Sur2p	2	3.7979	0.3308	1806.41	1805.109	1	504.8	50 N.L1R4P1K2E1S1L1L1P1E1M1S1D1G1V1L1.A
	VDB200W/	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to	2	2 2202	0.0006	1701 17	1790 771	1	749.4	
gilos2050511e11NF_010565.11	IDR299W	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to	2	3.3302	0.2330	1701.17	1702.771		740.4	
gi 6320505 ref NP_010585.1	YDR299W	Brefeldin A; Bfr2p Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to	2	3.0579	0.2348	1768.31	1769.017	1	1166	66.66667 D.CANGRLPELISPVVKD.S
gi 6320505 ref NP_010585.1	YDR299W	Brefeldin A; Bfr2p Essential protein possibly involved in secretion: multicopy suppressor of sensitivity to	3	4.308	0.3056	3184.01	3184.451	1	918.3	28.703705 S.L1A1D1Q2I1S1D111A111K2P1V1N2K2D1F1D111E1D1E1E1N2A1S1L1F1.Q
gi 6320505 ref NP_010585.1	YDR299W	Brefeldin A; Bfr2p	2	3.9047	0.3753	1786.47	1786.846	1	1422.9	71.42857 V.NKDFDIEDEENASLF.Q
gi 6320505 ref NP_010585.1	YDR299W	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to Brefeldin A; Bfr2p	2	3.6442	0.2789	2224.91	2224.429	1	934.2	55.555557 A.IKPVNKDFDIEDEENASLF.Q
		Peptidyl-prolyl cis-trans isomerase (cyclophilin) of the endoplasmic reticulum.								
gi 6320510 ref NP_010590.1	YDR304C	catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER; Cpr5p	2	3.8718	0.3103	2212.49	2211.587	1	800	58.333332 Y.I1E1N2V1K2T1D1S1R4N2M1P1V1K2E1V1I111V1.E
gi 6320510 ref NP_010590.1	YDR304C	Peptidyl-prolyl cis-trans isomerase (cyclophilin) of the endoplasmic reticulum, catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER; Cpr5p	2	3.3458	0.1512	1403.53	1402.708	4	596.5	68.181816 D.S1R4N2M1P1V1K2E1V1111V1.E
gi 6320510 ref NP_010590.1	YDR304C	Peptidyl-prolyl cis-trans isomerase (cyclophilin) of the endoplasmic reticulum, catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER; Cpr5p	3	4.087	0.1603	2184.02	2185.587	3	1243.8	41.666664 Y.IENVKTDSRNMPVKEVIIV.E
gi 6320510 ref NP_010590.1	YDR304C	Peptidyl-prolyl cis-trans isomerase (cyclophilin) of the endoplasmic reticulum, catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER; Cpr5p	2	4.352	0.1938	2185.61	2185.587	1	707.6	55.555557 Y.IENVKTDSRNMPVKEVIIV.E
		Peptidyl-prolyl cis-trans isomerase (cyclophilin) of the endoplasmic reticulum, catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues;								
gi 6320510 ref NP_010590.1	YDR304C	transcriptionally induced in response to unfolded proteins in the ER; Cpr5p Transcriptional repressor required for mitotic repression of middle sporulation-	2	4.2179	0.2007	1514.53	1514.824	1	1159.1	79.16667 D.SRNMPVKEVIIVE.S
gi 6320516 ref NP 010596.1	YDR310C	specific genes; involved in telomere maintenance, regulated by the pachytene checkpoint; Sum1p	3	4.0883	0.2302	3801.74	3802.141	1	518.3	23.387096 Q.WREWMFPHNETLPALGQDGINEDNLNETIDNM.L
		Transcriptional repressor required for mitotic repression of middle sporulation-								O W284E1W2M1E1P1H3N2E1T1L1P1A1L1G1O2D1G111N2E1D1N2L1N2E1T111D1
gi 6320516 ref NP_010596.1	YDR310C	checkpoint: Sum1p Transcriptional repressor required for mitotic repression of middle sporulation- specific genes; involved in telomere maintenance, regulated by the pachytene	3	3.9769	0.2508	3847.82	3847.141	1	614.1	22.580645 N2M1.L
gi 6320516 ref NP_010596.1	YDR310C	checkpoint; Sum1p Transcriptional repressor required for mitotic repression of middle sporulation-	2	5.3503	0.4202	2234.87	2234.476	1	1064.9	65 K.FHQIPSSPSNPVSQPAPVRTS.R
-1022054014ND 040500 41	VDD0400	specific genes; involved in telomere maintenance, regulated by the pachytene		2 5000	0 4040	4507.50	4520 000	-	240.2	
gil0320310[ter[NP_010390.1]	TDR310C	Low affinity glucose transporter of the major facilitator superfamily, expression is		2.5009	0.1010	1557.56	1550.062	5	219.5	50 V.NZETRZSTATSTNZQZGTATETETSTETVT.N
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p Low affinity glucose transporter of the major facilitator superfamily, expression is	1	2.4498	0.3406	1227.37	1228.446	1	494.8	66.66667 S.VQWRVPLGLC.F
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	1	2.63	0.1578	1308.52	1309.482	1	620	77.77778 L.MHDDQPFYKK.M
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	3.6679	0.2606	1282.23	1280.469	1	671.8	75 N.KVAPDHPFIQQ.E
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	3.5103	0.2711	1153.39	1152.338	2	864.8	77.77778 N.KVAPDHPFIQ.Q
gi 6320552 ref NP_010632.1	YDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions; Hxt3p	1	2.7881	0.3567	1330.77	1331.524	1	483.9	60.000004 N.S1V1Q2W2R4V1P1L1G1L1C1.F
gil6320552lrefINP_010632.1	YDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions: Hxt3p	2	3.0808	0.2446	1329.11	1331.524	1	647.3	70 N S1V1Q2W2B4V1P1L1G1L1C1 F
gil0020002[rol[N] _010002.1]	VDD0450	Low affinity glucose transporter of the major facilitator superfamily, expression is	-	0.7444	0.0500	4246.0	1015 504		404.7	
9ij0320332jreij/NP_010632.1	1003400	Low affinity glucose transporter of the major facilitator superfamily, expression is	1	2.1114	0.2000	1310.9	1313.524	I	404.7	UU.UUUUUH N.U VUWR VELULU.F
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p Low affinity glucose transporter of the major facilitator superfamily, expression is	2	3.3881	0.1985	1155.25	1155.385	1	957.6	83.33333 N.SVQWRVPLGL.N
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p Low affinity glucose transporter of the major facilitator superfamily, expression is	2	3.4626	0.2637	1170.05	1170.385	1	969.7	83.33333 N.S1V1Q2W2R4V1P1L1G1L1.C
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	3.2605	0.2624	1940.31	1941.163	1	801.4	60.000004 K.NYSNSVQWRVPLGLCF.A
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	3.39	0.3049	1297.11	1296.469	1	431.2	70 N.K2V1A1P1D1H3P1F1I1Q2Q2.E

gi 6320552 ref NP_010632.1	YDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions; Hxt3p	2	3.8048	0.405	1228.33	1228.446	1	1426	94.44444 S.VQWRVPLGLC.F
ail63205521refINP_010632_11	VDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions: Hy13p	1	2 5102	0 3299	1243 74	1243 446	1	373.2	61 11111 S V102W2R4V1P1I 1G1I 1C1 F
	1010400	Low affinity glucose transporter of the major acilitator superfamily, expression is		2.0102	0.0200	1240.14	12-10.440		010.2	
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p Low affinity glucose transporter of the major facilitator superfamily, expression is	1	2.9361	0.1536	1323.5	1324.482	1	819.9	77.77778 L.M1H3D1D1Q2P1F1Y1K2K2.M
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	3.1271	0.2703	1324.19	1324.482	2	1063.5	77.77778 L.M1H3D1D1Q2P1F1Y1K2K2.M
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	1	3.0054	0.2588	1279.98	1280.469	1	473.9	60.000004 N.KVAPDHPFIQQ.E
ail63205521refINP 010632.11	YDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions; Hxt3p	1	2.4139	0.304	1152.61	1152.338	1	456.3	66.66667 N.KVAPDHPFIQ.Q
5/(0220550)-+fND_040022.4	VDD0450	Low affinity glucose transporter of the major facilitator superfamily, expression is		2.0105	0.0045	4402.47	4402 700		250	
gij6320552/rei/iNP_010632.1/	TDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is	2	3.0195	0.2615	1493.47	1493.706	2	308	34. 100000 K. VIKVAPDHPFIQQ.E
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p Low affinity glucose transporter of the major facilitator superfamily, expression is	2	3.2032	0.2164	1327.39	1325.482	1	811.7	83.33333 L.M@HDDQPFYKK.M
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	3.7273	0.349	1154.23	1152.338	1	904	77.77778 N.KVAPDHPFIQ.Q
gi 6320552 ref NP_010632.1	YDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions; Hxt3p	2	3.703	0.2487	1168.97	1166.338	1	1101.3	83.33333 N.K2V1A1P1D1H3P1F1I1Q2.Q
gil6320552/refINP_010632.1	YDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions: Hxt3p	2	4.3966	0.3171	1513.61	1512,749	1	1578.1	87.5 S.K2V1N2K2V1A1P1D1H3P1F1I1Q2.Q
	VDD0450	Low affinity glucose transporter of the major facilitator superfamily, expression is	-	0.0000	0.0171	4004 5	1000.007	-	005.4	
gi 6320552 ret NP_010632.1	YDR345C	Induced in low or high glucose conditions; Hxt3p Low affinity glucose transporter of the major facilitator superfamily, expression is	1	2.2094	0.1855	1221.5	1222.387	/	235.1	55.555557 M.11F1V1P1E1S1P1R4Y1L1.V
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	3.0225	0.1869	1195.09	1194.308	1	700.7	81.25 L.M1H3D1D1Q2P1F1Y1K2.K
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	1	3.4043	0.1853	1296.72	1296.469	1	570.2	65 N.K2V1A1P1D1H3P1F1I1Q2Q2.E
gi 6320552 ref NP_010632.1	YDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions; Hxt3p	1	2.205	0.3341	1151.5	1152.338	1	493.9	66.66667 N.KVAPDHPFIQ.Q
ail63205521refINP_010632_11	VDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions: Hy13p	2	2 9934	0 2829	1321 75	1324 482	з	989	77 77778 M1H3D1D1O2P1E1V1K2K2 M
giloszosszirelini _010052.1	1010400	Low affinity glucose transporter of the major facilitator superfamily, expression is	2	2.3334	0.2023	1521.75	1324.402	5	303	
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p Low affinity glucose transporter of the major facilitator superfamily, expression is	1	2.8298	0.2752	1279.57	1280.469	1	559.6	65 N.KVAPDHPFIQQ.E
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	3.0746	0.2605	1494.29	1493.749	1	795.4	70.83333 S.KVNKVAPDHPFIQ.Q
gi 6320552 ref NP_010632.1	YDR345C	induced in low or high glucose conditions; Hxt3p	2	4.8127	0.3494	1641.79	1642.88	1	1113.4	76.92308 S.K2V1N2K2V1A1P1D1H3P1F111Q2Q2.E
gi 6320559 ref NP_010639.1	YDR352W	hypothetical protein; Ydr352wp	3	3.8525	0.1977	3253.61	3252.631	1	484.5	25.925926 A.T1V1G1H3E1P1K2P1L1L1P1E1L1V1E1N2G1E1L1L1R4E1E1E1D1M1I1Q2.G
gi 6320559 ref NP_010639.1	YDR352W	hypothetical protein; Ydr352wp	2	3.6968	0.308	1984.47	1985.288	1	538.2	50 V.GHEPKPLLPELVENGELL.R
gi 6320559 ref NP_010639.1	YDR352W	hypothetical protein; Ydr352wp	2	3.7292	0.3511	2184.49	2185.525	1	339.3	39.473686 A.TVGHEPKPLLPELVENGELL.R
gi 6320559 ref NP_010639.1	YDR352W	hypothetical protein; Ydr352wp	2	4.284	0.3517	2209.17	2209.525	1	528.2	50 A.T1V1G1H3E1P1K2P1L1L1P1E1L1V1E1N2G1E1L1L1.R
		Essential protein involved in nuclear export of Mss4p, which is a lipid kinase that								
		generates phosphatidylinositol 4,5-biphosphate and plays a role in actin cytoskeleton								
gi 6320568 ref NP_010648.1	YDR361C	organization and vesicular transport; Bcp1p	2	2.9918	0.1605	1486.37	1484.837	1	1087.3	75 N.MPPEVVPPLYKIT.L
		Essential protein involved in nuclear export of Mss4p, which is a lipid kinase that								
		generates phosphatidylinositol 4.5-biphosphate and plays a role in actin cytoskeleton								
ail6320568/refINP_010648_1	YDR361C	organization and vesicular transport. Bcp1p	2	3 91 18	0.3697	2223 49	2221 641	1	501.4	47.22222 S1E1R4 111N2M1P1P1E1V1V1P1P1 1Y1K2 1T1
giloczocoliciji i _crocici i	10110010	Essential protein involved in nuclear export of Mss4n, which is a linid kinase that	-	0.0110	0.0001	EEE0.10	2221.011		00111	
		reperates phosphatidylinositol 4 5-biphosphate and plays a role in actin cytoskeleton								
gi 6320568 ref NP 010648.1	YDR361C	organization and vesicular transport; Bcp1p	2	3.1174	0.2619	1150.29	1150.309	3	641.3	75 N.H3L1S1D1Y1V1K2Y1L1.Q
510000		Essential protein involved in nuclear export of Mss4p, which is a lipid kinase that								
		generates phosphatidylinositol 4,5-biphosphate and plays a role in actin cytoskeleton								
gi 6320568 ref NP_010648.1	YDR361C	organization and vesicular transport; Bcp1p	2	4.3136	0.393	1544.49	1544.62	1	928.8	70.83333 D.F1D1F1F1G1G1N2P1E1V1D1F1H3.A
ail62205721rofIND_010652.11	VDB265C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely	2	4 0112	0.2571	1049.27	1049.052	1	E10 1	
gil0320373[rei]NP_010033.1]	IDK303C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely	2	4.0112	0.3371	1940.37	1940.000	'	516.1	30.23 F.EURDFAIDFIQFERGI.Q
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p Nucleolar protein involved in pre-rRNA processing: depletion causes severely	2	4.6211	0.4125	1967.71	1969.053	1	736.6	56.25 F.E1D1H3D1F1A1I1D1P1T1Q2P1E1F1K2G1T1.Q
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p	2	3.8947	0.2713	2322.43	2323.477	1	980.6	55.263157 K.EVFEDHDFAIDPTQPEFKGT.Q
ail6320573/refINP_010653.1	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels: Est1p	2	3 7462	0 2738	2346 61	2347 477	1	385	39 473686 K E1V1E1E1D1H3D1E1A1I1D1P1T1O2P1E1E1K2G1T1 O
giloszosi oliciliti _010000.1	1010000	Nucleolar protein involved in pre-rRNA processing; depletion causes severely	2	0.1402	0.2700	2040.01	2041.411		000	
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p	2	3.5976	0.3246	1996.17	1996.046	2	335.7	44.11765 A.LEGGNEKSSEDKEETTIE.K
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p	2	3.7825	0.2879	2015.45	2017.046	1	442.5	44.11765 A.L1E1G1G1N2E1K2S1S1E1D1K2E1E1T1T1I1E1.K
ail6320573/refINP_010653.1	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels: Est1p	3	4.3134	0.2565	2583.8	2583.857	1	1036.6	36.25 K ERIVEDTETPDI EDPREKEVE E
	VDD0050	Nucleolar protein involved in pre-rRNA processing; depletion causes severely		4.407	0.0044	4070 74	1000 111		1000.0	
gi 6320573 ret NP_010653.1	1DR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely	2	4.137	0.3011	1870.71	1869.111	1	1086.2	75 E.R4M1Q2R4E1E1V1E1G1P1P1K2E1L1F1.Q
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p	3	3.907	0.1857	2610.47	2611.857	2	650.1	30.000002 K.E1R4I1V1E1D1T1F1T1P1D1L1E1D1P1R4F1K2E1V1F1.E
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p	2	4.0271	0.2346	1894.17	1894.956	3	823.8	60.000004 K.KETPNDEDEEVDMEIT.F
ail63205731refINP 010653.11	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	4.1908	0.2723	1914.23	1912.956	3	595.8	63.333332 K.K2E1T1P1N2D1E1D1E1E1V1D1M1E1I1T1.F
	VDD0050	Nucleolar protein involved in pre-rRNA processing; depletion causes severely	2	5 0047	0.005	0050 40	0047 477		0.40.7	
gilo320573[rei]NP_010653.1]	TDR305C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely	3	5.0017	0.205	2350.13	2347.477	I	646.7	40.789474 K.ETVTFTETDTR3DTFTATHDTPTTTQ2PTETFTK2GTTT.Q
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p Nucleolar protein involved in pre-rRNA processing: depletion causes severely	2	4.3992	0.352	2348.27	2347.477	1	684.3	50 K.E1V1F1E1D1H3D1F1A1I1D1P1T1Q2P1E1F1K2G1T1.Q
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p	2	3.5073	0.2158	2130.21	2131.208	3	312.6	47.058823 N.S1K2K2E1T1P1N2D1E1D1E1E1V1D1M1E1I1T1.F
gi 6320573 ref NP_010653.1	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	3.0419	0.3493	1746.27	1748.887	1	524.6	66.66667 N.RELEDFDKYFEKE.A
ail6320573/refINP_010653_1	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels: Est1p	3	4,7604	0.3029	1998 98	1999 094	1	1322.5	50 Q N2N2R4E1L1E1D1F1D1K2Y1E1E1K2E1 A
	VDDooco	Nucleolar protein involved in pre-rRNA processing; depletion causes severely	0	4 00-	0.0020	4000.00	4000.004		4044.4	
gijo320573[ret]NP_010653.1]	1DK365C	uecreased 165 rkNA levels; Est1p Nucleolar protein involved in pre-rRNA processing; depletion causes severely	2	4.927	0.392	1998.39	1999.094	1	1341.4	75 Q.NZNZK4E1L1E1D1F1D1K2Y1F1E1K2E1.A D.T1F1T1P1D1L1E1D1P1R4F1K2E1V1F1E1D1H3D1F1A1I1D1P1T1Q2P1E1F1K2C
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p Nucleolar protein involved in pre-rRNA processing: depletion causes severely	3	4.5837	0.3289	3811.88	3811.088	1	623	23.387096 1T1.Q
gi 6320573 ref NP_010653.1	YDR365C	decreased 18S rRNA levels; Esf1p	3	4.0951	0.2867	2464.64	2464.781	1	1235.8	47.368423 Q.KKERIVEDTFTPDLEDPRFK.E

gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.3488	0.1999	1299.69	1298.467	1	600.8	63.636364 K.N2A1N2D1L1P1K2L1V1E1G1L1.K
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.503	0.2553	1972.43	1973.329	1	449.7	50 F.L1L1A1D1P1K2I1Q2E1P1V1F1L1V1E1I1Q2.C
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	3	4.1302	0.2915	3058.94	3059.482	1	648.6	28.846153 F.L1L1A1D1P1K2I1Q2E1P1V1F1L1V1E1I1Q2C1P1E1Q2A1V1G1G1I1Y1.S
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.5904	0.4346	1792.49	1793.949	1	895.5	63.333332 M.G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.0232	0.287	1774.43	1773.949	1	714.8	60.000004 M.GRFVEPIDDCPAGNII.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.8322	0.396	2098.47	2098.353	1	681.2	52.77778 M.M1G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.4843	0.3755	1944.27	1944.161	1	916.9	58.823532 M.GRFVEPIDDCPAGNIIGL V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	3.1457	0.3044	1461.52	1462.587	1	363	58.333332 C.L1Q2D1L1E1H3D1H3A1G1V1P1L1.K
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.8665	0.4554	1443.52	1444.587	1	310.7	58.333332 C.LQDLEHDHAGVPL.K
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.0061	0.2356	1297.57	1297.578	1	997.7	75 K.KDEIPVLLEKL.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	2.9216	0.2969	1811.75	1811.948	1	564.8	57.14286 M.ADDYGWDVTDARKIW.C
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.3985	0.4404	1887.47	1887.109	1	966.2	65.625 G.RFVEPIDDCPAGNIIGL.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.0536	0.1856	2213.83	2214.486	1	240.9	47.368423 M.M\$G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1V1.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.2507	0.3994	2042.47	2043.293	1	971.1	58.333332 M.GRFVEPIDDCPAGNIIGLV.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.4412	0.3272	2066.29	2066.293	1	617	55.555557 M.G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1V1.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.9713	0.3376	1777.61	1777.037	1	1285.6	62.5 A.L1R4V1T1D1G1A1L1V1V1V1D1T1I1E1G1V1.C
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.7581	0.3175	2109.65	2110.348	1	970.4	62.5 R.HGMKEEVPGWQEYYDKL
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.1407	0.3325	2427.35	2427.752	1	607.4	45.238094 C.L1Q2D1L1E1H3D1H3A1G1V1P1L1K2I1S1P1P1V1V1A1Y1.R
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.1573	0.244	1588.65	1588.929	1	1378.1	79.16667 N.F1K2K2D1E1I1P1V1L1L1E1K2L1.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.6935	0.3111	1688.63	1687.032	1	2001.2	84.61539 M.NFKKDEIPVLLEKL.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	5.1458	0.2974	1704.45	1705.032	1	2455.2	84.61539 M.N2F1K2K2D1E1I1P1V1L1L1E1K2L1.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.7872	0.4096	2106.49	2107.33	1	542.4	52.941177 K.KWTNKDTDAEGKPLERAF.N
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.2595	0.1534	1475.29	1473.672	9	286.1	63.636364 T.RKDEQERGITIK.S

gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.2686	0.1779	1353.79	1354.649	1	108.2	63.636364 A.L1G1E1R4I1K2P1V1V1V111N2.K
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	3	3.8984	0.1826	2455.28	2456.899	1	1105.1	36.25 M.VAFTVDQMRSLMDKVTNVRNM.S
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.9572	0.2608	2499.83	2499.803	1	455.2	45 K.KWTNKDTDAEGKPLERAFNMF.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.8804	0.3057	1343.62	1344.516	1	267	65 L.SKSPNKHNRIY.L
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	2.9159	0.2175	1134.27	1134.407	2	896.7	93.75 F.ILDPIFRLF.T
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.2039	0.1527	1147.15	1146.407	4	937.7	93.75 F.I1L1D1P111F1R4L1F1.T
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.3552	0.3232	1799.41	1797.923	1	666.7	56.666668 E.Q2L1Y1E1G1P1A1D1D1A1N2C1I1A1I1K2.N
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.349	0.4527	1926.53	1926.142	1	809.9	59.375 M.M1G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.7286	0.2441	1744.41	1745.01	4	513.7	50 L.A1D1P1K2I1Q2E1P1V1F1L1V1E1I1Q2.C
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.4824	0.2443	1725.51	1727.01	1	965.4	60.714287 L.ADPKIQEPVFLVEIQ.C
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.2111	0.2977	2173.83	2174.486	1	428	42.105263 M.MGRFVEPIDDCPAGNIIGLV.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.8425	0.3218	2074.73	2075.353	1	574.4	44.444447 M.MGRFVEPIDDCPAGNIIGL.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	5.1534	0.4646	1966.59	1966.161	1	863	58.823532 M.G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.8367	0.4513	1906.41	1908.109	1	826	59.375 G.R4F1V1E1P111D1D1C1P1A1G1N21111G1L1.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	3	4.0851	0.3386	1943.39	1944.161	1	828.6	47.058823 M.GRFVEPIDDCPAGNIIGL.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.5062	0.4272	2006.41	2008.241	1	755.5	58.823532 G.R4F1V1E1P111D1D1C1P1A1G1N2I1I1G1L1V1.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.8321	0.351	1987.89	1986.241	1	860.1	58.823532 G.RFVEPIDDCPAGNIIGLV.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.0512	0.3243	1595.61	1596.734	1	1042.3	73.07692 N.K2D1T1D1A1E1G1K2P1L1E1R4A1F1.N
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.1694	0.2948	1446.35	1444.587	1	619.7	79.16667 C.LQDLEHDHAGVPLK
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.2201	0.2218	1465.41	1462.587	1	625.9	79.16667 C.L1Q2D1L1E1H3D1H3A1G1V1P1L1.K
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.5251	0.2341	1932.55	1935.155	1	472.2	57.14286 G.M1K2E1E1V1P1G1W2Q2E1Y1Y1D1K2L1
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.5906	0.3356	1710.49	1710.968	1	788.5	71.42857 Q.G1P1N2Y1V1P1G1K2K2D1D1L1F111K2.A
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.7937	0.3512	2210.71	2211.416	1	743.4	52.77778 W.T1N2K2D1T1D1A1E1G1K2P1L1E1R4A1F1N2M1F1.I

gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.0796	0.1916	1969.61	1970.207	3	335	43.75 N.KDTDAEGKPLERAFNMF.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	6.2237	0.342	2132.79	2133.33	1	813.9	55.88235 K.K2W2T1N2K2D1T1D1A1E1G1K2P1L1E1R4A1F1.N
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.9446	0.2488	2132.69	2133.348	1	1094.4	65.625 R.H3G1M1K2E1E1V1P1G1W2Q2E1Y1Y1D1K2L1
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	3	4.2253	0.1848	1686.86	1687.032	1	2364	63.461536 M.NFKKDEIPVLLEKL.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.2466	0.1978	1407.85	1408.727	7	81.7	54.166668 Q.ALGERIKPVVVIN.K
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.7416	0.2648	2379.57	2381.627	1	915	55.263157 K.K2W2T1N2K2D1T1D1A1E1G1K2P1L1E1R4A1F1N2M1.F
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.3309	0.2837	2351.79	2352.627	1	924.4	55.263157 K.KWTNKDTDAEGKPLERAFNM.F
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.3153	0.2853	2530.27	2529.803	1	788.3	50 K.K2W2T1N2K2D1T1D1A1E1G1K2P1L1E1R4A1F1N2M1F1.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	3	5.217	0.3828	2527.43	2529.803	1	1056.1	40 K.K2W2T1N2K2D1T1D1A1E1G1K2P1L1E1R4A1F1N2M1F1.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	3.0221	0.2911	1363.68	1364.516	1	246.1	60.000004 L.S1K2S1P1N2K2H3N2R4I1Y1.L
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.1225	0.1575	1541.47	1542.673	1	333.2	72.72727 E.E1V1P1G1W2Q2E1Y1Y1D1K2L1
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.0795	0.2032	1528.39	1527.673	1	216.5	68.181816 E.EVPGWQEYYDKL-
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	2.9716	0.165	1431.49	1428.596	3	578.2	66.66667 Y.L1K2A1E1P1I1D1E1E1V1S1L1A1.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.4976	0.3297	1413.63	1414.596	5	268	45.833336 Y.LKAEPIDEEVSLA.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.6228	0.2782	1502.77	1500.72	1	628.3	66.66667 L.A1D1P1K2I1Q2E1P1V1F1L1V1E1.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.4157	0.3419	1282.42	1283.467	1	458.2	59.090908 K.NANDLPKLVEGL.K
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.4893	0.1658	1300.11	1298.467	1	1562.1	81.818184 K.N2A1N2D1L1P1K2L1V1E1G1L1.K
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.1346	0.3162	1484.67	1483.791	3	663.1	62.5 F.LLADPKIQEPVFL.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.7183	0.2256	1412.23	1410.536	1	1407.3	81.818184 Y.SEMSDEDVKEIK.Q
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.7772	0.3412	1564.47	1565.631	1	739.6	57.692307 M.G1R4F1V1E1P1I1D1D1C1P1A1G1N2.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.4104	0.2925	1383.69	1384.632	1	241	59.090908 L.L1A1D1P1K2I1Q2E1P1V1F1L1.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.4194	0.2532	1599.13	1598.88	2	579.8	69.230774 L.LADPKIQEPVFLVE.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.6444	0.3596	1498.21	1498.791	1	920.3	70.83333 F.L1L1A1D1P1K2I1Q2E1P1V1F1L1.V

gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.5627	0.1611	1497.72	1498.791	1	348.7	62.5 F.L1L1A1D1P1K2I1Q2E1P1V1F1L1.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.3244	0.2924	1728.35	1729.039	1	784.4	71.42857 F.L1L1A1D1P1K2I1Q2E1P1V1F1L1V1E1.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.8355	0.282	1713.35	1712.039	1	403.6	57.14286 F.LLADPKIQEPVFLVE.I
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.2486	0.3566	1584.47	1582.924	1	661.6	57.692307 F.LLADPKIQEPVFLV.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.3591	0.2621	1667.01	1666.841	1	1012.8	73.07692 Y.SEMSDEDVKEIKQK.T
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.0227	0.4436	1904.19	1905.142	1	1204.5	62.5 M.MGRFVEPIDDCPAGNII.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.1106	0.4563	2112.41	2114.353	1	936.7	55.555557 M.M\$G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.6858	0.446	2089.93	2091.353	1	909.9	50 M.M@GRFVEPIDDCPAGNIIGL.V
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.0833	0.4235	2198.87	2198.486	1	648	44.736843 M.M1G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1V1.G
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.9122	0.156	1293.77	1294.583	3	1135.5	88.88889 M.F1I1L1D1P111F1R4L1F1.T
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.2689	0.2141	1559.15	1558.88	1	527.5	72.72727 F.N2M\$F111L1D1P111F1R4L1F1.T
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.2759	0.2386	1622.21	1622.772	1	686	61.538464 K.K2W2T1N2K2D1T1D1A1E1G1K2P1L1.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.1199	0.3015	1604.27	1603.772	1	972.6	76.92308 K.KWTNKDTDAEGKPL.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.0693	0.3716	1691.47	1691.968	1	708	67.85714 Q.GPNYVPGKKDLFIK.A
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.6654	0.1839	1283.47	1281.583	1	1223.2	88.88889 M.FILDPIFRLF.T
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	3	3.8177	0.2021	1705.43	1705.032	1	1598.3	50 M.N2F1K2K2D1E1I1P1V1L1L1E1K2L1.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.4424	0.318	1704.61	1705.032	1	985.5	69.230774 M.N2F1K2K2D1E1I1P1V1L1L1E1K2L1.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	3	3.9836	0.2142	1687.55	1687.032	1	1831	53.846157 M.NFKKDEIPVLLEKL.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.1369	0.3038	1542.01	1542.88	1	1419	72.72727 F.N2M1F111L1D1P111F1R4L1F1.T
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	3	5.1121	0.216	2132.63	2133.33	1	1480.5	48.52941 K.K2W2T1N2K2D1T1D1A1E1G1K2P1L1E1R4A1F1.N
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.4224	0.2588	1571.85	1572.929	1	1276	75 N.FKKDEIPVLLEKL.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.4877	0.267	1687.89	1687.032	1	2219.5	84.61539 M.NFKKDEIPVLLEKL.E
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.234	0.1776	1659.51	1656.789	2	377	58.333332 K.EEVPGWQEYYDKL

gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.7426	0.3493	1344.68	1344.516	1	283.7	65 L.SKSPNKHNRIY.L
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	2.9473	0.3515	1344.23	1344.516	1	456	65 L.SKSPNKHNRIY.L
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	3.2488	0.3243	1477.7	1478.676	1	236.6	59.090908 A.L1S1K2S1P1N2K2H3N2R4I1Y1.L
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	3.1137	0.363	1457.83	1457.676	1	215.8	54.545456 A.LSKSPNKHNRIY.L
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	3.1557	0.3351	1549.53	1550.754	1	257	54.166668 T.A1L1S1K2S1P1N2K2H3N2R4I1Y1.L
gi 6320593 ref NP_010673.1	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	1	2.6437	0.2782	1527.72	1528.754	1	223.2	50 T.ALSKSPNKHNRIY.L
ail6320614 refINP_010694.1	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15o	3	4.0565	0.2382	1985.75	1985.282	1	865.3	43.333332 V.S11/E1E1K2N2R4Y1V1E1E1V11/K21/L1.E
gil6320614/refINP_010694.11	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element: Pdr15p	2	4 3677	0 3828	2312 61	2313 356	1	578	52 380955 O EKHRPGDIENNAGSSPDSATTE K
	VDD 400W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr p, Pdr3p and Pdr8p transmission provides the stress the section of Pdr p. Pdr3p and Pdr8p transmission provides the stress the section of Pdr p. Pdr3p and Pdr8p transmission provides the stress the section of Pdr p. Pdr3p and Pdr8p transmission provides the stress the section of Pdr p. Pdr3p and Pdr8p transmission provides the stress the section of Pdr p. Pdr3p and Pdr8p transmission provides the stress transmission p. Pdr3p and Pdr8p transmission of Pdr p	2	4.5024	0.0020	4004.04	4000.000		4202.2	
gij6320614 ret NP_010694.1	YDR406VV	Transcription regulators; promoter contains a PDR responsive element; Pdr15p ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p	3	4.5831	0.2285	1964.81	1963.282	2	1393.2	55 V.SIEEKNRYVEEVIKILE
gi 6320614 ret NP_010694.1	YDR406W	transcription regulators; promoter contains a PDR responsive element; Pdr15p ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p	2	3.9554	0.3438	1782.41	1780.008	1	1378.7	/1.4285/ K.GTRVPQTPKDMAEYW.L
gi 6320614 ref NP_010694.1	YDR406W	transcription regulators; promoter contains a PDR responsive element; Pdr15p ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p	2	4.4145	0.4566	1798.75	1801.008	1	1547.7	71.42857 K.G1T1R4V1P1Q2T1P1K2D1M1A1E1Y1W2.L
gi 6320614 ref NP_010694.1	YDR406W	transcription regulators; promoter contains a PDR responsive element; Pdr15p ATP binding cassette (ABC) transporter of the plasma membrane; general stress	2	3.0307	0.2232	2035.35	2037.298	1	404.2	50 K.GTRVPQTPKDM@AEYWLQ.S
gi 6320614 ref NP_010694.1	YDR406W	response ractor implicated in ceilular detoxification; target or Pdri p, Pdrsp and Pdrsp transcription regulators; promoter contains a PDR responsive element; Pdr15p ATP binding cassette (ABC) transporter of the plasma membrane; general stress	2	3.6585	0.2608	1988.91	1988.335	1	541.8	56.25 K.GLRLLKPSKEEDTFQIL.K
gi 6320614 ref NP_010694.1	YDR406W	response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	2	3.3324	0.2535	2010.11	2011.335	1	374.2	46.875 K.G1L1R4L1L1K2P1S1K2E1E1D1T1F1Q2I1L1.K
gi 6320614 ref NP_010694.1	YDR406W	response factor implicated in cellular detoxification; target of Pdrl p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	2	4.3167	0.3436	1992.63	1993.146	1	842.8	55.88235 A.V1G1A1Y1P1G1N2D1Y1V1L1G1D1D1F1L1K2E1.S
gi 6320614 ref NP_010694.1	YDR406W	A I P binding Cassette (ABC) transporter of the plasma memorane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	2	3.256	0.3075	2489.87	2488.731	1	238.3	37.5 V.QEELDWMEKNLPGRSKEPTAE.E
gi 6320614 ref NP_010694.1	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	1	2.3514	0.1683	1017.49	1018.16	1	469.6	78.57143 S.KSEAIFHW.R
gi 6320614 ref NP_010694.1	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdrl p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	2	2.916	0.1951	1338.21	1338.508	1	908.7	77.77778 Y.WRSPDYLWSK.F
gi 6320614 ref NP_010694.1	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	2	3.6158	0.2429	1502.51	1501.684	1	1008.2	80 Q.YWRSPDYLWSK.F
gi 6320614 ref NP_010694.1	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	1	2.7648	0.2615	1500.58	1501.684	1	318	70 Q.YWRSPDYLWSK.F
gi 6320614 ref NP_010694.1	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	1	2.8492	0.1991	1353.47	1354.508	5	241.3	72.22222 Y.W2R4S1P1D1Y1L1W2S1K2.F
gi 6320614 ref NP_010694.1	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	2	3.0327	0.2108	2043.53	2041.282	1	807.8	57.14286 R.L1F1Q2Q2Y1W2R4S1P1D1Y1L1W2S1K2.F
gi 6320614 ref NP_010694.1	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	1	2.5722	0.2369	1313.69	1314.531	3	106	55 L.NVEQRKRLTIG.V

gi 6320624 ref NP_010704.1	YDR416W	Component of the spliceosome complex involved in pre-mRNA splicing; involved in regulation of cell cycle progression; similar to Drosophila crooked neck protein; Sy11p	2	3.3212	0.2506	2218.61	2219.505	1	732.1	50 Q.S1L1K2V1P1Y1P1Y1I1E1D1L1E1E1I1Y1L1N2.W
gi 6320624 ref NP_010704.1	YDR416W	Component of the spliceosome complex involved in pre-mRNA splicing; involved in regulation of cell cycle progression; similar to Drosophila crooked neck protein; Syf1p	2	3.0154	0.1775	2001.63	1999.268	1	478.4	50 L.KVPYPYIEDLEEIYLN.W
gi 6320624 ref NP_010704.1	YDR416W	Component of the spliceosome complex involved in pre-mRNA splicing; involved in regulation of cell cycle progression; similar to Drosophila crooked neck protein; Sy11p Protein component of the large (605) ribosomal subunit, nearly identical to Rp112Ap;	2	3.4425	0.3099	2197.45	2199.505	1	610.5	47.058823 Q.SLKVPYPYIEDLEEIYLN.W
gi 6320625 ref NP_010706.1	YDR418W	rpf12a rpf12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpf12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpf12Ap;	1	2.6504	0.2574	1032.45	1032.182	4	393.2	55.555557 K.KVGEDIAKAT.K
gi 6320625 ref NP_010706.1	YDR418W	to E. coil L11 and rat L12 ribosomal proteins; Rp12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp12Ap;	2	3.7758	0.2926	2564.57	2564.811	1	652.1	47.727272 R.VDFKNPHDIIEGINAGEIEIPEN
gi 6320625 ref NP_010706.1	YDR418W	rp12a rp12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins: Rp12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp12Ap;	1	2.2064	0.2766	1524.52	1525.704	2	351.9	53.846157 D.FKNPHDIIEGINAG.E
gi 6320625 ref NP_010706.1	YDR418W	rp12a rp12o double mutant exhibits slow growth and slow translation; has similarity to E. coli L10 and rat L12 ribosomal proteins; Rp112bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112Ap; rp113b rp11b durble mutant achibits (buogramuth and lowut replations has rightfore);	2	3.0439	0.1705	2972.57	2973.19	1	209.9	32 V.G1C1R4V1D1F1K2N2P1H3D1111E1G111N2A1G1E111E111P1E1N2
gi 6320625 ref NP_010706.1	YDR418W	(p) 124 (p) 120 double mutant exhibits stow growth and stow translation, has similarly to E. coli L1 and rat L12 ribosomal proteins; Rp112bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112Ap; m113b m110b double mutant achibits plaug around and plaus translations has righter the m113b m110b double mutant achibits plaus around and plaus translations has righter the m113b m110b double mutant achibits plaus around and plaus translations has righter the m113b m110b double mutant achibits plaus around and plaus translations has righter the m113b m110b double mutant achibits plaus around and plaus translations has righter the m113b m110b double mutant achibits plaus around and plaus translations has righter the m113b m110b double mutant achibits plaus around and the m113b m110b m11	2	4.7655	0.4088	1920.69	1921.113	1	1282.6	65.625 C.R4V1D1F1K2N2P1H3D1111E1G111N2A1G1.E
gi 6320625 ref NP_010706.1	YDR418W	(p) 124 prize double motant exhibits solve growth and slow translation, has similarly to E. coli L1 and rat L12 ribosomal proteins; Rp112bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112bp; e1132 en1132 double mutant achibits claw growth and claw trapelations has similarly.	2	3.9466	0.2409	1898.91	1896.113	1	1303.7	65.625 C.RVDFKNPHDIJEGINAG.E
gi 6320625 ref NP_010706.1	YDR418W	to E. coil L1 and rat L2 losomal proteins; Rp112bp Protein component of the large (605) ribosomal subunit, nearly identical to Rp112Ap; m12a m12b double mutat advibite (eval group and ellow transferitor) has elliptic	2	3.6854	0.1782	2298.47	2299.514	1	838.2	50 Q.SVGCRVDFKNPHDIIEGINAG.E
gi 6320625 ref NP_010706.1	YDR418W	(p) 124 prize double motant exhibits solve growth and slow translation, has similarly to E. coli L1 and rat L12 ribosomal proteins; Rp112bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112bp; e1132 en1132 double mutant achibits claw growth and claw trapelations has similarly.	2	4.5681	0.3976	2272.73	2270.463	1	1094.8	55.263157 Q.S1V1G1C1R4V1D1F1K2N2P1H3D11111E1G111N2A1.G
gi 6320625 ref NP_010706.1	YDR418W	(p) 12a pP/12b output industrie amounds sow grown and sow manistration, nas similarity to E. coli L11 and rat L12 ribosomal proteins; Rp112b pp. Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112bp; m112a m12b double mutant exhibits color warguith and slow translation; bas similarity.	2	3.9087	0.4478	1837.71	1839.061	1	1118	63.333332 C.RVDFKNPHDIJEGINA.G
gi 6320625 ref NP_010706.1	YDR418W	(p) La ph/Lb output initial exhibits and projections (and the constraints) in the constraint of the constraint of the large (60S) ribosomal provident subunit, nearly identical to Rp12Ap; Protein component of the large (60S) ribosomal subunit, nearly identical to Rp12Ap; n12a n12b double mutant exhibits color war growth and slow translation; has similarity.	1	2.4288	0.1862	961.67	962.197	7	396.1	55.555557 S.A1A1L1A1P1K2I1G1P1L1.G
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 risksmanlar sort with the sort rationation, in a similarity to E. coli L11 and rat L12 risksmanlar proteins; Rp112bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112Ap; m12a m12b double mutant exhibits elsw growth and show transition; has similarity	2	3.2908	0.2044	1582.55	1583.741	4	438.5	53.846157 V.DFKNPHDIIEGINA.G
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12r lossonal proteins; Rp112bp Protein component of the large (605) ribosomal subunit, nearly identical to Rp112Ap; m112cm112c double avoid a subunit, nearly identical to Rp112Ap;	2	4.7711	0.3991	2464.65	2465.679	1	955.7	54.761906 V.DFKNPHDIIEGINAGEIEIPEN
gi 6320625 ref NP_010706.1	YDR418W	(p) 12a iprize output initial exhibits solve growth and solve translation, has similarly to E. coli L11 and rat L12 ibosomal proteins; Rp112b, Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112b; m112a m12b double mutant arbitritis clow growth and slow translation; has similarly.	2	3.4054	0.2639	2491.09	2493.679	1	375.6	38.095238 V.D1F1K2N2P1H3D1I11E1G1I1N2A1G1E111E111P1E1N2
gi 6320625 ref NP_010706.1	YDR418W	(p) Lat p)/LB or that is the second and a proteins; Rp12bp to E, coli L11 and rat L12 ribosomal proteins; Rp12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp12Ap; rn12a rn12b double mutant exhibits solve month and slow translation: has similarity.	2	4.8864	0.3207	2379.31	2377.59	1	826.4	55 D.F1K2N2P1H3D1111E1G111N2A1G1E111E111P1E1N2
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; RpI12bp Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap; rpI12a rpI12b double mutant exhibits slow growth and slow translation; has similarity	2	4.1232	0.358	2350.65	2350.59	1	719.2	52.499996 D.FKNPHDIIEGINAGEIEIPEN
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rp12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112Ap; m12a m12b double mutant exhibits (sow growth and slow translation; bas similarity	2	3.5404	0.3129	3158.97	3161.4	4	232.1	25.925926 Q.S1V1G1C1R4V1D1F1K2N2P1H3D1111E1G111N2A1G1E111E111P1E1N2
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rp12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp112Ap; m12a m12b double mutant exhibits (sow growth and slow translation; bas similarity	2	3.2052	0.1772	3122.79	3124.4	1	458.4	33.333336 Q.SVGCRVDFKNPHDIIEGINAGEIEIPEN
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits (slow growth and slow translation; has similarity	2	3.2542	0.2118	1527.39	1525.704	3	743.8	65.38461 D.FKNPHDIIEGINAG.E
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; RpI12bp Protein component of the large (605) ribosomal subunit, nearly identical to RpI12Ap; rol12a rol12b double mutant exhibits slow growth and slow translation: has similarity	1	3.0853	0.2929	1467.62	1468.652	1	597.4	62.5 D.FKNPHDIIEGINA.G
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rol12a rol12b double mutant exhibits slow growth and slow translation; has similarity	3	4.0125	0.2162	2972.87	2973.19	1	377	31 V.G1C1R4V1D1F1K2N2P1H3D1111E1G111N2A1G1E111E111P1E1N2
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity	2	3.8616	0.1747	2720.65	2720.999	4	224	30.434782 C.RVDFKNPHDIIEGINAGEIEIPEN
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; ml12a ml12b double mutant exhibits low growth and slow translation; has similarity	3	3.8104	0.2509	3158.84	3161.4	2	340.9	25.925926 Q.S1V1G1C1R4V1D1F1K2N2P1H3D11111E1G111N2A1G1E111E111P1E1N2
gi 6320625 ref NP_010706.1	YDR418W	(a) Explicitly and rate 12 ribosomal proteins; Rpl12bp to E: coli L11 and rat L12 ribosomal proteins; Rpl12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; ml12a ml12b double mutant exhibits (sow growth and slow translation; bas similarity ml2ar ml2b double mutant exhibits.	3	3.8882	0.2706	3122.51	3124.4	1	513.5	32.407406 Q.SVGCRVDFKNPHDIIEGINAGEIEIPEN
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rol12a rol12b double mutant exhibits slow growth and slow translation: has similarity	3	4.4613	0.3418	2753.6	2753.999	1	585.5	39.130436 C.R4V1D1F1K2N2P1H3D1111E1G111N2A1G1E111E111P1E1N2
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rp1/2bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rp1/2Ap; rp1/2a rp1/2b double mutant exhibits slow growth and slow translation: has similarity	2	3.6203	0.2298	1789.37	1790.982	1	529.4	60.714287 C.R4V1D1F1K2N2P1H3D1111E1G111N2.A
gi 6320625 ref NP_010706.1	YDR418W	to E. coil 11 and rat L12 ribosomal proteins; Rp120b Protein component of the large (60S) ribosomal subunit, nearly identical to Rp12Ap; rm12a rm12b double mutant exhibits slow growth and slow translation: has eximilarity	2	4.2064	0.4492	2056.51	2056.252	1	1266.8	64.70589 V.GCRVDFKNPHDIIEGINA.G
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.2013	0.5068	2139.21	2140.304	1	988.5	52.77778 V.G1C1R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1.E

		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.2784	0.3182	2328.15	2328.514	1	933.3	50 Q.S1V1G1C1R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1.E
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.5519	0.4539	2239.85	2242.463	1	1319.5	57.894737 Q.SVGCRVDFKNPHDIIEGINA.G
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.1694	0.2582	2753.85	2753.999	2	182.4	30.434782 C.R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1E1I1E1I1P1E1N2
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.4692	0.3247	2058.87	2056.252	1	511.1	47.058823 G.CRVDFKNPHDIIEGINAG.E
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.5941	0.2973	1532.39	1532.762	1	456.4	53.571426 L.G1L1S1P1K2K2V1G1E1D1I1A1K2A1T1.K
		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.7196	0.3451	1515.55	1514.762	2	576.4	60.714287 L.GLSPKKVGEDIAKAT.K
		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.4567	0.3239	1766.75	1767.982	1	518.5	60.714287 C.RVDFKNPHDIIEGIN.A
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.8973	0.4401	2081.69	2082.252	1	1569.2	64.70589 V.G1C1R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1.G
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.1096	0.3579	1865.35	1863.061	1	1079.3	66.66667 C.R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1.G
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.8559	0.3469	2112.51	2113.304	1	1065.5	55.555557 V.GCRVDFKNPHDIIEGINAG.E
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.187	0.2939	1653.53	1653.878	1	856.7	57.692307 C.RVDFKNPHDIIEGI.N
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; RpI12bp	2	3.8611	0.2889	1672.55	1674.878	1	1318.8	76.92308 C.R4V1D1F1K2N2P1H3D1I1I1E1G1I1.N
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI12Ap;								
gi 6320625 ref NP_010706.1	YDR418W	to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.7827	0.3072	1871.21	1871.069	1	896.9	56.666668 V.GCRVDFKNPHDIIEGI.N
ail63206651refINP 010745.1	YDR457W	E3 ubiquitin ligase of the hect-domain class; has a role in mRNA export from the nucleus and may regulate transcriptional coactivators; Tom1p	2	4.004	0.3021	1837.77	1839.098	1	1012.8	67.85714 K F1H3L1P1S1F1D1E1D1D1L1M1K2I1L1 S
		E3 ubiquitin ligase of the hect-domain class; has a role in mRNA export from the		0.00.40	0.0004	4705.05	1704.000		5 40 7	
gil6320665 ret NP_010745.1	YDR457W	E3 ubiquitin ligase of the hect-domain class; has a role in mRNA export from the	2	2.9243	0.2901	1705.65	1704.889	2	546.7	53.846157 L.KDMESEDPDYYKSE.V
gi 6320665 ref NP_010745.1	YDR457W	nucleus and may regulate transcriptional coactivators; Tom1p	2	3.4037	0.2239	1675.41	1673.921	2	727.7	69.230774 F.HLPSFDEDDLMKIL.S
		transcription initiation, required for nucleotide excision repair factor s complexes, involved in								
gi 6320668 ref NP_010748.1	YDR460W	similar to mammalian CAK and TFIIH subunit; Tfb3p	2	4.2711	0.2917	1669.25	1670.929	1	2013.4	91.66667 N.K2Y1L1E1E1V1E1D11111Y1K2L1.D
		transcription initiation, required for nucleotide excision repair; ring finger protein								
gi 6320668 ref NP_010748.1	YDR460W	similar to mammalian CAK and TFIIH subunit; Tfb3p Protein component of the large (60S) ribosomal subunit, nearly identical to Rol27Ap	2	3.9331	0.2099	1655.17	1655.929	1	2126.1	87.5 N.KYLEEVEDIIYKL.D
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	2	3.0254	0.2999	1309.79	1308.52	1	389.2	63.636364 K.VVIVKPHDEGSK.S
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	2	3.6056	0.2369	1698.97	1698.855	1	918.4	73.07692 E.T1F1E1Q2P1S1Q2R4E1E1A1K2K2V1.V
ail6320670/refINP_010759_1	VDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI27Ap and bas similarity to rat L 27 ribosomal protein: RpI27bp	2	3 7085	0 2664	2058.49	2059 277	5	271.2	46 875 T E1T1E1E102P1S102R4E1E1A1K2K2V1V1K2 K
giloszoorojicijini _ororos.ij	1 DIGHT IN	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap	2	0.7000	0.2004	2000.40	2000.211	0	271.2	
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap	2	3.7563	0.2824	1904.43	1905.161	2	290.6	46.666668 E.TFEQPSQREEAKKVVK.K
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	2	4.4802	0.1771	2190.13	2189.451	1	363.6	52.941177 T.E1T1F1E1Q2P1S1Q2R4E1E1A1K2K2V1V1K2K2.A
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	2	3.8092	0.2328	2056.65	2059.335	1	569.6	59.375 E.T1F1E1Q2P1S1Q2R4E1E1A1K2K2V1V1K2K2.A
ail6320670/refINP_010759_1	VDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI27Ap and bas similarity to rat L 27 ribosomal protein: RpI27bp	1	2 4538	0 2406	932 69	932 186	з	373 3	71 42857 K K2V1V111V1K2P1H3 D
gil0320079161141 _010733.11	101(4711)	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap		2.4000	0.2400	332.03	332.100	5	575.5	11.42037 K.N2 V V 11 V INZE 1113.D
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap	2	4.0049	0.3944	1776.03	1777.033	1	664.5	66.66667 K.VVIVKPHDEGSKSHPF.G
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	2	4.0883	0.4789	1796.69	1799.033	1	712.1	70 K.V1V1I1V1K2P1H3D1E1G1S1K2S1H3P1F1.G
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	2	3.841	0.2836	2161.75	2162.451	4	283.5	47.058823 T.ETFEQPSQREEAKKVVKK.A
ail63206791refINP 010759.11	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI27Ap and has similarity to rat L27 ribosomal protein: RpI27bp	2	2.9788	0.1822	1438.29	1436.695	5	223.1	62.5 K KVVIVKPHDEGSK S
		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap		0.0574	0.0050	4007.40	1000 101	_		
gi 6320679 ret NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap	2	3.2574	0.2652	1927.19	1929.161	1	334.3	50 E.11F1E1Q2P1S1Q2R4E1E1A1K2K2V1V1K2.K
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	3	4.3056	0.2376	2062.31	2059.335	6	428.6	34.375 E.T1F1E1Q2P1S1Q2R4E1E1A1K2K2V1V1K2K2.A
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	3	4.0122	0.3048	1797.41	1799.033	1	625.3	41.6666664 K.V1V1I1V1K2P1H3D1E1G1S1K2S1H3P1F1.G
ail63206791refINP 010759.11	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI27Ap and has similarity to rat L27 ribosomal protein: RpI27bp	2	2,9542	0.1756	1677.25	1677.855	1	587.8	61.538464 E.TEEOPSOREEAKKV.V
		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap		4 00 4 0	0.0507	0400	0100 151		004.0	
giloszopvalteilMP_010759.1	10K4/1W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap	3	4.0916	0.∠587	2192	2109.451	4	304.8	30.233234 I.ETTFTETQ2FTSTQ2K4ETETATK2K2V1V1K2K2.A
gi 6320679 ref NP_010759.1	YDR471W	and has similarity to rat L27 ribosomal protein; Rpl27bp	2	3.5566	0.2523	2032.67	2033.335	1	418.7	53.125 E.TFEQPSQREEAKKVVKK.A
		Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated								
gi 6320689 ref NP_010769.1	YDR481C	by levels or inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	1	3.1871	0.3202	1592.6	1593.774	1	433.1	53.846157 Q.HVNDLPIDDILTLD.E

gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	4.2481	0.2878	1723.83	1720.92	2	950.5	67.85714 F.NQHVNDLPIDDILTL.D
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	1	3.3099	0.2955	1495.77	1494.685	8	465.3	50 Q.H3V1N2D1L1P1I1D1D1I1L1T1L1.D
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.6575	0.2714	2266.87	2267.411	1	576.9	47.22222 F.ADNDIPFEIDRDEKEYPSL.K
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	1	2.7828	0.2975	1477.63	1478.685	8	472.9	54.166668 Q.HVNDLPIDDILTLD
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.5512	0.3388	2651.21	2652.831	2	335	33.333336 F.ADNDIPFEIDRDEKEYPSLKEQ.V
gi 6320689 ref NP 010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	2.9979	0.2213	2541.47	2542.761	1	561.8	45 L.FADNDIPFEIDRDEKEYPSLK.E
ail6320680/refINP_010760.11	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho8(0, Pho81, and Pho85, denhosphortdes phosphotrosyl particles; Pho8n	2	4 0938	0 2912	2800 77	2800.008	1	389.2	
	VDD4040	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p,	2	4.0000	0.2312	2000.11	2000.000		440.7	
gi 6320689 ret NP_010769.1	YDR481C	Pho80p, Pho81p and Pho85p; dephosphorytates phosphotyrosyl peptides; Pho8p Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p,	2	3.3785	0.2496	2438.45	2439.587	2	449.7	44./36843 L.F1A1D1N2D111P1F1E1I1D1R4D1E1K2E1Y1P1S1L1.K
gi 6320689 ref NP_010769.1	YDR481C	Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated	2	3.9284	0.3251	1522.79	1522.655	1	714.1	81.818184 D.RDEKEYPSLKEQ.V
gi 6320689 ref NP_010769.1	YDR481C	by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.1422	0.3272	1728.05	1730.986	1	668.4	57.14286 T.H3Q2L1G1E1Y1P1L1G1R4V1V1D1L1L1.M
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	4.118	0.3941	1962.81	1965.284	1	458.7	53.125 A.T1H3Q2L1G1E1Y1P1L1G1R4V1V1D1L1L1M1.G
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.2121	0.3748	1940.69	1942.284	1	354.3	50 A.THQLGEYPLGRVVDLLM.G
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	4.0357	0.3095	1862.63	1863.179	1	645.8	63.333332 T.H3Q2L1G1E1Y1P1L1G1R4V1V1D1L1L1M1.G
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.0091	0.3093	1574.37	1571.857	6	397.4	54.166668 F.IKHEILEKDLGIY.D
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	4.0724	0.3706	1832.41	1833.96	1	464.7	56.666668 L.K2S1Y1N2G1A1I1G1V1D1P1H3H3R4P1C1.G
ail6320689/refINP 010769.11	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80o. Pho81o and Pho85o: dephosphorvlates phosphotvrosvi oeptides: Pho8o	2	3.1016	0.2357	1204.71	1205.298	1	872.5	88.88899 A.I1G1V1D1P1H3H3R4P1C1.G
3 1		Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p,								
gi 6320689 ref NP_010769.1	YDR481C	Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated	3	4.66	0.2517	2828.42	2830.008	1	1025.1	35.227272 L.F1A1D1N2D111P1F1E111D1R4D1E1K2E1Y1P1S1L1K2E1Q2.V
gi 6320689 ref NP_010769.1	YDR481C	by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.8012	0.3458	2301.83	2301.51	1	605.6	52.63158 L.I1H3L1D1D1N2A1N2A1I1Q2D1K2L1N2D1M1V1S1F1.R
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.936	0.3751	2273.33	2274.51	1	816	50 L.IHLDDNANAIQDKLNDMVSF.R
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.1624	0.1658	1712.23	1709.986	1	596.1	60.714287 T.HQLGEYPLGRVVDLL.M
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.1651	0.2691	1369.39	1368.578	1	768.1	68.181816 T.HQLGEYPLGRVV.D
gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.4753	0.3938	1840.81	1841.179	1	578.7	53.333336 T.HQLGEYPLGRVVDLLM.G
	VDB4040	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, De200, De21a and De26, deabhard international internatione international international int	~	2 7404	0.2550	1050 75	1957 000	4	670.0	
gilo320009[tet[NP_010769.1]	10K4810	Filooop, Filoo Ip and Photop; dephosphorylates phosphotyrosyl peptides; Pho8p	2	3.1424	0.2552	1000.75	1007.009	1	0/3.2	00.000004 F.NZQ2E3V IN2D1L1P111D1D111L111L1D1.E

gi 6320689 ref NP_010769.1	YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	1	3.3097	0.2849	1493.58	1494.685	2	446.8	50 Q.H3V1N2D1L1P1I1D1D1I1L1T1L1.D
ail6320680/rofIND_010760_1		Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho8p, Pho8p, Pho81, and Pho8p, depheroproduce phosphotycocit oparidae; Pho8p,	2	2 9646	0 1749	1405.27	1404 685	5	118 7	
gilos200691e114F_010769.1	VDD 400W	Photop, Photop and Photop, deprosphorylates photophotylogy peptides, Photop	2	2.9040	0.1749	1495.27	1494.000	5	440.7	
gij6320691 ref NP_010771.1	YDR483W	Alpha 1,2-mannosyltransferase of the Goigi Involved in protein mannosylation; Kre2p	2	3.566	0.3504	2157.21	2158.254	1	635.2	52.941177 F.SDIGYHHPPYDNCPLDKE.V
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	4.2152	0.3828	2447.15	2446.563	1	631.6	50 F.S1D111G1Y1H3H3P1P1Y1D1N2C1P1L1D1K2E1V1Y1.N
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	3.3304	0.221	2155.53	2155.414	1	636.8	56.666668 E.LLEEYDWYWRVEPDIK.L
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	3.6011	0.3588	2431.71	2431.75	1	638.1	52.941177 E.LLEEYDWYWRVEPDIKLY.C
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	3	4.0171	0.1893	2563.37	2560.865	1	605.5	33.333336 H.ELLEEYDWYWRVEPDIKLY.C
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	3	4.3083	0.2968	2586.11	2585.865	2	670.3	30.555555 H.E1L1L1E1E1Y1D1W2Y1W2R4V1E1P1D1I1K2L1Y1.C
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	3.0921	0.3393	2560.07	2560.865	1	342.4	41.666664 H.ELLEEYDWYWRVEPDIKLY.C
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	3.101	0.2862	2584.55	2585.865	1	438.5	41.6666664 H.E1L1L1E1E1Y1D1W2Y1W2R4V1E1P1D1I1K2L1Y1.C
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	1	2.6706	0.2336	1537.45	1536.669	1	237.3	63.636364 W.R4S1P1A1Y1R4E1Y1F1D1T1L1.D
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	1	3.2349	0.2931	1453.63	1454.743	1	683.2	70 K.I1N2K2K2F1P1Y1P1W2V1F1.L
qi 6320691 ref NP 010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	1	3.0266	0.2185	1441.79	1439.743	1	564.2	65 K.INKKFPYPWVF.L
gil6320691/refINP_010771.1	YDR483W	Alpha1.2-mannosyltransferase of the Golgi involved in protein mannosylation. Kre2p	2	4.3743	0.151	2203.09	2202.502	1	586.2	44.11765 T.SMDFIKKNPEYLDENNI M.S
gil63206911refINP_010771_1	YDR483W	Alpha 1,2 mannosyltransferase of the Golai involved in protein mannosylation; Kre2n	-	2 3038	0 1881	1211 54	1212 48	2	546.8	
=:::::::::::::::::::::::::::::::::::::	VDD400W		2	2.0000	0.0400	1420.05	1212.40	-	054.7	
gilo320691[rei]NP_010771.1]	TDR463W	Alpha 1,2-mannosyltransierase of the Golgi involved in protein mannosylation; Kre2p	2	3.0011	0.3126	1439.65	1439.743		854.7	
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	4.4527	0.1858	2226.33	2225.502	1	739	47.058823 T.S1M1D1F111K2K2N2P1E1Y1L1D1E1N2N2L1M1.S
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	3.6614	0.2517	2284.71	2284.53	1	550.4	46.875 H.ELLEEYDWYWRVEPDIK.L
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	4.2687	0.3479	2420.27	2420.563	1	497.1	44.736843 F.SDIGYHHPPYDNCPLDKEVY.N
gi 6320691 ref NP_010771.1	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p Cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins, acidification of the vacuolar lumen, and assembly of the vacuolar H+-	2	3.274	0.1715	1453.41	1454.743	1	841.1	75 K.I1N2K2K2F1P1Y1P1W2V1F1.L
gi 6320703 ref NP_010783.1	YDR495C	ATPase; Vps3p Cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins, acidification of the vacuolar lumen, and assembly of the vacuolar H+-	2	3.4093	0.1877	2070.73	2072.178	1	545.3	53.125 T.S1C1E1E1S1E111D1N2I1E1D1Q2L1K2K2L1.A
gi 6320703 ref NP_010783.1	YDR495C	ATPase; Vps3p Cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins, acidification of the vacuolar lumen, and assembly of the vacuolar H+-	2	3.9107	0.3434	2050.57	2051.178	1	734.6	59.375 T.SCEESEIDNIEDQLKKL.A
gi 6320703 ref NP_010783.1	YDR495C	ATPase; Vps3p Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the FR: required for N- and Q-divcosvlation in the Golgi but not in the FR: forms a	2	3.5216	0.2905	1830.61	1829.118	1	477.8	53.571426 K.N2Y1P1R4N2V111V1E1F1P1Y1111A1.E
gi 6320706 ref NP_010786.1	YDR498C	complex with the cytosolic Tip20p; Sec20p Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER: required for N- and O-colversvatiation in the Goldi but not in the ER: forms a	2	4.9148	0.3046	2858.27	2860.014	1	1195.6	47.826088 A.IANEHNDEEEEIEFEDLVNIIESK.V
gi 6320706 ref NP_010786.1	YDR498C	are city required for A direct speeds atom in the cost of the first rate in the city of ci	2	4.4782	0.2607	2889.61	2890.014	1	649.3	43.47826 A.I1A1N2E1H3N2D1E1E1E1E1I1E1F1E1D1L1V1N2I1I1E1S1K2.V
gi 6320706 ref NP_010786.1	YDR498C	are city required for maline groups data in the Cost of the first male city for the cost of the city o	2	4.84	0.4095	2673.77	2675.776	1	1124.1	54,761906 A.NEHNDEEEEIEFEDLVNIIESK.V
gi 6320706 ref NP_010786.1	YDR498C	complex with the cytosolic Tip20p; Sec20p Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER: required for N- and O-olycosystation in the Goldi but not in the ER: forms a	2	4.5753	0.3542	2561.79	2561.672	1	675.8	45 N.EHNDEEEEIEFEDLVNIIESK.V
gi 6320706 ref NP_010786.1	YDR498C	complex with the cytosolic Tip20p; Sec20p Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-qlycosylation in the Golgi but not in the ER; forms a	3	4.5893	0.2114	2860.64	2860.014	1	884.9	34.782608 A.IANEHNDEEEEIEFEDLVNIIESK.V
gi 6320706 ref NP_010786.1	YDR498C	complex with the cytosolic Tip20p; Sec20p Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes	2	3.2225	0.2829	2104.63	2105.089	1	930.6	56.25 A.NEHNDEEEEIEFEDLVN.I
gi 6320715 ref NP_010795.1	YDR507C	autophosphorylation; similar to Kcc4p and Hsl1p; Gin4p Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes	3	4.0218	0.3256	2498.18	2495.682	1	954.2	33.75 Q.K2G1E1F1E1M1P1S1D1D1E1I1S1R4E1A1Q2D1L1I1R4.K
gi 6320715 ref NP_010795.1	YDR507C	autophosphorylation; similar to Kcc4p and Hsl1p; Gin4p Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes	2	3.7836	0.2629	2326.31	2327.619	1	494.1	44.736843 T.D1N2L1H3L1P1I1L1P1P1L1N2G1D1N2E1L1R4K2Q2.N
gi 6320715 ref NP_010795.1	YDR507C	autophosphorylation; similar to Kcc4p and Hsl1p; Gin4p Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes	3	4.2216	0.2094	1819.82	1821.054	1	1033.9	50 L.V1E1R4G1P1L1P1E1H3E1A111R4F1F1.R
gi 6320715 ref NP_010795.1	YDR507C	autophosphorylation; similar to Kcc4p and Hsl1p; Gin4p Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes	2	3.6939	0.1929	1819.81	1821.054	1	543.6	50 L.V1E1R4G1P1L1P1E1H3E1A111R4F1F1.R
gi 6320715 ref NP_010795.1	YDR507C	autophosphorylation; similar to Kcc4p and Hsl1p; Gin4p Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes	2	3.4116	0.2954	1935.63	1935.214	1	683	53.333336 L.L1V1E1R4G1P1L1P1E1H3E1A111R4F1F1.R
gi 6320715 ref NP_010795.1	YDR507C	autophosphorylation; similar to Kcc4p and Hsl1p; Gin4p Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes	3	4.3772	0.2681	1935.32	1935.214	1	1954	51.666664 L.L1V1E1R4G1P1L1P1E1H3E1A1I1R4F1F1.R
gi 6320715 ref NP_010795.1	YDR507C	autophosphorylation; similar to Kcc4p and Hsl1p; Gin4p	2	3.3838	0.3542	1910.93	1911.214	1	987.5	56.666668 L.LVERGPLPEHEAIRFF.R

gi 6320715 ref NP_010795.1	YDR507C	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes autophosphorylation; similar to Kcc4p and Hs1fp; Gin4p	3	4.0581	0.3812	2162.51	2165.477	1	933.6	41.17647 F.N2L1L1V1E1R4G1P1L1P1E1H3E1A111R4F1F1.R
gi 6320715 ref NP_010795.1	YDR507C	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes autophosphorylation; similar to Kcc4p and Hs1tp; Gin4p	3	4.9491	0.3498	2326.04	2327.619	1	1231.7	43.421055 T.D1N2L1H3L1P1I1L1P1P1L1N2G1D1N2E1L1R4K2Q2.N
gi 6320715 ref NP_010795.1	YDR507C	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes autophosphorylation; similar to Kcc4p and Hs1p; Gin4p	2	4.222	0.3776	2326.73	2327.619	1	836.7	52.63158 T.D1N2L1H3L1P111L1P1P1L1N2G1D1N2E1L1R4K2Q2.N
ail6320715/refINP 010795.1	YDR507C	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes autophosphorvlation; similar to Kcdv and Hs1to: Girdo	2	3.2728	0.2443	2298.43	2297.619	2	372.1	39.473686 T.DNLHLPILPPLNGDNELRKQ.N
gil6320715lrefINP_010795.1	YDR507C	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes autophosphorylation: similar to KorAp and Hs10: Gin4o	2	3.8492	0.3777	1797.89	1798.054	1	978.8	64 28571 L.VERGPLPEHEAIREE.R
gil6320726lrefINP_010806.1	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of pdf1p: may interact with nascent polyneptides in the ER: Eur1p	2	3.3772	0.2067	1771.73	1768.964	1	412.2	50 L SIHLPNTTEPILEDGN V
gil6320726lrefINP_010806.1	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polyneptides in the ER: Europ	1	3.4856	0.2382	1551.57	1552,783	8	202.4	50 K R4F1A1P111Y1E1E111A1N2V1L1 A
gil6320726lrefINP_010806.1	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pd110; may interact with nascent polyneotides in the ER: Euro10	2	3.5176	0.2784	1555.35	1552,783	-	291.6	70 83333 K R4F1A1P111Y1E1E111A1N2V1L1 A
gil6320726/refINP_010806.1	YDR518W	Protein disulfied is more as the endoplasmic reticulum lume 1.1, e.g. overlaps with that of efforts may interact with nearcont polynomials in the EP. Euron	-	4 053	0.313	3329	3329.836	1	688.2	
gil6320726/rofINP_010806.1	VDR518W	Protein disulfide isomerase of the endoplasmic reticulum lume, function overlaps with that of Pdfac may informed with respond to knowing is the EP. Europe	2	3 5756	0.010	1776.43	1779.043	1	491.7	
	VDD540W	Protein disulfide isomerase of the endoplasmic reticulum lume, Exc. Eugin p with that dr Patrip, isomerase of the endoplasmic reticulum lume, Exc. Eugin p	2	3.5756	0.29	4700.44	1779.043	1	491.7	
	VDD540W	Protein disulfide isomerase of the endoplasmic reticulum lume, Exc. Eugin p with that dr Patrip, isomerase of the endoplasmic reticulum lume, Exc. Eugin p	2	3.0355	0.152	4525.27	4525 702	1	202.0	
gilp320726[ref[NP_010806.1]	VDR518W	with that of Politip, insertion with nascent polypepudes in the ER, Euglip Protein disulfice isomerase of the endoplasmic reticulum lumen, function polarity with what of Delta some view something another the polarities in the ER. Europe	2	3.3036	0.2454	1752.21	1751 025	1	302.0	
	VELODOC	with that of Portp, they interact with hascent polypepudes in the EK, Eugrip Beta submit of the oligosaccharyl transferase (OST) glycoprotein complex, required	2	2.9386	0.2703	1752.21	1751.035	1	209.3	
gil6320835[ref]NP_010914.1]	YEL002C	Tor N-linked glycosylation of proteins in the endoplasmic reticulum; wop to Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required	1	3.0222	0.4292	1386.65	1387.581	1	237.5	SU T.GEFILPDRHGVF.T
gi 6320835 ref NP_010914.1	YEL002C	for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required	1	3.3171	0.3988	1404.55	1404.581	1	326.1	54.545456 1.G1E1F111L1P1D1R4H3G1V1F1.I
gi 6320835 ref NP_010914.1	YEL002C	for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p Reta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required	1	2.8831	0.2189	1347.67	1346.529	9	130.3	55 G.E1F111L1P1D1R4H3G1V1F1.T
gi 6320835 ref NP_010914.1	YEL002C	For N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p	2	2.9829	0.1912	1859.35	1857.098	4	337.3	50 Y.D1K2E1Q2R4L1F1D1N2I1I1V1F1P1T1.K
gi 6320835 ref NP_010914.1	YEL002C	for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p	2	4.1126	0.1881	2064.51	2064.393	3	507.2	50 A.LLENREQIVPILNAPRTS.F
gi 6320835 ref NP_010914.1	YEL002C	Beta subunit of the oligosaccharyl transferase (US1) glycoprotein complex; required for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p	2	3.1385	0.2689	2264.81	2265.607	4	174.3	35.294117 D.L1Y1D1K2E1Q2R4L1F1D1N2I1I1V1F1P1T1K2.G
gi 6320835 ref NP_010914.1	YEL002C	Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p	2	3.0236	0.1831	1609.73	1610.894	8	245.1	50 E.Q2R4L1F1D1N2I1I1V1F1P1T1K2.G
gi 6320835 ref NP_010914.1	YEL002C	Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p	3	6.0028	0.242	2349.98	2349.654	3	1259.8	42.105263 Y.D1K2E1Q2R4L1F1D1N2l1l1V1F1P1T1K2G1G1K2N2.L
gi 6320835 ref NP_010914.1	YEL002C	Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p	3	5.068	0.267	3101.57	3100.499	1	911.4	32.692307 T.STTVDLYDKEQRLFDNIIVFPTKGGKN.L
gi 6320835 ref NP_010914.1	YEL002C	Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p	3	4.811	0.2482	2348.45	2349.654	2	982	36.842106 Y.D1K2E1Q2R4L1F1D1N2I1I1V1F1P1T1K2G1G1K2N2.L
gi 6320835 ref NP_010914.1	YEL002C	Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for	2	3.5003	0.2948	2350.03	2349.654	2	209.7	34.210526 Y.D1K2E1Q2R4L1F1D1N2l1l1V1F1P1T1K2G1G1K2N2.L
gi 6320824 ref NP_010903.1	YEL013W	the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p Phosphorvlated vacuolar membrane protein that interacts with Ata13p, required for	2	5.0375	0.4044	2014.93	2016.169	1	884.8	52.941177 H.NDKVEDLVKNDDDIINGV.R
gi 6320824 ref NP_010903.1	YEL013W	the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nv11p to form nucleus-vacuole junctions; Vac8p Phosphorylated vacuolar membrane protein that interacts with Ato13p, required for	2	4.0156	0.3042	2171.53	2172.357	3	281.2	47.22222 H.NDKVEDLVKNDDDIINGVR.K
gi 6320824 ref NP_010903.1	YEL013W	the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Ny1p to form nucleus-vacuole junctions; Vac8p Phosphorytated vacuolar membrane protein that interacts with Ato13p, required for	1	3.1044	0.1705	1380.78	1381.699	5	554.4	63.636364 Q.VSREVLEPILIL.L
gi 6320824 ref NP_010903.1	YEL013W	the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Ny1p to form nucleus-vacuole junctions; Vac8p Phosphorytated vacuoler membrane protein that interacts with Atri13p, required for	1	2.6276	0.1636	1394.86	1396.699	5	510.2	63.636364 Q.V1S1R4E1V1L1E1P1I1L11L1.L
gi 6320824 ref NP_010903.1	YEL013W	the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Ny1p to form nucleus-vacuole junctions; Vac8p Phosphorytated vacuolar membrane protein that interacts with Atro13p. required for	1	2.6989	0.2454	1509.83	1510.858	4	390.8	50 Q.V1S1R4E1V1L1E1P1I1L11L1L1L1Q
gi 6320824 ref NP_010903.1	YEL013W	the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	2	3.318	0.1611	1410.99	1410.726	2	794.4	72.72727 V.S1R4E1V1L1E1P1I1L1I1L1L1.Q

		Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for								
gil6320824lrofIND_010003_11	VEL 013W	the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form	2	3 1071	0 1626	1307 57	1305 726	1	853.2	77 27273 \/ SPE\/I EPII II I O
gilo320624[tet]INF_010903.1]	TELOISW	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for	2	3.1071	0.1020	1397.57	1393.720	'	000.2	11.2/2/3 V.SREVLEFILILLQ
		the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form								
gi 6320824 ref NP_010903.1	YEL013W	nucleus-vacuole junctions; Vac8p Phoenboulated vacualar membrane protein that interacts with Ata13p, required for	2	3.4592	0.1521	1494.31	1494.858	1	1102.1	75 Q.VSREVLEPILILL.Q
		the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form								
gi 6320824 ref NP_010903.1	YEL013W	nucleus-vacuole junctions; Vac8p	1	3.2179	0.2193	1295.56	1296.566	4	638	70 V.S1R4E1V1L1E1P1I1L1I1L1.L
		Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for								
gil6320824/refINP 010903.1	YEL013W	nucleus-vacuole iunctions: Vac8p	1	3.0339	0.1659	1282.73	1282.566	3	705.4	70 V.SREVLEPILILL
51		Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in								
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
ail6320813/refINP_010892.1	YEL022W	Gea2p	2	3.4083	0.1708	2003.27	2004.257	1	576.8	50 N.KIEIPTNEMESVEELIE.G
2/1		Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in	-							
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
ail6320813/refINP 010892.1	YEL022W	Gea2p	3	5.3746	0.2945	2581.31	2579.956	1	1275.1	43.18182 N.K2I1E1I1P1T1N2E1M1E1S1V1E1E1L1I1E1G1G1L1L1P1L1.L
		Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in								
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
ail6320813/refINP 010892.1	YEL022W	Gea2p	2	3.7712	0.1986	2812.89	2810.219	1	766.2	41.6666664 N.K2I1E1I1P1T1N2E1M1E1S1V1E1E1L1I1E1G1G1L1L1P1L1L1N2.S
51		Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in								
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
ail6320813/refINP_010892.1	YEL022W	cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	3	4,1091	0.2477	2783.33	2782.219	1	743.6	34.375 N.KIEIPTNEMESVEELIEGGLUPLUN.S
51		Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in								
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
gil6320813lrefINP_010892_1	YEI 022W	cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2n	2	3 0428	0 2341	2782 13	2782 219	1	1013.9	43 75 N KIEIPTNEMESVEELIEGGU PU N S
giloozoo iolioiliu _010002.11	LEGEL	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in	-	0.0120	0.2011	2102.10	2702.210	·	1010.0	
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
gil6320813lrofINP_010892_11	YEI 022W	cytoskeleton organization; similar to but not functionally redundant with Gea1p;	2	3 4739	0 3282	1564 19	1564 751	1	321.5	62.5 S G1H3K2I1D1K2E1N2P1Y1K2K2S1 I
giloozoo ioliciliai _010002.11	TELOZZW	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in	-	0.4700	0.0202	1004.10	1004.701		021.0	
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
gil6320813lrofIND_010802_11	VEI 022W/	cytoskeleton organization; similar to but not functionally redundant with Gea1p;	3	4 0001	0 2751	2554.40	2554 956	1	064.2	
giloszoo15/rei/14/_010052.1/	TLLOZZVV	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in	5	4.3031	0.2751	2004.40	2334.930		304.2	
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
gil6320813lrofIND_010802_11	VEI 022W/	cytoskeleton organization; similar to but not functionally redundant with Gea1p;	2	3 6319	0 2325	2780.01	2782 210	1	021.8	
giloszoorsiteiliar_010032.1	TLLOZZVV	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in	2	3.0310	0.2323	2700.91	2702.219		321.0	
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
dil63208131rofIND_010802_11	VEI 022W/	cytoskeleton organization; similar to but not functionally redundant with Gea1p;	2	4 5562	0 3947	2149.05	21/0 386	1	636.3	
giloozoo ioliciliai _010002.11	TELOZZW	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in	-	4.0002	0.0047	2140.00	2143.000		000.0	
		vesicular transport between the Golgi and ER, Golgi organization, and actin								
dil63208131rofIND_010802_11	VEI 022W/	cytoskeleton organization; similar to but not functionally redundant with Gea1p;	2	3 28/6	0 2034	1660 11	1650 777	1	777 1	77 27273 C C1N2H3K2D1E1D1E1W2V1I 1D1 P
giloozoo iolioiliu _010002.11	LEGEL	P-type ATPase, ion transporter of the ER membrane involved in ER function and	-	0.2010	0.2001	1000.11	1000.111	·		
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	4.2087	0.3558	1782.07	1779.988	1	425.2	60.000004 S.EDNLQLDGVDKIAVLH.G
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.9604	0.3876	1802.35	1800.988	1	853.9	70 S.E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1H3.G
		P-type AI Pase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2n degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.0508	0.2359	1548.19	1548.604	1	471.3	66.66667 S.KIDDLNRDDVESE.L
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
gil6320804lrefINP_010883_1	YEI 031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1: Sof1p	2	3 8498	0 1578	1674 43	1672 873	1	788.2	67 85714 A V1E1E1A1N2S1K2P1V1E1V1I1K2P1N2 G
giloo2000 ilioiliti _010000.11		P-type ATPase, ion transporter of the ER membrane involved in ER function and	-	0.0100	0.1070	107 1110	1012.010	·	100.2	
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spt1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	2.9503	0.1774	1543.57	1540.723	1	565.6	70.83333 F.HCPLKDDAIETIK.M
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.7305	0.3658	2046.33	2047.149	1	515.8	56.25 S.K2I1D1D1L1N2R4D1D1V1E1S1E1L1T1F1N2.G
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.7273	0.4725	2423.33	2422.567	1	983.5	60.000004 F.RDVEETVSIPFDPSKDTFDHS.K
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
gil6320804lrofINP_010883_11	YEI 031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; conters sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	2	3 8655	0 3656	2106 39	2105 259	1	593.9	55 88235 F R4D1//1F1F1T1//1S1I1P1F1D1P1S1K2D1T1F1 D
giloo20004[ici]i4i _010000.1]	TELOOTW	P-type ATPase, ion transporter of the ER membrane involved in ER function and	-	0.0000	0.0000	2100.00	2100.200		000.0	
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spt1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	4.0582	0.4572	2082.65	2083.259	1	824	64.70589 F.RDVEETVSIPFDPSKDTF.D
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.2424	0.1505	2367.59	2367.595	1	499.4	47.368423 L.L1F1R4D1V1E1E1T1V1S1I1P1F1D1P1S1K2D1T1F1.D
		P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis: required for regulating Hmg2p degradation: confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.6258	0.3484	2369.91	2367.536	1	459.6	50 S.K2I1D1D1L1N2R4D1D1V1E1S1E1L1T1F1N2G1F1L1.I
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
ail6320804/ref/NP 010883 1	YEL031W	caz+ nomeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	2	3,5886	0.2904	1947.57	1947,149	2	291.2	44.444447 Q.V1T1P1P1E1H3K2S1D1I1P1P1P1P1D1G1G1A1L1.A
of a second second		P-type ATPase, ion transporter of the ER membrane involved in ER function and	-					-		
ail6320804/refIND 010882 41	YEI 031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia faringes KK1; Spf1p	2	3 6101	0.3664	2764 70	2764 140	1	320.0	36 & VEEANSKEVEVIKENGI SEKKEADI A S
8-1005000-110-114F_010003.1	1 2200 1 11	a miles town (owner) produced by Fronia rannoad titer, oprip	4	0.0131	0.0004	2104.13	2104.143	'	020.0	SCALLERINGIN VEVIN HOLDENN ADEA.O

		P-type ATPase ion transporter of the FR membrane involved in FR function and								
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.7582	0.3859	2795.57	2796.149	1	503.6	42 A.V1E1E1A1N2S1K2P1V1E1V111K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
ail6320804/refINP 010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.278	0.2491	2517.75	2518.826	2	241	35 T.EIYKLEPREPQVDLEKEFAPS.L
31		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	2.9128	0.2157	2290.13	2290.639	1	378.3	38.88889 K.RLYGENSFDIPIPTFMELF.K
		P-type A I Pase, ion transporter of the EK membrane involved in EK function and								
gi 6320804 ref NP 010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.9788	0.3858	1748.41	1748.935	1	1336.5	76.92308 L.WHENEQVFSSPKFL.V
51		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.4732	0.3243	2134.63	2137.375	3	225.2	41.17647 Y.K2L1E1P1R4E1P1Q2V1D1L1E1K2E1F1A1P1S1.L
		P-type A I Pase, ion transporter of the ER membrane involved in ER function and								
ail6320804/refINP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	2	3.5894	0.3038	2424.69	2424.8	1	674.6	50 E.SIKLRPSEDNLQLDGVDKIAVLH
3.1		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.7396	0.3108	1805.45	1804.075	1	745.8	64.28571 F.H3C1P1L1K2D1D1A1I1E1T111K2M1L1.N
		P-type A I Pase, ion transporter of the EK membrane involved in EK function and Ca2+ homeostasis: required for regulating Hmg2p degradation: confers sensitivity to								
ail6320804/refINP 010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	2	3.7166	0.2547	2450.85	2453.8	2	425.8	42.857143 E.S1I1K2L1R4P1S1E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1.H
51		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								S.G1E1S1T1P1L1L1K2E1S1I1K2L1R4P1S1E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	5.2104	0.4016	3557.87	3559.017	1	1085.9	29.032257 H3.G
		P-type ATPase, for transporter of the ER memorane involved in ER function and Ca2+ homeostasis: required for regulating Hmg2n degradation: confers sensitivity to								
ail6320804/refINP 010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	3	4.9693	0.3726	3515.9	3517.017	1	994.1	28.225807 S.GESTPLLKESIKLRPSEDNLQLDGVDKIAVLH.G
3.1		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.6899	0.2959	2841.69	2843.166	1	494	39.130436 K.GAPETIRERLSDIPKNYDEIYKSF.T
		P-type A I Pase, ion transporter of the EK membrane involved in EK function and								
ail6320804/refINP 010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	2	3.8926	0.2799	2874.87	2876.166	2	344.4	34.782608 K.G1A1P1E1T1I1R4E1R4L1S1D1I1P1K2N2Y1D1E1I1Y1K2S1F1.T
3.1		P-type ATPase, ion transporter of the ER membrane involved in ER function and	_					_	• • • • •	
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	3.9766	0.32	2842.28	2843.166	1	433.3	27.173912 K.GAPETIRERLSDIPKNYDEIYKSF.T
		P-type A I Pase, ion transporter of the EK membrane involved in EK function and								
ail6320804/refINP 010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	2	4.3459	0.3663	2593.43	2593.941	3	472.4	40.909092 E.S1I1K2L1R4P1S1E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1H3.G
3.1		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.7487	0.3392	2560.89	2561.941	1	667	45.454548 E.SIKLRPSEDNLQLDGVDKIAVLH.G
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
ail6320804/refINP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	2	3.3313	0.1938	2650.69	2651.993	2	403.5	36.95652 E.S1I1K2L1R4P1S1E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1H3G1.G
giloozooo ilioiltii _oroooo.ii	12200111	P-type ATPase, ion transporter of the ER membrane involved in ER function and	-	0.0010	0.1000	2000.00	2001.000	-	100.0	
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	7.1236	0.3669	2591.63	2593.941	1	1193.3	43.18182 E.S1I1K2L1R4P1S1E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1H3.G
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
ail6320804/refINP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	3	6.0182	0.4419	2559.5	2561.941	1	1003.6	39.772728 E.SIKLRPSEDNI QLDGVDKIAVLH G
3.1		P-type ATPase, ion transporter of the ER membrane involved in ER function and	-					-		
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.8348	0.3498	2516.57	2517.803	7	330.3	36.842106 E.T1I1R4E1R4L1S1D1I1P1K2N2Y1D1E1I1Y1K2S1F1.T
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
ail6320804/refINP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	3	4.0209	0.2916	2923.4	2923,296	1	600.2	30,208334 A. VKGAPETIRERLSDIPKNYDEIYKS F
gileo2000 ilioiltit _010000.11	12200111	P-type ATPase, ion transporter of the ER membrane involved in ER function and	0		0.2010	2020.1	2020.200	·	000.2	
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.696	0.4217	3108.11	3106.472	1	590.1	29 A.V1K2G1A1P1E1T1I1R4E1R4L1S1D111P1K2N2Y1D1E1I1Y1K2S1F1.T
		P-type A Pase, ion transporter of the ER membrane involved in ER function and								
ail6320804/refINP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	3	3.9815	0.32	3070.4	3070.472	1	481	28 A.VKGAPETIRERI SDIPKNYDEIYKSE.T
3.1		P-type ATPase, ion transporter of the ER membrane involved in ER function and	-					-		
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.517	0.253	1652.69	1653.873	1	883.6	60.714287 A.VEEANSKPVEVIKPN.G
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
gil6320804/refINP_010883_1	YEI 031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	2	4 8356	0.3426	1718 77	1716 944	1	1397.2	76 6666641 VKLEDGDIVGDPMEKA T
gileo2000 ilioiltit _010000.11	12200111	P-type ATPase, ion transporter of the ER membrane involved in ER function and	-		0.0120			·	1001.2	
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.2744	0.2176	2254.33	2253.436	1	699.1	50 L.F1R4D1V1E1E1T1V1S1I1P1F1D1P1S1K2D1T1F1.D
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
ail6320804/refINP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	3	5.225	0.227	3578.27	3580.778	1	773.1	26.666668 1.K
3.1		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.1232	0.2934	3541.79	3540.778	4	402.6	20.833332 A.GKSDDNQLLFRDVEETVSIPFDPSKDTFDHS.K
		P-type At Pase, for transporter of the EK membrane involved in EK function and								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1: Spf1p	3	6.2318	0.4017	2795.15	2796.149	1	2138.8	40 A.V1E1E1A1N2S1K2P1V1E1V1I1K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
0. · · · · · · · · · · · · · · · · · · ·		P-type ATPase, ion transporter of the ER membrane involved in ER function and	-							
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.1732	0.246	2236.01	2233.53	1	685.3	50 K.LRPSEDNLQLDGVDKIAVLH.G
		Ca2+ homeostasis: required for regulating Hmg2p degradation: confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.5545	0.3777	2235.23	2233.53	1	1003.6	40.789474 K.LRPSEDNLQLDGVDKIAVLH.G

		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	6.0907	0.3616	2690.81	2691.057	1	953.4	39.130436 K.ESIKLRPSEDNLQLDGVDKIAVLH.G
		P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to		0.0100	0.4740	0044.00	0044.044			
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.0169	0.1712	2311.23	2311.641	2	441.3	40 E.SIKLRPSEDNLQLDGVDKIAV.L
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; conters sensitivity to a killer toxin; (SMKT) produced by Pichia farinosa KK1; Spr1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.8936	0.3918	1784.55	1785.075	1	1246	71.42857 F.HCPLKDDAIETIKML.N
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; conters sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	3	4.5582	0.2874	1787.66	1785.075	1	2024.2	57.14286 F.HCPLKDDAIETIKML.N
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATsae, ion transporter of the ER membrane involved in ER function and	2	4.0403	0.3893	2338.69	2339.694	1	586.4	47.368423 Y.KLEPREPQVDLEKEFAPSLL.N
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required tor regulating Hmg2p degradation; conters sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.8275	0.3367	2843.51	2843.166	1	492.7	39.130436 K.GAPETIRERLSDIPKNYDEIYKSF.T
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.6863	0.3478	2560.49	2561.941	1	467.5	38.636364 E.SIKLRPSEDNLQLDGVDKIAVLH.G
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	3	6.4952	0.4864	2560.49	2561.941	1	1769.2	48.863636 E.SIKLRPSEDNLQLDGVDKIAVLH.G
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	4.2157	0.3964	2593.81	2593.941	2	341.8	34.090908 E.S111K2L1R4P1S1E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1H3.G
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.7372	0.2805	2487.57	2488.803	4	435.2	39.473686 E.TIRERLSDIPKNYDEIYKSF.T
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.0314	0.2563	1387.71	1388.576	2	860.3	79.16667 L.VKLEDGDIVGDPM.E
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.8638	0.2384	1401.49	1402.576	1	863.8	79.16667 L.V1K2L1E1D1G1D111V1G1D1P1M1.E
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	4.653	0.3578	1544.03	1544.705	1	1430.2	83.33333 F.F1F1M1D1D1K2P1S1D111S1V1Q2.Q
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	4.172	0.3574	1529.51	1529.705	1	1380.8	83.33333 F.FFMDDKPSDISVQ.Q
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type APpase, ion transporter of the ER membrane involved in ER function and	2	3.9267	0.3492	1629.59	1630.812	1	556.1	57.692307 R.W2N2Q2P1Q2P1P1V1P1E1P111A1H3.L
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	3	4.0564	0.2946	2793.86	2796.149	1	1015.9	32 A.V1E1E1A1N2S1K2P1V1E1V1I1K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.5612	0.2755	1734.09	1734.944	1	730.6	60.000004 L.V1K2L1E1D1G1D111V1G1D1P1M1E1K2A1.T
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.0428	0.2035	1711.43	1710.822	3	309.7	50 T.V1S111P1F1D1P1S1K2D1T1F1D1H3S1.K
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.3568	0.3634	2109.49	2111.227	3	206	38.235294 Q.SKIDDLNRDDVESELTFN.G
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	3	4.7951	0.2649	2449.28	2449.567	1	1057.7	36.25 F.R4D1V1E1E1T1V1S1I1P1F1D1P1S1K2D1T1F1D1H3S1.K
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	3	4.4345	0.2859	2424.59	2422.567	1	950.4	33.75 F.RDVEETVSIPFDPSKDTFDHS.K
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	4.0834	0.27	1930.53	1931.045	1	707.4	56.666668 S.K2I1D1D1L1N2R4D1D1V1E1S1E1L1T1F1.N
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.0319	0.2476	2052.35	2053.279	1	244.3	39.473686 L.QVTPPEHKSDIPPPPDGGAL.A
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.9756	0.2344	2545.45	2545.826	1	341.9	42.5 T.E1I1Y1K2L1E1P1R4E1P1Q2V1D1L1E1K2E1F1A1P1S1.L
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.4806	0.1994	1558.49	1557.723	1	597.5	70.83333 F.H3C1P1L1K2D1D1A111E1T111K2.M
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	3	3.9777	0.1506	2363.3	2363.706	1	610.7	33.333336 A.N2S1K2P1V1E1V111K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmq2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	4.8324	0.3648	2362.65	2363.706	1	457.4	45.238094 A.N2S1K2P1V1E1V111K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.7069	0.4363	2112.51	2113.375	1	290.3	50 Y.KLEPREPQVDLEKEFAPS.L
gi 6320804 ref NP_010883.1	YEL031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase, ion transporter of the ER membrane involved in ER function and	2	3.4408	0.3336	2049.87	2051.361	1	539.9	46.875 L.K2R4L1Y1G1E1N2S1F1D11P111P1T1F1M1.E
gi 6320804 ref NP_010883.1	YEL031W	Caz+ nomeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.492	0.4154	2363.55	2365.694	1	644.8	50 Y.K2L1E1P1R4E1P1Q2V1D1L1E1K2E1F1A1P1S1L1L1.N

		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
ail6320804/refINP_010883.11	YEI 031W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	з	4 2661	0 2965	2641.49	2630 011	1	637	32 142857 K G141P1E1T111R4E1R4I 1S1D111P1K2N2Y1D1E111Y1K2 S
gil0320004[rei]INF_010003.1]	TELUSIW	P-type ATPase, ion transporter of the ER membrane involved in ER function and	3	4.2001	0.2905	2041.49	2039.911	'	037	32.142037 R.GIATETETTTIR4ETR4E131D11F1R2N211D1E11111R2.3
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p P-type ATPase ion transporter of the EP membrane involved in EP function and	3	4.1685	0.1881	2876.21	2876.166	1	574.5	29.347824 K.G1A1P1E1T1I1R4E1R4L1S1D1I1P1K2N2Y1D1E1I1Y1K2S1F1.T
		Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.3043	0.3043	2216.27	2215.504	1	1067.6	43.055553 A.V1K2G1A1P1E1T111R4E1R4L1S1D111P1K2N2Y1.D
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
gi 6320804 ref NP_010883.1	YEL031W	a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.2202	0.2583	2837.18	2836.217	1	420.6	28.260868 A.VKGAPETIRERLSDIPKNYDEIYK.S
		P-type ATPase, ion transporter of the ER membrane involved in ER function and								
ail62200041rofIND_010002_11	VEL 021W	Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to	2	4 5094	0 2472	2057 27	2059 206	1	511.0	
gil0320004[rei]NF_010003.1]	TELUSIW	Protein involved in DNA replication: component of the Mcm2-7 hexameric complex	3	4.0004	0.3473	2957.27	2936.290	1	511.9	29.100000 A.VIN2GIAIFTETTIIN4EIK4EIGIDIIIFIN2N2TIDIEIIITIN2SI.F
gi 6320803 ref NP_010882.1	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	2	3.8156	0.3492	2207.85	2209.417	1	553.9	50 S.LFERINEELPEEEKFSAQ.E
ail62208021rofIND_010892.11	VEL 022W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex	2	7 7702	0 5202	2425.00	2420 207	1	1061.9	A.N2Y1N2D1D1Q2D1D1A1D1E1R4D1L1L1G1D1D1D1D1D1D1D1L1E1K2E1K2K2A1/
gilo520005[rei]Nr_010002.1]	TLL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex	J	1.1132	0.5505	3433.30	5450.507		1001.0	34.402730 1.3
gi 6320803 ref NP_010882.1	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	3	5.2933	0.393	4226.21	4227.325	1	914.2	22.368422 L.AVGEDADINPEEHSNSGAGVENEGEDDEDHVFEKFNPLL.Q
ail63208031rofIND_010882.11	VEI 032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex	2	7 7000	0.5406	4273 67	1275 325	1	1466.3	L.A1V1G1E1D1A1D111N2P1E1E1H3S1N2S1G1A1G1V1E1N2E1G1E1D1D1E1D1H: 25.657806 \/1E1E1K2E1N2B11414.0
gilo520005[rei]Nr_010002.1]	TLL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex	5	1.1035	0.3400	42/ 3.07	4210.020	'	1400.5	
gi 6320803 ref NP_010882.1	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	2	3.731	0.2572	2272.35	2272.612	1	380.6	52.77778 H.RYLPPGYLEGEPVRERLNL.S
ail63208031rofIND_010882.11	VEI 032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex	2	4 8418	0 4423	2017 10	2017 007	1	1200.2	62.5 A G1//1E1N/2E1G1E1D1D1E1D1H3//1E1E1K/2E1 N
gilo520005[rei]Nr_010002.1]	TLL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex	2	4.0410	0.4423	2017.13	2017.007		1203.2	
gi 6320803 ref NP_010882.1	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	2	4.4117	0.4343	2553.03	2555.847	1	771.6	47.727272 R.S1I1D1V111L1D1D1D1L1V1D1K2T1K2P1G1D1R4V1N2V1V1.G
ail6320803/refINP_010882_1	YEI 032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex; Mcm3p	3	5 0259	0 2856	2557 34	2555 847	1	1082 1	36 363636 R S111D1V1111 1D1D1D11 1V1D1K2T1K2P1G1D1R4V1N2V1V1 G
giloozoooliciini _010002.11	12200211	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex	0	0.0200	0.2000	2007.04	2000.047		1002.1	
gi 6320803 ref NP_010882.1	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	3	4.3448	0.2734	2526.17	2526.847	1	887.9	34.090908 R.SIDVILDDDLVDKTKPGDRVNVV.G
ail6320803/refINP_010882.1	YEI 032W	Protein involved in DINA replication; component of the Mcm2-7 nexameric complex that binds chromatin as a part of the pre-replicative complex; Mcm3p	3	5 0958	0 2242	2913 29	2916 228	1	766.3	32 A G1Q2I 1P1R4S1I1D1V1I1I 1D1D1D1I 1V1D1K2T1K2P1G1D1R4V1N2 V
giloozooolioilui _01000211	LEGOLI	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex	0	0.0000	0.2212	2010.20	2010.220	·	100.0	
gi 6320803 ref NP_010882.1	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	3	4.0376	0.299	2879.9	2880.228	9	413.1	25 A.GQLPRSIDVILDDDLVDKTKPGDRVN.V
ail63208031refINP 010882.11	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	3	6.1882	0.3065	3117.08	3116.493	1	1162.7	28.703705 A.G1Q2L1P1R4S1I1D1V1I1L1D1D1D1L1V1D1K2T1K2P1G1D1R4V1N2V1V1.G
		Protein involved in DNA replication; component of the Mcm2-7 hexameric complex								
gi 6320803 ref NP_010882.1	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	3	6.1066	0.2953	3078.44	3078.493	1	1352.8	31.48148 A.GQLPRSIDVILDDDLVDKTKPGDRVNVV.G
gi 6320803 ref NP_010882.1	YEL032W	that binds chromatin as a part of the pre-replicative complex; Mcm3p	2	4.6141	0.4288	2300.97	2301.612	1	528	61.11111 H.R4Y1L1P1P1G1Y1L1E1G1E1P1V1R4E1R4L1N2L1.S
		Translation initiation factor eIF-5A, promotes formation of the first peptide bond;								
ail63208011refINP_010880_11	YEL034W	similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification: expressed under aerobic conditions: Hyp2p	2	4 494	0 4547	2338 43	2338 52	1	722 7	47 61905 L MNMDGDTKDDVKAPEGELGDSL O
giloozooo ilioiluu _oroooo.ii	12200111	Translation initiation factor eIF-5A, promotes formation of the first peptide bond;	-		0.1011	2000.10	2000.02	·		
-100000041 (IND_040000-41		similar to and functionally redundant with Anb1p; undergoes an essential	•		0.0470	0005.05	0000 50		000 7	
gil6320801 [ref]NP_010880.1]	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond:	3	4.1942	0.2472	2365.25	2363.52	1	999.7	36.904/62 L.MIN2MIDIGIDITIK2DIDIVIK2AIPIEIGIEILIGIDISILI.Q
		similar to and functionally redundant with Anb1p; undergoes an essential								
gi 6320801 ref NP_010880.1	YEL034W	hypusination modification; expressed under aerobic conditions; Hyp2p	3	3.8517	0.2894	2231.57	2231.328	1	929.5	35 M.N2M1D1G1D1T1K2D1D1V1K2A1P1E1G1E1L1G1D1S1L1.Q
		similar to and functionally redundant with Anb1p; undergoes an essential								
gi 6320801 ref NP_010880.1	YEL034W	hypusination modification; expressed under aerobic conditions; Hyp2p	2	5.3857	0.5058	2230.41	2231.328	1	1134.5	55 M.N2M1D1G1D1T1K2D1D1V1K2A1P1E1G1E1L1G1D1S1L1.Q
		I ranslation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anh1n; undergoes an essential								
gi 6320801 ref NP_010880.1	YEL034W	hypusination modification; expressed under aerobic conditions; Hyp2p	1	2.686	0.1723	1126.58	1127.24	3	403.6	66.66667 K.KLEDLSPSTH.N
		Translation initiation factor eIF-5A, promotes formation of the first peptide bond;								
ail63208011refINP_010880_11	YEL034W	similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	1	2 8257	0 1892	1139 48	1140 24	1	391.9	66 66667 K K2I 1E1D1I 1S1P1S1T1H3 N
giloo2000 fileinti _010000.1	1 ELCO4W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond;	'	2.0207	0.1002	1100.40	1140.24		001.0	
-100000041 (IND_040000-41		similar to and functionally redundant with Anb1p; undergoes an essential	•	4 0000	0.0040	0000 50	0000 004		000.4	
gil6320801 [ref]NP_010880.1]	YEL034W	nypusination modification; expressed under aerobic conditions; Hyp2p Translation initiation factor eIF-5A, promotes formation of the first peotide bond:	3	4.0392	0.2643	2338.58	2339.631	1	808.4	38.157894 K.K2L1E1D1L1S1P1S111H3N2M\$E1V1P1V1V1K2K4N2.E
		similar to and functionally redundant with Anb1p; undergoes an essential								
gi 6320801 ref NP_010880.1	YEL034W	hypusination modification; expressed under aerobic conditions; Hyp2p	3	4.1086	0.2286	2339.93	2338.52	1	1836.2	42.857143 L.MNMDGDTKDDVKAPEGELGDSL.Q
		i ransiation initiation factor eiF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential								
gi 6320801 ref NP_010880.1	YEL034W	hypusination modification; expressed under aerobic conditions; Hyp2p	2	5.5073	0.4427	2362.23	2363.52	1	1117.7	50 L.M1N2M1D1G1D1T1K2D1D1V1K2A1P1E1G1E1L1G1D1S1L1.Q
		Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein;								
ail63207991refINP 010878.11	YEL036C	nas a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol: Anp1p	1	2.5787	0.3216	1253.58	1254.462	4	182.3	55.555557 N.V1W2R4P1L1P1D1W2L1G1.N
51		Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein;								
ail6220700/rofIND_010979_1	VEL 026C	has a role in retention of glycosyltransferases in the Golgi; involved in osmotic	2	4 5196	0.2595	1979 05	1977 140	1	502.2	64 29674 N V/4W/2D 4D11 4D4 D1W/21 4C 4N/214 C/2D4 V4 D
gil0320799[rei]NF_010676.1]	TEL030C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein;	2	4.0100	0.3365	10/0.95	10/7.149	'	093.3	04.2037110.V1W2R4F1E1F1D1W2E1G1021102F111.D
		has a role in retention of glycosyltransferases in the Golgi; involved in osmotic								
gi 6320799 ref NP_010878.1	YEL036C	sensitivity and resistance to aminonitrophenyl propanediol; Anp1p Subunit of the alpha-1.6 mannosyltransferase complex: type II membrane protein:	2	3.4293	0.3508	2632.45	2634.006	1	490.7	42.857143 Q.GIFKPYVPDFKNTPSVEFYDLR.N
		has a role in retention of glycosyltransferases in the Golgi; involved in osmotic								
gi 6320799 ref NP_010878.1	YEL036C	sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	3.7075	0.3291	2661.55	2662.006	1	706.1	50 Q.G111F1K2P1Y1V1P1D1F1K2N2T1P1S1V1E1F1Y1D1L1R4.N
		has a role in retention of glycosyltransferases in the Goloi: involved in osmotic								
gi 6320799 ref NP_010878.1	YEL036C	sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	3.5637	0.2214	1524.25	1524.643	1	779.4	77.27273 K.I1W2E1I1G1F1E1D1V1R4D1Q2.W
		Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein;								
gi 6320799 ref NP_010878.1	YEL036C	sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	2.9741	0.2791	1369.87	1370.566	4	538.9	60.000004 N.V1W2R4P1L1P1D1W2L1G1N2.I
		Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein;								
gi 6320799 ref NP_010878.1	YEL036C	nas a role in relention or grycosyntansierases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenvl propanediol: Anp1p	2	3.9023	0.3474	1854.35	1855.149	1	557	60.714287 N.VWRPLPDWLGNIQPY.D

		Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein;								
gi 6320799 ref NP_010878.1	YEL036C	has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein;	2	3.0089	0.1599	2249.25	2249.571	1	392.5	38.88889 Q.GIFKPYVPDFKNTPSVEFY.D
gi 6320799 ref NP_010878.1	YEL036C	has a role in retention of glycoxyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	3.2001	0.2462	2270.97	2271.571	2	510	41.6666664 Q.G1I1F1K2P1Y1V1P1D1F1K2N2T1P1S1V1E1F1Y1.D
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.5992	0.4191	2391.75	2393.674	1	1096.3	57.14286 N.A1S111P1K2T1P1E1D111S111L1P1V1N2D1E1P1G1Y1L1.Q
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	3.2342	0.3276	2196.75	2199.375	1	455.7	50 L.S1A1V1R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1.G
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.5525	0.4479	2355.79	2357.559	1	755.4	52.499996 L.S1A1V1R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1G1V1.S
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.4268	0.4801	2329.81	2330.559	1	1437.8	62.5 L.SAVRDHLEKDYPFPVVEGDGV.S
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	3.5939	0.3243	2503.67	2503.832	1	810.1	52.380955 A.VRDHLEKDYPFPVVEGDGVSIM.G
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.282	0.4575	2530.43	2531.832	1	494.4	40.476192 A.V1R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1G1V1S111M1.G
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.5894	0.4515	2405.57	2404.7	1	1041	52.499996 V.RDHLEKDYPFPVVEGDGVSIM.G
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.4211	0.417	2429.83	2431.7	1	503.5	42.5 V.R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1G1V1S1I1M1.G
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.568	0.3893	2690.59	2691.989	1	517.1	41.304348 L.S1A1V1R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1G1V1S1I1M1.G
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.5118	0.3887	2664.71	2661.989	1	582	41.304348 L.SAVRDHLEKDYPFPVVEGDGVSIM.G
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred lis substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	3.7085	0.3664	2249.53	2248.512	1	735.2	47.368423 R.DHLEKDYPFPVVEGDGVSIM.G
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred lis substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	3.1194	0.2231	1580.17	1580.868	1	858.6	66.66667 Q.IIV1F1E1P1T1F1P1I1N2E1K2M1.V
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred tis substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	3.654	0.2995	2521.73	2523.805	1	303.8	34.090908 N.A1S111P1K2T1P1E1D111S111L1P1V1N2D1E1P1G1Y1L1Q2.D
gi 6320793 ref NP_010872.1	YEL042W	mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred lits substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	3	4.419	0.2079	2526.11	2523.805	3	472.5	29.545454 N.A1S111P1K2T1P1E1D111S111L1P1V1N2D1E1P1G1Y1L1Q2.D
gi 6320793 ref NP_010872.1	YEL042W	Transferred tis substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP- Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	4.7234	0.3903	2449.55	2451.726	1	420.4	40.476192 A.S111P1K2T1P1E1D111S111L1P1V1N2D1E1P1G1Y1L1Q2.D
gi 6320793 ref NP_010872.1	YEL042W	Transferred tis substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP- Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	3.836	0.2951	2499.67	2497.805	1	626	47.727272 N.ASIPKTPEDISILPVNDEPGYLQ.D
gi 6320793 ref NP_010872.1	YEL042W	Transferred tis substrate; Gda1p Guanosine diphosphatase located in the Golgi, involved in the transport of GDP- Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-	2	3.7612	0.4068	2296.87	2298.595	1	471.7	42.5 A.SIPKTPEDISILPVNDEPGYL.Q
gi 6320793 ref NP_010872.1	YEL042W	mannose into the coigi lumen by converting GUP to GWP after mannose is transferred tis substrate; Gda1p Subuni D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- 47Dpc of V17D=coiet	2	4.9232	0.3845	2371.55	2369.674	1	827.3	52.380955 N.ASIPKTPEDISILPVNDEPGYL.Q
gi 6320784 ref NP_010863.1	YEL051W	A I Pase (V-A I Pase), an electrogenic proton pump round throughout the endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis; Vma8p Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-	2	3.4256	0.3009	2445.29	2447.462	1	489.2	45.238094 K.R4D1R4A1E1Q2D1A1S1E1V1A1A1D1E1E1P1Q2G1E1T1L1.V
gi 6320784 ref NP_010863.1	YEL051W	endomembrane system; plays a role in the coupling folding intrograduatine endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis; Vma8p Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase). an electrocenic coroton pump found throughout the	2	4.1064	0.3353	2416.49	2417.462	1	715.8	45.238094 K.RDRAEQDASEVAADEEPQGETL.V
gi 6320784 ref NP_010863.1	YEL051W	endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis; Vma8p Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrocenic proton pump found throuchout the	3	4.9268	0.2657	1965.47	1965.12	1	1194.1	48.214287 N.S1E1L1D1E1L1D1R4E1E1F1Y1R4L1K2.K
gi 6320784 ref NP_010863.1	YEL051W	endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis; Vma8p	2	2.9226	0.277	1278.43	1278.494	1	929.6	75 N.AIEHVIIPRTE.N
gi 6320764 ref NP_010843.1	YEL071W	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and reduced in cells grown with glutamate as the sole nitrogen source, located in the cytoplasm; Dld3p	1	3.8286	0.1941	1259.54	1260.395	1	593.2	77.77778 F.L1H3D1H3D1H3I1F1P1L1.D
gi 6320764 ref NP_010843.1	YEL071W	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and reduced in cells grown with glutamate as the sole nitrogen source, located in the cytoplasm; Dld3p	2	3.0967	0.1907	1362.13	1364.509	4	340	63.636364 F.L1K2D1T1T1D1S1K2L1I1S1E1.G
gi 6320764 ref NP_010843.1	YEL071W	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and reduced in cells grown with glutamate as the sole nitrogen source, located in the cytoplasm; Dld3p	2	3.8587	0.1565	1996.51	1997.254	1	414	53.333336 L.K2D1L1P1F1P1L1E1N2Q2H3N2F1Y1V1L1.I
gi 6320764 ref NP_010843.1	YEL071W	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and reduced in cells grown with glutamate as the sole nitrogen source, located in the cytoplasm; Dld3p	2	3.1894	0.208	1343.81	1346.524	9	649.4	85 F.T1K2Q2I1E1D1L1L1E1P1F1.V

		D-lactate dehydrogenase, part of the retrograde regulon which consists of genes								
gi 6320764 ref NP_010843.1	YEL071W	grown with glutamate as the sole nitrogen source, located in the cytoplasm; Dld3p	1	3.1985	0.2111	1244.47	1244.395	2	462.2	72.22222 F.LHDHDHIFPL.D
ail6320839/refINP_010918.1	YER003C	Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P: required for early steps in protein mannosylation: Pmi40p	2	3.72	0.1811	1944.71	1943.164	1	813.7	56.25 S.KNSPSDENKPDLPELIQ.R
giloozooolioilui _orooroiri	1210000	Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and	-	0.12	0.1011		1010.101		01011	
gi 6320839 ref NP_010918.1	YER003C	mannose-6-P; required for early steps in protein mannosylation; Pmi40p Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and	2	3.5301	0.2725	2131.59	2132.331	1	1068.5	58.333332 F.IAPHLPVDLEAEDEAFTTY.R
gi 6320839 ref NP_010918.1	YER003C	mannose-6-P; required for early steps in protein mannosylation; Pmi40p	2	3.0818	0.1678	1713.37	1712.866	1	586.3	53.571426 F.F1I1A1P1H3L1P1V1D1L1E1A1E1D1E1.A
gi 6320844 ref NP_010923.1	YER007C-A	hypothetical protein; Tma20p	2	3.612	0.2594	1800.71	1801.09	4	531.2	57.14286 K.QYPKIEDVIDELIPK.K
gil6320844/ref/NP_010923.1	YER007C-A	hypothetical protein; Tma20p	3	5.0639	0.1924	2030.39	2028.397	2	1220.2	30 L.VKQTPKIEDVIDELIPK.K 40 27778 L.V1K2O2Y1P1K2I1E1D1V111D1E1L11P1K2K2S1 O
ail6320844/ref/NP_010923.1	YER007C-A	hypothetical protein: Tma20p	3	4.597	0.24	2049.53	2049.397	1	1508	50 L.V1K2Q2Y1P1K2I1E1D1V1I1D1E1L1I1P1K2.K
gi 6320844 ref NP_010923.1	YER007C-A	hypothetical protein; Tma20p	2	4.8687	0.3188	2048.93	2049.397	1	1317.5	71.875 L.V1K2Q2Y1P1K2I1E1D1V1I1D1E1L1I1P1K2.K
gi 6320844 ref NP_010923.1	YER007C-A	hypothetical protein; Tma20p	2	4.8063	0.3537	2026.77	2028.397	1	1173.3	68.75 L.VKQYPKIEDVIDELIPK.K
gi 6320844 ref NP_010923.1	YER007C-A	hypothetical protein; Tma20p	3	5.0705	0.1933	2245.49	2243.649	1	1476.6	44.444447 L.VKQYPKIEDVIDELIPKKS.Q
gi 6320844 ref NP_010923.1	YER007C-A	nypotnetical protein; I mazup Camma subunit of the translation initiation factor eIE2, involved in the identification	2	3.0214	0.1563	1821.05	1819.09	3	233.7	57.14286 K.Q2Y1P1K2I1E1D1V111D1E1L111P1K2.K
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	2	3.7206	0.2672	1731.41	1732.897	4	541.5	50 F.D1V1N2K2P1G1A1E1I1E1D1L1K2G1G1V1A1.G
		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
	VEDOOFIN	of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-		4 0005	0.0504	44.40.0	44.45.400		105 1	
gil6320863[ref]NP_010942.1]	YER025W	Met; Gc011p Gamma subunit of the translation initiation factor eIE2 involved in the identification	3	4.8325	0.3564	4142.6	4145.439	1	465.4	20./1428/ L.EEDGETEEEKKKKEFEEGGGLPEQPLNPDF5KLNPL.5
		of the start codon: binds GTP when forming the ternary complex with GTP and tRNAi-								E.T1G1L1E1E1D1G1E1T1E1E1E1K2R4K2R4E1E1E1E1G1G1G1L1P1E1Q2P1L1N2
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	3	4.8658	0.3872	4465.16	4467.756	1	576	21.052631 P1D1F1S1K2L1N2P1L1.S
		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	3	4.2523	0.1869	4315.43	4315.651	1	599.4	20.945946 T.GLEEDGETEEEKRKREFEEGGGLPEQPLNPDFSKLNPL.S
		of the start codon: hinds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP 010942.1	YER025W	Met; Gcd11p	2	3.4733	0.2316	1441.53	1439.695	2	798.6	66.66667 F.KLGDEIEIRPGIV.T
51000		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	2	3.013	0.2939	1835.93	1837.151	1	931.6	63.333332 V.F1K2L1G1D1E111E111R4P1G111V1T1K2.D
		of the start codon; hinds GTP when forming the ternary complex with GTP and tRNAi.								
ail63208631refINP 010942.11	YER025W	Met: Gcd11p	2	3.6006	0.2765	1712.39	1712.897	1	826.1	59.375 F.DVNKPGAEIEDLKGGVA.G
51000		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	3	4.8537	0.3099	1713.26	1712.897	1	1261.1	50 F.DVNKPGAEIEDLKGGVA.G
		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
ail6320863/refINP_010942.1	YER025W	Met: Gcd11p	2	3.5773	0.3098	1442.61	1444.641	1	780.1	66.66667 L.G1D1E1I1E1I1R4P1G1I1V1T1K2 D
giloo20000101111 _010012111	121102011	Gamma subunit of the translation initiation factor eIF2, involved in the identification	-	0.0770	0.0000			·	100.1	
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	2	3.8499	0.2944	1946.55	1947.152	1	1015.2	58.333332 R.SFDVNKPGAEIEDLKGGVA.G
		Gamma subunit of the translation initiation factor eIF2, involved in the identification of the start coden; binds GTP when forming the ternary complex with GTP and tPNA.								
ail6320863/refINP_010942.1	YER025W	Met: Gcd11p	2	3.5301	0.2702	1428.33	1427.641	1	702.5	66.66667 L.GDEIEIRPGIVTK.D
3.1		Gamma subunit of the translation initiation factor eIF2, involved in the identification	-							
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	2	3.3117	0.1904	1967.21	1969.152	1	742.7	52.77778 R.S1F1D1V1N2K2P1G1A1E111E1D1L1K2G1G1V1A1.G
		Gamma subunit of the translation initiation factor eIF2, involved in the identification of the start codon; binds GTP when forming the tergary complex with GTP and tRNAi.								
ail6320863/refINP_010942.1	YER025W	Met: Gcd11p	3	4.82	0.3617	4419.71	4416.756	1	703.4	23.026316 F.TGLEEDGETEEEKRKREFEEGGGLPEOPLNPDESKLNPLS
510000		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	2	3.4262	0.2107	1498.55	1496.629	1	772.7	66.66667 R.HVSFVDCPGHDIL.M
		Gamma subunit of the translation initiation factor eIF2, involved in the identification of the start coden; binds GTP when forming the ternary complex with GTP and tPNA.								
ail6320863/refINP_010942.1	YER025W	Met: Gcd11p	2	4.5985	0.3934	1667.93	1668.974	1	1139.3	71.42857 F.KLGDEIEIRPGIVTK.D
3.1		Gamma subunit of the translation initiation factor eIF2, involved in the identification	-							
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	2	2.9027	0.28	1626.59	1626.957	1	608.1	57.692307 K.TIPVPPRDFMISPR.L
		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
gil6320863[refINP_010942.1]	YER025W	Met: Gcd11p	2	3 6124	0 2776	1274 05	1273 355	1	652.4	80 V S1E1V1D1C1P1G1H3D111 1 M
giloo20000101111 _010012111	121102011	Gamma subunit of the translation initiation factor eIF2, involved in the identification	-	0.0121	0.2770	121 1.00	1210.000	·	002.1	
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	2	4.6766	0.2917	1533.95	1534.663	2	1376.6	73.07692 R.SFDVNKPGAEIEDL.K
		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
ail6320863/refINP_010942.1	YER025W	Met: Gcd11p	2	3,7446	0.429	2125.61	2125.294	1	627.9	50 N.GNLEPVGEPDIVEETEVVAQ.E
3.1		Gamma subunit of the translation initiation factor eIF2, involved in the identification	-							
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	2	4.7041	0.3742	1937.47	1937.203	1	1017.8	64.70589 G.GGLPEQPLNPDFSKLNPL.S
		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
gil6320863[refINP_010942.1]	YER025W	Met: Gcd11p	2	3 6517	0 2058	1241 91	1242 403	1	1302.6	80 E K2I 1G1D1E1I1E1I1B4P1G1 I
giloo20000101111 _010012111	121102011	Gamma subunit of the translation initiation factor eIF2, involved in the identification	-	0.0011	0.2000	1211.01	12 12:100	·	1002.0	
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								L.E1E1D1G1E1T1E1E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	3	4.4816	0.2585	3864.23	3865.059	1	513.9	24.21875 S1K2L1.N
		Gamma subunit of the translation initiation factor eIF2, involved in the identification								
ail6320863/ref/NP 010942 1	YER025W	Met: Gcd11p	3	5,4849	0.4245	4036.46	4037.271	1	688.8	25.735294 D1F1S1K2L1.N
21		Gamma subunit of the translation initiation factor eIF2, involved in the identification	-							
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p	3	3.9123	0.3327	3991.13	3991.271	1	660.7	22./9411/ I.GLEEDGETEEEKRKREFEEGGGLPEQPLNPDFSKL.N

		Gamma subunit of the translation initiation factor eIF2, involved in the identification of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-								LE1E1D1G1E1T1E1E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p Gamma subunit of the translation initiation factor eIF2, involved in the identification of the standard high CTD when forming the transport and write CTD and (DUM)	3	5.2932	0.3297	4190.96	4193.439	7	266.7	
gi 6320863 ref NP_010942.1	YER025W	Met; Gcd11p Gamma subunit of the translation initiation factor eIF2, involved in the identification	3	5.3736	0.3808	4364.87	4365.651	1	940.1	22.972973 D1F1S1K2L1N2P1L1.S
gi 6320863 ref NP_010942.1	YER025W	of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi- Met; Gcd11p Gamma subunit of the translation initiation factor eIF2, involved in the identification	3	5.7324	0.4671	3066.08	3068.352	1	1254.2	34 E.E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1.N
gi 6320863 ref NP_010942.1	YER025W	of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi- Met; Gcd11p Gamma subunit of the translation initiation factor eIF2, involved in the identification	3	5.1896	0.487	3029.36	3031.352	1	939.8	31 E.EEKRKREFEEGGGLPEQPLNPDFSKL.N
gi 6320863 ref NP_010942.1	YER025W	of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi- Met; Gcd11p Gamma subunit of the translation initiation factor eIF2, involved in the identification	3	6.2829	0.4438	3398.3	3396.732	1	897.2	25.892857 E.E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1N2P1L1.S
gi 6320863 ref NP_010942.1	YER025W	of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi- Met; Gcd11p Gamma subunit of the translation initiation factor eIF2, involved in the identification	3	5.0611	0.4301	3356.12	3355.732	4	628.7	24.107143 E.EEKRKREFEEGGGLPEQPLNPDFSKLNPL.S
gi 6320863 ref NP_010942.1	YER025W	of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi- Met; Gcd11p Gamma subunit of the translation initiation factor eIF2, involved in the identification	2	4.0335	0.166	1887.41	1887.167	1	665.7	64.28571 Q.T1V1R4F1K2D1E1L1E1R4N2I1T111K2.L
		of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-	•	0.44	0.0400	1000 17	1000 107			
gi 6320863 ref NP_010942.1 gi 6320890 ref NP_010969.1	YER025W YER049W	Met; Gcd11p bypothetical protein: Tpa1p	2	3.44 5.8479	0.2169	2489.25	2487 677	2	541.5 1354.4	57.14286 Q. I VRFKDELERNI I IK.L 67.5 W Y1H3I1P1Q2V1G1E1E1G1Y1I1P1G1E1E1E1A1W2V1R4 N
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	3.8848	0.3456	1586.51	1585.795	1	1155.1	67.85714 L.LKSNPDIIDAVLEGT.L
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	3.0892	0.3177	1700.71	1698.954	2	757.9	53.333336 L.LKSNPDIIDAVLEGTL.C
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	5.4444	0.4319	2460.67	2459.677	1	1328.6	65 W.YHIPQVGEEGYIPGEEEAWVR.N
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	4.1853	0.306	1883.55	1885.093	1	735.4	57.14286 N.V1L1E1D1F1E1F1P1K2D1E1R4N2I1L1.S
gi[6320890]ref[NP_010969.1]	YER049W	hypothetical protein; I pa1p	2	3.7852	0.2275	2065.89	2066.275	3	448.6	43.75 E.SNVLEDFEFPKDERNIL.S 50 O G1W2Y1H3H2H02V4G1E1E1G1Y1H2HG1E1E1E1A1W2V4P4 N
gi[6320890]ref[NP_010969.1]	YER049W	hypothetical protein: Tpa1p	2	4 5709	0.4405	2701.89	2702 942	1	1074.4	52 272724 O GWYHIPOVGEEGYIPGEEEAWVR N
gil6320890/refINP_010969.1	YER049W	hypothetical protein; Tpa1p	2	4.585	0.2895	2350.65	2349.623	1	761.6	50 K.G1E1K2E1R4N2S1K2Q2I1S1L1E1E1D1K2I1K2G1M1.F
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	3.5004	0.2812	1421.47	1422.538	1	392.6	77.27273 E.G1Y1I1P1G1E1E1E1A1W2V1R4.N
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	4.055	0.3157	2193.61	2191.318	2	805.3	50 Y.RADDSGDSVLINDPPAWNTF.N
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	3.3952	0.2443	1662.25	1661.855	1	656.1	69.230774 S.GLDWDDLSRLPNLF.K
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	4.437	0.3871	2218.41	2217.318	2	804.7	52.63158 Y.R4A1D1D1S1G1D1S1V1L11N2D1P1P1A1W2N2T1F1.N
gi[6320890]ref[NP_010969.1]	YER049W	hypothetical protein; Tpa1p	2	5 7654	0.2086	2486.83	2487.677	1	1380.6	65 W Y1H311P102V1G1E1E1G1Y111P1G1E1E1E1A1W2V1R4.N
gi 6320890 ref NP 010969.1	YER049W	hypothetical protein; Tpa1p	2	4.6386	0.3462	2458.89	2459.677	1	1255.7	62.5 W.YHIPQVGEEGYIPGEEEAWVR.N
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	3	4.0278	0.3054	2457.62	2459.677	2	1071.6	43.75 W.YHIPQVGEEGYIPGEEEAWVR.N
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	3.1722	0.199	1052.15	1052.266	1	912.7	87.5 F.F1K2V1L1P1G1F1S1F1.H
gi 6320890 ref NP_010969.1	YER049W	hypothetical protein; Tpa1p	2	4.137	0.5269	2700.85	2702.942	1	939.6	50 Q.GWYHIPQVGEEGYIPGEEEAWVR.N
gi[6320890]ref[NP_010969.1]	YER049W	hypothetical protein; I pa1p	3	3 8468	0.3191	2702.84	2702.942	1	928.6	39.772728 Q.GWYHIPQVGEEGYIPGEEEAWVR.N 53.125 P.L1E1P1S111L1P1N2V1P1H3S1D1P1S1A1K2 L
gil6320890/refINP_010969.1	YER049W	hypothetical protein; Tpa1p	2	3 1744	0.3317	1818.89	1820.098	8	374.5	43 75 R I EPSIL PNVPHSDPSAK I
310020000101111 _010000.11	12101011	Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; excression regulated by Cor4o and the general control of amine acid synthesis:	-	0.1111	0.0011	1010.00	1020.000	Ū	07.1.0	
gi 6320893 ref NP_010972.1	YER052C	Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	2	5.4586	0.4276	2183.93	2185.478	1	1975.5	65.789474 F.G1G1T1S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p According kingas (L. considerate 4. B. transformac); outpelapping accurate that establishes	3	4.2309	0.376	2161.49	2160.478	1	1395.5	42.105263 F.GGTSVGKFPVQIVDDIVKHY.S
		Aspartate kinase (L-aspartate 4+-ratisterase), cytoplasmic enzyme mar catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis;								
gi 6320893 ref NP_010972.1	YER052C	Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	2	3.4905	0.2562	1944.03	1945.269	1	1075.1	62.5 T.SVGKFPVQIVDDIVKHY.S
	VEDOFOC	expression regulated by Gcn4p and the general control of amino acid synthesis;	2	F 0700	0.0574	4000 07	4007.000		0407.0	
gilos20695[rel[i4F_010972.1]	TERUSZC	Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; provided by Conde and the general control of amino activity provide the state of the st	3	5.9700	0.3371	1900.37	1907.209	I	2127.0	57.6125 1.51 VIG IK2F IF IVIG211VIDIDITIVIK26511.5
gi 6320893 ref NP_010972.1	YER052C	Hom3p Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	3	5.2121	0.3569	2184.47	2185.478	1	1054	38.157894 F.G1G1T1S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes	2	4.114	0.3682	1721.55	1721.006	1	1263.3	76.92308 G.K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	the miss step in the cohmon partway tor methodine and oreonine busynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes	3	4.9283	0.3642	1878.35	1879.191	1	1321.4	48.333332 S.V1G1K2F1P1V1Q2I1V1D1D111V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	4.4502	0.3452	1969.77	1967.269	1	1465	68.75 T.S1V1G1K2F1P1V1Q2I1V1D1D111V1K2H3Y1.S
	VEDOCOO	Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis;	~	4 0000	0.040	4700 50	4700 000		4700.0	
gijo320893[ret]NP_010972.1]	TERU52C	rouncy Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis:	3	4.2663	0.3424	1782.59	1782.093	1	1789.9	DD I.DVGKFYVUIVDUIVKH.Y
gi 6320893 ref NP_010972.1	YER052C	Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	3	5.9198	0.3609	1805.12	1803.093	1	2335.8	63.333332 T.S1V1G1K2F1P1V1Q2I1V1D1D111V1K2H3.Y
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	4.667	0.3873	2184.31	2185.478	1	987.6	52.63158 F.G1G1T1S1V1G1K2F1P1V1Q2I1V1D1D111V1K2H3Y1.S

		Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Con4p and the general control of amino acid synthesis;								
gi 6320893 ref NP_010972.1	YER052C	Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	3	3.9542	0.4123	1701.53	1702.006	1	1091.8	55.76923 G.KFPVQIVDDIVKHY.S
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes	3	5.4368	0.3631	1720.28	1721.006	1	806.1	50 G.K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	4.7073	0.2294	1779.02	1779.058	1	784.1	51.785713 V.G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
		Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Con4p and the general control of amino acid synthesis;								
gi 6320893 ref NP_010972.1	YER052C	Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	2	3.5527	0.2238	1781.13	1779.058	1	996.9	57.14286 V.G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control or amino acid synthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first ten is the compare pathwar for methologic and therearing bioenthesis;	3	4.7456	0.4131	1944.62	1945.269	1	1246.8	48.4375 T.SVGKFPVQIVDDIVKHY.S
gi 6320893 ref NP_010972.1	YER052C	are mas skep in due och infor parway'r on reennol me aro finedonie biograficesis; expression regulated by Con4p and the general control of amino acid ynthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes	2	4.6431	0.3418	1965.83	1967.269	1	1429.2	68.75 T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320893 ref NP 010972.1	YER052C	the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	5.5896	0.3531	1967.9	1967.269	1	1218.3	48.4375 T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
		Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Con4p and the general control of amino acid synthesis;								
gi 6320893 ref NP_010972.1	YER052C	Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	2	4.1528	0.2264	1625.63	1624.773	1	1007.7	66.66667 Q.E1S1E1F1Q2D11111E1V111R4Q2.D
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	2	3.3043	0.1973	1606.71	1606.773	1	1057.2	66.66667 Q.ESEFQDIIEVIRQ.D
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	3	4.237	0.4032	1615.1	1614.882	1	647.6	48.076923 V.G1K2F1P1V1Q2I1V1D1D111V1K2H3.Y
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first sten in the common nathway for methionine and threonine biosynthesis;	2	3.7301	0.392	1802.27	1803.093	1	706.5	53.333336 T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3.Y
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes	3	5.7132	0.4253	1967.24	1967.269	1	1359.6	50 T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Aspartate kinase (I -aspartate 4-P-transferase): cytoplasmic enzyme that catalyzes	3	4.3502	0.2559	1720.55	1721.006	1	700.1	48.076923 G.K2F1P1V1Q2I1V1D1D111V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	the first step in the common pathway for methonine and threonine biosynthesis; expression regulated by Gon4p and the general control of amino acid synthesis; Hom3p	2	3.2295	0.2878	1720.69	1721.006	1	716.6	57.692307 G.K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
		Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Ccn4p and the general control of amino acid synthesis;								
gi 6320893 ref NP_010972.1	YER052C	Hom3p Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	3	4.816	0.3865	1759.34	1759.058	1	934.6	48.214287 V.GKFPVQIVDDIVKHY.S
gi 6320893 ref NP_010972.1	YER052C	Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis;	3	5.1842	0.409	1776.35	1779.058	1	1234.4	58.928574 V.G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320893 ref NP_010972.1	YER052C	expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p Purine-cvtosine permease, mediates purine (adenine, quanine, and hypoxanthine)	2	4.6214	0.3593	1969.47	1967.269	1	1268.9	65.625 T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi 6320897 ref NP_010976.1	YER056C	and cytosine accumulation; Fcy2p Purine-cytosine permease mediates purine (adenine, quanine, and hypoxanthine)	1	2.2119	0.224	1200.6	1201.365	7	323.7	60.000004 Q.DLEKRSPVIGS.S
gi 6320897 ref NP_010976.1	YER056C	and cytosine accumulation; Fcy2p	2	2.9823	0.3492	2112.57	2113.234	1	309.4	41.666664 E.T1K2G1V1E1P1V1T1E1D1E1K2T1D1D1S1I1L1N2.A
gi 6320897 ref NP_010976.1	YER056C	and cytosine accumulation; Fcy2p	2	4.6746	0.4081	1932.17	1931.065	1	358.8	63.333332 Y.N2I1D1D1W2D1N2W2E1H3L1P1I1G1I1A1.G
gi 6320897 ref NP_010976.1	YER056C	Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine accumulation; Fcy2p	1	2.9645	0.2025	1215.53	1216.365	1	438.2	70 Q.D1L1E1K2R4S1P1V1I1G1S1.S
		Protein that is processed in the mitochondrion to yield acetylglutamate kinase and N-								
ail6320913/refINP_010002_1	YER060W/	acetyl-gamma-glutamyl-phosphate reductase, which catalyze the 2nd and 3rd steps in argining biosynthesis; enzymes form a complex with Arg2n; Arg5 6n	1	2 7426	0 2508	1162 47	1162 303	1	454 7	66 66667 Y H3V1G1I 1Y1P1I1V1I 1H3 G
gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.4103	0.1536	1465.95	1466.601	1	954.1	72.72727 Y.D1L1K2E1D1I1T1D1F1D1K2L1.S
gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	1	2.8125	0.1902	1415.63	1416.648	2	188.6	54.545456 N.S1L1N2P1V1R4Q2P1F1V1L1Q2.E
gijo320924jretjNP_011003.1 gij6320924jretjNP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Emp29p The authentic, non-tagged protein was localized to the mitochondria: Emp29p	1 2	3.6545 3.0153	0.2553	1452.63	1452.601 1398.648	1 1	588.3 923.9	77.27273 N.SLNPVRQPFVLQ.E
gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.8935	0.3635	2318.27	2319.492	1	581.7	50 E.DIYDGETNPDLQNRWKIGPS.V
gi 6320924 ref NP_011003.1 gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	1	2.6082	0.3351	1395.65	1396.673	1	226.4	54.166668 A.KAPDGKILPPVFN.K 54.545456 L RIPYPI ENENTLIS
gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.0131	0.3233	1710.15	1709.896	2	655.2	57.692307 L.RIPYPLENENTLSY.R
gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.5523	0.3291	1685.55	1685.961	1	945.5	65.38461 F.ILRIPYPLENENTL.S
gi 6320924 ref NP_011003.1 gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.9686	0.3565	1607.43 1624 51	1607.732 1624 732	1	1249.2 1021 8	73.07692 L.MKDWDPLIEDGSSN.Q 69 230774 L M1K2D1W2D1P1L111E1D1G1S1S1N2 O
gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	1	3.2587	0.2659	1451.38	1452.601	1	633.5	68.181816 Y.DLKEDITDFDKL.S

gi 6320924 ref NP_011003.1 gi 6320924 ref NP_011003.1 gi 6320924 ref NP_011003.1	YER080W YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p The authentic, non-tagged protein was localized to the mitochondria; Fmp29p The authentic non-tagged protein was localized to the mitochondria; Fmp29p	1 2 2	3.9773 3.7111 3.0052	0.1714 0.179	1466.62 1452.07	1466.601 1452.601 1396.673	1 2 1	600.4 1066.7	63.636364 Y.D1L1K2E1D111T1D1F1D1K2L1.S 77.27273 Y.DLKEDITDFDKL.S 65.65657 A KADDKII EDIYUSI K
gi 6320924 ref NP_011003.1	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fing29p Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis, forms	2	2.9594	0.2038	1978.15	1979.246	1	410.5	60.00000 Q.HQWEKKLNDNNPKLIT.A
gi 6320935 ref NP_011014.1	YER090W	multirunctional netero-oligomeric antiranilate synthase indole-3-giycerol prosphate synthase enzyme complex with Trg3p; Trp2p Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis, forms	2	3.9629	0.2468	1845.39	1845.082	3	730.7	53.125 T.I1K2T1G1P1T1E1G1I1E1T1D1P1L1E1I1L1.E
gi 6320935 ref NP_011014.1	YER090W	multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp3p; Trp2p Abundant cubunit of the purclear page complex (NPC), present on both sides of the	2	3.6231	0.2494	1826.57	1827.082	6	593.7	46.875 T.IKTGPTEGIETDPLEIL.E
gi 6320952 ref NP_011031.1	YER105C	NPC, has similarity to Nup170p; Nup157p	2	3.8618	0.3566	1530.59	1531.663	1	951.2	69.230774 L.SRIIENSEGNVELA.K
gi 6320952 ref NP_011031.1	YER105C	NPC, has similarity to Nup170p; Nup157p	2	3.7284	0.3619	1550.17	1550.663	1	983.4	73.07692 L.S1R4I1I1E1N2S1E1G1N2V1E1L1A1.K
gi 6320952 ref NP_011031.1	YER105C	NPC, has similarity to Nup170p; Nup157p	1	2.589	0.1793	1530.66	1531.663	1	282	50 L.SRIIENSEGNVELA.K
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	2	3.674	0.227	2202.31	2202.388	1	499.3	47.058823 L.SFRDRNTPILDNPDYYSK.G
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	3	4.064	0.2618	1778.57	1776.045	9	829.2	41.07143 G.KTTRDTDVVFPVHFL.M
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	2	2.9037	0.3916	1773.85	1776.045	1	541.3	50 G.KTTRDTDVVFPVHFL.M
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	1	2.4126	0.3159	1363.74	1364.715	1	598.6	58.333332 T.KLIPSIPGGKLIQ.K
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	2	3.1748	0.2326	2226.73	2227.701	1	402.7	37.5 S.N2L1A1N2L1L1P1T1K2L1I1P1S1I1P1G1G1K2L1I1Q2.K
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	2	3.7637	0.2707	1828.73	1829.918	1	818.8	56.25 Y.GEAGNTIESELRDVTTH.V
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	3	3.9325	0.2742	1796.03	1797.045	1	1046.2	44.642857 G.K2T1T1R4D1T1D1V1V1F1P1V1H3F1L1.M
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	2	3.0994	0.339	1775.39	1776.045	1	808.1	60.714287 G.KTTRDTDVVFPVHFL.M
gi 6320952 ref NP_011031.1	YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	2	3.3646	0.1561	1380.03	1380.715	2	745.9	70.83333 T.K2L111P1S111P1G1G1K2L111Q2.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.7926	0.3014	2054.33	2055.276	1	956.7	62.5 A.H3L1P1L1N2T1G1F1E1E1Y1N2P1I1F1E1L1.I
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.713	0.2218	2318.53	2317.628	1	831.1	55.555557 A.H3L1P1L1N2T1G1F1E1E1Y1N2P1I1F1E1L111M\$.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.7024	0.2821	2387.25	2389.706	4	507.6	42.105263 L.A1H3L1P1L1N2T1G1F1E1E1Y1N2P1I1F1E1L111M\$.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.7378	0.2167	2350.39	2349.706	5	231.7	42.105263 L.AHLPLNTGFEEYNPIFELIM.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.5076	0.2125	2371.43	2373.706	2	384.2	44.736843 L.A1H3L1P1L1N2T1G1F1E1E1Y1N2P1I1F1E1L1I1M1.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.3227	0.3188	2476.09	2477.88	1	292.8	35 L.AHLPLNTGFEEYNPIFELIMK.L
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.5066	0.2881	2407.93	2406.802	1	223.8	36.842106 A.HLPLNTGFEEYNPIFELIMK.L
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	3	4.4628	0.2999	2479.34	2477.881	1	1903.2	42.5 L.AHLPLNTGFEEYNPIFELIMK.L
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	3	4.3829	0.2148	2409.5	2406.802	1	1443.9	38.157894 A.HLPLNTGFEEYNPIFELIMK.L
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	3	4.6581	0.3281	2502.41	2503.88	1	1019	37.5 L.A1H3L1P1L1N2T1G1F1E1E1Y1N2P1I1F1E1L1I1M1K2.
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.3842	0.2748	1402.49	1404.519	1	1280.8	72.72727 L.TTDLQDEVAKFH.E
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	1	2.586	0.2324	1231.83	1232.422	7	197.4	55.555557 T.NETPRIIEIF.S
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.4845	0.2205	1074.37	1074.349	1	879.9	87.5 F.LKTILPEIF.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.3656	0.2235	2243.35	2241.514	7	222.5	33.333336 L.A1H3L1P1L1N2T1G1F1E1E1Y1N2P1I1F1E1L1I1.M

gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.3575	0.1711	2461.23	2462.866	2	271.1	40 L.LAHLPLNTGFEEYNPIFELIM.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	5.1449	0.395	1757.77	1758.979	1	1272.8	67.85714 F.H3E1E1Y1L1P1L1111D11111D1S1A1.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.537	0.2131	1906.17	1907.155	1	728	50 K.F1H3E1E1Y1L1P1L1II1D1II1D1S1A1.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.6629	0.3029	1888.77	1889.155	1	1166.4	63.333332 K.FHEEYLPLIIDIIDSA.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	4.292	0.4346	2278.53	2278.628	1	372.9	55.555557 A.HLPLNTGFEEYNPIFELIM.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	4.4503	0.404	1740.79	1741.979	1	1495.2	71.42857 F.HEEYLPLIIDIIDSA.K
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.117	0.163	1669.89	1670.9	1	1212.5	65.38461 F.HEEYLPLIIDIIDS.A
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.4167	0.1715	1674.73	1675.75	7	640.9	57.14286 L.AAEDDEATREIIDRA.Y
gi 6320956 ref NP_011035.1	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	1	2.5505	0.2067	1245.58	1246.422	4	226.5	61.11111 T.N2E1T1P1R4I1I1E1I1F1.S
qi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.956	0.416	1905.31	1906.143	1	608.5	59.375 N.EKEVPAEPETQPPVQVK.K
ail6320966/ref/NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositid auxotrophy above 34 degrees C. VAP homolog: Scs2p.	2	4.0512	0.3361	2536.63	2537.783	1	312.2	38.636364 Q ENKETVEPVVQDSEPKEVPAVVN E
ail6320966/ref/NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositid auxotrophy above 34 degrees C. VAP homolog: Scs2p.	2	4.5555	0.3168	1734.95	1736.018	1	1127.4	67.85714 R. DKFL VITLPSPYDLN G
gil6320966/refINP_011046.1	VER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes insist auxotrophy above 34 depress C VAP bomolog: Scs2p	2	4 1508	0 2245	1926 51	1927 143	1	497.5	56.25 N E1K2E1V1P141E1P1E1T102P1P1V102V1K2 K
gij6520966/ref/NP_011046_1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes insisti auxotrophy above 34 decrees C, VAP homolog; Scs2p	-	4 3432	0.1643	3170.54	3171 529	2	582.3	
gij0020000[10][H]_011046.1]	VER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, diagraphia equase insettle unstractive bears 24 degraes C. VAB homelog: Sec2o	2	4.0769	0.0070	3160.07	2171 520	1	226.7	
	YER 120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing,	2	4.0268	0.2273	3169.97	3171.529	,	330.7	
gilb320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing,	2	4.9478	0.1531	2642.57	2643.956	1	475.2	39.130436 K.EIVIPIAIVIVINZEIKZEIVIPIAIEIPIEIIIUZPIPIVIUZVIKZ.K
gi 6320966 ref NP_011046.1	YER120W	disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing,	1	2.893	0.2162	1405.55	1406.666	5	336.2	59.090908 R.D1K2F1L1V111T1L1P1S1P1Y1.D
gi 6320966 ref NP_011046.1	YER120W	disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Op11p, also involved in telomeric silencing,	2	3.3699	0.2307	1750.63	1753.018	1	920.4	60.714287 R.D1K2F1L1V111T1L1P1S1P1Y1D1L1N2.G
gi 6320966 ref NP_011046.1	YER120W	disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing,	2	4.2277	0.1983	2012.75	2013.323	1	1153.1	61.764706 R.D1K2F1L1V111T1L1P1S1P1Y1D1L1N2G1K2A1.V
gi 6320966 ref NP_011046.1	YER120W	disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing,	2	4.7605	0.3106	1942.65	1941.244	1	881.2	65.625 R.D1K2F1L1V11T1L1P1S1P1Y1D1L1N2G1K2.A
gi 6320966 ref NP_011046.1	YER120W	disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.742	0.2185	1396.35	1393.666	1	1672.5	81.818184 R.DKFLVITLPSPY.D
gi 6320966 ref NP_011046.1	YER120W	Integrate removance protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.8366	0.3299	2726.43	2727.042	1	239.9	34.090908 L.T1E1E1P1A1A1D1F1K2C1R4D1K2F1L1V1I1T1L1P1S1P1Y1.D
gi 6320966 ref NP_011046.1	YER120W	Integral EX membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opitp, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.8477	0.3636	2698.39	2699.042	1	498.4	43.18182 L.TEEPAADFKCRDKFLVITLPSPY.D

gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.7903	0.2194	1921.31	1921.244	2	693.6	53.125 R.DKFLVITLPSPYDLNGK.A
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.3734	0.3349	2897.53	2899.253	3	182.6	31.25 L.G1L1T1E1E1P1A1A1D1F1K2C1R4D1K2F1L1V111T1L1P1S1P1Y1.D
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.6067	0.2844	2868.35	2869.253	3	259.5	33.333336 L.GLTEEPAADFKCRDKFLVITLPSPY.D
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	3	4.8005	0.2946	3431.06	3433.831	1	767.6	27.586206 L.G1L1T1E1E1P1A1A1D1F1K2C1R4D1K2F1L1V1I1T1L1P1S1P1Y1D1L1N2G1K2.A
gi]6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	3	3.9579	0.3112	3394.88	3396.831	1	803.3	25.862068 L.GLTEEPAADFKCRDKFLVITLPSPYDLNGK.A
gi]6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.9889	0.2338	2564.57	2565.783	1	247.1	38.636364 Q.E1N2K2E1T1V1E1P1V1V1Q2D1S1E1P1K2E1V1P1A1V1V1N2.E
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	3	4.2617	0.2528	1905.77	1906.143	6	574.8	35.9375 N.EKEVPAEPETQPPVQVK.K
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	4.6436	0.2742	2614.13	2614.956	1	585.9	41.304348 K.EVPAVVNEKEVPAEPETQPPVQVK.K
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	3	4.9992	0.2678	2644.04	2643.956	1	1103.7	32.608696 K.E1V1P1A1V1V1N2E1K2E1V1P1A1E1P1E1T1Q2P1P1V1Q2V1K2.K
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	2.9274	0.1868	1409.09	1406.666	2	651.4	68.181816 R.D1K2F1L1V1I1T1L1P1S1P1Y1.D
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	3	5.0318	0.3578	3170.9	3171.529	1	1009.9	31.25 Q.DSEPKEVPAVVNEKEVPAEPETQPPVQVK.K
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	3	4.9291	0.3116	3205.58	3206.529	1	922.4	30.357143 Q.D1S1E1P1K2E1V1P1A1V1V1N2E1K2E1V1P1A1E1P1E1T1Q2P1P1V1Q2V1K2.K
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.8098	0.2574	3170.81	3171.529	1	404.3	33.92857 Q.DSEPKEVPAVVNEKEVPAEPETQPPVQVK.K
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	3	4.8069	0.3546	4425.98	4424.903	1	668.3	21.153847 Q.ENKETVEPVVQDSEPKEVPAVVNEKEVPAEPETQPPVQVK.K
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	3	4.827	0.315	3229.34	3226.62	1	754	31.48148 L.TEEPAADFKCRDKFLVITLPSPYDLNGK.A
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	1	2.9577	0.2203	1392.7	1393.666	8	348.9	59.090908 R.DKFLVITLPSPY.D
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.4172	0.2304	1406.05	1406.666	3	1186.9	72.72727 R.D1K2F1L1V1I1T1L1P1S1P1Y1.D
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	2	3.0553	0.2124	1710.39	1709.992	1	612.5	61.538464 K.CRDKFLVITLPSPY.D
gi 6320966 ref NP_011046.1	YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p ADB discuting forter CTBreas adjustment particle (APE CAD) involved in EP Colori	2	3.1259	0.2277	1729.65	1727.992	3	449.1	50 K.C1R4D1K2F1L1V111T1L1P1S1P1Y1.D
gi 6320969 ref NP_011048.1	YER122C	transport; shares functional similarity with Gcs1p; Glo3p	2	4.4845	0.3885	2976.33	2977.98	1	533.2	38 N.S1K2G1N2N2N2N2S1I1D1D111N2T1Q2P1D1E1F1N2D1F1L1N2D1T1.S
gi 6320969 ref NP_011048.1	YER122C	ADP-HDUSYIAtion factor G i Pase activating protein (ARF GAP), involved in ER-Golgi transport; shares functional similarity with Gcs1p; Glo3p	1	2.3724	0.2439	1591.34	1592.631	1	232.9	45.833336 T.S1K2E1N2S1V1D1D1F1F1S1N2W2.Q
gi 6320969 ref NP_011048.1	YER122C	AUP-ribosylation factor GTPase activating protein (ARF GAP), involved in ER-Golgi transport; shares functional similarity with Gcs1p; Glo3p	2	3.8512	0.3866	1592.23	1592.631	1	1296.2	79.16667 T.S1K2E1N2S1V1D1D1F1F1S1N2W2.Q
gi 6320969 ref NP_011048.1	YER122C	ADP-ribosylation factor GTPase activating protein (ARF GAP), involved in ER-Golgi transport; shares functional similarity with Gcs1p; Glo3p	2	3.8392	0.3951	2942.59	2942.98	1	556	36 N.SKGNNNNSIDDINTQPDEFNDFLNDT.S
gi 6320969 ref NP_011048.1	YER122C	ADP-ribosylation factor GTPase activating protein (ARF GAP), involved in ER-Golgi transport; shares functional similarity with Gcs1p; Glo3p	1	2.6082	0.209	1592.65	1592.631	1	213.7	45.833336 T.S1K2E1N2S1V1D1D1F1F1S1N2W2.Q
gi 6320969 ref NP_011048.1	YER122C	ADP-ribosylation factor GTPase activating protein (ARF GAP), involved in ER-Golgi transport; shares functional similarity with Gcs1p; Glo3p	2	3.6992	0.3596	1592.21	1592.631	1	1543.4	83.33333 T.S1K2E1N2S1V1D1D1F1F1S1N2W2.Q
gi 6320972 ref NP_011051.1	YER125W	Ubiquitin-protein ligase involved in ubiquitin-mediated protein degradation; plays a role in heat shock element (HSE)-mediated gene expression and multivesicular body sorting; contains a hect (homologous to E6-AP carboxyl terminus) domain; Rsp5p	2	3.6758	0.3827	1602.35	1601.771	1	1203.7	79.16667 N.RVDLPQYVDYDSM.K

gi 6320972 ref NP_011051.1	YER125W	Ubiquitin-protein ligase involved in ubiquitin-mediated protein degradation; plays a role in heat shock element (HSE)-mediated gene expression and multivesicular body sorting; contains a hect (homologous to E6-AP carboxyl terminus) domain; Rsp5p	2	4.4909	0.351	1862.73	1863.052	1	1735.9	78.57143 C.FNRVDLPQYVDYDSM.K
gi 6320972 ref NP_011051.1	YER125W	Ubiquitin-protein ligase involved in ubiquitin-mediated protein degradation; plays a role in heat shock element (HSE)-mediated gene expression and multivesicular body sorting; contains a hect (homologous to E6-AP carboxyl terminus) domain; Rsp5p	2	4.8755	0.4334	1884.27	1883.052	1	1397.8	71.42857 C.F1N2R4V1D1L1P1Q2Y1V1D1Y1D1S1M1.K
gi 6320972 ref NP_011051.1	YER125W	Ubiquitin-protein ligase involved in ubiquitin-mediated protein degradation; plays a role in heat shock element (HSE)-mediated gene expression and multivesicular body sorting; contains a hect (homologous to E6-AP carboxyl terminus) domain; Rsp5p	2	3.0755	0.3128	1519.23	1517.719	2	293.7	66.66667 F.R4S1Q2P1A1L1R4I1L1P1G1Q2C1.H
gi 6320972 ref NP_011051.1	YER125W	Ubiquitin-protein ligase involved in ubiquitin-mediated protein degradation; plays a role in heat shock element (HSE)-mediated gene expression and multivesicular body sorting; contains a hect (homologous to E6-AP carboxyl terminus) domain; Rsp5p	2	4.488	0.4623	1626.35	1626.72	1	863.6	60.000004 L.S1K2L1P1S1S1S1P1H3S1Q2A1P1S1G1H3.T
gi 6320972 ref NP_011051.1	YER125W	Ubiquitin-protein ligase involved in ubiquitin-mediated protein degradation; plays a role in heat shock element (HSE)-mediated gene expression and multivesicular body sorting; contains a hect (homologous to E6-AP carboxyl terminus) domain; Rsp5p	2	3.1462	0.2036	1517.39	1515.814	1	371.3	68.181816 M.RQTPEDLKKRLM.I
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	2	4.774	0.4224	2076.57	2076.271	1	1365.2	61.764706 R.GSKPGQQVDLEENEIRYL.C
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	2	3.2165	0.1951	2246.79	2248.714	1	577.7	44.444447 R.S111F111K2Q2P111L1L1E1L1E1A1P111K211C1.G
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	2	4.9054	0.475	2100.51	2101.271	1	1244.7	61.764706 R.G1S1K2P1G1Q2Q2V1D1L1E1E1N2E111R4Y1L1.C
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	2	3.8505	0.1937	1661.83	1662.97	9	606.8	58.333332 L.A1Y1K2I1K2Y1P1E1N2F1F1I1L1.R
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	2	3.0236	0.2161	1646.69	1646.97	1	739.8	58.333332 L.AYKIKYPENFFIL.R
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	1	2.5123	0.2146	1407.74	1408.536	2	334.8	65 Q.V1D1L1E1E1N2E1I1R4Y1L1.C
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	1	2.3409	0.2475	1331.49	1332.428	3	424.8	55 L.W2S1D1P1D1K2D111V1G1W2.S
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	2	2.9717	0.1644	1213.73	1214.395	3	772.8	81.25 C.Y1K2I1K2Y1P1E1N2F1.F
gi 6320980 ref NP_011059.1	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by	2	3.1669	0.1808	1399.31	1399.763	1	328.7	54.545456 K.ARSIFIKQPILL.E
gi 6320983 ref NP_011062.1	YER136W	regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by multiple dissociation of CDP from the Cord/Action family of CTP binding	2	3.7156	0.2178	1205.65	1204.416	1	930.7	80 L.G1P1I1E1E1K2F1M1G1I1A1.E
gi 6320983 ref NP_011062.1	YER136W	Proteins: Golf p GDP dissociation inhibitor, regulates veside traffic in secretory pathways by	2	3.0051	0.1956	1952.97	1952.186	5	240.3	46.666668 Q.GLDLDKNTMDEVYYKF.G
gi 6320983 ref NP_011062.1	YER136W	regulating the dissociation of GDP from the Sec4/yptrab family of GTP binding proteins; Gdf p GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by	2	3.065	0.1701	1617.29	1616.883	7	461.2	46.42857 Y.K2V1P1A1N2E1I1E1A1I1S1S1P1L1M1.G
gi 6320983 ref NP_011062.1	YER136W	regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdf p GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by	2	3.6431	0.3089	1706.29	1706.934	1	557	67.85714 S.TIIETDKPHIELEPA.F
gi 6320983 ref NP_011062.1	YER136W	regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p High affinity iron permease involved in the transport of iron across the plasma	2	4.0523	0.3461	1725.39	1724.934	1	828.8	75 S.T1I1I1E1T1D1K2P1H3I1E1L1E1P1A1.F
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	2	4.9951	0.3267	1688.25	1686.788	1	1370.4	80.769226 A.K2M1E1N2I1N2F1N2E1D1G1E1I1N2.V
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	2	3.1568	0.2447	1143.13	1142.319	2	646.9	81.25 K.H3L1N2P1G1Y1W2I1K2.N
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	2	4.651	0.2872	1926.39	1927.173	2	739.9	64.28571 K.N2K2K2K2Q2E1L1T1E1E1Q2K2R4Q2L1.F
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	1	2.8777	0.1739	1271.39	1272.493	1	417.6	66.66667 L.K2H3L1N2P1G1Y1W2I1K2.N
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	1	2.6657	0.1794	1141.6	1142.319	1	522.6	68.75 K.H3L1N2P1G1Y1W2I1K2.N
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	2	3.9922	0.3056	2012.45	2013.056	1	337.5	53.333336 Y.H3V1N2C1C1N2P1E1L1D1N2G1W2D1I1F1.N
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	1	2.4537	0.2027	1510.71	1510.672	1	180.5	59.090908 Q.E1L1T1E1E1Q2K2R4Q2L1F1A1.K
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	2	3.8078	0.2556	1900.33	1901.151	1	458.9	50 K.K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1A1.K
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	2	4.4463	0.2581	1828.37	1829.072	1	717.1	65.38461 K.K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1.A
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p	1	2.8586	0.2072	1143.64	1142.319	1	520.4	68.75 K.H3L1N2P1G1Y1W2I1K2.N

		High affinity iron permasse involved in the transport of iron across the plasma								
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p	2	3.2037	0.2636	1140.65	1142.319	1	676.3	81.25 K.H3L1N2P1G1Y1W2I1K2.N
gi 6320993 ref NP_011072.1	YER145C	High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p	2	3.3997	0.2658	1257.77	1258.423	1	640	72.22222 K.H3L1N2P1G1Y1W2I1K2N2.K
ail63209931refINP 011072.11	YER145C	High affinity iron permease involved in the transport of iron across the plasma membrane: forms complex with Fet3p: expression is regulated by iron: Ftr1p	1	2.64	0.2121	1128.57	1128.319	1	529.8	68.75 K.HLNPGYWIK.N
=ilc220002i+=fIND_011070.4i	VED4450	High affinity iron permease involved in the transport of iron across the plasma	2	4 4020	0.0000	1000.05	4004 472	4	4014.0	
gi 6320993 ret NP_011072.1	YER145C	High affinity iron permease involved in the transport of iron across the plasma	2	4.1839	0.3903	1900.85	1901.173	1	1014.9	/1.4285/ K.NKKKQELTEEQKKQL.F
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p High affinity iron permease involved in the transport of iron across the plasma	2	5.79	0.3759	2029.61	2031.325	1	784.9	66.66667 K.K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1A1K2.M
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p	2	4.9055	0.3165	2074.59	2075.35	1	1034.6	66.66667 K.N2K2K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1.A
gi 6320993 ref NP_011072.1	YER145C	membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p	3	4.4537	0.3015	2146.91	2147.429	1	908.2	45.3125 K.N2K2K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1A1.K
gil6320993/refINP_011072.1	YER145C	High affinity iron permease involved in the transport of iron across the plasma membrane: forms complex with Fet3p; expression is regulated by iron; Etr1p	2	2.9981	0.1744	1143.15	1142.319	1	663.2	81,25 K.H3L1N2P1G1Y1W2I1K2 N
3-1022000021-st[ND_044070.4]	VED4450	High affinity iron permease involved in the transport of iron across the plasma	-	0.700	0.0000	4444 54	44.40.040		500.0	
gi 6320993 ret NP_011072.1	YER145C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and	1	2.792	0.2262	1141.51	1142.319	1	520.2	68.75 K.H3L1N2P1G1Y1W2I1K2.N
gil6320997/refINP_011076.1	YER149C	low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth: Pea2p	2	3,7207	0.3501	1784.05	1781.145	1	909.7	60.000004 K.GIDIKPIPLDDPVKFL.K
3.1		Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and								
gi 6320997 ref NP_011076.1	YER149C	localizes to sites of polarized growth; Pea2p	2	3.9117	0.455	1799.67	1799.145	1	493.4	50 K.G1I1D1I1K2P1I1P1L1D1D1P1V1K2F1L1.K
		Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx: forms polarisome complex with Bni1p, Bud6p, and Spa2p;								
gi 6320997 ref NP_011076.1	YER149C	localizes to sites of polarized growth; Pea2p	3	4.8548	0.2709	1930.28	1929.32	1	1334.2	45.3125 Q.K2G111D111K2P111P1L1D1D1P1V1K2F1L1.K
		low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p;								
gi 6320997 ref NP_011076.1	YER149C	localizes to sites of polarized growth; Pea2p Colled-coll polarisome protein required for polarized morphogenesis, cell fusion, and	2	4.5507	0.4403	2260.85	2261.688	1	491.2	47.368423 N.S1I1Q2K2G1I1D111K2P1I1P1L1D1D1P1V1K2F1L1.K
		low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p;								
gi 6320997 ref NP_011076.1	YER149C	localizes to sites of polarized growth; Pea2p Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and	3	4.2542	0.2217	2237.57	2237.688	1	873	35.526314 N.SIQKGIDIKPIPLDDPVKFL.K
ail6320007/refINP_011076.1	VER149C	low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth: Pea2p.	2	3 0318	0 2516	1928.01	1020 32	1	539.7	50 O K2G111D111K2P111P11 1D1D1P1V1K2E1L1 K
gilos20397 [rei]14F_011070.1]	TEICI490	Colled-coil polarisome protein required for polarized morphogenesis, cell fusion, and	2	3.0310	0.2310	1320.01	1929.92		555.1	
gi 6320997 ref NP_011076.1	YER149C	low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	2	3.7274	0.3033	2237.81	2237.688	1	723.4	47.368423 N.SIQKGIDIKPIPLDDPVKFL.K
		Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx forms polarisome complex with Bni1p, Bud6p, and Spa2p;								
gi 6320997 ref NP_011076.1	YER149C	localizes to sites of polarized growth; Pea2p	3	4.2135	0.327	2237.3	2237.688	2	837.7	34.210526 N.SIQKGIDIKPIPLDDPVKFL.K
		Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p;								
gi 6320997 ref NP_011076.1	YER149C	localizes to sites of polarized growth; Pea2p Colled-coll polarizome protein required for polarized morphogenesis, cell fusion, and	2	4.196	0.4499	2236.55	2237.688	1	769.5	50 N.SIQKGIDIKPIPLDDPVKFL.K
		low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p;								
gi 6320997 ref NP_011076.1	YER149C	localizes to sites of polarized growth; Pea2p Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and	3	4.4886	0.2964	1930.25	1929.32	1	1352.7	43.75 Q.K2G111D111K2P111P1L1D1D1P1V1K2F1L1.K
ail6320007/refINP_011076.1	VER149C	low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth: Pea2p.	3	4 2707	0.39	2258 75	2261 688	1	860.7	35 526314 N S11102K2G111D111K2P111P11 1D1D1P1V1K2E11 1 K
giloszossi licilitä _011010.11	TERT-50	Colled-coil polarisone protein required for polarized morphogenesis, cell fusion, and	0	4.2707	0.00	2200.70	2201.000		000.7	
gi 6320997 ref NP_011076.1	YER149C	low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	2	3.0921	0.1682	1929.79	1929.32	4	201.8	40.625 Q.K2G1I1D1I1K2P1I1P1L1D1D1P1V1K2F1L1.K
		Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain;								
gi 6321012 ref NP_011091.1	YER164W	component of both the SAGA and SILK complexes; Chd1p	2	3.0638	0.2567	2450.33	2449.717	1	329.9	36.842106 T.DYKADIDWDDIIPEEELKKL.Q
		Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain;								
gi 6321012 ref NP_011091.1	YER164W	component of both the SAGA and SILK complexes; Chd1p	2	3.5233	0.1689	1854.67	1857.111	1	1130.3	71.42857 D.IDWDDIIPEEELKKL.Q
		contains a chromo domain, a helicase domain and a DNA-binding domain;								
gi 6321012 ret NP_011091.1	YER164W	component of both the SAGA and SILK complexes; Chd1p Nucleosome remodeling factor that functions in regulation of transcription elongation;	2	4.5715	0.3186	2170.55	2171.452	1	1151.7	58.823532 Y.KADIDWDDIIPEEELKKL.Q
gil6321012 refINP_011091.1	YER164W	contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SILK complexes; Chd1p	2	3.4589	0.1775	1671.11	1670.803	2	476.8	61.538464 D.H3E1N2S1P1D1S1N2D1E1V1E1L1L1.S
34		Nucleosome remodeling factor that functions in regulation of transcription elongation;								
gi 6321012 ref NP_011091.1	YER164W	component of both the SAGA and SILK complexes; Chd1p	2	5.2781	0.4656	2295.53	2297.632	1	1275	52.499996 F.G1N2L1K2E1I1L1D1E1L1I1A1D1G1T1L1P1V1K2S1F1.E
		Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain;								
gi 6321012 ref NP_011091.1	YER164W	component of both the SAGA and SILK complexes; Chd1p	2	3.9548	0.435	2276.13	2273.632	1	339.6	37.5 F.GNLKEILDELIADGTLPVKSF.E
		contains a chromo domain, a helicase domain and a DNA-binding domain;								
gi 6321012 ref NP_011091.1	YER164W	component of both the SAGA and SILK complexes; Chd1p Nucleosome remodeling factor that functions in regulation of transcription elongation:	2	3.1375	0.1795	1654.85	1652.803	1	444.7	61.538464 D.HFNSPDSNDFVFLL.S
ail62210121cofIND_011001_1	VED164W	contains a chromo domain, a helicase domain and a DNA-binding domain;	2	4 4210	0.2656	2440.22	2440 717	2	702 7	
gilosz to tzitelitár _011031.1	ILI(104W	Nucleosome remodeling factor that functions in regulation of transcription elongation;	5	4.4213	0.2000	2443.22	2449.717	2	102.1	34.210320 F.D HADDWDDIII EEEEINE.Q
gi 6321012 ref NP 011091.1	YER164W	contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SILK complexes; Chd1p	2	5.3895	0.3538	2041.75	2039.377	1	2623.4	66.66667 F.GNLKEILDELIADGTLPVK.S
		Nucleosome remodeling factor that functions in regulation of transcription elongation;								
gi 6321012 ref NP_011091.1	YER164W	component of both the SAGA and SILK complexes; Chd1p	2	4.2784	0.2937	1928.15	1928.119	1	1047	64.28571 A.KDCVHEEEKNRKEIL.E
		Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain;								
gi 6321012 ref NP_011091.1	YER164W	component of both the SAGA and SILK complexes; Chd1p	2	3.7185	0.1532	1951.45	1952.119	1	1403.5	75 A.K2D1C1V1H3E1E1E1K2N2R4K2E1I1L1.E
	VEDACAN	contains a chromo domain, a helicase domain and a DNA-binding domain;	0	0.0050	0.07	4504.07	4505 000		000.0	
gilo321012[rei]NP_011091.1]	IERI64W	component or both the SAGA and SILK complexes; Und1p	2	3.3053	0.27	1004.37	1505.622	1	996.2	10 V.ONDIVEEVLERA.K

		Nucleosome remodeling factor that functions in regulation of transcription elongation;								
ail6221012[rof[NID_011001_1]		contains a chromo domain, a helicase domain and a DNA-binding domain;	2	2 7260	0 2420	1071.67	1072 100	2	969.6	
gil6321012[rei]NP_011091.1]	TER 164W	Poly(A) binding protein, part of the 3'-end RNA-processing complex, mediates	2	3.7309	0.2438	19/1.0/	1972.199	3	868.6	50.000000 A.DIDWDDIIPEEELKKL.Q
		interactions between the 5' cap structure and the 3' mRNA poly(A) tail, involved in								
gi 6321013 ref NP_011092.1	YER165W	control of poly(A) tail length, interacts with translation factor eIF-4G; Pab1p	1	2.2454	0.1724	1065.36	1066.159	8	253.4	68.75 K.NLHPDIDNK.A
		Poly(A) binding protein, part of the 3'-end RNA-processing complex, mediates								
ail6321013/refINP_011092.1	YER165W	interactions between the 5 cap structure and the 3 mRNA poly(A) tail, involved in control of poly(A) tail length, interacts with translation factor eIE-4G. Pab1p	2	2 9874	0 3849	2293.83	2295 659	1	551.4	45 Y G1V1M1P1P1R4G1V1P1F1N2G1P1N2P1Q2Q2M1N2P1M1 G
gilooz i o i oli oli i i <u>_</u> o i i ooz.i i	121110011	Poly(A) binding protein, part of the 3'-end RNA-processing complex, mediates	-	2.007	0.0010	2200.00	2200.000	·	00111	
		interactions between the 5' cap structure and the 3' mRNA poly(A) tail, involved in								
gi 6321013 ref NP_011092.1	YER165W	control of poly(A) tail length, interacts with translation factor eIF-4G; Pab1p	2	3.0657	0.382	2013.91	2015.091	6	217.4	40.625 N.LDDSVDDEKLEEEFAPY.G
		Poly(A) binding protein, part of the 3'-end RNA-processing complex, mediates								
ail6321013/refINP_011092.1	YER165W	control of poly(A) tail length interacts with translation factor eIF-4G: Pab1p	2	3 6444	0 3149	2148 19	2149 195	1	248.4	41 17647 K N2I 1D1D1S1V1D1D1E1K2I 1E1E1E1E1A1P1Y1 G
3.1		Poly(A) binding protein, part of the 3'-end RNA-processing complex, mediates	_							
		interactions between the 5' cap structure and the 3' mRNA poly(A) tail, involved in								
gi 6321013 ref NP_011092.1	YER165W	control of poly(A) tail length, interacts with translation factor eIF-4G; Pab1p	2	4.4227	0.4326	2129.09	2129.195	1	443.9	55.88235 K.NLDDSVDDEKLEEEFAPY.G
		interactions between the 5' can structure and the 3' mRNA poly(A) tail involved in								
gi 6321013 ref NP 011092.1	YER165W	control of poly(A) tail length, interacts with translation factor eIF-4G; Pab1p	1	2.513	0.2022	1154.61	1155.404	2	317	68.75 Q.KKNERMHVL.K
		Non-essential P-type ATPase that is a potential aminophospholipid translocase,								
		localizes to the plasma membrane and late exocytic or early endocytic membranes,								
gi 6321014 ref NP_011093.1	YER166W	likely involved in protein transport; Dnf1p	3	5.295	0.3135	3367.67	3366.859	6	354.3	24.038462 V.Y1Y1N2M1P1L1P1K2D1M1I1D1E1E1G1N2P1I1M1Q2Y1P1R4N2K2I1R4.T
		localizes to the plasma membrane and late exocytic or early endocytic membranes.								
gi 6321014 ref NP_011093.1	YER166W	likely involved in protein transport; Dnf1p	2	5.0717	0.3185	1872.51	1872.134	1	626.3	59.375 S.C1I1V1K2I1P1G1L1N2P1G1D1E1P1R4A1L1.L
		Non-essential P-type ATPase that is a potential aminophospholipid translocase,								
		localizes to the plasma membrane and late exocytic or early endocytic membranes,								
gi 6321014 ref NP_011093.1	YER166W	likely involved in protein transport; Dnf1p	3	4.7164	0.3495	2442.8	2441.595	1	1203.1	38.75 H.G1H3F1D1H3Y1P1P1G1Y1D1P1T1D1P1N2R4P1K2V1T1.K
		localizes to the plasma membrane and late exocytic or early endocytic membranes.								
gi 6321014 ref NP_011093.1	YER166W	likely involved in protein transport; Dnf1p	3	4.4596	0.4559	3528.8	3530.069	7	298.2	22.321428 V.YYNMPLPKDMIDEEGNPIMQYPRNKIRTT.K
		Non-essential P-type ATPase that is a potential aminophospholipid translocase,								
	VEDICON	localizes to the plasma membrane and late exocytic or early endocytic membranes,	•	0.0070	0 101 1	0570 74	0574 000		770.0	
gil6321014[ref]NP_011093.1]	YER166W	IKely Involved in protein transport, Unt1p Non-essential P-type ATPase that is a potential aminophospholipid translocase	3	6.0678	0.4214	3570.74	3571.069	1	770.3	32.142857 V.Y1Y1N2M1P1L1P1K2D1M1I1D1E1E1G1N2P1I1M1Q2Y1P1R4N2K2I1R41111.K
		localizes to the plasma membrane and late exocytic or early endocytic membranes,								
gi 6321014 ref NP_011093.1	YER166W	likely involved in protein transport; Dnf1p	2	3.6777	0.3352	1976.09	1978.154	1	451	56.25 T.A1I1E1D1R4L1Q2D1G1V1P1D1C1I1E1L1L1.A
		Non-essential P-type ATPase that is a potential aminophospholipid translocase,								
ail6321014/rofINP_011093_1	VEP166W	localizes to the plasma membrane and late exocytic or early endocytic membranes,	3	3 8383	0 3001	1712 12	1710 006	1	1370.0	50 C 11\/1K211P1C11 1N/2P1C1D1E1P1P4A11 1
gil0321014[lei]14F_011033.1]	LICIOUV	Non-essential P-type ATPase that is a potential aminophospholipid translocase.	5	3.0302	0.3001	1712.12	17 10.330	'	1373.3	
		localizes to the plasma membrane and late exocytic or early endocytic membranes,								
gi 6321014 ref NP_011093.1	YER166W	likely involved in protein transport; Dnf1p	3	4.7771	0.3407	3057.92	3058.512	1	673.9	34.375 V.YYNMPLPKDMIDEEGNPIMQYPRNK.I
		Non-essential P-type ATPase that is a potential aminophospholipid translocase,								
gil6321014/refINP_011093_1	YER166W	localizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport: Dnf1p	3	5 1501	0.3681	2647 22	2648 056	1	1003.5	39 285713 N M1P1I 1P1K2D1M1I1D1E1E1G1N2P1I1M102Y1P1R4N2K2 I
giloozion inolina _orrooo.ii	121110011	Non-essential P-type ATPase that is a potential aminophospholipid translocase,	Ũ	0.1001	0.0001	2011.22	2010.000	·	1000.0	
		localizes to the plasma membrane and late exocytic or early endocytic membranes,								
gi 6321014 ref NP_011093.1	YER166W	likely involved in protein transport; Dnf1p	2	4.1681	0.4065	2441.21	2441.595	2	475.1	42.5 H.G1H3F1D1H3Y1P1P1G1Y1D1P1T1D1P1N2R4P1K2V1T1.K
		Non-essential P-type A Pase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exocytic or early endocytic membranes								
gi 6321014 ref NP_011093.1	YER166W	likely involved in protein transport; Dnf1p	3	4.2106	0.2705	3162.98	3164.683	1	777.9	31 Y.YNMPLPKDMIDEEGNPIMQYPRNKIR.T
		Non-essential P-type ATPase that is a potential aminophospholipid translocase,								
	VEDICON	localizes to the plasma membrane and late exocytic or early endocytic membranes,	0	4 7000	0.0000	0000 54	0007.050		040.4	
gil6321014[ref]NP_011093.1]	YER166W	IKely Involved in protein transport; Untip RNA-dependent ATPase RNA belicase involved in the facilitation and disruption of	3	4.7089	0.2606	3326.51	3327.859	2	318.1	25 V.YYNMPLPKDMIDEEGNPIMQYPRNKIR.I
		snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs								
gi 6321020 ref NP_011099.1	YER172C	to activate the spliceosome for catalysis; Brr2p	2	3.4024	0.2573	2151.65	2150.404	1	572.4	52.941177 Q.GVWDVDNPLRQIPHFNNK.I
		RNA-dependent ATPase RNA helicase involved in the facilitation and disruption of								
ail6321020/rofINP_011000_1	VEP172C	snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs to activate the spliceocome for catalysis: Brr2p	3	4 4521	0.2548	2/15 8	2/13 766	1	866.2	36 25 T K2E1S1N2D1A111D1D1V111D11 1E1K211K2E1D1E1S1 S
gil0321020[10]101 _011033.1]	TER 1720	RNA-dependent ATPase RNA helicase involved in the facilitation and disruption of	5	4.4321	0.2340	2413.0	2413.700		000.2	
		snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs								
gi 6321020 ref NP_011099.1	YER172C	to activate the spliceosome for catalysis; Brr2p	3	4.6398	0.2438	2390.54	2388.766	1	904.4	35 T.KFSNPAIPPVIDLEKIKFDES.S
		RNA-dependent A I Pase RNA helicase involved in the facilitation and disruption of								
ail6321020/refINP_011099.1	YER172C	to activate the spliceosome for catalysis: Brr2p	2	3.5458	0.4079	2178.03	2179.404	1	516.1	52.941177 Q.G1V1W2D1V1D1N2P1L1R4Q2I1P1H3F1N2N2K2 J
3.1										
		E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct								
gi 37362644 ret NP_011105.2	YER178W	oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.5023	0.2677	2388.13	2388.544	4	228.3	38.095238 T.DKKAPEDIEGSDTVQIELPESS.F
		E1 aloha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct								
gi 37362644 ref NP_011105.2	YER178W	oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.2712	0.358	2416.23	2413.544	1	785.5	47.61905 T.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1.F
ail37362644/rofINP_011105_2	VED178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct	2	3 701	0.235	3116.97	3117 301	1	755 5	
gij3/302044[lei]i4[_011103.2]	ILI(I/OW	ondative decarboxylation of pyruvate to acetyr-con, regulated by glucose, r da tp	2	5.751	0.200	3110.07	5117.501	'	755.5	30.0003 N. TERRAR EDIEGOET VOIEER EGGI EGT.W
		E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct								
gi 37362644 ref NP_011105.2	YER178W	oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.441	0.395	2912.79	2915.091	1	687.9	40 T.DKKAPEDIEGSDTVQIELPESSFESY.M
		E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct								
gi 37362644 ref NP_011105.2	YER178W	oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.8901	0.2966	2941.47	2944.091	3	600	38 T.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.M
=		, , , , , , , , , , , , , , , , ,								
ail27262644iroftND_044465_0	VED170W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct	2	E 7000	0.444	2017.05	2015 004		1101.0	
yijor 302044[ter]NP_011105.2]	IERI/8W	oxidative decarboxytation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	5.7628	0.411	2917.85	2915.091	1	1191.9	JZ I.UNNAPEDIEGODI VQIELPEOOFEDY.M
		E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct								
gi 37362644 ref NP_011105.2	YER178W	oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.668	0.1972	3116.72	3117.301	1	1093.9	31.48148 K.TTDKKAPEDIEGSDTVQIELPESSFESY.M

gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	6.0923	0.3806	2946.08	2944.091	1	1492.1	36 T.D1K2K2A1P1E1D111E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.0941	0.2391	3054.98	3055.455	1	705.8	33.333336 Y.DKSARKYVDEQVELADAAPPPEAKLSILF
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.3203	0.2159	2671.17	2671.828	3	372.5	36.95652 K.KAPEDIEGSDTVQIELPESSFESY.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.873	0.3477	2864.84	2867.047	1	732.3	31 K.TTDKKAPEDIEGSDTVQIELPESSFE.S
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.8681	0.3277	2664.21	2664.836	1	853.1	45.652176 T.DKKAPEDIEGSDTVQIELPESSFE.S
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.1162	0.2436	3118.71	3117.301	1	595.1	33.333336 K.TTDKKAPEDIEGSDTVQIELPESSFESY.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.0416	0.4516	3146.91	3148.301	1	692	37.037037 K.T1T1D1K2K2A1P1E1D111E1G1S1D1T1V1Q211E1L1P1E1S1S1F1E1S1Y1.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.5706	0.3712	2534.89	2535.721	1	356.5	36.363636 T.DKKAPEDIEGSDTVQIELPESSF.E
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.9263	0.2917	2917.81	2915.091	1	682.1	42 T.DKKAPEDIEGSDTVQIELPESSFESY.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	6.2393	0.3727	2942.12	2944.091	1	1223.1	32 T.D1K2K2A1P1E1D111E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.9217	0.2513	2943.83	2944.091	1	698.7	42 T.D1K2K2A1P1E1D111E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	5.9228	0.4604	3116.54	3117.301	1	922.9	30.555555 K.TTDKKAPEDIEGSDTVQIELPESSFESY.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.3307	0.1702	3148.94	3148.301	3	620.7	25 K.T1T1D1K2K2A1P1E1D111E1G1S1D1T1V1Q211E1L1P1E1S1S1F1E1S1Y1.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	5.5033	0.3702	2914.97	2915.091	1	1153.9	32 T.DKKAPEDIEGSDTVQIELPESSFESY.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.0805	0.2709	3245.3	3245.475	1	600.5	25 L.KTTDKKAPEDIEGSDTVQIELPESSFESY.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.2916	0.3046	1248.75	1250.326	1	828.1	77.77778 R.G1R4I1P1E1D1T1W2D1F1.K
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.989	0.3432	3116.39	3117.301	1	1484.5	34.25926 K.TTDKKAPEDIEGSDTVQIELPESSFESY.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	4.1912	0.2902	2942.97	2944.091	1	566.7	36 T.D1K2K2A1P1E1D111E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.5929	0.2513	2690.91	2691.836	1	565.2	39.130436 T.D1K2K2A1P1E1D111E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1.S
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.5809	0.2068	2916.38	2915.091	1	1128	30.000002 T.DKKAPEDIEGSDTVQIELPESSFESY.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.2093	0.2957	2944.19	2944.091	1	772.1	27.000002 T.D1K2K2A1P1E1D111E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.M
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	3	4.594	0.2857	1642.97	1640.805	1	2418.8	60.416668 R.G1R411P1E1D1T1W2D1F1K2K2Q2.G
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.0632	0.1538	1621.41	1620.805	1	875.6	66.66667 R.GRIPEDTWDFKKQ.G
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.3882	0.1738	1640.17	1640.805	1	905	66.666667 R.G1R4I1P1E1D1T1W2D1F1K2K2Q2.G
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.1816	0.2961	2346.51	2347.594	1	244.1	44.444447 T.E1T1P1T1L1R4G1R4I1P1E1D1T1W2D1F1K2K2Q2.G
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	2	3.1587	0.2564	2505.09	2507.751	1	325.5	40 K.G1T1E1T1P1T1L1R4G1R4I1P1E1D1T1W2D1F1K2K2Q2.G
gi 37362644 ref NP_011105.2	YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p Vacular methrage protein juvolved in vacular control protection to acetyl-CoA.	2	3.0842	0.172	2318.37	2318.594	5	204.3	38.88889 T.ETPTLRGRIPEDTWDFKKQ.G
nii14318518/refiNID 116651 11		functions as regulator of vacuolar H-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vhc2n	2	3 1057	0 1976	1027 53	1926 136	1	576 9	
9ij 140 100 10j teljivr_1 1003 I. I	11 L00411	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaparones; involved in porticin localization and new transporter involved in the protein localization and new transporter	2	3.1837	0.1070	1321.00	1320.130	I	510.0	UNDUCT THE DE DINGDI NER. I
gi 14318518 ref NP_116651.1	YFL004W	oraperones, involved in protein localization and non-autophagic vacuolar fusion; Vtc2p	2	3.4057	0.2105	1857.71	1858.953	3	483.4	50 A.G1R4D1L1E1R4L1E1E1D1F1S1E1I1Q2.N

		Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion;								
gi 14318518 ref NP_116651.1	YFL004W	Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter	3	4.4492	0.3728	2602.4	2604.783	1	758.5	33.75 R.WDDSDESKFVEELDKELEKVY.G
gi 14318518 ref NP_116651.1	YFL004W	chaperones, involved in protein localization and non-aduptragic vacuolar usion; Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a reoulator of vacuolar H+-ATPase activity and vacuolar transporter	2	3.0232	0.3103	2630.55	2629.783	1	319.3	37.5 R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi 14318518 ref NP_116651.1	YFL004W	chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation;	3	4.9956	0.3098	2630.45	2629.783	1	1081.6	38.75 R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi 14318518 ref NP_116651.1	YFL004W	functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Vacuolar membrane protein involved in vacuolar polynoposphate accumulation;	3	4.3172	0.3458	3008.96	3008.34	1	595.2	31.52174 F.W2L1P1D1L1E1T1D111R4Q2D1P1K2Q2A1Y1E1E1E1K2K2K2L1.L
gi 14318518 ref NP_116651.1	YFL004W	functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p	3	3.9237	0.1876	3252.44	3252.674	2	490.7	28 F.W2L1P1D1L1E1T1D111R4Q2D1P1K2Q2A1Y1E1E1E1K2K2K2L1L1K2.G
oil14219549[ocf]ND_116651_1]		Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion;	2	2.0450	0 2201	1400 70	1400 701	1	1164.4	77 27272 K LI2D4 K21 424 D4 K24 D4 C41/4 K2 C
gij 143 163 16]10[0P_116651.1]	TFL004W	Viczp Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion;	2	3.9459	0.3201	1490.79	1492.731	I	1164.4	11.21213 K.H3U IKZLI Y IP IKZY IP ISI V IKZ.S
gi 14318518 ref NP_116651.1	YFL004W	Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter	1	2.8738	0.3486	1474.65	1475.731	1	514.2	63.636364 K.HDKLYPKYPSVK.S
gi 14318518 ref NP_116651.1	YFL004W	chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter	2	3.9494	0.333	1474.93	1475.731	1	1635.5	81.818184 K.HDKLYPKYPSVK.S
gi 14318518 ref NP_116651.1	YFL004W	chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter	2	2.9969	0.2072	2086.75	2089.312	1	572	59.375 F.WLPDLETDIRQDPKQAY.E
gi 14318518 ref NP_116651.1	YFL004W	chaperones; involved in protein localization and non-autophagic vacualar fusion; Vtc2p Vacualar membrane protein involved in vacualar polyphosphate accumulation; functions as a regulator of vacualar H+-ATPase activity and vacualar transporter	2	3.2932	0.195	2417.63	2418.57	2	568	44.736843 W.DDSDESKFVEELDKELEKVY.G
gi 14318518 ref NP_116651.1	YFL004W	chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter	2	3.754	0.317	2630.99	2629.783	1	632	45 R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi 14318518 ref NP_116651.1	YFL004W	chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accurularitor; functione con crounters of results H. A Tabas a dividu cod usoucler transporter	3	3.8164	0.2431	2606.51	2604.783	1	784	33.75 R.WDDSDESKFVEELDKELEKVY.G
gi 14318518 ref NP_116651.1	YFL004W	chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation;	2	3.5353	0.3716	2603.73	2604.783	2	365.3	40 R.WDDSDESKFVEELDKELEKVY.G
gi 14318518 ref NP_116651.1	YFL004W	functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation;	3	4.1943	0.3303	2627.42	2629.783	1	741.6	32.5 R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi 14318518 ref NP_116651.1	YFL004W	functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p	2	3.0077	0.281	2628.79	2629.783	1	289.8	35 R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
ail14318518 ref NP 116651.1	YFL004W	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2o	2	3.7909	0.3784	2604.17	2604.783	1	580.2	45 R.WDDSDESKFVEELDKELEKVY.G
		Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion;								
gi 14318518 ref NP_116651.1	YFL004W	Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones: involved in protein localization and non-autophanic vacuolar fusion;	3	4.728	0.265	2561.57	2561.91	1	663.2	31.818182 M.G1V1D1S1E1E1E1E1E11HE1L1P1P1G1V1K2K2P1L1N2L1L1K2.N
gi 14318518 ref NP_116651.1	YFL004W	Vtc2p Vtc2p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter	3	3.8923	0.1735	3123.11	3122.5	2	506.6	28.125 F.W2L1P1D1L1E1T1D111R4Q2D1P1K2Q2A1Y1E1E1E1K2K2K2L1L1.K
gi 14318518 ref NP_116651.1	YFL004W	chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p Subunit of the multiprotein cohesin complex, essential protein involved in chromosome seareaation and in double-strand DNA break repair. SMC chromosomal	1	2.8876	0.2547	1009.44	1010.228	1	356.9	78.57143 L.R4H3L1P1V1L1V1Y1.A
gi 14318514 ref NP_116647.1	YFL008W	ATPase family member, binds DNA with a preference for DNA with secondary structure; Smc1p Subunit of the multiprotein cohesin complex, essential protein involved in	2	3.4741	0.2923	1730.17	1728.853	1	592.1	57.692307 F.D1Y1V1S1D1H3L1D1A111Y1R4E1L1.T
gi 14318514 ref NP_116647.1	YFL008W	chromosome segregation and in double-strand DNA break repair, SMC chromosomal ATPase family member, binds DNA with a preference for DNA with secondary structure; Smc1p Subunit of the multiprotein cohesin complex, essential protein involved in	2	3.1187	0.3332	1979.75	1979.135	1	690.2	60.000004 K.T1F1D1Y1V1S1D1H3L1D1A1I1Y1R4E1L1.T
gi 14318514 ref NP_116647.1	YFL008W	chromosome segregation and in double-strand DNA break repair; SMC chromosomal ATPase family member, binds DNA with a preference for DNA with secondary structure; Smc1p Subunit of the multiprotein cohesin complex, essential protein involved in	2	3.4585	0.2808	1879.85	1877.029	1	690.5	60.714287 T.F1D1Y1V1S1D1H3L1D1A1I1Y1R4E1L1.T
gi 14318514 ref NP_116647.1	YFL008W	chromosome segregation and in double-strand DNA break repair, SMC chromosomal ATPase family member, binds DNA with a preference for DNA with secondary structure; Smc1p	2	3.6131	0.3982	1957.45	1958.135	1	1272	60.000004 K.TFDYVSDHLDAIYREL.T

		Subunit of the multiprotein cohesin complex, essential protein involved in								
		ATPase family member, binds DNA with a preference for DNA with secondary								
gi 14318514 ref NP_116647.1	YFL008W	structure; Smc1p Protein involved in folding of mitochondrially synthesized proteins in the	2	4.0848	0.2809	1842.33	1842.102	1	968.2	71.42857 K.YHNDLIEKEIQPKIT.E
		mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the								
gi 14318504 ref NP_116638.1	YFL016C	DnaJ family of molecular chaperones; Mdj1p Protein involved in folding of mitochondrially synthesized proteins in the	2	3.5505	0.2804	1834.29	1835.02	1	293.3	53.571426 K.K2Y1H3P1D111N2K2E1P1D1A1E1K2K2.F
		mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the								
gi 14318504 ref NP_116638.1	YFL016C	DnaJ family of molecular chaperones; Mdj1p Protein involved in folding of mitochondrially synthesized proteins in the	2	3.3399	0.1965	2356.39	2357.572	3	202.1	41.6666664 Q.K2Q2E1E1E1K2H3A1K2K2D1D1D1N2T1L1K2R4L1.E
		mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the								
gi[14318504]ret[NP_116638.1]	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the	2	3.5137	0.3135	2846.91	2848.142	1	514.1	34.615387 1.VDLPHGLQDGDVVRIPGQGSYPDIAVE.A
-14424050414ND 44002041	VEL 04CC	mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the	2	2 4704	0.0044	2464.04	2402 544	2	440.4	
gi 14310304 101 14F_110030.1	TFLUIDC	Protein involved in folding of mitochondrially synthesized proteins in the	2	3.4791	0.3044	3101.91	3103.311	2	412.4	31.034461 K. TH VDLFHGLQDGDVVKIFGQG31FDIAVE.A
ail14318504lrefINP 116638 1	YEI 016C	mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the Dna.I family of molecular chaperones: Mdi1n	3	4 6942	0 2543	2326.88	2326 572	2	658.9	
gift to root in only in _ rootoor if	11 20100	Protein involved in folding of mitochondrially synthesized proteins in the	0	1.0012	0.2010	2020.00	2020.072	-	000.0	
qi 14318504 ref NP 116638.1	YFL016C	mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	2	3.6045	0.3482	1812.73	1813.02	1	872.8	71.42857 K.KYHPDINKEPDAEKK.F
		Protein involved in folding of mitochondrially synthesized proteins in the								
gi 14318504 ref NP_116638.1	YFL016C	DnaJ family of molecular chaperones; Mdj1p	2	3.6955	0.3384	1886.71	1888.044	1	807.8	52.941177 L.QDGDVVRIPGQGSYPDIA.V
		Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix: localizes to the mitochondrial inner membrane; member of the								
gi 14318504 ref NP_116638.1	YFL016C	DnaJ family of molecular chaperones; Mdj1p	2	4.0609	0.2407	1942.75	1941.194	1	410.9	56.666668 A.KKYHPDINKEPDAEKK.F
		Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme.								
gi 14318501 ref NP_116635.1	YFL018C	complexes; Lpd1p	1	2.2409	0.1638	968.32	969.083	1	368.4	71.42857 K.EDHILDVK.N
		Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme								
gi 14318501 ref NP_116635.1	YFL018C	complexes; Lpd1p	2	3.1002	0.282	1266.47	1264.381	1	517.2	75 R.GRLVIDDQFNS.K
		the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme								
gi 14318501 ref NP_116635.1	YFL018C	complexes; Lpd1p Dibydrolingamide debydrogenase, the lingamide debydrogenase component (F3) of	2	2.9448	0.3588	1528.83	1529.69	2	705.9	62.5 K.RNDDKNVVEIVVE.D
		the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme								
gi 14318501 ref NP_116635.1	YFL018C	complexes; Lpd1p Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of	1	2.7102	0.2565	1528.71	1529.69	2	202.5	50 K.RNDDKNVVEIVVE.D
- 1440405041 (ND 440005-41		the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme			0.0000	4000.05	1000.000		1500.0	
gi 14318501 ret NP_116635.1	YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of	2	4.4618	0.2622	1802.25	1802.083	1	1528.3	/1.42857 R.LVIDDQENSKEPHIK.V
ail14318501/rofIND 116635 1	VEI 018C	the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme	2	3 1679	0.2477	1657 67	1657 964	1	469.9	
gi 1431030 (reiliar_110033.1)	II LOIDO	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of	2	3.1070	0.2477	1037.07	1037.004		400.0	33.040137 A.M.MDDMAVVEIVVE.D
ail14318501/refINP 116635.1	YFL018C	the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes: Lpd1p	2	3.9151	0.1658	2040.15	2041.323	1	933.4	62.5 R.G1R4I 1V111D1D102E1N2S1K2E1P1H3I1K2 V
	VEL 00714/	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer,	_		0.0000	0075 50	0077.544		505.5	
gi 14318481 161 10P_116616.1	TFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer,	2	4.1044	0.3602	2275.59	2277.514	2	535.5	44.730843 K.GTTTEGAELVDSVMDVIRRE.A
gi 14318481 ref NP_116616.1	YFL037W	which polymerizes to form microtubules; Tub2p Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer	2	3.7738	0.3078	2725.63	2726.899	1	534.7	41.304348 K.G1H3Y1T1E1G1A1E1L1V1D1S1V1M1D1V1I1R4R4E1A1E1G1C1.D
gi 14318481 ref NP_116616.1	YFL037W	which polymerizes to form microtubules; Tub2p	2	3.4986	0.2188	2694.31	2694.899	6	280.4	30.434782 K.GHYTEGAELVDSVMDVIRREAEGC.D
ail14318481 refINP 116616.1	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules: Tub2p	2	3.5586	0.2633	1878.19	1879.135	1	864.1	56.666668 T.S1I1Q2E1L1F1K2R4V1G1D1Q2F1S1A1M1.F
		Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer,		4 0005	0.0040	0005 77	0005 544		055.7	
gi 14318481 ret NP_116616.1	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer,	2	4.2825	0.2946	2305.77	2305.514	1	655.7	50 K.G1H3Y111E1G1A1E1L1V1D1S1V1M1D1V111R4R4E1.A
gi 14318481 ref NP_116616.1	YFL037W	which polymerizes to form microtubules; Tub2p Reta-tubulin: associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimor	2	3.9469	0.3901	1512.41	1511.637	1	786.4	81.818184 T.YHGHDDIQKERL.N
gi 14318481 ref NP_116616.1	YFL037W	which polymerizes to form microtubules; Tub2p	2	3.7783	0.3883	1533.03	1532.637	1	880.4	86.36364 T.Y1H3G1H3D1D111Q2K2E1R4L1.N
ail14318481 refINP 116616.1	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules: Tub2p	2	4.424	0.2905	1888.39	1888.049	1	1143.8	71.42857 T.YHGHDDIQKERLNVY.F
		Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer,		0 7704	0.4057	4040.57	4040.040		454 7	70 57440 MADAFAMAU0404 T
gi 14318481 ret NP_116616.1	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer,	1	2.7761	0.1957	1012.57	1012.216	1	451.7	78.57143M1R4E1111H311S1.1
gi 14318481 ref NP_116616.1	YFL037W	which polymerizes to form microtubules; Tub2p Beta-tubulin: associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimen	3	3.8381	0.2067	2756.57	2754.995	1	620.1	29.166666 E.GAELVDSVMDVIRREAEGCDSLQGF.Q
gi 14318481 ref NP_116616.1	YFL037W	which polymerizes to form microtubules; Tub2p	2	2.9274	0.1894	1193.25	1192.45	1	741.6	77.77778 A.VNLVPFPRLH.F
ail14318481/refINP_116616.1	YEI 037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules: Tub2p	2	3 0993	0 1794	1630.01	1627 717	1	723 9	62.5 A F1W2F1T111C1G1F1H3G1L1D1F1 N
		Actin, structural protein involved in cell polarization, endocytosis, and other	-	0.0000						
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	2	3.1264	0.2551	1578.29	1578.759	1	868.8	69.230774 S.SIEKSYELPDGQVI. I
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p	1	2.8715	0.333	1577.57	1578.759	1	787.8	61.538464 S.SIEKSYELPDGQVI.T
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p	1	2.8989	0.2537	1593.56	1594.759	1	723.8	57.692307 S.S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1.T
ail14318479/refINP 116614 1	YEI 039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions: Act1n	1	2 4338	0.332	1267 56	1268 471	1	325	65 D LAGRDI TDYLM K
	11 20000	Actin, structural protein involved in cell polarization, endocytosis, and other		2.4000	0.002	1207.00	1200.471		020	
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	2	2.9991	0.2786	2044.21	2045.232	2	385.8	44.444447 Q.S1S1S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1.N
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p	2	4.1944	0.4095	1851.75	1850.076	1	838.8	62.5 S.SIEKSYELPDGQVITIG.N
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p	1	3.0594	0.3019	1535.5	1536.723	1	356.3	53.846157 E.K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1.N
ai 14318479 refINP 116614 1	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cvtoskeletal functions: Act1p	2	3.6767	0.3796	1791.71	1793.024	1	678.8	56,666668 S.SIEKSYELPDGQVITI.G
		Actin, structural protein involved in cell polarization, endocytosis, and other	-							
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p	2	3.9143	0.325	1530.05	1530.573	1	1535	80.769226 M.G1Q2K2D1S1Y1V1G1D1E1A1Q2S1K2.R

	Actin, structural protein involved in cell polarization, endocytosis, and other								
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	3.3064	0.4308	1385.52	1386.418	1	205.1	63.636364 Q.E1Y1D1E1S1G1P1S1I1V1H3H3.K
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	2	3.9947	0.4073	1490.37	1489.582	1	1184.8	83.33333 S.KQEYDESGPSIVH.H
gi 14318479 ref NP_116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.1305	0.3296	1488.59	1489.582	1	685.1	70.83333 S.KQEYDESGPSIVH.H
gil14318479lrefINP_116614.1 YEL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions: Act1p	2	4 2639	0.3296	1628 43	1626 723	1	908.7	76 92308 S KOEYDESGPSIVHH K
	Actin, structural protein involved in cell polarization, endocytosis, and other	-	0.0074	0.0007	4077.0	4070 504		000.4	
gi[14318479][ei]NP_116614.1 TFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other	1	2.9974	0.3327	1377.0	1378.384	2	200.1	54.545450 L.K4V IAIP IE IE IE3P IV IL IL II I.E
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	3.0652	0.3007	1275.59	1276.479	3	301.6	60.000004 L.R4V1A1P1E1E1H3P1V1L1L1.T
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	3	4.4611	0.3722	3244.91	3246.552	1	403.1	23.214285 Q.S1S1S111E1K2S1Y1E1L1P1D1G1Q2V111T111G1N2E1R4F1R4A1P1E1A1L1.F
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	1	3.0667	0.1782	1598.72	1599.871	9	196	50 T.AEREIVRDIKEKL.C
gi 14318479 ref NP_116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	4.2042	0.2773	1781.51	1782.01	1	1051.7	73.07692 T.A1E1R4E1I1V1R4D1I1K2E1K2L1C1.Y
gil14318479lrefINP_116614.1 YEL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions: Act1n	3	4 6001	0 2795	1783 46	1782 01	1	1131 1	51 923077 T A1E1R4E1I1V1R4D111K2E1K2I 1C1 Y
	Actin, structural protein involved in cell polarization, endocytosis, and other		0.0750	0.2700	4 470 70	1171 740			
gi[14318479 ret NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	3.2759	0.3671	14/3./3	14/4./43	1	367.8	58.333332 E.LRVAPEEHPVLLT.E
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocvtosis, and other	1	3.2734	0.3323	1491.68	1492.743	1	481	62.5 E.L1R4V1A1P1E1E1H3P1V1L1L1T1.E
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	1	2.9794	0.2495	1372.65	1373.638	1	765.6	63.636364 E.LRVAPEEHPVLL.T
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	1	3.1398	0.3494	1389.77	1390.638	1	682.1	63.636364 E.L1R4V1A1P1E1E1H3P1V1L1L1.T
gi 14318479 ref NP 116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.1099	0.3646	1862.33	1863.114	1	326.4	50 L.TEAPMNPKSNREKMTQ.I
	Actin, structural protein involved in cell polarization, endocytosis, and other	1	2 9204	0.2976	1104 55	1105 269	2	215	
	Actin, structural protein involved in cell polarization, endocytosis, and other		2.0294	0.2070	1164.55	1103.300	2	215	
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	2.6386	0.2865	1200.53	1200.368	4	189.9	55.555557 L.R4Y1P111E1H3G111V1T1.N
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocutosis, and other	1	2.9402	0.2979	1398.64	1399.633	1	514.8	68.181816 L.TLRYPIEHGIVT.N
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	1	3.2998	0.3343	1416.66	1416.633	1	428.9	63.636364 L.T1L1R4Y1P111E1H3G1I1V1T1.N
gi 14318479 ref NP_116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	2.9522	0.338	1860.57	1861.115	1	370.6	53.571426 T.TAEREIVRDIKEKLC.Y
gil14318479lrefINP 116614.1 YEL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions: Act1p	2	2,9933	0.1861	1578.69	1579.816	1	409.2	68.181816 E.R4E111V1R4D111K2E1K2L1C1.Y
	Actin, structural protein involved in cell polarization, endocytosis, and other	-	2.0007	0.4704	1200 50	4000 077	-	440.0	
gi[14318479][ei]NP_116614.1 TFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other	1	3.2007	0.1734	1399.59	1399.077	1	140.2	60.000004 E.REIVRDINERL.C
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	2.652	0.1612	1298.6	1299.472	4	233.2	60.000004 L.RYPIEHGIVTN.W
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin structural pratain involved in cell polarization, and octasis, and other	2	3.5133	0.2259	2092.65	2093.397	1	682.6	53.125 T.AEREIVRDIKEKLCYVA.L
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	2	3.0983	0.3432	2702.81	2705.043	1	278.6	36.95652 E.KSYELPDGQVITIGNERFRAPEAL.F
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	2	3.1421	0.2806	1402.43	1401.692	3	662.1	68.181816 K.VKIIAPPERKYS.V
ail14318479/refINP 116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cvtoskeletal functions: Act1p	2	2.9554	0.2555	1461.75	1459.731	1	575	72.72727 K.IIAPPERKYSVW.I
	Actin, structural protein involved in cell polarization, endocytosis, and other	2	2 0022	0.1626	2521 47	2520.024	1	207.6	
gi[14316479][e][NF_110614.1] TFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other	2	3.0933	0.1020	2551.47	2030.934		207.0	32.3 I.EAFININFRSINKERINI QIINFETFIN
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	3.0335	0.3316	1520.62	1520.723	1	291.6	46.153847 E.KSYELPDGQVITIG.N
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin structural pratain involved in cell polarization, and octasis, and other	2	3.0806	0.3462	1511.25	1512.573	1	489.1	65.38461 M.GQKDSYVGDEAQSK.R
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	2	4.0479	0.3935	1648.27	1646.723	1	698	65.38461 S.K2Q2E1Y1D1E1S1G1P1S1I1V1H3H3.K
gi 14318479 ref NP_116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.8456	0.3244	1360.74	1361.584	1	254	54.545456 L.RVAPEEHPVLLT.E
ail14318479/refINP 116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cvtoskeletal functions: Act1p	2	3.3071	0.3772	1511.31	1511.654	1	1012.4	80 T.NWDDMEKIWHH.T
ail14318470[rof[ND_116614.1]_VEL030C	Actin, structural protein involved in cell polarization, endocytosis, and other	1	3 3335	0.2688	1520 77	1530 654	1	138.0	
	Actin, structural protein involved in cell polarization, endocytosis, and other		0.0000	0.2000	1323.77	1330.034		430.9	
gl[14318479]ref[NP_116614.1] YFL039C	cytoskeletal functions; Actip Actin, structural protein involved in cell polarization, endocytosis, and other	2	3.1275	0.2424	1454.33	1454.725	1	584.7	12.12121 A.GRDETDYLM@KILS
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	2.7056	0.2844	1202.73	1203.343	1	212.3	72.22222 G.NERFRAPEAL.F
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	3	4.0942	0.1588	3071.3	3070.396	1	533.5	25.961538 S.S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1N2E1R4F1R4A1P1E1A1L1.F
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	2	3.7981	0.2277	1781.35	1782.01	1	680.5	65.38461 T.A1E1R4E1I1V1R4D1I1K2E1K2L1C1.Y
gi 14318479 ref NP_116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.4278	0.3397	1754.37	1754.897	1	550.9	60.714287 S.KQEYDESGPSIVHHK.C
ail14318470irafiND 116614.11 VEL030C	Actin, structural protein involved in cell polarization, endocytosis, and other	2	2 060	0.2062	1476 30	1476 731	3	475 1	68 181816 K 1111 A1D1D1E1D4K2V1S1\/4\//2 1
	Actin, structural protein involved in cell polarization, endocytosis, and other	2	2.303	0.2002	1470.33	1470.751		475.1	
gi[14318479]ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	2	3.1177	0.2481	2153.39	2153.537	1	365.3	47.058823 T.EAPMNPKSNREKMTQIMF.E
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization. endocvtosis. and other	3	4.172	0.3909	2089.07	2086.361	1	970.6	40.789474 A.GFAGDDAPRAVFPSIVGRPR.H
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Actip	1	2.4109	0.2658	1236.57	1237.372	1	336.4	75 T.NWDDMEKIW.H
gi 14318479 ref NP_116614.1 YFL039C	cytoskeletal functions; Act1p	2	3.9872	0.321	1593.67	1594.759	1	686.9	65.38461 S.S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1.T
gi 14318479 ref NP_116614.1 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.346	0.1755	1577.6	1578.759	2	566.2	53.846157 S.SIEKSYELPDGQVI.T
ail14318479/refINP 116614 11 YEL0390	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions: Act to	2	3,7191	0.233	1580.03	1578,759	1	823 7	73.07692 S.SIEKSYELPDGQVLT
21	·····	-		2.200					

		Action structured protein involved in cell polorization, and putching and other								
gi 14318479 ref NP_116614.1	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.3054	0.2749	1537.99	1536.723	1	549.4	61.538464 E.K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1.N
gi 14318479 ref NP 116614.1	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.0693	0.2268	1535.58	1536.723	1	292.9	46.153847 E.K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1.N
gil14318479lrefINP 116614.1	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cvtoskeletal functions: Act1p	2	4.9296	0.2635	1869.31	1869.076	1	726.2	59.375 S.S.111E1K2S1Y1E1L1P1D1G1Q2V111T111G1 N
gil14218470 rofIND 1166141	VEL 020C	Actin, structural protein involved in cell polarization, endocytosis, and other stacklottel functions. Actin	-	2 5254	0.2104	1057.02	1057 154	1	001.0	
gi 14316479 101 14F_110014.1	TFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other	2	3.3234	0.2104	1957.95	1957.154		021.3	
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	3.0946	0.3196	1511.58	1511.654	1	433.6	70 T.NWDDMEKIWHH.T
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	1	2.9394	0.2494	1219.58	1220.343	1	237.3	72.22222 G.N2E1R4F1R4A1P1E1A1L1.F
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p	1	3.0299	0.2373	1260.64	1260.479	1	339.6	65 L.RVAPEEHPVLL.T
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act p	2	3.8142	0.3469	1687.93	1688.931	1	360.5	70.83333 A.EREIVRDIKEKLC.Y
gi 14318479 ref NP_116614.1	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.203	0.1583	1529.59	1528.792	1	446.1	77.27273 A.EREIVRDIKEKL.C
gi 14318479 ref NP_116614.1	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.9925	0.3943	1757.75	1760.01	1	791.6	65.38461 T.AEREIVRDIKEKLC.Y
gil14318479lrefINP 116614 1	YEL 039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions: Act1n	2	2 9745	0 2065	1699.01	1700 976	6	396.4	50 T TAEREIVRDIKEKI C
	VELODOC	Actin, structural protein involved in cell polarization, endocytosis, and other	-	2.07.10	0.2000	1000.01	4002.400	4	000.1	
gi 14318479 rei NP_116614.1	TFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other	2	3.8340	0.274	1922.29	1923.180	1	806.1	04.200/TT.AEKEIVKDIKEKLUT.V
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	2	2.916	0.2963	1852.53	1852.107	1	346.7	69.230774 A.EREIVRDIKEKLCY.V
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p Actin, structural protein involved in cell polarization, endocytosis, and other	2	3.0346	0.2975	2023.83	2024.291	1	491.8	53.333336 T.TAEREIVRDIKEKLCY.V
gi 14318479 ref NP_116614.1	YFL039C	cytoskeletal functions; Act1p	2	3.5121	0.2102	1237.05	1237.372	1	682.4	87.5 T.NWDDMEKIW.H
gi 14318477 ref NP_116612.1	YFL041W	role in iron transport; Fet5p	2	3.2625	0.2422	1936.05	1937.026	1	551.8	57.14286 A.F11111H3D1P1E1E1P1F1E1Y1D1H3E1.R
gi 14318477 ref NP_116612.1	YFL041W	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport; Fet5p	2	3.9945	0.3293	2393.85	2395.623	1	976.7	55.263157 F.N2G1E1W2P1L1P1D1I1H3V1E1K2G1D1R4V1E1L1Y1.L
gi 14318477 ref NP 116612.1	YFL041W	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport; Fet5p	2	3.4424	0.2562	2366.89	2367.623	1	967	50 F.NGEWPLPDIHVEKGDRVELY.L
gil14318477/refINP_116612.1	YEL 041W	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport. Fet5p	2	4 2002	0.41	2527 37	2527 77	1	786	55 263157 & F1I11H3D1P1E1E1P1E1E1Y1D1H3E1R4V1I1T1L1 S
sil44040477i=fND_440042.1	VELOAAW	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a	-	9.4000	0.2054	4425 50	4400 007		070.7	
gi 14318477 rei NP_116612.1	TFL041VV	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a		3.1200	0.3854	1435.56	1430.097		212.1	58.333332 N.GLPRQPEPLPKGF. I
gi 14318477 ref NP_116612.1	YFL041W	role in iron transport; Fet5p Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a	1	3.1748	0.3286	1455.61	1454.697	2	229.6	54.166668 K.G1L1P1R4Q2P1E1P1L1P1K2G1F1.T
gi 14318477 ref NP_116612.1	YFL041W	role in iron transport; Fet5p Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a	3	4.1422	0.157	2529.92	2527.77	2	792.2	31.578945 A.F1I1I1H3D1P1E1E1P1F1E1Y1D1H3E1R4V1I1T1L1.S
gi 14318477 ref NP_116612.1	YFL041W	role in iron transport; Fet5p	2	3.821	0.3436	2499.55	2500.77	1	781.9	55.263157 A.FIIHDPEEPFEYDHERVITL.S
gi 14318476 ref NP_116611.1	YFL042C	Putative protein of unknown function; YFL042C is not an essential gene; Yfl042cp	2	3.579	0.2105	2536.39	2536.756	1	439.3	47.5 F.K2S1V1P1K2D1D1R4L1L1D1D1F1N2C1G1L1N2R4E1L1.L
gi 14318476 ref NP_116611.1	YFL042C	Putative protein of unknown function; YFL042C is not an essential gene; Yfl042cp	3	4.3722	0.1768	3092.18	3093.399	1	819.9	29.1666666 T.F1K2S1V1P1K2D1D1R4L1L1D1D1F1N2C1G1L1N2R4E1L1L1Y1Q2.G
gi 14318476 ref NP_116611.1	YFL042C	Putative protein of unknown function; YFL042C is not an essential gene; Yfl042cp	3	4.4497	0.2688	2943.38	2945.223	1	560.3	25 F.K2S1V1P1K2D1D1R4L1L1D1D1F1N2C1G1L1N2R4E1L1L1Y1Q2.G
gi 14318476 ref NP_116611.1	YFL042C	Putative protein of unknown function; YFL042C is not an essential gene; Yfl042cp	3	4.0916	0.2341	2908.88	2910.223	1	491.3	23.913044 F.KSVPKDDRLLDDFNCGLNRELLYQ.G
		Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid								
gi 14318526 ref NP_116659.1	YFR004W	couples the deubiquitination and degradation of proteasome substrates; Rpn11p	2	3.7226	0.1553	1896.69	1897.056	1	375.6	57.14286 R.I1E1E1E1K2E1L1T1E1E1E1L1K2T1R4.Y
		Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid;								
gi 14318526 ref NP_116659.1	YFR004W	couples the deubiquitination and degradation of proteasome substrates; Rpn11p	3	5.5971	0.3198	2032.91	2033.243	1	1625.4	48.333332 K.RIEEEKELTEEELKTR.Y
gil14318526 ref NP_116659.1	YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiguitination and degradation of proteasome substrates: Rpn11p	3	6.1164	0.2684	2274.71	2275.495	2	2049.3	51,47059 Y.S1K2R4I1E1E1E1K2E1L1T1E1E1E1L1K2T1R4 Y
git 1010020[10][11 _ 110000.1]		Matellangetages subunit of the 10S regulation of probability ages and ages and a	0	0.1101	0.2001		2210.100	-	201010	
gi 14318526 ref NP_116659.1	YFR004W	couples the deubiquitination and degradation of proteasome substrates; Rpn11p	2	5.7388	0.245	2273.65	2275.495	4	1099.7	61.764706 Y.S1K2R4I1E1E1E1K2E1L1T1E1E1E1L1K2T1R4.Y
		Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid;								
gi 14318526 ref NP_116659.1	YFR004W	couples the deubiquitination and degradation of proteasome substrates; Rpn11p	2	3.2285	0.2653	1619.15	1618.679	1	408.4	53.846157 A.D1T1G1R4D1D1T1K2E1T1V1Y1I1S1.S
gil14318526lrefINP_116659.11	YER004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiquitination and degradation of proteasome substrates: Rpn11p	2	6 1302	0 2521	2056 51	2057 243	1	1981.3	80 K R4I1E1E1E1K2E1I 1T1E1E1E1I 1K2T1R4 Y
git 1010020[10][11 _ 110000.1]		Matellangetages subunit of the 10S regulation of probability ages and ages and a	-	0.1002	0.2021	2000.01	2001.210		1001.0	
gi 14318526 ref NP_116659.1	YFR004W	couples the deubiquitination and degradation of proteasome substrates; Rpn11p	3	6.6353	0.3444	2276.09	2275.495	1	2647	52.941177 Y.S1K2R4I1E1E1E1K2E1L1T1E1E1E1L1K2T1R4.Y
		Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid;								
gi 14318526 ref NP_116659.1	YFR004W	couples the deubiquitination and degradation of proteasome substrates; Rpn11p Positive regulator of the Gcp2p kinase activity, forms a complex with Gcp1p;	2	5.9526	0.2657	2274.59	2275.495	3	1324.6	61.764706 Y.S1K2R4I1E1E1E1K2E1L1T1E1E1E1L1K2T1R4.Y
gi 14318531 ref NP_116664.1	YFR009W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	2	3.3207	0.1619	1877.21	1876.999	3	431	57.14286 K.K2L1D1N2E1R4E1D1L1D1N2H3L1I1Q2.I
gi 14318531 ref NP_116664.1	YFR009W	proposed to stimulate Gon2p activation by an uncharged tRNA; Gon20p	2	4.6528	0.4746	1762.37	1762.883	1	590.7	64.28571 L.H3V1E1Q2E1L1R4G1D1D1T1K2A1L1Q2.S
gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	2	3.8758	0.3974	1739.35	1739.883	1	465.6	60.714287 L.HVEQELRGDDTKALQ.S
gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	2	4.3681	0.1608	1691.69	1689.928	1	889.6	73.07692 F.K2F1P1E1C1D1K2L1S1P1P1I1I1Q2.L
ail14318531 refINP 116664 1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA: Gcn20p	3	4,8118	0.3335	3802.34	3804.333	1	885.7	L.E1K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1K2F1P1E1C1D1K2L1S1P1P1I1I1Q2L 27.419355 1.Q
gil14318531/refIND 116664.1	YER000W/	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tBNA. Gcn20p	2	4 2492	0.3516	2262.12	2263 602	ว	434 4	47 22222 K K2I 1E1K2I 1P1V1I 1E1P1P1E102D1K2T1I4D1E1 K
sil 4040504 setting_110004.1	VEDOCOVI	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p;	2	4.0007	0.0000	2202.13	2200.002	2	+34.4	K.K2L1E1K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1K2F1P1E1C1D1K2L1S1P1P1I1
yij 14310531 [ref]NP 110004.1	1 F KUU9W	proposed to sumulate GCn2p activation by an Uncharged TKINA; GCn20D	3	4.0097	U.2884	3934.58	3934.507	1	00/	23.4373 IQZ.L

gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	2	3.3036	0.2823	1633.19	1632.752	1	425	61.538464 L.H3V1E1Q2E1L1R4G1D1D1T1K2A1L1.Q
gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	2	3.0464	0.2122	1675.45	1672.928	1	475.9	57.692307 F.KFPECDKLSPPIIQ.L
gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	3	5.471	0.2973	3289.64	3291.746	1	865.4	30.769232 K.K2L1E1K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1K2F1P1E1C1D1K2L1.S
gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	3	4.6663	0.155	3559.31	3560.058	1	841.3	27.586206 E.K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1K2F1P1E1C1D1K2L1S1P1P1I1I1Q2.L
gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	2	3.5036	0.3184	1805.49	1804.088	1	990.9	67.85714 F.K2F1P1E1C1D1K2L1S1P1P11111Q2L1.Q
gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	3	3.8712	0.1997	3653.84	3653.173	2	336.4	24.166666 L.EKLPVLEPPEQDKTIDFKFPECDKLSPPIIQ.L
gi 14318531 ref NP_116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	3	5.4955	0.3907	3689.87	3690.173	1	592.5	L.E1K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1K2F1P1E1C1D1K2L1S1P1P1I1I1Q2 25 L
gi 14318531 ref NP 116664.1	YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	2	3.8823	0.3537	2241.17	2240.602	1	461.5	50 K.KLEKLPVLEPPEQDKTIDF.K
		Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin								E.N2Y1R4P1S1N2G1G1R4G1S1F1D1D1D1E1D1D1Y1Y1D1D1D1D1Y1Y1N2D1I1P1
gi 15530184 ref NP_219497.1	YFR024C-A	polymerization; Lsb3p Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of	3	6.4361	0.4595	3934.1	3932.805	1	648.3	30.46875 S1S1F1.S
gil15530184/refINP_219497.1	YFR024C-A	human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization: Lsb3p	3	5.4341	0.2983	2911.04	2911.854	1	603.2	36.904762 S.R4N2R4W2A1D1D1E1Y1D1D1Y1D1D1D1Y1E1S1G1Y1R4R4 G
34		Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin	-							
gi 15530184 ref NP_219497.1	YFR024C-A	polymerization; Lsb3p Protein containing a C-terminal SH3 domain; binds Las17n, which is a homolog of	2	3.9633	0.1995	2875.01	2875.854	1	288.3	38.095238 S.RNRWADDEYDDDDDYESGYRR.G
ail15530184/refINP 219497 1	YER024C-A	human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization: I shan	2	3 7626	0 1807	2910.33	2911 854	5	319.2	35 714287 S R4N2R4W2A1D1D1E1Y1D1D1Y1D1D1D1Y1E1S1G1Y1R4R4 G
gi10000104101141 _210401.11	1110240 //	Protein phosphatase required for mitatic evit located in the puckablus until liberated	2	0.7020	0.1007	2010.00	2311.004	5	010.2	00.7 H201 0.1(H121(H121(H121(H121(H121(H121(H121(H1
ai142195511rofIND 116694.11	VEROSEC	by the FEAR and Mitotic Exit Network in anaphase, enabling it to act on key	2	2 1 2 0 2	0 2007	1064.91	1064 142	1	606.9	
gi 14318551 fei NP_116684.1	TFRU28C	Substrates to effect a decrease in CDK/B-cyclin activity and mitotic exit; Cdc14p	2	3.1292	0.2907	1904.01	1964.143	1	090.0	
	VED.000	by the FEAR and Mitotic Exit Network in anaphase, enabling it to act on key		5 0500	0.4705	0070.05	0070 047		4000 5	
gi 14318551 ret NP_116684.1	YFR028C	substrates to effect a decrease in CDK/B-cyclin activity and mitotic exit; Cdc14p	2	5.8539	0.4735	2073.25	2073.317	1	1932.5	70.588234 Q.HEDEIFEDGTCPDESIVK.N
		Protein phosphatase required for mitotic exit; located in the nucleolus until liberated by the FEAR and Mitotic Exit Network in anaphase, enabling it to act on key								
gi 14318551 ret NP_116684.1	YFR028C	substrates to effect a decrease in CDK/B-cyclin activity and mitotic exit; Cdc14p	2	3.8175	0.4272	2093.17	2094.317	1	739.5	50 Q.H3L1D1L111F1E1D1G111C1P1D1L1S111V1K2.N
		Protein phosphatase required for mitotic exit; located in the nucleolus until liberated by the FEAR and Mitotic Exit Network in anaphase, enabling it to act on key								
gi 14318551 ref NP_116684.1	YFR028C	substrates to effect a decrease in CDK/B-cyclin activity and mitotic exit; Cdc14p Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has	2	3.667	0.3723	1945.13	1945.143	1	1023.8	59.375 Q.HLDLIFEDGTCPDLSIV.K
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has	2	5.2108	0.4664	1749.01	1750.851	1	1456.4	68.75 R.G1V1A1M1N2P1V1D1H3P1H3G1G1G1N2H3Q2.H
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has	2	3.0924	0.1832	1211.29	1211.45	5	494.2	63.636364 A.GGGRVDKPLLKA.G
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has	1	3.2419	0.2175	1211.62	1211.45	1	552.6	59.090908 A.GGGRVDKPLLKA.G
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has	2	3.3366	0.3065	1496.51	1497.588	1	338.8	61.538464 A.MNPVDHPHGGGNHQ.H
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has	2	3.3467	0.2139	1045.37	1045.189	1	357.2	92.85714 K.RNSWPKTR.G
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has	2	3.2015	0.2254	1690.63	1688.834	1	358	57.692307 G.H3N2P1D1E1N2K2T1R4V1R4L1P1S1.G
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has	2	4.5291	0.4438	1723.55	1724.851	1	1244.7	65.625 R.GVAMNPVDHPHGGGNHQ.H
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap Protein component of the large (60S) ribosomal subjust identical to Rpl2Bp and has	2	3.298	0.3277	1519.49	1520.588	1	487.9	65.38461 A.M1N2P1V1D1H3P1H3G1G1G1N2H3Q2.H
gi 14318555 ref NP_116688.1	YFR031C-A	similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	2	3.239	0.3676	1819.09	1818.964	1	277.4	53.333336 G.H3N2P1D1E1N2K2T1R4V1R4L1P1S1G1A1.K
gi 6321437 ref NP_011514.1	YGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	1	2.4588	0.1767	1287.64	1286.372	9	401.5	55 M.H3G1Q2N2P1D1I1Y1D1I1V1.N
ail6321437/rofINP_011514_1	VGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove	2	3 568	0 3061	1604 30	1604 759	1	420.1	61 538/6/ A S1D1M1H3C1O2N2D1D111V1D111V1 N
gilosz1457 lieliter_011514.1	IGEOOTC	C.3 starol dehydrogenase, catalyzes the second of three steps required to remove	2	5.500	0.5001	1004.55	1004.755		420.1	
gi 6321437 ref NP_011514.1	YGL001C	two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	1	2.7515	0.233	1357.6	1358.525	2	500.9	65 Q.F1F1D111N2P1K2P1D111H3.I
	VOI 0010	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove		0.0050	0.005	1015 50	1010 001		4 400 0	
gi 6321437 ret NP_011514.1	YGL001C	two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	2	3.6958	0.265	1645.59	1646.884	1	1492.8	71.42857 L.LGYTPRVGIEEGINK.T
gi 6321437 ref NP_011514.1	YGL001C	C-3 sterol denydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	2	3.3536	0.2851	1753.57	1750.992	1	219.6	57.692307 Q.Q2F1F1D111N2P1K2P1D111H311F1.D
gi 6321437 ref NP_011514.1	YGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	2	3.2111	0.31	1605.59	1603.861	1	714	70.83333 Q.FFDINPKPDIHIF.D
gi 6321437 ref NP_011514.1	YGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	2	3.2457	0.2989	1620.01	1620.861	1	585.3	66.66667 Q.F1F1D111N2P1K2P1D111H311F1.D
gi 6321437 ref NP_011514.1	YGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	2	3.587	0.2702	1606.63	1604.846	2	524.8	50 A.G1I1F1G1P1G1D1R4Q2L1V1P1G1L1R4.Q
gi 6321437 ref NP_011514.1	YGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	2	3.0604	0.2032	1586.23	1586.759	3	284.1	53.846157 A.SPMHGQNPDIYDIV.N
gi 6321437 ref NP_011514.1	YGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	3	4.3431	0.307	1604.54	1604.846	4	890.3	44.642857 A.G1I1F1G1P1G1D1R4Q2L1V1P1G1L1R4.Q

		C-3 stored dehydrogenase, catalyzes the second of three stops required to remove								
gi 6321437 ref NP_011514.1	YGL001C	two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	3	3.9009	0.2424	1604.66	1604.846	3	741.2	41.07143 A.G1I1F1G1P1G1D1R4Q2L1V1P1G1L1R4.Q
gi 6321437 ref NP_011514.1	YGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	2.9146	0.1627	1606.31	1604.846	1	623.6	57.14286 A.G111F1G1P1G1D1R4Q2L1V1P1G1L1R4.Q
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	5.053	0.4455	2189.71	2189.349	1	1075.2	63.88889 G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.4081	0.4595	2165.61	2166.349	1	835.6	58.333332 G.EARPVPEEYLQTDPSYGLT.S
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase. pumps protons out of the cell: maior regulator of	2	4.6052	0.3773	2248.45	2247.401	1	844	57.894737 A.G1E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.0936	0.2904	2333.79	2335.479	1	788.1	55 A.G1E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1S1.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.8799	0.349	2548.93	2547.913	1	593.4	50 N.T1A1V1V111R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D111L1.Q
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	3.8542	0.2991	3074.42	3073.317	1	589.3	26.724138 N.IYNAERLGLGGGGDMPGSELADFVENADGF.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.6637	0.3595	2249.73	2247.597	1	467.6	50 V.VIRDGQLVEIPANEVVPGDIL.Q
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.5762	0.4451	2996.49	2997.176	1	1056	41.37931 Y.NAERLGLGGGGDMPGSELADFVENADGFAE.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.3676	0.4955	2828.47	2829.982	1	1182	50 Y.N2A1E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of membrane blased environment of the D0 membrane protocols of the dot of the D0 membrane protocols of the D0	2	5.5138	0.4975	2796.39	2796.982	1	1598.3	55.555557 Y.NAERLGLGGGGDMPGSELADFVENADGF.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.6803	0.4193	1759.47	1760.811	1	932.3	64.28571 K.TVEEDHPIPEDVHEN.Y
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pri and plasma memorane potential, part of the P2 subgroup of calcon- transporting ATPases, Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.3084	0.5001	2294.45	2295.381	1	1174.2	58.333332 K.TVEEDHPIPEDVHENYENK.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.4984	0.4098	2166.49	2167.207	1	690.2	55.88235 K.TVEEDHPIPEDVHENYEN.K
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.1009	0.3321	1522.51	1522.671	1	506.8	60.000004 E.R4L1G1L1G1G1G1G1D1M\$P1G1S1E1L1A1.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplastine primitioplastine memorane potential, part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catoplasmic alt-and plasma asombrane potential; board of the D2 subgroup of cation-	2	3.2265	0.2518	1418.55	1416.592	1	1033.6	78.57143 E.RLGLGGGGDMPGSELA
gi 6321430 ref NP_011507.1	YGL008C	events and a particular termination protonal, part of the 12 staggraph of earlier transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the ell; major regulator of catcolarging atH and plasma argumpang potential; part of the P3 subgraph of earlier	2	4.1385	0.3594	2036.51	2037.233	1	818.3	61.764706 E.ARPVPEEYLQTDPSYGLT.S
gi 6321430 ref NP_011507.1	YGL008C	cytoplashing pranic plasher memorane potential, part of the 2 subgroup of calcon- transporting ATPases; Pm1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catcolarem alt-and plasma areampang potential; board of the D2 subgroup of calcon-	2	6.2826	0.4671	2222.25	2221.403	1	763.4	54.761906 A.ERLGLGGGGDMPGSELADFVEN.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplashing pranic plasher memorane potential, part of the 2 subgroup of calcon- transporting ATPases; Pm1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catcolarem alt-and plasma areampang potential; board of the D2 subgroup of calcon-	2	5.3432	0.3938	2446.41	2445.808	1	921.5	56.81818 T.A1V1V111R4D1G1Q2L1V1E111P1A1N2E1V1V1P1G1D111L1.Q
gi 6321430 ref NP_011507.1	YGL008C	eyopasitie pranic plasma memorare potential, part of the 22 subgroup of calcon- transporting ATases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catcalcare bit and plasma membrane potential; bard of the D2 subgroup of calcon-	2	5.406	0.3477	2295.13	2292.482	1	618.3	43.18182 A.ERLGLGGGGDMPGSELADFVENA.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplashing pranto plasma memorana potential, part of the 22 subgroup of calcon- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic HH and plasma membrane potential: part of the P2 subgroup of calcon-	2	4.723	0.3113	2589.91	2588.02	1	847.2	52.173912 A.VVIRDGQLVEIPANEVVPGDILQL.E
gi 6321430 ref NP_011507.1	YGL008C	eyopasitie pranic plasma memorare potential, part of the 22 subgroup of calcon- transporting ATases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catcalcare bit and plasma membrane potential; bard of the D2 subgroup of calcon-	3	5.4401	0.2249	2620.94	2618.02	1	1211.1	35.869564 A.V1V111R4D1G1Q2L1V1E111P1A1N2E1V1V1P1G1D111L1Q2L1.E
gi 6321430 ref NP_011507.1	YGL008C	eyopasitie pranic plasma memorare potential, part of the 22 subgroup of calcon- transporting ATases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catcalcare bit and plasma membrane potential; bard of the D2 subgroup of calcon-	3	4.2727	0.2074	2589.83	2588.02	1	919.7	36.95652 A.VVIRDGQLVEIPANEVVPGDILQL.E
gi 6321430 ref NP_011507.1	YGL008C	cytoplashing praning plasma presiminarian potential, part of the 22 subgroup of calcon- transporting ATPases; Pm1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catcalcaria eH and plasma membrane potential; out of the D2 subgroup of calcon-	2	3.7307	0.424	3031.41	3032.176	2	293.8	24.13793 1.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplashing praning plasma presiminarian potential, part of the 22 subgroup of calcon- transporting ATPases; Pm1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catcalcaria eH and plasma membrane potential; out of the D2 subgroup of calcon-	2	4.1553	0.279	2811.85	2811.994	1	558.4	33.333336 A.ERLGLGGGGDMPGSELADFVENADGFAE.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplashing praning plasma presiminarian potential, part of the 22 subgroup of calcon- transporting ATPases; Pm1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of catcalcaria eH and plasma membrane potential; out of the D2 subgroup of calcon-	2	4.4259	0.467	2842.11	2843.994	1	514.3	31.48148 A.E1R4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.V
gi 6321430 ref NP_011507.1	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic oH and plasma membrane potential: part of the Cell; major regulator of cytoplasmic oH and plasma membrane potential: part of the PS subgroup of cation.	3	5.4295	0.4325	2641.64	2641.799	1	2259.1	37 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
gi 6321430 ref NP_011507.1	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytonlasmic of H and plasma membrane potential: part of the 29 approximation of cytonlasmic of H and plasma membrane potential: part of the P3 approximation of cytonlasmic of H and plasma membrane potential: part of the P3 approximation of cytonlasmic of H and plasma membrane potential: part of the P3 approximation of cytonlasmic of H and plasma membrane potential: part of the P3 approximation of cytonlasmic of H and plasma membrane potential: part of the P3 approximation of cytonlasmic of H and plasma membrane potential: part of the P3 approximation of cytonlasmic of H and plasmic of H and P3 approximation of the P3 approximation of cytonlasmic of H and P3 approximation of H and P3 approximation of cytonlasmic of H and P3 approximation of H and P3 approximation of cytonlasmic of cyto	2	5.392	0.4153	2614.65	2611.799	1	1021.8	44 A.ERLGLGGGGDMPGSELADFVENADGF.A
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	3	4.5372	0.2913	2614.58	2611.799	1	2365.4	38 A.ERLGLGGGGDMPGSELADFVENADGF.A

		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	5.3766	0.4611	2641.39	2641.799	1	644.5	44 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
		cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.2881	0.3161	3071.21	3073.317	1	435.5	32.75862 N.IYNAERLGLGGGGDMPGSELADFVENADGF.A
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0 7400	0.0050	4505 70	1500.074		000	
gij6321430 ret NP_011507.1	YGL008C	transporting AI Pases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of citoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	3.7432	0.3258	1505.73	1506.671	4	689	63.333332 E.K4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1.D
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.0774	0.4926	1487.17	1487.671	1	593.4	63.333332 E.RLGLGGGGDMPGSELA.D
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+ATPase, pumps protons out of the cell: major regulator of	2	3.3583	0.3085	1251.39	1249.465	1	1314.5	85 Q.MADEKESLVVK.F
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.9924	0.5157	2421.85	2423.555	1	1640.8	63.15789 L.KTVEEDHPIPEDVHENYENK.V
ail6321430/rofIND_011507_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	3	5 1003	0 2774	2075 21	2075 161	1	607.2	40.625 L K2T1\/1E1E1D1H3D1I1D1E1D1\/1H3E1N2Y1 E
gilosz 1400/10/14/ _011001.1	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	5	0.1000	0.2114	2070.21	2070.101	·	007.2	
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.2306	0.2368	1502.55	1502.674	4	374.1	62.5 V.VESPEGERIVCVK.G
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cutoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+ATPase, pumps protons out of the cell; major regulator of	1	3.5582	0.2529	1215.53	1216.34	1	315.2	72.22222 LE1F1H3P1F1D1P1V1S1K2.K
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H + ATPase, pumpe protone out of the cells major regulator of	1	3.3522	0.3862	1505.6	1506.671	1	290.5	53.333336 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
		cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	3.1361	0.4644	1486.66	1487.671	1	310.9	53.333336 E.RLGLGGGGDMPGSELA.D
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
-:::C2244201{IND_04450741	VOLODOC	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0.0004	0.0040	4 440 55	4446 500	-	005.0	
gij6321430/ret/NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	1	2.9604	0.2949	1416.55	1416.592	5	285.8	53.5/1426 E.RLGLGGGGDMPGSEL.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.061	0.2348	1146.47	1146.37	1	585.8	77.77778 G.SIVDELKKTL.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP 011507.1	YGL008C	transporting ATPases: Pma1p	2	3.2313	0.1586	1160.51	1158.37	1	598.6	77.77778 G.S1I1V1D1E1L1K2K2T1L1.A
51		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0.0004	0.0044	4505.04	1500 700		407.0	
gi 6321430 ret NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	2	3.0281	0.3044	1505.81	1503.736	1	467.2	61.538464 G.SIVDELKKTLANTA.V
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.9853	0.1644	2618.49	2618.02	2	750.6	47.826088 A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								T 41/4/(4/10/01/01/01/01/10/01/10/01/10/01/10/01/10/01/10/01/10/01/10/01/10/01/10/01/10/01/10/01/10/01/10/01/0
ail6321430/refINP 011507.1	YGL008C	transporting ATPases: Pma1p	3	5.4371	0.3045	4057.97	4059.593	1	753.7	23.648647 P1T1D1G1R4I1V1.T
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6221420/rofIND_011E07_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	E 0692	0.2051	2714 12	0710 070	1	1000 6	22 652947 E B4I 4041 404040404040404046454541 4A4D4541/454N2A4D40454A454 V
gil0321430[rei]NF_011507.1]	IGLUUGC	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	5.0002	0.2951	2/14.12	2/13.0/0		1220.0	53.053647 E.R4EIGIEIGIGIGIGIGIDIMIFIGISTEILIAIDIFIVIEINZAIDIGIFIAIEI.V
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	5.2444	0.3944	2485.53	2482.684	1	2021.9	56.25 E.RLGLGGGGDMPGSELADFVENADGF.A
		Plasma memorane H+-A I Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.6785	0.2978	1569.65	1568.637	1	545.3	57.14286 M.PGSELADFVENADGF.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/rofIND_011507_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	5 2010	0 5343	2713 20	2713 979	1	1518.0	46 153847 E P4I 1611 1616161616101M1P161S1E1I 1A1D1E1V1E1N2A1D161E1A1E1 V
giloo21400[101141_011001.1]	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-	0.2010	0.0040	2110.20	2110.010		1010.0	
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+ ATPase, pumps protons out of the cell: major regulator of	1	2.7129	0.2811	1583.42	1584.637	3	279.6	46.42857 M.P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
		cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	3	5.1942	0.4124	2484.95	2482.684	1	1684.5	38.541664 E.RLGLGGGGDMPGSELADFVENADGF.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507_1	VGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases: Pma1p	з	6 7227	0 3985	2511 44	2511 684	1	2107.8	39 583336 E R4I 1G1I 1G1G1G1G1G1D1M1P1G1S1E1I 1A1D1E1V1E1N2A1D1G1E1 A
giloo21400[101141_011001.1]	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	0	0.7227	0.0000	2011.44	2011.004		2107.0	
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrana HL ATPase, pumpa protopa out of the cells major regulator of	2	3.6276	0.4345	3153.41	3154.435	1	233.1	30.000002 E.RLGLGGGGDMPGSELADFVENADGFAEVFPQ.H
		cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.7683	0.1533	1429.54	1430.632	3	444.8	63.636364 K.V1L1E1F1H3P1F1D1P1V1S1K2.K
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507_1	YGI 008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases: Pma1p	2	5 9946	0 4767	2512 29	2511 684	1	1841 4	56 25 E R4I 1G1I 1G1G1G1G1G1D1M1P1G1S1E1I 1A1D1E1V1E1N2A1D1G1E1 A
giloo21400[101141_011001.1]	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-	0.0040	0.4707	2012.20	2011.004		1041.4	
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.859	0.3615	2441.33	2441.749	1	346.4	35.714287 N.K2L1S1L1H3E1P1Y1T1V1E1G1V1S1P1D1D1L1M1L1T1A1.C
		cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.1995	0.4095	2417.55	2416.749	1	636.1	47.61905 N.KLSLHEPYTVEGVSPDDLMLTA.C
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507_1	YGL008C	cytoptasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases: Pma1p	2	3,4294	0.239	1561 25	1560 806	3	571.6	62.5 K.V1L1E1E1H3P1E1D1P1V1S1K2K2 V
aurer 1001011 _01100111			4	0.1204	0.200			0	0.1.0	
		Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of								
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		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	4.2271	0.4645	1754.61	1755.067	1	843.1	67.85714 K.SLKQYPKAKDALTKY.K
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.5338	0.2848	2759.65	2760.132	1	385.3	33.333336 L.TKNKLSLHEPYTVEGVSPDDLMLTA.C
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.291	0.273	1421.73	1422.671	3	113.4	55 T.SDEVLKRRKKY.G
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.9207	0.241	1201.59	1202.425	2	452.5	70 R.K2K2K2G1L1D1A1I1D1K2A1.F
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gil6321430/refINP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	3	4,2392	0.3021	3186.44	3185.614	1	587.3	27.777779 LEFHPEDPVSKKVTAVVESPEGERIVCVK G
3-1		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-							
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	0	2 2002	0.0050	4070.00	4070 447	2	C10 1	
gilo321430[rei]ivr_011307.1]	1GL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.2003	0.3356	10/0.09	10/9.117	2	610.4	50 R.DGQLVEIFANEVVFGDILQ
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ret NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	1	2.3272	0.2606	1023.34	1024.036	1	420.3	62.5 A.D1F1V1E1N2A1D1G1F1.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.3186	0.1882	1186.71	1185.469	1	449.4	61.11111 M.FFVGPIQFVM.E
		cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.0444	0.273	1372.41	1372.518	4	453.4	66.66667 L.EDGTVIPTDGRIV.T
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.1359	0.3633	1460.47	1461.579	1	806.3	66.66667 T.A1V1V1E1S1P1E1G1E1R4I1V1C1.V
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gil6321430/refINP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4,1923	0.2678	1846.55	1844.029	1	644.6	65.625 L.QLEDGTVIPTDGRIVTE.D
3-1		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	_							
ail62214201rofIND_011E07_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	4 2442	0 2094	1962 61	1965 020	1	666.0	
gil0321430[rei]ivr_011307.1]	1GL006C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.2442	0.3964	1003.01	1865.029		000.9	65.625 E.Q2LTEIDIGTTVITIFTTIDIGTR4TVITIET.D
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		4 5070	0.0040	1005 17	4000 000		005.4	
gi 6321430 ret NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.5373	0.3846	1635.47	1632.808	1	685.1	71.42857 L.Q2L1E1D1G111V111P111D1G1R4I1V1.1
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Please membrane H. ATPase, numbe protone out of the cells major regulator of	2	4.1802	0.2814	2690.03	2690.098	1	592.3	41.666664 T.A1V1V111R4D1G1Q2L1V1E111P1A1N2E1V1V1P1G1D111L1Q2L1.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.37	0.3231	1618.57	1616.786	1	639.2	50 A.ERLGLGGGGDMPGSELA.D
		Plasma membrane H+-A Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.4466	0.1725	1563.41	1564.708	1	679.9	60.000004 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.2741	0.3558	2279.51	2277.427	2	389.3	39.473686 G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1S1.D
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP 011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4.0462	0.3767	1902.25	1901.052	1	663.1	52.77778 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1.V
3.1		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gil6321430/rofIND_011507_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	6 3042	0 4206	2248 57	2247 403	1	720.1	52 380955 A E1R4I 1G1I 1G1C1C1C1C1D1M1R1G1S1E1I 1A1D1E1V1E1N2 A
gilosz1430/rei/Mr_011307.1]	TGL000C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	0.3342	0.4200	2240.07	2247.403	'	725.1	
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		4 0040	0.0000	007474	0070 507		505.0	
gijo321430/rei[NP_011507.1]	IGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.0010	0.2926	2274.71	22/3.59/		505.6	50 V.VIIIR4DIGIQ2EIVIEIIIPIAIN2EIVIVIPIGIDIIIEI.Q
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	2	3.2806	0.1711	1842.59	1842.941	1	947.3	52.77778 L.G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.4359	0.3068	2319.51	2319.482	1	439.6	38.636364 A.E1R4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1.D
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	6.1596	0.4726	2513.71	2511.684	1	2255.3	58.333332 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
		Plasma membrane H+-A Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	3	4.3238	0.4133	2656.22	2657.799	1	1134.4	31 A.E1R4L1G1L1G1G1G1G1D1M\$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	5.4497	0.4729	2657.41	2657.799	1	1025	42 A.E1R4L1G1L1G1G1G1G1D1M\$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP 011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	1	2.6392	0.2081	1038.58	1038.293	2	455.3	62.5 F.FVGPIQFVM.E
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507_1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	6 1747	0 4699	2642 75	2641 799	1	1351.2	48 A E1R4I 1G1I 1G1G1G1G1G1D1M1P1G1S1E1I 1A1D1E1V1E1N2A1D1G1E1 A
gilooz i ioolioiliii _orroorrii	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-	0.11 11	0.1000	2012.10	2011.00		100112	
ail6321430/refIND_011507_4	YGI 008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases: Pma1p	2	4 3002	0 2724	1969 47	1060 267	1	760.3	58 823532 G O2I 1V1E1I1D1A1N2E1V1V1P1C1D111I 1O2I 1 E
91002 140010110F_011007.1	101000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.3082	0.2131	1303.47	1303.207	'	100.5	OUR CONTRACTOR CONTRACTOR OF A CONTRACTOR OFTA CONT
	VOLCOOO	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	~	0 4044	0 100-	0000 07	0007 007		4750.0	
gijo321430[ret]NP_011507.1]	rGL008C	uansporung ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	6.4014	0.4927	2239.37	2237.337	1	1758.3	จข.ขขขขช L.G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	6.2003	0.5011	2214.45	2213.337	1	1627.8	56.81818 L.GLGGGGDMPGSELADFVENADGF.A

		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP 011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4.7356	0.3215	2348.65	2346.729	1	1084.7	61,904762 A.VVIRDGQLVEIPANEVVPGDIL.Q
9.100-1.001.001.00 _0.0000.01		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gil6321430/rofIND_011507_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3 2233	0 2216	1106 22	1106 /60	1	1195 3	83 33333 M E1E11/1G1P111O2E1//1M1 E
giloo21400[101141_011001.1]	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	0.2200	0.2210	1150.20	1150.405		1100.0	
-100044001(IND-04450741	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0.0000	0 4705	1105 57	4400 400		457.0	
gil6321430/ret/NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	1	2.2302	0.1735	1195.57	1196.469	1	457.2	61.11111 M.F1F1V1G1P111Q2F1V1M1.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+ATPase, pumps protons out of the cell; major regulator of	2	3.2639	0.3472	1518.09	1519.674	2	300.9	62.5 V.V1E1S1P1E1G1E1R4I1V1C1V1K2.G
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	3	6.2375	0.4112	2320.88	2321.381	1	2223.1	48.61111 K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.V
		Plasma membrane H+-A Pase, pumps protons out of the cell; major regulator of cvtoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.7079	0.4037	1302.74	1303.433	4	230.2	53.846157 E.RLGLGGGGDMPGSE.L
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.5913	0.3176	1318.47	1320.433	8	222	53.846157 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1.L
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP 011507.1	YGL008C	transporting ATPases; Pma1p	2	3.8429	0.4462	1603.93	1602.759	1	537.6	59.375 E.RLGLGGGGDMPGSELAD.F
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507_1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	5 9716	0 4285	2262.69	2263 403	1	1226.9	54 761906 & E1R4I 1G1I 1G1G1G1G1G1D1M\$P1G1S1E1I 1A1D1E1V1E1N2 A
gilooz i ioolioilui _oriooriii	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-	0.07.10	0.1200	2202.00	2200.100	· ·	1220.0	
ail6221420IrofIND_011507.1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	2 6750	0 1910	2402 12	2402 729	2	212.0	25 71 4297 \/ \/114 P4P1C1O2L4\/4E414P1A4N2E4\/4\/4P1C1P1414L4O2L
gil0321430[lei]NF_011307.1]	IGLUUGC	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.07.59	0.1019	2403.13	2403.728	2	312.9	35./1426/ V.VIIIR4DIGIQ2EIVIEIIIFIAIN2EIVIVIFIGIDIIIEIQ2.L
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ret NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: maior regulator of	2	3.4081	0.3673	2034.09	2035.305	1	635.8	58.333332 I.RDGQLVEIPANEVVPGDIL.Q
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	2	5.2241	0.3724	2306.55	2305.455	1	1185.4	52.272724 E.R4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1.G
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.6691	0.3941	2302.63	2303.595	1	684.2	50 I.R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	5.2285	0.3773	2628.57	2627.799	1	591.1	40 A.ERLGLGGGGDM@PGSELADFVENADGF.A
		Plasma membrane H+-A Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.6301	0.2685	1368.56	1368.495	1	493.1	59.090908 A.GLSDWVDFGVIC.G
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cutoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.4887	0.3164	2516.89	2517.887	1	593.5	43.18182 V.V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.9549	0.3374	2064.87	2065.126	1	662.1	42.5 L.G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP 011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4.227	0.3604	2614.69	2611.799	1	876.3	40 A.ERLGLGGGGDMPGSELADFVENADGF.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507_1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4 9937	0.3288	2588 77	2588 02	1	810.2	50 A VVIRDGOI VEIPANEVVPGDILOL E
gilooz i ioolioilui _oriooriii	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-		0.0200	2000.11	2000.02	· ·	010.2	oo har the ode ten hare the obledele
ail6221420IrofIND_011507.1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	1	2 402	0.2502	1264 70	1265 560	-	202.0	
gilos21450/101/107.1	IGLUUGC	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	1	2.492	0.2502	1304.70	1303.309	5	302.9	45.653530 I.FAINEVVFGDILQLE
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ret NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: maior regulator of	1	2.9994	0.2341	1381.93	1380.569	1	479.4	58.333332 I.P1A1N2E1V1V1P1G1D111L1Q2L1.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	3	5.5851	0.2271	2616.5	2618.02	1	1108.7	41.304348 A.V1V111R4D1G1Q2L1V1E111P1A1N2E1V1V1P1G1D111L1Q2L1.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	3	4.5814	0.2899	2587.22	2588.02	7	568.8	30.434782 A.VVIRDGQLVEIPANEVVPGDILQL.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	5.2071	0.4869	1752.53	1749.936	1	1226	73.52941 E.RLGLGGGGDMPGSELADF.V
		cvtoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	5.4743	0.156	2619.55	2618.02	1	887.8	50 A.V1V111R4D1G1Q2L1V1E111P1A1N2E1V1V1P1G1D111L1Q2L1.E
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	6.2073	0.5407	1772.33	1770.936	1	1629.2	79.411766 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1.V
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.365	0.4127	1509.33	1506.671	2	840.6	70 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.6288	0.3274	2057.71	2059.233	1	993.8	64.70589 E.A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cycopiasmic pri and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3.3152	0.2371	1419.17	1416.592	1	925.1	75 E.RLGLGGGGDMPGSEL.A
– .		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP 011507.1	YGL008C	cycopiasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4.0031	0.298	1717.89	1717.028	2	855.7	56.25 A.A1D111V1F1L1A1P1G1L1S1A11111D1A1L1.K
/										

		Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3.6757	0.3078	1701.45	1700.028	1	1128.7	65.625 A.ADIVFLAPGLSAIIDAL.K
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430 refINP 011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4.0582	0.4519	1487.29	1487.671	1	950.2	70 E.RLGLGGGGDMPGSELA.D
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3.5315	0.2311	1432.45	1434,592	1	935.9	75 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1.A
gilooz i loolioiliti _oriooriil	.020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-	0.0010	0.2011	1102.10	1101.002		000.0	
ail6321430/refINP_011507_1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	3 1349	0 1695	1035 17	1033 086	2	771.2	
gilo321430[rei]14: _011307.1]	IGLOUDE	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.1545	0.1035	1055.17	1033.000	2	111.2	01.5 E.AVDIATI GDQ.1
ail6221420/rofIND_011E07_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	2 2406	0.2156	1045 71	1046 086	2	772.0	97 5 L A1//1D1//2U2/1C1D1O2 T
gilo321430/rei/inP_011507.1	IGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.2490	0.2156	1045.71	1046.086	3	113.9	87.5 LATVIDIKZH3TIGIDIQ2.1
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	2	3.906	0.3139	1319.13	1318.427	2	618	70.83333 M.T1G1D1G1V1N2D1A1P1S1L1K2K2.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	1	2.6697	0.287	1248.52	1249.465	3	509.4	60.000004 Q.MADEKESLVVK.F
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.5267	0.1938	1392.58	1392.596	1	107.7	59.090908 N.Q2M1A1D1E1K2E1S1L1V1V1K2.F
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.2045	0.2932	1966.45	1966.028	1	428.5	53.333336 E.EDHPIPEDVHENYENK.V
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.3159	0.3604	1988.09	1989.028	1	544.4	60.000004 E.E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.V
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP 011507.1	YGL008C	transporting ATPases; Pma1p	2	4.5526	0.3475	2218.31	2219.276	1	1287.6	61.764706 T.V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.V
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	5.6678	0.475	2074.23	2075.161	1	1382.6	65.625 L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1.E
3.1		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-							
ail6321430/refINP_011507_1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	5 0485	0 5013	2051.07	2052 161	1	1617 7	
	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	0.0400	0.0010	2001.07	2002.101		1017.7	
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	0	4 0000	0.4000	0.400.04	2402 502		c 20 2	
gilo321430/rei/inP_011507.1	IGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.2030	0.4266	2492.91	2493.592		028.Z	47.5 K.11VTETETDTH3PTTPTETDTVTH3ETN2TTETN2K2VTAT.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	1	2.355	0.1638	1032.57	1033.21	2	371.5	68.75 G.SIVDELKKT.L
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	3.3552	0.3543	1203.54	1203.34	2	315.8	72.22222 L.EFHPFDPVSK.K
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	3.3367	0.4155	1505.66	1506.671	1	355.8	56.666668 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
		Plasma memorane H+-A Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.9072	0.2169	1417.65	1416.592	2	320.3	57.14286 E.RLGLGGGGDMPGSEL.A
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	3.6008	0.5161	1488.84	1487.671	1	353.4	56.666668 E.RLGLGGGGDMPGSELA.D
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.1088	0.3375	1934.47	1936.128	1	554.7	53.125 E.ARPVPEEYLQTDPSYGL.T
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430 refINP 011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4.2196	0.2764	1956.43	1957.128	1	703.6	59.375 E.A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1.T
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	5.436	0.525	1786.23	1786.936	1	1312.8	79.411766 E.R4L1G1L1G1G1G1G1G1D1M\$P1G1S1E1L1A1D1F1.V
gilooz i loolioiliti _oriooriil	.020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-	0.100	0.020	1100.20	1100.000		1012.0	
ail6321/30/rofINP_011507_1	VGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	5 0524	0.5347	2134 57	2122 288	1	2242.2	72 5 E P/I 1011 101010101010101010151511 1010151//15100 0
gilos21430/101/10F_011507.1	IGLUUGC	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	0.9024	0.5547	2134.37	2133.200		2242.2	72.5 E.R4EIGTEIGIGIGIGIGIDIMOFIGISTEIEIAIDIFIVIEINZ.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	0	5 0000	0.4000	0407.57	24.00 200		4000	
gilo321430/rei/inP_011507.1	IGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.6933	0.4896	2107.57	2108.288		1623	10 E.RLGLGGGGDM@PGSELADFVEN.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	3.4484	0.4294	1863.49	1865.069	1	512.8	47.22222 E.RLGLGGGGDM@PGSELADFV.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	2	6.5195	0.4779	2117.37	2117.288	1	1322.9	67.5 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	5.9348	0.4672	2091.55	2092.288	1	1671.5	77.5 E.RLGLGGGGDMPGSELADFVEN.A
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	6.2265	0.3511	2003.01	2001.184	1	836	65.789474 E.R4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1.N
		Plasma membrane H+-ALPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.6024	0.3585	1979.53	1978.184	1	760.1	63.15789 E.RLGLGGGGDMPGSELADFVE.N
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.5831	0.3588	2496.73	2494.681	1	409.9	40.476192 L.EDGTVIPTDGRIVTEDCFLQID.Q

		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+ATPase, pumps protons out of the cell-major regulator of	2	3.3435	0.2815	2523.17	2520.681	1	266.6	35.714287 LE1D1G1T1V111P1T1D1G1R4I1V1T1E1D1C1F1L1Q2I1D1.Q
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of advalgement is bit and plasma membrane potential; and of the P3 subgroup of entire	2	4.1058	0.1649	2172.23	2173.464	1	699.4	52.63158 V.I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1.Q
gi 6321430 ref NP_011507.1	YGL008C	Programme provide the international protection of the second protection	2	3.6566	0.2748	1849.15	1849.069	1	435.4	50 E.RLGLGGGGDMPGSELADFV.E
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.901	0.4663	1868.45	1871.069	1	1324.4	72.22222 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1.E
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.2275	0.2659	2148.45	2148.464	1	795.4	57.894737 V.IRDGQLVEIPANEVVPGDIL.Q
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase. pumps protons out of the cell: maior regulator of	2	4.8872	0.4233	2280.45	2278.455	1	695	43.18182 E.RLGLGGGGDMPGSELADFVENAD.G
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H_+ATPase, pumps protons out of the cell: major regulator of	3	4.2546	0.3264	2186.87	2189.367	2	773.8	30.952381 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1.D
	VCLOORC	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	4 40 47	0.0045	2000 74	2000 070		105.0	
gij6321430/ret NP_011507.1	YGL008C	transporting A Pases; Fmarp Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	4.1647	0.3815	2696.71	2698.878	1	495.6	30.769232 E.KLGLGGGGDM@PGSELADFVENADGFAE.V
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	4.6563	0.3336	2497.61	2498.684	1	1196.1	43.75 E.RLGLGGGGDM@PGSELADFVENADGF.A
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytrolasmic pH and plasma membrane potential; part of the P2 subarrun of cation-	2	4.1984	0.4845	2727.61	2729.878	1	730.2	36.53846 E.R4L1G1L1G1G1G1G1D1M\$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.V
gi 6321430 ref NP_011507.1	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of enterland the cell major regulator of plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of enterland cell and other acceptence patiential beat of the D0 sub-regulator of enterland cell and other acceptence patiential beat of the D0 sub-regulator of enterland cell and other acceptence patiential beat of the D0 sub-regulator of enterland cell and other acceptence patiential beat of the D0 sub-regulator of enterland cell and other acceptence patiential beat of the D0 sub-regulator of enterland cell and the D0 sub-regulator of the D0 sub-regulator of enterland cell and the D0 sub-regulator of the D0 sub-regulator of enterland cell and the D0 sub-regulator of the D0 sub-regulator of enterland cell and the D0 sub-regulator of the D0 sub-regulator of enterland cell and the D0 sub-regulator of the D0 sub-regulator of enterland cell and the D0 sub-regulator of the D0 sub-regulator of enterland cell and the D0 sub-regulator enterland cell and the D0 sub-regu	2	3.2968	0.3602	2582.11	2583.763	1	268.3	28 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1.E
gi 6321430 ref NP_011507.1	YGL008C	Programme provide the providet	3	5.9485	0.3954	2713.91	2713.878	1	1362.5	35.576923 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.V
gi 6321430 ref NP_011507.1	YGL008C	cycoptastine pri and plasma memorane polential, part of the P2 subgroup of callon- transporting ATPases, Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	4.4571	0.4071	2681.96	2682.878	1	1205.5	33.653847 E.RLGLGGGGDMPGSELADFVENADGFAE.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic PH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	4.4412	0.3383	4244.12	4242.814	1	452.6	17.948719 T.AVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGRIVTE.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.2951	0.5394	2715.89	2713.878	1	1353.1	44.230766 E.R4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.8468	0.4298	2189.33	2189.367	1	1432.6	61.904762 E.R4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.6226	0.4634	2527.51	2527.684	1	1510.7	52.083332 E.R4L1G1L1G1G1G1G1G1D1M\$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.565	0.381	2484.97	2482.684	1	2298.6	60.416668 E.RLGLGGGGDMPGSELADFVENADGF.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.0423	0.2745	1247.91	1248.323	2	325.9	70 E.S1L1A1V1D1K2H3Y1G1D1Q2.T
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	6.1799	0.4322	2451.39	2451.555	1	2246.9	65.789474 L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.5391	0.347	2195.51	2194.276	1	1613.8	67.64706 T.VEEDHPIPEDVHENYENK.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.2568	0.3814	2323.27	2321.381	1	1058.5	52.77778 K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	5.5737	0.4735	2293.28	2295.381	1	2179.7	48.61111 K.TVEEDHPIPEDVHENYENK.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.3125	0.3257	1604.39	1601.807	1	572.2	57.692307 A.VVESPEGERIVCVK.G
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase. pumps protons out of the cell: maior regulator of	1	2.9138	0.1685	1345.62	1346.514	7	244.9	60.000004 L.E1F1H3P1F1D1P1V1S1K2K2.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, numes protons out of the cell: major regulator of	2	4.5266	0.4292	1690.73	1691.885	1	1045.1	64.28571 T.A1V1V1E1S1P1E1G1E1R4I1V1C1V1K2.G
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, nums protons out of the cell: maior regulator of	2	4.0493	0.4455	1670.83	1672.885	1	1471.2	71.42857 T.AVVESPEGERIVCVK.G
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons cut of the cell: major regulator of	2	3.7301	0.4181	1772.43	1773.99	1	1069	60.000004 V.TAVVESPEGERIVCVK.G
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic inclusion internet mass, painty protons out on the cell, integrin regulation of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: maior regulator of	2	4.3877	0.3833	1792.55	1793.99	1	1140.3	60.000004 V.T1A1V1V1E1S1P1E1G1E1R4I1V1C1V1K2.G
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4.2	0.3389	2809.75	2809.946	1	484.6	41.304348 K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2V1A1E1L1A1.S

		Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	1	2.6246	0.1557	1415.34	1415.632	4	434.6	63.636364 K.VLEFHPFDPVSK.K
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.938	0.3039	1430.99	1430.632	1	860.3	77.27273 K.V1L1E1F1H3P1F1D1P1V1S1K2.K
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.017	0.1868	1987.45	1987.155	1	411.2	50 A.R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.3142	0.4077	2206.55	2205.367	1	921.9	52.380955 E.R4L1G1L1G1G1G1G1G1D1M\$P1G1S1E1L1A1D1F1V1E1N2A1.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase numps protons out of the cell: major regulator of	2	3.805	0.4006	2180.01	2179.367	1	494.8	38.095238 E.RLGLGGGGDM@PGSELADFVENA.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the PS subgroup of cation- transporting ATPases; Pma1p	2	5.3931	0.4716	2164.97	2163.367	1	1385.1	64.28571 E.RLGLGGGGDMPGSELADFVENA.D
gi 6321430 ref NP_011507.1	YGL008C	relation internotation (FFA) race, pumps protonts out or the cent, major regulation or cytoplasmic pH and plasma membrane potential; part of the P2 subport of cation- transporting ATPases; Pma1p	3	5.2648	0.4704	2524.73	2527.684	1	1955.8	37.5 E.R4L1G1L1G1G1G1G1D1M\$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
gi 6321430 ref NP_011507.1	YGL008C	Presima memorane new Al Pase, pumps protons out or the cen, major regulation or cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3.0929	0.3199	2658.07	2659.098	2	499.5	39.583336 T.AVVIRDGQLVEIPANEVVPGDILQLE
gi 6321430 ref NP_011507.1	YGL008C	events an animotane m-A1 Pase, pumps protons out or the cen, major regulator or cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3.0213	0.1711	2906.43	2908.307	1	371.2	32.692307 A.N2T1A1V1V111R4D1G1Q2L1V1E111P1A1N2E1V1V1P1G1D111L1Q2L1.E
gi 6321430 ref NP_011507.1	YGL008C	Plasma membrane H+-A1 Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	3	4.8472	0.3926	2498.93	2498.684	1	1876.2	37.5 E.RLGLGGGGDM@PGSELADFVENADGF.A
ail6321430/refINP 011507.1	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases: Pma1p	2	4.0695	0.3156	2793.13	2792.203	1	563	40 N.T1A1V1V111R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D111L1Q2L1.E
gil6221420[rof[NID_011507_1]	VCI 008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPacage: Denote	-	E 220E	0.2042	4210.22	4210 725	4	010 7	A.VIVIIIR4D1G102L1V1E1I1P1A1N2E1V1V1P1G1D1I1L102L1E1D1G1T1V1I1P1
	VOLODOC	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	3	5.2505	0.2943	4219.22	4219.755		010.7	
gi 6321430 ret NP_011507.1	YGL008C	transporting AI Pases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	3	4.8383	0.4035	4173.65	4171.735	1	1087.4	24.342104 A. VVIRDGQLVEIPANEVVPGDILQLEDG1 VIP1DGRIV1E.D
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	1	2.2223	0.1956	1211.72	1210.274	1	436.2	60.000004 E.L1A1D1F1V1E1N2A1D1G1F1.A
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	3	4.4574	0.3109	4114.94	4113.698	1	494.8	23.026316 N.TAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGRIV.T
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cutoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation.	3	5.1959	0.4286	2480.45	2482.684	1	1775.6	39.583336 E.RLGLGGGGDMPGSELADFVENADGF.A
gi 6321430 ref NP_011507.1	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	6.7465	0.3552	2511.8	2511.684	1	2552.9	42.708336 E.R4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
gi 6321430 ref NP_011507.1	YGL008C	cytopiasmic pH and piasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	6.1231	0.3847	3988.7	3987.514	1	760.8	A.VIVIIR401G102L1V1E111P1A1N2E1V1V1P1G10111L102L1E101G111V11P1 24.305555 T1D1G1R4I1V1.T
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	4.4591	0.3189	4280.03	4277.802	1	860.9	A.NZT1A1V1V111R4D1G1Q2L1V1E111P1A1N2E1V1V1P1G1D111L1Q2L1E1D1G1T1 22.435898 V111P1T1D1G1R4I1V1.T
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.3472	0.4003	3190.87	3190.435	1	467.5	E.R4L1G1L1G1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1V1F1P 35 1Q2.H
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+ATPase, pumps protons out of the cell; major regulator of	3	5.8191	0.416	3152.99	3154.435	1	545.2	30.833334 E.RLGLGGGGDMPGSELADFVENADGFAEVFPQ.H
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.2735	0.1645	1467.97	1466.754	5	339.3	63.636364 F.D1R4L1M1N2G1K2P1M1K2E1K2.K
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	6.0632	0.3211	2451.86	2451.555	1	3717.4	57.894737 L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.1231	0.3239	1192.53	1191.413	1	1279.6	80 K.GLDAIDKAFLK.S
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase. pumps protons out of the cell: major regulator of	3	4.5097	0.349	4162.88	4161.698	1	963.1	N.T1A1V1V11R4D1G102L1V1E1I1P1A1N2E1V1V1P1G1D1I1L102L1E1D1G1T1V1 23.684212 IIP1T1D1G1R4I1V1.T
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P22-sbagroup of cation- transporting ATPases; Pma1p Plasma membrane Hu-ATPase, numes protons out of the cell: major regulator of	3	5.1408	0.4037	3941.69	3941.514	1	711.1	25 A. VVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGRIV.T
gi 6321430 ref NP_011507.1	YGL008C	relation inclination for the relation points proton of the doministry of regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, nums protons out of the cell maior regulator of	2	3.5927	0.214	1335.93	1334.587	1	840.5	81.818184 K.K2G1L1D1A111D1K2A1F1L1K2.S
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	3.0849	0.2825	1319.65	1319.587	1	995.7	81.818184 K.KGLDAIDKAFLK.S
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	3.3824	0.21	1559.89	1560.806	1	559.4	62.5 K.V1L1E1F1H3P1F1D1P1V1S1K2K2.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	2.9106	0.2372	2330.21	2327.704	1	247.6	33.333336 A.A1D111V1F1L1A1P1G1L1S1A1111D1A1L1K2T1S1R4Q2.I

		Plasma membrane H+-ATPase numps protons out of the cell: major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	1	3.051	0.2285	1559.54	1560.806	1	425.9	58.333332 K.V1L1E1F1H3P1F1D1P1V1S1K2K2.V
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cycoplasmic pri and plasma memorane potential, part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.2274	0.269	1543.47	1543.806	1	855.7	70.83333 K.VLEFHPFDPVSKK.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	1	2.8486	0.272	1542.65	1543.806	1	568.2	62.5 K.VLEFHPFDPVSKK.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	5.0042	0.2417	2888.06	2888.179	1	1264.9	32.692307 Q.T1F1S1S1S1T1V1K2R4G1E1G1F1M1V1V1T1A1T1G1D1N2T1F1V1G1R4.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.4516	0.2304	1627.31	1624.905	1	1164	70.83333 Q.I1S1L1T1E1N2W2L1I1F1I1T1R4.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	1	2.5571	0.1598	1062.58	1063.285	8	408.7	68.75 K.SLKQYPKAK.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	4.202	0.1648	2851.85	2853.179	1	1032.5	30.769232 Q.TFSSSTVKRGEGFMVVTATGDNTFVGR.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.7098	0.3389	2177.37	2175.459	1	371.5	44.736843 T.R4A1A1G1P1F1W2S1S1I1P1S1W2Q2L1A1G1A1V1F1.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.0764	0.3088	2108.53	2109.451	1	275.5	37.5 A.A1R4S1A1A1D111V1F1L1A1P1G1L1S1A11111D1A1L1.K
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	4.8557	0.3957	2346.47	2343.663	1	1568	38.095238 S.TVKRGEGFMVVTATGDNTFVGR.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.478	0.3769	2343.59	2343.663	1	469.1	45.238094 S.TVKRGEGFMVVTATGDNTFVGR.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	1	2.7192	0.1748	1241.64	1242.393	1	431	66.66667 R.K2R4G1E1G1H3W2E111L1.G
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	6.0346	0.4266	2373.71	2373.663	1	2008.5	40.476192 S.T1V1K2R4G1E1G1F1M1V1V1T1A1T1G1D1N2T1F1V1G1R4.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	5.5935	0.4078	2517.11	2517.82	1	1818.2	40.217392 S.T1V1K2R4G1E1G1F1M1V1V1T1A1T1G1D1N2T1F1V1G1R4A1A1.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part or the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of advantage of the protocol state of the ADP constraint of the trans-	3	4.4035	0.2963	2484.53	2485.82	1	1737.7	41.304348 S.TVKRGEGFMVVTATGDNTFVGRAA.A
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part or the P2 subgroup or cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of autonomic and and phore accombing exploration act of the AD	2	3.1142	0.2755	1762.49	1761.127	1	403.4	43.75 L.R4Y1T1L1G111T1111G1V1P1V1G1L1P1A1.V
gi 6321430 ref NP_011507.1	YGL008C	cycipitastinic pri anicipitastinia memorarile potentinal, part or the PZ subgroup or cation- transporting ATPasses; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cataolastinic biL and plasma, asombrang, patotalic) act of the AP	2	3.6767	0.3196	2013.39	2014.373	1	610.1	42.105263 A.RSAADIVFLAPGLSAIIDAL.K
gi 6321430 ref NP_011507.1	YGL008C	cyclopiastic primaric plasma memorane potential, part of the riz sougroup of calculation transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cdrollasmic HL and plasma membrane potential: part of the P2 subgroup of calcula-	2	3.4395	0.379	2038.81	2037.373	1	514.4	42.105263 A.R4S1A1A1D111V1F1L1A1P1G1L1S1A11111D1A1L1.K
gi 6321430 ref NP_011507.1	YGL008C	cyclopiastic primaric plasma memorane potential, part of the riz sougroup of calculation transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cdrollasmic HL and plasma membrane potential: part of the P2 subgroup of calcula-	2	3.0517	0.3433	1555.53	1556.863	1	627.8	79.16667 L.M1N2G1K2P1M1K2E1K2K2S1T1R4.S
gi 6321430 ref NP_011507.1	YGL008C	cytophaning promo public international potential, part of the Liz baggiog of calculation transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the CP subroun of cation- cutoplasmic oH and plasma membrane potential: part of the CP subroun of cation-	2	3.608	0.1537	1574.73	1575.928	1	637.9	75 F.DRLMNGKPMKEKK.S
gi 6321430 ref NP_011507.1	YGL008C	expensions processing ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of extrolasmic cell and plasma membrane potential; part of the P2 subrorup of cation-	2	3.749	0.2348	1506.17	1506.671	2	740.9	63.333332 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cvtoolasmic oH and plasma membrane potentiai: part of the P2 suboroup of cation-	2	3.6337	0.3797	1488.37	1487.671	1	572.5	63.333332 E.RLGLGGGGDMPGSELA.D
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cvtoolasmic oH and plasma membrane potentiai: part of the P2 suboroup of cation-	2	3.0246	0.2108	1973.83	1973.084	4	273.3	43.75 A.G1E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1.G
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cvtoolasmic oH and plasma membrane potentiai: part of the P2 suboroup of cation-	1	2.7347	0.1609	1403.54	1404.52	1	264.2	59.090908 A.G1E1A1R4P1V1P1E1E1Y1L1Q2.T
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	1	2.6209	0.3179	1387.58	1388.52	1	392.7	68.181816 A.GEARPVPEEYLQ.T
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	1	2.8051	0.2079	1331.65	1331.468	4	184.8	60.000004 G.EARPVPEEYLQ.T
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	1	2.3873	0.236	1273.56	1274.389	3	189.3	55 A.G1E1A1R4P1V1P1E1E1Y1L1.Q
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic, pH and plasma membrane potential; part of the P2 subgroup of cation-	2	2.9718	0.1747	1275.45	1274.389	2	533.9	70 A.G1E1A1R4P1V1P1E1E1Y1L1.Q
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	1	2.2622	0.1667	1202.46	1203.337	2	213.3	61.11111 G.EARPVPEEYL.Q
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.5237	0.2125	1614.97	1614.852	1	608.3	67.85714 T.A1V1V111R4D1G1Q2L1V1E1I1P1A1N2.E

		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3.4799	0.3942	2008.09	2009.136	1	714.5	55.88235 A.GEARPVPEEYLQTDPSYG.L
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3.2647	0.2619	1971.75	1973.084	1	330.5	46.875 G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1.L
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4.0932	0.3271	1912.33	1915.033	1	803.9	63.333332 G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1.G
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430 refINP 011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	3	4.2059	0.3298	2189.72	2189.349	1	708.5	37.5 G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
3/1		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507_1	YGI 008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	4 6328	0 3743	2123.31	2122 296	1	797 9	58 333332 A GEARPVPEEYLOTDPSYGL T
gilooz i loofiolful _o i loofiolful	1020000	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	-	1.0020	0.07 10	2120.01	2122.200	·	101.0	
ail6221420IrofIND_011507_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	E 1900	0 2025	2097.07	2097 244	1	070.2	
gil0321430[101]NF_011507.1]	1GL006C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.1699	0.3925	2007.97	2007.244	'	970.5	
ail6221420kofIND_011507_1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	2 9205	0.2410	2029 15	2020 222	1	505	
gilb321430/rei/NP_011507.1	IGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.8295	0.3419	2028.15	2029.322	'	505	52.77778 A.VIVIIIR4DIGIQ2EIVIEIIIPIAIN2EIVIVIPIGI.D
- 10004 4001 - (INID: 044 507 4)	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		1 00 10	0.440	0004 70	0000 404		700.4	
gil6321430/ret/NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.3919	0.412	2224.73	2223.401	1	769.1	55.263157 A.GEARPVPEETLQTDPSTGLT.S
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ret NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	3.6553	0.1688	2030.63	2029.248	1	1100.6	58.333332 R.D1G1Q2L1V1E111P1A1N2E1V1V1P1G1D111L1Q2.L
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, numps protons out of the cell: major regulator of	2	5.1626	0.4324	2189.27	2189.349	1	996.7	61.11111 G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	3.6726	0.3306	1782.21	1780.811	1	638.4	53.571426 K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2.Y
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell: major regulator of	2	2.9231	0.3649	1593.53	1594.634	1	721	66.66667 E.EDHPIPEDVHENY.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+ATPase, pumps protons out of the cells major regulator of	2	4.4543	0.4292	2191.25	2191.207	1	1412.3	64.70589 K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2.K
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.3909	0.4159	1924.09	1923.987	1	1062.2	63.333332 K.TVEEDHPIPEDVHENY.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.751	0.432	1945.27	1944.987	1	859.7	56.666668 K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1.E
		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	3.135	0.1944	1345.54	1346.468	5	131.2	50 G.E1A1R4P1V1P1E1E1Y1L1Q2.T
		Plasma memorane H+-A I Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	2.9633	0.1577	1441.61	1442.64	5	325.7	58.333332 V.V1I1R4D1G1Q2L1V1E1I1P1A1N2.E
		Plasma memorane H+-A I Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.7195	0.1787	1672.85	1672.888	4	523	67.85714 A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1.V
		Plasma membrane H+-A I Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.9197	0.2988	1635.61	1636.786	1	957.5	62.5 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
		Plasma membrane H+-A Pase, pumps protons out of the cell; major regulator of cvtoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.8077	0.4506	2064.83	2065.244	1	1255	67.64706 G.EARPVPEEYLQTDPSYGL.T
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.3769	0.3602	2003.87	2005.322	1	389	50 A.VVIRDGQLVEIPANEVVPG.D
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	5.5414	0.3939	2420.25	2417.808	1	1137.7	61.363636 T.AVVIRDGQLVEIPANEVVPGDIL.Q
		Plasma membrane H+-A Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	5.4073	0.427	2373.45	2373.729	1	889.1	57.14286 A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1.Q
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.8161	0.3862	2520.15	2518.913	1	529.4	45.652176 N.TAVVIRDGQLVEIPANEVVPGDIL.Q
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	3.118	0.223	1261.44	1262.465	1	687.9	70 Q.M1A1D1E1K2E1S1L1V1V1K2.F
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	1	2.7229	0.258	1248.39	1249.465	1	607.5	65 Q.MADEKESLVVK.F
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	3.8879	0.3118	1909.53	1910.985	1	885.3	60.000004 L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2.Y
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of action								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	2	4.9021	0.2629	1508.45	1508.7	1	1323.2	87.5 L.N2Q2M1A1D1E1K2E1S1L1V1V1K2.F
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of action								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	3	6.0691	0.3926	2451.65	2451.555	1	2268.6	46.05263 L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.V
		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation.								
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p	3	5.3803	0.3683	2422.79	2423.555	1	2073.7	46.05263 L.KTVEEDHPIPEDVHENYENK.V

		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	5.7719	0.4294	2073.47	2075.161	1	1479.1	65.625 LK2T1V1E1E1D1H3P111P1E1D1V1H3E1N2Y1.E
		Plasma memorane H+-A I Pase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential: part of the P2 subgroup of cation-								
gi 6321430 ref NP_011507.1	YGL008C	Programme prime present memorane potential, part of the P2 subgroup of calloine transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.649	0.2395	2623.19	2623.766	1	281.1	35.714287 LK2T1V1E1E1D1H3P111P1E1D1V1H3E1N2Y1E1N2K2V1A1.E
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.6473	0.3335	1842.07	1842.882	1	756.5	57.14286 T.V1E1E1D1H3P111P1E1D1V1H3E1N2Y1.E
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase numps protons out of the cell: major regulator of	2	3.1426	0.4158	1302.73	1303.433	1	684	76.92308 E.RLGLGGGGDMPGSE.L
gi 6321430 ref NP_011507.1	YGL008C	vabilitation in the second sec	1	2.8753	0.3638	1302.36	1303.433	1	238.4	53.846157 E.RLGLGGGGDMPGSE.L
gi 6321430 ref NP_011507.1	YGL008C	vabilitation in the second sec	1	3.0808	0.184	1417.57	1418.593	2	400.5	59.090908 Y.D1N2A1P1Y1S1P1K2P1V1K2W2.N
gi 6321430 ref NP_011507.1	YGL008C	relation include the time area points provide or of the contribution or guidater of cytoplasmic pH and plasms membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	1	3.0087	0.2655	1402.55	1402.593	1	395.6	59.090908 Y.DNAPYSPKPVKW.N
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	2	3.1095	0.3507	1504.33	1503.671	1	479.9	56.666668 E.RLGLGGGGDM@PGSELA.D
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	1	2.5086	0.1925	1277.53	1278.449	1	523.4	65 M.A1D1E1K2E1S1L1V1V1K2F1.V
gi 6321430 ref NP_011507.1	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	1	3.8317	0.3033	1433.54	1434.592	1	432.3	64.28571 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1.A
ail6321430/refINP_011507.1	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transnorting ATPases: Pma10	1	3.4927	0.5199	1486.67	1487.671	1	262.6	50 F. RI GLGGGGDMPGSELA.D
ail6221420trofIND_011507.1	VCLOORC	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPage; Dep1.		2 091	0.2270	2057 80	2050 205		E1E 9	
	VOLODO	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	3.901	0.3279	2037.89	2009.000		515.6	T.A1VV111R401G102L1V1E11P1A1N2E1V1V1P1G1D111L102L1E1D1G1T1V11
gij6321430[rei]NP_011507.1]	TGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	3	4.4905	0.2225	4292.42	4291.814		505.6	19.230/7 PTTDTGTK4IIVTTET.D
gi 6321430 ref NP_011507.1	YGL008C	transporting AT Pases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	4.5537	0.4609	2683.33	2682.878	1	1385.7	46.153847 E.RLGLGGGGDMPGSELADFVENADGFAE.V
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	3	4.9779	0.3772	2712.11	2713.878	1	1294.6	33.653847 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.V
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	4.5428	0.4464	2422.35	2423.555	1	1085.3	60.526318 L.KTVEEDHPIPEDVHENYENK.V
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cvtoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	1	3.1453	0.2153	1332.55	1331.514	2	281.5	65 L.EFHPFDPVSKK.V
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cvtoolasmic oH and olasma membrane potential: part of the P2 subgroup of cation-	2	2.9311	0.2511	1402.17	1402.593	9	497.1	63.636364 Y.DNAPYSPKPVKW.N
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subarroup of cation-	2	4.2542	0.3642	1769.95	1769.007	1	1009.2	71.42857 A.I1A1Y1D1N2A1P1Y1S1P1K2P1V1K2W2.N
gi 6321430 ref NP_011507.1	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytonlasmic oH and plasma membrane notential; part of the PS subrorup of cation-	2	3.6587	0.3016	1428.37	1430.632	1	697.9	72.72727 K.V1L1E1F1H3P1F1D1P1V1S1K2.K
gi 6321430 ref NP_011507.1	YGL008C	Propriorities of the public transporting that are provided by the provided of the test of test	2	3.0859	0.1583	1873.31	1871.056	1	390.3	50 F.G1W2W2S1E1N2W2T1D1I1V1T1V1V1R4.V
gi 6321430 ref NP_011507.1	YGL008C	Provide the second seco	2	3.4791	0.2776	1409.55	1406.668	1	873.8	75 S.LTENWLIFITR.A
gi 6321430 ref NP_011507.1	YGL008C	exception and present present present and present and present and present and present present and present present and present	1	3.1081	0.1543	1559.57	1560.806	2	447.9	58.333332 K.V1L1E1F1H3P1F1D1P1V1S1K2K2.V
gi 6321430 ref NP_011507.1	YGL008C	Provide the provided the provid	1	2.7446	0.2994	1542.63	1543.806	1	590.9	62.5 K.VLEFHPFDPVSKK.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma memorane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.7002	0.2806	1546.53	1543.806	1	887.3	75 K.VLEFHPFDPVSKK.V
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	4.6149	0.3304	2453.93	2454.856	2	794.5	32.142857 A.V1V1E1S1P1E1G1E1R4I1V1C1V1K2G1A1P1L1F1V1L1K2.T
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+ATPase, pumps protons out of the cell; major regulator of	1	2.3987	0.2291	1195.54	1196.469	1	626.6	66.66667 M.F1F1V1G1P1I1Q2F1V1M1.E
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	2.9276	0.295	1195.43	1196.469	1	1037.7	77.77778 M.F1F1V1G1P111Q2F1V1M1.E
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.7997	0.4109	2145.47	2145.296	1	735.9	58.333332 A.G1E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1.T
gi 6321430 ref NP_011507.1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases; Pma1p	1	2.2839	0.2518	1460.45	1461.579	3	349.7	45.833336 T.A1V1V1E1S1P1E1G1E1R4I1V1C1.V

		Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of								
ail6321430/refINP_011507_1	YGL008C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation- transporting ATPases: Pma1p	2	3 1325	0 2034	1308.63	1308 567	1	460.8	80 N G1K2P1M1K2E1K2K2S1T1R4 S
gilo321430[rei]14F_011307.1]	TGL000C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	5.1525	0.2034	1300.03	1300.307		400.0	00 N.O NZP IM NZE NZNZOTI N4.0
ail6221420/rofIND_011507.1		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	1	2 2646	0 2226	1441 69	1440 671	2	100	55 T \$1D151/41 1K2D4D4K2K2X1 C
gilo21430[rei]14F_011307.1]	TGL000C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of		2.3040	0.2330	1441.00	1442.071	2	103	33 1.31D1E171E17214(4)(2)(2)1.3
ail6221420/rofIND_014507.41		cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	2 445	0.2494	1400.05	1501 77	1	056.7	
gilo321430[ter]NF_011507.1]	1GL006C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.445	0.3401	1499.93	1501.77		950.7	09.230/74 A.ASKKKKGLDAIDKA.F
-: 10204 4201 (IND 044507 4)	VCI 000C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0.0500	0 0000	4500 70	4504 77		250	
gilo321430[rei]NP_011507.1]	IGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	1	2.9528	0.3282	1500.76	1501.77	1	350	53.646157 A.ASRKKKGLDAIDKA.F
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0 7005	0 4745	1500.00	1500 77		400.0	
gij6321430[ref]NP_011507.1]	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	1	2.7935	0.1745	1520.69	1522.77	2	403.3	57.692307 A.A1S1R4K2K2K2G1L1D1A111D1K2A1.F
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0 0001	0.0040	4504.05	1500.000	-		
gij6321430[ref]NP_011507.1]	YGL008C	transporting ATPases; Pma1p Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	1	2.6021	0.3043	1594.85	1592.882	5	96.9	45.833336 T.SDEVLKRRKKYGL.N
-: 10204 4201 4IND 044507 41	VCI 000C	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-	2	4 4705	0.0004	0000 75	0000 500		450.4	
gilo321430[rei]NP_011507.1]	IGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	4.1725	0.3064	2208.75	2209.533	1	452.4	52.941177 Y.DINZAIPITISIPIKZPIVIKZWZNZEIPIR4EIWZ.G
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		4 000 4	0.0004	0000 7	0000 500		000.0	
gij6321430[ref]NP_011507.1]	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	4.6894	0.3981	2206.7	2209.533	1	809.6	41.17647 Y.D1NZA1P1Y1S1P1K2P1V1K2W2N2L1P1R4L1W2.G
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0.045	0.0700	0101 50	0400 500		170.0	
gij6321430[ref]NP_011507.1]	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.645	0.3729	2181.53	2182.533	1	479.9	52.941177 Y.DNAPYSPKPVKWNLPRLW.G
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0.0070	0 0707	0100.00	0400 500		007.0	
gij6321430[ref]NP_011507.1]	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	3	3.8872	0.2787	2180.63	2182.533	1	687.2	39.705883 Y.DNAPYSPKPVKWNLPRLW.G
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0 1010	0.0070	0074 07	0070 700		005.0	
gij6321430[ref]NP_011507.1]	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of	2	3.1813	0.3078	23/1.2/	2373.709	1	295.8	44.444447 A.Y1D1N2A1P1Y1S1P1K2P1V1K2W2N2L1P1R4L1W2.G
	VOI 0000	cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-		0.01.10	0.0454	0070.00	0070 700		550 7	
gij6321430[ref]NP_011507.1]	YGL008C	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants	3	3.8148	0.2454	2373.02	2373.709	1	558.7	40.27778 A.Y1D1N2A1P1Y1S1P1K2P1V1K2W2N2L1P1R4L1W2.G
gi 6321426 ref NP_011503.1	YGL012W	are viable, but lack ergosterol; Erg4p	2	4.0888	0.2085	1730.09	1729.974	1	729.6	67.85714 Q.GEEKKSKQPVNFLPQ.G
gi 6321426 ref NP_011503.1	YGL012W	are viable, but lack ergosterol; Erg4p	2	3.4601	0.3542	1968.75	1970.189	1	588.3	46.875 Q.GKWLKPNEIEYEFGGTT.G
ail6321426/rofIND_011503_1	VGI 012W/	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants	2	3 0680	0 2238	1080.63	1001 180	1	370 /	40 625 O C1K2W2I 1K2P1N2E1I1E1X1E1E1C1C1C1T1T1 C
gilooz i izolioiliti _orriooorij	10201211	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants	-	0.0000	0.2200	1000.00	10011100	•	0.0.1	
gi 6321426 ref NP_011503.1	YGL012W	are viable, but lack ergosterol; Erg4p C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants	2	3.2942	0.3303	1209.37	1208.406	1	598.9	81.25 F.F1E1V1R4L1P1W2F1T1.L
gi 6321426 ref NP_011503.1	YGL012W	are viable, but lack ergosterol; Erg4p	2	3.4525	0.3258	1755.47	1755.056	9	360	46.42857 Y.D1F1F1M1G1A1P1L1N2P1R4W2G1I1L1.D
gi 6321426 ref NP_011503.1	YGL012W	c-24(28) steroi reductase, catalyzes the final step in ergosteroi biosynthesis; mutants are viable, but lack ergosterol; Erg4p	2	2.9107	0.1987	1309.93	1308.566	1	673.2	77.77778 F.FEVRLPWFTL.Y
gi 6321426 ref NP 011503.1	YGL012W	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants are viable, but lack ergosterol; Erg4p	1	2.3119	0.1644	1324.01	1325.615	1	534.7	63.636364 F.MGAPLNPRWGIL.D
ail6221426irofIND_011502.1	VCI 012W	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants	2	2 0297	0 2021	1000.07	1225 615	1	1022.2	
gilo321420[10]14F_011503.1]	IGLUIZW	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants	2	2.9307	0.2031	1323.07	1323.015	1	1023.3	00.30304 F.INGAFLINFRWGILD
gi 6321426 ref NP_011503.1	YGL012W	are viable, but lack ergosterol; Erg4p C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants	2	4.0371	0.1621	1750.67	1750.974	1	546.1	57.14286 Q.G1E1E1K2K2S1K2Q2P1V1N2F1L1P1Q2.G
gi 6321426 ref NP_011503.1	YGL012W	are viable, but lack ergosterol; Erg4p	2	3.2321	0.2355	1489.45	1490.791	2	447.8	66.66667 F.F1M1G1A1P1L1N2P1R4W2G1I1L1.D
gi 6321426 ref NP_011503.1	YGL012W	are viable, but lack ergosterol; Erg4p	2	3.3418	0.2731	1475.27	1472.791	1	476.3	70.83333 F.FMGAPLNPRWGIL.D
gil6321426lrefINP_011503.11	YGL012W	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants are viable, but lack ergosterol: Erg4p	2	3.3813	0.1831	1865.83	1867.154	1	413.2	60.000004 Q.M1S1G1D1K2T1G1R4K2T1F1P1F1L1P1Y1.Q
3.1		C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants								
gi 6321426 ref NP_011503.1	YGL012W	are viable, but lack ergosterol; Erg4p Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster	2	4.0675	0.2775	1844.91	1846.154	1	494.6	60.000004 Q.MSGDKTGRKTFPFLPY.Q
		proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of								
gi 6321425 ref NP_011502.1	YGL013C	multidrug resistance genes; Pdr1p Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster	3	5.2023	0.1587	3486.47	3483.829	8	402.1	25 S.NIDDSKINCLLPKNFRDVGFLDNRDFIEN.V
		proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of								
gi 6321425 ref NP_011502.1	YGL013C	multidrug resistance genes; Pdr1p Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster	3	5.6455	0.3092	1971.41	1971.188	1	1833.9	48.333332 V.G1F1L1D1N2R4D1F111E1N2V1H3L1V1R4.R
		proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of								
gi 6321425 ret NP_011502.1	YGL013C	Member of the PUF protein family, which is defined by the presence of Pumilio	3	4.959	0.2342	1946.87	1945.188	1	1409.1	45 V.GFLDNRDFIENVHLVR.R
		homology domains that confer RNA binding activity; preferentially binds mRNAs								
gi 6321424 ret NP_011501.1	YGL014W	Member of the PUF protein family, which is defined by the presence of Pumilio	2	3.4688	0.3143	1899.81	1899.202	1	766.9	63.333332 F.HILPPQQNTPPPPWLY.S
		homology domains that confer RNA binding activity; preferentially binds mRNAs								
gi 6321424 ref NP_011501.1	YGL014W	encoding nucleolar ribosomal RNA-processing factors; Puf4p Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	2	3.619	0.3182	1920.37	1921.202	1	702.8	56.666668 F.H3I1L1P1P1Q2Q2N2T1P1P1P1P1W2L1Y1.S
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p	2	3.1259	0.2593	1707.03	1706.808	1	493.7	62.5 L.D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p	1	3.415	0.2434	1581.86	1582.896	1	448.8	65.38461 A.E1V1L1P1K2L1G1P1K2I1G1W2D1L1.R
gi 6321412 ref NP 011489.1	YGL026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis; Trp5p	1	2.6166	0.2963	1564.6	1565.896	2	253.5	50 A.EVLPKLGPKIGWDL.R
ail6321412/refINP_011489_11	YGI 026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis: Tro5o	2	3 1795	0 3742	2256 53	2257 444	1	366.8	41 17647 E 111 1D1E1E1D1E1N2H3K2H3P111R4E1G1D1E1 G
	. 010200	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	-	0.000	0.0172	0545.00	0547		000.0	
gijo321412jref NP_011489.1	YGLU26C	control system of amino acid biosynthesis; I rp5p Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	2	3.8328	0.3832	2515.43	2517.734	1	940	อบ ห.หzeามายายายายายายาหวห3ห2H3P111R4F1G1D1F1.G
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	2	3.099	0.471	1336.63	1338.565	3	321.9	63.636364 S.A1I1G1P1H3P1Y1P1T1L1V1R4.T
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p	2	3.0357	0.1979	1415.39	1413.719	4	528.6	66.66667 Q.ARNEGVTVPIILM.G

		The second								
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p	3	4.6792	0.1707	2518.25	2517.734	1	1681.2	40.789474 K.K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1G1D1F1.G
gi 6321412 ref NP_011489.1	YGL026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis; Trp5p	3	4.6268	0.268	2195	2195.417	1	876.9	42.1875 K.K2E111L1D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gi 6321412 ref NP 011489.1	YGL026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis; Trp5p	2	3.8124	0.3648	2194.43	2195.417	1	466.1	50 K.K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gil6321412lrefINP_011489_1	YGI 026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis; Tro5p	1	2 6625	0 2296	1051.38	1052 164	4	345.4	55 555557 G S1A111G1P1H3P1Y1P1T1 I
gil6321412 rof NR_011489.1	VGL026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general		2 208	0.3116	963.44	064.086	1	416.7	62.5.5.5.111/G104H304V4D4T41
	VOL 0000	Tryptophan systems and biosynthesis, hpop	1	2.200	0.0170	303.44	304.000		410.7	
gij6321412 ret NP_011489.1	YGL026C	Control system of amino acid biosynthesis; Trp5p Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	2	3.7036	0.3478	2065.41	2065.243	1	429.5	53.333336 K.ETITLTDTETFTDTETN2H3K2H3P1T1K4F1.G
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	2	3.3083	0.2803	2039.57	2040.243	1	388.5	53.333336 K.EILDEFDENHKHPIRF.G
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	1	3.5271	0.3036	1351.56	1352.648	1	344.3	68.181816 A.E1V1L1P1K2L1G1P1K2I1G1W2.D
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p	1	3.1591	0.2598	1336.6	1337.648	1	325.4	68.181816 A.EVLPKLGPKIGW.D
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p	2	3.2736	0.3268	1910.63	1911.127	1	602.1	57.14286 E.ILDEFDENHKHPIRF.G
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p	2	4.5666	0.4409	1932.83	1935.127	1	723.3	57.14286 E.I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gi 6321412 ref NP_011489.1	YGL026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis; Trp5p	3	4.6323	0.2741	2194.34	2195.417	4	641.4	37.5 K.K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gil6321412/refINP_011489.1	YGL026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis; Tro5p	2	5.0405	0.463	2193.63	2195.417	1	1467.3	65.625 K K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gil6321412/rofINE_011489.1	VGL026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	2	4 4255	0.363	2167 77	2168 /17	1	1005.6	
gilosz1412 rel 141_011409.1	VOL 0000	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	2	4.4200	0.000	2107.77	2100.417	'	1035.0	
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	3	4.3081	0.4277	2509.22	2509.827	3	549.6	30.263159 A.NVKKEILDEFDENHKHPIRF.G
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general	3	5.1722	0.3787	2543.42	2541.827	1	2499.5	48.684208 A.N2V1K2K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gi 6321412 ref NP_011489.1	YGL026C	control system of amino acid biosynthesis; Trp5p Ribosomal protein L30 of the large (60S) ribosomal subunit, pearly identical to	2	5.1802	0.3634	2540.71	2541.827	1	1233.4	57.894737 A.N2V1K2K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gi 6321407 ref NP_011484.1	YGL031C	RpI24Bp and has similarity to rat L24 ribosomal protein; not sential for translation but may be required for normal translation rate; RpI24ap	1	2.4168	0.2218	1289.65	1290.478	1	237.6	77.77778 K.E1R4R4S1L1K2P1E1V1R4.K
		Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to Rpl24Bp and has similarity to rat L24 ribosomal protein; not essential for translation								
gi 6321407 ref NP_011484.1	YGL031C	but may be required for normal translation rate; Rpl24ap Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to	1	2.497	0.2831	1166.69	1166.382	1	305.8	72.22222 A.K2I1Y1P1G1R4G1T1L1F1.V
gi 6321407 ref NP_011484.1	YGL031C	but may be required for normal translation rate; Rpl24ap	2	3.3825	0.2145	1966.61	1967.297	1	326	53.333336 A.S1L1D1L1I1K2E1R4R4S1L1K2P1E1V1R4.K
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+)								
gi 6321401 ref NP 011478.1	YGL037C	salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p	2	3.3242	0.1951	1774.39	1775.052	2	251.5	50 L.T1V1P1K2G1E1E1L1I1N2P1I1S1D1L1M1.Q
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+)								
ail6221401/rofIND_041479.1	VCI 027C	salvage pathway, required for life span extension by calorie restriction; PNC1	2	2 02 42	0 194	2024 51	2025 242	4	410 E	
gilo32140111e111476.11	IGE03/C	expression responds to an known sumuli that extend replicative life span, Fricip	2	2.9343	0.104	2034.51	2033.342	4	412.0	41.000004 L.GT3TETTTV IFTR2GTETETETTINZFTT3TDTETWIT.Q
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1								
gi 6321401 ref NP_011478.1	YGL037C	expression responds to all known stimuli that extend replicative life span; Pnc1p	3	5.0026	0.4158	3056.39	3058.456	1	614.7	32 T.V1L1L1D1Y1T1R4P111S1D1D1P1E1V111N2K2V1K2E1E1L1K2A1H3.N
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1								
gi 6321401 ref NP_011478.1	YGL037C	expression responds to all known stimuli that extend replicative life span; Pnc1p	2	3.9899	0.3473	2422.57	2423.577	1	330	42.5 Y.T1Y1H3S1P1R4P1G1D1D1S1T1Q2E1G1I1L1W2P1V1H3.C
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+)								
gi 6321401 ref NP_011478.1	YGL037C	salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p	2	4.3695	0.3293	2582.51	2584.716	1	556.4	40.476192 Y.T1Y1H3S1P1R4P1G1D1D1S1T1Q2E1G1I1L1W2P1V1H3C1.V
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+)								
ail6321401/refINP_011478_1	YGL037C	salvage pathway, required for life span extension by calorie restriction; PNC1	2	4 2105	0 3027	2552 41	2553 716	1	703.2	
giloo214011101141_011410.11	1020070		2	4.2100	0.0021	2002.41	2000.710		100.2	
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1								
gi 6321401 ref NP_011478.1	YGL037C	expression responds to all known stimuli that extend replicative life span; Pnc1p	3	4.9997	0.4122	2586.65	2584.716	1	755.8	32.142857 Y.T1Y1H3S1P1R4P1G1D1D1S1T1Q2E1G1I1L1W2P1V1H3C1.V
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1								
gi 6321401 ref NP_011478.1	YGL037C	expression responds to all known stimuli that extend replicative life span; Pnc1p	3	4.1487	0.4661	2552.66	2553.716	1	1071.7	36.904762 Y.TYHSPRPGDDSTQEGILWPVHC.V
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+)								
gi 6321401 ref NP_011478.1	YGL037C	expression responds to all known stimuli that extend replicative life span; PnC1	3	3.9326	0.3107	2088.23	2088.365	1	672.1	45.588234 T.VLLDYTRPISDDPEVINK.V
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+)								
ail6321401/refINP 011478.1	YGL037C	salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span: Pnc1p	2	4.1742	0.1581	2113.71	2111.365	1	658.1	58.823532 T.V1L1L1D1Y1T1R4P1I1S1D1D1P1E1V1I1N2K2.V
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+)		_					-	
ail6221404 tofND_044472_1	VOL0070	salvage pathway, required for life span extension by calorie restriction; PNC1	2	4 4704	0 400 4	2202 50	2202 577	4	050 7	
gijo321401[rei]NP_011478.1]	TGL03/C	expression responds to all known sumuli that extend replicative life span; Phc1p	3	4.4701	0.4981	2392.58	2393.577	1	953.7	33 T. ITROPREGUDO I QEGILWPVM.G
		Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1								
gi 6321401 ref NP_011478.1	YGL037C	expression responds to all known stimuli that extend replicative life span; Pnc1p	2	4.3795	0.4682	2392.87	2393.577	1	909.8	50 Y.TYHSPRPGDDSTQEGILWPVH.C

gi 6321401 ref NP_011478.1	YGL037C	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p	3	4.8834	0.4249	2583.14	2584.716	1	1276.4	40.476192 Y.T1Y1H3S1P1R4P1G1D1D1S1T1Q2E1G1I1L1W2P1V1H3C1.V
gi 6321401 ref NP_011478.1	YGL037C	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p	2	3.7049	0.3097	2553.43	2553.716	1	454.2	42.857143 Y.TYHSPRPGDDSTQEGILWPVHC.V
gi 6321401 ref NP_011478.1	YGL037C	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p	2	4.6175	0.3276	2582.53	2584.716	1	532.1	38.095238 Y.T1Y1H3S1P1R4P1G1D1D1S1T1Q2E1G1I1L1W2P1V1H3C1.V
gi 6321401 ref NP_011478.1	YGL037C	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p	2	3.0936	0.2585	1642.45	1642.86	2	425.6	60.714287 L.T1V1P1K2G1E1E1L111N2P111S1D1L1.M
gi 6321401 ref NP_011478.1	YGL037C	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p	3	4.5829	0.475	2392.91	2393.577	1	986.5	36.25 Y.TYHSPRPGDDSTQEGILWPVH.C
gi 6321401 ref NP_011478.1	YGL037C	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p Protein associated with the mitochondrial nucleoid; putative mitochondrial ribosomal	3	4.4419	0.3437	2556.23	2553.716	1	934.5	36.904762 Y.TYHSPRPGDDSTQEGILWPVHC.V
gi 6321369 ref NP_011447.1	YGL068W	protein with similarity to E. coli L7/L12 ribosomal protein; required for normal respiratory growth; Mp1p Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp	2	3.4169	0.2998	2064.63	2065.291	1	345.5	50 T.TTTAPSHKDDVRPVDPKIS.K
gi 6321362 ref NP_011439.1	YGL076C	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); RPI7ap Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp	2	3.8165	0.3206	1425.93	1425.622	2	1106.5	75 L.SIDDLIHEIITVG.P
gi 6321362 ref NP_011439.1	YGL076C	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); R9/7ap Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp	3	4.7334	0.1697	1679.36	1678.88	1	1262.7	53.571426 L.S1I1D1D1L111H3E1I1I1T1V1G1P1H3.F
gi 6321362 ref NP_011439.1	YGL076C	and has similarity to E. con L23 and rat L7 motosomal proteins, contains a conserved C+terminal Nucleic acid Binding Domain (NDB2); R977ap Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp and has similarity to E. con L33 motosomal subunit, nearly identical to RpI7Bp and has similarity to E. con L34 motosomal subunit, nearly identical to RpI7Bp	2	4.5013	0.4571	1476.83	1476.642	1	1874.8	83.33333 I.D1D1L1I1H3E1111T1V1G1P1H3.F
gi 6321362 ref NP_011439.1	YGL076C	and mas similarity to E. Con Cash and C. Thousandar proteins, contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); RpTrap Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp and has similarity to F. coli 13 and ret 12 ribosomal proteins: contains a conserved	3	4.6253	0.2736	1660.7	1659.88	1	978.6	50 L.SIDDLIHEIITVGPH.F
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to F_ coli 130 and rat 12 ribosomal proteins: contains a conserved	2	4.1165	0.4118	1462.31	1459.642	1	1708.4	79.16667 I.DDLIHEIITVGPH.F
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to F_ coli 130 and rat 12 ribosomal proteins: contains a conserved	2	3.5253	0.3629	1016.31	1016.146	1	1290.5	93.75 I.H3E1111T1V1G1P1H3.F
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved	2	3.4359	0.2985	1003.33	1003.146	1	1302.6	93.75 I.HEIITVGPH.F
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved	3	3.9432	0.2414	1573.46	1572.801	2	1162.8	53.846157 S.IDDLIHEIITVGPH.F
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved	2	4.5195	0.3942	1662.45	1659.88	1	1718.8	75 L.SIDDLIHEIITVGPH.F
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved	2	3.3973	0.2841	1129.81	1130.305	1	1196.4	88.88889 L.11H3E11111T1V1G1P1H3.F
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S); hobsomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved	3	4.8698	0.2077	1591.28	1590.801	1	1669.9	57.692307 S.I1D1D1L111H3E11111TV1G1P1H3.F
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rplrap Protein component of the large (60S) rhosomal subunit, nearly identical to RpI7Bp and has similarity to E, coli L30 and rat L7 ribosomal proteins; contains a conserved	2	4.1948	0.3563	1359.61	1360.553	1	1466.8	
ail6321362/refINP_011439.1	YGL076C	C-terminal router add bilding bortian (UCDE), Kpr ag Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Bioring Domain (NIDB2): EDIZa.	2	4 9026	0.2392	1678 23	1678.88	1	1674.4	60.30304 D.D.Incill VGFn.F
ail6321362/refINP 011439.1	YGL076C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C+terminal Nucleic acid Bindino Domain (NDB2): Ro17ap	2	3.4425	0.4238	1572.77	1572.801	1	1128	65.38461 S.IDDLIHEIITVGPH.F
gi 6321362 ref NP_011439.1	YGL076C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rp17ap	2	2.9824	0.1821	1791.91	1793.039	1	615.4	53.333336 I.L1S111D1D1L111H3E11111T1V1G1P1H3.F
gi 6321362 ref NP_011439.1	YGL076C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp and has similarity to E, coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); RpI7ap	3	4.5	0.311	1957.76	1957.23	1	1210.8	48.4375 L.S111D1D1L111H3E1111T1V1G1P1H3F1K2.Q
gi 6321362 ref NP_011439.1	YGL076C	Protein component or the large (pos) noosonial suburin, nearly identical to Rpi/Rp and has similarity to E. coli 130 and rat 1.2 ribosonial proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpi/Rap Protein component of the Jarae (BOS); thosenal suburin; nearly identical to Rn/Rp.	3	4.8666	0.384	2277.23	2275.544	1	1427.1	38.157894 L.S111D1D1L111H3E11111T1V1G1P1H3F1K2Q2A1N2.N
gi 6321362 ref NP_011439.1	YGL076C	and has similarity to E. coli 130 and rat L7 ribosomal solution, recently contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (605) ribosomal solutini. nearly identical to RnI7Bn	3	4.1256	0.3475	2064.02	2063.361	1	942.9	41.17647 L.SIDDLIHEIITVGPHFKQ.A
gi 6321362 ref NP_011439.1	YGL076C	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp	3	4.3352	0.2576	2087.39	2087.361	1	736.4	39.705883 L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2Q2.A
gi 6321362 ref NP_011439.1	YGL076C	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.6858	0.3451	2064.59	2063.361	1	903.4	50 L.SIDDLIHEIITVGPHFKQ.A

		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp								
gil6321362[rofIND_011430_1]	VGI 076C	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved	2	3 6010	0 2721	2273 77	2275 544	1	018.0	50 S1101011111H3E1111T1\/1G1D1H3E1K2O2A1N2 N
gilosz1302[rei]rar_011435.1]	TGL070C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp	2	3.0313	0.2721	2213.11	2275.544		510.5	
	VOI 0700	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved		0 400 4	0.4000	0457.04	0450.44		4500	
gilo321362[rei]NP_011439.1]	IGL076C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp	2	0.1004	0.4683	2157.61	2159.44	1	1269	61.11111 E.STIDIDIETIIH3ETITTI VIGIPIH3FTK2Q2AT.N
		and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp	3	6.3176	0.3907	2159.9	2159.44	1	1931.7	51.38889 L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2Q2A1.N
		and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	3.8923	0.2851	1957.22	1957.202	1	1118	43.75 I.D1D1L111H3E1111T1V1G1P1H3F1K2Q2A1.N
		and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	5.9998	0.459	2135.51	2134.44	1	1323.5	45.833336 L.SIDDLIHEIITVGPHFKQA.N
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI/Bp and has similarity to E, coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.993	0.3951	2247.8	2248.544	1	1738.6	44.736843 L.SIDDLIHEIITVGPHFKQAN.N
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	4.5393	0.4783	2132.91	2134.44	1	1311.1	55.555557 L.SIDDLIHEIITVGPHFKQA.N
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp								
gi 6321362 ref NP 011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.3302	0.3227	1935.26	1935.23	1	843.8	43.75 L.SIDDLIHEIITVGPHFK.Q
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp								
ail6321362 ref NP_011439.1	YGL076C	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	4.8379	0.5189	1659.81	1659.88	1	1846.7	75 L.SIDDLIHEIITVGPH.E
gilooz rooziroliti _orriboriti	1020100	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp	-	1.0010	0.0100	1000.01	1000.00		101011	
gil6321362[rofIND_011430_1]	VGI 076C	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved	2	5 2497	0.4806	1676 31	1679.99	1	1700.0	75 \$1/1D1D11111H3E11111T1\/1G1D1H3 E
gilosz1302[rei]rar_011435.1]	TGL070C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp	2	5.2407	0.4030	10/0.51	1070.00		1730.3	
	VOI 0700	and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved		4 5045	0 4707	1070	1070.00		700	
gilb321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpi7ap Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp	3	4.5815	0.1787	1679	1678.88	2	786	48.214287 L.S111D1D1L111H3E1111111V1G1P1H3.F
		and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp	3	4.3871	0.2391	1660.25	1659.88	2	1464.9	50 L.SIDDLIHEIITVGPH.F
		and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap Protein component of the large (60S) ribosomal subunit, pearly identical to Rpl7Bp	2	3.0791	0.3431	2135.67	2134.44	3	445.1	36.11111 L.SIDDLIHEIITVGPHFKQA.N
		and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.5348	0.2862	2135.84	2134.44	1	623.2	33.333336 L.SIDDLIHEIITVGPHFKQA.N
		and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.1653	0.1728	1678.7	1678.88	1	923.8	46.42857 L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3.F
		and has similarity to E, coli L30 and rat L7 ribosomal subunit, nearly identical to Rpi/Bp								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.1941	0.3254	1660.67	1659.88	1	928.1	44.642857 L.SIDDLIHEIITVGPH.F
		Protein component of the large (60S) ribosomal subunit, nearly identical to RpI7Bp and has similarity to F_coli L30 and rat L7 ribosomal proteins; contains a conserved								
gi 6321362 ref NP_011439.1	YGL076C	C-terminal Nucleic acid Binding Domain (NDB2); RpI7ap	2	3.1571	0.4018	1658.05	1659.88	1	847.2	53.571426 L.SIDDLIHEIITVGPH.F
ail6321360/refINP_011437_1	YGI 078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: Dbp3p	1	2 8622	0 1508	1581 7	1582 736	1	439.6	58 333332 K G1E1E1E1D111K2N2I111R4E1T1 D
	TOLOTOO	Putative ATP-dependent RNA helicase of the DEAD-box family involved in		2.0022	0.1000	1001.7	1002.700		400.0	
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Butative ATB dependent BNA believes of the DEAD bey family involved in	2	3.9298	0.2782	1580.53	1582.736	1	1281.8	75 K.G1F1E1E1D111K2N2I111R4E1T1.D
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	3	4.525	0.3017	3821.06	3823.199	1	894.3	27.272728 Q.SEALTSLPQSDIDEYFKENEIAVEDSLDLALRPL.L
-:::C2042C01{IND_044427_4	VCI 070C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	2 00 40	0.0055	4005.00	4005 405		45405	
gilb321360 ref NP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	3	3.9846	0.2955	1935.92	1935.185	1	1540.5	50 M.LEKGFEEDIKNIIRET.D
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	2	3.821	0.3234	2231.99	2233.43	1	628.7	47.22222 M.L1E1K2G1F1E1E1D111K2N2I1I1R4E1T1D1A1S1.K
ail6321360/refINP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: Dbp3p	2	3.2596	0.2721	2277.75	2279.473	1	335.1	44.444447 K.G1F1E1E1D111K2N2I1I1R4E1T1D1A1S1K2R4Q2.T
3.1		Putative ATP-dependent RNA helicase of the DEAD-box family involved in	-							
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Putative ATP-dependent RNA belicase of the DEAD-box family involved in	2	3.3944	0.2811	2491.19	2492.792	1	470.8	42.5 M.LEKGFEEDIKNIIRETDASKR.Q
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	3	5.7082	0.311	2843.99	2844.19	1	475.2	33.695652 H.K2K2E1K2K2G1E1K2E1V1E1V1P1E1K2E1S1E1K2K2P1E1P1T1.S
gil6321360/rofIND_011437_1	VGI 078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: Dbp3p	2	2 0732	0.2610	23/6 13	2345 475	1	518 /	
gilosz1300[rei]rar_011437.1]	TGL070C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	2.3732	0.2013	2340.13	2343.473		510.4	30 Q.SDIDE IT REINEIXVEDSEDE.X
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	1	2.9138	0.336	1563.6	1564.736	1	473.4	58.333332 K.GFEEDIKNIIRET.D
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	1	2.7767	0.2542	1581.7	1582.736	3	361.7	50 K.G1F1E1E1D1I1K2N2I1I1R4E1T1.D
	VOI 0700	Putative ATP-dependent RNA helicase of the DEAD-box family involved in		0 5005	0.0014	1500.00	1501 700		1050.0	
gilb321360 ref NP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	3.5305	0.3014	1563.63	1564.736	1	1258.2	70.83333 K.GFEEDIKNIIRET.D
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	3	4.1447	0.2697	2583.53	2583.842	2	632.5	32.142857 K.E1K2K2G1E1K2E1V1E1V1P1E1K2E1S1E1K2K2P1E1P1T1.S
ail6321360/refINP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: Dbp3p	3	5.2481	0.1635	1473.35	1472,725	1	2020.5	68,181816 K.RKVVDEEVIEKK.K
3.1		Putative ATP-dependent RNA helicase of the DEAD-box family involved in	-							
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Putative ATP-dependent RNA belicase of the DEAD-box family involved in	2	3.5143	0.3162	1470.11	1472.725	1	921.5	77.27273 K.RKVVDEEVIEKK.K
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	3	4.6352	0.2089	2841.74	2842.173	1	657.8	31.25 K.KEKKGEKEVEVPEKESEKKPEPTSA.V
ail6321360/refIND 011427 11	YGI 078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	4 4212	0 2050	2544 10	2545 01	1	625	47.5 M T1K2E1E1I101D1K2K2R4K2\/1\/1D1E1E1\/111E1K2K2K2
910021000101111F_011437.1	10100	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	4.4212	0.2909	2044.18	2040.91	I	020	
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Butative ATE-dependent BNA belieges of the DEAD how family involved in	3	4.7691	0.191	2544.32	2545.91	1	834.5	37.5 M.T1K2E1E1I1A1D1K2K2R4K2V1V1D1E1E1V111E1K2K2.K
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	3	7.0119	0.3557	2813	2812.19	1	2224.9	40.217392 H.KKEKKGEKEVEVPEKESEKKPEPT.S
ail6221260/rofIND 011107 1	VCI 0700	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	4	2 5400	0.0700	1000 7	1006 505	2	550 F	
91032130011e11NP_011437.1	IGLU/OC	nuosomai uidgenesis, uupop	1	2.0120	0.2139	1220.7	1220.000	2	000.0	UU U.N.FENE I FIQAV.A

gi 6321360 ref NP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	1	3.0063	0.2137	1541.67	1542.732	7	221	53.846157 L.NGANQPVPEDLIKF.G
gi 6321360 ref NP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.2714	0.165	1774.49	1775.024	1	780.9	60.000004 N.V1L1N2G1A1N2Q2P1V1P1E1D1L1I1K2F1.G
gi 6321360 ref NP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	4.3594	0.3666	1993.57	1991.26	1	834.2	52.941177 L.V1N2V1L1N2G1A1N2Q2P1V1P1E1D1L1I1K2F1.G
gil6321360/refINP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: Dbp3p	1	2,7953	0.2608	1564.54	1564,736	1	448.1	62.5 K GEEDIKNIRET D
gil6321360/rofINP_011437.1	VGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: Dba3p	1	2 0166	0.2000	1591.67	1582 736	1	371.0	
sil0321300 ref NP_011437.1	VCL070C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in		4.0000	0.205	4504.05	4502.730	,	4402.2	
gil6321360 ref NP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	4.0232	0.2658	1581.65	1582.736	1	1403.3	75 K.G1F1E1E1D111K2N2I11R4E111.D
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	3.9554	0.3023	1563.69	1564.736	1	1350.4	75 K.GFEEDIKNIIRET.D
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	4.3844	0.454	1702.37	1704.964	1	1467.9	76.92308 M.LEKGFEEDIKNIIR.E
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	2	5.6219	0.4241	1954.69	1957.185	1	1932.4	73.333336 M.L1E1K2G1F1E1E1D111K2N2I111R4E1T1.D
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Db9p Puteting ATB description PDA belieses of the DEAD box family involved in	2	3.7464	0.199	1490.39	1490.725	1	785.5	77.27273 K.R4K2V1V1D1E1E1V111E1K2K2.K
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p	3	5.5481	0.2984	2413.97	2415.736	1	1585.3	44.736843 M.T1K2E1E1I1A1D1K2K2R4K2V1V1D1E1E1V1I1E1K2.K
gi 6321360 ref NP_011437.1	YGL078C	Putative A I P-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.5687	0.2642	2387.25	2387.736	1	718.6	55.263157 M.TKEEIADKKRKVVDEEVIEK.K
gi 6321360 ref NP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	4.5614	0.3084	2414.47	2415.736	1	749.3	57.894737 M.T1K2E1E1I1A1D1K2K2R4K2V1V1D1E1E1V1I1E1K2.K
ail6321360/refINP 011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: Dbp3p	3	5.6653	0.3075	2545.04	2545.91	1	1354.6	42.5 M.T1K2E1E1I1A1D1K2K2R4K2V1V1D1E1E1V1I1E1K2K2.K
gil6321360/rofIND_011437_1	VGI 078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: Dbo3n	2	4 8034	0.3762	2545.65	2545.01	1	1033.2	57.5 M T1K2E1E111A1D1K2K2P4K2\/1\/1D1E1E1\/11E1K2K2K
gij0321300 iei NF_011437.1	1010700	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	4.0304	0.5702	2545.05	2545.51		750.4	
gil6321360 ref NP_011437.1	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	4.2148	0.2518	2515.69	2515.91	1	753.4	52.499996 M. I KEEIADKKRKVVDEEVIEKK.K
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Putative ATP-dependent RNA helicase of the DEAD-box family involved in	1	2.7293	0.2079	1067.64	1068.293	1	576.2	75 S.K2F1P1K2P1T1P1I1Q2.A
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Putative ATP-dependent RNA helicase of the DEAD-box family involved in	1	2.6492	0.2311	1056.61	1056.293	6	459.6	68.75 S.KFPKPTPIQ.A
gi 6321360 ref NP_011437.1	YGL078C	ribosomal biogenesis; Dbp3p Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for	2	4.1119	0.3011	1945.59	1945.291	1	538.9	60.000004 F.F1K2D1V1D1L1T1K2K2P1K2K2I1T1F1D1
ail62012411rofIND_011419_1		nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by	2	4 6504	0.2546	1027.25	1027 166	2	659.2	
gilo321341 iei NF_011418.1	IGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for	2	4.0394	0.5540	1937.33	1937.100	2	036.3	55.00235 C.GTVT3TETDTVTETDTGTATETVTTTK2FTK2K4LT.A
gi 6321341 ref NP_011418.1	YGL097W	Cdc28p; Srm1p	2	3.8781	0.214	1912.77	1914.166	1	704.5	55.88235 C.GVSEDVEDGALVTKPKRL.A
		Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by								
gi 6321341 ref NP_011418.1	YGL097W	Cdc28p; Srm1p Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for	2	3.1193	0.2302	2054.57	2053.362	1	360	47.058823 Q.L1A1P1G1K2D1H3I1L1F1L1D1E1E1G1M1V1F1.A
ail6321341/refINP_011418_1	YGL097W	nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	3 4141	0.3036	1918 27	1919 202	1	545 5	59 375 L APGKDHILELDEEGMVE A
gilosz to 4 filolitat _011410.1	10E03/W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for	2	0.4141	0.0000	1310.27	1010.202		040.0	
gi 6321341 ref NP_011418.1	YGL097W	Cdc28p; Srm1p	2	3.6918	0.4301	1739.81	1739.762	3	472	53.571426 K.LSDEDAEKRADEMDD
		Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by								
gi 6321341 ref NP_011418.1	YGL097W	Cdc28p; Srm1p Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for	2	3.368	0.1869	1624.13	1622.757	1	813.4	69.230774 L.G1P1F1E1D1D1T1E1V1P1T1R4I1K2.N
ail6321341/refINP 011418.1	YGL097W	nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc280; Srm1p	2	3.402	0.3279	1766.61	1766.989	1	503.6	60.714287 F.EVGIPKDNLPEYTYK.D
5100 0 101 =0 0 1		Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleostical semic trafficking of macromolecules; potentially phosphon/atted by								
gi 6321341 ref NP_011418.1	YGL097W	Cdc28p; Srm1p	2	4.3671	0.3551	1578.49	1578.811	1	1386.2	76.92308 A.KIPRESFPPLAEGH.K
		Nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by								
gi 6321341 ref NP_011418.1	YGL097W	Cdc28p; Srm1p Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for	2	4.2305	0.2664	1597.83	1598.811	1	1613.6	80.769226 A.K2I1P1R4E1S1F1P1P1L1A1E1G1H3.K
gi 6321341 ref NP 011418.1	YGL097W	nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	1	2.6237	0.392	1577.71	1578.811	1	414.3	69.230774 A.KIPRESFPPLAEGH.K
		Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by								
gi 6321341 ref NP_011418.1	YGL097W	Cdc28p; Srm1p	1	2.294	0.2327	1597.65	1598.811	1	188.8	50 A.K2I1P1R4E1S1F1P1P1L1A1E1G1H3.K
gi 6321339 ref NP_011416.1	YGL099W	release of Nm3p from 60S subunits in the cytoplasm; Lsg1p	2	3.2125	0.2812	2179.35	2176.607	1	309.5	40 S.KAPNEPLLPPLPGQPPLINIG.L
gi 6321339 ref NP_011416.1	YGL099W	release of Nmd3p from 60S subunits in the cytoplasm; Lsg1p	2	3.6189	0.3177	2197.29	2198.458	1	604.6	58.823532 A.RQKENAIEYLPDGEMRFT.T
gi 6321339 ref NP_011416.1	YGL099W	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the release of Nmd3p from 60S subunits in the cytoplasm; Lsg1p	2	4.5554	0.3927	2223.69	2225.458	1	863.2	67.64706 A.R4Q2K2E1N2A1I1E1Y1L1P1D1G1E1M1R4F1T1.T
gi 6321339 ref NP 011416.1	YGL099W	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the release of Nmd3p from 60S subunits in the cytoplasm; Lsg1p	2	3.0696	0.2366	2288.67	2289.767	2	293	35.714287 S.KAPNEPLLPPLPGQPPLINIGL.V
gil6321339/refINP_011416.1	YGL099W	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the release of Nmd3p from 60S subunits in the cytoplasm. Lsdp	2	3.0869	0.2644	1668.87	1668.711	3	484.9	46.666668 Q.T1K2S1R4D1E1G1G1N2G1D1J1P1T1A1Q2 E
gil6321330/refIND_011416_1	YGL000W/	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the release of Nmdap from 60S subunits in the autoplasm. Leaf p	-	3 606	0.2520	2203 55	2201 607	2	200.3	40 S K241P1N2F1P1 11 1P1P4 1P4C402P1P4 114N24C4
silo201200aleellNP_011410.1	VOLOCOW	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the	2	0.000	0.2028	2203.00	2201.007	3	230.3	
gilo321339[ref]NP_011416.1]	YGL099W	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the	2	3.758	0.3235	2314.41	2315./6/	2	297.2	30.099230 S.KZATPINZETPILILIPTPILIPTGIQ2PTPILITN2HGLLIV
gi 6321339 ref NP_011416.1	YGL099W	release of Nmd3p from 60S subunits in the cytoplasm; Lsg1p Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the	2	3.1834	0.2209	1590.65	1590.733	1	614	62.5 Y.N2A1A1E1D1L1D1R4D1F1F1K2M1.N
gi 6321339 ref NP_011416.1	YGL099W	release of Nmd3p from 60S subunits in the cytoplasm; Lsg1p Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the	2	3.5036	0.4149	2092.57	2093.474	1	603.4	44.736843 L.SKAPNEPLLPPLPGQPPLIN.I
gi 6321339 ref NP_011416.1	YGL099W	release of Nmd3p from 60S subunits in the cytoplasm; Lsg1p	2	3.2261	0.2895	2026.61	2029.396	1	506.1	50 S.K2A1P1N2E1P1L1L1P1P1L1P1G1Q2P1P1L1I1N2.I

		Putative GTPase involved in 60S ribosomal subunit biogenesis: required for the								
gil6321330/rofIND_011416_1		release of Nmd3p from 60S subunits in the cutoplasm. Leato	2	3 3002	0 3130	2004 21	2006 306	1	374 1	
gilo321339[rei]NP_011416.1]	1GL099W	Riberenzel entria 1.00 of the large (COC) siberenzel entriality in the similarity to E coli	2	3.3992	0.3139	2004.21	2006.396		374.1	41.000004 S.KAPNEPLLPPLPGQPPLIN.I
		Ribosofial plotein E29 of the large (603) hosofial subulit, has similarity to E. con								
		L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can								
gi 6321335 ret NP_011412.1	YGL103W	mutate to cycloheximide resistance; Rpl28p	2	3.4221	0.1643	2300.65	2301.653	2	317.4	41.17647 N.L1D1K2L1W211L111P1E1D1K2R4D1Q2Y1L1K2.S
		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli								
		L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can								
gi 6321335 ref NP_011412.1	YGL103W	mutate to cycloheximide resistance; Rpl28p	2	3.0526	0.2242	1387.65	1388.681	1	653.8	80 H.F1W2K2P1V1L1N2L1D1K2L1.W
		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli								
		L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can								
ail6321335/refINP_011412.1	YGL103W	mutate to cycloheximide resistance: Rpl28p	2	2,9492	0.2095	1374.45	1373.681	1	624.1	75 H.FWKPVLNLDKL.W
3.1		Ribosomal protein $1/29$ of the large (60S) ribosomal subunit has similarity to E coli	-							
		115 and rot 1 27 a rise and rate rate way have partial standards and rot in the								
-:::C2242251#IND_044442.41	VCI 400W	E 15 and fat E27a ribosofiai proteins, may have peptidy transletase activity, can	0	2 0000	0.0400	4007 75	4000 40	7	074 5	
gilo321335[rei]NP_011412.1]	IGL103W	Pilate to cycloneximide resistance, Rpi26p	2	3.0666	0.2168	1207.75	1208.49		874.5	80 K.GTR4HPTN2VTPTVTHVTKZ.A
		Ribosomal protein L29 of the large (605) ribosomal subunit, has similarity to E. coll								
		L15 and rat L2/a ribosomal proteins; may have peptidyl transferase activity; can								
gi 6321335 ref NP_011412.1	YGL103W	mutate to cycloheximide resistance; Rpl28p	1	2.5446	0.2674	1248.73	1249.542	2	336.8	59.090908 L.GKGRIPNVPVIV.K
		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli								
		L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can								
gi 6321335 ref NP_011412.1	YGL103W	mutate to cycloheximide resistance; Rpl28p	1	2.8527	0.2813	1265.76	1266.542	4	334.9	59.090908 L.G1K2G1R4I1P1N2V1P1V11V1.K
		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli								
		L15 and rat L27a ribosomal proteins: may have peptidyl transferase activity: can								
ail6321335/refINP_011412.1	YGL103W	mutate to cycloheximide resistance: Rpl28p	2	3.8382	0.3109	1826.37	1827.072	1	597.6	65.38461 L.W2T1L11P1E1D1K2R4D1Q2Y1L1K2.S
3.1		Ribosomal protein 1.29 of the large (60S) ribosomal subunit has similarity to E coli	-							
		1 15 and rat 1 27a ribosomal proteins: may have pentidul transferase activity: can								
ail6221225[rofIND_011412_1]	VCI 102W	mutoto to quelobovimido registence: Bpl29p	4	2 2167	0 1597	1122 54	1122 240	2	E0E 9	
gijo321335[rei]NP_011412.1]	IGL103W	Pilate to cycloneximide resistance, Rpi26p		2.2107	0.1567	1132.54	1132.348	2	595.8	66.75 H.FWKPVLNLD.K
		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli								
		L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can								
gi 6321335 ref NP_011412.1	YGL103W	mutate to cycloheximide resistance; Rpl28p	2	3.5322	0.3326	1914.35	1915.15	1	676	57.14286 L.W2T1L11P1E1D1K2R4D1Q2Y1L1K2S1.A
		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli								
		L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can								
ail6321335/refINP_011412.1	YGL103W	mutate to cycloheximide resistance: Rpl28p	2	3.3826	0.2976	1806.57	1806.072	1	735.9	69.230774 L WTLIPEDKRDQYLK S
3.1		Ribosomal protein 1.29 of the large (60S) ribosomal subunit has similarity to E coli	-							
		1 15 and rat 1 27a rises and proteins; may have pentidul transferase activity; can								
-:::C2242251{IND_044442.41	VCI 400W	E lo and la E27 a ribosoma proteins, may have peptidy transletase activity, can	2	4 4004	0 4504	4200.0	4000 004	-	4407.0	
gilo321335[rei]NP_011412.1]	FGL103W	mutate to cycloneximide resistance; Rpi28p	3	4.4001	0.1561	1300.9	1300.001	5	1197.8	67.5 H.FTW2K2PTVTLINZLIDTKZLT.W
		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli								
		L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can								
gi 6321335 ref NP_011412.1	YGL103W	mutate to cycloheximide resistance; Rpl28p	1	2.2002	0.179	1372.57	1373.681	1	734.5	70 H.FWKPVLNLDKL.W
		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli								
		L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can								
ail6321335/refINP 011412.1	YGL103W	mutate to cycloheximide resistance: Rpl28p	2	3.1902	0.2312	1395.87	1396.716	1	831.9	62.5 L.G1K2G1R4I1P1N2V1P1V1I1V1K2.A
3.1		Protein that binds tRNA and methionyl- and dutamyl-tRNA synthetases (Mes1p and								
		Gusto) delivering tRNA to them stimulating catalysis and ensuring their localization								
ail62212221rofIND_011410_1		to the autoplanming have to ment, summaring data solds, and channing their localization	2	4 7762	0 2226	2022.04	2022 252	1	600 F	20 907503 C C151N3D4D4K3\/45154\/454D4D4K3D454K3A4C1D4K3\/4545454C154C
gil0521555[rei]147_011410.1]	IGLI03W	Directory that high a RNA and mathematic and alutamut RNA authors (Maa1a and	5	4.7703	0.3320	3022.34	3022.232	'	030.5	
		Fible in that binds trive and methody and globally trive synthetases (west pland								
		Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization								
gi 6321333 ref NP_011410.1	YGL105W	to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	3	4.2874	0.3192	1572.59	1573.789	1	1096.5	47.916664 N.HDLDLPHEVIEKK.K
		Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and								
		Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization								
gi 6321333 ref NP_011410.1	YGL105W	to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	2	5.0023	0.4503	2397.67	2397.69	1	1758.8	71.05263 N.DGLEVIFKDEEEKDHPVRKL.T
		Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and								
		Gusto, delivering tRNA to them, stimulating catalysis, and ensuring their localization								
ail6321333/refINP_011410_1	YGI 105W	to the cytoplasm: also hinds quadrunley nucleic acids: Arcin	2	4 9571	0 4314	2425 45	2425 69	1	1035	55 263157 N D1G1I 1E1V11E1K2D1E1E1E1K2D1H3P1V1R4K2I 1 T
giloo21000/101111_011410.11	IGEI00	Direct of options, also binds qualitational and alutamid (PNA authorses (Mooth and	2	4.5571	0.4014	2420.40	2420.00		1000	
		Fible in that binds trive and methody and globally trive synthetases (west pland								
		Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization								
gi 6321333 ret NP_011410.1	YGL105W	to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	3	5.1259	0.3562	1592.3	1592.789	1	1580.3	60.416668 N.H3D1L1D1L1P1H3E1V1I1E1K2K2.K
		Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and								
		Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization								
gi 6321333 ref NP_011410.1	YGL105W	to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	2	3.7918	0.213	1929.21	1930.168	1	641.2	60.000004 L.EINHDLDLPHEVIEKK.K
		Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and								
		Gusto, delivering tRNA to them, stimulating catalysis, and ensuring their localization								
ail6321333/refINP_011410_1	YGI 105W	to the cytoplasm: also hinds quadrunley nucleic acids: Arcin	3	4 8982	0 3601	2397.2	2307 60	1	1657 7	
giloo21000/101111_011410.11	ICEICON	Direct of options, also binds quadrupick indicate adds, Articip	0	4.0302	0.0001	2001.2	2007.00		1007.1	40.703+7+N.DOLEVII NDELENDII VIINE.T
		Frotein that binds trivia and methody and global any -trivia synthetases (wes p and								
		Gus (p), delivering triva to them, sumulating catalysis, and ensuring their localization								
gi 6321333 ret NP_011410.1	YGL105W	to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	2	3.2836	0.2553	2357.47	2355.673	4	186.6	40.476192 N.H3D1L1D1L1P1H3E1V111E1K2K2K2K2A1P1A1G1G1A1A1.D
gi 6321331 ref NP_011408.1	YGL107C	Mitochondrial protein required for sporulation; Rmd9p	2	4.0251	0.1655	2346.51	2344.728	1	471	44.444447 A.ESFFDKIINDEMPYKIILQ.V
gi 6321331 ref NP_011408.1	YGL107C	Mitochondrial protein required for sporulation; Rmd9p	2	4.2364	0.1722	2239.27	2237.597	1	716.6	52.941177 A.E1S1F1F1D1K2I1I1N2D1E1M1P1Y1K2I1I1L1.Q
ail6321331/refINP 011408.1/	YGL107C	Mitochondrial protein required for sporulation: Rmd9p	2	3.8353	0.275	1713.65	1712.938	1	914.8	60.714287 T.TTEDDIKVPKPLENL.K
gil6321331 refINP_011408.1	YGL107C	Mitochondrial protein required for sporulation: Rmd9p	2	3,2402	0.2158	2361.79	2359.598	1	604.9	44,736843 L GSIDNTNNEEILDRWLELVK.K
gil6321331/refINP_011408.1	YGL107C	Mitochondrial protein required for sporulation: Rmd9n	2	3 5432	0.1781	2217 35	2216 597	1	896.9	
gil6321331/rofIND_011408.1	VGL 107C	Mitochondrial protein required for sporulation; Rmd9p	2	3 4453	0.2880	1/18/17	1417 643	1	610.3	
gil032133111e11NF_011408.11	IGE10/C	Milochondhai protein required for spordiation, Kindsp	2	3.4405	0.2009	1410.47	1417.043		010.3	10.65555 N.SERDISDDIEIGK.V
		Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation								
gi 6321326 ref NP_011403.1	YGL112C	of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	2	3.3725	0.2495	1743.67	1743.025	1	470.9	53.571426 L.I1N2E1P1L1P1Q2V1P1R4L1P1T1F1T1.T
		Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation								
ail6321326/refINP_011403_1	YGI 112C	of RNA polymerase II and in chromatin modification, similar to histone H4: Taf6n	2	3 4798	0.4288	1950 59	1950 119	1	551.4	63 333332 K GEKVTDEDKEKLLERC G
giloo21020/101111 _011400.11	TOLITZO	of refer polymenase in and in emoniation notation, similar to instone rife, ratop	2	0.4750	0.4200	1000.00	1550.115		001.4	00.000002 A.OEAV IDEDAEALEERO.O
		Suburit (CO UDA) of TEUD and CACA complement involved in terroregistics initiation								
		Subunit (60 KDa) of TFIID and SAGA complexes, involved in transcription initiation								
gi 6321326 ref NP_011403.1	YGL112C	of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	3	4.0658	0.2474	3014.12	3016.348	1	663.6	27.083334 Y.L1D1E1E1E1V1D1F1D1R4L111N2E1P1L1P1Q2V1P1R4L1P1T1F1.T
		Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation								
gi 6321326 ref NP 011403.1	YGL112C	of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	3	5.2013	0.3975	3280.97	3282.629	1	857.7	30.769232 Y.Y1L1D1E1E1E1V1D1F1D1R4L1I1N2E1P1L1P1Q2V1P1R4L1P1T1F1T1.T
		Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation								
gil6321326/refINP_011403_1	YGL112C	of RNA polymerase II and in chromatin modification similar to histone H4. Tafeo	3	4,9675	0.3902	3446 81	3446 805	1	1109 1	31.48148 V.Y1Y1L1D1E1E1E1V1D1E1D1R4I 1I1N2E1P1I 1P1O2V1P1R4I 1P1T1E1T1 T
5-1-02 (020) of (1 _01 +00.1]			0		0.0002	00.01	0			
		Subunit (60 kDa) of TEIID and SAGA complexes, involved in transprintion initiation								
dile201206 roftND 044400 4	VCI 1400	of DNA polymoroad II and in observation modification initiation initiation	2	4 40 4	0.040	2400 77	2400 020		740	
giju321320[rei]INP_011403.1]	IGL1120	or non-polymerase in and in chromatin modification, similar to historie FI4; Taf6p	3	4.404	0.346	3400.11	3400.032	1	/10	
		Subunit (60 kDa) of THID and SAGA complexes, involved in transcription initiation	-							
100010001	YG1 112C	or KNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	3	5.4297	U.284	3526.01	3524.875	1	10/6.6	2/.6/85/ Y.YILIDIE1E1E1VIDIE1DIR4L1IN2E1P1L1P1Q2V1P1R4L1P1T1F1T1T1H3.W

gi 6321326 ref NP_011403.1	YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	3	5.7301	0.4129	3687.14	3689.051	1	930.9	27.586206 V.Y1Y1L1D1E1E1E1V1D1F1D1R4L111N2E1P1L1P1Q2V1P1R4L1P1T1F1T1T1H3.W
gi 6321326 ref NP_011403.1	YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	3	5.1411	0.3456	3747.23	3748.183	1	819.4	25.833332 S.VYYLDEEEVDFDRLINEPLPQVPRLPTFTTH.W
gi 6321326 ref NP_011403.1	YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	2	3.711	0.1883	2266.39	2265.594	1	349.4	41.6666664 A.I1I1Q2N2P1N2L1N2D1I1R4V1S1Q2P1P1F1I1R4.G
gi 6321326 ref NP_011403.1	YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	3	6.3214	0.4912	3486.95	3485.875	1	1391.9	32.142857 Y.YLDEEEVDFDRLINEPLPQVPRLPTFTTH.W
gi 6321326 ref NP_011403.1	YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	2	3.5784	0.4156	1722.39	1723.025	1	920.2	64.28571 L.INEPLPQVPRLPTFT.T
gi 6321326 ref NP_011403.1	YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	3	4.0863	0.2762	3082.82	3084.453	4	389.7	29 Y.LDEEEVDFDRLINEPLPQVPRLPTFT.T
gi 6321326 ref NP_011403.1	YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	3	5.8232	0.4289	3249.59	3247.629	1	2540.8	42.307693 Y.YLDEEEVDFDRLINEPLPQVPRLPTFT.T
gi 6321326 ref NP_011403.1	YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p RNA belgense in the DEALbex family involved in engages of the larity intro from	2	3.4169	0.2993	2234.97	2235.594	9	271.7	36.11111 A.IIQNPNLNDIRVSQPPFIR.G
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p	2	3.4195	0.4045	2135.75	2136.455	1	729	55.555557 Y.FNDAPLLAVPGRTYPVELY.Y
gi 6321318 ref NP 011395.1	YGL120C	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from the spliceosome; Prp43p	2	3.8156	0.3406	1474.77	1475.596	1	940.2	75 F.LTGEDEIEDAVRK.I
=102042401==fNID_044205_41	VCI 4000	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from	0	0.0704	0.0474	4000.00	4000 755		705 7	
gij6321318 ret NP_011395.1	YGL120C	the spliceosome; Prp43p RNA helicase in the DEAH-box family, involved in release of the lariat-intron from	2	3.6764	0.2474	1606.29	1606.755	1	785.7	61.538464 F.L111G1E1D1E1I1E1D1A1V1R4K2I1.S
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p RNA boliceoso in the DEAH-box family, involved in release of the larist-introp from	2	3.4712	0.344	1586.71	1588.755	1	835.9	61.538464 F.LTGEDEIEDAVRKI.S
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p	2	3.3218	0.4022	1734.65	1735.94	1	850.2	60.714287 L.SKQHPLPSEEPLVHH.D
ail6321318 refINP 011395.1	YGL120C	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from the spliceosome: Prp43p	2	3.2806	0.3295	1674.19	1675.833	1	442	53.571426 F.LTGEDEIEDAVRKIS.L
	VCI 4000	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from	2	4 00 40	0.0007	0407.70	0407.004		004.0	
gilo321318[rei]INP_011395.1]	IGL120C	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from	3	4.0249	0.2997	2107.76	2107.331	1	824.8	44.11765 A.EELSKQAPLPSEEPLVAA.D
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p RNA helicase in the DEAH-box family, involved in release of the lariat-intron from	2	3.7584	0.339	2106.39	2107.331	1	419.9	47.058823 A.EELSKQHPLPSEEPLVHH.D
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p	3	5.7557	0.4209	2754.95	2755.016	1	1262.7	34.782608 A.EELSKQHPLPSEEPLVHHDAGEFK.G
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p	2	3.4631	0.206	2482.93	2483.819	1	269	40 Q.R4Y1F1N2D1A1P1L1L1A1V1P1G1R4T1Y1P1V1E1L1Y1.Y
ail6321318/refINP_011395_1	YGI 120C	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from the spliceosome: Pro43p.	2	3 3108	0 1797	2454 03	2455 819	1	305.8	
	1021200	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from	-	0.0100	0.1757	2404.00	2400.010		000.0	
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p RNA helicase in the DEAH-box family, involved in release of the lariat-intron from	2	3.071	0.3511	1761.57	1758.94	1	307.2	53.571426 L.S1K2Q2H3P1L1P1S1E1E1P1L1V1H3H3.D
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p	2	3.6805	0.3699	2156.61	2159.455	1	802.2	55.555557 Y.F1N2D1A1P1L1L1A1V1P1G1R4T1Y1P1V1E1L1Y1.Y
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p	2	3.4066	0.2494	1383.13	1382.529	7	383.4	63.636364 T.V1K2D1N2Q2D1V1L1I1H3P1S1.T
ail6321318/refINP 011395.11	YGL120C	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from the spliceosome: Prp43p	1	2.2834	0.2557	1203.43	1204.313	4	350.7	55 F.A1H3P1D1G1D1H3I1T1L1L1.N
	X014000	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from		0.0000	0.0004	1100 77	4470.055		1000 7	
gi 6321318 ret NP_011395.1	YGL120C	the spliceosome; Prp43p RNA helicase in the DEAH-box family, involved in release of the lariat-intron from	2	3.2696	0.3201	1169.77	1170.355	1	1069.7	83.33333 K.K2L1G111D1D1L1V1H3F1.D
gi 6321318 ref NP_011395.1	YGL120C	the spliceosome; Prp43p	2	4.1602	0.4674	2132.11	2133.331	1	616.3	50 A.E1E1L1S1K2Q2H3P1L1P1S1E1E1P1L1V1H3H3.D
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	3.9525	0.3185	1960.61	1961.293	1	595.3	50 L.L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	3.807	0.4289	1936.91	1938.293	1	871.9	56.25 L.LPGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	3	4.087	0.2587	1847.36	1847.133	1	1380.9	50 L.P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	3.5004	0.2639	2653.75	2652.095	1	269.2	36.363636 F.Q2I111D1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	3	4.1695	0.2613	3980.12	3977.685	1	344.6	E.I1F1L1H3S1L1P1V1K2E1F1Q2I1I1D1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q 20.454546 2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	3	5.1787	0.4137	1825.13	1825.133	1	1632.5	53.333336 L.PGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	3.2129	0.1847	2406.97	2407.805	2	389.9	37.5 I.IID1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	3.6047	0.1807	2266.95	2267.646	1	939.1	55.263157 I.DTLLPGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	4.9403	0.3692	1846.49	1847.133	1	1396.6	66.66667 L.P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	3.5064	0.327	2896.91	2898.388	1	377.7	37.5 K.EFQIIDTLLPGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	3.6287	0.3704	2152.51	2152.557	1	497.7	52.77778 D.TLLPGLQDEVMNIKPVQKQ.T

gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	3.2317	0.2345	2619.95	2622.095	1	357	40.909092 F.QIIDTLLPGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	4.3545	0.4031	1825.41	1825.133	1	1328.3	66.66667 L.PGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	3	5.1853	0.3525	3459.11	3461.048	1	980.2	28.448275 H.S1L1P1V1K2E1F1Q2I1I1D1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	3	5.5466	0.2322	3424.88	3423.048	3	595.8	25 H.SLPVKEFQIIDTLLPGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	4.3506	0.3299	2520.41	2521.965	1	459.9	45.238094 Q.1111D1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	4.3225	0.3758	2492.57	2493.965	1	663.5	50 Q.IIDTLLPGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	4.8036	0.3099	1847.91	1847.133	1	1085.4	63.333332 L.P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	2	4.5354	0.3939	1824.63	1825.133	1	1119.9	63.333332 L.PGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	3	3.9535	0.2957	2897.72	2898.388	2	287.8	25 K.EFQIIDTLLPGLQDEVMNIKPVQKQ.T
gi 6321315 ref NP_011392.1	YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coll 55 and rat S2 ribosomal proteins; Rps2p N-terminally acetylated protein component of the large (60S) ribosomal subunit,	2	4.3325	0.3243	2072.85	2075.452	1	613.3	58.823532 T.L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi 6321303 ref NP_011380.1	YGL135W	nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp N-terminally acetylated protein component of the large (60S) ribosomal subunit,	2	4.9649	0.4107	1794.65	1796.958	1	1905.5	76.6666664 A.G1K2F1P1T1P1V1S1H3N2D1D1L1Y1G1K2.V
gi 6321303 ref NP_011380.1	YGL135W	neardy identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp N-terminally acetylated protein component of the large (60S) ribosomal subunit,	2	4.0703	0.3907	1774.91	1775.958	1	1179.7	70 A.GKFPTPVSHNDDLYGK.V
gi 6321303 ref NP_011380.1	YGL135W	nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp N-terminally acetylated protein component of the large (60S) ribosomal subunit,	2	4.5818	0.3675	1977.07	1976.196	1	525.4	58.823532 A.GKFPTPVSHNDDLYGKVT.D
gi 6321303 ref NP_011380.1	YGL135W	nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp N-terminally acetylated protein component of the large (60S) ribosomal subunit,	2	4.872	0.4386	2001.53	1999.196	1	471.4	55.88235 A.G1K2F1P1T1P1V1S1H3N2D1D1L1Y1G1K2V1T1.D
gi 6321303 ref NP_011380.1	YGL135W	nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp N-terminally acetylated protein component of the large (60S) ribosomal subunit,	2	4.8205	0.4013	1875.17	1875.091	1	1476.1	68.75 A.GKFPTPVSHNDDLYGKV.T
gi 6321303 ref NP_011380.1	YGL135W	nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp N-terminally acetylated protein component of the large (60S) ribosomal subunit,	2	4.6807	0.309	1895.75	1897.091	1	1576.7	68.75 A.G1K2F1P1T1P1V1S1H3N2D1D1L1Y1G1K2V1.T
gi 6321303 ref NP_011380.1	YGL135W	nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-	3	3.9467	0.2502	1999.49	1999.211	9	363.8	36.764706 S.K2A1G1K2F1P1T1P1V1S1H3N2D1D1L1Y1G1K2.V
gi 6321301 ref NP_011378.1	YGL137W	to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta ¹ -COP; Sec27p Essential beta ¹ -coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-	2	3.8119	0.3514	1956.63	1957.188	1	455.6	52.941177 E.EAIENVLPNVEGKDSLTK.I
gi 6321301 ref NP_011378.1	YGL137W	to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta ¹ -COP; Sec27p Essential beta ¹ -coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-	1	2.3417	0.309	1309.77	1308.607	1	456.8	59.090908 F.AVFHPTLPIIIS.G
gi 6321301 ref NP_011378.1	YGL137W	to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta ¹ -COP; Sec27p Essential beta ¹ -coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-	3	4.02	0.164	2788.07	2788.083	1	851.6	32.291664 L.T1L1R4G1E111E1E1A111E1N2V1L1P1N2V1E1G1K2D1S1L1T1K2.I
gi 6321301 ref NP_011378.1	YGL137W	to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-	2	4.4536	0.4564	2019.63	2021.261	1	1197.2	62.5 R.S1D1R4V1K2G111D1F1H3P1T1E1P1W2V1L1.T
gi 6321301 ref NP_011378.1	YGL137W	to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-	2	3.2554	0.285	2354.61	2354.63	1	268.1	44.736843 F.SNRSDRVKGIDFHPTEPWVL.T
gi 6321301 ref NP_011378.1	YGL137W	to-Ex transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi- CD, the transport into the COPI coatomer, involved in ER-to-Golgi and Golgi-	3	4.9053	0.4856	4136.6	4139.254	1	548	25 N.SEAVEAEKKEEEAPQQQQSEQQPEQGEAVPEPVEEES
gi 6321301 ref NP_011378.1	YGL137W	to-Ex transport, contains work domains that mediate dargo selective interactions, 45% sequence identity to mammalian beta'-COP; Sec27p Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi- ED beta tector protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-	3	5.5636	0.5593	4251.26	4253.358	1	766.4	26.35135 S.NSEAVEAEKKEEEAPQQQQSEQQPEQGEAVPEPVEEES
gi 6321301 ref NP_011378.1	YGL137W	to-Ex transport, contains work domains that mediate cargo selective interactions, 45% sequence identity to mammalian beta-COP; Sec27p Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi- to ER transport, perpise that mediate that mediate cargo aclocities in paralities;	1	2.9204	0.1773	1425.63	1426.6	2	484	59.090908 K.G1I1D1F1H3P1T1E1P1W2V1L1.T
gi 6321301 ref NP_011378.1	YGL137W	to-Ex transport, contains work domains that mediate cargo selective interactions, 45% sequence identity to mammalian beta'-COP; Sec27p Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi- ED beta transport. W/D to do the coatomer, involved in ER-to-Golgi and Golgi-	1	2.5769	0.3	1249.58	1250.528	1	349.5	55 A.V1F1H3P1T1L1P1I1111S1.G
gi 6321301 ref NP_011378.1	YGL137W	to-Ex transport, contains work domains that mediate cargo selective interactions, 45% sequence identity to mammalian beta'-COP; Sec27p Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi- ED beta transport. W/D to do the coatomer, involved in ER-to-Golgi and Golgi-	1	2.9395	0.359	1236.74	1237.528	1	371.6	55 A.VFHPTLPIIIS.G
gi 6321301 ref NP_011378.1	YGL137W	to-co-transport, contains work opinians intermediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi- ED beta-transport. W/0 to do-contains.	2	3.0415	0.2185	1784.73	1784.969	1	665.5	60.714287 R.SDRVKGIDFHPTEPW.V
gil6321301/refINP_011379_1	YGI 137W	45% sequence identity to mammalian beta'-COP: Sec276	2	3 6055	0 282	1997 60	1997 261	1	1383.0	68 75 R SDRVKGIDEHPTEPWVL T
gi 6321299 ref NP 011376.1	YGL139W	Putative protein of unknown function; localized to the mitochondrion; Flc3p	1	2.8199	0.2299	1396.57	1397.54	2	414.8	50 Q.FCPVHPGNIQID.S
gi 6321299 ref NP_011376.1	YGL139W	Putative protein of unknown function; localized to the mitochondrion; FIc3p	1	3.0268	0.2807	1412.5	1413.54	1	545	54.545456 Q.F1C1P1V1H3P1G1N2I1Q2I1D1.S
gi 6321299 ref NP_011376.1	YGL139W	Putative protein of unknown function; localized to the mitochondrion; FIc3p	2	3.8396	0.2528	1627.23	1626.676	1	499	66.66667 V.F1N2P1D1D1R4S1L1H3Y1D1L1D1.M
gi 6321299 ref NP_011376.1	YGL139W	Putative protein of unknown function; localized to the mitochondrion; Flc3p	2	3.7199	0.3334	1692.09	1692.782	1	1098	69.230774 F.DVVFNPDDRSLHYD.L
gijo321299 ret NP_011376.1	YGL139W	Putative protein of unknown function; localized to the mitochondrion; Flc3p	2	3.2572	0.2585	1920.31	1921.03	1	734	56.666668 F.DVVFNPDDRSLHYDLD.M

And the state of the state o			ATPase that forms a large complex, containing actin and soveral actin-related								
Mark Mark<	discontacting of the state	XCI 150C	proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in	2	2 9560	0.2726	1094 10	1095 221	1	790.9	
International sector	gilosz1269/rei/lvr_011565.1	TGLISUC	ATPase that forms a large complex, containing actin and several actin-related	2	3.0009	0.3720	1904.19	1903.331	1	700.0	55.00235 N.NGIEVEDEEKI GLEFEEL.N
apple biological biologi	gi 6321289 ref NP_011365.1	YGL150C	proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p ATPase that forms a large complex, containing actin and several actin-related	2	4.2893	0.1598	2002.69	2005.331	1	1096.6	61.764706 K.K2G111P1V1E1D1F1P1K2T1G1L1F1P1E1P1L1.N
added states in the first and advancements of states in the states the states in the states in the states in th	gi 6321289 ref NP_011365.1	YGL150C	proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p ATPase that forms a large complex, containing actin and several actin-related	2	3.4078	0.2835	2340.43	2341.712	1	442.1	50 K.KGIPVEDFPKTGLFPEPLNKN.F
Automatical and a set of the order or	gi 6321289 ref NP_011365.1	YGL150C	proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p ATPase that forms a large complex, containing actin and several actin-related	2	3.5143	0.3014	2230.01	2227.608	2	571.7	44.736843 K.KGIPVEDFPKTGLFPEPLNK.N
Automate of the set o	gi 6321289 ref NP_011365.1	YGL150C	proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p ATPase that forms a large complex, containing actin and several actin-related	2	3.7423	0.3226	2250.55	2251.608	1	584.6	44.736843 K.K2G11P1V1E1D1F1P1K2T1G1L1F1P1E1P1L1N2K2.N
generation gene generation generation	gi 6321289 ref NP_011365.1	YGL150C	proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p ATPase that forms a large complex, containing actin and several actin-related	3	4.0897	0.2659	2367.05	2367.712	2	883.9	32.5 K.K2G111P1V1E1D1F1P1K2T1G1L1F1P1E1P1L1N2K2N2.F
Bit	gi 6321289 ref NP_011365.1	YGL150C	proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases, Ino80p ATPase that forms a large complex, containing actin and several actin-related	2	3.1846	0.2481	1875.05	1875.157	3	343.2	40.625 K.G1I1P1V1E1D1F1P1K2T1G1L1F1P1E1P1L1.N
approximate of the second measurement and the second measurement of the second	gi 6321289 ref NP_011365.1	YGL150C	proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p Peroxisomal membrane protein that is a central component of the peroxisomal protein import machineau; interacts with DT14 (PacyFa) and PTS2 (PacyFa)	3	4.1009	0.305	2226.44	2227.608	1	1013.6	39.473686 K.KGIPVEDFPKTGLFPEPLNK.N
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	gi 6321285 ref NP_011362.1	YGL153W	protein import indumery, interacts with FTST(FEXAP) and FTSZ(FEXAP) peroxisomal matrix protein signal recognition factors and membrane receptor Pext3p; Pext4p Peroxisomal membrane protein that is a central component of the peroxisomal	2	3.5222	0.3558	1778.19	1779.025	1	308.3	60.000004 M.K2E1P1K2K2D1G1I1V1G1D1E1V1S1K2K2.I
	gi 6321285 ref NP 011362.1	YGL153W	protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p: Pex14p	2	4.4644	0.3552	1910.29	1911.218	1	922.5	68.75 A.M1K2E1P1K2K2D1G111V1G1D1E1V1S1K2K2.I
BIB212 State (HP _ 21132.1) VG1 State Pactage (HP _ 21132.1) Pactage (HP _ 21132.1)	3 1		Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (PexSp) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor								
1225239949P-011322 701.00 Production from the second control of the personand interpret encloses encloses of the personand interpret encloses enclose	gi 6321285 ref NP_011362.1	YGL153W	Pex13p; Pex14p Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p)	2	4.1553	0.2424	1888.31	1889.218	1	393	56.25 A.MKEPKKDGIVGDEVSKK.I
Bits 2258	gi 6321285 ref NP_011362.1	YGL153W	peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p)	3	4.0491	0.2486	1910.96	1911.218	6	511.2	40.625 A.M1K2E1P1K2K2D1G1I1V1G1D1E1V1S1K2K2.I
$g_{12222}g_{122}g_{$	gi 6321285 ref NP_011362.1	YGL153W	peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery interacts with PTS1 (Pex5n) and PTS2 (Pex7n)	3	4.3174	0.3336	1890.14	1889.218	1	805	43.75 A.MKEPKKDGIVGDEVSKK.I
inspection with models and PTS (Peck) and PTS (Peck) 2 2.0	gi 6321285 ref NP_011362.1	YGL153W	protein import indiviniely, interacts with FTS (FEX30) and FTS2 (FEX70) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p Peroxisomal membrane protein that is a central component of the peroxisomal	2	3.5665	0.3763	2232.73	2234.595	1	619.7	52.941177 Y.EAMPPTLPHRDWKDYFVM.A
$ \begin{array}{l l l l l l l l l l l l l l l l l l l $	gi 6321285 ref NP_011362.1	YGL153W	protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p	2	3.0769	0.2516	2257.57	2259.595	4	276.4	38.235294 Y.E1A1M1P1P1T1L1P1H3R4D1W2K2D1Y1F1V1M1.A
gls2125/jell/PD_011342 Full-based of the DEAD lock family, required for 185 rRNA 3 4.602 0.815 3816.20 1 20.01 2424242 K KEDDREKTTENDSPAKEEKSGNDDG(LKPVTNT_SKEDIGDIG(LFVTNT_SKEDIGDIG))	gi 6321267 ref NP_011344.1	YGL171W	ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis; Rok1p	1	2.2004	0.2503	1160.4	1161.43	2	439	61.11111 E.GEFKPPIIIF.L
Bioscience Bioscie	gi 6321267 ref NP_011344.1	YGL171W	ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis; Rok1p	3	4.0627	0.3195	3816.23	3817.069	1	341.9	24.242424 S.KVEDDREKTTENDSPNKEEKSGNDDGLIKPVITN.T
approximation APP-dependent RNA helicase of the DZ box family: required for 185 rRNA synthesis: Rxhip approximation: Rxhip approxim	gi 6321267 ref NP_011344.1	YGL171W	ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis; Rok1p	3	4.6744	0.3648	3860.96	3863.069	1	270.1	S.K2V1E1D1D1R4E1K2T1T1E1N2D1S1P1N2K2E1E1K2S1G1N2D1D1G1L1I1K2P1 24.242424 V111T1N2.T
ATP-dependent RNA helicase of the DEAD box family: required for 1SS rRNA gi[821267/ref[NP_011342]VGL170VGR170	gi 6321267 ref NP_011344.1	YGL171W	ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis; Rok1p	2	3.413	0.2517	1445.35	1442.609	1	1223	81.818184 L.IFDEADKLFDKT.F
gils321265/relNP_011342.11VGL1730 <td>gi 6321267 ref NP_011344.1 </td> <td>YGL171W</td> <td>ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis; Rok1p</td> <td>2</td> <td>3.0391</td> <td>0.1742</td> <td>1400.49</td> <td>1398.738</td> <td>1</td> <td>988.1</td> <td>77.27273 S.I1M1M1D1P1V1R4V1111G1H3.K</td>	gi 6321267 ref NP_011344.1	YGL171W	ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis; Rok1p	2	3.0391	0.1742	1400.49	1398.738	1	988.1	77.27273 S.I1M1M1D1P1V1R4V1111G1H3.K
glig3212g5/gli[NP_01132.1]VGL1732 <td></td> <td></td> <td>Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P)</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>			Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P)								
Big 321265 [ref [NP_011342.1]VGL 73CEvolutionally-conserved 5.3 exonuclease component of cytoplasmic processing (P) and telomere maintenance; Kem1p24.33780.40252189.592191.43911849.669.44444 LA1K2G1L1D102D111E1F1D1L151K2P1FTTP1FLQg [3521265 [ref [NP_011342.1]YGL 73CEvolutionally-conserved 5.3 exonuclease component of cytoplasmic processing (P) filamentous growth, nibosomal RNA maturation, and telomere maintenance; Kem1p34.09980.2962764.672766.119320.528.40999 LP1D1E1E111P1TL1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.Kg [3521265 [ref [NP_011342.1]YGL 73CEvolutionally-conserved 5.3 exonuclease component of cytoplasmic processing (P) filamentous growth, nibosomal RNA maturation, and telomere maintenance; Kem1p34.58890.30973687.473687.1322420.8LQ2E1K2L1S1P1D1L1P1D1E1E111P1TL1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.Kg [3521265 [ref [NP_011342.1]YGL 73CEvolutionally-conserved 5.3 exonuclease component of cytoplasmic processing (P) filamentous growth, nibosomal RNA maturation, and telomere maintenance; Kem1p35.28390.42773687.1322420.8LQ2E1K2L1S1P1D1L1P1D1E1E111P1TL1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.Kg [3621265 [ref [NP_011342.1]YGL 70Evolutionally-conserved 5.3 exonuclease component of cytoplasmic processing (P) fodes involved in mRNA decary, plays a role in microtubule-mediated processes, filamentous growth, nibosomal RNA maturation, and telomere maintenance; Kem1p35.28390.42773112.5939.52.335 ES1V1V1N2E1D1E1R4Y1K2E1R4G1P111P111E1E1E1F1P1L1N2S1K2.Vg [3621265 [ref [NP_011342.1]YGL	gi 6321265 ref NP_011342.1	YGL173C	bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	3.9866	0.2882	2177.11	2176.428	1	983.9	60.526318 L.SKVGNDIPVLEDLFPDTSTK.D
gig321265/ref NP_011342.1YGL1730Follower and the conserved 5-3' econculcases component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p34.69990.2962766.179320.528.40909 L.P1D1E1E11IP1T1L1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.Kgi[6321265]ref NP_011342.1YGL1730Follamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p34.58990.30973687.473687.1322420.8LQ2E1K2L1S1P1D1L1P1D1E1E11IP1T1L1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.gi[6321265]ref NP_011342.1YGL1730Follamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p35.28390.42773112.523112.39193.5S5 E.S1V1V1N2E1D1E1R4Y1K2E1R4G1P11IP1I1E1E1F1P1L1N2S1K2.Vgi[6321265]ref NP_011342.1YGL1730YGL1730Follomere maintenance; Kem1p35.28390.42773112.523112.39193.535 E.S1V1V1N2E1D1E1R4Y1K2E1R4G1P11IP1I1E1E1F1P1L1N2S1K2.Vgi[6321265]ref NP_011342.1YGL1730YGL1730YGL1730YGL1730155.3372.22222 K.HINVGIPVKF.E	gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	4.3378	0.4025	2189.59	2191.439	1	1849.6	69.44444 L.A1K2G1L1D1Q2D111E1F1D1L1S1K2P1F1T1P1F1.Q
gi[6321265]ref[NP_011342.1]YGL173CEvolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) tilamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p34.58890.30973687.473687.1322420.8LQ2E1K2L1S1P1D1L1P1D1E1E111P1TL1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.gi[6321265]ref[NP_011342.1]YGL173CFoldies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p34.58890.30973687.473687.1322420.8LQ2E1K2L1S1P1D1L1P1D1E1E11P1TL1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.gi[6321265]ref[NP_011342.1]YGL173CFoldies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p35.28390.42773112.523112.391939.535 E.S1V1V1N2E1D1E1R4Y1K2E1R4G1P111P11E1E1E1F1P1L1N2S1K2.Vgi[6321265]ref[NP_011342.1]YGL173CFoldies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p13.03550.3781124.671552.372.22222 K.HINVGIPVKF.Egi[6321265]ref[NP_011342.1]YGL173CFoldionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p25.8650.4934212.17211.135111475.369.44444 S.K2V1G1N2D111P1V1L1E1D1L1F1P1D1TS1TK2D	gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	3	4.0998	0.296	2764.67	2766.11	9	320.5	28.40909 L.P1D1E1E1I1P1T1L1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.K
gi[6321265]ref[NP_011342.1] YGL173C Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p 3 5.283 0.4277 3112.2 3112.39 1 939.5 35 E.S1V1V1N2E1D1E1R4Y1K2E1R4G1P11IP11IE1E1E1F1P1L1N2S1K2.V gi[6321265]ref[NP_011342.1] YGL173C Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p 1 3.035 0.3718 1124.66 1124.371 1 552.3 72.22222 K.HINVGIPVKF.E gi[6321265]ref[NP_011342.1] YGL173C Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p 1 3.0355 0.3718 1124.66 1124.371 1 552.3 72.22222 K.HINVGIPVKF.E gi[6321265]ref[NP_011342.1] YGL173C Filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p 2 5.8645 0.4934 2112.17 2111.35 1 1475.3 69.44444 S.K2V1G1N2D111P1V1L1E1D1L1F1P1D1T1S1T1K2.D	gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	3	4.5889	0.3097	3687.47	3687.132	2	420.8	LQ2E1K2L1S1P1D1L1P1D1E1E1I1P1T1L1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1. 20 K
Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p 1 3.0355 0.3718 1124.66 1124.371 1 552.3 72.22222 K.HINVGIPVKF.E Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p 2 5.8645 0.4934 2112.17 2111.35 1 1475.3 69.44444 S.K2V1G1N2D11P1V1L1E1D1L1F1P1D1T1S1T1K2.D	gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	3	5.2839	0.4277	3112.52	3112.39	1	939.5	35 E.S1V1V1N2E1D1E1R4Y1K2E1R4G1P1I1P1I1E1E1E1F1P1L1N2S1K2.V
Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, gij6321265/ref[NP_011342.1] YGL173C filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p 2 5.8645 0.4934 2112.17 2111.35 1 1475.3 69.44444 S.K2V1G1N2D11P1V1L1E1D1L1F1P1D1T1S1T1K2.D	gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	1	3.0355	0.3718	1124.66	1124.371	1	552.3	72.22222 K.HINVGIPVKF.E
	gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	5.8645	0.4934	2112.17	2111.35	1	1475.3	69.44444 S.K2V1G1N2D111P1V1L1E1D1L1F1P1D1T1S1T1K2.D

gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	5.2583	0.4609	2168.01	2169.439	1	1502.7	61.11111 L.AKGLDQDIEFDLSKPFTPF.Q
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	3	3.9986	0.2628	3076.25	3076.39	1	1177.6	35 E.SVVNEDERYKERGPIPIEEEFPLNSK.V
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	3.2045	0.3892	1138.21	1138.371	1	876	83.33333 K.H3I1N2V1G111P1V1K2F1.E
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	5.1004	0.5037	2089.95	2089.35	1	1070.2	63.88889 S.KVGNDIPVLEDLFPDTSTK.D
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	4.3141	0.3915	2198.19	2199.428	1	684.2	47.368423 L.S1K2V1G1N2D1I1P1V1L1E1D1L1F1P1D1T1S1T1K2.D
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	2.9167	0.2501	1767.57	1766.996	5	304.6	58.333332 K.EYRQTFPDFFFRL.S
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	4.5201	0.3261	2276.65	2275.631	1	1058.8	58.333332 T.V1E1K2K2F1L1D1S1E1P1T1I1G1K2E1R4L1Q2M1.D
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	1	3.2069	0.4337	1137.49	1138.371	1	522.4	72.22222 K.H3I1N2V1G1I1P1V1K2F1.E
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	3.4424	0.1814	1378.91	1378.546	1	684.8	83.33333 Y.R4Q2T1F1P1D1F1F1F1R4.L
gi 6321265 ref NP_011342.1	YGL173C	Evolutionarily-conserved 5-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	2	3.1343	0.2005	1801.01	1799.974	1	590.8	53.571426 L.DQDIEFDLSKPFTPF.Q
gi 6321243 ref NP_011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn2p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	1	2.4767	0.1907	1355.52	1356.649	1	508	68.181816 K.K2S1D1V1I1F1P1I1L1I1P1T1.L
ail6321243/refINP_011320_1	YGI 195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA: Gcn1p	1	3 1211	0 2748	1413 56	1414 627	2	459 5	58 3333321 G1K2P111E1D11 1D1K2111S141 G
sil0221240[ref[NP_011220.1]	VOLADEW	Positive regulator of the Gcn2p activation by an anomal ged which, Gon2p;		0.1211	0.2020	4200.04	4000 007	2	400.0	
gij6321243 rei NP_011320.1	IGL 195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn2p;		2.8206	0.2832	1398.01	1399.627	0	409.3	54. TOODOO L.G.RPIEDLUNISA.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	1	3.0639	0.3135	1599.55	1599.865	1	605	53.571426 F.SLGKPIEDLDKIISA.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	1	2.7986	0.2022	1472.52	1470.809	1	313.5	54.166668 K.K2S1D1V111F1P111L111P1T1L1.L
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.0811	0.2627	1456.57	1456.809	1	644.6	70.83333 K.KSDVIFPILIPTL.L
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	1	2.7736	0.2517	1457.7	1456.809	2	281.3	50 K.KSDVIFPILIPTL.L
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.8402	0.2295	2024.05	2025.356	1	1025.4	68.75 L.VERLGEEQFPDLIPRLL.D
gi 6321243 ref NP_011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.9453	0.4369	2416.77	2417.798	1	318	35.714287 Y.V111E111L1P1N2I1L1K2N2L1G1D1A1V1P1E1V1R4D1A1.T
gil6321243/refINP 011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.3857	0.2543	2624.65	2625.999	2	390.8	36.363636 L.G1A1L1V1E1R4L1G1E1E1Q2F1P1D1L1I1P1R4L1L1D1T1L1.S
gil6321243[rof[NP_011320_1]	VCI 105W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn2p;	-	4 7044	0.2242	2505.26	2505 000	1	1362.3	
	VOLACEW	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	5	4.7344	0.2242	2030.20	2000.000		1302.5	
gilb321243[rei]NP_011320.1]	IGE 195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn2p;	2	2.9001	0.2172	2810.33	2012.101		367.9	30.434782 F.VIVIN2DIEILILIK2SILIFIPILIFIN2Q2DIDISIGILIK4LIFI.A
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.8699	0.3601	2283.03	2281.784	1	793.9	55 K.KSDVIFPILIPTLLAPPIDAF.R
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.6251	0.2778	2247.19	2247.47	1	441.6	44.444447 S.N2T1D1T1T1L1E1D1L1T1K2L1I1D1E1I1F1K2N2.I
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.3834	0.2344	1495.57	1496.719	1	834.9	77.27273 A.V1L1E1R4L1P1N2F1F1D1K2T1.V
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gonzp activation by an uncharged tRNA; Gonzp	2	3.9495	0.1802	1817.59	1819.107	1	714.9	67.85714 E.R4L1G1E1E1Q2F1P1D1L111P1R4L1L1.D
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	1	3.3777	0.2889	1498.69	1499.773	1	677.2	62.5 F.S1C1L1R4D1P1V1I1P1I1K2L1A1.A
gi 6321243 ref NP_011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	1	2.7301	0.35	1482.67	1482.773	1	608.3	62.5 F.SCLRDPVIPIKLA.A
ail63212431refINP 011320.11	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn2p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	4.0442	0.3203	2312.13	2312.544	1	475.6	52.63158 L.NWEDISPVLEKGTRESHVSK.R
gil6321243lrefINP_011320_1	YGI 195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA: Gcn1p	1	2 4574	0 1572	1287 42	1288 521	1	422.6	61 111111 E1Y1K2K2P1E1E1I1G1E1 S
sil0221240[ref[NP_011220.1]	VOLADEW	Positive regulator of the Gcn2p activation by an anomal ged which, Gon2p;		4.0500	0.1072	4440.50	4444.070		705 4	
9100212401011110P_011320.1	NOL 199W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn2pp;	1	4.0000	0.2010	1413.38	1414.0/3		1 33.4	
gijb321243 ret NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.5393	0.3085	1400.27	1399.673	1	922.3	12.12/2/ E.KAKPLEPILDQF.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	1	3.8093	0.252	1399.69	1399.673	1	679.4	63.636364 E.KAKPLEPILDQF.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn2p	1	3.0324	0.2492	1573.64	1574.902	1	426.3	57.692307 M.S1K2K2S1D1V11F1P111L11P1T1.L
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity forms a complex with Gcn20p;	2	2.9201	0.1696	1414.39	1414.673	2	744.4	68.181816 E.K2A1K2P1L1E1P111L1D1Q2F1.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.9275	0.1998	1354.49	1354.649	3	1196.7	75 S.K2I1L1I1E1I1P1L1T1H3Y1.E

		Positive regulator of the Gen2n kinase activity forms a complex with Gen20n.								
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.6926	0.2369	1340.55	1340.649	2	1241	80 S.KILIEIPLTHY.E
ail6321243 refINP 011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	1	2.574	0.3313	1557.88	1558.902	1	421.9	57.692307 M.SKKSDVIFPILIPT.L
34eee.e.		Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;								
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	1	3.2493	0.2933	1353.51	1354.649	1	861.7	75 S.K2I1L1I1E1I1P1L1T1H3Y1.E
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	4.1466	0.1887	1689.31	1689.061	4	546.6	60.714287 M.S1K2K2S1D1V1I1F1P1I1L1I1P1T1L1.L
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.4727	0.2163	1672.41	1672.061	4	549.4	60.714287 M.SKKSDVIFPILIPTL.L
ail622121212tofND_011220_1	VCI 10FW	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	2 11 17	0.2127	1471 10	1470 900	1	690.2	70 00000 // //00104//41454041414140474141
gil0321243[rei]INP_011320.1]	IGLI95W	Positive regulator of the Gcn2p activation by an uncharged tRNA, Gcmp Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.1147	0.2127	1471.19	1470.009		000.2	70.03333 K.K231D1WIIIF1F11E11F111E1.E
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.1013	0.336	1398.71	1399.627	1	483.8	62.5 L.GKPIEDLDKIISA.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	3	3.9481	0.1728	2026.43	2025.356	1	2492.4	51.5625 L.VERLGEEQFPDLIPRLL.D
gil6321243 refINP_011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA: Gcn1p	1	2.2485	0.1928	1518.72	1518,795	1	261.3	59.090908 Q.ELEYKKPEFIGE S
	NOI 405111	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;		0.0000	0.0000	1700.05	1717.000		507.0	
gi 6321243 ret NP_011320.1	YGL195W	Proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.0893	0.3036	1720.25	1/1/.962	1	527.3	61.538464 S.HNSNLFEEYIPKLL.V
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity forms a complex with Gcn20p;	2	3.0057	0.2936	1285.91	1288.521	1	932.1	77.77778 L.F1Y1K2K2P1E1F1I1G1F1.S
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.1722	0.2988	1397.07	1399.673	1	817.2	68.181816 E.KAKPLEPILDQF.G
ail6321243/refINP_011320_1	YGI 195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA: Gcn1p	1	3 705	0.3163	1398 59	1399 673	1	921 1	72 72727 E KAKPI EPILDOE G
gilooz iz iojioijiti _01102011		Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;		0.100	0.0100	1000.00	1000.070	÷	02111	
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	1	3.8013	0.2047	1413.72	1414.673	1	636.4	63.636364 E.K2A1K2P1L1E1P1I1L1D1Q2F1.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	4.6377	0.283	1673.65	1674.963	1	1469.3	76.92308 Y.K2E1K2A1K2P1L1E1P1I1L1D1Q2F1.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.9184	0.2897	1821.31	1820.139	1	949.3	67.85714 F.YKEKAKPLEPILDQF.G
ail622121212tofND_011220_1	VCI 10FW	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	2 71	0 1716	1209 47	1200 507	2	600.0	
gil0321243[rei]INP_011320.1]	IGLI95W	Positive regulator of the Gcn2p activation by an uncharged tRNA, Gcmp Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.71	0.1716	1290.47	1299.397	3	090.9	60 L.RRVDRFTLERL.V
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.4415	0.3212	1546.37	1544.761	2	663	66.66667 L.G1E1E1Q2F1P1D1L1I1P1R4L1L1.D
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3	0.2248	1079.49	1077.275	1	704.3	81.25 F.CLEIGLKPF.L
ail6321243 refINP 011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	1	2.8979	0.1627	1544.68	1544.761	8	279.7	45.833336 L.G1E1E1Q2F1P1D1L1I1P1R4L1L1.D
		Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	0.45.44	0.0057	4000 54	4500.005		447.0	
gi 6321243 ret NP_011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn2p;	2	3.1541	0.2657	1600.51	1599.865	1	447.9	57.14286 F.SLGKPIEDLDKIISA.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity forms a complex with Gcn20p;	2	4.6487	0.2325	1817.73	1819.107	1	632.6	64.28571 E.R4L1G1E1E1Q2F1P1D1L1I1P1R4L1L1.D
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	4.0612	0.3307	1798.95	1797.107	1	778.4	71.42857 E.RLGEEQFPDLIPRLL.D
gil6321243 refINP_011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA: Gcn1p	3	4.597	0.1554	1819.22	1819.107	3	824.6	48.214287 E.R4L1G1E1E1O2E1P1D1L1I1P1R4L1L1.D
34eee.e.		Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	-							
gi 6321243 ret NP_011320.1	YGL195W	Proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	3.6643	0.2749	1400.45	1399.673	1	1444	86.36364 E.KAKPLEPILDQF.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.5995	0.1576	1413.71	1414.673	1	869.1	72.72727 E.K2A1K2P1L1E1P1I1L1D1Q2F1.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	1	4.0511	0.2482	1413.51	1414.673	1	790.6	68.181816 E.K2A1K2P1L1E1P1I1L1D1Q2F1.G
gil6321243/refINP_011320.1	YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA: Gcn1p	1	3.9343	0.3593	1398.69	1399.673	1	906	72,72727 E.KAKPLEPILDOF.G
34eee.e.		Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;								
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p;	2	4.3572	0.2756	1656.51	1656.963	1	1593.5	76.92308 Y.KEKAKPLEPILDQF.G
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	3.0876	0.2523	1533.47	1531.839	1	461.6	70.83333 L.LLEGEKRSPFVKK.D
gi 6321243 ref NP_011320.1	YGL195W	proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	2	4.1548	0.4341	1986.35	1987.315	1	1156.7	60.000004 N.F1Y1K2E1K2A1K2P1L1E1P1I1L1D1Q2F1.G
ail6321243/refINP_011320_1	YGI 195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA: Gcn1p	2	3 0823	0.3092	1966 13	1967 315	1	674.2	63 333332 N EYKEKAKPI EPILDOE G
gilooz iz iolioiliti _o i iozoiii			-	0.0020	0.0002	1000.10	1007.010	·	07.1.2	
		Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion								
gi 6321232 ref NP_011309.1	YGL206C	structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.966	0.3978	2494.31	2495.748	1	326.9	42.857143 Y.QKETTDIFFPPDATNDFPIAVQ.V
		Clathrin heavy chain, subunit of the major coat protein involved in intracellular								
ail62212221rofIND_011200_1		protein transport and endocytosis; two heavy chains form the clathrin triskelion	1	2 260	0 1797	1174 55	1172 205	1	462.6	
gilo321232[rei]NP_011309.1]	IGL200C	structural component, the light chain (GLCT) is thought to regulate function, Cherp		3.309	0.1767	1174.55	1175.595		402.0	11.11116 L.ERIILEF SFF.IN
		Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion								
gi 6321232 ref NP_011309.1	YGL206C	structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	4.3392	0.2323	1961.65	1963.219	1	906.8	59.375 L.E1K2I1I1L1E1P1S1P1F1N2E1N2V1A1L1Q2.G
		Clathrin heavy chain, subunit of the major coat protein involved in intracellular								
-102040201{IND_044200.41	VCI 2000	protein transport and endocytosis; two heavy chains form the clathrin triskelion	2	2 5202	0.0004	4050 50	4900 404	2	704.0	
gilo321232[rei]NP_011309.1]	FGL206C	structural component; the light chain (CECT) is thought to regulate function; ChcTp	2	3.5363	0.2961	1000.09	1860.121	3	/31.3	56.6666666 F.LIKZDIAINZETEIDIQZEIPIEIVIIIVICI.D
		Clathrin heavy chain, subunit of the major coat protein involved in intracellular								
gi 6321232 ref NP_011309.1	YGL206C	structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.063	0.1949	1962.41	1963.089	1	430.3	53.333336 N.N2S1P1E1K2F1L1K2E1N2D1Q2Y1D1T1L1.D
		Clathrin heavy chain, subunit of the major coat protein involved in intracellular								
alleggigggingfND_044000_t	VOLDOCO	protein transport and endocytosis; two heavy chains form the clathrin triskelion	4	2 1402	0 1007	1540.00	1550 007	4	945 7	
gijosz12szjrei/NP_011309.1	TGL206C	Subdural component; the light chain (CLCT) is thought to regulate function; Chc1p	1	3.1193	0.1937	1049.00	100.007	1	845.7	04.2007 I L.NZINZI I QZA IP IPIGIAIII SIPIII LILI.Y
		Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion								
gi 6321232 ref NP_011309.1	YGL206C	structural component; the light chain (CLC1) is thought to regulate function; Chc1p	1	3.3091	0.3081	1531.56	1532.867	1	962.2	67.85714 L.KNIQAPPGAISPILL.Y

gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.2171	0.2938	1377.11	1374.608	1	993.8	77.27273 F.S1K2S1D1N2L1P1L111K2P1F1.L
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	1	3.1586	0.2768	1373.6	1374.608	1	480	59.090908 F.S1K2S1D1N2L1P1L111K2P1F1.L
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	2.9937	0.3248	2006.49	2009.184	1	709.3	56.25 K.EDKLECSEELGDIVKPF.D
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	4.2	0.2027	1941.43	1942.219	1	812.4	56.25 L.EKIILEPSPFNENVALQ.G
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	4.1788	0.2548	1545.65	1544.773	2	749.6	75 N.K2E1E1T111E1L1A1R4P1V1L1Q2.Q
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.7637	0.2458	1527.65	1526.773	4	644.1	66.66667 N.KEETIELARPVLQ.Q
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	3	5.2474	0.2939	2272.46	2272.517	1	998.5	48.61111 W.L1K2E1D1K2L1E1C1S1E1E1L1G1D1I1V1K2P1F1.D
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	6.1032	0.3668	2252.75	2250.517	1	1804.2	75 W.LKEDKLECSEELGDIVKPF.D
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.0234	0.3117	1534.43	1532.867	1	750.8	53.571426 L.KNIQAPPGAISPILL.Y
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	5.9866	0.4624	2271.39	2272.517	1	1840.8	69.44444 W.L1K2E1D1K2L1E1C1S1E1E1L1G1D1I1V1K2P1F1.D
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	3	4.1551	0.2024	3406.58	3404.767	1	509.5	21.428572 W.L1K2E1D1K2L1E1C1S1E1E1L1G1D111V1K2P1F1D1T1T1L1A1L1A1C1Y1L1.R
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	4.4793	0.3874	2142.79	2143.361	1	1956.5	67.64706 L.RIIEIDHDASLPSQYQKE.T
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.2935	0.2291	2633.79	2634.955	3	256.9	37.5 Y.REIERIVKDNNVYDPERVKNF.L
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.0044	0.1774	2667.91	2669.955	1	214.2	37.5 Y.R4E111E1R4I1V1K2D1N2N2V1Y1D1P1E1R4V1K2N2F1.L
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.637	0.2689	2524.03	2521.748	2	267.3	38.095238 Y.Q2K2E1T1T1D1I1F1F1P1P1D1A1T1N2D1F1P1I1A1V1Q2.V
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.868	0.3889	1839.83	1841.121	1	1249.1	70 F.LKDANLEDQLPLVIVC.D
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	2	3.5305	0.2288	1373.73	1374.608	2	851.6	72.72727 F.S1K2S1D1N2L1P1L111K2P1F1.L
gi 6321232 ref NP_011309.1	YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p Subunit of the heterordimeric FACT complex (Spt1fba-Poh3b) (aclitates RNA	2	3.2825	0.2578	1550.39	1550.867	1	1826.3	82.14286 L.K2N2I1Q2A1P1P1G1A111S1P111L1L1.Y
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p Suburit of the heterodimetic EACT complex (Su16o-Poh3n) facilitates ENA	1	2.3204	0.2266	1387.47	1388.519	1	506.1	65 M.KSLQDDPYQFF.L
gi 6321231 ref NP_011308.1	YGL207W	Dolumin or activation intervention of configure (prover configure), toulnated and Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p Subunit of the heterordiner FACT complex (Snt16p-Pol30), facilitates RNA	2	3.1782	0.2341	1925.75	1927.23	3	581.2	50 A.K2L1S1D1K2l1E1N2K2l1D1D1V1K2F1L1.K
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA	2	3.9969	0.3434	1907.95	1906.23	1	1006.2	63.333332 A.KLSDKIENKIDDVKFL.K
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p Subunit of the heterodimeric FACT complex (Spt16p-Pob3o). facilitates RNA	2	2.9719	0.2768	1656.61	1656.876	1	622	61.538464 V.QIPLDETEPPRFLT.N
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA	2	4.1296	0.2453	1942.65	1942.176	1	793.8	59.375 L.ADTVQIPLDETEPPRFL.T
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	2	4.4125	0.2722	1502.45	1502.841	1	1001.6	79.16667 Q.T1I1I1L1P1I1Y1G1R4P1V1P1F1.H

		Subunit of the beterodimeric EACT complex (Spt16p-Pob3p) facilitates RNA								
gi 6321231 ref NP_011308.1	YGL207W	Polymeras I transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p Subunit of the betarroffmenic FACT complex (Spt16p-Dot2n) facilitates RNA	1	2.7458	0.1719	1500.91	1502.841	4	298.1	62.5 Q.T11111L1P111Y1G1R4P1V1P1F1.H
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; St16p	3	3.8176	0.2589	1502.42	1502.841	1	1232.9	56.25 Q.T1111L1P111Y1G1R4P1V1P1F1.H
gi 6321231 ref NP_011308.1	YGL207W	Subunit of the heterodiment FACT complex (Sph top-FUSD), addited NVA Polymerase Il transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p Subunit of the heterodiment; FACT complex (Sqt16p-Poh2n) facilitates RNA	2	4.0281	0.3827	1488.11	1486.841	1	903.4	75 Q.TIILPIYGRPVPF.H
gi 6321231 ref NP_011308.1	YGL207W	Suburit of the heterodinetic FACE complex (Sph GPT 002), facilitates NMA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Sph Gp Suburit of the heterodinetic FACE complex (Soft Gp. Debta), facilitates DNA	2	2.9464	0.1759	1388.67	1385.736	1	608.7	72.72727 T.IILPIYGRPVPF.H
gi 6321231 ref NP_011308.1	YGL207W	Subunit of the hearson ment have structure; Spt16p Subunit of the hearson ment and the hearson ment of the structure; Spt16p Subunit of the hearson ment FACT complex (Spt16p Data) facilitates RNA	2	3.9595	0.273	1870.25	1871.097	2	640.5	60.000004 A.DTVQIPLDETEPPRFL.T
gi 6321231 ref NP_011308.1	YGL207W	Polymeraeas II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Sp116p Subunit of the heterordimetic FACT complex (So116p-Pol3n) facilitates RNA	2	3.182	0.1599	1962.45	1963.176	1	355.1	40.625 L.A1D1T1V1Q2I1P1L1D1E1T1E1P1P1R4F1L1.T
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Sp116p Subunit of the heterodimeric FACT complex (So116p-Pob3p), facilitates RNA	1	3.1659	0.1954	1582.8	1583.872	4	189.2	46.153847 A.TKVPSKPDRNSKIL.R
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p. Subunit of the heterodimeric FACT complex (Spt16p-Po3p), facilitates RNA	3	4.358	0.2889	3154.04	3155.492	1	543.7	30.555555 N.NEEEDNNKKKSSPATKVPSKPDRNSKIL.R
gi 6321231 ref NP_011308.1	YGL207W	Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	1	2.571	0.2746	1400.89	1401.692	2	258.5	54.545456 N.ILKPGRTPKEVY.E
gi 6321206 ref NP_011283.1	YGL231C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; Ygl231cp	2	3.0554	0.1507	1443.83	1442.66	4	631.9	63.636364 N.AKGDWLPWERIA.H
ail6321206/refINP 011283.1	YGL231C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; Yql231cp	2	3.7721	0.3934	1742.05	1742.977	1	950.5	73.07692 N.AKGDWLPWERIAHY.N
gil6321206/rofINE_011283.1	VGL231C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	4 0204	0.3832	1763 57	1764 977	1	021 7	
	IGL23IC	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	4.0204	0.3032	1703.57	1704.977		921.7	
gi 6321206 ref NP_011283.1	YGL231C	localizes to the endoplasmic reticulum; Ygl231cp Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	3.2582	0.2113	2238.51	2237.569	1	586	47.22222 M.GLIPNAKGDWLPWERIAHY.N
gi 6321206 ref NP_011283.1	YGL231C	localizes to the endoplasmic reticulum; Ygl231cp Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation;	1	2.3231	0.2948	1387.66	1388.584	5	250.4	50 D.W2L1P1W2E1R4I1A1H3Y1.N
gi 6321198 ref NP_011276.1	YGL238W	Cse1p Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p),	2	3.6302	0.3779	1914.71	1916.048	1	689.6	60.000004 L.KNDYVDLDNLEEISTF.G
gi 6321198 ref NP_011276.1	YGL238W	homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p),	2	4.0714	0.413	1980.65	1981.337	1	746.6	55.88235 F.I1K2T1D1S1S111F1P1D1L1V1P1V1L1G111F1.Q
gi 6321198 ref NP_011276.1	YGL238W	Nonloig of melazoan CAS protein, required of accurate chromosome segregation, Csefp Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p),	2	3.3348	0.2928	3172.75	3174.4	1	214.6	28 N.VIT1L1R4E1E1D1V1E1L1F1E1D1D1P1I1E1Y1I1R4R4D1L1E1G1S1.D
gi 6321198 ref NP_011276.1	YGL238W	nomining of metazoan CAS protein, required of accurate chromosome segregation, Csefp Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), under the protein that mediates the nuclear export of importin alpha (Srp1p),	2	3.1099	0.2454	1430.49	1428.703	1	571.4	70 A.V1T1R4I1P1K2Y1F1E1I1F1.N
gi 6321198 ref NP_011276.1	YGL238W	nomining of metazoan CAS protein, required of accurate chromosome segregation, Csefp Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), under the protein that mediates the nuclear export of importin alpha (Srp1p),	2	4.4688	0.4465	2143.71	2143.312	1	884.3	55.88235 A.NLKNDYVDLDNLEEISTF.G
gi 6321198 ref NP_011276.1	YGL238W	nomining of metazoan CAS protein, required of accurate chromosome segregation, Csefp Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), under the protein that mediates the nuclear export of importin alpha (Srp1p),	2	3.397	0.1554	2164.81	2165.312	1	281.7	41.17647 A.N2L1K2N2D1Y1V1D1L1D1N2L1E1E1I1S1T1F1.G
gi 6321198 ref NP_011276.1	YGL238W	nomolog of metazoan CAS protein, required on accurate chromosome segregation, CSet p Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), boralear of metazoan CAS exterior accurate chromesome approximation;	2	3.0536	0.2751	3138.55	3139.4	1	228.8	28 N.VTLREEDVELFEDDPIEYIRRDLEGS.D
gi 6321198 ref NP_011276.1	YGL238W	nomiolog or metazoan CAS protein, required or accurate chromosome segregation, CSet p Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), boralear of metazoan CAS exterior accurate chromesome approximation;	2	3.7387	0.2953	1515.19	1513.687	7	653.1	62.5 S.EKPFDPLPEIDVN.N
gi 6321198 ref NP_011276.1	YGL238W	Cose1p Karyopherin, responsible for nuclear import of Spt15p, histones H2A and H2B, and Nag1r, aming targing a bawe similarity to those of dube importing carticularly	2	3.4845	0.2315	1667.21	1664.84	1	798.8	65.38461 S.I1A1D1S1D1F1P1D1R4W2P1T1L1L1.S
gi 6321196 ref NP_011273.1	YGL241W	Certp; localization is primarily nuclear; Kap114p Karyopherin, responsible for nuclear import of Spt15p, histones H2A and H2B, and	2	2.9194	0.3314	2020.17	2020.293	1	390.5	43.75 F.LKKKPNDGFLPDEINQY.L
gi 6321196 ref NP_011273.1	YGL241W	Nap1p; amino terminus shows similarity to those of other importins, particularly Cse1p; localization is primarily nuclear; Kap114p GlutamyI+RNA synthetase (GluRS), forms a complex with methionyI-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	2	4.5454	0.3606	2042.67	2043.293	1	602	53.125 F.L1K2K2K2P1N2D1G1F1L1P1D1E1I1N2Q2Y1.L
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1n) and 4rc1n; complex formation increases the cataluitic efficiency.	2	3.4057	0.2498	1599.93	1598.707	4	283.6	57.692307 F.T1E1E1M1K2N2G1T1E1E1G1L1K2N2.C
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p GlutamyI-tRNA synthetase (GluRS), forms a complex with methionyI-tRNA	2	3.5545	0.2064	2692.45	2694.863	1	931.8	45.454548 F.DDTNPSKEKEEFQDSILEDLDLL.G
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Guttamut/RNA synthetase (GluPS) forms a complex with mathicaul+DNA	3	4.9535	0.2674	2723.03	2721.863	1	1112.7	40.909092 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
ail37362640/refIND_011260.21	YGI 245W	Guany-river synthetase (Gurs), roms a complex with methionyl-triVia synthetase (Mest p) and Arctp; complex formation increases the califyic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Curst n	2	3 3991	0 2700	2720 47	2721 863	1	430 5	
9101 002040[101[14F_011203.2]	. 0124010	Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mest p) and Arctp; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cvtoplasm:	2	0.0001	0.2109	2120.41	2121.000		-00.0	
gi 37362649 ref NP_011269.2	YGL245W	Gus1p	3	4.3741	0.2706	2692.07	2694.863	1	1100.9	40.909092 F.DDTNPSKEKEEFQDSILEDLDLL.G

ail37362649/refINP_011269.21	YGI 245W	Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Glustn	2	3 011	0 2785	2839 97	2842 039	2	413.3	
9101002010[10].tt _011200.2]		Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both PBV suppletaces and ensure their correct localization to the optoplace:	-	0.011	0.2100	2000.01	2012.000	-	110.0	
gi 37362649 ref NP_011269.2	YGL245W	Gustp Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	3	4.9311	0.3563	2479.76	2477.773	1	599.1	36.842106 Q.W2M1V1D1K2D1L1V1G1N2W2D1D1P1R4F1P1T1V1R4.G
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gustp Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mestin) and Arctin; complex formation increases the catalytic efficiency	3	5.1085	0.2568	2719.22	2721.863	1	1346.9	43.18182 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA	2	4.2135	0.3345	2724.31	2721.863	1	508.6	40.909092 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p GlutamyI-tRNA synthetase (GluRS), forms a complex with methionyI-tRNA	2	4.0967	0.3482	2312.41	2313.48	1	777	55.555557 L.ITKDRLEEDESFEDFLTPQ.T
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Clutamul/RNA synthetases (CluPS) forms a complex with methionul-tPNA	2	3.5463	0.3792	2500.55	2501.755	1	562	40.476192 Y.K2D111V1V1D1K2D1D1A1D1V111N2V1D1E1E1V1T1L1M1.D
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p	2	3.4452	0.1656	2695.25	2694.863	1	604	43.18182 F.DDTNPSKEKEEFQDSILEDLDLL.G
oil37362640/offNP_011260.21	XGI 245W	Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm;	3	3 080	0 179	3257 63	3258 546	2	402.2	
gij37302049 tet 14F_011209.2	TGL245W	GutamyI-tRNA synthetase (GluRS), forms a complex with methionyI-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm;	3	3.969	0.178	3237.03	3236.340	3	492.2	23 LITTIK4F 1010 FT 192F 131K2E 1K2E 1E1F 1Q2013 THE LEDIE 101E 101E 101E
gi 37362649 ref NP_011269.2	YGL245W	Gustp GlutamyI-RNA synthetase (GluRS), forms a complex with methionyI-tRNA synthetase (Mestp) and Arctp; complex formation increases the catalytic efficiency of both RNA synthetases and ensures their correct localization to the cutoplasm;	2	4.8896	0.464	1855.27	1854.017	1	744.7	70 T.Y1D1F1C1V1P1I1V1D1A1I1E1G1V1T1H3.A
gi 37362649 ref NP_011269.2	YGL245W	Gustp Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	2	3.9885	0.3403	1873.43	1874.953	1	497.5	64.28571 D.R4L1E1E1D1E1S1F1E1D1F1L1T1P1Q2.T
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	2	3.9411	0.3487	1855.41	1855.953	1	606.4	67.85714 D.RLEEDESFEDFLTPQ.T
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1n) and Arctin: complex formation increases the catalytic efficiency.	2	3.412	0.1999	1376.39	1378.574	1	1390.8	90 Q.W2M1V1D1K2D1L1V1G1N2W2.D
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p GlutamyI-tRNA synthetase (GluRS), forms a complex with methionyI-tRNA	2	4.1673	0.2788	2376.41	2377.455	2	310.4	39.473686 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1.D
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arc1p; complex tormation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p GlutamyI-tRNA synthetase (GluRS), forms a complex with methionyI-tRNA	2	4.5755	0.3168	2351.91	2353.455	1	950	52.63158 F.DDTNPSKEKEEFQDSILEDL.D
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Clutamul-IRNA synthetase (GluBS) forms a complex with mathionul-IRNA	3	5.0757	0.3337	1828.52	1828.029	2	1749	51.666664 A.DTKDVVPVDLVDFDHL.I
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arch; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p	3	5.5584	0.2503	1848.11	1847.029	1	2220.9	53.333336 A.D1T1K2D1V1V1P1V1D1L1V1D1F1D1H3L1.I
gi 37362649 ref NP_011269.2	YGL245W	Glutamyl-tRNA synthetase (GluK3), forms a complex with metmonyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p	2	3.2127	0.2725	2041.65	2042.293	1	471.9	47.058823 A.DTKDVVPVDLVDFDHLIT.K
oil37362640/coflNP_011260.21	VGI 245W	Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Cure to	2	3 2155	0 1743	2064 57	2063 203	1	677	
gij5/302049161[4r_011203.2]	TOL243W	Gutamyl-IRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm;	2	3.2133	0.1743	2004.37	2003.233		0//	
gi 37362649 ref NP_011269.2	YGL245W	Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cvtoolasm:	2	3.0151	0.2055	1166.21	1165.332	2	728.9	77.77778 K.LNLEGDFKKT.K
gi 37362649 ref NP_011269.2	YGL245W	Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	2	3.3465	0.264	1875.43	1873.968	1	382.2	53.571426 L.ITKDRLEEDESFEDF.L
gi 37362649 ref NP_011269.2	YGL245W	or oom twwa synthetases and ensures their correct localization to the cytoplasm; Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	2	3.5988	0.1939	2525.51	2525.632	4	360.7	35 R.F1D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1.D
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mosta) and color complex formation of the complex f	2	4.3268	0.3626	1828.53	1828.029	1	1130.5	73.333336 A.DTKDVVPVDLVDFDHL.I
gi 37362649 ref NP_011269.2	YGL245W	of both RNA synthetases and ensures their correct localization to the cytoplasm; Gus1p	2	3.9713	0.2591	2693.01	2694.863	1	892.8	45.454548 F.DDTNPSKEKEEFQDSILEDLDLL.G

		Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mest p) and Arc1p; complex formation increases the catalytic efficiency of both rRNA synthetases and ensures their correct localization to the cytoplasm;								
gi 37362649 ref NP_011269.2	YGL245W	Gus1p GustapURNA synthetase (GluRS), forms a complex with methionyl-IRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	2	3.7434	0.2676	2719.65	2721.863	1	587.1	40.909092 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S111L1E1D1L1D1L1L1.G
gi 37362649 ref NP_011269.2	YGL245W	or both trive synthetases and ensures their context localization to the cytoplasm; Gust p Glutamyl-RNA synthetase (GluRS), forms a complex with methionyl-IRNA synthetase (Mes10) and Arcto: complex formation increases the catalytic efficiency	3	4.9671	0.2802	2844.65	2842.039	1	1039.2	36.95652 R.FDDTNPSKEKEEFQDSILEDLDLL.G
gi 37362649 ref NP_011269.2	YGL245W	of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA	3	5.3001	0.2423	2872.28	2870.039	1	1351.5	36.95652 R.F1D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p GlutamyLRNA synthetase (GluRS) forms a complex with methionyLIRNA	3	5.1059	0.2745	2723.12	2721.863	1	832.6	38.636364 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi 37362649 ref NP_011269.2	YGL245W	synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p	2	3.7556	0.2518	2251.37	2249.477	1	587.3	47.22222 N.PSKEKEEFQDSILEDLDLL.G
		GlutamyI-RNA synthetase (GluRS), forms a complex with methionyI-IRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both RNA synthetases and ensures their correct localization to the cytoplasm;								
gi 37362649 ref NP_011269.2	YGL245W	Gustp GlutamyHRNA synthetase (GluRS), forms a complex with methionyHRNA synthetase (Mest p) and Arc1p; complex formation increases the catalytic efficiency of hoth BND, washtetance and exempt their ancred lecentration to the actentioner.	2	3.4875	0.2875	1251.07	1251.515	1	829.3	80 F.NKKVIDPIAPR.H
gi 37362649 ref NP_011269.2	YGL245W	Gustp Gustp Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mest p) and Arc1p; complex formation increases the catalytic efficiency of both tBNA authotocos and neurone their parcent localization to the partnetaem;	3	5.11	0.209	2696.75	2694.863	2	1043.7	36.363636 F.DDTNPSKEKEEFQDSILEDLDLL.G
gi 37362649 ref NP_011269.2	YGL245W	Gustp Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	1	2.2541	0.1614	1250.65	1251.515	4	258.9	60.000004 F.NKKVIDPIAPR.H
gi 37362649 ref NP_011269.2	YGL245W	of both tKNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency	2	4.7844	0.2934	1848.35	1847.029	1	954.2	66.666667 A.D1T1K2D1V1V1P1V1D1L1V1D1F1D1H3L1.I
gi 37362649 ref NP_011269.2	YGL245W	or both tKNA synthetases and ensures their correct localization to the cytoplasm; Gus1p Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokinase during growth on glucose; functions in the nucleus to	2	4.1526	0.3973	1838.41	1836.017	1	547.8	63.333332 T.YDFCVPIVDAIEGVTH.A
gi 6321184 ref NP_011261.1	YGL253W	repress expression of HXK1 and GLK1 and to induce expression of its own gene; Hxk2p Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokinase during growth on glucose; functions in the nucleus to	2	5.4264	0.443	2341.41	2340.419	1	1691.4	63.88889 A.RIEEDPFENLEDTDDLFQN.E
gi 6321184 ref NP_011261.1	YGL253W	repress expression of HXK1 and GLK1 and to induce expression of its own gene; Hxk2p Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokinase during growth on glucose; functions in the nucleus to	2	6.2893	0.4134	2366.47	2365.419	1	1640.3	66.66667 A.R4I1E1E1D1P1F1E1N2L1E1D1T1D1D1L1F1Q2N2.E
gi 6321184 ref NP_011261.1	YGL253W	repress expression of HXK1 and GLK1 and to induce expression of its own gene; Hxk2p Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol;	2	4.2932	0.4761	2929.49	2932.026	1	830.6	45.652176 A.R4I1E1E1D1P1F1E1N2L1E1D1T1D1D1L1F1Q2N2E1F1G1I1N2.T
gi 6321184 ref NP_011261.1	YGL253W	predominant hexokinase during growth on glucose; functions in the nucleus to repress expression of HXK1 and GLK1 and to induce expression of its own gene; Hxk2p Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol;	2	4.3893	0.3992	2643.69	2643.711	1	1352.3	55 A.R4I1E1E1D1P1F1E1N2L1E1D1T1D1D1L1F1Q2N2E1F1.G
gi 6321184 ref NP_011261.1	YGL253W	predominant hexokinase during growth on glucose; functions in the nucleus to repress expression of HXK1 and GLK1 and to induce expression of its own gene; Hxk2p Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol;	2	4.051	0.3825	2900.25	2901.026	1	1085.5	45.652176 A.RIEEDPFENLEDTDDLFQNEFGIN.T
gi 6321184 ref NP_011261.1	YGL253W	predominant hexokinase during growth on glucose; functions in the nucleus to repress expression of HXK1 and GLK1 and to induce expression of its own gene; Hxk2p	1	2.441	0.2448	1399.59	1400.74	5	505.4	58.333332 K.KGGNIPMIPGWVM.E
gi 6321464 ref NP_011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	1	3.6734	0.2868	1395.56	1396.643	1	291.2	63.636364 L.E1K2E1G11111K2P111S1K2H3.S
gi 6321464 ref NP_011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	3	5.3444	0.3345	2342.93	2343.619	1	936.3	48.52941 L.D1Q2E1K2Y1D1R4I1L1K2E1V1P1T1Y1R4Y1V1.S
gi 6321464 ref NP_011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	3	4.8837	0.2438	2318.48	2316.619	1	581.8	39.705883 L.DQEKYDRILKEVPTYRYV.S
gi 6321464 ref NP_011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	3	5.2488	0.2602	2673.77	2672.07	1	1066.3	40 A.V1I1L1D1Q2E1K2Y1D1R4I1L1K2E1V1P1T1Y1R4Y1V1.S
gi 6321464 ref NP_011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	1	3.2917	0.3419	1378.67	1379.643	1	306	63.636364 L.EKEGIIKPISKH.S
gi 6321464 ref NP 011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	1	2.2657	0.2754	1524.66	1525.788	3	235.2	45.454548 E.KYDRILKEVPTY.R
gil6321464lrefINP_011541_1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat \$25 ribosomal protein; Rps25ap	2	3 3722	0 278	1545 67	1542 788	1	558.8	72 72727 E K2Y1D1R4I1I 1K2E1V1P1T1Y1 R
gil6321464/rofIND_011541.1	VCR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp	2	2 2970	0.270	2674.27	2672.07	1	201.6	
gil6321464/ref/NP_011541.1	VCR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp	2	2 1794	0.2309	26/0 72	2012.01	1	241.4	
gij6321464 rei NP_011541.1	YGRU27C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp	2	3.1784	0.2396	2040.73	2042.07	1	341.4	37.5 A.VILDQERTURILEVPTTRTV.5
yijo321464jreijNP_011541.1	rGRU2/C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp	2	3.23/1	0.2306	1907.53	1907.284	1	346.7	
gi 6321464 ref NP_011541.1	YGR027C	and has similarity to rat S25 ribosomal protein; Rps25ap Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp	2	3.5058	0.2765	1381.21	1379.643	1	512.5	63.636364 L.EKEGIIKPISKH.S
gi 6321464 ref NP_011541.1	YGR027C	and has similarity to rat S25 ribosomal protein; Rps25ap Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp	3	4.5966	0.1642	2342.6	2343.619	1	781.1	42.647057 L.D1Q2E1K2Y1D1R4I1L1K2E1V1P1T1Y1R4Y1V1.S
gi 6321464 ref NP_011541.1	YGR027C	and has similarity to rat S25 ribosomal protein; Rps25ap Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp	2	3.6807	0.3148	2341.89	2343.619	1	251.3	41.17647 L.D1Q2E1K2Y1D1R4I1L1K2E1V1P1T1Y1R4Y1V1.S
gi 6321464 ref NP_011541.1	YGR027C	and has similarity to rat S25 ribosomal protein; Rps25ap	2	3.3206	0.2114	2672.75	2672.07	1	311.2	37.5 A.V1I1L1D1Q2E1K2Y1D1R4I1L1K2E1V1P1T1Y1R4Y1V1.S

gi 6321464 ref NP_011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	3	5.8017	0.3031	2672.24	2672.07	1	1120.2	41.25 A.V111L1D1Q2E1K2Y1D1R4I1L1K2E1V1P1T1Y1R4Y1V1.S
gi 6321464 ref NP_011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	2	3.2081	0.2819	2343.03	2343.619	2	234.1	41.17647 L.D1Q2E1K2Y1D1R4I1L1K2E1V1P1T1Y1R4Y1V1.S
gi 6321464 ref NP_011541.1	YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap Catabitic subunit of 1.3 Jobta.ducan surphase, has similarity to an alternate catabitic	3	4.1323	0.3472	2639.99	2642.07	6	541.7	28.75 A.VILDQEKYDRILKEVPTYRYV.S
gi 6321469 ref NP_011546.1	YGR032W	catayid: subunit (Fstp (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p Cratavid: subunit of 1.3-beta-ducan synthase, has similarity to an alternate catalytic	2	3.1083	0.1963	1493.41	1491.745	1	1012.9	72.72727 L.LYRVENPEIVQM.F
gi 6321469 ref NP_011546.1	YGR032W	subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p Catalytic subunit of 1.3-beta-olucan synthase, has similarity to an alternate catalytic	2	4.0015	0.3834	1768.27	1766.865	1	766.3	62.5 Q.LSGNPILGDGKSDNQNH.A
gi 6321469 ref NP_011546.1	YGR032W	subunit, Fks1p (Gestp); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic	2	3.0169	0.2088	2347.71	2348.59	1	364.5	41.666664 L.CVYDRDKPITDVLYPIGCY.N
gi 6321469 ref NP_011546.1	YGR032W	subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic	2	2.9656	0.2172	1563.73	1564.698	2	451.7	68.181816 L.REIIREDDQFSR.V
gi 6321469 ref NP_011546.1	YGR032W	subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic units of the synthesis and the synthesis of the synthesis and the synthesy	1	2.6272	0.2875	1170.4	1171.257	1	505.4	66.66667 L.HYGHPDFINA.T
gi 6321469 ref NP_011546.1	YGR032W	subunit, Fks1p (Issc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit Cells (Cent of Decidence).	1	2.3429	0.2088	1212.63	1213.422	2	207.5	66.66667 L.TPHYAERILL.S
gi 6321469 ref NP_011546.1	YGR032W	subunit, rks1p (issc1p); kho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit. Etada (cond-b): Abd a central to the routenton submit involved in cell until where the conduction of the conduction submit is routen of the cell until submit. Etada (cond-b): Abd a central to the routenton submit is routen of the cell until the cell until submit is routened by the central submit is routened by the cell until submit is routened by the central submit is routened by the cell until submit is routened by the central submit is routened by the cell until submit is routened by the central submit is routened by the	1	2.8608	0.2275	1377.63	1378.586	1	503	60.000004 L.YRVENPEIVQM.F
gi 6321469 ref NP_011546.1	YGR032W	suburit, rks/p (sscrp), kno p encodes the regulatory suburit, involved in cell wait synthesis and maintenance; Gsc2p Catalytic suburit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic suburit Ecto (Cscr0): Plog a cenceder the regulatory suburit involved in cell wall	1	2.8873	0.2571	1393.45	1394.586	3	470.9	60.000004 L.Y1R4V1E1N2P1E111V1Q2M1.F
gi 6321469 ref NP_011546.1	YGR032W	subunit, rks/p (9sc/p), kito/p encodes the regulatory subunit, involved in cell wait synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit Fkst0 (Ssc1p). Bhota encodes the regulatory subunit involved in cell wall	2	3.9674	0.4052	1926.27	1926.143	1	798.1	66.66667 Y.DRDKPITDVLYPIGCY.N
gi 6321469 ref NP_011546.1	YGR032W	subduint, in an P (Gosp), runs 9 shocks in Eigeniany subduint, involved in term main synthesis and maintenance; Gosp shocks and the similarity to an alternate catalytic Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit. Fixsto (Gscho): Rohot encodes the regulatory subunit involved in cell wall	2	4.2798	0.4519	1947.33	1946.143	1	649	63.333332 Y.D1R4D1K2P1I1T1D1V1L1Y1P1I1G1C1Y1.N
gi 6321469 ref NP_011546.1	YGR032W	subdim; harfy (solid); the second second second second second in the second sec	1	2.9719	0.3987	1429.28	1430.612	1	505.3	70 Q.LHPVEWDCFVK.D
gi 6321469 ref NP_011546.1	YGR032W	synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit. Fxs1o (Gsc1o): Rho1o encodes the regulatory subunit: involved in cell wall	1	3.0722	0.3968	1445.4	1445.612	1	618.2	65 Q.L1H3P1V1E1W2D1C1F1V1K2.D
gi 6321469 ref NP_011546.1	YGR032W	synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit. Fxs1o (Gsc1o): Rho1o encodes the regulatory subunit: involved in cell wall	1	3.0987	0.3196	1299.85	1300.417	1	560.5	65 K.L1H3Y1G1H3P1D1F1I1N2A1.T
gi 6321469 ref NP_011546.1	YGR032W	synthesis and maintenance; Gsc29 Synthesis and maintenance; Gsc29 Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit. Fkst0 (Gsc10): Rhoto encodes the reouldorv subunit involved in cell wall	1	3.5637	0.2957	1401.5	1402.522	1	617.7	68.181816 K.L1H3Y1G1H3P1D1F111N2A1T1.F
gi 6321469 ref NP_011546.1	YGR032W	synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fxs1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall	1	2.8802	0.3853	1284.67	1284.417	1	767.1	70 K.LHYGHPDFINA.T
gi 6321469 ref NP_011546.1	YGR032W	synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fxs1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall	2	3.2833	0.2581	1585.79	1586.698	1	513.8	72.72727 L.R4E1111R4E1D1D1Q2F1S1R4.V
gi 6321469 ref NP_011546.1	YGR032W	synthesis and maintenance; Gsc2p Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit. Fxs1o (Gsc1o): Rho1o encodes the requilatory subunit: involved in cell wall	3	4.2841	0.2523	2292.56	2289.614	1	1248.9	45.833336 V.M1E1D1G1T1R4L111D1L1P1A1E1E1R4Y1L1K2L1.G
gi 6321469 ref NP_011546.1	YGR032W	synthesis and maintenance; Gsc2p Protein component of the large (60S) ribosomal subunit, nearly identical to RpI26Ap and has similarity to E. coll L24 and rat L26 ribosomal proteins: binds to 5.85 rRNA:	1	2.2789	0.2659	1063.52	1064.236	1	434.8	78.57143 A.H3W2Q2A1P1L1L1W2.F
gi 6321471 ref NP_011548.1	YGR034W	Rpl/26bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coll L24 and rat L26 ribosomal proteins: binds to 5.85 rRNA:	1	2.3302	0.1872	1337.7	1337.565	1	286.1	60.000004 L.HLDKDRKALIQ.R
gi 6321471 ref NP_011548.1	YGR034W	Rpl26bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E, coll L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA;	2	3.6219	0.1889	1354.29	1356.565	2	438	70 L.H3L1D1K2D1R4K2A1L111Q2.R
gi 6321471 ref NP_011548.1	YGR034W	Rpl26bp Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E, coll L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA;	2	3.0937	0.3168	1651.09	1651.95	1	267.9	61.538464 K.ALPIRRDDEVLVVR.G
gi 6321471 ref NP_011548.1	YGR034W	Rpl26bp Mitogen-activated protein kinase (MAPK) involved in signal transduction pathways	1	2.8709	0.2524	1208.74	1209.434	1	452.3	72.22222 K.LHLDKDRKAL.I
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p Mitogen-activated protein kinase (MAPK) involved in signal transduction pathways	2	4.6232	0.4846	2747.25	2747.908	1	720.9	47.61905 M.Y1H3D1P1S1D1E1P1E1Y1P1P1L1N2L1D1D1E1F1W2K2L1.D
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	2	4.3132	0.4508	2721.69	2720.908	1	1058.5	54.761906 M.YHDPSDEPEYPPLNLDDEFWKL.D
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p Mitogen-activated protein kinase (MAPK) involved in signal transduction pathways	3	4.7886	0.3071	2722.46	2720.908	1	1182.3	36.904762 M.YHDPSDEPEYPPLNLDDEFWKL.D
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	3	4.1145	0.2791	2852.45	2852.101	1	906.7	34.090908 A.MYHDPSDEPEYPPLNLDDEFWKL.D
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	2	3.0723	0.3143	1953.35	1952.325	1	360.5	50 A.NLPMRPPLPWETVWSK.T
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	3	5.2794	0.2341	2749.64	2747.908	1	1341.3	40.476192 M.Y1H3D1P1S1D1E1P1E1Y1P1P1L1N2L1D1D1E1F1W2K2L1.D
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	2	4.5208	0.4788	2746.39	2747.908	1	826.1	52.380955 M.Y1H3D1P1S1D1E1P1E1Y1P1P1L1N2L1D1D1E1F1W2K2L1.D
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	2	3.0116	0.1908	1569.19	1568.859	1	315.5	54.166668 A.N2L1P1M1R4P1P1L1P1W2E1T1V1.W
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	2	3.08	0.2672	1736.07	1735.097	1	579.6	57.14286 Y.IANLPMRPPLPWETV.W
gi 6321477 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	2	3.9582	0.4701	1754.61	1757.072	1	329.3	57.692307 A.N2L1P1M1R4P1P1L1P1W2E1T1V1W2.S

gi 6321477 ref NP_011554.1	YGR040W	Mitogen-activated protein kinase (MAPK) involved in signal transduction pathways that control filamentous growth and pheromone response; Kss1p Mitogen-activated protein kinase (MAPK) involved in signal transduction pathways the sector bit for the sector sector bit of the transport of the sector sector bit of the sector sector bit of the sector sector bit of the sector	2	3.7661	0.3184	1945.67	1943.31	1	601.5	60.000004 Y.I1A1N2L1P1M1R4P1P1L1P1W2E1T1V1W2.S
gi 63214/7 ref NP_011554.1	YGR040W	that control filamentous growth and pheromone response; Kss1p	2	3.5595	0.3513	1922.17	1921.31	1	316.1	43.333332 Y.IANLPMRPPLPWETVW.S
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	3	4.1576	0.3355	1397.9	1397.618	1	1652	54.545456 T.VRGPKAEEILER.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	2	3.434	0.4064	1397.53	1397.618	1	902.9	81.818184 T.VRGPKAEEILER.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	2	3.2091	0.2694	1518.45	1518.723	3	524.9	66.66667 V.T1V1R4G1P1K2A1E1E1I1L1E1R4.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	2	3.3937	0.3657	1618.35	1618.855	1	433.1	53.846157 H.V1T1V1R4G1P1K2A1E1E111L1E1R4.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	2	3.7922	0.223	1418.33	1416.618	1	1038	81.818184 T.V1R4G1P1K2A1E1E1I1L1E1R4.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	2	3.5509	0.1889	1600.19	1597.855	1	478.3	57.692307 H.VTVRGPKAEEILER.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	3	4.5689	0.1534	1416.65	1416.618	1	1660.4	56.81818 T.V1R4G1P1K2A1E1E111L1E1R4.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	3	4.1011	0.1691	1397.48	1397.618	1	938.8	50 T.VRGPKAEEILER.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	2	3.2169	0.3183	1396.75	1397.618	1	922.8	77.27273 T.VRGPKAEEILER.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	3	4.3368	0.3014	1517.84	1518.723	1	1568.1	52.083332 V.T1V1R4G1P1K2A1E1E1I1L1E1R4.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	2	3.068	0.1937	1789.71	1791.067	2	490.2	53.333336 H.V1T1V1R4G1P1K2A1E1E111L1E1R4G1L1.K
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp	1	2.2486	0.1962	1221.57	1222.415	2	518.3	65 L.G1I1K2Y1D1P1S1I1G1I1F1.G
gi 6321522 ref NP_011599.1	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; RpI11bp Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	1	2.419	0.2086	1209.55	1210.415	2	548.8	60.000004 L.GIKYDPSIGIF.G
gi 6321523 ref NP_011600.1	YGR086C	with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	5.618	0.4142	2216.27	2217.201	1	1171.6	61.11111 E.P1E1Q2E1E1E1G1A1V1E1E1H3E1Q2V1G1H3Q2Q2.S
gi 6321523 ref NP_011600.1	YGR086C	with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lendo to down service hand stress resistance with a protein and with Lendo to down service hand stress resistance with a protein and down service and stress resistance with a protein and stress resistance with a protein and down service and stress resistance with a phase and down service	2	5.6185	0.4481	2189.31	2190.201	1	1210.1	66.66667 E.PEQEEEGAVEEHEQVGHQQ.S
gi 6321523 ref NP_011600.1	YGR086C	With Lspip to down-regulate heat states resistance via regulation on the Pk2 p and Ypk1p pathways; phosphorylated by Pk1p and Pkk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with J sch to down-regulate heat stress resistance via regulation of the Pkc1p and	3	4.4581	0.369	2500.22	2500.855	1	1881.6	46.25 L.KYKDPQSPKIEVLEQELVRAE.A
gi 6321523 ref NP_011600.1	YGR086C	Minitopip ip or other ingulate hards in the part of th	3	4.3913	0.291	2531	2529.855	2	690.6	32.5 L.K2Y1K2D1P1Q2S1P1K2I1E1V1L1E1Q2E1L1V1R4A1E1.A
gi 6321523 ref NP_011600.1	YGR086C	Ypk1p pathways: phosphorylated by Phk1p and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and	2	4.2993	0.3682	2500.33	2500.855	1	637.4	55 L.KYKDPQSPKIEVLEQELVRAE.A
gi 6321523 ref NP_011600.1	YGR086C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and	2	3.9387	0.2374	2528.59	2529.855	1	701	55 L.K2Y1K2D1P1Q2S1P1K2l1E1V1L1E1Q2E1L1V1R4A1E1.A
gi 6321523 ref NP_011600.1	YGR086C	Ypktp pathways; phosphorylated by Phktp and Phk2p; Piltp Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and	2	2.9642	0.1923	1737.95	1738.789	1	581	58.333332 S.E1L1D1D1Q2F111D1R4Y1D1Q2Y1.R
gi 6321523 ref NP_011600.1	YGR086C	Ypktp pathways: phosphorylated by Phktp and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and	2	4.7574	0.397	1650.43	1649.706	1	1242.7	64.28571 W.GLENDDDVSDITDKL.G
gi 6321523 ref NP_011600.1	YGR086C	Ypktp pathways: phosphorylated by Phktp and Phk2p: Piltp Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and	2	4.9604	0.4026	1665.59	1666.706	1	1970.6	75 W.G1L1E1N2D1D1D1V1S1D1I1T1D1K2L1.G
gij6321523 ref NP_011600.1	YGR086C	rpxtp partways: phosphorylated by Phktp and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Victa pathways: phosphorylated by Bktch and Pkk2p; Pil1p	2	3.3997	0.3015	1/22.25	1/20.789	1	/33.2	
gij6321523[ref[NP_011600.1]	VGPOREC	Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Vhc1p patware: hosphonolated ku blk1p and Pkk2p. Plife.	2	2 2614	0.3952	2004.00	1422 645	I E	312.1 120	63 636364 K V1K2D1P1()254P1K214E1/41 4 E
91002102010110F_011000.1	1010000	rpk ip patimayo, phoophoryiatou by rink ip alla Flikzp, Flitp		2.0011	0.1704	1401.00	1402.040	U	4 02	00.000004 N. FINZD IF NZZO IF INZITETVIELE

		Long obein have reasonably inhibitor of protein kineses Rkh1p and Rkh2p, acts along								
gi 6321523 ref NP_011600.1	YGR086C	Long chain base-responsive initiation of protein kinases Pkrinp and Pkrizp, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p, Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	1	3.6638	0.2835	1561.78	1562.819	1	663.3	66.66667 L.K2Y1K2D1P1Q2S1P1K2I1E1V1L1.E
gi 6321523 ref NP_011600.1	YGR086C	with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	3.3673	0.1616	1544.97	1545.819	1	640.9	70.83333 L.KYKDPQSPKIEVL.E
gi 6321523 ref NP_011600.1	YGR086C	with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	1	3.3529	0.2138	1545.82	1545.819	1	533.7	58.333332 L.KYKDPQSPKIEVL.E
gi 6321523 ref NP_011600.1	YGR086C	with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	3.427	0.1941	1658.75	1658.979	4	582.3	61.538464 Y.LKYKDPQSPKIEVLE
gi 6321523 ref NP_011600.1	YGR086C	with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pl1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	4.9953	0.4064	1830.27	1830.999	1	846.2	62.5 L.L1E1L1L1D1D1S1P1V1T1P1G1E1T1R4P1A1.Y
gi 6321523 ref NP_011600.1	YGR086C	with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	4.7872	0.4783	1810.43	1810.999	1	1122.8	68.75 L.LELLDDSPVTPGETRPA.Y
gi 6321523 ref NP_011600.1	YGR086C	with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pli1p	2	3.9839	0.3617	1646.17	1646.72	1	1015.6	66.66667 Y.E1V1S1E1L1D1D1Q2F1I1D1R4Y1.D
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	2	3.3342	0.2054	1646.21	1644.85	1	472.9	61.538464 L.F1T1P1G1L1K2D1Y1D1F1V1V1D1L1.R
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	2	4.3517	0.2498	1530.81	1532.765	1	1269.9	81.818184 K.K2S1F1D1D1L1Y1K2I1I1F1Q2.M
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	1	2.6554	0.4313	1406.92	1407.612	1	354.4	62.5 F.HNFLPLPNLPSSA.K
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	1	2.3056	0.1978	1263.71	1264.455	1	472	70 F.H3N2F1L1P1L1P1N2L1P1S1.S
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	1	2.7348	0.287	1250.05	1249.455	1	577.5	70 F.HNFLPLPNLPS.S
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	1	2.2395	0.2078	1388.31	1389.634	3	403.5	60.000004 K.KSFDDLYKIIF.Q
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	2	3.0859	0.2088	1537.41	1535.786	1	518	57.692307 F.HNFLPLPNLPSSAK.T
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	2	3.2642	0.3039	1553.35	1554.786	2	509	57.692307 F.H3N2F1L1P1L1P1N2L1P1S1S1A1K2.T
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	2	3.9828	0.2639	1899.69	1901.003	1	697.6	66.66667 L.D1L1V1K2P1E1D1D111R4D1T1F1E1T1S1.I
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	2	3.95	0.3107	1879.47	1881.003	5	326.8	46.666668 L.DLVKPEDDIRDTFETS.I
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	2	3.0511	0.2126	1401.63	1402.634	1	798.6	80 K.K2S1F1D1D1L1Y1K2I11F1.Q
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	2	3.5662	0.3247	1517.35	1517.765	2	939.8	72.72727 K.KSFDDLYKIIFQ.M
gi 6321527 ref NP_011604.1	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p Component of the RNA polymerase II holoenzyme. phosphorytated in response to	2	2.9835	0.294	1364.51	1364.686	4	447.1	65 L.LTMPKELFEKK.D
gi 6321534 ref NP_011611.1	YGR097W	oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p Component of the RNA polymerase II holoenzyme, phosphorylated in response to	3	4.6834	0.3009	3035.27	3036.32	2	490	25.925926 F.L1T1D1I1D1E1T1T1N2T1I1T1D1P1F1T1T1A1P1R4G1P1K2K2A1Q2P1A1.Q
gi 6321534 ref NP_011611.1	YGR097W	oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p Component of the RNA polymerase II holoenzyme, phosphorvlated in response to	2	3.3438	0.3183	2931.83	2934.304	1	185.7	29.1666666 K.E1F111L1P1E1T1D1E1R4S1P1Y1F1I1N2V1P111P1K2A1Q2P1T1.S
gi 6321534 ref NP_011611.1	YGR097W	oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p Component of the RNA polymerase II holoenzyme, phosphorvlated in response to	3	4.713	0.3161	3001.49	3001.32	3	510.7	25.925926 F.LTDIDETTNTITDPFTTAPRGPKKAQPA.Q
gi 6321534 ref NP_011611.1	YGR097W	oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p Component of the RNA polymerase II holoenzyme, phosphorvlated in response to	2	3.3056	0.3358	1760.33	1758.974	1	582.2	57.14286 Q.HGIISKPPAFEWDNF.V
gi 6321534 ref NP_011611.1	YGR097W	oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p Component of the RNA polymerase II holoenzyme, phosphorylated in response to	2	3.1308	0.3077	1712.35	1712.882	1	388	61.538464 F.I1L1P1E1T1D1E1R4S1P1Y1F11N2.V
gi 6321534 ref NP_011611.1	YGR097W	oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p Component of the RNA polymerase II holoenzyme, phosphorylated in response to	2	3.379	0.3042	1970.17	1971.201	1	458.4	43.75 H.G11111S1K2P1P1A1F1E1W2D1N2F1V1T1Q2.H
gi 6321534 ref NP_011611.1	YGR097W	oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p Cvtrolasmic GTPase-activation protein for Ynt/Rab transport GTPases Ynt6p.	2	3.9692	0.3561	2355.77	2355.617	1	568.9	44.736843 Q.E1L1Q2H3G1111S1K2P1P1A1F1E1W2D1N2F1V1T1.Q
gi 6321537 ref NP_011614.1	YGR100W	Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function; Mdr1p Cvtoolsam; GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p	2	3.6369	0.2591	2023.91	2021.188	1	665.1	55.88235 K.YKLPANENILEDTNAEVS.F
gi 6321537 ref NP_011614.1	YGR100W	Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function; Mdr1p Cvtoolasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p	2	3.9872	0.3753	1890.81	1892.208	1	576.5	50 N.AALDPTHPKVIDLPTFR.M
gi 6321537 ref NP_011614.1	YGR100W	Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function; Mdr1p	2	3.9527	0.2718	1917.23	1915.208	9	516.7	53.125 N.A1A1L1D1P1T1H3P1K2V1I1D1L1P1T1F1R4.M

		Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p,								
ail6321537/rofIND_011614_1	VGP100W	Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Color secretory function: Mdr1p	2	3 1206	0 2151	18/1 00	19/3 13	1	567 3	53 333336 A A1I 1D1D1T1H3D1K2\/111D1I 1D1T1E1D4 M
gil0321337 [rei]INF_011014.1]	IGRIUUW	Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p,	2	3.1200	0.2131	1041.99	1043.13		507.5	55.555556 A.ATEIDTETTTISETK2VITIDTETETTTETK4.W
		Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of	-							
gi 6321537 ref NP_011614.1	YGR100W	Golgi secretory function; Mdr1p Nucleolar protein involved in rPNA processing and 60S ribocomal subunit	2	4.2468	0.1802	2206.25	2206.455	1	659.8	55.555557 M.NQIELPTGVTIDEEKYKVE.Q
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	3.0065	0.2407	2332.29	2330.548	9	181.2	36.842106 R.QEDSLLKLDPTEIEEDVKVE.S
		Nucleolar protein involved in rRNA processing and 60S ribosomal subunit								
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p Nucleolar protein involved in rPNA processing and 60S ribosomal subunit	3	4.9747	0.1998	2331.02	2330.548	1	1417.6	39.473686 R.QEDSLLKLDPTEIEEDVKVE.S
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	3	4.9274	0.2547	4522.4	4523.524	1	633.4	22.222223 E1T1E1L1D1T1F1.E
		Nucleolar protein involved in rRNA processing and 60S ribosomal subunit								
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	3.429	0.1684	2732.15	2731.929	6	306.5	36.363636 L.E1S1R4Q2E1D1S1L1L1K2L1D1P1T1E111E1E1D1V1K2V1E1.S
ail6321540/refINP 011617.1	YGR103W	biogenesis: constituent of several different pre-ribosomal particles: Nop7p	2	3.0615	0.2569	1809.73	1809.09	1	929.5	64.28571 F.KFPENIPSDVDFRIM.L
51		Nucleolar protein involved in rRNA processing and 60S ribosomal subunit								
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	3	3.8777	0.366	2746.73	2747.995	1	629.9	30.681818 L.D1H3I1I1K2E1R4Y1P1S1F1P1D1A1I1R4D1I1D1D1A1L1N2.M
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	3	4.2228	0.2921	2878.58	2880.187	1	830.4	28.260868 L.D1H3I1I1K2E1R4Y1P1S1F1P1D1A1I1R4D1I1D1D1A1L1N2M1.L
		Nucleolar protein involved in rRNA processing and 60S ribosomal subunit								
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	4.3227	0.3429	1708.67	1705.997	1	1526.9	82.14286 N.KYLPGEALPPHLSPW.G
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	3	4.6195	0.1886	2353.64	2353.548	2	764	31.578945 R.Q2E1D1S1L1L1K2L1D1P1T1E1I1E1E1D1V1K2V1E1.S
		Nucleolar protein involved in rRNA processing and 60S ribosomal subunit								
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p Nucleolar protein involved in rRNA processing and 60S ribosomal subunit	2	3.4169	0.29	2264.41	2265.464	3	294.2	41.6666664 K.E1R4Y1P1S1F1P1D1A1I1R4D1I1D1D1A1L1N2M1.L
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	3.5801	0.2055	1829.73	1829.09	1	952	64.28571 F.K2F1P1E1N2I1P1S1D1V1D1F1R4I1M1.L
		Nucleolar protein involved in rRNA processing and 60S ribosomal subunit								
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	3.0297	0.2224	1518.67	1516.642	1	718.9	66.66667 K.LDPTEIEEDVKVE.S
gi 6321540 ref NP 011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	3.4258	0.2401	1727.19	1724.997	1	967.1	67.85714 N.K2Y1L1P1G1E1A1L1P1P1H3L1S1P1W2.G
		Nucleolar protein involved in rRNA processing and 60S ribosomal subunit								
gi 6321540 ref NP_011617.1	YGR103W	biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	4.8058	0.4135	1819.29	1820.101	1	1427	80 A.NKYLPGEALPPHLSPW.G
ail6321540/refINP 011617.1	YGR103W	biogenesis: constituent of several different pre-ribosomal particles: Nop7p	2	5.2126	0.4405	1841.35	1841.101	1	1486.1	76.6666664 A.N2K2Y1L1P1G1E1A1L1P1P1H3L1S1P1W2.G
51		Essential protein that interacts with histones and is involved in nucleosome								
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	2	3.2456	0.1907	1479.55	1479.67	1	670	68.181816 Q.DIYDLEDLKKNL.M
ail6321552 refINP 011631.1	YGR116W	disassembly and reassembly during transcription elongation; Sot6p	2	3.3178	0.311	2464.31	2465.569	1	303.1	36.11111 S.W2N2E1K2R4Q2K2Y1E1D1L1E1H3D1Q2L1D1S1T1.R
31		Essential protein that interacts with histones and is involved in nucleosome								
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	3	6.7143	0.4254	4436.72	4437.422	1	1429.8	25.657896 F.GDGHDYDWALEIENEELENGNDNNEAEEEEIDEETGAIK.S
ail6321552 refINP 011631.1	YGR116W	disassembly and reassembly during transcription elongation; Sot6p	3	7,7503	0.504	4484.84	4485.422	1	2360	28.947369 I1D1E1E1T1G1A111K2.S
31		Essential protein that interacts with histones and is involved in nucleosome								
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	2	3.2003	0.1866	1645.57	1642.847	1	2075.8	87.5 Q.K2Y1N2D1L1D1Q2I1I1V1E1Y1L1.Q
gi 6321552 ref NP 011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	3	4.0351	0.2083	2863.58	2866.14	1	837.7	33.695652 Y.K2I1V1D1N2P1F1D1K2T1N2P1E1K2F1E1D1T1L1D1N2I1I1Q2.S
		Essential protein that interacts with histones and is involved in nucleosome								
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	2	3.6749	0.2298	2864.71	2866.14	3	486.9	39.130436 Y.K2I1V1D1N2P1F1D1K2T1N2P1E1K2F1E1D1T1L1D1N2I1I1Q2.S
gi 6321552 ref NP 011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	2	3.5636	0.1934	1626.49	1626.847	1	1999.6	79.16667 Q.KYNDLDQIIVEYL.Q
31		Essential protein that interacts with histones and is involved in nucleosome								
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	2	2.9153	0.2561	2089.21	2089.359	2	269.3	41.17647 Q.NSERAAQEFPNKPPLVKY.C
gi 6321552 ref NP 011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	3	4.0128	0.2321	3135.02	3132.148	1	700.5	27.083334 L.DELDDFIEDDEFSDEDDETRQRRIQ.E
		Essential protein that interacts with histones and is involved in nucleosome								
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	3	4.6285	0.2894	3168.41	3168.148	1	808.6	30.208334 L.D1E1L1D1D1F1I1E1D1D1E1F1S1D1E1D1D1E1T1R4Q2R4R4I1Q2.E
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	2	3.6072	0.2334	2833.87	2835.14	2	499.2	36.95652 Y.KIVDNPFDKTNPEKFEDTLDNIIQ.S
		Essential protein that interacts with histones and is involved in nucleosome								
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	3	4.1783	0.225	2463.77	2465.569	1	1032	41.666664 S.W2N2E1K2R4Q2K2Y1E1D1L1E1H3D1Q2L1D1S1T1.R
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	2	3.8922	0.2834	2434.69	2435.569	1	576.6	50 S.WNEKRQKYEDLEHDQLDST.R
		Essential protein that interacts with histones and is involved in nucleosome								
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	2	3.7931	0.3083	2464.47	2465.569	1	561	50 S.W2N2E1K2R4Q2K2Y1E1D1L1E1H3D1Q2L1D1S1T1.R
gi 6321552 ref NP_011631.1	YGR116W	disassembly and reassembly during transcription elongation; Spt6p	3	3.9505	0.3635	2233.1	2233.489	1	863.7	34.210526 Q.HQIHPPVDHPSSKPVEVIES.I
		Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine								
gi 6321563 ref NP_011640.1	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	3.0312	0.2171	2127.11	2128.389	1	415.8	53.125 T.DEPDVKPYLPEEILWRQ.K
gi 6321563 ref NP_011640.1	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	3.3541	0.2156	1709.87	1710.968	4	449.3	61.538464 L.E1A1R4V1P1F1L1D1K2D1F1L1Q2L1.C
		Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine								
gi 6321563 ref NP_011640.1	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	3.0354	0.2107	1881.67	1883.179	1	600.5	50 W.G1L1E1A1R4V1P1F1L1D1K2D1F1L1Q2L1.C
gi 6321563 ref NP_011640.1	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	4.2454	0.1944	1671.97	1669.912	1	1765.9	87.5 A.R4V1P1F1L1D1K2D1F1L1Q2L1C1.M
		Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine								
gi 6321563 ref NP_011640.1	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	2.9448	0.2227	1650.69	1651.912	1	422.8	70.83333 A.RVPFLDKDFLQLC.M
gi 6321563 ref NP_011640.1	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	3.9533	0.3131	2151.45	2151.389	1	618.7	62.5 T.D1E1P1D1V1K2P1Y1L1P1E1E1I1L1W2R4Q2.K
		Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine								
gilb321563[ref]NP_011640.1]	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Ash2p Asparagine synthetase isozyme of Ash1p; catalyzes the synthesis of L-asparagine	2	2.9105	0.2585	2470.37	2471.688	1	285.9	47.368423 F.D11111D1E1P1D1V1K2P1Y1L1P1E1E111L1W2R4Q2.K
gi 6321563 ref NP_011640.1	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	4.9511	0.4326	1877.49	1879.076	1	928.9	71.42857 D.W2L1D1E1K2R4I1P1S1T1P1V1D1Y1H3.A
	VOD404W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine	~	4 5500	0.4046	0400.00	0400 504		4070	
gijusz i sosjreijiNP_011640.1	IGR 124W	Asparagine synthetase, isozyme of Asn1p; catalvzes the synthesis of L-asparagine	3	4.0582	0.1842	2109.68	2109.524	1	1070	40.000204 G.WHNZHUTP INZETRZWITTRZPTRZETGTR4HET.K
gi 6321563 ref NP_011640.1	YGR124W	from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	3.5087	0.189	1378.01	1378.614	1	1444.8	80 A.RVPFLDKDFLQ.L
gil6321563[rof[NID_044640.4]	VCP124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine	2	4 4400	0 1640	1508 20	1509 772	0	1252.2	77 27273 A R4V/101E11 101K201E11 1021 1 C
gi 6321595 ref NP_011672.1	YGR124W	Pta1p Interacting protein; Pti1p	2	4.4193	0.1649	1491.29	1492.871	9 8	540.2	54.166668 N.L1S1K2I1P1P1L1Q2L11E1I11.S
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	3.3069	0.2544	1793.89	1793.157	1	657.7	53.333336 Q.NLSKIPPLQLIEIISN.L

gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	4.3413	0.1808	1679.73	1679.053	4	934.3	64.28571 L.SKIPPLQLIEIISNL.K
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	4.2893	0.3195	1694.49	1697.053	1	1120.6	71.42857 L.S1K2I1P1P1L1Q2L1I1E1I1I1S1N2L1.K
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	3.7594	0.2306	1794.49	1792.213	1	1037.5	63.333332 N.LSKIPPLQLIEIISNL.K
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	3.5325	0.2045	1926.59	1927.316	2	644.9	50 Q.N2L1S1K2I1P1P1L1Q2L1I1E1I1I1S1N2L1.K
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	2.9121	0.2499	1904.79	1906.316	1	653.9	46.875 Q.NLSKIPPLQLIEIISNL.K
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	3.2815	0.2447	1568.37	1565.894	1	1546.9	76.92308 L.SKIPPLQLIEIISN.L
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	2.9454	0.1576	1581.53	1582.894	1	608.2	53.846157 L.S1K2I1P1P1L1Q2L1I1E1I1I1S1N2.L
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	3.7177	0.1629	1365.45	1364.712	1	813.1	77.27273 L.SKIPPLQLIEII.S
gi 6321595 ref NP_011672.1	YGR156W	Pta1p Interacting protein; Pti1p	2	4.0767	0.2104	1378.59	1378.712	1	839.1	77.27273 L.S1K2I1P1P1L1Q2L1I1E1I1I1.S
		Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the								
		conversion of phosphatidylethanolamine to phosphatidylcholine during the								
gi 6321596 ref NP_011673.1	YGR157W	methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	4.2997	0.3259	2034.97	2033.28	1	817.4	59.375 N.T1T1T1P1E1L1F1E1K2D1L1T1E1F1L1T1K2.V
		Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the								
		conversion of phosphatidylethanolamine to phosphatidylcholine during the								
gi 6321596 ref NP_011673.1	YGR157W	methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	4.2966	0.4255	2228.73	2228.527	1	1348.3	55.88235 L.NWKMPIELYNGDDWIGLY.K
		Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the								
		conversion of phosphatidylethanolamine to phosphatidylcholine during the								
gi 6321596 ref NP_011673.1	YGR157W	methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	4.4009	0.4824	2135.51	2135.423	1	973.8	56.25 N.W2K2M1P1I1E1L1Y1N2G1D1D1W2I1G1L1Y1.K
		Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the								
		conversion of phosphatidylethanolamine to phosphatidylcholine during the								
gi 6321596 ref NP_011673.1	YGR157W	methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	3.1608	0.2573	1207.33	1206.434	1	647.5	75 L.N2W2K2M1P1I1E1L1Y1.N
		Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the								
		conversion of phosphatidylethanolamine to phosphatidylcholine during the								
gi 6321596 ref NP_011673.1	YGR157W	methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	3.1787	0.2223	1195.23	1194.434	1	870.6	87.5 L.NWKMPIELY.N
		Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the								
		conversion of phosphatidylethanolamine to phosphatidylcholine during the								
gi 6321596 ref NP_011673.1	YGR157W	methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	5.4345	0.4652	2249.77	2251.527	1	1599.9	58.823532 L.N2W2K2M1P1I1E1L1Y1N2G1D1D1W2I1G1L1Y1.K
		Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA								
gi 6321599 ref NP 011675.1	YGR159C	processing and ribosome biogenesis; Nsr1p	1	2.7987	0.2702	1310.67	1311.437	4	229.9	60.000004 F.NADRDAIFELF.A
510000		Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA								
ail6321599/refINP 011675.1	YGR159C	processing and ribosome biogenesis: Nsr1p	1	2.6706	0.1727	1325.59	1326.437	1	290.1	65 F.N2A1D1R4D1A111F1E1L1F1.A
3.1		Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA								
gil6321599/refINP_011675_1	YGR159C	processing and ribosome biogenesis: Nsr1p	2	3 1309	0 1767	1336 23	1334 488	2	459	72 22222 S W2S111D1D1E1W2I 1K2K2 E
giloo21000[ici]i4i _011010.1]	101(1000	Nucleolar protein that binds nuclear localization sequences required for pre-rRNA	2	0.1000	0.1707	1000.20	1004.400	2	400	
ail6321599/refINP_011675_1	VGR159C	processing and ribosome biogenesis: Nsr1p	2	4 2671	0.4575	2246 53	2244 509	1	530.6	47 368423 W SIDDEWI KKEEEHIGGVIGA R
giloo21000[ici]i4i _011010.1]	101(1000	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	2	4.2071	0.4070	2240.00	2244.000		000.0	
ail6321599/refINP_011675_1	VGR159C	processing and ribosome biogenesis: Ner1p	2	4 0411	0 3192	1825.49	1824 046	1	1165.7	
giloo21000[ici]i4i _011010.1]	101(1000	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	2	4.0411	0.0102	1020.40	1024.040		1100.7	
gil6321599/refINP_011675_1	YGR159C	processing and ribosome biogenesis: Nsr1p	2	4 1713	0.3019	1849 53	1847 046	1	982 1	63 333332 V S1V1R4I1P1T1H3P1E1T1E1O2P1K2G1E1 G
gilooz recelicititi _errererit	10111000	Nucleolar protein that binds nuclear localization sequences required for pre-rRNA	-		0.0010	1010.00	10111010		002.1	
ail6321599/refINP_011675_1	VGR159C	processing and ribosome biogenesis: Nsr1p	2	4 8883	0.4	2403 29	2400 696	1	1322.1	52 499996 W SIDDEWI KKEEEHIGGVIGAR V
gilooz recelicititi _errererit	10111000	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	-		0.1	2100.20	2100.000		TOLL	
gil6321599/refINP_011675_1	YGR159C	processing and ribosome biogenesis: Nsr1p	3	4 036	0 2503	1824 65	1824 046	3	715.3	45 V SVRIPTHPETEOPKGE G
gilooz recelicititi _errererit	10111000	Nucleolar protein that binds nuclear localization sequences required for pre-rRNA	0	1.000	0.2000	102 1100	102 110 10	0	1 10.0	
gil6321599/refINP_011675_1	YGR159C	processing and ribosome biogenesis: Nsr1p	2	3 5538	0.3253	2173 77	2173 43	1	580.3	50 W SIDDEWI KKEEEHIGGVIG A
3.1		Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	-							
ail6321599/refINP_011675_1	VGR159C	processing and ribosome biogenesis: Nsr1p	3	4 2413	0.262	1637 27	1637 836	1	1394.8	57 692307 V RIPTHPETEOPKGE G
giloo21000[ici]i4i _011010.1]	101(1000	Nucleolar protein that binds nuclear localization sequences required for pre-rRNA	0	4.2410	0.202	1007.27	1007.000		1004.0	
ail6321599/refINP_011675_1	VGR159C	processing and ribosome biogenesis: Nsr1p	з	3 8846	0 2165	2938.07	2030 106	1	312	29 K FIDGRPINCOM@STSKPAGNNDRAKKEG
giloo21000[ici]i4i _011010.1]	101(1000	Nucleolar protein that binds nuclear localization sequences required for pre-rRNA	0	0.0040	0.2100	2000.07	2000.100		012	
gil6321599/refINP_011675_1	YGR159C	processing and ribosome biogenesis: Nsr1p	2	3 5031	0.3136	1823 43	1824 046	1	732.2	56 666668 V SVRIPTHPETEOPKGE G
giloo21000[101]11 _01101011]	10111000	Nucleolar protein that hinds nuclear localization sequences, required for pre-rRNA	-	0.0001	0.0100	1020.10	10211010	•	102.2	
gil6321599/refINP_011675_1	YGR159C	processing and ribosome biogenesis: Nsr1p	2	3 1938	0 2844	1636 63	1637 836	1	723.4	65 38461 V RIPTHPETEOPKGE G
giloo21000[101]11 _01101011]	10111000	Nucleolar protein that hinds nuclear localization sequences, required for pre-rRNA	-	0.1000	0.2011	1000.00	1001.000	•	120.1	
ail6321500/rofIND_011675_1	VCP150C	processing and ribosome biogenesis: Ner1p	2	3 2586	0 2200	1322.21	1320 488	1	811.5	
gil0521555[rei]14F_011075.1]	101(1550	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	2	3.2300	0.2335	1322.21	1320.400		011.5	00.00009 S.WSIDDEWERR.E
ail6321599/refINP_011675_1	VGR159C	processing and ribosome biogenesis: Nsr1p	2	3 6149	0 3623	2196 37	2197 43	1	409.4	41 666664 W S1I1D1D1E1W2I 1K2K2E1E1E1H3I1G1G1V1I1G1 A
gil0521555[rei]14F_011075.1]	101(1550	Nucleolar protein that hinds nuclear localization sequences, required for pre-rPNA	2	3.0143	0.3023	2130.37	2137.45		403.4	41.000004 W.STITDTDTETW2EIN2R2EITTETHSHGTGTVTHGT.A
ail6321500/rofIND_011675_1	VCP150C	processing and ribosome biogenesis: Ner1p	2	1 1724	0 3460	2128 63	2120 378	1	485.2	50 W/ S111D1D1E1W2I 1K2K2E1E1E1H3I1C1C1V111 C
gil0321399[rei]ivF_011075.1]	IGK159C	Nucleolar protein that hinds nucleon localization acquishes required for the rPNA	2	4.1724	0.3409	2130.03	2139.370	'	403.2	50 W.3111D1D1E1W2E1K2K2E1F1E1H3H313131111.3
	VOD4500	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	2	2 0000	0.0050	0447.44	0440 070		201 5	
gil6321599[rei]NP_011675.1]	IGR 1590	processing and hoosome biogenesis; hisrip	2	3.8086	0.3956	2117.11	2110.378		301.5	44.11765 W.SIDDEWLKKEFERIGGVI.G
	VOD4500	Nucleolar protein that binus nuclear localization sequences, required for pre-initia	0	2 00 20	0.0470	0007.05	2200 500		c24	
gil0321399[rei]ivF_011075.1]	IGK159C	Nucleolar protein that hinds publicar legalization acquisition required for pro rBNA	2	3.9020	0.3476	2207.33	2209.009	'	034	42.105203 W.3111D1D1E1W2E1K2K2E1F1E1H311G1G1V111G1A1.K
ail6221E00IrofIND_01167E_1	VCP150C	nucleolar protein that binds nuclear localization sequences, required for pre-IRNA	2	4 9674	0.0776	1627.24	1627 926	1	11/7 1	
gil6321599[rei]NP_011675.1]	IGR 1590	processing and housene biogenesis; his rip	3	4.2071	0.2776	1637.24	1037.030		1147.1	53.840157 V.RIPTHPETEQPKGF.G
ail6221E00IrofIND_01167E_1	VCP150C	nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	2	4 1014	0.2107	1000 50	1924.046	2	050.7	
gil0321399[rei]ivF_011075.1]	IGK159C	Nucleolar protein that hinds nucleon localization acquishes required for the rPNA	3	4.1014	0.3107	1022.02	1024.040	2	959.7	40.333332 V.3VKIFTHEELEQEKOF.0
	VOD4500	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	2	0.0004	0.000	4007.45	4007.000		C02 4	
gil6321599[rei]NP_011675.1]	IGR 1590	processing and hoosome biogenesis; instrip	2	3.2931	0.293	1637.45	1037.830	1	603.4	05.36401 V.RIPTHPETEQPKGF.G
	VOD4500	Nucleolar protein that binus nuclear localization sequences, required for pre-initia	0	2 64 00	0.0575	4057 70	4050.000		770 5	
gil6321599[rei]NP_011675.1]	IGR 1590	processing and housene biogenesis; his rip	2	3.6109	0.3575	1657.79	1000.000		118.5	09.230774 V.R4IIPTTTH3PTETTTETQ2PTR2GTFT.G
ail6221E00IrofIND_01167E_1	VCP150C	nucleolar protein that binds nuclear localization sequences, required for pre-rRNA	2	2 9656	0.2617	1000.05	1924.046	1	021.0	
gil0321399[rei]ivF_011075.1]	IGK159C	processing and hoosome biogenesis, rish tp	2	3.0000	0.3017	1022.00	1024.040	'	921.9	03.333332 V.3VRIFTHELEQEROF.0
		Translation initiation factor of E4C, suburit of the mDNA and binding protein complex.								
		(a)E4E) that also contains a E4E (Cda22a), consistent with the part (A) his disc								
-:::C224.004	VOD4COW	(eIF4F) that also contains eIF4E (Cocosp); associates with the poly(A)-binding		0.0700	0.0700	4000.00	4000 544		250.0	
gil6321601[rei]NP_011678.1]	IGR 162W	protein Pabilp, also interacts with eiF4A (Tilitp); homologous to Til4632p; Til4631p		2.3728	0.2738	1308.02	1309.514		359.6	54.545456 L.KDATPIEDVFSF.N
		Translation initiation factor aIE4C, automit of the mBNA can binding protain complex								
		(a)E4E) that also contains a)E4E (Cda22a), according to the high the part (A) binding								
	VOD4COW	(eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding	0	4 005 4	0.0477	0070.04	0070 500		4000.4	
giju321001[rei[NP_011078.1]	1 GR 102W	protent rap ip, also interacts with eir 4A (Till Ip); nomologous to Til4632p; Til4631p	2	4.0004	0.3477	2312.21	2312.302	1	1030.1	JI. 19200 E. OAF VEFOEWVNEE I EVAE I EVA.N
		Translation initiation factor eIE4C, subunit of the mDNA can binding protois according								
		(elE4E) that also contains elE4E (Cdc33p); associates with the poly(A)-binding								
dil6321601/ref/ND_011679_1	YGR162M	notein Pah1n, also interacts with eIF44 (Tif1n); homologous to Tif4622n; Tif4624n	2	4 2886	0 2059	2307 61	2397 502	1	720 5	47 61905 E S141P1\/1P1P1S1E1O2\/1K2E1E1T1E1\/1A1E1T1E1O2S1 N
9100210011c11076.1	10110210	proton i ao ip, also interacis with en 4A (111 p), nonologous to 1114032p, 1114031p	2	4.2000	0.2900	2007.01	2001.002	1	120.0	TO THE REPORT OF THE
		Translation initiation factor eIE4G, subunit of the mRNA can-binding protein complex								
		(eIF4F) that also contains eIF4F (Cdc33p); associates with the poly(A)-hinding								
		(and a set of the set			0.0500	0000 75	0000 400		050 5	
ail6321601 refINP 011678 1	YGR162W	DIDIEIN PAD D. AISO INTERACIS WITH EIF4A (LITID)' NOMOLOGOUS TO LIT46320' LIT46320	2	4,4016	0.3583	223875	2236.493	1	9535	57.894737 L.MKDLTDSPSEETLESVVETT N
gi 6321601 ref NP_011678.1	YGR162W	protein Pab1p, also interacts with eiF4A (Tir1p); nomologous to Tir4632p; Tir4631p	2	4.4016	0.3583	2238.75	2236.493	1	953.5	57.894737 L.MKDLTDSPSEETLESVVELL.N

gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.8996	0.3094	2067.33	2067.304	1	447.3	55.88235 E.EKREDDKPKEEVAPLVPS.A
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.5987	0.3549	2089.67	2091.304	1	511.3	50 E.E1K2R4E1D1D1K2P1K2E1E1V1A1P1L1V1P1S1.A
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.2536	0.2582	2375.05	2375.725	2	191.2	31.818182 A.GSAPANPIPVEEKSPVPTKIEIT.T
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	5.3937	0.354	3383.21	3383.648	1	560.1	27.5 K.TKPAEEKSAEPEVKQETPAEEGEQGEKGQIK.E
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	4.8364	0.477	2056.07	2057.309	1	782.6	61.764706 K.LAPDGKTELLDKDEVERK.M
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.3754	0.3254	2400.91	2401.725	1	276.2	31.818182 A.G1S1A1P1A1N2P1I1P1V1E1E1K2S1P1V1P1T1K2I1E1I1T1.T
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	4.8273	0.2578	3046.13	3046.315	1	874.9	37 Q.KEREEKTEGKENKEVPVQEETKSAIE.S
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	5.7101	0.1673	3472.79	3472.751	1	572	30.357143 K.K2Q2Q2K2E1R4E1E1K2T1E1G1K2E1N2K2E1V1P1V1Q2E1E1T1K2S1A1I1E1.S
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.8304	0.385	2178.19	2179.293	1	735.3	52.63158 E.S1A1P1V1P1P1S1E1Q2V1K2E1E1T1E1V1A1E1T1E1.Q
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.9235	0.4215	2156.57	2157.293	1	870.8	60.526318 E.SAPVPPSEQVKEETEVAETE.Q
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	5.1631	0.451	3013.55	3014.183	1	1408.4	32.407406 K. TKPAEEKSAEPEVKQETPAEEGEQGEKG.Q
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	6.2073	0.5094	3047.33	3048.183	1	1436.1	34.25926 K.T1K2P1A1E1E1K2S1A1E1P1E1V1K2Q2E1T1P1A1E1E1G1E1Q2G1E1K2G1.Q
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.5839	0.3379	1622.41	1623.803	1	512.6	57.692307 F.NYPEGIEGPDIKYK.K
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	7.107	0.3018	3420.83	3422.648	1	1828.1	K.T1K2P1A1E1E1K2S1A1E1P1E1V1K2Q2E1T1P1A1E1E1G1E1Q2G1E1K2G1Q2I1 39.166668 K2.E
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	4.9311	0.3576	2611.34	2610.965	1	683.1	29.347824 K. VVKELNPDITDETNEGKTGPKLVL.H
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	4.0188	0.2218	3173.21	3174.446	1	542.4	29.807693 Q.QKEREEKTEGKENKEVPVQEETKSAIE.S
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	4.2802	0.1776	3210.05	3212.446	2	480.8	29.807693 Q.Q2K2E1R4E1E1K2T1E1G1K2E1N2K2E1V1P1V1Q2E1E1T1K2S1A111E1.S
ail6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1o. also interacts with eIF4A (Tif1o): homologous to Tif4632p: Tif4631p	3	5.1479	0.3484	3430.91	3430.751	1	431	25 K.KOQKEREEKTEGKENKEVPVQEETKSAIE.S
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	3	5.1734	0.4674	2701.49	2704.051	1	377.5	32.954548 K K2T1E1K2K2L1A1P1D1G1K2T1E1L1L1D1K2D1E1V1E1R4K2.M
gi 6321601 ref NP 011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.3055	0.2679	1802.29	1803.052	3	382.6	50 D.KLPTNEDGTPLEPEMM.S
gi 6321601 ref NP_011678.1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	2	3.0542	0.314	1384.79	1382.514	1	1254.3	81.818184 L.K2D1A1T1P111E1D1V1F1S1F1.N
ail6321601/ref/NP_011678_1	YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pablic also interacts with eIF4A (Tif1a): homologues to Ti4632b.	-	2.7447	0.3437	1381 61	1382 514	1	583.9	68 181816 L K2D1A1T1P11E1D1V1E1S1E1 N
gi 6321611 ref NP_011688.1	YGR172C	Integral membrane protein required for the biogenesis of ER-derived COPII transport vesicles; interacts with Yif1p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p	2	2.9601	0.1883	1678.35	1678.882	1	424.9	53.571426 K.GYPHEPPLLEEIGIN.F

		Integral membrane protein required for the biogenesis of ER-derived COPII transport								
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with rinp and yos1p; iocalizes to the Goigi, the ER, and COPII vesicles; Yip1p Integral membrane protein required for the biogenesis of ER-derived COPII transport	2	3.6831	0.2495	2017.43	2017.24	1	450.3	52.941177 L.S1T1K2G1Y1P1H3E1P1P1L1L1E1E1I1G1I1N2.F
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with Yif1p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p Integral membrane protein required for the biogenesis of ER-derived COPII transport	2	3.7661	0.3818	1847.31	1845.059	1	939.4	60.000004 K.G1Y1P1H3E1P1P1L1L1E1E1I1G1I1N2F1.D
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with Yi11p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p Integral membrane protein required for the biogenesis of ER-derived COPII transport	2	3.2748	0.2214	1697.93	1696.882	2	337.5	50 K.G1Y1P1H3E1P1P1L1L1E1E1I1G1I1N2.F
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with Yif1p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p Integral membrane protein required for the biogenesis of ER-derived COPII transport	2	3.4393	0.297	1824.67	1826.059	1	1388.7	66.66667 K.GYPHEPPLLEEIGINF.D
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with Yi11p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p Integral membrane protein required for the biogenesis of ER-derived COPII transport	2	3.8087	0.2889	1995.11	1995.24	1	501.4	44.11765 LSTKGYPHEPPLLEEIGIN.F
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with Yi11p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p Integral membrane protein required for the biogenesis of ER-derived COPII transport	2	4.2327	0.4165	2143.13	2142.416	1	1079.4	58.333332 LSTKGYPHEPPLLEEIGINF.D
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with Yi11p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p Integral membrane protein required for the biogenesis of ER-derived COPII transport	2	4.2072	0.4555	2165.43	2165.416	1	919.6	52.77778 LS1T1K2G1Y1P1H3E1P1P1L1L1E1E1I1G1I1N2F1.D
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with Yi11p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p Integral membrane protein required for the biogenesis of ER-derived COPII transport	2	2.9754	0.1566	1403.23	1400.821	2	711.6	54.545456 H.I1I1T1K2T1K2M\$V1L1I1P1I1.R
gi 6321611 ref NP_011688.1	YGR172C	vesicles; interacts with Yif1p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p Protein with similarity to mammalian developmentally regulated GTP-binding protein;	1	2.3634	0.2448	1116.77	1117.481	3	374.6	75 T.KMVLIPIRF.G
gi 6321612 ref NP_011689.1	YGR173W	Rbg2p	2	4.5723	0.2724	2091.21	2090.168	1	1661	68.75 L.V1R4D1D1Q2C1T1I1D1D1F1I1D1V1I1N2E1.Q
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	4.2774	0.2733	2220.19	2220.298	1	1094.6	64.70589 L.V1R4D1D1Q2C1T111D1D1F111D1V111N2E1Q2.H
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	4.7744	0.2787	2197.33	2196.298	1	1640.1	73.52941 L.VRDDQCTIDDFIDVINEQ.H
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.5169	0.3222	1386.91	1387.576	1	1038	72.72727 A.SLEKELENVGIR.L
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.0476	0.179	2798.85	2800.907	7	190.7	30.952381 L.V1R4D1D1Q2C1T1I1D1D1F1I1D1V1I1N2E1Q2H3R4N2Y1.V
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.0506	0.2392	2766.41	2766.907	3	243.1	28.57143 L.VRDDQCTIDDFIDVINEQHRNY.V
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	3	4.2116	0.3244	1946.33	1946.27	1	1231.4	40.625 M.GIIDKIKAIEEEMARTQ.K
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	3	4.6815	0.381	1969.79	1969.27	1	1689.3	42.1875 M.G1I1I1D1K2I1K2A1I1E1E1E1M1A1R4T1Q2.K
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.9675	0.3359	1966.95	1969.27	1	481.4	53.125 M.G1I1I1D1K2I1K2A1I1E1E1E1M1A1R4T1Q2.K
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.2904	0.277	1406.53	1404.576	1	1099.7	72.72727 A.S1L1E1K2E1L1E1N2V1G1I1R4.L
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	3	6.3114	0.4004	2802.53	2800.907	1	1408.5	40.476192 L.V1R4D1D1Q2C1T111D1D1F111D1V111N2E1Q2H3R4N2Y1.V
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.1306	0.2868	1617.25	1614.842	1	793.9	73.07692 Q.RASLEKELENVGIR.L
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.1432	0.2586	1636.07	1636.842	1	290.3	46.153847 Q.R4A1S1L1E1K2E1L1E1N2V1G111R4.L
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	3	4.1961	0.2742	1967.75	1969.27	1	1883.7	43.75 M.G1I1I1D1K2I1K2A1I1E1E1E1M1A1R4T1Q2.K
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.6496	0.3153	1966.33	1969.27	1	755.6	50 M.G1I1I1D1K2I1K2A1I1E1E1E1M1A1R4T1Q2.K
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	3.5394	0.2502	1943.37	1946.27	1	1280.6	59.375 M.GIIDKIKAIEEEMARTQ.K
gi 6321612 ref NP_011689.1	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	2	4.0663	0.2974	2067.37	2068.168	1	967.7	59.375 L.VRDDQCTIDDFIDVINE.Q
		Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific								
gi 6321614 ref NP_011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	3.8965	0.3255	2025.77	2027.239	3	358.4	52.941177 L.KDLVKDGNDKVLEDSTIH.I
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	2.9064	0.2307	1992.61	1993.221	1	462.4	53.125 K.KIGDLDFSDREKVLDELL
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	3.3066	0.1617	2013.93	2015.221	2	347.5	50 K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1.L
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	3	4.051	0.3318	2410.88	2409.645	4	415.2	31.578945 K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1Y1.H
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	3	4.5019	0.322	2522.27	2521.786	1	811.6	38.75 K.KIGDLDFSDREKVLDELLDYH.F
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	3.4063	0.305	2546.85	2549.786	1	586.7	45 K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1Y1H3.F
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	4.3478	0.3286	2520.55	2521.786	1	1001.3	55 K.KIGDLDFSDREKVLDELLDYH.F
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	2.9595	0.1949	2826.35	2828.078	2	262.8	31.818182 K.K211G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1Y1H3F1E1.R
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinatine: Erg1p Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	3.0173	0.2781	2797.59	2798.078	1	373.8	36.363636 K.KIGDLDFSDREKVLDELLDYHFE.R
gi 6321614 ref NP_011691.1	YGR175C	prays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	3	3.9583	0.1883	2555.36	2555.806	1	468.6	31.578945 L.DFSDREKVLDELLDYHFERK.S

		Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;								
gi 6321614 ref NP_011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	3.4106	0.1892	1510.37	1510.731	1	401.5	75 A.K2V1D1I1D1G1R4G1K2V1E1F1K2.A
		Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;								
ail6321614 refINP 011691.1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine: Erg1p	2	4,7908	0.382	2267.89	2268.572	1	814.5	65.789474 E.KLKDLVKDGNDKVLEDSTIH.I
		Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;								
ail6321614/refINP_011691_1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinatine: Erg1p	3	4 9349	0.3893	3083.81	3082 44	1	842 1	27 083334 K KIGDI DESDREKVI DELI DYHEERK S
gilooz to tilioitat _ottoottil	1011100	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	0	1.0010	0.0000	0000.01	0002.111		0.2.1	
ail62216141rofIND_011601_1	VCB175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific	2	2 2607	0 2211	1661 42	1650 942	1	976 E	
gilo321014[rei]NP_011091.1]	IGR1/5C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	3.3007	0.3211	1001.43	1009.042	1	676.S	67.89714 F.RKELHPDHVF1VGSS.F
		plays an essential role in the ergosterol-biosynthesis pathway and is the specific								
gi 6321614 ref NP_011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p Squalene enovidase, catalyzes the enovidation of squalene to 2.3-ovidosqualene:	2	3.1311	0.1766	2633.11	2634.066	4	348.5	34.090908 W.MIKDVQPFIPKSLRPSFDEAVSQ.G
		plays an essential role in the ergosterol-biosynthesis pathway and is the specific								
gi 6321614 ref NP_011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p	2	4.3182	0.4063	2386.65	2384.645	1	384	50 K.KIGDLDFSDREKVLDELLDY.H
		plays an essential role in the ergosterol-biosynthesis pathway and is the specific								
gi 6321614 ref NP_011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p	3	5.5372	0.2989	2295.26	2295.572	1	2019.3	43.421055 L.K2D1L1V1K2D1G1N2D1K2V1L1E1D1S1T1I1H3I1K2.D
		Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific								
gi 6321614 ref NP_011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p	2	4.6105	0.3188	2267.09	2268.572	1	997.9	55.263157 L.KDLVKDGNDKVLEDSTIHIK.D
		Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;								
gi 6321614 ref NP 011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p	3	4.1938	0.4046	2795.36	2798.078	1	832.3	32.954548 K.KIGDLDFSDREKVLDELLDYHFE.R
		Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;								
ail6321614/refINP_011691_1	YGR175C	plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinatine: Erg1p	2	4 1663	0.3001	1694 15	1694 833	4	516.8	57 142861 K2D1I 1V1K2D1G1N2D1K2V1I 1E1D1S1 T
gilosz to talicitat _011001.1	101(1100	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	4.1000	0.0001	1004.10	1004.000	-	010.0	
	VOD4750	plays an essential role in the ergosterol-biosynthesis pathway and is the specific	0	0 5 475	0.0040	0045.07	0045 400		407.4	
gilo321014[rei]NP_011091.1]	IGR1/5C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene;	2	3.5475	0.3013	2245.07	2240.409	1	407.1	44.444447 K.K2IIGIDIEIDIFISIDIR4EIK2VILIDIEILILIDI.1
		plays an essential role in the ergosterol-biosynthesis pathway and is the specific								
gi 6321614 ref NP_011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p Squalene enoxidase, catalyzes the enoxidation of squalene to 2.3-oxidosqualene:	2	4.1517	0.3273	2407.73	2409.645	2	383.3	44.736843 K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1Y1.H
		plays an essential role in the ergosterol-biosynthesis pathway and is the specific								
gi 6321614 ref NP_011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p	2	4.0817	0.3211	1918.59	1917.167	1	517.5	56.25 E.KLKDLVKDGNDKVLEDS.T
		plays an essential role in the ergosterol-biosynthesis pathway and is the specific								
gi 6321614 ref NP_011691.1	YGR175C	target of the antifungal drug terbinafine; Erg1p	2	4.1901	0.2205	1940.73	1939.167	2	428.4	53.125 E.K2L1K2D1L1V1K2D1G1N2D1K2V1L1E1D1S1.T
ail6321626/refINP_011703_1	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm. Hoh1p	3	6 238	0 4952	4230.08	4230 582	1	1336.6	A.S1A1K2D1S1E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I1 30 000002 P1A1I1I1C1 C
2-1		Protein of unknown function with similarity to human HMG1 and HMG2; localizes to	-							
gi 6321626 ref NP_011703.1	YGR187C	the cytoplasm; Hgh1p Protein of unknown function with similarity to human HMG1 and HMG2: localizes to	3	5.3845	0.4691	4187.9	4187.582	1	715.8	25 A.SAKDSEIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C S 41K2D1S1E111D1E1E1D1M1E1N211P1D1E111021111P1E1D1K2E1R4D1P111P1
gi 6321626 ref NP_011703.1	YGR187C	the cytoplasm; Hgh1p	3	6.7544	0.4816	4140.65	4142.504	1	1282.5	28.676472 A11111C1.C
ail62216261rofIND_011702_1	VCB107C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to	2	E 4061	0.2254	4027.04	4020 425	1	1675.0	
gilo32102010110F_011703.1	IGKIO/C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to	3	5.4001	0.2234	4027.01	4029.425	'	1075.2	20.707078 A.RDSEIDEEDMFNLFDELQLLFEDRERDFIFAIIG.C
gi 6321626 ref NP_011703.1	YGR187C	the cytoplasm; Hgh1p	3	5.4103	0.487	4098.65	4100.504	1	998.7	26.470589 S.AKDSEIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C
ail63216261refINP 011703.11	YGR187C	Protein of unknown function with similarity to numan HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	5.1858	0.4063	3551.54	3550.793	1	984.2	31.034481 K.D1S1E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I1P1A1.I
51		Protein of unknown function with similarity to human HMG1 and HMG2; localizes to								
gi 6321626 ref NP_011703.1	YGR187C	the cytoplasm; Hgh1p Protein of unknown function with similarity to human HMG1 and HMG2 [,] localizes to	3	4.8777	0.3518	3900.77	3901.251	1	916.2	25.78125 K.DSEIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C K D1S1E1I1D1E1E1D1M1E1N2I 1P1D1E1I 102I 1I 1P1E1D1K2E1R4D1P1I1P1A1I1
gi 6321626 ref NP_011703.1	YGR187C	the cytoplasm; Hgh1p	3	5.2919	0.3766	3938.21	3940.251	1	988.6	27.34375 1C1.C
ail62216261rofIND_011702_1	VCB107C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to	2	4 1002	0.2204	2712.6	2714 046	1	E24	
gilo321020[1010F_011703.1]	IGRIDIC	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to	3	4.1095	0.2394	3/13.0	3714.040	'	554	S.A1K2D1S1E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P111P1
gi 6321626 ref NP_011703.1	YGR187C	the cytoplasm; Hgh1p	3	6.5124	0.4602	3754.1	3753.046	1	1576.1	30.645163 A1.I
gi 6321626 ref NP 011703.1	YGR187C	Protein of unknown function with similarity to numan HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	5.8102	0.4151	4068.95	4070.425	1	1527.7	A.K2D1S1E111D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1K4D1P111P1A: 31.060606 I1I1C1.C
		Protein of unknown function with similarity to human HMG1 and HMG2; localizes to								S.E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I1P1A1I1I1C1
gi 6321626 ref NP_011703.1	YGR187C	the cytoplasm; Hgh1p Protein of unknown function with similarity to human HMG1 and HMG2 [,] localizes to	3	3.8805	0.2576	3734.54	3736.084	2	503.9	20.833332 C
gi 6321626 ref NP_011703.1	YGR187C	the cytoplasm; Hgh1p	3	4.7264	0.3059	3700.1	3699.084	1	600.3	23.333334 S.EIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C
ail62216261rofIND_011702_1	VCB107C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to	2	4 5007	0 2247	2516.65	2514 702	1	700	
gilo32102010110F_011703.1	IGKIO/C	the cytopiash, right p	3	4.3007	0.3347	3310.03	5514.795	'	133	27.300200 R.DSEIDEEDMFNLFDELQLLFEDRERDFIFA.I
		Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and								
gil6321631/refINP_011708.1	YGR192C	gluconeogenesis; tetramer that catalyzes the reaction of glyceraidenyde-3-phosphate to 1.3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.4521	0.3697	1710.25	1708.967	1	724.7	60.000004 LAKVINDAEGIEEGLMT.T
5100 00 10 1 <u>-</u>										
		Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and glyconeogenesis: tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate								
gi 6321631 ref NP_011708.1	YGR192C	to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	2.3528	0.2078	1211.58	1212.42	1	367.2	55 A.L1S1R4P1N2V1E1V1V1A1L1.N
		Chronoldohudo 2 phoephote dehudrogeneges jestiume 2 jeurohued in alueohueje and								
		gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate								
gi 6321631 ref NP_011708.1	YGR192C	to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.325	0.2093	1594.69	1595.79	1	899.2	69.230774 M.GVNEEKYTSDLKIV.S
		Glyceraldehyde-3-phosphate dehydrogenase. isozvme 3. involved in alvcolvsis and								
		gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate								
gi 6321631 ref NP_011708.1	YGR192C	to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.6141	0.3794	1682.41	1680.074	1	616.6	56.666668 K.KVVITAPSSTAPMFVM.G
		Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and								
ail6321631/rofIND_044700_4	VCP102C	gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate	2	3 202	0.2010	160F F0	1607 074	4	007 9	60 000004 K K2)/1/11T101D1C1C1T101D1M4E4//4M4 C
910021001101110F_011708.1	1011920	to 1,0 010 priospriogrycerate, detected in the cytopidstil ditu cell-wall, 10113p	2	3.382	0.2919	1033.38	1031.014	1	501.0	

gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.9968	0.3271	2287.81	2286.62	1	625.8	50 N.C1L1A1P1L1A1K2V1I1N2D1A1F1G1I1E1E1G1L1M1T1.T
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.2988	0.3929	1296.17	1294.423	1	701.2	80 S.H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	3	4.9171	0.2588	1699.43	1698.939	1	2157.1	63.461536 K.L1N2K2E1T1T1Y1D1E111K2K2V1V1.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	3.107	0.4297	1276.53	1277.423	1	422.3	65 S.HDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	3.2876	0.3036	1293.51	1294.423	1	616.2	75 S.H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.6707	0.1982	1384.47	1382.501	1	839.1	81.818184 V.S1H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.9608	0.2679	1280.37	1277.423	1	1068.6	85 S.HDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	3.7438	0.3838	1481.49	1482.633	2	614.5	66.66667 E.V1S1H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	3.3662	0.2748	1463.56	1463.633	1	630.6	66.66667 E.VSHDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.1696	0.3977	1483.97	1482.633	1	937	75 E.V1S1H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.586	0.4109	2142.59	2143.367	1	721.9	52.63158 D.S1T1G1V1F1K2E1L1D1T1A1Q2K2H3I1D1A1G1A1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.1777	0.3061	1354.19	1354.577	1	1036.2	72.72727 T.R4V1V1D1L1V1E1H3V1A1K2A1
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.0234	0.3565	1464.51	1463.633	1	471.5	66.66667 E.VSHDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	5.867	0.4011	1807.89	1809.113	1	889.3	75 K.LNKETTYDEIKKVVK.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	3	4.4222	0.2814	1880.84	1880.192	1	1168.7	48.333332 K.LNKETTYDEIKKVVKA.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	5.2546	0.422	1880.63	1880.192	1	1017.3	70 K.LNKETTYDEIKKVVKA.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.5933	0.3128	1973.63	1973.271	1	920	65.625 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1K2A1A1.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.0846	0.3171	1195.39	1194.39	1	1039.1	80 R.V1V1D1L1V1E1H3V1A1K2A1
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.429	0.3304	1182.07	1180.39	1	1323.8	90 R.VVDLVEHVAKA
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.5144	0.1956	1611.77	1612.79	1	736.9	65.38461 M.G1V1N2E1E1K2Y1T1S1D1L1K2I1V1.S
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	3.2257	0.4282	1276.48	1277.423	1	445.1	65 S.HDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	2.98	0.3444	1293.64	1294.423	1	400.1	60.000004 S.H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.9645	0.3891	1483.97	1482.633	1	549.1	66.66667 E.V1S1H3D1D1K2H3I1I1V1D1G1K2.K

gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	2.9798	0.3483	1481.58	1482.633	1	496.6	54.166668 E.V1S1H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.2359	0.3357	1652.41	1649.801	1	1010.7	67.85714 A.GEVSHDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	3	4.1807	0.2337	1668.47	1670.801	1	665.3	48.214287 A.G1E1V1S1H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.203	0.2982	1581.03	1581.806	1	1263.8	75 K.LNKETTYDEIKKV.V
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.2301	0.4276	1292.23	1294.423	1	800.1	80 S.H3D1D1K2H3l1l1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.0822	0.3866	1277.35	1277.423	1	719.4	80 S.HDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.2363	0.4341	1363.93	1364.501	1	1000.2	81.818184 V.SHDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	2.8955	0.3457	1462.6	1463.633	1	452.6	58.333332 E.VSHDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	3	4.1333	0.3861	1806.44	1809.113	1	1083.7	51.785713 K.LNKETTYDEIKKVVK.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	5.3832	0.3862	1899.75	1901.192	1	926.5	66.66667 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1K2A1.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.2393	0.2134	1278.35	1278.497	1	493.3	68.181816 M.V1R4V1A1I1N2G1F1G1R4I1G1.R
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	6.1302	0.3751	1828.55	1829.113	1	945.9	75 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1K2.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	3	4.4223	0.3725	1336.97	1336.577	1	1578.1	59.090908 T.RVVDLVEHVAKA
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	2.9523	0.1556	1055.21	1054.275	1	746.1	83.33333 K.AVGKVLPELQ.G
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.1355	0.2645	1654.29	1654.745	1	547.8	65.38461 A.T1Y1Q2E1R4D1P1A1N2L1P1W2G1S1.S
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	2.9311	0.2297	1104.09	1104.252	3	197	66.66667 M.A1F1R4V1P1T1V1D1V1S1.V
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.6405	0.3546	1669.49	1670.801	1	942.4	67.85714 A.G1E1V1S1H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	2.7042	0.2044	1481.39	1482.575	1	484.4	58.333332 A.G1E1V1S1H3D1D1K2H3I1I1V1D1.G
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.1662	0.3537	1297.39	1294.423	1	653.3	80 S.H3D1D1K2H3l1l1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.0112	0.4027	1276.57	1277.423	1	672.1	80 S.HDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.2276	0.2071	1356.13	1354.543	9	738.5	80 N.KETTYDEIKKV.V
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.7102	0.3114	1698.35	1698.939	1	651.8	69.230774 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.0594	0.1756	2262.53	2263.62	3	291.8	32.5 N.CLAPLAKVINDAFGIEEGLMT.T

gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	2.6531	0.437	1276.49	1277.423	1	406.8	60.000004 S.HDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.748	0.3018	1462.49	1463.633	1	919.9	75 E.VSHDDKHIIVDGK.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.1021	0.4074	1482.43	1482.633	1	452.5	66.66667 E.V1S1H3D1D1K2H3I1I1V1D1G1K2.K
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	1	4.1317	0.1921	1598.94	1598.85	2	714.2	66.66667 N.K2E1T1T1Y1D1E111K2K2V1V1K2.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	4.4712	0.3171	1671.27	1670.929	1	854	76.92308 N.K2E1T1T1Y1D1E111K2K2V1V1K2A1.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.8658	0.378	1654.53	1652.929	1	699.9	61.538464 N.KETTYDEIKKVVKA.A
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	2	3.3666	0.3766	1423.79	1424.597	1	311.1	72.72727 S.H3D1D1K2H3I1I1V1D1G1K2K2.I
gi 6321631 ref NP_011708.1	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by	2	3.6718	0.2825	2128.55	2129.286	1	398.3	47.22222 A.T1Q2K2T1V1D1G1P1S1H3K2D1W2R4G1G1R4T1A1.S
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pvruvate dehydrogenase (PDH) complex, plavs a structural role in the complex by	2	3.7192	0.3257	1374.35	1374.533	1	1725.7	80 N.SKYFDPIFEDL.V
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by	2	3.5935	0.2102	1704.49	1702.93	1	690	65.38461 N.S1K2Y1F1D1P1I1F1E1D1L1V1T1L1.S
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by	3	4.3206	0.1981	2029.88	2029.344	4	1350.3	48.4375 S.SVRPVEKNLPEKNEYIL.A
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by	2	3.1324	0.3739	2212.61	2213.582	1	333.7	41.666664 S.SVRPVEKNLPEKNEYILAL.N
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by	2	4.346	0.3423	2053.13	2053.344	1	519	59.375 S.S1V1R4P1V1E1K2N2L1P1E1K2N2E1Y1I1L1.A
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by	2	4.2022	0.2737	2030.53	2029.344	1	668.2	62.5 S.SVRPVEKNLPEKNEYIL.A
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by	1	2.3449	0.1712	1373.66	1374.533	1	724	60.000004 N.SKYFDPIFEDL.V
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex plays a structural role in the complex by	2	3.5412	0.2353	1690.63	1687.93	1	619	61.538464 N.SKYFDPIFEDLVTL.S
gi 6321632 ref NP_011709.1	YGR193C	binding and positioning E3 to the dihydrolipon pupped accordance of the accordance of pointing and positioning E3 to the dihydrolipon mide acetyltransferase (E2) core; Pdx1p Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the outenless in a purchase pattern: VCB108W is an essential agency.	2	4.2346	0.2921	2028.59	2029.344	1	571.2	59.375 S.SVRPVEKNLPEKNEYIL.A
gi 6321637 ref NP_011714.1	YGR198W	Var198wp Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	3.8723	0.2688	2317.71	2317.637	1	345.7	45 M.P1N2S1N2V1R4I1P1P1T1V1P1S1K2I1I1D1V1V1D1Q2.A
gi 6321637 ref NP_011714.1	YGR198W	localizes to the cytopiasm in a punctate pattern; YGR 196W is an essential gene; Yqr198Wp Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	2	3.8648	0.307	2291.47	2289.637	1	340.8	45 M.PNSNVRIPPTVPSKIIDVVDQ.A
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histiidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	1	3.1107	0.3802	1411.55	1412.64	1	519.7	54.166668 L.K2L1L1T1P1V1P1S1D1I1D1I1S1.R
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	1	2.7603	0.397	1397.79	1398.64	1	515.4	58.333332 L.KLLTPVPSDIDIS.R
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	1	3.2487	0.1608	1371.59	1372.562	1	217.6	54.166668 G.R4S1D1I1V1G1S1P1V1A1E1L1L1.K
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	1	2.9195	0.2564	1355.64	1356.562	2	245	58.333332 G.RSDIVGSPVAELL.K
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	2	4.5309	0.2724	1782.39	1780.926	1	876.3	64.28571 Q.K2T1N2P1D1D1L1T1P1E1E1I1N2K2F1.A
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	1	3.0962	0.3989	1373.74	1374.684	1	680.6	65.38461 Y.VHLITPVPGGVGPM.T

		Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single								
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymioylate, methionine, and histidine; Ade3p	2	4.9327	0.4608	1930.65	1931.136	1	986.1	58.333332 L.K2S1H3G1G1A1P1D1V1K2P1G1Q2P1L1P1S1A1Y1.T
		cytoplasmic trifunctional enzyme C1-tetrahydrotolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine,								
gi 6321643 ref NP_011720.1	YGR204W	and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidvlate, methionine.	2	3.0696	0.1597	1374.29	1372.562	2	621.2	66.66667 G.R4S1D111V1G1S1P1V1A1E1L1L1.K
gi 6321643 ref NP_011720.1	YGR204W	and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	2	3.6995	0.317	2273.11	2273.599	4	526.5	42.105263 H.G1111V1Q2L1P1L1P1A1H3L1D1E1D1R4I1T1S1R4.V
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of punnes, thymidylate, methionine, and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	2	3.5691	0.2712	2244.11	2244.599	1	923	50 H.GIIVQLPLPAHLDEDRITSR.V
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	3	4.342	0.2596	3492.41	3492.833	1	500.3	22.413794 R.Y1V1D1Q2L1N2E1D1P1H3T1H3G1I1I1V1Q2L1P1L1P1A1H3L1D1E1D1R4I1T1.S
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of punnes, thymidylate, methionine, and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	2	4.0758	0.2881	1486.41	1486.724	1	839.4	73.07692 A.N2V1R4Q2P1S1L1G1P1T1L1G1V1K2.G
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	2	4.4235	0.4125	1469.63	1466.724	1	969.8	76.92308 A.NVRQPSLGPTLGVK.G
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p Cvtoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single	2	4.0206	0.2704	1696.25	1694.881	1	1430.3	68.75 L.K2S1H3G1G1A1P1D1V1K2P1G1Q2P1L1P1S1.A
gi 6321643 ref NP_011720.1	YGR204W	carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p Essential protein with two zinc fingers, present in the nucleus of growing cells but	2	3.9079	0.4607	1675.71	1672.881	1	1131.2	62.5 L.KSHGGAPDVKPGQPLPS.A
gi 6321650 ref NP_011727.1	YGR211W	relocates to the cytoplasm in starved cells via a process mediated by Cpr1p; binds to translation elongation factor eEF-1 (Tef1p); Zpr1p Essential protein with two zinc fingers, present in the nucleus of growing cells but	2	3.9711	0.4022	1807.27	1806.999	1	645.4	61.538464 N.S1W2I1E1Y1K2P1G1E1P1Q2H3K2W2.S
gi 6321650 ref NP_011727.1	YGR211W	relocates to the cytoplasm in starved cells via a process mediated by Cpr1p; binds to translation elongation factor eEF-1 (Tef1p); Zpr1p	2	2.9975	0.1619	1384.27	1382.704	1	614.7	80 T.SIPYFREIIIM.S
gi 6321657 ref NP_011734.1	YGR218W	the nucleus; Crm1p	2	3.5861	0.4012	1653.85	1654.814	1	1302.7	71.42857 Q.IKEVGGDPTDYLFAE.D
gi 6321657 ref NP_011734.1	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus; Crm1p	2	3.8242	0.3859	2201.55	2199.47	1	442.8	52.941177 L.KQEWPQNWPEFIPELIGS.S
gi 6321657 ref NP_011734.1	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus; Crm1p	2	4.0811	0.1707	2285.67	2286.549	1	703.2	52.77778 L.KQEWPQNWPEFIPELIGSS.S
gi 6321657 ref NP_011734.1	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus; Crm1p	2	3.419	0.2385	2308.77	2311.549	3	507.3	44.444447 L.K2Q2E1W2P1Q2N2W2P1E1F1I1P1E1L1I1G1S1S1.S
gi 6321657 ref NP_011734.1	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus; Crm1p	2	2.9209	0.1707	1408.55	1408.701	1	426.9	70 A.LNPEYMKRFPL.K
gi 6321657 ref NP_011734.1	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus; Crm1p	2	3.4193	0.2819	1269.69	1269.483	1	826	77.77778 M.SKEFEQIFKL.C
gil6321657/refINP 011734.1	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus: Crm1p	2	3.8628	0.2705	1468.21	1468.62	4	416.4	62.5 Q.I1K2E1V1G1G1D1P1T1D1Y1L1F1.A
gil6321657lrefINP_011734_1	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus: Crm1p	2	3 3141	0.3432	1732 31	1732 846	1	611.8	
gi 6321657 ref NP_011734_1	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus: Crm1p	2	3.3806	0.283	1751 43	1750 846	1	711.9	70 83333 K D1F1T1F1Y1P1F1H3R4V1F1F1Y1 K
9/002/00///0/// _0///0///	10121011	Cyclin.dependent kinase (CDK) inhibitor regulates Pho80n-Dho85n and Pol7n-	-	0.0000	0.200		1100.010	•	11110	
gi 6321672 ref NP_011749.1	YGR233C	Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	4.0639	0.2909	1571.41	1570.753	1	998.5	75 H.L1T1L1D1D111D1E1K21111H3Q2.R
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.4028	0.3008	2243.95	2245.602	1	460.8	44.444447 R.V1Y1F1P1T1D1K2E1I1D1T1I1P1I1K2I1S1P1F1.I
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.5155	0.2752	1780.59	1780.982	1	747	56.666668 S.TTGKFVGDTPNCLKEL.A
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.506	0.3124	1904.81	1907.257	1	424.9	50 A.T1V1V1S1I1Q2P1I1F1T1R4D1G1P1L1K2L1.N
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.1516	0.2536	2550.67	2551.919	1	494.3	38.095238 V.S1I1Q2P11F1T1R4D1G1P1L1K2L1N2D1E1T1L1H3I1L1.L
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.3534	0.193	2521.25	2521.919	1	270.7	33.333336 V.SIQPIFTRDGPLKLNDETLHILL
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.607	0.3534	2223.59	2224.602	7	266.6	33.333336 R.VYFPTDKEIDTIPIKISPF.I
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	2.9831	0.1501	1891.79	1892.248	3	617.2	53.333336 L.DYQIIFPYPGNPLKII.N
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.9096	0.2659	1632.85	1632.895	1	1341.6	76.92308 T.D1K2E1I1D1T1I1P1I1K2I1S1P1F1.I
gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.5638	0.2473	1486.17	1484.741	1	1137.8	68.181816 L.NWKQPNFPVLLQ.M

gi 6321672 ref NP_011749.1	YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p- Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	2	3.2754	0.1963	1615.67	1616.957	2	614	61.538464 Q.I1I1F1P1Y1P1G1N2P1L1K2I1I1N2.Y
gi 6321673 ref NP_011750.1	YGR234W	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; Yhb1p	2	3.5867	0.2682	2138.33	2139.34	1	456.2	53.125 K.E1L1E1H3R4D1D1M1I1H3Y1E1P1F1G1P1K2.M
gi 6321673 ref NP_011750.1	YGR234W	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; Yhb1p	2	3.0097	0.3237	1962.67	1960.171	1	467.6	60.714287 L.KELEHRDDMIHYEPF.G
gi 6321673 ref NP_011750.1	YGR234W	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; Yhb1p	2	3.0786	0.2991	2114.39	2114.34	1	392.7	50 K.ELEHRDDMIHYEPFGPK.M
gi 6321673 ref NP_011750.1	YGR234W	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; Yhb1p	2	4.1882	0.1997	2243.89	2242.514	1	733.7	52.941177 L.KELEHRDDMIHYEPFGPK.M
gi 6321673 ref NP_011750.1	YGR234W	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; Yhb1p	2	4.416	0.3654	2268.49	2269.514	1	747.9	55.88235 L.K2E1L1E1H3R4D1D1M11H3Y1E1P1F1G1P1K2.M
gi 6321673 ref NP_011750.1	YGR234W	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; Yhb1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.9121	0.3097	2187.93	2188.457	1	206.9	53.125 M.LEEQVKCNPNRPIYWIQ.S
gi 6321679 ref NP_011756.1	YGR240C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Plk1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.0076	0.277	1956.17	1957.067	9	215.3	38.235294 H.GEKVPTVEHEDDSAAVIC.V
gi 6321679 ref NP_011756.1	YGR240C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	5.2227	0.4965	1977.17	1978.067	1	527.9	61.764706 H.G1E1K2V1P1T1V1E1H3E1D1D1S1A1A1V1I1C1.V
gi 6321679 ref NP_011756.1	YGR240C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.4725	0.2414	1358.41	1358.64	2	376.6	80 L.E1N2K2I1IIR4M1P1L1V1E1.S
gi 6321679 ref NP_011756.1	YGR240C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pk1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	4.2369	0.3513	1746.43	1744.94	1	1143.9	70 T.TVKDDGSELLPVSDRL.N
gi 6321679 ref NP_011756.1	YGR240C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Phtp Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	2.9408	0.2831	1908.57	1906.078	1	653.6	53.333336 Y.S1A1L1E1R4I1C1E1M1V1D1Y1I1D1A1T1.A
gi 6321679 ref NP_011756.1	YGR240C	Indispensable for anaerooic growin, activated by tructose-2,o-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; PK1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.5232	0.3911	1698.13	1700.858	2	315	61.538464 F.R4H3E1W2P1S1L1V1D1E1L1V1A1E1.G
gi 6321679 ref NP_011756.1	YGR240C	Indispensation for anaerobic growin, activated by indicase-2,o-bispriosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pktp Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indicased for anaerobic activity activated by functione, 26 Alpharburgheba and	2	3.5824	0.346	1680.19	1680.858	1	307	57.692307 F.RHEWPSLVDELVAE.G
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pktp AMP, mutation inhibits glucose induction of cell cycle-related genes; Pktp Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indisenseshal for anaerchie growth a criticated by furures. ² Abitempenbate and	2	3.4861	0.2309	1419.57	1420.535	1	1056.6	80 N.L1W2E1N2E1T1N2V1E1L1R4.K
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pk1p AMP, mutation inhibits glucose induction of cell cycle-related genes; Pk1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indisenesshells for anaerohic growth a critizated by fructores-26 Aibinschate and	2	3.8047	0.2401	1408.37	1407.518	1	1128.7	80 H.G1K2W2Q2D1E1L1K2E1V1C1.Q
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pik1p AMP, mutation inhibits glucose induction of cell cycle-related genes; Pik1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indiscensable for anaerobic growth, activated by fructose-2.6-bibshosbhate and	2	5.3357	0.34	1763.55	1764.94	1	1089.2	70 T.T1V1K2D1D1G1S1E1L1L1P1V1S1D1R4L1.N
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indiscensable for anaerobic growth. activated by fructose-2.6 bibshosbhate and	2	3.3375	0.2368	1538.35	1537.648	1	1112.3	81.818184 H.G1K2W2Q2D1E1L1K2E1V1C1Q2.R
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p Alpha subunit of heterooctameric phosphof/ructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2.6-bisphosphate and	1	2.2415	0.227	1379.92	1381.531	5	272.2	60.000004 F.RHEWPSLVDEL.V
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; PR1p Alpha subunit of heterocidameric phosphoffuctokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,8-bisphosphate and	2	3.9696	0.2346	1397.73	1398.531	1	1209.5	85 F.R4H3E1W2P1S1L1V1D1E1L1.V
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and	2	5.123	0.2324	1921.67	1923.257	1	1374.8	66.66667 T.D1L1N2K2I1V1E1K2F1P1K2Q2A1E1K2L1.S
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and	2	4.5214	0.2925	1901.51	1901.257	1	1226.5	66.66667 T.DLNKIVEKFPKQAEKL.S
gi 6321679 ref NP_011756.1	YGR240C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-	3	4.5484	0.2015	2087.09	2087.292	1	997.3	42.1875 L.K2E1N2F1R4H3D1K2G1E1N2R4N2G1K2L1L1.V
gi 6321693 ref NP_011770.1	YGR254W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	1	3.0795	0.214	1515.62	1516.717	2	645.5	57.692307 Q.T1A1E1E1A1L1D1L1I1V1D1A1I1K2.A
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoen/pyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	1	2.8605	0.3586	1500.52	1501.717	3	498.3	57.692307 Q.TAEEALDLIVDAIK.A
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.1711	0.2585	1476.49	1475.771	1	1271.2	83.33333 S.KTSPYVLPVPFLN.V
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.6144	0.3323	1502.67	1501.717	1	1645.3	73.07692 Q.TAEEALDLIVDAIK.A
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	5.2994	0.3147	1515.89	1516.717	1	2429	84.61539 Q.T1A1E1E1A1L1D1L1I1V1D1A111K2.A
		Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-								
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gi 6321693 ref NP_011770.1	YGR254W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	2.9072	0.221	1250.37	1248.508	4	586.9	75 S.KTSPYVLPVPF.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	1	2.9783	0.2112	1474.79	1475.771	1	299.1	66.66667 S.KTSPYVLPVPFLN.V
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	5.138	0.3857	2342.09	2339.522	1	1024.6	55.555557 K.RYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	2.9865	0.2872	1791.55	1793.141	2	614.9	53.333336 K.S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1.N
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.0486	0.2616	1702.73	1705.063	1	899.2	64.28571 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1.N
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.0117	0.3204	1686.97	1688.063	1	792.8	64.28571 S.KTSPYVLPVPFLNVL.N
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.4132	0.2458	2290.17	2289.72	2	657.6	45 L.ADLSKSKTSPYVLPVPFLNVL.N
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.0179	0.2423	2216.93	2218.642	1	417.2	36.842106 A.DLSKSKTSPYVLPVPFLNVL.N
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.504	0.268	2312.05	2313.72	1	576.3	42.5 L.A1D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1.N
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.4323	0.1757	2845.37	2846.226	1	581.3	29.807693 L.A1D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1.G
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.244	0.2076	2296.31	2295.621	4	378.5	35.714287 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1.G
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	5.4397	0.3309	2236.41	2237.569	1	1776.9	60.000004 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1.G
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.043	0.3319	2613.53	2614.889	1	422.7	45 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.4834	0.3277	2644.23	2641.889	1	407.3	45 L.M\$K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.0596	0.2673	2495.39	2493.697	1	649.5	40.789474 M.K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.1217	0.4389	2470.45	2467.697	1	402.1	47.368423 M.KRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.5866	0.3156	2626.16	2625.889	1	774.3	40 L.M1K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	2.9678	0.1985	2711.13	2712.049	1	287.5	38.095238 S.LMKRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.6371	0.2648	2256.67	2257.508	1	440.9	47.22222 D.GKYDLDFKNPNSDKSKWLT.G
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.9012	0.3103	2612.66	2614.889	1	1461	45 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.818	0.4115	2596.88	2598.889	1	846.8	42.5 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.2089	0.294	2712.92	2712.049	1	438.5	32.142857 S.LMKRYPIVSIEDPFAEDDWEAW.S
ai 6321693 ref NP 011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dlyconeogenesis; expression is repressed in response to glucose; Eno1o	2	4.2894	0.3873	2537.61	2539.911	1	581.7	39.583336 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L1.A

gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.0753	0.3475	2512.31	2509.911	1	959.5	33.333336 S.KTSPYVLPVPFLNVLNGGSHAGGAL.A
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.0078	0.3533	2742.95	2740.049	1	643.4	33.333336 S.L1M1K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	5.1492	0.3524	2482.43	2482.755	1	840.5	57.5 G.KYDLDFKNPNSDKSKWLTGPQ.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.8196	0.3232	2599.49	2598.889	1	564.1	52.499996 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.2203	0.162	2737.71	2740.049	1	206.3	33.333336 S.L1M1K2R4Y1P111V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.515	0.2068	2723.73	2724.045	1	307.2	34.782608 D.GKYDLDFKNPNSDKSKWLTGPQLA.D
gi 6321693 ref NP_011770.1	YGR254W	Enolase 1, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.9062	0.3197	2628.41	2625.889	1	574.6	55 L.M1K2R4Y1P1I1V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
ail6321693lrefINP 011770.11	YGR254W	Enclase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dlyconeogenesis; expression is repressed in response to olucose; Enoto	1	2.5545	0.277	1463.68	1463.76	1	497	62.5 S.KSKTSPYVLPVPF.L
oil6321693/refINP_011770_1	YGR254W	Enclase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during disconcengenesis: expression is represent in response to durose. Encl	2	3 8589	0 171	1796 11	1797 101	1	608.1	53 3333361 S1K2S1K2T1S1P1Y1V11 1P1V1P1F11 1N2 V
oil6321603/rofIND_011770_1	VGP254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during durong generative supersion is correspond to generative supersion of the reverse reaction	-	3.0769	0.335	1576.89	1576 010	1	535.6	57 692907 S KSKTSPV// DV/DEL N
-:::C224.C021#ND_044770.4	VOD254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	1	3.0769	0.335	0400.00	0400.007	1	333.0	
gilo321093[rei]NP_011770.1]	rGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	3.3051	0.3136	2493.03	2493.697	I	352	42.105203 M.K.2R41 IP IIT VISITIE ID IP IF IATE ID ID IWZE IATW2.5
gi 6321693 ref NP_011770.1	YGR254W	during gluconeogenesis; expression is repressed in response to glucose; Eno1p Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	3	6.2507	0.3046	3149.75	3148.568	1	1039.9	30.000002 1.A A.D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L1.
gi 6321693 ref NP_011770.1	YGR254W	during gluconeogenesis; expression is repressed in response to glucose; Eno1p Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-	3	4.7384	0.3059	3074.57	3076.489	1	673.7	25.862068 A
gi 6321693 ref NP_011770.1	YGR254W	during gluconeogenesis; expression is repressed in response to glucose; Eno1p Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-	1	3.6069	0.2722	1515.7	1516.717	1	1095.5	61.538464 Q.T1A1E1E1A1L1D1L1I1V1D1A1I1K2.A
gi 6321693 ref NP_011770.1	YGR254W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p Enolase I. a phosphopyruvate hydratase that catalyzes the conversion of 2-	1	3.0555	0.3415	1500.72	1501.717	1	878.2	57.692307 Q.TAEEALDLIVDAIK.A
gi 6321693 ref NP_011770.1	YGR254W	hosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.7107	0.4756	1712.83	1710.75	1	839.9	61.538464 V.SIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	phosphoglycerate to phosphoen/pyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	1	2.2309	0.1512	1248.54	1248.508	6	441.4	65 S.KTSPYVLPVPF.L
gi 6321693 ref NP_011770.1	YGR254W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.0147	0.2993	1248.37	1248.508	3	652.2	80 S.KTSPYVLPVPF.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	2.9922	0.1575	1260.35	1260.508	2	621.5	80 S.K2T1S1P1Y1V1L1P1V1P1F1.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	1	3.1461	0.2013	1491.83	1490.771	1	360.4	66.66667 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2.V
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.9522	0.1817	1493.41	1490.771	1	1136.5	79.16667 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2.V
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	1	2.3595	0.1623	1360.59	1361.667	4	444.2	59.090908 S.KTSPYVLPVPFL.N
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.744	0.3745	1501.41	1501.717	1	2279.1	80.769226 Q.TAEEALDLIVDAIK.A

gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycorrate to phosphoenlopyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	5.0579	0.2969	1514.75	1516.717	1	2284.9	84.61539 Q.T1A1E1E1A1L1D1L111V1D1A111K2.A
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.2894	0.3515	2364.89	2363.522	1	1119.6	44.44447 K.R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.766	0.4775	2339.57	2339.522	1	903.3	43.055553 K.RYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	5.9392	0.3854	2362.09	2363.522	1	882.3	52.77778 K.R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.0729	0.2728	1567.13	1568.806	1	264.6	62.5 L.EMRDGDKSKWMGK.G
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.584	0.3642	2069.15	2067.243	1	1184.1	46.875 D.G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.6972	0.415	2067.03	2067.243	1	1166.3	68.75 D.G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.4615	0.3899	2266.35	2266.472	1	827.2	52.77778 E.FFKDGKYDLDFKNPNSDKS.K
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.715	0.3974	2638.97	2641.889	1	1341.7	41.25 L.M\$K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.0255	0.3834	2613.95	2614.889	1	949.3	43.75 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.2119	0.2812	2599.25	2598.889	1	914	41.25 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.7208	0.4427	2601.87	2598.889	1	479.2	50 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.5541	0.3244	2541.17	2539.807	1	1747.9	40.476192 D.GKYDLDFKNPNSDKSKWLTGPQ.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	5.2148	0.4373	2538.27	2539.807	1	1236.1	54.761906 D.GKYDLDFKNPNSDKSKWLTGPQ.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	5.3868	0.4366	2567.69	2569.807	1	1131.6	54.761906 D.G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2L1T1G1P1Q2.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	7.3066	0.5244	2571.62	2569.807	1	2575.8	45.238094 D.G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2L1T1G1P1Q2.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.6499	0.3173	2756.72	2756.049	1	612.7	33.333336 S.L1M\$K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.1006	0.3101	2490.83	2493.697	1	304.6	42.105263 M.K2R4Y1P111V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.2537	0.3561	2613.61	2614.889	1	526.9	47.5 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.9558	0.3649	2625.05	2625.889	1	460.5	50 L.M1K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.0293	0.3205	2494.07	2493.697	1	610	40.789474 M.K2R4Y1P111V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.0003	0.214	3700.67	3698.128	1	384.9	25 M.KRYPIVSIEDPFAEDDWEAWSHFFKTAGIQI.V
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	3.8866	0.1639	3740.24	3739.128	2	237.3	M.K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2S1H3F1F1K2T1A1G1I1Q2I 19.166666 1.V

gi 6321693 ref NP_011770.1	YGR254W	Enclase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconseogenesis; expression is repressed in response to glucose; Eno1p	3	4.719	0.2578	2466.5	2467.697	1	662.7	40.788474 M.KRYPIVSIEDPFAEDDWEAW.S
ail63216931refINP_011770_11	YGR254W	Enclase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during duronegraphics: expression is represent in response to duronse. English	3	6 1698	0 4314	2611 85	2609 859	1	1238.2	40 F F1F1K2D1G1K2Y1D11 1D1F1K2N2P1N2S1D1K2S1K2W2 I
	YOD054W	Enolase I, a phosphopyrruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyrruvate during glycolysis and the reverse reaction	0	4.040	0.4014	2011.00	2003.005		200.2	
gij6321693 ref NP_011770.1	YGR254W	during gluconeogenesis; expression is repressed in response to glucose; Eno1p Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	4.919	0.4962	2607.63	2609.859	1	662.6	50 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2.L
gi 6321693 ref NP_011770.1	YGR254W	during gluconeogenesis; expression is repressed in response to glucose; Eno1p Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-	2	4.667	0.4151	2582.75	2580.859	1	664	50 E.FFKDGKYDLDFKNPNSDKSKW.L
gi 6321693 ref NP_011770.1	YGR254W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.6595	0.3044	1563.85	1566.838	1	1108.7	80.769226 L.S1K2S1K2T1S1P1Y1V1L1P1V1P1F1.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	6.1221	0.2542	2626.25	2625.889	1	846.7	46.25 L.M1K2R4Y1P111V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	5.2083	0.3763	3079.37	3077.423	1	1326.5	34 E.FFKDGKYDLDFKNPNSDKSKWLTGPQ.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	1	3.3001	0.2649	1477.6	1478.76	1	540.5	62.5 S.K2S1K2T1S1P1Y1V1L1P1V1P1F1.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.1976	0.2297	1777.11	1778.101	1	619.3	53.333336 L.SKSKTSPYVLPVPFLN.V
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.7107	0.1716	1706.65	1709.023	1	949.7	75 S.K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2.V
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.0694	0.2877	1666.49	1663.998	1	820.7	67.85714 L.SKSKTSPYVLPVPFL.N
qi 6321693 ref NP 011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	3.8124	0.281	3205.01	3206.538	1	413.2	24.038462 S.EFFKDGKYDLDFKNPNSDKSKWLTGPQ.L
ail6321693/refINP 011770.1	YGR254W	Enclase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dlyconeogenesis: expression is repressed in response to olucose: Eno1p	3	4.136	0.212	2613.92	2614.889	1	565	35 L.M@KRYPIVSIEDPFAEDDWEAW.S
ail6321693/ref/NP_011770.1	YGR254W	Enclase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during divencegonesis: expression is repressed in response to diverse: Engly	3	6.6877	0.5112	2569.37	2569.807	1	2556.4	45 238094 D.G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2L1T1G1P1O2.L
ail6321693/refINP_011770.11	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during diverse transcent is represent in response to during the reverse reaction	3	6 3575	0.4843	2538.95	2539 807	1	2386.3	
	YOD254W	Enolase I, a phosphopyrruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyrruvate during glycolysis and the reverse reaction	5	0.0010	0.4043	2330.53	2559.007	'	2300.3	
gi 6321693 ret NP_011770.1	YGR254W	during gluconeogenesis; expression is repressed in response to glucose; Eno1p Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-	2	4.9616	0.4011	2538.53	2539.807	1	1181.6	54.761906 D.GKYDLDFKNPNSDKSKWLTGPQ.L
gi 6321693 ref NP_011770.1	YGR254W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	6.3468	0.4113	2513.45	2511.755	1	2487.3	46.25 G.K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2L1T1G1P1Q2.L
gi 6321693 ref NP_011770.1	YGR254W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.5111	0.3256	2597.09	2598.889	1	439.8	32.5 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.4475	0.2047	2624.37	2625.889	1	305.4	40 L.M1K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.5097	0.2515	2796.08	2795.123	3	613.9	29.545454 E.FFKDGKYDLDFKNPNSDKSKWLT.G
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	4.5596	0.2617	2625.08	2625.889	1	628.9	35 L.M1K2R4Y1P111V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	4.2446	0.3172	2598.83	2598.889	1	360.7	42.5 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	3	6.6383	0.4514	3113.54	3112.423	1	1553.9	36 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2L1T1G1P1Q2.L

gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.5062	0.3662	3111.85	3112.423	1	327.5	34 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2L1T1G1P1Q2.L
gi 6321693 ref NP_011770.1	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	2	3.0634	0.2207	1690.57	1691.023	1	607.3	60.714287 S.KSKTSPYVLPVPFLN.V
gi 6321694 ref NP_011771.1	YGR255C	Putative flavin-dependent monooxygenase, involved in ubiquinone (Coenzyme Q) biosynthesis; located on the matrix side of the mitochondrial inner membrane; Coq6p	3	4.2877	0.4002	2840.21	2838.158	1	835	32.608696 T.LVDMVDLKDKLSDFYNSPPDYFTN.R
gi 6321694 ref NP_011771.1	YGR255C	Putative flavin-dependent monooxygenase, involved in ubiquinone (Coenzyme Q) biosynthesis; located on the matrix side of the mitochondrial inner membrane; Coq6p	2	3.4143	0.2513	1578.25	1575.823	1	581.3	57.14286 T.GPIAHLPMPENNATL.V
gi 6321694 ref NP_011771.1	YGR255C	Putative flavin-dependent monooxygenase, involved in ubiquinone (Coenzyme Q) biosynthesis; located on the matrix side of the mitochondrial inner membrane; Coq6p Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline	1	2.4227	0.2081	1378.46	1378.484	2	351.3	54.545456 K.HSDPNDPLSWPL.V
gi 6321700 ref NP_011777.1	YGR261C	phosphatase to the vacuole via the alternate pathway, exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline	2	4.7687	0.2643	1738.21	1738.83	1	621	70 T.E1V1G1E1T1G1N2D111R4E1G1A1E1L1K2.D
gi 6321700 ref NP_011777.1	YGR261C	phosphatase to the vacuole via the alternate pathway, exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline	1	2.3169	0.1586	1402.78	1403.578	5	196.3	54.545456 L.RFAENDPNLTLL.S
gi 6321700 ref NP_011777.1	YGR261C	phosphatase to the vacuole via the alternate pathway; exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline	3	4.7304	0.2852	4086.98	4088.393	1	803.6	24.264706 S.SEGSPRSCPLPDKYNEIEYPSYEVVNDPDLDLFLQ.S
gi 6321700 ref NP_011777.1	YGR261C	prospnatase to the vacuole via the airemate patriway, exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline observements to the user poulsi the observate and where write in bette a densile and	3	5.3579	0.3139	4129.28	4130.393	1	1033.4	25.735294 1L1F1L1Q2.S
gi 6321700 ref NP_011777.1	YGR261C	prospiratase to the vacuole via the alternate pathway, exists in both cytosolic and peripherally associated membrane-bound pools; ApI6p	2	3.1477	0.2147	2302.49	2303.493	1	363.8	44.44447 R.SCPLPDKYNEIEYPSYEVV.N
gi 6321705 ref NP_011782.1	YGR266W	Protein of unknown function;predicted to contain a single transmembrane domain; localized to both the mitochondrion and the plasma membrane; Ygr266wp	1	3.3173	0.2048	1487.56	1488.668	5	321.7	59.090908 K.R4N2W2S1D1111P111E1N2L1.L
gi 6321705 ref NP_011782.1	YGR266W	Protein of unknown function;predicted to contain a single transmembrane domain; localized to both the mitochondrion and the plasma membrane; Ygr266wp	2	4.1296	0.4017	2320.31	2319.415	1	535.2	50 N.EFNGDVELLDDLNDHWCAR.H
gi 6321705 ref NP_011782.1	YGR266W	Protein of unknown function, predicted to contain a single transmembrane domain; localized to both the mitochondrion and the plasma membrane; Ygr266wp	2	5.7349	0.5074	1848.69	1848.019	1	1857.3	83.33333 H.HFDLETDEDAVPIFAK.E
gi 6321705 ref NP_011782.1	YGR266W	Protein of unknown function, predicted to contain a single transmembrane domain; localized to both the mitochondrion and the plasma membrane; Ygr266wp	3	4.6863	0.3113	1750.28	1751.06	1	956.6	46.153847 T.R4I1I1E1E1P1T1K2D1V1R4L111F1.N
gi 6321705 ref NP_011782.1	YGR266W	Protein of unknown function, predicted to contain a single transmembrane domain; localized to both the mitochondrion and the plasma membrane; Ygr266wp	2	6.135	0.4924	1867.27	1867.019	1	2023.2	83.33333 H.H3F1D1L1E1T1D1E1D1A1V1P111F1A1K2.E
gi 6321705 ref NP_011782.1	YGR266W	Protein of unknown function;predicted to contain a single transmembrane domain; localized to both the mitochondrion and the plasma membrane; Ygz266wp GTP-cyclohydrolase L catalyzes the first sten in the fail: cacity biosynthetic pathway;	2	3.9116	0.2077	2543.81	2544.822	2	639.6	47.5 M.SEEKEKENTRIIEEPTKDVRLI
gi 6321706 ref NP_011783.1	YGR267C	Fol2p	2	3.4632	0.2461	1776.21	1776.855	8	228.6	57.692307 Q.RAEETEEEEKERIQ.R
gi 6321706 ref NP_011783.1	YGR267C	GTP-cyclohydrolase I, catalyzes the first step in the folic acid biosynthetic pathway; Fol2p	2	4.1801	0.3985	2141.79	2143.341	1	392.2	41.6666664 Y.T1L1N2P1P1V1E1R4D1G1F1S1W2P1S1V1G1T1R4.Q
gil6321706/refINP_011783.1	YGR267C	GTP-cyclohydrolase I, catalyzes the first step in the folic acid biosynthetic pathway; Fol2p	2	3.9226	0.3239	2072.09	2073.235	1	577.3	52.941177 T.S1P1Y1T1L1N2P1P1V1E1R4D1G1F1S1W2P1S1.V
gil6221710/rofIND_011797.1	VCP271W	Putative RNA helicase related to Ski2p, involved in translation inhibition of non-	2	4 226	0.210	2504.42	2505 50	1	000.4	
gilo321710/rei/NP_011787.1	IGR271W	Putative RNA helicase related to Ski2p, involved in translation inhibition of non-	2	4.320	0.319	2504.43	2505.59	I	990.4	52.03 136 L.STQ2DTR4N2DTW2DTDTTFFETETFTR2DTTSTFTAT.Q
gi 6321710 ref NP_011787.1	YGR271W	poly(A) mRNAs; required for repressing propagation of dsRNA viruses; Slh1p Putative RNA helicase related to Ski2p, involved in translation inhibition of non-	2	3.4369	0.2449	1505.85	1505.751	1	866.5	72.72727 Q.KQELEKELLDFL.G
gi 6321710 ref NP_011787.1	YGR271W	poly(A) mRNAs; required for repressing propagation of dsRNA viruses; SIh1p Putative RNA belicase related to Ski2p, involved in translation inhibition of non-	2	4.059	0.2548	1793.33	1795.04	1	609.1	57.14286 S.K2I1S1L1P1D1F1D1D1E1L1K2K2V1Q2.K
gi 6321710 ref NP_011787.1	YGR271W	poly(A) mRNAs; required for repressing propagation of dsRNA viruses; Slh1p	2	3.805	0.1755	2364.51	2363.737	1	875.2	47.368423 E.ELQFSLINDALGLRYDMVHK.L
gi 6321710 ref NP_011787.1	YGR271W	poly(A) mRNAs; required for repressing propagation of dsRNA viruses; SIh1p	2	3.794	0.3588	2477.19	2478.59	1	753.5	42.105263 L.SQDRNDWDDIFEEFKDISFA.Q
gi 6321710 ref NP_011787.1	YGR271W	Putative RNA helicase related to Ski2p, involved in translation inhibition of non- poly(A) mRNAs; required for repressing propagation of dsRNA viruses; Slh1p	2	3.0024	0.2414	2099.43	2101.319	2	291.9	40.625 E.S1T1F1T1D1E1F1E1L1P1M1W2D1P1H3V1K2.T
ail6321720/refINP 011797.11	YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin: Yor1p	2	3.625	0.1991	1517.27	1516.648	2	564.9	66.66667 M.LKDRDGPEDLEKT.S
5-100247001-s-fND_044707.4	VODOMW	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	_	5.0700	0.4050	0474.04	0474 500	-	4570.7	
gilo321720[rei]NP_011797.1]	IGR201W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	2	5.0736	0.4959	2474.01	2474.090	I	15/2./	55 C.SFEWEDTELINDAIEEARGEAR.D
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	3	4.3591	0.1592	3000.35	3002.367	1	522.4	32.692307 Q.S1L1L1E1A1P1E1D1D1P1N2Q2M1I1E1M1K2P1S1P1G1F1D1P1K2L1A1.L
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	2	3.3407	0.2696	2296.89	2297.344	2	285.9	38.88889 C.S1F1E1W2E1D1Y1E1L1N2D1A111E1E1A1K2G1E1.A
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycic; Yor1p	2	3.3729	0.3136	1724.21	1724.926	1	652.1	65.38461 S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1.M
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p	2	3.6662	0.2336	2524.65	2525.897	1	820.6	47.5 S.YRKPEMTPPESWPSMGEIIFE.N
gi 6321720 ref NP_011797.1	YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin; Yor1p	2	4.3654	0.4158	2396.49	2396.781	1	751.7	55.263157 S.YRKPEMTPPESWPSMGEIIF.E
ail6321720/refINP 011797.11	YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin: Yor1p	2	4.0109	0.3653	1857.53	1857.118	1	597.7	60.714287 S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1.G
ail6321720/ref/NP_011797_1	YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	2	3 0262	0 2505	2638 69	2640	1	352.5	45 238094 S YRKPEMTPPESWPSMGEIIEEN V
ail6221720[rof]ND_044707_1	VCD004W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	<u>_</u>	3 3050	0.2000	2000.03	2040	· •	107.4	
9103217201011797.1	VODCO IV	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	2	3.3239	0.2024	2007.07	2000	o	19/.1	
gij6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	2	4.4277	0.2736	2421.39	2421.781	1	732.2	52.63158 S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1G1E1I1I1F1.E
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p	2	3.7766	0.4121	2737.75	2739.133	1	674.1	43.18182 S.YRKPEMTPPESWPSMGEIIFENV.D

		Bloome membrane transporter of the ATB binding acceptte (ABC) family, mediated								
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p	2	3.9593	0.3671	2765.71	2768.133	1	589.5	38.636364 S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1G1E1I1I1F1E1N2V1.D
gi 6321720 ref NP 011797.1	YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin; Yor1p	3	4.6253	0.2618	2766.74	2768.133	2	807	31.818182 S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1G1E1I1I1F1E1N2V1.D
ail6321720/refINP_011797.1	YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin; Yor1p	3	4.356	0.2919	2257.67	2257.592	8	602	40.27778 H.SKKIPEVPOTDDERKIYPL F
3.1000.0001 (1010.000.000)		Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	-					-		
gi 6321720 ret NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	2	3.0622	0.2485	1240.61	1242.536	3	/16.1	70 F.A1Y1R4P1G1L1P111V1L1K2.N
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	3	4.1508	0.315	2999.54	3001.398	1	768.5	30.208334 S.YRKPEMTPPESWPSMGEIIFENVDF.A
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p	3	4.3575	0.3915	2170.19	2170.514	1	571	38.235294 S.KKIPEVPQTDDERKIYPL.F
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p	2	3.7668	0.2145	2194.63	2195.514	1	640.1	52.941177 S.K2K2I1P1E1V1P1Q2T1D1D1E1R4K2I1Y1P1L1.F
gi 6321720 ref NP_011797.1	YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin; Yor1p	3	4.3739	0.4367	3033.77	3032.398	1	693.9	27.083334 S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1G1E1I1I1F1E1N2V1D1F1.A
ail6321720/refINP 011797.1	YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin: Yor1p	2	3.0088	0.2355	1227.75	1226.295	1	1213.2	88.88889 O.TRIVEEEGDC T
gil6221720/rofIND_011707_1	VCD291W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	-	4 4099	0.274	2062 77	2065 24	4	611.4	
gilo321720161NF_011737.11	101(2011)	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	2	4.4300	0.574	2003.77	2005.54		011.4	
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates	2	4.0937	0.3894	2041.01	2042.34	1	536.1	56.25 K.KIPEVPQTDDERKIYPL.F
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p Plasma membrane transporter of the ATP-hinding cassette (ARC) family, mediates	2	3.1291	0.2305	1488.71	1489.801	1	1003.4	70.83333 V.DFAYRPGLPIVLK.N
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p	2	3.135	0.2006	1588.51	1588.933	4	431.2	53.846157 N.VDFAYRPGLPIVLK.N
gi 6321720 ref NP_011797.1	YGR281W	export of many different organic anions including oligomycin; Yor1p	2	3.5113	0.3215	2550.39	2551.897	1	592.3	45 S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1G1E1I1I1F1E1.N
		Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain								
gi 6321724 ref NP_011801.1	YGR285C	and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p Cutosolic ribosome associated chaperone that acts together with Ssz1p and the Ssb	1	2.3217	0.2502	1396.47	1397.484	1	285.6	55 H.TWSEFERIEAE.K
	VODAAFO	proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain		4.0500		0400.04	0107.0		050.0	
gil6321724 ret NP_011801.1	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb	2	4.6503	0.4181	2186.31	2187.3	1	958.8	61.11111 N.VIK211V1D1E1S1N2V1D1P1D1E1L1L1F1D111E1.L
gi 6321724 ref NP 011801.1	YGR285C	proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p	2	3.6589	0.3904	1957.29	1956.994	1	653.6	53.125 K.T1V1D1E1S1N2V1D1P1D1E1L1L1F1D1T1E1.L
5100 101 20 00 1		Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb								
gi 6321724 ref NP_011801.1	YGR285C	and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p	2	3.2707	0.1588	1658.03	1658.762	1	572.7	70.83333 H.T1W2S1E1F1E1R4I1E1A1E1K2N2.V
		Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain								
gi 6321724 ref NP_011801.1	YGR285C	and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb	2	3.0264	0.2397	2094.13	2095.282	3	344.3	47.058823 C.D1F1V1A1D1V1P1P1P1K2K2G1T1D1Y1D1F1Y1.E
ail6221724/rofIND_011801_1	VCD20EC	proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain	2	2 4017	0.2964	1641 42	1620 762	1	261	
gil6321724[rei]NP_011801.1]	IGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb	2	3.4917	0.2864	1641.43	1039.702	I	301	02.5 H. IWSEFERIEAENN.V
gi 6321724 ref NP_011801.1	YGR285C	proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p	2	2.985	0.2375	2074.51	2075.282	3	261.3	44.11765 C.DFVADVPPPKKGTDYDFY.E
		Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins as a chaperone for pascent polypentide chains; contains a Dna I domain								
gi 6321724 ref NP_011801.1	YGR285C	and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p	2	3.2798	0.2836	1398.15	1397.484	1	1000.1	80 H.TWSEFERIEAE.K
		proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain								
gi 6321724 ref NP_011801.1	YGR285C	and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb	2	3.3753	0.3628	1819.91	1820.991	1	569.1	56.666668 N.VKTVDESNVDPDELLF.D
ail6321724/refINP_011801_1	YGR285C	proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain and functions as a l-protein partner for Ssh1n and Ssh2n; Zuo1n	2	3 9391	0.3644	2037 91	2037 185	1	1123.2	64 70589 N VKTVDESNVDPDELLEDT E
giloo2112 ilioilui _01100111	10112000	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb	-	0.0001	0.0011	2007.01	20011100	·	1120.2	
gi 6321724 ref NP_011801.1	YGR285C	and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p	1	2.5975	0.24	1396.57	1397.484	2	333.7	55 H.TWSEFERIEAE.K
		Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)- coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to								
gi 6321784 ref NP_011860.1	YHL003C	Lac1p; Lag1p Ceramide synthese component involved in synthesis of ceramide from C26/acvl)-	2	3.4881	0.2373	1649.33	1648.915	1	733.1	70.83333 M.Y1R4T1Y1P1V111T1N2P1F1L1F1.K
		coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to								
gi 6321784 ref NP_011860.1	YHL003C	Lac1p; Lag1p Mitochondrial ribosomal protein of the small subunit: Mrp4p	2	2.9705	0.233	1758.91	1760.089	1	434.7 547.4	53.846157 M.YRTYPVITNPFLFK.I
gil6321782[ref NP_011859.1]	YHL004W	Mitochondrial ribosomal protein of the small subunit; Mrp4p	2	3.5254	0.2416	1777.09	1776.039	1	470.1	57.14286 H.KDIFYPPLPENITVE.S
gi 6321782 ref NP_011859.1	YHL004W	Mitochondrial ribosomal protein of the small subunit; Mrp4p	2	2.9284	0.1968	1746.39	1746.958	3	528.6	53.333336 S.LVTYPIPGNDDSLRSV.N
gi 6321782 ref NP_011859.1	YHL004W	Mitochondrial ribosomal protein of the small subunit; Mrp4p	2	3.7171	0.4138	2146.79	2147.346	1	610.8	50 D.SEPSLVTYPIPGNDDSLRSV.N
		Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to F								
gi 6321772 ref NP_011848.1	YHL015W	coli S10 and rat S20 ribosomal proteins; Rps20p	2	3.1861	0.3178	1561.71	1562.834	1	514.4	62.5 H.K2R4Y111D1L1E1A1P1V1Q2I1V1.K
		Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E.								
gi 6321772 ref NP_011848.1	YHL015W	coli S10 and rat S20 ribosomal proteins; Rps20p	1	3.5675	0.3716	1561.68	1562.834	1	497	58.333332 H.K2R4Y1I1D1L1E1A1P1V1Q2I1V1.K
		Protein component of the small (40S) ribosomal subunit; overproduction suppresses								
gi 6321772 ref NP_011848.1	YHL015W	coli S10 and rat S20 ribosomal proteins; Rps20p	1	3.2007	0.3476	1543.68	1544.834	1	487.7	58.333332 H.KRYIDLEAPVQIV.K
		Protein component of the small (40S) ribosomal subunit; overproduction suppresses								
-:::C204770I{IND_044040_4	VUI 045W	mutations affecting RNA polymerase III-dependent transcription; has similarity to E.	0	2 2202	0.0004	4544 70	4544.004		c 00 0	
gijuuz 1772 ji ei jiNP_011048.1	11101500	Protein component of the small (40S) ribosomal subunit; overproduction subpresses	2	3.3203	0.2801	1044.73	1044.034	I	028.3	
		mutations affecting RNA polymerase III-dependent transcription; has similarity to E.								
gi 6321772 ref NP_011848.1	YHL015W	coli S10 and rat S20 ribosomal proteins; Rps20p	1	2.9161	0.3223	1561.79	1562.834	2	308.9	45.833336 H.K2R4Y1I1D1L1E1A1P1V1Q2I1V1.K
		Protein component of the small (405) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E								
gi 6321772 ref NP_011848.1	YHL015W	coli S10 and rat S20 ribosomal proteins; Rps20p	1	3.0557	0.3622	1544.86	1544.834	2	326.7	50 H.KRYIDLEAPVQIV.K
gi 6321766 ref NP_011842.1	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	2.9753	0.3091	1839.73	1841.117	1	583.3	56.666668 L.HTDLPFLENVPGFQIL.Q
gi 6321766 ref NP_011842.1	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	3.2446	0.2805	1885.83	1887.142	1	646.6	53.333336 H.YANKDLPLHTDLPFLE.N
gijb321766 ret NP_011842.1	YHL021C	i ne autnentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	3.046	0.2102	2592.85	2592.998	5	280	31.818182 Y.ANKULPLHTULPFLENVPGFQIL.Q

ail6321766/refINP 011842.1	YHL021C	The authentic, non-tagged protein was localized to the mitochondria: Fmp12p	2	3.6753	0.2853	2436.41	2433.815	1	855.5	50 N.K2D1L1P1L1H3T1D1L1P1F1L1E1N2V1P1G1F1Q2I1L1.Q
gil6321766/refINP_011842_1	YHL021C	The authentic non-tagged protein was localized to the mitochondria: Emp12p	2	3 9771	0 2358	2401 45	2401 724	1	415.6	42.5 H YANKDI PI HTDI PEI ENVPGE O
silcood 700 relinit _011042.1	VIII 024C	The authentic, non-tagged protein was localized to the mitochondra, Thip 12p	2	3.3771	0.2000	2401.45	2401.724		705.0	
gilo321766[rei]INP_011642.1]	THLUZIC	The authentic, non-tagged protein was localized to the mitochondra; Frip 12p	2	4.1017	0.3619	2755.05	2/50.1/4		705.6	41.304348 R. TANKDEPERTDEPFEENVPGPQIE.Q
gi 6321766 ref NP_011842.1	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	4.2144	0.3549	2522.67	2521.919	1	570.6	42.857143 A.NKDLPLHTDLPFLENVPGFQIL.Q
gi 6321766 ref NP 011842.1	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	4.0429	0.2087	2784.49	2786.174	1	556.9	39.130436 H.Y1A1N2K2D1L1P1L1H3T1D1L1P1F1L1E1N2V1P1G1F1Q2I1L1.C
gil6321766/refINP_011842_1	VHI 021C	The authentic pon-tagged protein was localized to the mitochondria: Emp12p	2	4 3351	0 3053	2409.63	2407 815	1	956	57.5 N KDI PLHTDI PELENVPGEOILO
sil0004700irclini _0140404	VIII.024C	The authentic, non tagged protein was localized to the mitchendria, The 12p	2	9.0001	0.0000	4500.57	4504 705		004.4	
gi 6321766 ret NP_011842.1	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	3.6041	0.2993	1530.57	1531.795	2	934.4	12.12121 K.LKFLEEKFPHDK
gi 6321766 ref NP_011842.1	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	3.768	0.2664	1652.03	1652.888	1	1472.9	76.92308 A.NKDLPLHTDLPFLE.N
gil6321766/refINP_011842.1	YHL021C	The authentic, non-tagged protein was localized to the mitochondria: Emp12p	2	3.6412	0.3439	2528.25	2529.855	1	625.7	40.476192 H.YANKDLPLHTDLPELENVPGEQ.
sil0004704iastND_0440404i	VIII.0000C	Detain resulted for a secondation. Deddda	-	2.070	0.4504	4000.05	4050.005		4075.0	
gilo321764[rei]NP_011640.1]	THLU23C	Protein required for sporulation; Rmd i fp	2	3.270	0.1564	1360.25	1359.695		12/5.8	11.21213 S.KFP3LP3LPIFL.5
gi 6321764 ref NP_011840.1	YHL023C	Protein required for sporulation; Rmd11p	2	3.1903	0.2348	1372.67	1372.695	1	902.3	68.181816 S.K2F1P1S1L1P1S1L1P1I1F1L1.S
gil6321764/refINP_011840_1	YHL023C	Protein required for sporulation: Rmd11p	3	3 9664	0 1776	2159 21	2161 489	1	973.4	36 764706 O N2E1E1E1K2M1P1N2E1K2L1O2P1V1L1R4G1S1 Y
giloo2 in o ili oili il _o ino io. il		Nuclearly since the second state is a state in the second state with small suclear	0	0.0001	0.1170	2100.21	21011100		010.1	
		Nucleolar single-strand nucleic acid binding protein; associates with small nuclear								
gi 6321753 ref NP_011829.1	YHL034C	RNAs; Sbp1p	3	6.4183	0.3851	2822.21	2819.893	1	1569.4	39.130436 D.V1A1V1I1R4P1E1N2D1E1E1E1I1E1Q2E1T1G1S1E1E1K2Q2E1
		Nucleolar single-strand nucleic acid binding protein: associates with small nuclear								
-: 102047521fND_044000_41	VUI 024C	DNA: Chata	2	5 0000	0 4070	0040 57	0040.004	4	0004	
gilo321753[ter]INF_011629.1]	THL034C	KNAS, SUPTP	2	0.0000	0.4370	2010.07	2010.001		2231	01.904702 A.VIKFENDEEEIEQEIGSEERQE.
		Nucleolar single-strand nucleic acid binding protein; associates with small nuclear								
gi 6321753 ref NP 011829.1	YHL034C	RNAs; Sbp1p	2	6.234	0.3802	2645.51	2647.681	1	2025.2	59.523808 A.V1I1R4P1E1N2D1E1E1E1I1E1Q2E1T1G1S1E1E1K2Q2E1
5100 00101 <u>=</u> 0 0001		Nuclealar single-strand nucleic acid binding protein: associates with small nuclear								
	XIIII 00.40	Duke of a state straid nucleic acid binding protein, associates with small nuclear	~	4 4 4 9 9	0.000	0700 47	0700 000		000 7	
gilo321753[rei]iNP_011629.1]	THL034C	RNAS; SDPTP	2	4.1400	0.309	2/00.4/	2100.093		922.7	45.052176 D.VAVIRPENDEEEIEQETGSEERQE
		Nucleolar single-strand nucleic acid binding protein; associates with small nuclear								
gil6321753/refINP_011829_1	YHI 034C	RNAs: Shp1p	2	5 4252	0.3805	2340.69	2341 616	1	908.9	61 11111 V1K2E1P1T1K2I1D1E1D1N2I1K2E1N2Y1D1T1K2 V
gilooz in oplicitititi _o inozoniti	11120010	Nuels los cierto atrand avaleia esid biadine proteia, esseciates with exall avalees	-	0.1202	0.0000	2010.00	2011.010		000.0	
		Nucleolal single-strand nucleic acid binding protein, associates with small nuclear								
gi 6321753 ref NP_011829.1	YHL034C	RNAs; Sbp1p	2	3.8039	0.3079	2103.49	2104.146	1	454.4	44.11765 A.VIRPENDEEEIEQETGSE.E
		Nucleolar single-strand nucleic acid binding protein; associates with small nuclear								
ail6321753[rofIND_011820_1]		PNAs: Sho1o	2	3 0111	0 3396	1/51 07	1452 604	1	508.7	
gilo321735[rei]NF_011023.1]	11120340	Navas, Supply	2	5.0111	0.5500	1431.57	1432.004		500.7	30.333332 1.3DE V3 VEIT INET. 1
		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein								
gi 6321748 ref NP 011824.1	YHL039W	localizes to the cytoplasm; Yhl039wp	2	3.8381	0.4184	2068.79	2069.409	1	671.3	52.941177 N.EKFSPKPDQALIRVPETL.L
		Putative protein of unknown function: green fluorescent protein (GEP)-fusion protein								
	VIII 00004/	a dative protein of an low Million and the protein (Grif) has on protein	~	4 7004	0 4005	0007.04	0000 045		504.4	
gi 6321748 ret NP_011824.1	YHL039W	localizes to the cytoplasm; YhiU39wp	2	4.7381	0.4095	2307.81	2309.645	1	581.4	52.63158 F.V1N2E1K2F1S1P1K2P1D1Q2A1L111R4V1P1E111L1.L
		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein								
ail6321748/refINP_011824_1	YHI 039W	localizes to the cytoplasm: Ybl039wp	3	3 937	0 2986	2283 35	2282 645	2	1253 7	39 473686 F VNEKESPKPDOALIRVPETLI
gilooz 1140/10/141_011024.11	THEODOW		0	0.507	0.2000	2200.00	2202.040	2	1200.1	SS. Froudor I. Merillion Repeated in the Denterror Ere.e
		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein								
gi 6321748 ref NP_011824.1	YHL039W	localizes to the cytoplasm; Yhl039wp	2	4.5049	0.301	2281.97	2282.645	1	803.8	55.263157 F.VNEKFSPKPDQALIRVPETL.L
		Putative protein of unknown function: green fluorescent protein (GEP)-fusion protein								
-: C204740 (ND 0440044)	VI II 020W/		0	2 445	0.0040	0004.07	0000 045		075 4	
gilo321746[rei]NP_011624.1]	1 HL039W	localizes to the cytoplasm, thiosowp	2	3.115	0.2049	2261.97	2282.845		275.4	39.473666 F.VNEKFSPKPDQALIKVPETLL
		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein								
ail6321748/refINP 011824.1	YHL039W	localizes to the cytoplasm; Yhl039wp	3	4.6475	0.3534	2306.75	2309.645	1	959.4	36.842106 F.V1N2E1K2F1S1P1K2P1D1Q2A1L1I1R4V1P1E1T1L1.L
5111 III = III I		Transporter, member of the ARN family of transporters that specifically recognize								
		That spotter, member of the virth farming of that spotters that spotter any recognize								
		siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin,								
gi 6321747 ref NP_011823.1	YHL040C	ferrirhodin, and related siderophores; Arn1p	2	3.9598	0.3859	1985.77	1985.213	1	598.5	56.666668 K.D1N2D1P1I1L1D1W2F1E1K2L1P1S1K2F1.T
		Transporter, member of the ARN family of transporters that specifically recognize								
		ridiopolitica, monipoli o internativa farma politica de constructiva de la construcción de la constru Construcción de la construcción de la constr								
		siderophore-iron chelates; responsible for uptake of iron bound to remirubin,								
gi 6321747 ref NP_011823.1	YHL040C	ferrirhodin, and related siderophores; Arn1p	3	4.6521	0.343	2093.45	2093.387	1	1616.1	43.75 T.KDNDPILDWFEKLPSKF.T
		Transporter, member of the ARN family of transporters that specifically recognize								
		siderophore-iron chalates; responsible for untake of iron bound to ferringhin								
		siderophore-iron cherates, responsible for uptake of non bound to remitabilit,								
al 6221747 rof ND 011022 1	YHL040C	ferrirhodin, and related siderophores; Arn1p	3	5.0469	0.3661	2114.99	2115.387	1	1013	42.1875 T.K2D1N2D1P1I1L1D1W2F1E1K2L1P1S1K2F1.T
gilo321747 [rei]ivF_011623.1]										
gilo321747 [lei]NF_011823.1]		Transporter, member of the ARN family of transporters that specifically recognize								
gilosz 1747 frei fivr_011625. 1		Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates: responsible for untake of iron bound to ferrirubin								
		Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin,								
gi 6321747 ref NP_011823.1	YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p	3	5.5645	0.4295	3311.48	3310.596	1	1906.3	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T
gi 6321747 ref NP_011823.1	YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Arn Ip Transporter, member of the ARN family of transporters that specifically recognize	3	5.5645	0.4295	3311.48	3310.596	1	1906.3	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.1
gi 6321747 ref NP_011823.1 gi 6321747 ref NP_011823.1	YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrinubin, ferrinubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore; iron chelates; responsible for untake of iron bound to ferrinubin.	3	5.5645	0.4295	3311.48	3310.596	1	1906.3	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T
gi 6321747 ref NP_011823.1 =::::::::::::::::::::::::::::::::::::	YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, torible of the development of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, torible of the development of the ARN family of the development of the development of the ARN family of the development of the developmen	3	5.5645	0.4295	3311.48	3310.596	1	1906.3	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.1
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1]	YHL040C YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p	3 3	5.5645 5.4854	0.4295 0.3397	3311.48 3280.7	3310.596 3278.596	1	1906.3 892.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T
gi 6321747 ref NP_011823.1 gi 6321747 ref NP_011823.1 gi 6321747 ref NP_011823.1	YHL040C YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize for iron of the ARN family of transporters that specifically recognize transporter, member of the ARN family of transporters that specifically recognize	3 3	5.5645 5.4854	0.4295 0.3397	3311.48 3280.7	3310.596 3278.596	1	1906.3 892.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.1 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T
gi 6321747 ref NP_011823.1 gi 6321747 ref NP_011823.1 gi 6321747 ref NP_011823.1	YHL040C YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrinubin, ferrinubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrinubin, ferrinubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrinubin, ferrinubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for untake of iron bound to ferrinubin.	3 3	5.5645 5.4854	0.4295 0.3397	3311.48 3280.7	3310.596 3278.596	1	1906.3 892.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1]	YHL040C YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, end related siderophores; Am1p	3 3	5.5645 5.4854	0.4295	3311.48 3280.7	3310.596 3278.596	1	1906.3 892.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.1 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T
gij6321747/ref/NP_011823.1/ gij6321747/ref/NP_011823.1/ gij6321747/ref/NP_011823.1/ gij6321747/ref/NP_011823.1/	YHL040C YHL040C YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p	3 3 2	5.5645 5.4854 4.329	0.4295 0.3397 0.4725	3311.48 3280.7 1962.29	3310.596 3278.596 1965.213	1	1906.3 892.7 955.3	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011826.1]	YHL040C YHL040C YHL040C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	3 3 2 2	5.5645 5.4854 4.329 3.2618	0.4295 0.3397 0.4725 0.261	3311.48 3280.7 1962.29 1390.97	3310.596 3278.596 1965.213 1388.592	1 1 1 1	1906.3 892.7 955.3 1209.1	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q
gij6321747 ref NP_011823.1 gij6321747 ref NP_011823.1 gij6321747 ref NP_011823.1 gij6321747 ref NP_011823.1 gij6321790 ref NP_01186.1 gij6321790 ref NP_01186.1	YHL040C YHL040C YHL040C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function.	3 3 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868	0.4295 0.3397 0.4725 0.261 0.2164	3311.48 3280.7 1962.29 1390.97 1627.75	3310.596 3278.596 1965.213 1388.592 1628.82	1 1 1 1	1906.3 892.7 955.3 1209.1 724.9	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.V1Y151E1E1V1L1D1F111E1R4L1.F
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter-inon chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Utative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	3 3 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3092	0.4295 0.3397 0.4725 0.261 0.2164	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41	3310.596 3278.596 1965.213 1388.592 1628.82	1 1 1 1 1	1906.3 892.7 955.3 1209.1 724.9 982.1	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.Y1Y1S1E1E1Y1L1D1F111E1R4L1.F 66 66667 Y SEEU / DEED EV E
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHL040C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	3 3 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992	0.4295 0.3397 0.4725 0.261 0.2164 0.1984	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862	1 1 1 1 1 1	1906.3 892.7 955.3 1209.1 724.9 982.1	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2E1Y1D1S111L1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F111E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	3 3 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995	1 1 1 1 1 1 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.Y1Y1S1E1E1Y1L1D1F111E1R4L1.F 66.66667 Y.SEEVLDFIEELFK.E 64.26571 E.A1L1R4H3L1P1E1L1G1T1M1P1G111F1.G
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	3 3 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527 0.3978	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519	1 1 1 1 1 1 2	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S11L1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F11F1R4L1.F 66.666667 Y.SEEVLDFIERLFK.E 64.28571 E.A1L1R4H3L1P1E1L1G1T1M1P1G11F1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011826.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	3 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527 0.3978 0.3699	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1655 59	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519	1 1 1 1 1 1 1 2	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.Y1Y1S1E1E1Y1L1D1F11E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.26571 E.A1L1R4H3L1P1E1L1G1T1M1P1G111F1.G 38.88899 A.VRDEALRHLPELGTMPGIF.G 64.26571 E.A1L1R4H3L1P1E1L1G1TMPIF.G 64.26571 E.A1L1R4H3L1P1E1L1G1TMPIF.G 64.26571 E.A1L1R4H3L1P1E1L1G1TMPIF.G
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown f	3 3 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527 0.3978 0.3699	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1655.59	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519 1652.995	1 1 1 1 1 1 1 2 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2E1Y1D1S11L1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F11F1F1.Q 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.A1L1R4H3L1P1E1L1G1T1M1P1G111F1.G 38.8889A V.RDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown f	3 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527 0.3978 0.3699	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1655.59	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519 1652.995	1 1 1 1 1 1 1 2 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.Y1Y1S1E1E1Y1L1D1F11E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.26571 E.AL1:R4H3L1P1E1L1G1T1M1P1G111F1.G 38.88899 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown f	3 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527 0.3978 0.3699	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1655.59	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519 1652.995	1 1 1 1 1 1 2 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2E1Y1D1S11L1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F11F1F1.Q 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.A1L1R4H3L1P1E1L1G1T1M1P1G111F1.G 38.88890 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp STP-binding alpha subunit of the heterotirmer G protein that couples to pheromone receptors; negatively requirements pathway by sequestering Ghrefajamama	3 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527 0.3978 0.3699	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1655.59	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519 1652.995	1 1 1 1 1 1 2 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.Y1Y1S1E1E1Y1L1D1F11E1R4L1.F 66.66667 Y.SEEVLDFIEELFK.E 64.26571 E.ALLR4H3L1P1E1L1G1T1M1P1G111F1.G 38.88899 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by trigenine and enderine receptore; mentioned miterine contents; contents and contents and contents and contents and the contents and the content contents and contents and contents and contents and contents and the content contents and the content content content and content content contents and content contents and content conten	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527 0.3978 0.3699	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1655.59	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519 1652.995	1 1 1 1 1 1 2 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F11E1R4L1.F 66.66667 Y.SEEVLDFIREFK.E 64.28571 E.A1L1R4H3L1P1E1L1G1T1M1P1G111F1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321792]ref]NP_011868.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, terrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein duknown function, localizes to the mito	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992 3.0198	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1984 0.3699 0.256	3311.48 3280.7 1962.29 1390.97 1628.41 1678.75 1628.41 1675.59 1678.33	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519 1652.995	1 1 1 1 1 1 2 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.Y1Y1S1E1E1Y1L1D1F11E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.ALLR4H3L1P1E1L1G1T1M1P1G111F1.G 38.88899 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR003C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Bitter protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992 3.0198	0.4295 0.3397 0.4725 0.261 0.2164 0.1527 0.3978 0.3699 0.256	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1655.59 1678.33	3310.596 3278.596 1965.213 1388.592 1628.82 1627.862 1672.995 2152.519 1652.995	1 1 1 1 1 1 2 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9	37.5 E.Y111E1D1G1E1Y1V1D1T1K2D1N2D1P111L1D1W2F1E1K2L1P1S1K2F1.T 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S111L1E1T1F1.Q 62.5 A.Y1Y1S1E1E1V1L1D1F11E1R4L1.F 66.666667 Y.SEEVLDFIERLFK.E 64.28571 E.A1L1R4H3L1P1E1L1G1T1M1P1G111F1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N
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gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR005C YHR005C YHR005C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the h	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.6433 3.2992 3.0198 3.5348 2.6062	0.4295 0.3397 0.4725 0.261 0.2164 0.1527 0.3978 0.3699 0.256 0.2352 0.2352	3311.48 3280.7 1962.29 1390.97 1627.75 1628.71 1671.87 2152.51 1675.59 1678.33 1699.89 1314.5	3310.596 3278.596 1965.213 1388.592 1628.82 1672.995 2152.519 1652.995 1679.738 17700.738 1314.569	1 1 1 1 1 2 1 1 1 2	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.7 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 63.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S1HL1E1T1F1.Q 62.5 A.Y1Y1S1E1E1V1L1D1F1HE1KL1.F 66.66667 Y.SEEVLDFIREFK.E 64.28571 E.A1L1R4H3L1P1E1L1G1T1M1P1G1HF1.G 38.88899 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L
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gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321792]ref]NP_011866.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR005C YHR005C YHR005C YHR005C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Bittive protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the hete	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1488	0.4295 0.3397 0.4725 0.261 0.2164 0.1527 0.3978 0.3699 0.256 0.2352 0.2352 0.2306 0.1743 0.1766	3311.48 3280.7 1962.29 1390.97 1627.75 1628.75 1678.33 1679.89 1678.33 1699.89 1314.5 1326.55 1309.33	3310.596 3278.596 1965.213 1388.592 1628.82 1672.995 2152.519 1652.995 1679.738 1700.738 1314.569 1326.569 1308.567	1 1 1 1 2 1 1 2 1 1 1 1 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.7 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 80.R_1K2F1Y1D1S1HL1E1T1F1.0 82.5 A.V1Y1S1E1F1V1L1D1F1H1E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.AIL1R4H3L1P1E1L1G1TMPG1F.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F1H1L1F1.L
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gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR005C YHR005C YHR005C YHR005C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1488	0.4295 0.3397 0.4725 0.261 0.2164 0.1527 0.3978 0.3699 0.256 0.2352 0.2352 0.2306 0.1743 0.1766	3311.48 3280.7 1962.29 1390.97 1627.75 1628.71 1671.87 2152.51 1675.59 1678.33 1699.89 1314.5 1326.55 1309.33	3310.596 3278.596 1965.213 1388.592 1628.82 1672.995 2152.519 1652.995 1679.738 1700.738 1314.569 1326.569 1308.567	1 1 1 1 2 1 1 2 1 1 1 1 1 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.7 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 80.R_1K2F1Y1D1S1HL1E1T1F1.0 82.5 A.V1Y1S1E1F1V1L1D1F1H1E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.AIL1R4H3L1P1E1L1G1TM1P1G1HF1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F1HL1F1.L
gij6321747 ref NP_011823.1 gij6321747 ref NP_011823.1 gij6321747 ref NP_011823.1 gij6321747 ref NP_011823.1 gij6321790 ref NP_011866.1 gij6321790 ref NP_011866.1 gij6321790 ref NP_011866.1 gij6321792 ref NP_011866.1 gij6321792 ref NP_011868.1	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR005C YHR005C YHR005C YHR005C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1488	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.1527 0.3978 0.3699 0.256 0.2352 0.2352 0.2306 0.1743 0.1766	3311.48 3280.7 1962.29 1390.97 1628.41 1671.87 2152.51 1655.59 1678.33 1699.89 1314.5 1326.55 1309.33	3310.596 3278.596 1965.213 1388.592 1628.82 1627.395 1652.995 1679.738 1700.738 1314.569 1326.569 1308.567	1 1 1 1 1 1 2 1 1 2 1 1 1	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5 1023.7	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.3 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 80.RL1K2E1Y1D1S1HL1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F1H1E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.ATL1R4H3L1P1E1L1G1T1M1P1G1H1F1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F1HL1F1.L
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1]	 YHL040С YHL040С YHR003С YHR003С YHR003С YHR003С YHR003С YHR005С 	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubdin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulate	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1488 2.9374	0.4295 0.3397 0.4725 0.261 0.2164 0.1527 0.3978 0.3699 0.256 0.2352 0.2352 0.2352 0.2306 0.1743 0.1766	3311.48 3280.7 1962.29 1390.97 1627.75 1628.71 1671.87 2152.51 1675.59 1678.33 1699.89 1314.5 1326.55 1309.33 1937.69	3310.596 3278.596 1965.213 1388.592 1628.82 1672.995 2152.519 1652.995 1679.738 1700.738 1314.569 1326.569 1308.567 1939.22	1 1 1 1 1 2 1 1 2 1 1 1 3	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5 1023.7 299.6	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.7 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 80.R_1K2F1Y1D1S1HL1E1T1F1.0 82.5 A.V1Y1S1E1F1V1L1D1F1H1E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.AIL1R4H3L1P1E1L101T1M1P1G1HF1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F1H1L1F1.L 83.33333 S.K2W2F1K2D1T1P1F1H1L1F1.L
gi[6321792]ref]NP_011823.1] gi]6321747]ref]NP_011823.1] gi]6321747]ref]NP_011823.1] gi]6321747[ref]NP_011823.1] gi]6321790]ref]NP_011866.1] gi]6321790[ref]NP_011866.1] gi]6321790[ref]NP_011866.1] gi]6321792[ref]NP_011866.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR005C YHR005C YHR005C YHR005C YHR005C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am 1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am 1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am 1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am 1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive r	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1492 3.1488 2.9374	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.3699 0.256 0.2352 0.2352 0.2306 0.1743 0.1766 0.1534	3311.48 3280.7 1962.29 1390.97 1628.41 1671.87 2152.51 1655.59 1678.33 1699.89 1314.5 1326.55 1309.33 1937.69	3310.596 3278.596 1965.213 1388.592 1628.82 1672.995 2152.519 1679.738 1700.738 1314.569 1326.569 1308.567 1939.22	1 1 1 1 1 2 1 1 2 1 1 1 3	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5 1023.7 299.6	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.7 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 83.333332 K.DNDPILDWFEKLPSKF.T 80 R.L1K2F1Y1D1S1HL1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F1H1E1R4L1.F 66.66667 Y.SEEVLDFIERFK.E 64.28571 E.A1L1R4H3L1P1E1L1G1T1M1P1G1H1F1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F1HL1F1.L 83.33333 S.K2W2F1K2D1T1P1F1HL1.F1.L
gi[6321792]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR005C YHR005C YHR005C YHR005C YHR005C YHR005C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1488 2.9374	0.4295 0.3397 0.4725 0.261 0.2164 0.1527 0.3978 0.3699 0.256 0.2352 0.2352 0.2352 0.2306 0.1743 0.1766	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1675.59 1678.33 1699.89 1314.5 1326.55 1309.33 1937.69	3310.596 3278.596 1965.213 1388.592 1628.82 1672.995 2152.519 1652.995 1679.738 1700.738 1314.569 1326.569 1308.567 1939.22	1 1 1 1 1 2 1 1 2 1 1 1 1 3	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5 1023.7 299.6	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.7 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 80.R_1K2F1Y1D1S1HL1E1T1F1.0 82.5 A.V1Y1S1E1F1V1L1D1F1HE1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.AIL1R4H3L1P1E1L1G1T1M1P1G1HF1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F1H1L1F1.L 83.33333 S.K2W2F1K2D1T1P1F1H1L1F1.L
gi[6321747]ref]NP_011823.1] gi]6321747]ref]NP_011823.1] gi]6321747[ref]NP_011823.1] gi]6321747[ref]NP_011823.1] gi]6321790[ref]NP_011866.1] gi]6321790[ref]NP_011866.1] gi]6321790[ref]NP_011866.1] gi]6321790[ref]NP_011866.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1] gi]6321792[ref]NP_011868.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR003C YHR005C YHR005C YHR005C YHR005C YHR005C YHR005C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the h	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1492 3.1488 2.9374	0.4295 0.3397 0.4725 0.261 0.2164 0.1984 0.3699 0.256 0.2352 0.2352 0.2306 0.1743 0.1766 0.1534	3311.48 3280.7 1962.29 1390.97 1628.41 1671.87 2152.51 1655.59 1678.33 1699.89 1314.5 1326.55 1309.33 1937.69	3310.596 3278.596 1965.213 1388.592 1628.82 1672.995 2152.519 1679.738 1700.738 1314.569 1326.569 1308.567 1939.22	1 1 1 1 1 2 1 1 2 1 1 1 3	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5 1023.7 299.6	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.7 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 83.333332 K.DNDPILDWFEKLPSKF.T 80.RL1K2F1Y1D1S1HL1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F1H1E1R4L1.F 66.66667 Y.SEEVLDFIERFK.E 64.28571 E.A1L1R4H3L1P1E1L1G1T1M1P1G1H1F1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 64.28571 E.ALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F1HL1F1.L 83.33333 S.K2W2F1K2D1T1P1F1HL1.F1.L
gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321747]ref]NP_011823.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321790]ref]NP_011866.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1] gi[6321792]ref]NP_011868.1]	YHL040C YHL040C YHR003C YHR003C YHR003C YHR003C YHR005C YHR005C YHR005C YHR005C YHR005C YHR005C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirubin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1488 2.9374 3.5271	0.4295 0.3397 0.4725 0.261 0.2164 0.1527 0.3978 0.3699 0.256 0.2352 0.2352 0.2352 0.2306 0.1743 0.1766 0.1534	3311.48 3280.7 1962.29 1390.97 1627.75 1628.41 1671.87 2152.51 1678.33 1699.89 1314.5 1326.55 1309.33 1937.69	3310.596 3278.596 1965.213 1388.592 1628.82 1625.862 1672.995 2152.519 1652.995 1679.738 1700.738 1314.569 1326.569 1308.567 1939.22 1296.596	1 1 1 1 1 2 1 1 2 1 1 1 3 3	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5 1023.7 299.6	37.5 E.Y1HE1D1G1E1Y1V1D1T1K2D1N2D1P1HL1D1W2F1E1K2L1P1S1K2F1.7 27.884615 E.YIEDGEYVDTKDNDPILDWFEKLPSKF.T 80.R_1K2F1Y1D1S1HL1E1T1F1.0 82.5 A.Y1Y1S1E1F1V1L1D1F1H1E1R4L1.F 66.66667 Y.SEEVLDFIERLFK.E 64.28571 E.AIL1R4H3L1P1E1L1G1TH1P1G1HF1.G 38.88889 A.VRDEALRHLPELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F1H1L1F1.L 83.33333 S.K2W2F1K2D1T1P1F1H1L1F1.L 84.6666668 K.S1M1P1HR4K2Y1F1P1D1Y1Q2G1R4V1G1.D
gij6321747 [ref]NP_011823.1] gij6321747 [ref]NP_011823.1] gij6321747 [ref]NP_011823.1] gij6321747 [ref]NP_011823.1] gij6321790 [ref]NP_011866.1] gij6321790 [ref]NP_011866.1] gij6321790 [ref]NP_011866.1] gij6321792 [ref]NP_011866.1] gij6321792 [ref]NP_011868.1] gij6321792 [ref]NP_011868.1] gij6321792 [ref]NP_011868.1] gij6321792 [ref]NP_011868.1] gij6321792 [ref]NP_011868.1] gij6321792 [ref]NP_011868.1] gij6321792 [ref]NP_011868.1] gij6321792 [ref]NP_011868.1]	 YHL040С YHL040С YHR003С YHR003С YHR003С YHR003С YHR003С YHR003С YHR005С 	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Am1p Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp Putative protein of unknown function, localizes to the mitochondria; Yhr003cp GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p GTP-binding alpha subunit of the h	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5.5645 5.4854 4.329 3.2618 2.9868 3.3992 3.1709 3.6433 3.2992 3.0198 3.5348 2.6062 3.1492 3.1492 3.1488 2.9374 3.5271	0.4295 0.3397 0.4725 0.261 0.2164 0.1527 0.3978 0.3699 0.256 0.2352 0.2352 0.2306 0.1743 0.1766 0.1534 0.3143	3311.48 3280.7 1962.29 1390.97 1628.41 1671.87 2152.51 1655.59 1678.33 1699.89 1314.5 1326.55 1309.33 1937.69 1296.03	3310.596 3278.596 1965.213 1388.592 1628.82 1672.995 2152.519 1679.738 1700.738 1314.569 1326.569 1308.567 1939.22 1296.596	1 1 1 1 1 2 1 1 2 1 1 3 3	1906.3 892.7 955.3 1209.1 724.9 982.1 625.9 381.6 699.7 560.9 515.5 416.6 793.5 1023.7 299.6 793.1	37.5 E.Y1I1E1D1G1E1Y1V1D1T1K2D1N2D1P1I1L1D1W2F1E1K2L1P1S1K2F1." 27.884615 E.Y1EDGEYVDTKDNDPILDWFEKLPSKF.T 80.R_L1K2F1Y1D1S1I1L1E1T1F1.Q 62.5 A.V1Y1S1E1E1V1L1D1F1I1E1R4L1.F 66.66667 Y.SEEVLDFIERFK.E 64.28571 E.ALLR4H3L1P1E1L1G1T1M1P1G111F1.G 38.88889 A.VRDEALRH.PELGTMPGIF.G 57.14286 S.NVKSDTDRDAETVTQ.N 57.14286 S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N 66.66667 K.WFKDTPFILF.L 83.33333 K.W2F1K2D1T1P1F111L1F1.L 83.33333 S.K2W2F1K2D1T1P1F111L1.F 46.6666688 K.S1M1P111R4K2Y1F1P1D1Y1Q2G1R4V1G1.D 72.72727 M.VTLPTGPAKIIW.E

gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	2	3.2226	0.223	1858.83	1857.993	1	425.5	69.230774 Y.E1F1F1E1E1C1Q2K2K2Y1G1D111F1.S
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	2	3.1062	0.2526	1842.51	1840.993	6	183.9	53.846157 Y.EFFEECQKKYGDIF.S
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	2	3.6809	0.3665	2563.53	2564.9	1	755.2	42.857143 Y.SDLDKGFTPINFVFPNLPLEHY.R
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	2	4.1274	0.3106	2594.75	2591.9	1	686.3	40.476192 Y.S1D1L1D1K2G1F1T1P1I1N2F1V1F1P1N2L1P1L1E1H3Y1.R
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	2	4.7419	0.4514	2597.75	2597.949	1	572.6	47.5 L.LHLAERPDVQQELYEEQMRVL.D
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	2	3.5447	0.241	1569.81	1570.885	3	333.1	53.846157 M.V1T1L1P1T1G1P1A1K2I1I1W2E1K2.R
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	2	4.1439	0.3576	2117.45	2118.414	1	626.3	58.823532 L.KWHYPEGKTVPPPDFTSM.V
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	1	2.3241	0.1505	1353.51	1354.502	1	490	63.636364 Y.SDLDKGFTPINF.V
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	1	2.6227	0.2952	1367.43	1368.502	1	458.7	63.636364 Y.S1D1L1D1K2G1F1T1P1I1N2F1.V
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	1	2.5569	0.2726	1228.5	1229.421	4	393.4	61.11111 F.VFPNLPLEHY.R
gi 6321795 ref NP_011871.1	YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg1p	1	2.239	0.288	1242.47	1242.421	1	391.1	61.11111 F.V1F1P1N2L1P1L1E1H3Y1.R
gi 6321796 ref NP_011872.1	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2p	1	2.413	0.1557	1361.73	1362.612	1	605.2	70 T.KVTLPDLKWDF.G
ail6321796/refINP_011872.1	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2p	2	3.2541	0.2437	1360.95	1362.612	1	1122.7	80 T.KVTLPDLKWDE.G
gil6321796/refINP_011872_1	VHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2n	2	3 3756	0 1852	2378 51	2378 73	3	419.4	
	111100000	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity;	-	0.0700	0.1002	2070.01	2010.10		- 15.4	
gi 6321796 ret NP_011872.1	THR008C	S002p Manganese-containing superoxide dismutase; protects cells against oxygen toxicity;	2	3.8503	0.2551	2192.13	2193.547	1	645.2	50 T.KVTLPDLKWDFGALEPYIS.G
gi 6321796 ref NP_011872.1	YHR008C	Sod2p Manganese-containing superoxide dismutase; protects cells against oxygen toxicity;	1	2.8556	0.3187	1361.77	1362.612	1	667.4	70 T.KVTLPDLKWDF.G
gi 6321796 ref NP_011872.1	YHR008C	Sod2p Manganese-containing superoxide dismutase: protects cells against oxygen toxicity:	2	3.6735	0.3208	1361.89	1362.612	1	1629.6	90 T.KVTLPDLKWDF.G
gi 6321796 ref NP_011872.1	YHR008C	Sod2p Manganese-containing superovide dismutase: protects cells against ovugen tovicity:	2	3.0961	0.179	1101.29	1100.346	1	1366.3	87.5 T.KVTLPDLKW.D
gi 6321796 ref NP_011872.1	YHR008C	Sod2p	1	2.4069	0.1601	1099.57	1100.346	1	538.7	68.75 T.KVTLPDLKW.D
gi 6321808 ref NP_011884.1	YHR020W	Putative protein of unknown function, has similarity to proline-tRNA ligase; YHR020W is an essential gene; Yhr020wp	2	4.2651	0.4196	1891.57	1891.146	1	1307	66.66667 L.EARIPEILEEMQGDLF.K
gi 6321808 ref NP_011884.1	YHR020W	Putative protein of unknown function, has similarity to proline-tRNA ligase; YHR020W is an essential gene; Yhr020wp	2	3.7486	0.357	1563.47	1563.924	1	874	76.92308 Y.ELKGIPIRIELGPK.D
ail6321808/refINP_011884.1	YHR020W	Putative protein of unknown function, has similarity to proline-tRNA ligase; YHR020W is an essential gene: Yhr020wp	2	4.6637	0.3957	1910.67	1911.146	1	1158.2	63.333332 L E1A1R4I1P1E1I1L1E1E1M1Q2G1D1L1E1.K
gil6321808/rofINE_011884_1		Putative protein of unknown function, has similarity to proline-tRNA ligase;	2	3 4624	0 2030	1606.41	1606 788	1	525.8	70 83333 S D4//41 151K251K2D1H3//151G151 A
gilosz roodreinar _0 r roo4. n	111102000	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may	2	3.4024	0.2333	1000.41	1000.700	I	525.0	
gi 6321816 ref NP_011892.1	YHR027C	participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	3	4.5315	0.3344	2940.41	2940.953	1	497.1	25.961538 K.SSDKDATTDGKNDDEEEEKEAGIVDEL.A
gi 6321816 ref NP_011892.1	YHR027C	participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	5.7354	0.362	2042.43	2041.068	1	1560.5	70.588234 D.G1K2N2D1D1E1E1E1E1K2E1A1G111V1D1E1L1.A
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	3.4518	0.3144	2765.75	2766.797	2	307	35.416664 S.DKDATTDGKNDDEEEEKEAGIVDEL.A
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	3.9688	0.2553	1965.63	1963.191	1	531.6	59.375 K.E1L1N2L1T1G1P1K2V1P1E1D111Y1K2S1H3.L
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	5.2643	0.4001	2093.49	2093.365	1	1174.6	61.764706 A.K2E1L1N2L1T1G1P1K2V1P1E1D1I1Y1K2S1H3.L
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	4.317	0.3684	2069.33	2069.365	1	1406.8	70.588234 A.KELNLTGPKVPEDIYKSH.L

gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	1	2.8986	0.3616	1409.78	1410.622	2	293	65 L.KFLRPTYPDLC.S
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	1	2.3632	0.1574	1424.5	1425.622	5	249.4	60.000004 L.K2F1L1R4P1T1Y1P1D1L1C1.S
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	3.4815	0.2507	1424.49	1425.622	5	812.5	70 L.K2F1L1R4P1T1Y1P1D1L1C1.S
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	3	4.5279	0.3219	3420.02	3419.603	1	745.5	25.862068 E.QVNEPTKNEEAEIEVDEMEVDAEGEEVEVK.A
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	3	5.3218	0.3162	3454.07	3454.603	1	904.8	E.Q2V1N2E1P1T1K2N2E1E1A1E1I1E1V1D1E1M1E1V1D1A1E1G1E1E1V1E1V1K2. 28.448275 A
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	3	4.2301	0.2063	2092.7	2093.365	8	700.8	38.235294 A.K2E1L1N2L1T1G1P1K2V1P1E1D111Y1K2S1H3.L
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	3	4.2125	0.2313	2068.16	2069.365	1	1233.1	44.11765 A.KELNLTGPKVPEDIYKSH.L
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	3.8268	0.3281	2141.71	2140.444	1	301.6	44.444447 L.AKELNLTGPKVPEDIYKSH.L
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	3.8611	0.2387	2162.97	2165.444	1	336.1	44.444447 L.A1K2E1L1N2L1T1G1P1K2V1P1E1D1I1Y1K2S1H3.L
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	3	5.4316	0.2506	3001.43	3002.349	1	1101.3	35.416664 E.KQTPNKKDKKKEEEEQLSEEDAKLK.T
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	3	6.9913	0.2988	3686.45	3687.028	1	1416.9	Q.S1Q2I1S1P1E1K2Q2T1P1N2K2K2D1K2K2K2E1E1E1E1Q2L1S1E1E1D1A1K2L1K 31.666666 2.T
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	4.636	0.4334	2019.31	2020.068	1	1138.9	67.64706 D.GKNDDEEEEKEAGIVDEL.A
gi 6321816 ref NP_011892.1	YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine- rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	2	3.1458	0.2125	1428.57	1425.622	5	532.6	70 L.K2F1L1R4P1T1Y1P1D1L1C1.S
gi 6321823 ref NP_011899.1	YHR034C	Protein of unresolved function; may function in protein folding and/or rRNA processing, interacts with a chaperone (Hsp82p), two chromatin remodeling factors (Rvb1p, Rvb2p) and two rRNA processing factors (Rrp43p, Nop58p); Pih1p	2	3.0528	0.2937	1738.65	1738.947	1	531.2	53.571426 N.VCHSPLVPKPEVDFN.A
gi 6321823 ref NP_011899.1	YHR034C	Protein of unresolved function; may function in protein folding and/or rRNA processing, interacts with a chaperone (Hsp82p), two chromatin remodeling factors (Rvb1p, Rvb2p) and two rRNA processing factors (Rrp43p, Nop58p); Pih1p	2	4.2052	0.321	2702.51	2703.954	1	606.9	43.47826 N.L1K2Q2A1P1A1P1A1P1A1P1H3E1Q2Q2E1D1V1P1E1Y1E1V1K2.M
gi 6321823 ref NP_011899.1	YHR034C	Protein of unresolved function; may function in protein folding and/or rRNA processing, interacts with a chaperone (Hsp82p), two chromatin remodeling factors (Rvb1p, Rvb2p) and two rRNA processing factors (Rrp43p, Nop58p); Pih1p	3	5.5297	0.4623	2703.08	2703.954	1	1068.5	38.04348 N.L1K2Q2A1P1A1P1A1P1A1P1H3E1Q2Q2E1D1V1P1E1Y1E1V1K2.M
gi 6321823 ref NP_011899.1	YHR034C	Protein of unresolved function; may function in protein folding and/or rRNA processing, interacts with a chaperone (Hsp82p), two chromatin remodeling factors (Rvb1p, Rvb2p) and two rRNA processing factors (Rrp43p, Nop58p); Pih1p	2	3.0781	0.2534	1810.17	1810.97	2	307.3	46.666668 L.I1E1N2K2A1P1N2S1K2P1D1R4F1S1P1S1.Y
gi 6321827 ref NP_011903.1	YHR038W	Mitochondrial ribosome recycling factor, essential for mitochondrial protein synthesis and for the maintenance of the respiratory function of mitochondria; Rrf1p	2	4.149	0.2591	1977.99	1979.244	1	486.3	53.125 A.NLNLTPERVPNNDLQLK.V
gi 6321827 ref NP_011903.1	YHR038W	Mitochondrial ribosome recycling factor, essential for mitochondrial protein synthesis and for the maintenance of the respiratory function of mitochondria; Rrf1p	2	3.731	0.2553	2210.25	2211.378	2	676.4	47.22222 S.S1T1P1T1E1K2V1E1E1D1E1I1D1V1N2E1L1L1K2.K
gi 6321827 ref NP_011903.1	YHR038W	Mitochondrial ribosome recycling factor, essential for mitochondrial protein synthesis and for the maintenance of the respiratory function of mitochondria; Rrf1p	2	3.7297	0.2181	2187.37	2189.378	1	633.9	47.22222 S.STPTEKVEEDEIDVNELLK.K
gi 6321827 ref NP_011903.1	YHR038W	Mitochondrial ribosome recycling factor, essential for mitochondrial protein synthesis and for the maintenance of the respiratory function of mitochondria; Rrf1p	2	3.4652	0.2287	2005.33	2005.244	1	700.9	53.125 A.N2L1N2L1T1P1E1R4V1P1N2N2D1L1Q2L1K2.V
gi 6321832 ref NP_011908.1	YHR042W	NAUP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.2887	0.4176	1664.09	1662.868	1	466.7	61.538464 L.A1V1W2P1S1N2P1L1E1K2V1E1Q2F1.L
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.2458	0.3419	1293.59	1292.481	1	809.9	75 M.I1G1P1G1T1G1V1A1P1F1R4G1F1.I
gi 6321832 ref NP_011908.1	YHR042W	NAUP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.8838	0.3445	1594.35	1592.85	1	915.8	73.07692 S.N2F1R4L1P1S1N2P1S1T1P1V1I1M1.I
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	1	3.4212	0.264	1572.73	1573.85	1	191.9	57.692307 S.NFRLPSNPSTPVIM.I
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	3.1726	0.3287	2062.03	2063.144	1	487.5	56.666668 S.RNTDDFLYQDEWPEYA.K
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	3	6.1011	0.4459	2796.53	2796.233	1	799.2	36.458336 F.NLDPETIFDLKPLDPTVKVPFPTPT.T

gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.6682	0.2836	1574.67	1573.85	1	864.2	73.07692 S.NFRLPSNPSTPVIM.I
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.7511	0.4429	1454.61	1455.565	1	1104.6	81.818184 L.KDELHLDEQEAK.F
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	1	3.457	0.2983	1593.64	1592.85	1	209.9	61.538464 S.N2F1R4L1P1S1N2P1S1T1P1V1I1M1.I
gi 6321832 ref NP 011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.3866	0.3715	2010.57	2010.257	1	1061.2	62.5 G.DHLAVWPSNPLEKVEQF.L
gil6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.964	0.3406	2821.83	2824.233	1	496.2	37.5 F.N2L1D1P1E1T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gil6321832 ref NP_011908_1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg110; Ncp1p	2	4 1988	0.3766	2594.61	2593 97	1	612.4	43 18182 D1P1E1T11E1D11 1K2P11 1D1P1T1V1K2V1P1E1P1T1P1T1 T
gil6321832 ref NP_011008_1	VLD042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	4 1500	0.3101	2476 40	2000.01	4	440	
gilosz1652 1e1 14F_011906.1	1004200	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	4.1509	0.3101	2470.49	2477.001		449	
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	3.2109	0.2681	2568.19	2568.97	1	223.6	34.090908 L.DPETIFDLKPLDPTVKVPFPTPT.T
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	3	5.289	0.3288	3097.52	3098.549	1	896.4	35.185184 F.N2L1D1P1E1T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T111G1.A
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	3.3995	0.2933	2750.93	2752.197	3	308	33.333336 D.P1E1T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T111G1.A
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cvtochrome P450 reductase: involved in ergosterol biosynthesis: associated	2	4.5019	0.2931	3099.13	3098.549	1	351	33.333336 F.N2L1D1P1E1T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T111G1.A
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	3	5.4848	0.2762	3207.98	3209.707	1	1575.4	32.75862 F.NLDPETIFDLKPLDPTVKVPFPTPTTIGAA.I
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	4.1749	0.35	3170.71	3170.628	3	244.4	28.57143 F.N2L1D1P1E1T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T111G1A1.A
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	3.9595	0.1961	3139.71	3138.628	2	348.1	35.714287 F.NLDPETIFDLKPLDPTVKVPFPTPTTIGA.A
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	3	4.339	0.2224	3054.26	3056.569	2	486.4	27.884615 S.IFNLDPETIFDLKPLDPTVKVPFPTPT.T
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.498	0.2481	1890.07	1891.115	1	723	56.666668 A.E1T1N2L1P1V1H3Y1D1L1N2G1P1R4K2L1.F
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.9586	0.3371	2035.45	2033.257	1	706	59.375 G.D1H3L1A1V1W2P1S1N2P1L1E1K2V1E1Q2F1.L
gil6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	3	7.0388	0.4504	2822.3	2824.233	1	1000.7	37.5 F.N2L1D1P1F1T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gil6321832 ref NP_011908_1	VHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	4 2901	0 3724	2700 10	2796 233	1	581.2	
gil0321032[ref]NP_011300.1]	VUD042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	9.2301	0.0754	2/33.13	2/ 50.255	,	000.0	
gilb321832 rel NP_011908.1	THR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	3.1845	0.2751	2453.37	2453.661		200.0	LS1A1A1G1A111R4L1G1K2L1G1E1A1D1D1G1A1G1T1T1D1E1D1Y1M1A1W2K2D
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	3	4.0231	0.2485	3780.38	3783.118	1	754.1	25 S111L1E1V1L1.K
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	4.3065	0.3273	1869.57	1867.115	2	336	53.333336 A.ETNLPVHYDLNGPRKL.F
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cvtochrome P450 reductase: involved in ergosterol biosynthesis: associated	2	3.2424	0.2737	2199.61	2199.474	1	169.4	50 A.ETNLPVHYDLNGPRKLFAN.Y
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase: involved in ergosterol biosynthesis: associated	2	3.963	0.399	2168.47	2169.394	1	467.3	44.444447 H.Y1L1P1S1H3Q2L1N2R4N2A1D1G1I1Q2L1G1P1F1.D
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	4.3617	0.4027	2142.71	2141.394	1	1099.3	61.11111 H.YLPSHQLNRNADGIQLGPF.D
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	3.6733	0.192	1838.93	1841.116	1	409.6	56.666668 R.R4S1N2F1R4L1P1S1N2P1S1T1P1V1I1M1.I
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	3.3862	0.1808	1435.51	1434.592	1	1297.4	75 Q.L1N2R4N2A1D1G111Q2L1G1P1F1.D
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	3.5192	0.3069	1574.43	1573.85	1	1308.4	76.92308 S.NFRLPSNPSTPVIM.I
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	1	2.4944	0.1689	1572.6	1573.85	3	139.8	50 S.NFRLPSNPSTPVIM.I
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.2346	0.2686	1575.31	1573.789	1	437.2	62.5 A.VWPSNPLEKVEQF.L
gi 6321832 ref NP 011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.5763	0.2356	1591.05	1590.789	2	552	66.66667 A.V1W2P1S1N2P1L1E1K2V1E1Q2F1.L
gil6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11b; Ncp1p	1	2,9291	0.3486	1572.68	1573.789	1	530.2	54 166668 A VWPSNPL EKVEQE L
gil6321832/rofINE_011008_1		NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	3 9/77	0 3 2 3 0	1647.43	1644 868	1	594.6	
gil6321832 ref NP_011008_1	VLD042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	2 5 4 1 1	0.0200	1572.10	1572.05	4	947 5	
gilb321832 rel NP_011908.1	THR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	3.5411	0.3726	1573.19	1573.65		847.5	09.230774 S.NFRLPSNPSTPVIM.I
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	3.8334	0.3467	1886.89	1885.208	1	626.9	56:25 F.D1L1K2P1L1D1P111V1K2V1P1F1P111P1111.1
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	3.7242	0.172	2077.47	2077.364	5	504.1	47.058823 F.N2L1D1P1E1T111F1D1L1K2P1L1D1P1T1V1K2.V
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	3	4.929	0.4333	2708.33	2708.129	1	852	34.782608 N.L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-cytochrome P450 reductase: involved in ergosterol biosynthesis: associated	2	4.9644	0.2801	2823.29	2824.233	1	483.8	37.5 F.N2L1D1P1E1T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	4.2837	0.4853	2793.87	2796.233	1	513.9	39.583336 F.NLDPETIFDLKPLDPTVKVPFPTPT.T
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	3.8373	0.3367	1757.67	1758.027	1	302.5	50 L.AVWPSNPLEKVEQFL.S
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	3	6.1186	0.4311	2795.21	2796.233	1	1071.8	37.5 F.NLDPETIFDLKPLDPTVKVPFPTPT.T
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	3	5.9672	0.4812	2827.22	2824.233	1	511.3	31.25 F.N2L1D1P1E1T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	1	2.9661	0.26	1572.7	1573.85	1	193.1	57.692307 S.NFRLPSNPSTPVIM.I
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.9919	0.3799	2249.17	2249.649	1	533.7	47.368423 E.T111F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi 6321832 ref NP 011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	3	4.6939	0.3862	2477.93	2477.881	1	528.9	34.523808 D.P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gil6321832 ref NP_011908_1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11b; Nep1p	3	3,963	0,2765	2928.02	2926.338	2	509.3	28 F.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T1 I
		2 0 0 1 1 1	- 1							

		NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated								
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p NADP-outochrome P450 reductase: involved in ergosterol biosynthesis: associated	2	3.6395	0.4487	2039.29	2039.291	1	372.3	50 A.E1T1N2L1P1V1H3Y1D1L1N2G1P1R4K2L1F1.A
gi 6321832 ref NP_011908.1	YHR042W	and coordinately regulated with Erg11p; Ncp1p	2	4.7877	0.4545	2485.43	2486.892	1	1098.9	54.347824 S.NFRLPSNPSTPVIM@IGPGTGVAPF.R
gi 6321832 ref NP_011908.1	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.8272	0.3266	2514.35	2515.892	1	747.8	45.652176 S.N2F1R4L1P1S1N2P1S1T1P1V1I1M\$I1G1P1G1T1G1V1A1P1F1.R
ail62219221rofIND_011009_1		NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated	2	2 4944	0.2604	2014 52	2014 201	1	202.9	
gijo321632[rei]NP_011908.1]	THR042W	Essential protein that interacts with proteasome components and has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles;	2	3.4844	0.3694	2014.53	2014.291	1	393.8	53.125 A.ETNEPVITIDENGERKEF.A
gi 6321843 ref NP_011919.1	YHR052W	Cic1p Essential protein that interacts with proteasome components and has a potential role	2	3.0963	0.1673	1831.97	1831.971	2	316.4	57.14286 K.NLLEDDEEELKKDLQ.L
gi 6321843 ref NP_011919.1	YHR052W	in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles; Cic1p Essential protein that interacts with proteasome components and has a potential role	2	5.2564	0.2404	1588.53	1589.737	3	1264.7	79.16667 N.LLEDDEEELKKDL.Q
gi 6321843 ref NP_011919.1	YHR052W	in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles; Cic1p	2	3.8468	0.3682	1918.17	1919.067	1	554	63.333332 K.KDKIEETHEDDMVTID.G
gi 6321843 ref NP_011919.1	YHR052W	in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles; Cic1p	2	4.4442	0.2972	1939.11	1939.067	1	408	60.000004 K.K2D1K211E1E1T1H3E1D1D1M1V1T1I1D1.G
ail62218421-afIND 011010.1	VUDOEDW	Essential protein that interacts with proteasome components and has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles;	2	2 0221	0.2702	2028 60	2020 401	F	266.9	44 17617 V C1T4D1\/4C1T4D1C1V2E4V2V2V2\/414E4V2V2 C
gilosz to4sitetilite_011919.1	THRUSZW	Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome- associated complex that binds the ribosome via the Zuo1p subunit; also involved in electronic four peristance via concurrent activation of PDP1 and PDP5; binds ATP;	Z	2.9231	0.2792	2036.09	2039.401	5	200.0	41.17047 N.STITETVISTIETISTKZE INZNZNZVITETINZNZ.S
gi 37362658 ref NP_011931.2	YHR064C	Ssz1p	1	2.5995	0.2556	1524.7	1525.783	1	824.2	61.538464 A.KAELDPLDIDAVLL.T
		Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome- associated complex that binds the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP;								
gi 37362658 ref NP_011931.2	YHR064C	Ssz1p Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome-	2	4.6754	0.4275	2397.57	2398.635	1	1732.5	54.761906 A.YINPKNDVDVIANPDGERAIPS.A
	100000	associated complex that binds the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP;								
gi 37362658 ref NP_011931.2	YHR064C	SS21p Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome- associated complex that binds the ribosome via the Zuo1p subunit: also involved in	3	7.4273	0.5089	3167.9	3166.596	1	1497.3	34.82143 5.011101410161114161411102221011101N21121H3L1K2K22111G1L11G1.A
ail373626581rofIND_011031_2	VHP064C	pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP;	1	2 8538	0 1784	1/61 72	1462 732	1	105 5	54 545456 O L 111 D 4N/2D1K/2N/2T1111N/2E1 D
gij57502050[tel[t4F_011951.2]	11110040	Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome- associated complex that binds the ribosome via the Zuo1p subunit; also involved in		2.0000	0.1704	1401.72	1402.732	1	199.9	
gi 37362658 ref NP_011931.2	YHR064C	Ssz1p	2	4.1804	0.3101	2235.63	2235.459	1	893.7	52.499996 Y.INPKNDVDVIANPDGERAIPS.A
		Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome- associated complex that binds the ribosome via the Zuo1p subunit; also involved in plaintonic drug resistance via sequential activation of PDR1 and PDR5 binds ATP.								
gi 37362658 ref NP_011931.2	YHR064C	Ssz1p	3	6.3259	0.5474	3130.61	3131.596	1	1799.3	35.714287 S.DYDADELAEALQPVIVNTPHLKKPIGLIG.A
		associated complex that binds the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation of PDR1 and PDR5: binds ATP:								
gi 37362658 ref NP_011931.2	YHR064C	Ssz1p Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome-	2	3.0492	0.2187	1442.95	1443.732	3	502.9	59.090908 Q.LIRNPKNTIINF.R
ail37362658/refINP_011931.2	VHR064C	associated complex that binds the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP;	2	A 77AA	0.4253	2260.69	2263.459	1	905.8	50 V 11N2D1K2N2D1\/4D1\/41141N2D1D1C1E1R44111D1S1 4
gij57502050[tel[t4F_011951.2]	11110040	Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome- associated complex that binds the ribosome via the Zuo1p subunit; also involved in	2	4.7744	0.4200	2200.03	2203.435		303.0	
gi 37362658 ref NP_011931.2	YHR064C	pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP; Ssz1p Hor270 statis that interacts with Zua1a (a Dae Lhamelac) to farm a ribecome	2	4.917	0.3588	2425.89	2427.635	1	1843.2	57.14286 A.Y1I1N2P1K2N2D1V1D1V111A1N2P1D1G1E1R4A111P1S1.A
		associated complex that binds the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP;								
gi 37362658 ref NP_011931.2	YHR064C	Ssz1p Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome-	2	3.3711	0.271	1721.71	1722.994	4	179.6	53.846157 L.Q2Q2L111R4N2P1K2N2T1111N2F1.R
ail272626581cofIND_044024.21		associated complex that binds the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP;	2	2 7709	0.2942	1571.00	1571 962	2	462.6	
gij3/302036 tel NF_011931.2	THR004C	OS2 IP	2	3.7706	0.2042	1571.09	1571.003	2	402.0	00.0000/ Q.QEIKNENN HINE.K
gi 37362659 ref NP_011932.2	YHR065C	return motive in trave processing, required to maturation to the 335 printary transcript of pre-rRNA and for cleavage leading to mature 185 rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	2	4.0277	0.1641	2219.69	2218.53	1	555.1	52.77778 M.DEADRLLDMEFGPVLDRILK
ail37362650/rafIND_011032.21	VHP065C	Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to of L-d which is a DRAD have RNA dependent ATRese with believe activity. Protocol	2	4 0471	0 1721	2244 53	2243 53	1	680.1	58 222222 M D1E1A1D1D4111 D1M1E1E1C1D1V111 D1D4111 1 K
gij5/502059/16/(WF_011952.2)	11110030		2	4.0471	0.1751	2244.55	2245.55		003.1	
gi 37362659 ref NP_011932.2	YHR065C	Protein involved in rKNA processing; required for maturation of the 3SS primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	3	3.9216	0.3234	2216.78	2218.53	1	898.2	40.27778 M.DEADRLLDMEFGPVLDRILK
		Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA: homelyague to								
gi 37362659 ref NP_011932.2	YHR065C	eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	2	3.3432	0.1949	2451.15	2448.855	1	567.5	45 L.VMDEADRLLDMEFGPVLDRIL.K
gi 37362659 refINP 011932.2	YHR065C	Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity: Rm3n	3	4.0931	0.2465	2474.99	2475.855	8	1208.9	38.75 L.V1M1D1E1A1D1R4L1L1D1M1E1F1G1P1V1L1D1R4l1L1.K
51		Protein involved in rRNA processing: required for maturation of the 35S primory	0					0		
gi 37362659 ref NP_011932.2	YHR065C	reascript of pre-rRNA and for cleavage leading to mature 185 rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	2	3.5889	0.2556	1567.59	1568.696	7	295.3	53.846157 L.R4D1S1V1D1K2A1N2G1E1V1V1M1E1.M

gi 37362659 ref NP_011932.2	YHR065C	Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	2	3.2605	0.1938	2219.23	2218.53	3	483.4	50 M.DEADRLLDMEFGPVLDRIL.K
gi 37362659 ref NP_011932.2	YHR065C	Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	2	3.4037	0.2504	2474.79	2475.855	1	720.4	50 L.V1M1D1E1A1D1R4L1L1D1M1E1F1G1P1V1L1D1R4I1L1.K
gi 37362659 ref NP_011932.2	YHR065C	Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	3	5.2718	0.1803	2476.76	2475.855	3	1466	42.5 L.V1M1D1E1A1D1R4L1L1D1M1E1F1G1P1V1L1D1R4I1L1.K
gi 37362659 ref NP_011932.2	YHR065C	Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	2	3.0277	0.3238	1517.51	1518.811	1	753.6	62.5 L.LDMEFGPVLDRIL.K
gi 37362659 ref NP_011932.2	YHR065C	Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	2	3.4088	0.1574	1513.17	1514.819	1	784.8	79.16667 K.K2L1P1K2E1S1V1D1K2N2I1I1L1.T
gi 6321863 ref NP_011939.1	YHR072W	2,3-epoxide, a step in ergosterol biosynthesis; Erg7p	1	2.6452	0.3052	1277.55	1278.448	5	256.9	55 S.SERLFEGIDVL.L
gi 6321863 ref NP_011939.1	YHR072W	Lanosterol synthase, an essential enzyme that catalyzes the cyclization of squalene 2,3-epoxide, a step in ergosterol biosynthesis; Erg7p	1	2.7134	0.2973	1477.66	1478.685	5	296.9	54.166668 M.ISSERLFEGIDVL.L
gil6321863lrefINP_011939.1	YHR072W	Lanosterol synthase, an essential enzyme that catalyzes the cyclization of squalene 2.3-epoxide, a step in ergosterol biosynthesis: Erg7p	2	3.356	0.2785	1923.35	1924,213	1	1065.4	67.85714 S.C1A111E1Y1P1S1Y1R4E1L1E1P111K2 A
gil6321863lrefINP_011939_1	VHR072W	Lanosterol synthase, an essential enzyme that catalyzes the cyclization of squalene	2	3 4961	0 2545	1905 11	1905 213	1	571 5	57 14286 S CALEVPSYRELEDIK A
gilosz rocoliciji (* _0**********************************	1111(0721)	Serine-threonine kinase and endorbionuclease; transmembrane protein that initiates	2	0.4001	0.2040	1000.11	1303.210	,	571.5	
gi 6321870 ref NP_011946.1	YHR079C	the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p Serine-threonine kinase and endonibonuclease; transmembrane protein that initiates the unfolded nortein response signal by regulation synthesis of Hac1p through HAC1	1	3.8493	0.3746	1559.52	1560.864	1	242.7	65.38461 A.R4W2V1S1P1T1F1P1G1111V1G1L1.F
gi 6321870 ref NP_011946.1	YHR079C	mRNA splicing; Ire1p Serine-threenine kinase and endoribonuclease: transmembrane protein that initiates	2	4.4124	0.3949	1933.47	1933.314	1	405.8	53.125 L.SKIGFMPEKEIPIVESK.S
gi 6321870 ref NP_011946.1	YHR079C	Commer Virtedmine the analysis of the second three second	2	3.5082	0.3532	1559.75	1560.864	1	917.4	69.230774 A.R4W2V1S1P1T1F1P1G11111V1G1L1.F
gi 6321870 ref NP_011946.1	YHR079C	the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p Soriae through a discourse and and ribenuclease; transmembrane protein that initiates	2	3.6302	0.251	1864.83	1865.235	1	887.2	60.000004 S.K2I1G1F1M1P1E1K2E1I1P1I1V1E1S1K2.S
gi 6321870 ref NP_011946.1	YHR079C	the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p Serine-threonine kinase and endoribonuclease; transmembrane protein that initiates	2	2.982	0.3995	1542.27	1542.864	1	1349.4	76.92308 A.RWVSPTFPGIIVGL.F
gi 6321870 ref NP_011946.1	YHR079C	the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent	2	3.825	0.3306	1560.35	1560.864	1	939.7	69.230774 A.R4W2V1S1P1T1F1P1G1I1I1V1G1L1.F
gi 6321880 ref NP_011956.1	YHR088W	of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p Nucleolar protein involved in the assembly of the large ribosomal subunit: constituent	2	4.2193	0.3798	2095.09	2097.254	1	816.8	59.375 E.T111N2K2E1V1E1G1D1E1D1D1L1M1R4Y1F1.N
gi 6321880 ref NP_011956.1	YHR088W	of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent	3	5.255	0.423	2769.95	2767.954	1	1104	34.523808 T.R4V1Y1D1E1T111N2K2E1V1E1G1D1E1D1D1L1M1R4Y1F1.N
gi 6321880 ref NP_011956.1	YHR088W	of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p Nucleolar parterin involved in the assembly of the large ribosomal subunit: constituent	2	3.7455	0.2694	2766.89	2767.954	1	531.7	42.857143 T.R4V1Y1D1E1T111N2K2E1V1E1G1D1E1D1D1L1M1R4Y1F1.N
gi 6321880 ref NP_011956.1	YHR088W	of 66S pre-libosomal patients ductions of an energy incontainability on auto- of 66S pre-libosomal patients; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p Nucleals protein involved in the assembly of the large ribosomal subunit constituent	3	4.4292	0.2367	1714.64	1714.974	1	779.9	53.846157 L.T1F111H3L1P1E1G1P1T1F1Y1F1K2.L
gi 6321880 ref NP_011956.1	YHR088W	of 66S pre-ribosomal protect in the assembly of the large incoming which is thought to bind RNA; Rpf1p	3	4.8584	0.2475	1700.36	1697.974	1	920.3	53.846157 L.TFIHLPEGPTFYFK.L
gi 6321880 ref NP_011956.1	YHR088W	reduction protein involved in the assembly of the target involved in subdinit, constituent of 66S pre-robosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p Nucleolar protein involved in the assembly of the large ribosomal subunit constituent	2	4.2997	0.2176	1713.79	1714.974	1	481	65.38461 LT1F111H3L1P1E1G1P1T1F1Y1F1K2.L
gi 6321880 ref NP_011956.1	YHR088W	of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p Nucleolar protein involved in the assembly of the large ribosomal subunit: constituent	2	3.3583	0.2938	2318.17	2319.458	1	388.8	47.22222 Y.DETINKEVEGDEDDLMRYF.N
gi 6321880 ref NP_011956.1	YHR088W	of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p	2	3.1043	0.1935	2345.61	2343.458	3	304.5	44.444447 Y.D1E1T111N2K2E1V1E1G1D1E1D1D1L1M1R4Y1F1.N
gi 6321881 ref NP_011957.1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	2	3.6741	0.3154	1570.77	1569.841	1	1235.8	75 N.TKIPYFNAPIYLE.N
gi 6321881 ref NP_011957.1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	1	2.2127	0.2917	1355.51	1356.453	1	248.8	50 F.LHPCEGDIVCR.S
gi 6321881 ref NP_011957.1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	1	2.4344	0.3858	1371.5	1372.454	1	384.3	60.000004 F.L1H3P1C1E1G1D1I1V1C1R4.S
gi 6321881 ref NP 011957.1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	1	2.3677	0.319	1304.52	1305.473	1	450.6	60.000004 T.SFKEGDKFYIA.A
gil6321881/refINP 011957.1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA: Gar1p	2	3.258	0.3458	1441.23	1440.725	1	1195.5	77.27273 N.TKIPYENAPIYL.E
gil63218811refINP_011957.1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA: Garto	2	4,7546	0.3155	2128.83	2126.46	1	522.3	58 823532 R. SINTKIPYENAPIYI ENK T
gil6321881/refINP_011957_1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA: Gar1o	2	3,7443	0.1504	1712.55	1711.014	2	894.8	73.07692 T.KIPYFNAPIYLENK.T
gil6321881/refINP_011957_1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA: Gar1o	2	5.6138	0.3403	2019.13	2019,286	-	1479.5	71.875 R.S111N2T1K211P1Y1F1N2A1P111Y1L1E1N2 K
gil6321881/refINP_011957_1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA: Garth	2	5.1016	0.3628	1999 97	1998,286	1	1385.6	65.625 R. SINTKIPYENAPIYLEN K
gil6321881/refINP_011957_1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA: Garth	2	4.2578	0.3684	1886 71	1884,182	1	1088.3	66.66667 R SINTKIPYENAPIYLE N
gi 6321881 ref NP_011957.1	YHR089C	Protein component of the H/ACA sonCNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	2	3.4056	0.205	1482.19	1482.736	1	797.2	72.72727 T.K2I1P1Y1F1N2A1P1I1Y1L1E1.N

gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p	2	3.2631	0.2866	1455.61	1454.725	1	988.4	77.27273 N.T1K2I1P1Y1F1N2A1P1I1Y1L1.E
ail63218811refINP 011957.11	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA: Gar1p	1	2.6751	0.1928	1440.17	1440.725	1	716.9	68.181816 N.TKIPYENAPIYL E
gil6321881/refINP_011957_1	VHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA: Garth	2	3 3653	0 202	1442 91	1440 725	2	801.9	
gilosz1001/reline_011957.1	11110030	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the	2	3.3033	0.232	1442.51	1440.725	2	001.9	
gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the	2	4.3605	0.2969	2147.65	2149.46	1	506.6	58.823532 R.S1I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1E1N2K2.T
gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p Protein component of the H/ACA snoRNP pseudouridy/ase complex, involved in the	3	3.937	0.3091	2063.54	2061.382	1	1014.1	43.75 S.I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1E1N2K2.T
gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p	2	3.1488	0.2935	1929.87	1931.208	1	968.4	60.000004 S.I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1E1N2.K
gi 6321881 ref NP_011957.1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	2	5.0077	0.3629	1901.55	1903.182	1	1098.8	66.66667 R.S1I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1E1.N
ail63218811refINP 011957.11	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	2	4,459	0.4252	1772.99	1773.067	1	1017.6	67.85714 R.S1I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1.E
gil6321881/rofIND_011057_1	VHP080C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rPNA. Carla	2	3 7351	0 /213	1753 37	1755 067	1	905.6	
gilosz1001/reijin _011957.1	11110030	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the	2	3.7331	0.4215	1755.57	1755.007		303.0	
gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the	1	3.1975	0.2846	1468.57	1468.736	3	619.9	63.636364 T.KIPYFNAPIYLE.N
gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p Protein component of the H/ACA snoRNP pseudouridvlase complex, involved in the	1	3.1332	0.2774	1583.35	1584.841	1	766.7	62.5 N.T1K2I1P1Y1F1N2A1P1I1Y1L1E1.N
gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p	2	3.5394	0.2591	1353.25	1352.62	1	1203.5	85 T.K2I1P1Y1F1N2A1P1I1Y1L1.E
gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p	2	2.9593	0.2697	1340.21	1339.62	1	981	80 T.KIPYFNAPIYL.E
gi 6321881 ref NP_011957.1	YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	1	3.138	0.2838	1439.6	1440.725	3	725.5	63.636364 N.TKIPYFNAPIYL.E
ail63218811refINP_011957_1	VHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA Garto	2	3 2414	0 3617	1796 21	1797 104	1	548 9	50 S INTKIPYENAPIVI E N
	11110030	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the	2	3.2414	0.3017	1730.21	1757.104		540.5	
gi 6321881 ref NP_011957.1	YHR089C	modification and cleavage of the 18S pre-rRNA; Gar1p Low-affinity glucose transporter of the major facilitator superfamily, expression is	2	3.1136	0.2055	1683.75	1684.988	1	//1.2	61.538464 S.I1N2 I1K2I1P1Y1F1N2A1P1I1Y1L1.E
ail63218861refINP 011962.11	YHR094C	induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting: Hxt1p	1	2.4498	0.3406	1227.37	1228.446	1	494.8	66.66667 S.VQWRVPLGLC.F
51		Low-affinity glucose transporter of the major facilitator superfamily, expression is								
gi 6321886 ref NP_011962.1	YHR094C	induced by Rxt2p in the presence of glucose and repressed by Rg1p when glucose is limiting; Hxt1p	3	4.2947	0.3285	3257.15	3256.573	1	718.4	27.777779 A.SWVPVSKRGADYNADDLMHDDQPFYKSL.F
		Low-affinity glucose transporter of the major facilitator superfamily, expression is induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose								
gi 6321886 ref NP_011962.1	YHR094C	is limiting; Hxt1p Low-affinity glucose transporter of the major facilitator superfamily, expression is	1	2.7881	0.3567	1330.77	1331.524	1	483.9	60.000004 N.S1V1Q2W2R4V1P1L1G1L1C1.F
ail62218961rofIND_011062_1		induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose	2	2 0909	0.2446	1220 11	1221 524	1	647.2	70 N 641/4020//2041/4041 4041 404 E
gilo321860[tel[NF_011962.1]	THR094C	Low-affinity glucose transporter of the major facilitator superfamily, expression is	2	3.0606	0.2440	1329.11	1331.324		047.3	70 N.STVTQ2W2R4VTFTETGTETGT.F
gi 6321886 ref NP_011962.1	YHR094C	induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting; Hxt1p	1	2.7114	0.2588	1316.9	1315.524	1	464.7	60.000004 N.SVQWRVPLGLC.F
		Low-affinity glucose transporter of the major facilitator superfamily, expression is induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose								
gi 6321886 ref NP_011962.1	YHR094C	is limiting; Hxt1p	2	3.3881	0.1985	1155.25	1155.385	1	957.6	83.33333 N.SVQWRVPLGL.N
		induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose								
gi 6321886 ref NP_011962.1	YHR094C	is limiting; Hxt1p Low-affinity glucose transporter of the major facilitator superfamily, expression is	2	3.4626	0.2637	1170.05	1170.385	1	969.7	83.33333 N.S1V1Q2W2R4V1P1L1G1L1.C
gil6321886/refINP_011962.1	YHR094C	induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting: Hxt1p	2	3.2605	0.2624	1940.31	1941.163	1	801.4	60.000004 K.NYSNSVQWRVPLGLCE A
2.1		Low-affinity glucose transporter of the major facilitator superfamily, expression is	_							
gi 6321886 ref NP_011962.1	YHR094C	induced by Hxk2p in the presence of glucose and repressed by Rg11p when glucose is limiting; Hxt1p	2	3.8048	0.405	1228.33	1228.446	1	1426	94.44444 S.VQWRVPLGLC.F
		Low-affinity glucose transporter of the major facilitator superfamily, expression is induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose								
gi 6321886 ref NP_011962.1	YHR094C	is limiting; Hxt1p	1	2.5102	0.3299	1243.74	1243.446	1	373.2	61.11111 S.V1Q2W2R4V1P1L1G1L1C1.F
	VUD004C	induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose	2	0.4007	0.4004	2200.20	2200 44		500	
gilo321886[rei]NP_011962.1]	THR094C	Low-affinity glucose transporter of the major facilitator superfamily, expression is	2	3.1007	0.1001	2299.39	2299.41	1	536	47.22222 K.R4GTATDTTTN2ATDTDTETMTH3DTDTQ2PTFTTTN2.S
gi 6321886 ref NP 011962.1	YHR094C	induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting; Hxt1p	2	3.7689	0.4607	1759.37	1759.968	1	908.7	69.230774 A.KVNKCPPDHPYIQY.E
		Low-affinity glucose transporter of the major facilitator superfamily, expression is								
gi 6321886 ref NP_011962.1	YHR094C	is limiting; Hxt1p	2	3.2771	0.2994	1513.89	1512.634	1	938.4	68.181816 D.D1L1M1H3D1D1Q2P1F1Y1K2S1.L
		induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose								
gi 6321886 ref NP_011962.1	YHR094C	is limiting; Hxt1p Low-affinity glucose transporter of the major facilitator superfamily, expression is	2	3.0225	0.1869	1195.09	1194.308	1	700.7	81.25 L.M1H3D1D1Q2P1F1Y1K2.K
ail6321886/rofIND_011062_1	VHP004C	induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting; Hxt1p	2	3 7522	0 1807	1533.67	1534 653	1	823.8	75 T P4I 1W2P1N2C1O2D1O2D1S1S1K2 C
gilo32100016114F_011902.1	11110340	Low-affinity glucose transporter of the major facilitator superfamily, expression is	2	3.7322	0.1037	1555.07	1554.055		023.0	
gi 6321886 ref NP_011962.1	YHR094C	induced by Hxk2p in the presence of glucose and repressed by Rg1p when glucose is limiting; Hxt1p	1	2.3207	0.1759	1419.75	1418.558	1	329.5	55 N.KCPPDHPYIQY.E
		Low-affinity glucose transporter of the major facilitator superfamily, expression is induced by Hxk2p in the presence of glucose and repressed by Rat1p when glucose								
gi 6321886 ref NP_011962.1	YHR094C	is limiting; Hxt1p	2	3.7342	0.2666	1595.97	1596.792	1	851.1	70.83333 A.KVNKCPPDHPYIQ.Y
	VUD0010	induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose	•	0.0007	0.0046	4770.04	4770 000		400.0	
gijo321886 ret NP_011962.1	THRU94C	Low-affinity glucose transporter of the major facilitator superfamily, expression is	2	3.2607	0.3043	1779.61	1779.968	1	486.9	57.092307 A.KZV1NZKZG1P1P1D1H3P1Y1I1Q2Y1.E
gi 6321886 ref NP_011962.1	YHR094C	induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting; Hxt1p	2	4.2802	0.3613	1615.37	1615.792	1	905.7	75 A.K2V1N2K2C1P1P1D1H3P1Y1I1Q2.Y

gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	2	4.0068	0.3754	2102.03	2101.245	1	795.6	53.125 N.K2A1W2Q2P1L1V1D1F1I1D1D1Q2H3D1S1Y1.M
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	3	4.7382	0.3562	2624.3	2622.871	1	852.1	37.5 N.KAWQPLVDFIDDQHDSYMRQE.Q
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	3	6.3367	0.3862	2654.39	2653.871	1	2018.2	50 N.K2A1W2Q2P1L1V1D1F1I1D1D1Q2H3D1S1Y1M1R4Q2E1.Q
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	1	3.405	0.2735	1325.46	1326.539	1	683.5	68.181816 T.G1H3G1L1K2P1I1D1I1E1T1M1.K
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	1	2.6954	0.172	1311.56	1311.539	1	755.3	63.636364 T.GHGLKPIDIETM.K
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	3	3.9653	0.2631	2523.62	2523.756	6	515.4	30.263159 N.K2A1W2Q2P1L1V1D1F1I1D1D1Q2H3D1S1Y1M1R4Q2.E
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	2	2.9186	0.1985	1313.49	1311.539	1	560	72.72727 T.GHGLKPIDIETM.K
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	2	3.8514	0.1582	1868.19	1869.037	2	504.2	64.28571 L.S1H3N2P1R4Y1K2E1E1E1N2A1L1K2K2.Y
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	2	3.8482	0.2763	1576.71	1575.761	1	1490	75 N.KAWQPLVDFIDDQ.H
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	2	2.9634	0.2773	1326.27	1326.539	2	362	63.636364 T.G1H3G1L1K2P1I1D1I1E1T1M1.K
gi 6321899 ref NP_011975.1	YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p SH3 domain protein implicated in the requilation of actin polymerization able to	3	3.9959	0.207	2033.12	2033.213	3	562.2	38.333332 L.S1H3N2P1R4Y1K2E1E1E1N2A1L1K2K2Y1.F
gi 6321906 ref NP_011982.1	YHR114W	error admitting polymerization machinery agrunting the SH3 domains, colocalizes with cortical actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p SH3 domain portain implicated in the resultation of actin polymerization patk to the second sec	2	4.1429	0.3036	2007.91	2009.199	1	728.8	58.823532 Y.V1Q2K2D1D1D1E1I1T1I1T1P1G1D1K2I1S1L1.V
gi 6321906 ref NP_011982.1	YHR114W	error advantary procent implementation machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p SH3 domain protein implementated in the requilation of actin polymerization, able to	2	3.2827	0.4267	2364.29	2364.619	1	194.6	44.736843 Q.DFVYKPSPVWHDDEKFAVPS.S
gi 6321906 ref NP_011982.1	YHR114W	recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las 17p, interacts with type I myosins; Bz21p SH3 domain portein implicated in the regulation of actin polymerization, able to	2	4.8505	0.2589	1761.35	1760.936	1	1731.4	70 Q.KDDDEITITPGDKISL.V
gi 6321906 ref NP_011982.1	YHR114W	recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p SH3 domain protein implicated in the regulation of actin polymerization, able to	2	3.2204	0.2734	2123.93	2125.354	1	233	52.941177 F.V1Y1K2P1S1P1V1W2H3D1D1E1K2F1A1V1P1S1.S
gi 6321906 ref NP_011982.1	YHR114W	recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p	2	3.3083	0.3513	2100.93	2102.354	2	183.8	50 F.VYKPSPVWHDDEKFAVPS.S
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	3.3238	0.2592	1624.41	1623.889	1	549.7	57.692307 L.KFPTLPEVPTFFAE.I
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	3.6927	0.3564	2355.33	2356.723	1	579.1	42.105263 F.FNETKLKFPTLPEVPTFFAE.I
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	4.8698	0.3843	2178.71	2177.529	1	777.7	52.941177 F.F1N2E1T1K2L1K2F1P1T1L1P1E1V1P1T1F1F1.A
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	3.994	0.342	2155.05	2156.529	1	668.8	50 F.FNETKLKFPTLPEVPTFF.A
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	3.0212	0.1582	1422.89	1423.695	1	595.7	63.636364 L.KFPTLPEVPTFF.A
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	3.2039	0.2792	1438.05	1436.695	6	479.2	59.090908 L.K2F1P1T1L1P1E1V1P1T1F1F1.A
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	1	2.4171	0.1539	1435.6	1436.695	1	505	59.090908 L.K2F1P1T1L1P1E1V1P1T1F1F1.A
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	1	2.5426	0.3262	1422.84	1423.695	1	617.1	63.636364 L.KFPTLPEVPTFF.A

gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	3.6348	0.2685	1549.63	1550.854	1	695.2	66.66667 K.L1K2F1P1T1L1P1E1V1P1T1F1F1.A
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	3.1192	0.2309	1536.45	1536.854	1	857.5	70.83333 K.LKFPTLPEVPTFF.A
gi 6321909 ref NP_011985.1	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	2	3.3712	0.3271	1912.05	1913.249	2	466.2	46.6666668 N.E1T1K2L1K2F1P1T1L1P1E1V1P1T1F1F1.A
ail6321924 ref NP 012000.1	YHR132C	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required for normal cell wall assembly: Ecm14p	2	3.3226	0.2111	1514.47	1514.689	1	1004.6	72.72727 K.K2E1T1K2Y1L1D1D1L1D1F1L1.V
cil6221024/rofIND_012000_1	VUD122C	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required	2	4 604	0.2216	2405.94	2405 715	1	757 4	
gilo321924[rei]NP_012000.1]	THR 1320	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required	2	4.004	0.3316	2405.61	2405.715	1	/5/.4	55.263157 K.KZETTIKZ TIELDIDIELDIFIELVIIIPIVIFINZPIDI.G
gi 6321924 ref NP_012000.1	YHR132C	for normal cell wall assembly; Ecm14p Putative metalloprotease with similarity to the zinc carboxypeptidase family, required	2	3.0697	0.2927	2602.11	2602.943	2	318.7	33.333336 K.KETKYLDDLDFLVIPVFNPDGY.A
gi 6321924 ref NP_012000.1	YHR132C	for normal cell wall assembly; Ecm14p Putative metalloprotease with similarity to the zinc carboxypeptidase family, required	2	4.1053	0.3672	2382.63	2382.715	1	580.8	50 K.KETKYLDDLDFLVIPVFNPD.G
gi 6321924 ref NP_012000.1	YHR132C	for normal cell wall assembly; Ecm14p	3	3.8887	0.25	2403.86	2405.715	6	428.6	32.894737 K.K2E1T1K2Y1L1D1D1L1D1F1L1V1I1P1V1F1N2P1D1.G
gi 6321925 ref NP_012001.1	YHR133C	one of two HMG-CoA iscenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIC proteins; Nsg1p Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p,	2	4.6197	0.4016	1833.67	1832.124	1	1418	70 K.NKIVAEPDMVPDWAVF.G
gi 6321925 ref NP_012001.1	YHR133C	one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; Nsg1p Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p,	2	4.4893	0.3191	1380.85	1379.686	1	1499.9	87.5 T.KKEAALPPLGNKL.G
gi 6321925 ref NP_012001.1	YHR133C	one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis, homolog of mammalian INSIG proteins; Nsg1p Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p,	2	3.9485	0.316	1868.77	1867.124	1	865.2	56.666668 K.N2K2I1V1A1E1P1D1M\$V1P1D1W2A1V1F1.G
gi 6321925 ref NP_012001.1	YHR133C	one of two HMG-COA isoenzymes that catalyze the rate-imiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; Nsg1p	2	4.9869	0.4236	1850.03	1851.124	1	972.4	63.333332 K.N2K2I1V1A1E1P1D1M1V1P1D1W2A1V1F1.G
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	3	5.132	0.383	2626.61	2628.947	1	736.7	32.954548 H.DLIYRDIKPDNFLIGRPGQPDAN.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	3	4.0948	0.2227	2126.99	2124.364	1	1044.9	43.055553 Y.RDIKPDNFLIGRPGQPDAN.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	3	5.5117	0.5002	2431.31	2431.699	1	876.8	36.25 L.I1Y1R4D111K2P1D1N2F1L111G1R4P1G1Q2P1D1A1N2.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.5842	0.1778	2432.47	2431.699	2	339.8	50 L.I1Y1R4D111K2P1D1N2F1L111G1R4P1G1Q2P1D1A1N2.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	1	2.3888	0.1539	1481.46	1480.704	1	376.1	54.166668 Y.K2I1L1N2G1T1P1N2I1P1Y1A1Y1.Y
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.4239	0.2146	2109.29	2106.349	1	707.2	47.058823 L.VIDLLGPSLEDLFDWCGR.K
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.5924	0.2082	2661.57	2661.947	1	240.6	40.909092 H.D1L111Y1R4D111K2P1D1N2F1L111G1R4P1G1Q2P1D1A1N2.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	4.9341	0.4492	1848.53	1848	1	998.9	67.85714 L.G1P1S1L1E1D1L1F1D1W2C1G1R4K2F1.S
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	4.0457	0.3409	2381.23	2381.7	1	835.3	50 L.VIDLLGPSLEDLFDWCGRKF.S
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	3	4.4597	0.3977	2660.66	2661.947	2	668.7	30.681818 H.D1L111Y1R4D111K2P1D1N2F1L111G1R4P1G1Q2P1D1A1N2.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	4.442	0.3637	2407.71	2406.7	1	922.8	52.63158 L.V111D1L1L1G1P1S1L1E1D1L1F1D1W2C1G1R4K2F1.S
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	3	4.617	0.2532	2152.1	2153.364	1	1259.3	44.444447 Y.R4D111K2P1D1N2F1L111G1R4P1G1Q2P1D1A1N2.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	3	4.6954	0.4311	2430.62	2431.699	1	936.1	36.25 L.I1Y1R4D111K2P1D1N2F1L111G1R4P1G1Q2P1D1A1N2.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.3499	0.1641	2399.03	2400.699	1	343.3	50 L.IYRDIKPDNFLIGRPGQPDAN.N

gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.3456	0.2391	2428.75	2431.699	4	330.6	45 L.I1Y1R4D1I1K2P1D1N2F1L1I1G1R4P1G1Q2P1D1A1N2.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	4.7633	0.3788	1570.13	1569.65	1	1485.6	79.16667 L.G1P1S1L1E1D1L1F1D1W2C1G1R4.K
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	4.2908	0.4292	1552.03	1552.65	1	1709.8	83.33333 L.GPSLEDLFDWCGR.K
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	1	2.2938	0.2699	1568.52	1569.65	1	318.3	50 L.G1P1S1L1E1D1L1F1D1W2C1G1R4.K
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.7933	0.3892	1798.69	1797.968	1	1176.2	67.85714 D.L1L1G1P1S1L1E1D1L1F1D1W2C1G1R4.K
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.3123	0.298	1781.13	1778.968	1	1144.1	64.28571 D.LLGPSLEDLFDWCGR.K
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.3794	0.3581	2128.57	2128.349	4	361.9	41.17647 L.V111D1L1L1G1P1S1L1E1D1L1F1D1W2C1G1R4.K
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	2	3.1841	0.2894	1399.13	1399.549	5	684.6	62.5 D.NFLIGRPGQPDAN.N
gi 6321927 ref NP_012003.1	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	3	5.3363	0.3544	2432.81	2431.699	2	828.1	33.75 L.11Y1R4D111K2P1D1N2F1L111G1R4P1G1Q2P1D1A1N2.N
nil6321927/refINP_012003_11	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking: provides an essential function overlapping with that of Yck2p; Yck1p	2	4 3614	0.371	1903 99	1904 22	1	413 5	
gi 6321940 ref NP 012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	5.0189	0.4488	1733.71	1735.046	1	930	61.764706 N.G1I1IIG1G1P1G1P1V1L1V1P1N2P1G1E1I1K2.E
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	3.3746	0.2909	1622.79	1624.834	1	625.5	57.692307 T.G1T1F1D1D1W2R4G1T1L1P1L1V1K2.T
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	4.7483	0.4348	2125.61	2126.368	1	1510.7	60.526318 S.SVTEKSPALPQADDPIVETK.E
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	3.8192	0.2084	1717.83	1718.945	1	766.7	64.28571 K.AKKDEEVFTLDPIVN.K
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	3.8646	0.3135	1988.89	1991.189	1	790.1	52.941177 T.N2V1S1K2E1A1P1G1N2F1H3I1L1P1I1D1Q2S1.A
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	3.51	0.3091	1754.79	1754.981	1	637.3	60.000004 N.KAPKLPLTDEQTAEGR.K
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	3	3.8302	0.3358	3454.58	3454.902	1	429.6	24.166666 K.AKKDEEVFTLDPIVNKAPKLPLTDEQTAEGR.K
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	3	4.9393	0.4487	1776.89	1776.981	1	889	45 N.K2A1P1K2L1P1L1T1D1E1Q2T1A1E1G1R4.K
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	3.2672	0.2593	1774.69	1776.981	1	625.8	60.000004 N.K2A1P1K2L1P1L1T1D1E1Q2T1A1E1G1R4.K
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	4.5391	0.3987	2067.79	2069.359	1	626.1	47.5 T.Q2S1N2G11111G1G1P1G1P1V1L1V1P1N2P1G1E111K2.E
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	4.2764	0.5138	2042.87	2044.359	1	569.1	
gi 6321940 ref NP_012016.1	VHP146W	Protein that binds to cruciform DNA structures; Crp1p	2	3.5823	0.4119	2340.51	2347.001	1	743.6	43.18182 1.0251N2G1111G1G1P1G1P1V1L1V1P1N2P1G1E11N2E1F1.1 64.28571 K A1K2K2D1E1E1\/1E1T1L1D1D111\/1N2 K
gi[6321940]refINP_012016.1	YHR146W	Protein that binds to cruciform DNA structures: Cro1p	2	5 1124	0.2007	1716.47	1715 046	1	1114.2	64 70589 N GIIGGPGPVI VPNPGEIK E
gil6321940/refINP_012016.1	YHR146W	Protein that binds to cruciform DNA structures: Crp1p	2	3.0468	0.3504	1603.77	1605.834	1	827.5	61.538464 T.GTFDDWRGTLPLVK.T
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	3.4759	0.2825	2321.63	2320.651	1	393	36.363636 T.QSNGIIGGPGPVLVPNPGEIKEF.T
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	5.4006	0.4213	2010.55	2013.338	1	1125.3	63.15789 N.G1I1I1G1G1P1G1P1V1L1V1P1N2P1G1E1I1K2E1F1.T
gi 6321940 ref NP_012016.1	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	4.7155	0.4507	1992.57	1991.338	1	625.6	50 N.GIIGGPGPVLVPNPGEIKEF.T
		Englace II a phosphonyruwate hydratase that catalyzes the conversion of 2-								
gi 6321968 ref NP_012044.1	YHR174W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	3.0795	0.214	1515.62	1516.717	2	645.5	57.692307 Q.T1A1E1E1A1L1D1L111V1D1A111K2.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	2.8605	0.3586	1500.52	1501.717	3	498.3	57.692307 Q.TAEEALDLIVDAIK.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.1711	0.2585	1476.49	1475.771	1	1271.2	83.33333 S.KTSPYVLPVPFLN.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.6144	0.3323	1502.67	1501.717	1	1645.3	73.07692 Q.TAEEALDLIVDAIK.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.2994	0.3147	1515.89	1516.717	1	2429	84.61539 Q.T1A1E1E1A1L1D1L111V1D1A111K2.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	2.9072	0.221	1250.37	1248.508	4	586.9	75 S.KTSPYVLPVPF.L
		England II a phosphonymytic hydrotoco that anti-lines the environment of a								
gi 6321968 ref NP_012044.1	YHR174W	phosphoglycerate to phosphoenolpyruvate nydratase that Catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	2.9911	0.2342	1339.57	1340.451	2	292.1	72.22222 L.E1M1R4D1E1D1K2S1K2W2.M
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	2.7482	0.2548	1323.46	1324.451	1	341.3	77.7778 L.EMRDEDKSKW.M

gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.7074	0.18	1718.27	1718.921	1	427.4	65.38461 L.E1M1R4D1E1D1K2S1K2W2M1G1K2G1.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.7763	0.3121	2008.37	2009.13	1	687.9	62.5 F.K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1.K
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.3333	0.2262	2024.57	2023.203	1	1327.8	51.666664 G.K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	2.9783	0.2112	1474.79	1475.771	1	299.1	66.66667 S.KTSPYVLPVPFLN.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.138	0.3857	2342.09	2339.522	1	1024.6	55.555557 K.RYPIVSIEDPFAEDDWEAW.S
ail6321968/refINP 012044.1/	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dluconeodenesis: expression is induced in response to alucose: Eno2o	2	2.9865	0.2872	1791.55	1793.141	2	614.9	53.333336 K.S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1.N
gil6321968/ref/NP_012044.1	YHR174W	Enclase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dlyconegoenesis: expression is induced in resonase to glucose: Enc2p	2	4.0486	0.2616	1702.73	1705.063	1	899.2	64 28571 S K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1 N
ail6321968/refINP_012044.11	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during durongengenesis: sergescient is induced in genones to glucose. Eno20	2	4 0117	0 3204	1686.97	1688.063	1	792.8	
gilos21900 101 14F_012044.1	10017400	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	4.0117	0.3204	1000.97	1088.005		792.0	04.20071 S.KISFIVLEVFFLINVLIN
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	3.7602	0.3372	1380.29	1380.562	1	409.1	75 M.RDEDKSKWMGK.G
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	3.7392	0.2675	1697.29	1697.921	1	427.5	65.38461 L.EMRDEDKSKWMGKG.V
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-	2	4.4164	0.2647	1659.97	1660.87	1	587	75 L.E1M1R4D1E1D1K2S1K2W2M1G1K2.G
gi 6321968 ref NP_012044.1	YHR174W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.7374	0.2671	1871.89	1872.042	1	832.5	66.66667 D.GKYDLDFKNPESDKSK.W
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.1418	0.3977	2022.05	2023.203	1	1612.4	76.666664 G.K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.4004	0.3104	2001.43	2001.203	1	1174	70 G.KYDLDFKNPESDKSKW.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.7188	0.2821	2060.35	2058.255	1	1248.6	68.75 D.GKYDLDFKNPESDKSKW.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.7077	0.4491	2303.81	2305.483	1	1460.6	61.11111 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1.K
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.2289	0.3877	2283.25	2281.483	1	1223.2	58.333332 E.FFKDGKYDLDFKNPESDKS.K
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.6064	0.3336	2238.86	2239.467	1	1064.3	42.647057 G.K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.5086	0.2517	3146.03	3146.407	1	840.9	32 A.S1S1E1F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP 012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	6.0035	0.3138	2969.6	2970.251	1	629.7	31.52174 S.E1F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
ail6321968/ref/NP_012044.1	YHR174W	Enclase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dluconeogenesis; expression is induced in response to glucose; Enc2p	2	4.5047	0.3397	2969.53	2970.251	1	374.2	39 130436 S E1F1F1K2D1G1K2Y1D1L1D1F1K2N2P1F1S1D1K2S1K2W2L1T1 G
3 100 00101 <u>-</u>		Enclase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphodycarta to aborehoorpolyruvate during disclosurie and the reverse reaction								
gi 6321968 ref NP_012044.1	YHR174W	prosprogrycerate to prosprogroup of the prosprogram of the reverse feation during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.4603	0.4167	2938.53	2939.251	1	451.8	39.130436 S.EFFKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enrouse III, a prosphopyruvate nydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.4132	0.2458	2290.17	2289.72	2	657.6	45 L.ADLSKSKTSPYVLPVPFLNVL.N

gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.0179	0.2423	2216.93	2218.642	1	417.2	36.842106 A.DLSKSKTSPYVLPVPFLNVL.N
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.2748	0.2733	1395.97	1398.562	1	552.6	75 M.R4D1E1D1K2S1K2W2M1G1K2.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.2498	0.4385	2300.55	2301.517	1	435	50 F.KDGKYDLDFKNPESDKSKW.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.4548	0.2075	2440.35	2441.677	5	307.9	42.105263 F.K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1.T
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.1663	0.2681	2329.49	2329.571	1	830	55.263157 D.GKYDLDFKNPESDKSKWLTG.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.7535	0.3252	2216.21	2215.467	1	804.5	58.823532 G.KYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.504	0.268	2312.05	2313.72	1	576.3	42.5 L.A1D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1.N
ail6321968/refINP 012044.1	YHR174W	Enclase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dlyconeogenesis; expression is induced in response to glucose; Enc2o	2	4.468	0.386	2447.67	2448.694	1	591.1	52.63158 F.FKDGKYDLDFKNPESDKSKW.L
ail6321968/refINP_012044.11	VHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during durongergenesis: expression is induced in response to duronger. Eno20	3	4 4323	0 1757	2845 37	2846 226	1	581 3	20 807603 41041 15162516271510191/11 101/101611 102/11 1026161511341 G
-:::coo40co::-=#ND_042044.41	VUD474W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	3	2.044	0.1737	2040.07	2040.220		370.5	
gilos21900 rei NP_012044.1	10R174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	3.244	0.2076	2290.31	2295.621	4	378.5	35./1420/ S.K211STP111VTLTP1VTP1F1LTN2VTLTN201G1STH5A1G1.G
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	5.4397	0.3309	2236.41	2237.569	1	1776.9	60.000004 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1.G
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.043	0.3319	2613.53	2614.889	1	422.7	45 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enoiase II, a prosphopyruvate nydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.4834	0.3277	2644.23	2641.889	1	407.3	45 L.M\$K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.0596	0.2673	2495.39	2493.697	1	649.5	40.789474 M.K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.1217	0.4389	2470.45	2467.697	1	402.1	47.368423 M.KRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.5866	0.3156	2626.16	2625.889	1	774.3	40 L.M1K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	2.9678	0.1985	2711.13	2712.049	1	287.5	38.095238 S.LMKRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	2.3481	0.1613	1153.46	1154.297	1	434.5	60.000004 A.G1H3D1G1K2V1K2I1G1L1D1.C
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	3.115	0.2539	1037.51	1038.208	1	418.8	61.11111 A.G1H3D1G1K2V1K2l1G1L1.D
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.8109	0.3668	2690.73	2691.959	1	518.3	45.238094 F.F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.4636	0.3444	2692.61	2691.959	1	565.2	33.333336 F.F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
		Enclase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-								
gi 6321968 ref NP_012044.1	YHR174W	priospriosprograde to priosproeniopyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.7952	0.3944	2623.07	2623.871	1	1559.6	42.5 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.8397	0.3672	2594.54	2595.871	1	1759.4	41.25 E.FFKDGKYDLDFKNPESDKSKW.L

gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glucolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.4786	0.4504	2621.11	2623.871	1	1043.1	52.499996 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.1285	0.4932	2594.55	2595.871	2	1000.5	52.499996 E.FFKDGKYDLDFKNPESDKSKW.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.3985	0.351	2866.77	2867.187	1	620.4	41.304348 E.FFKDGKYDLDFKNPESDKSKWLTG.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.9012	0.3103	2612.66	2614.889	1	1461	45 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.818	0.4115	2596.88	2598.889	1	846.8	42.5 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.2089	0.294	2712.92	2712.049	1	438.5	32.142857 S.LMKRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.2894	0.3873	2537.61	2539.911	1	581.7	39.583336 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L1.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.0753	0.3475	2512.31	2509.911	1	959.5	33.333336 S.KTSPYVLPVPFLNVLNGGSHAGGAL.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.0078	0.3533	2742.95	2740.049	1	643.4	33.333336 S.L1M1K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.1344	0.2998	1038.19	1038.208	1	613.4	77.77778 A.G1H3D1G1K2V1K2I1G1L1.D
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.0167	0.3645	2838.53	2840.135	1	612	45.454548 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.2208	0.4184	2808.77	2810.135	1	611.3	43.18182 E.FFKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.1731	0.2812	2812.76	2810.135	1	481.9	31.818182 E.FFKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.8196	0.3232	2599.49	2598.889	1	564.1	52.499996 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.2203	0.162	2737.71	2740.049	1	206.3	33.333336 S.L1M1K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.8334	0.2653	2839.04	2840.135	1	720.6	32.954548 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.9062	0.3197	2628.41	2625.889	1	574.6	55 L.M1K2R4Y1P111V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	2.5545	0.277	1463.68	1463.76	1	497	62.5 S.KSKTSPYVLPVPF.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.8589	0.171	1796.11	1797.101	1	608.1	53.333336 L.S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	3.0769	0.335	1576.88	1576.919	1	535.6	57.692307 S.KSKTSPYVLPVPFL.N
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.3651	0.3136	2493.03	2493.697	1	352	42.105263 M.K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	6.2507	0.3046	3149.75	3148.568	1	1039.9	L.A1D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L 30.000002 1.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.7384	0.3059	3074.57	3076.489	1	673.7	A.D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L1. 25.862068 A

gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoen/pyruvate during glucolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	3.6069	0.2722	1515.7	1516.717	1	1095.5	61.538464 Q.T1A1E1E1A1L1D1L1I1V1D1A1I1K2.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	3.0555	0.3415	1500.72	1501.717	1	878.2	57.692307 Q.TAEEALDLIVDAIK.A
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.7107	0.4756	1712.83	1710.75	1	839.9	61.538464 V.SIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	2.2309	0.1512	1248.54	1248.508	6	441.4	65 S.KTSPYVLPVPF.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.0147	0.2993	1248.37	1248.508	3	652.2	80 S.KTSPYVLPVPF.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	2.9922	0.1575	1260.35	1260.508	2	621.5	80 S.K2T1S1P1Y1V1L1P1V1P1F1.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	3.1461	0.2013	1491.83	1490.771	1	360.4	66.66667 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.9522	0.1817	1493.41	1490.771	1	1136.5	79.16667 S.K2T1S1P1Y1V1L1P1V1P1F1L1N2.V
ail6321968/refINP 012044.1	YHR174W	Enclase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dluconeogenesis; expression is induced in response to glucose; Enc2p	1	2.3595	0.1623	1360.59	1361.667	4	444.2	59.090908 S.KTSPYVLPVPFL.N
ail6321968/refINP_012044.1	YHR174W	Enclase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dluconeogenesis: expression is induced in resonase to glucose: Enc2o	2	4.744	0.3745	1501.41	1501.717	1	2279.1	80.769226 Q TAFFALDI IVDAIK A
ail6321968/refINP_012044_11	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during divencegonesis: expression is induced in resonase to glucose. Eno20	2	5 0579	0.2969	1514 75	1516 717	1	2284.9	84 61539 O T141E1E1411 1D11 111V1D14111K2 A
gil6321968/refINP_012044.11	VHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during durongengenesis: expression is induced in response to duronse. Eno20	-	5 2894	0.3515	2364.89	2363 522	1	1119.6	44 444447 K R4V10111V1S111E1D101E141E1D1D1W2E141W2 S
-:::::::::::::::::::::::::::::::::::::	VUD474W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	0	3.2034	0.0010	2304.03	2303.322	ļ	402.0	
gijo321968 rei NP_012044.1	100 IT 174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	2.996	0.1565	1471.01	1472.044	1	403.2	
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	2.9905	0.2143	1273.23	1273.429	2	725.2	75 L.LRIEEELGDKA.V
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphopyreparts to phosphophopyruvate during during during size and the reverse reaction	1	2.5924	0.2351	1287.43	1288.429	6	204.3	55 L.L1R4I1E1E1E1L1G1D1K2A1.V
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-	1	2.4704	0.2491	1272.52	1273.429	8	223.6	55 L.LRIEEELGDKA.V
gi 6321968 ref NP_012044.1	YHR174W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-	3	4.766	0.4775	2339.57	2339.522	1	903.3	43.055553 K.RYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II a phosphonyruvate bydratase that catalyzes the conversion of 2-	2	5.9392	0.3854	2362.09	2363.522	1	882.3	52.77778 K.R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	hosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.0629	0.3628	1639.77	1640.87	1	463.3	66.66667 L.EMRDEDKSKWMGK.G
gi 6321968 ref NP_012044.1	YHR174W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.013	0.3992	2326.43	2327.517	1	628.6	52.77778 F.K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enoiase II, a prosphopyruvate nydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.8325	0.3879	2021.77	2023.203	1	1363.7	73.333336 G.K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.0096	0.3552	2279.66	2281.483	1	1617.8	43.055553 E.FFKDGKYDLDFKNPESDKS.K
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.7431	0.2126	2197.49	2195.414	1	304.3	50 D.G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1.T

gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.2104	0.1781	3113.78	3113.407	1	871.4	30.000002 A.SSEFFKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	6.4593	0.3391	2970.23	2970.251	1	904.1	32.608696 S.E1F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	5.0407	0.4093	2969.07	2970.251	1	302.3	39.130436 S.E1F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.3613	0.2	2940.44	2939.251	2	483.2	27.173912 S.EFFKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	6.0382	0.2578	2328.47	2327.517	1	1513.7	45.833336 F.K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.5358	0.2076	2300.81	2301.517	1	1094.1	40.27778 F.KDGKYDLDFKNPESDKSKW.L
gil6321968/refINP 012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dluconeogenesis; expression is induced in resoonse to glucose: Eno2o	2	4.3851	0.4905	2514.13	2515.782	1	827.6	52.499996 F.KDGKYDLDFKNPESDKSKWLT G
gil6321968/refINP_012044_1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during dlycolysis and the reverses in its induced in resonase to glucose: Eno20	2	4 9037	0.4123	2541 91	2543 782	1	770.9	50 F K2D1G1K2V1D1I 1D1F1K2N2P1F1S1D1K2S1K2W2I 1T1 G
	VUD474W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	-	5 2442	0.2045	2402.50	2405 444		4047.4	
gijo321966 teijinP_012044.1	100174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	3	5.3112	0.3815	2193.56	2195.414	1	1247.4	
gi 6321968 ret NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction	2	4.2156	0.3455	2170.73	2171.414	1	887.9	52.941177 D.GKYDLDFKNPESDKSKWL.1
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- ohosphoqu/cerate to phosphoenolovruvate during d/vcolvsis and the reverse reaction	2	5.0011	0.3846	2475.79	2475.694	1	770.1	52.63158 F.F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-	2	4.4404	0.3026	2690.73	2691.959	1	512.9	42.857143 F.F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	pnospnoglycerate to pnospnoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-	2	4.2362	0.3683	2662.07	2662.959	1	364.4	42.857143 F.FKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.3058	0.2431	2665.16	2662.959	1	744.7	34.523808 F.FKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	bhoshoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.0784	0.2714	2596.58	2595.871	1	1301.3	38.75 E.FFKDGKYDLDFKNPESDKSKW.L
gi 6321968 ref NP_012044.1	YHR174W	phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.403	0.4094	2595.23	2595.871	1	487.6	47.5 E.FFKDGKYDLDFKNPESDKSKW.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	6.5303	0.4021	2620.94	2623.871	1	2112.4	46.25 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.715	0.3974	2638.97	2641.889	1	1341.7	41.25 L.M\$K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.0255	0.3834	2613.95	2614.889	1	949.3	43.75 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.2119	0.2812	2599.25	2598.889	1	914	41.25 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.7208	0.4427	2601.87	2598.889	1	479.2	50 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.0187	0.2468	2694.62	2691.959	2	467.5	29.761904 F.F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
qi 6321968 ref NP 012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose: Eno2o	2	5.3024	0.4588	2621.37	2623.871	1	894.9	50 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L

gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.2856	0.422	2839.07	2840.135	1	705.2	43.18182 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.9439	0.4251	2809.01	2810.135	1	673	45.454548 E.FFKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.6499	0.3173	2756.72	2756.049	1	612.7	33.333336 S.L1M\$K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.1006	0.3101	2490.83	2493.697	1	304.6	42.105263 M.K2R4Y1P1I1V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.2537	0.3561	2613.61	2614.889	1	526.9	47.5 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.9558	0.3649	2625.05	2625.889	1	460.5	50 L.M1K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	2.9559	0.2902	1038.63	1038.208	1	408.4	61.11111 A.G1H3D1G1K2V1K2I1G1L1.D
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.0293	0.3205	2494.07	2493.697	1	610	40.789474 M.K2R4Y1P1I1V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.0003	0.214	3700.67	3698.128	1	384.9	25 M.KRYPIVSIEDPFAEDDWEAWSHFFKTAGIQI.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	3.8866	0.1639	3740.24	3739.128	2	237.3	M.K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2S1H3F1F1K2T1A1G1I1Q2I 19.166666 1.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.719	0.2578	2466.5	2467.697	1	662.7	40.789474 M.KRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.6595	0.3044	1563.85	1566.838	1	1108.7	80.769226 L.S1K2S1K2T1S1P1Y1V1L1P1V1P1F1.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	6.1221	0.2542	2626.25	2625.889	1	846.7	46.25 L.M1K2R4Y1P1I1V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.3964	0.3268	2838.95	2840.135	1	753	31.818182 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	1	3.3001	0.2649	1477.6	1478.76	1	540.5	62.5 S.K2S1K2T1S1P1Y1V1L1P1V1P1F1.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.1976	0.2297	1777.11	1778.101	1	619.3	53.333336 L.SKSKTSPYVLPVPFLN.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.7107	0.1716	1706.65	1709.023	1	949.7	75 S.K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2.V
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.0694	0.2877	1666.49	1663.998	1	820.7	67.85714 L.SKSKTSPYVLPVPFL.N
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.8073	0.2457	2543.69	2543.782	1	1355.1	41.25 F.K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.5573	0.3308	2281.01	2281.483	1	1218.1	45.833336 E.FFKDGKYDLDFKNPESDKS.K
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.3847	0.2926	2441.84	2441.677	2	687.2	32.894737 F.K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1.T
gi 6321968 ref NP 012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose: Eno2o	2	5.2261	0.343	2237.65	2239.467	1	1849.6	67.64706 G.K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.714	0.3394	2296.51	2297.519	1	485.1	50 D.G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G

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gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a prosphopyruvate nydratase that catalyzes the conversion of 2- phosphoglycorate to phosphoen/pyruvate during glucolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.7856	0.2818	2275.28	2272.519	1	1337.7	45.833336 D.GKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.7369	0.4119	2194.73	2195.414	1	1618	47.058823 D.G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1.T
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.0347	0.3512	2968.75	2970.251	1	417	39.130436 S.E1F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.9935	0.2996	2970.92	2970.251	7	497	27.173912 S.E1F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.3305	0.3834	2407.99	2409.657	1	572.6	55.263157 E.FFKDGKYDLDFKNPESDKSK.W
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.6508	0.3964	2543.51	2543.782	1	752.1	50 F.K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.0158	0.3206	2414.03	2414.677	1	972	39.473686 F.KDGKYDLDFKNPESDKSKWL.T
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.302	0.2825	2436.5	2435.657	1	824.8	38.157894 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2.W
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.9009	0.4217	2622.68	2623.871	1	1426.9	41.25 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.L
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.3363	0.4141	2807.65	2810.135	1	921.1	47.727272 E.FFKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.8659	0.3869	2839.01	2840.135	1	845.5	36.363636 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.136	0.212	2613.92	2614.889	1	565	35 L.M@KRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.521	0.3773	2809.52	2810.135	1	882.1	35.227272 E.FFKDGKYDLDFKNPESDKSKWLT.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.401	0.3472	2839.31	2840.135	2	546.9	38.636364 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1T1.G
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.3043	0.2736	2737.51	2738.03	2	346.7	35.714287 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1.T
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	5.5183	0.3952	2739.44	2738.03	1	1445.7	38.095238 E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2L1.T
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.5572	0.4009	2707.67	2709.03	1	494.8	40.476192 E.FFKDGKYDLDFKNPESDKSKWL.T
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	3	4.5111	0.3256	2597.09	2598.889	1	439.8	32.5 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1	YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	3.4475	0.2047	2624.37	2625.889	1	305.4	40 L.M1K2R4Y1P111V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
		Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during durangenergies in evenergies in idvance is generate to a function.	3	4.5596	0.2617	2625.08	2625.889	1	628.9	35 L.M1K2R4Y1P111V1S111E1D1P1F1A1E1D1D1W2E1A1W2.S
gi 6321968 ref NP_012044.1	YHR174W	during gluconeogenesis, expression is induced in response to glucose, Enozp								
gi 6321968 ref NP_012044.1 gi 6321968 ref NP_012044.1	YHR174W YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	2	4.2446	0.3172	2598.83	2598.889	1	360.7	42.5 L.MKRYPIVSIEDPFAEDDWEAW.S
gi 6321968 ref NP_012044.1 gi 6321968 ref NP_012044.1 gi 6321968 ref NP_012044.1	YHR174W YHR174W YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2- phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p 6-phosphogluconate dehydrogenase (decarboxvlatino). catalyzes an NADPH	2	4.2446 3.0634	0.3172	2598.83 1690.57	2598.889 1691.023	1	360.7 607.3	42.5 L.MKRYPIVSIEDPFAEDDWEAW.S 60.714287 S.KSKTSPYVLPVPFLN.V

		6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH								
ail6321077/rofINP_012053_1		regenerating reaction in the pentose phosphate pathway; required for growth on D-	2	3 4975	0 3747	1762 33	1764.07	1	532.0	53 333336 E D1D1\/1D1G1K2B1I 1\/1E1K2I1M1D1T1A1 G
gil0321977 [rei]INP_012033.1]	THKIOSW	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	2	3.4675	0.3747	1702.33	1704.97	'	552.9	53.535350 F.DTDTVTDTGTKZFTETVTETKZHWIDTTTAT.G
	VUD400W	regenerating reaction in the pentose phosphate pathway; required for growth on D-	2	5 0000	0.0005	2020 77	2027 44		4054 7	
gilo321977 [rei]NP_012053.1]	THRIOSW	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	3	5.2902	0.2965	3036.77	3037.44	1	1251.7	35.576923 S.RVLPGPEVPRDAVRDREQFVDDLEQAL.1
	V(10400)W	regenerating reaction in the pentose phosphate pathway; required for growth on D-		0 4504	0.0045	0070.04	0070 44	-	000.4	
gi 6321977 ret NP_012053.1	YHR183W	giucono-deita-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxvlating), catalyzes an NADPH	2	3.4564	0.2315	3070.61	3072.44	5	386.1	28.846153 S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1L1.Y
	V(10400)W	regenerating reaction in the pentose phosphate pathway; required for growth on D-		0.0407	0.0770	0040 47	00.47 700		007.0	
gi 6321977 ret NP_012053.1	YHR183W	giucono-deita-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxvlating), catalyzes an NADPH	2	3.3497	0.2772	2646.47	2647.793	1	327.6	30.000002 S.G1V1S1G1G1E1E1G1A1R4Y1G1P1S1L1M1P1G1G1S1E1E1A1W2P1H3.
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ret NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxylating), catalyzes an NADPH	2	4.707	0.4091	2332.85	2334.547	1	814.1	57.894737 F.R4V1L1P1E1C1A1S1D1N2L1P1V1D1K2D1I1H3I1N2.W
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	2	3.2214	0.25	2827.47	2828.106	1	316.8	35.416664 K.V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1.L
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	3	6.2206	0.4175	2910.68	2912.112	1	955.4	33.333336 L.L1E1K2G1D111111D1G1G1N2S1H3F1P1D1S1N2R4R4Y1E1E1L1.K
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ret NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	2	3.4146	0.2404	2958.53	2958.28	9	340.3	30.000002 S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1.L
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxylating), catalyzes an NADPH	3	4.1599	0.2549	3073.88	3072.44	1	627.2	27.884615 S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1L1.Y
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	2	3.9361	0.3475	2922.83	2924.28	1	463.3	34 S.KVLPGPEVPKDAVKDREQFVDDLEQA.L
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	3	5.882	0.4334	2957.3	2958.28	1	1480	36 S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1.L
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxylating), catalyzes an NADPH	2	4.4042	0.4926	1877.03	1878.179	1	717.7	65.625 S.KVLPGPEVPKDAVKDRE.Q
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	3	4.1027	0.1985	3260.12	3260.634	1	430.8	26.85185 L.LEKGDIIIDGGNSHFPDSNRRYEELKKK.G
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	3	4.4706	0.2061	2852.9	2853.202	1	1496.7	37.5 S.KVLPGPEVPKDAVKDREQFVDDLEQ.A
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ret NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxylating), catalyzes an NADPH	2	2.9447	0.1838	2923.21	2924.28	9	330.2	30.000002 S.KVLPGPEVPKDAVKDREQFVDDLEQA.L
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ret NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxylating), catalyzes an NADPH	3	5.2671	0.3435	2922.41	2924.28	4	622.2	29 S.KVLPGPEVPKDAVKDREQFVDDLEQA.L
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ref NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxylating), catalyzes an NADPH	2	3.2328	0.1553	2883.67	2886.202	4	353	31.25 S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2.A
	V(10400)W	regenerating reaction in the pentose phosphate pathway; required for growth on D-	0	4 7050	0 4040	000470	0000 000		4000.0	
gi 6321977 ret NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehvdrogenase (decarboxylating), catalyzes an NADPH	3	4.7859	0.4013	2884.76	2886.202	1	1038.6	33.333336 S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2.A
		regenerating reaction in the pentose phosphate pathway; required for growth on D-								
gi 6321977 ret NP_012053.1	YHR183W	glucono-delta-lactone and adaptation to oxidative stress; Gnd1p 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH	2	3.5652	0.3316	2623.91	2625.955	1	387.5	38.636364 S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1.E
	V(10400)W	regenerating reaction in the pentose phosphate pathway; required for growth on D-		5 5000	0.000	0000 40	0050.00		007.0	
gilo321977[rei]NP_012053.1]	10810300	giucono-delta-lactorie and adaptation to oxidative stress; Grid ip	3	5.5293	0.392	2960.42	2958.28	1	007.0	34 S.KZVILIPIGIPIEIVIPIKZDIAIVIKZDIR4EIQZFIVIDIDILIEIQZAI.L
	VUD400W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl		0.005	0.004.0	4050 45	4050 004		457.4	
gil0321904[rei]INP_012000.1]	THKI90W	pyrophosphate moleties to form squalene in the steror biosynthesis pathway, Ergsp	1	2.925	0.2210	1230.43	1200.394	'	437.4	12.22222 T.DFESILIEFH.R
ail6321984/refINP_012060_1	VHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl	2	3 182	0 1993	2135 57	2137 345	1	425.4	47 058823 L D1T111E1D1D1M1S111E1H3D1L1K21D1L1L1 R
giloo21004[rel[14]_012000.1]	1111(1500		2	0.102	0.1555	2100.07	2107.040	·	420.4	
ail6321984/refINP_012060_1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl	2	3 6724	0.345	2633 75	2635 065	2	370.7	38 095238 E MEEMYODKI PPN/KPNETPIEL K
2/1/			_					-		
ail6321984 refINP 012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate mojeties to form squalene in the sterol biosynthesis pathway: Ero9p	2	4.2945	0.2972	2660.29	2662.065	1	406.9	40.476192 F.M1E1E1M1Y1Q2D1K2L1P1P1N2V1K2P1N2E1T1P1I1F1L1.K
gi 6321984 ref NP_012060.1	YHR190W	pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	4.5556	0.3593	2245.61	2245.642	1	701.8	55.555557 E.MYQDKLPPNVKPNETPIFL.K
		Formanyl dishaanhata formanyl transformaa (agualana aynthaaa), jajina two formanyl								
gi 6321984 ref NP_012060.1	YHR190W	pyrophosphate moleties to form squalene in the sterol biosynthesis pathway; Erg9p	3	3.9962	0.1771	2903.21	2904.119	1	597.1	29.545454 K.VKERSRYDDELVPTQQEEEYKFN.M
		Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl								
gi 6321984 ref NP_012060.1	YHR190W	pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.1595	0.1685	2481.59	2483.771	1	879.1	47.5 L.R4A1L1D1T111E1D1D1M1S111E1H3D1L1K2I1D1L1L1.R
		Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl								
gi 6321984 ref NP_012060.1	YHR190W	pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	3	4.4714	0.2073	1719.68	1719.031	4	897.8	50 H.KLKPEYQEVIKEIT.E
		Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl								
gi 6321984 ref NP_012060.1	YHR190W	pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	4.0409	0.3484	2267.53	2267.623	1	492.1	61.11111 M.Y1Q2D1K2L1P1P1N2V1K2P1N2E1T1P1I1F1L1K2.V
		Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl								
gi 6321984 ref NP_012060.1	YHR190W	pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.2372	0.2341	1279.83	1280.498	2	615.1	72.22222 A.V1I1R4E1L1H3P1E1L1R4.N

gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.8727	0.2456	2375.07	2373.816	1	534.4	55.263157 E.MYQDKLPPNVKPNETPIFLK.V
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	3	3.9965	0.231	2372.75	2373.816	1	1175.6	40.789474 E.MYQDKLPPNVKPNETPIFLK.V
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.5957	0.2832	2131.83	2129.513	2	374.3	43.75 H.K2L1K2P1E1Y1Q2E1V111K2E111T1E1K2M1.G
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	3	3.8122	0.193	2456.72	2456.771	1	906.2	33.75 L.RALDTIEDDMSIEHDLKIDLL.R
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.278	0.2685	1251.21	1250.394	1	1002	83.33333 T.DFESILIEFH.K
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.4277	0.2632	2241.63	2242.623	1	600.7	52.77778 M.YQDKLPPNVKPNETPIFLK.V
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	3	4.3667	0.2803	2375.36	2373.816	1	1314.7	42.105263 E.MYQDKLPPNVKPNETPIFLK.V
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	3	4.091	0.3167	2398.85	2399.816	1	1322.4	42.105263 E.M1Y1Q2D1K2L1P1P1N2V1K2P1N2E1T1P1I1F1L1K2.V
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.3262	0.2486	2372.65	2373.816	1	441.9	47.368423 E.MYQDKLPPNVKPNETPIFLK.V
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.013	0.2386	2231.13	2230.452	2	334.7	41.666664 L.RALDTIEDDMSIEHDLKID.L
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.3762	0.2539	1249.85	1250.394	1	1390.6	83.33333 T.DFESILIEFH.K
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	1	3.0812	0.2501	1249.49	1250.394	2	519	72.22222 T.DFESILIEFH.K
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	2	3.8298	0.2488	1728.47	1727.054	2	400.4	64.28571 D.K2L1P1P1N2V1K2P1N2E1T1P111F1L1.K
gi 6321984 ref NP_012060.1	YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p Protein comoonent of the small (405) ribosomal subuniti identical to Ros4Bp and has	2	3.4612	0.3623	1709.57	1708.054	1	400.7	53.571426 D.KLPPNVKPNETPIFL.K
gi 6321997 ref NP_012073.1	YHR203C	similarity to rat S4 ribosomal protein; Rps4bp	2	3.159	0.3116	1326.39	1325.461	3	603.9	75 H.RITDEEASYKL.G
gi 6321997 ref NP_012073.1	YHR203C	similarity to rat S4 ribosomal protein; Rps4bp	1	2.6893	0.2608	1317.04	1315.642	1	344.7	60.000004 H.KLRESLPLIVF.L
gil6321007/rofIND_012073_1	VHP203C	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has similarity to ret S4 ribosomal protein. Pps4bp	2	3 0034	0 4305	1375 23	1375 /3/	1	779	70 833331 \$10101110101015101019183
gilosz1997 lieiline_012073.1	THK2030	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has	2	3.9034	0.4305	1375.23	1375.434		110	70.03333 E.31010111ATETR4F131AT01F1H3.K
gi 6321997 ref NP_012073.1	YHR203C	similarity to rat S4 ribosomal protein; Rps4bp Protein component of the small (40S) ribosomal subunit: identical to Rps4Bp and has	1	2.9112	0.2271	1329.79	1330.642	2	356.8	60.000004 H.K2L1R4E1S1L1P1L1I1V1F1.L
gi 6321997 ref NP_012073.1	YHR203C	similarity to rat S4 ribosomal protein; Rps4bp Nuclear response regulator and transcription factor, part of a branched two- component signaling system: required for notimal induction of heat-shock genes in	3	4.844	0.3033	1394.24	1394.576	1	3840.1	77.27273 E.RHDGGFDLVHIK.D
gi 6322000 ref NP_012076.1	YHR206W	response to oxidative stress; involved in osmoregulation; Skn7p Nuclear response regulator and transcription factor, part of a branched two- component signaling system: required for notimal individing of heat-shock genes in	2	4.0246	0.3497	1599.45	1599.748	1	688.9	72.72727 Q.SWEFQHPEFRVH.Y
gi 6322000 ref NP_012076.1	YHR206W	response to oxidative stress; involved in osmoregulation; Skn7bc stress guide in Presponse to oxidative stress; involved in osmoregulation; Skn7b Mitochondrial branched-chain amino acid aminotransferase, homolog of murine FCA30: histoiku avarasead during logarithmic phase and represend during tationary	2	2.9466	0.348	1621.81	1620.748	1	364.7	54.545456 Q.S1W2E1F1Q2H3P1E1F1R4V1H3.Y
gi 6322002 ref NP_012078.1	YHR208W	phase; Bartip phase; Bartip Mitochondrial branched-chain amino acid aminotransferase, homolog of murine FC 439: binho expressed during logarithmic phase and repressed during stationary	2	3.3179	0.2579	1359.37	1356.564	1	988.2	77.27273 A.VVSPIKEIGWNN.E
gi 6322002 ref NP_012078.1	YHR208W	Echaosi mginy capicasco danny againima priodo ani represende danny datavirary phase; Batt p Mitochondrial branched-chain amino acid aminotransferase, homolog of murine EC 439: binhu expressed during logarithmic phase and represed during stationary	2	2.9471	0.2053	1445.51	1444.643	4	522.5	62.5 A.A1V1V1S1P111K2E111G1W2N2N2.E
gi 6322002 ref NP_012078.1	YHR208W	ECA20: http://www.ecaed.during.loganithmic.priase.and.repressed.during.gaturnery phase; Battp Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA20: http://www.ecaed.during.loganithmic.prior.edd.gaturnery.prior. ECA20: http://www.ecaed.during.loganithmic.prior.edd.gaturnery.prior. ECA20: http://www.ecaed.during.loganithmic.prior.edd.gaturnery.prior. ECA20: http://www.ecaed.during.loganithmic.prior.edd.gaturnery.prior. ECA20: http://www.ecaed.during.loganithmic.prior.edd.gaturnery.prior. ECA20: http://www.ecaed.during.loganithmic.prior.edd.gaturnery.prior. ECA20: http://www.ecaed.during.loganithmic.prior.edd.gaturnery.prior. ECA20: http://www.ecaed.during.loganithmic.prior.prior. ECA20: http://www.ecaed.gaturnery.prior. ECA20: http://w	2	3.3704	0.3561	1409.31	1409.533	1	623	72.72727 S.A1A1R4I1C1L1P1T1F1E1S1E1.E
gi 6322002 ref NP_012078.1	YHR208W	ECA20: bibliourement during logaritation and expressed during stationary phase; Bartip Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA20: bibliourement during logaritation action and texpressed during abarticator	2	3.677	0.2376	2483.97	2485.674	3	242.7	41.666664 A.R4D1K2L1D1P1Q2E1W2D111N2E1R4Y1Y1T111T1.E
gi 6322002 ref NP_012078.1	YHR208W	ECA39, finginy expressed during logarithmic phase and repressed during stationary phase; Batt p Mitochondrial branched-chain amino acid aminotransferase, homolog of murine	2	4.0378	0.2679	2456.53	2456.674	1	285.8	44.444447 A.RDKLDPQEWDINERYYTIT.E
gi 6322002 ref NP_012078.1	YHR208W	EUA39; nigni expressed during logarithmic phase and repressed during stationary phase; Bathp Mitochondrial branched-chain amino acid aminotransferase, homolog of murine	3	4.3978	0.3699	3120.41	3121.481	1	597.9	31.48148 A.V1V1S1P1I1K2E1I1G1W2N2N2E1D1I1H3V1P1L1L1P1G1E1Q2C1G1A1L1.T
gi 6322002 ref NP_012078.1	YHR208W	ECA39, nginy expressed during logarithmic phase and repressed during stationary phase; Bath Mitochondrial branched-chain amino acid aminotransferase, homolog of murine	2	3.7371	0.2761	3120.79	3121.481	1	275	27.777779 A.V1V1S1P111K2E1I1G1W2N2N2E1D111H3V1P1L1L1P1G1E1Q2C1G1A1L1.T
gi 6322002 ref NP_012078.1	YHR208W	Corvey, many expressed during logarithmic priase and repressed during stationary phase; Bart p Mitochondrial branched-chain amino acid aminotransferase, homolog of murine CO20b biblio unorecosed during logarithmic a boat or acid during and during the statistical during logarithmic in boat or acid during the during the Construction of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the statistical bart of the	1	2.4314	0.2151	1383.62	1384.629	1	543.3	54.166668 K.K2E1L1V1T1A1P1L1D1G1T1I1L1.E
gi 6322002 ref NP_012078.1	YHR208W	Corvey, many expressed during logarithmic priase and repressed during stationary phase; Bart p Mitochondrial branched-chain amino acid aminotransferase, homolog of murine CCA98: binbu expressed during logarithmic phase acid expressed during entities and the acid expressed for the phase of the phase of the phase of the phase is a stationary of the phase of the phase of the phase of the phase is a stationary of the phase of the phase of the phase of the phase is a stationary of the phase of the phase of the phase of the phase is a stationary of the phase of the phase of the phase of the phase is a stationary of the phase of the phase of the phase of the phase is a stationary of the phase of the phase is a stationary of the phase of the phase of the phase of the phase of the phase is a stationary of the phase of the phase of the phase of the phase of the phase is a stationary of the phase of the phase of the phase of the phase of the phase is a stationary of the phase of the pha	3	4.8311	0.4316	3085.43	3086.481	1	615.7	32.407406 A.VVSPIKEIGWNNEDIHVPLLPGEQCGAL.T
gi 6322002 ref NP_012078.1	YHR208W	Corvey, many expressed during logarithmic priase and repressed during stationary phase; Bart p Mitochondrial branched-chain amino acid aminotransferase, homolog of murine CCA20b bibliouroseance during logarithmic above and logaret of during the CCA20b bibliouroseance during logarithmic above and logaret of during the CCA20b bibliouroseance during logarithmic above and logaret of during the CCA20b bibliouroseance during logarithmic above and logaret of during the CCA20b bibliouroseance during logarithmic above and logaret of during logarithmic stationary and logarithmic above and logaret of during logarithmic above stationary and logarithmic above and logaret of during logarithmic above stationary and logarithmic above and logarithmic above stationary above and logarithmic above stationary above above stationary above above stationary above s	2	3.4672	0.2953	3120.37	3121.481	1	239.7	27.777779 A.V1V1S1P111K2E1I1G1W2N2N2E1D111H3V1P1L1L1P1G1E1Q2C1G1A1L1.T
gi 6322002 ref NP_012078.1	YHR208W	склюя, mgmy expressed during loganitrimic phase and repressed during stationary phase; Bat1p	3	4.897	0.2874	3123.74	3121.481	1	701.2	33.333336 A.V1V1S1P111K2E111G1W2N2N2E1D111H3V1P1L1L1P1G1E1Q2C1G1A1L1.T

		Mitochondrial branched-chain amino acid aminotransferase, homolog of murine								
gi 6322002 ref NP_012078.1	YHR208W	EUA39; nigniy expressed during logarithmic phase and repressed during stationary phase; Bart p Mitochondrial branched-chain amino acid aminotransferase, homolog of murine	2	3.5458	0.2236	2526.43	2527.753	2	223.4	39.473686 LARDKLDPQEWDINERYYTIT.E
gi 6322002 ref NP_012078.1	YHR208W	ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Batt p Mitochondrial branched-chain amino acid aminotransferase. homolog of murine	2	3.4653	0.3816	1374.27	1372.564	1	1317.8	81.818184 A.V1V1S1P111K2E111G1W2N2N2.E
gi 6322002 ref NP_012078.1	YHR208W	ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p Mitochondrial branched-chain amino acid aminotransferase. homolog of murine	1	2.4434	0.1876	1371.43	1372.564	2	222.3	54.545456 A.V1V1S1P111K2E111G1W2N2N2.E
gi 6322002 ref NP_012078.1	YHR208W	ECA39, highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	3.9975	0.2642	1384.29	1384.629	1	961	70.83333 K.K2E1L1V1T1A1P1L1D1G1T1I1L1.E
gi 6322180 ref NP_012255.1	YIL010W	Nuclear thiol peroxidase which functions as an alkyl-hydroperoxide reductase during post-diauxic growth; Dot5p	3	4.0064	0.2703	2162.75	2163.439	1	870.6	44.444447 L.E1E1E1E1S1K2L1A1P1I1S1T1P1E1V1P1K2K2K2.I
gi 6322180 ref NP_012255.1	YIL010W	Nuclear thiol peroxidase which functions as an alkyl-hydroperoxide reductase during post-diauxic growth; Dot5p	3	5.394	0.2666	2408.42	2407.772	1	470.8	38.75 L.E1E1E1E1S1K2L1A1P1I1S1T1P1E1V1P1K2K2K2l1K2.T
gi 6322180 ref NP_012255.1	YIL010W	post-diauxic growth; Dot5p	2	4.6529	0.4126	2406.71	2407.772	1	364.2	42.5 L.E1E1E1E1S1K2L1A1P1I1S1T1P1E1V1P1K2K2K2I1K2.T
gi 6322180 ref NP_012255.1	YIL010W	post-diauxic growth; Dot5p	3	4.475	0.3597	2383.61	2381.772	1	788.3	43.75 L.EEEESKLAPISTPEVPKKKIK.T
gi 6322180 ref NP_012255.1	YIL010W	Subunit of the cohesin complex, which is required for sister chromatid cohesion	3	3.9263	0.2994	2406.47	2407.772	1	381	40 L.E1E1E1E1S1K2L1A1P111S1T1P1E1V1P1K2K2K2I1K2.T
gi 6322163 ref NP_012238.1	YIL026C	during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p Subunit of the cohesin complex, which is required for sister chromatid cohesion	2	3.3408	0.1541	2290.25	2291.426	5	215.4	36.842106 Q.L1E1R4V1A1D1E1D1A1N2L1N2D1L1P1E1T1G1F1F1.E
gi 6322163 ref NP_012238.1	YIL026C	during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p Subunit of the cohesin complex, which is required for sister chromatid cohesion	2	3.8825	0.4056	2264.53	2266.426	1	680.8	55.263157 Q.LERVADEDANLNDLPETGFF.E
gi 6322163 ref NP_012238.1	YIL026C	during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p Subunit of the cohesin complex, which is required for sister chromatid cohesion	2	3.3804	0.1873	1678.15	1676.82	1	827.2	65.38461 L.GRDYPIEVDEELLQ.L
gi 6322163 ref NP_012238.1	YIL026C	during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p Subunit of the cohesin complex, which is required for sister chromatid cohesion	2	3.3418	0.2446	1934.47	1937.156	2	330.7	40 L.GRDYPIEVDEELLQLF.L
gi 6322163 ref NP_012238.1	YIL026C	during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p Subunit of the cohesin complex, which is required for sister chromatid cohesion	2	3.7013	0.2218	1696.23	1694.82	4	779.3	65.38461 L.G1R4D1Y1P11E1V1D1E1E1L1L1Q2.L
gi 6322163 ref NP_012238.1	YIL026C	during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p Subunit of the cohesin complex, which is required for sister chromatid cohesion	2	3.6659	0.2589	1397.25	1396.67	1	792.2	75 R.VIKEKFDEFIK.T
gi 6322163 ref NP_012238.1	YIL026C	during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p Subunit of the cohesin complex, which is required for sister chromatid cohesion	2	4.22	0.3323	2534.11	2531.888	1	584.3	45 L.F1K2K2I1V1D1D1T111M1E1N2P1E1P1N2K2K2N2I1Q2.K
gi 6322163 ref NP_012238.1	YIL026C	during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p Ubioutin-protein licase of the ER/nuclear envelope, required for degradation of	2	4.0184	0.2582	2502.53	2502.888	1	627.6	47.5 L.FKKIVDDTIMENPEPNKKNIQ.K
gi 6322159 ref NP_012234.1	YIL030C	Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an ma14 mutation; Ssm4p Ubiquitin-protein liaase of the ER/nuclear envelope, required for degradation of	3	5.0853	0.4095	3727.37	3728.838	1	705.2	T.L1D1E1H3A1V1D1E1N2E1V1E1E1V1E1H3D111P1E1R4D111N2N2A1P1V1N2N2I1 25.80645 N2:N
gi 6322159 ref NP_012234.1	YIL030C	Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an ma14 mutation; Ssm4p Ubiquitin-protein liaase of the ER/nuclear envelope, required for degradation of	3	4.8781	0.3055	3899.63	3899.047	1	356.1	21.969696 Q.NTLDEHAVDENEVEEVEHDIPERDINNAPVNNIN.N
gi 6322159 ref NP_012234.1	YIL030C	Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an ma14 mutation; Ssm4p Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of	3	5.0889	0.3712	3633.08	3633.919	1	519.7	25 Q.QNAINRPNAPVFIPPPAQNRAGNVDQDEQDFGAA.V
gi 6322159 ref NP_012234.1	YIL030C	Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an m14 mutation; Ssm4p Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of	2	3.1101	0.1815	1613.23	1613.981	1	1125.5	69.230774 M.FVPVTKDDKLLKPL.D
gi 6322159 ref NP_012234.1	YIL030C	Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an m14 mutation; Ssm4p Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of	3	4.2934	0.2961	3733.85	3733.051	1	442.6	25.735294 Q.QNAINRPNAPVFIPPPAQNRAGNVDQDEQDFGAAV.G
gi 6322159 ref NP_012234.1	YIL030C	Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an ma14 mutation; Ssm4p Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of	2	4.0155	0.3659	1541.55	1542.732	1	841	69.230774 M.M1L1D1G1S1S1P1Y1P1G1D1F1L1K2.S
gi 6322159 ref NP_012234.1	YIL030C	Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an ma14 mutation; Ssm4p	2	3.3515	0.3466	1526.57	1527.732	3	586.2	57.692307 M.MLDGSSPYPGDFLK.S
gi 6322159 ref NP_012234.1	YIL030C	Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an ma14 mutation; Ssm4p	3	4.9056	0.4192	3612.44	3614.678	1	688.2	L.D1E1H3A1V1D1E1N2E1V1E1E1V1E1H3D111P1E1R4D111N2N2A1P1V1N2N211N2 25.833332 .N
gi 6322156 ref NP_012231.1	YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	2	3.2198	0.2409	2067.79	2067.219	1	500.2	47.058823 K.IYQPGETIIREGDQGENF.Y
gi 6322156 ref NP_012231.1	YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	3	3.8659	0.2823	2411.57	2411.587	1	1309.1	40 L.DTKIYQPGETIIREGDQGENF.Y
gi 6322156 ref NP_012231.1	YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	2	3.6066	0.3503	2410.53	2411.587	1	836.4	52.499996 L.DTKIYQPGETIIREGDQGENF.Y
gi 6322156 ref NP_012231.1	YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	2	4.1552	0.3789	2438.09	2439.587	1	675.4	52.499996 L.D1T1K2I1Y1Q2P1G1E1T1I1I1R4E1G1D1Q2G1E1N2F1.Y
gi 6322156 ref NP_012231.1	YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	2	3.2744	0.3347	1688.27	1688.704	1	520.4	61.538464 S.G1F1N2L1D1P1H3E1Q2D1T1H3Q2Q2.A

gi]6322156 ref NP_012231.1	YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	3	4.4113	0.4045	2436.62	2439.587	1	1045.1	36.25 L.D1T1K2HY1Q2P1G1E1T1H1R4E1G1D1Q2G1E1N2F1.Y
gi 6322156 ref NP_012231.1	YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	2	4.5031	0.3444	1910.31	1911.103	1	780.5	70 K.N2I1V1L1F1P1E1P1E1E1S1F1S1R4P1Q2.S
gi 6322156 ref NP_012231.1	YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	2	3.0512	0.1806	2410.55	2411.587	2	362.3	40 L.DTKIYQPGETIIREGDQGENF.Y
gi 6322154 ref NP_012229.1	YIL035C	Alpha catalytic subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA2, CKB1 and CKB2, the many substrates include transcription factors and all RNA polymerases; Cka1p	2	3.1528	0.1858	1673.89	1674.991	2	629.4	60.714287 F.D1I1I1K2D1P1I1S1K2T1P1A1L1V1F1.E
gi 6322154 ref NP_012229.1	YIL035C	Alpha catalytic subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA2, CKB1 and CKB2, the many substrates include transcription factors and all RNA polymerases; Cka1p	1	2.2894	0.1787	1194.05	1194.419	2	491.9	72.22222 A.SRFFKGPELL.V
gi 6322154 ref NP_012229.1	YIL035C	Alpha catalytic subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA2, CKB1 and CKB2, the many substrates include transcription factors and all RNA polymerases; Cka1p	2	3.3995	0.2478	1790.17	1791.01	2	454.4	61.538464 F.E1Y1V1D1N2V1D1F1R4I1L1Y1P1K2.L
gi 6322154 ref NP_012229.1	YIL035C	Alpha catalytic subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA2, CKB1 and CKB2, the many substrates include transcription factors and all RNA polymerases; Cka1p	2	3.5206	0.2778	1708.37	1708.881	1	579.5	66.66667 K.Y1E111T1L1P1R4E1F1Y1D1M1D1.Q
ail6322148/refINP 012223.1	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles: Gvp36p	2	4.4012	0.3076	2316.41	2317.468	1	957.3	55 N.SFAEEPEAKPEVAEEEKPQTA.I
	N/II 0 4414	Golgi vesicle protein of unknown function; localizes to both early and late Golgi	-	4.0500	0.0004			Ż	070 5	
gi 6322148 ref NP_012223.1	YIL041W	vesicles; Gvp36p Golgi vesicle protein of unknown function; localizes to both early and late Golgi	2	4.3596	0.3304	2340.19	2341.468	1	879.5	52.499996 N.S1F1A1E1E1P1E1A1K2P1E1V1A1E1E1E1K2P1Q2T1A1.I
gi 6322148 ref NP_012223.1	YIL041W	vesicles; Gvp36p	3	5.9806	0.3076	2534.21	2533.813	1	1518.6	38.75 T.D1I1S1Q2L1P1R4E1Y1T1E1L1E1D1K2V1D1T1I1K2L1.I
gi 6322148 ref NP_012223.1	YIL041W	vesicles; Gvp36p	2	4.6041	0.2618	2532.77	2533.813	1	873.1	52.499996 T.D1I1S1Q2L1P1R4E1Y1T1E1L1E1D1K2V1D1T1I1K2L1.I
ail6222148/rofIND_012222_1	VII 041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi	2	4 40 47	0 1045	2280.44	2279 565	1	1120 E	
gilo322146/rei/iNP_012223.1/	TILU4TVV	Golgi vesicles; Gvp36p Golgi vesicle protein of unknown function; localizes to both early and late Golgi	3	4.4947	0.1945	2260.41	2278.303		1130.5	43.033533 I.SQLPRETTELEDKVDTIKLI
gi 6322148 ref NP_012223.1	YIL041W	vesicles; Gvp36p Galai vesicle protein of unknown function; localizes to both early and late Galai	3	5.5928	0.2148	2509.31	2506.813	6	1089.6	35 T.DISQLPREYTELEDKVDTIKL.I
gi 6322148 ref NP_012223.1	YIL041W	vesicles; Gvp36p	2	4.3644	0.2231	2531.63	2533.813	4	494.5	42.5 T.D1I1S1Q2L1P1R4E1Y1T1E1L1E1D1K2V1D1T1I1K2L1.I
gil6322148/refINP_012223.1	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles: Gvp36p	3	5,7541	0.3136	2532.29	2533.813	1	1082.4	35 T.D1I1S102L1P1R4E1Y1T1E1L1E1D1K2V1D1T1I1K2L1.I
	<u>_</u>	Golgi vesicle protein of unknown function; localizes to both early and late Golgi	-	4.0000	0.0075	0500.00	0500.040	Ż		
gi 6322148 ref NP_012223.1	YIL041W	Colgi vesicles; GVp36p Golgi vesicle protein of unknown function; localizes to both early and late Golgi	2	4.3608	0.2675	2533.69	2533.813	1	609.6	45 1.D111S1Q2L1P1R4E1Y111E1L1E1D1K2V1D11111K2L1.I
gi 6322148 ref NP_012223.1	YIL041W	vesicles; Gvp36p	2	4.0481	0.2456	2505.23	2506.813	6	394.9	40 T.DISQLPREYTELEDKVDTIKL.I
gi 6322146 ref NP_012221.1	YIL043C	cytochrome b reductase; Cbr1p	2	3.7898	0.2621	1503.81	1502.71	2	713.9	75 F.GLPHADDVLGLPIGQ.H
gil6322146/refINP_012221.1	YIL043C	cytochrome b reductase; Cbr1p	2	4.368	0.243	1661.45	1660.852	1	1413.9	73.333336 E.G1L1P1H3A1D1D1V1L1G1L1P111G102H3.
gi 6322146 ref NP_012221.1	YIL043C	cytochrome b reductase; Cbr1p	2	3.9497	0.323	2092.57	2093.477	1	1032	57.894737 F.GLPHADDVLGLPIGQHIVIK.A
gi 6322146 ref NP_012221.1	YIL043C	cytochrome b reductase; Cbr1p	2	3.5504	0.3187	1780.59	1778.061	1	501.9	56.25 Y.KFGLPHADDVLGLPIGQ.H
gi 6322146 ref NP_012221.1	YIL043C	cytochrome b reductase; Cbr1p	1	3.1064	0.2324	1502.61	1502.71	1	331.4	53.571426 F.GLPHADDVLGLPIGQ.H
gil6322146/refINP_012221.1	YIL043C	cytochrome b reductase; Cbr1p	2	3.1929	0.3466	1639.17	1639.852	2	215.8	42.657143 F.GTETPTH3ATDTDTVTETGTETPTHGTQ2.H 63.333332 E.GLPHADDVLGLPIGOH.I
giloozz 140/10/14/ _012221.11	1120400	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	2	0.1020	0.0400	1000.17	1000.002		504	
gi 6322136 ref NP_012211.1	YIL053W	biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2r isoform, osmotic stress; Rhr2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	3	5.875	0.3765	4125.8	4124.476	1	522.1	K.F1A1P1D1F1A1D1E1E1Y1V1N2K2L1E1G1E1I1P1E1K2Y1G1E1H3S1I1E1V1P1G 22.142857 1A1V1K2L1C1.N
gi 6322136 ref NP_012211.1	YIL053W	biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p Constitutively expressed isoform of DL-diversel-3-phosphatase; involved in diversel	1	2.2379	0.158	926.32	925.993	1	116.9	64.28571 K.N2H3E1S1I1R4V1G1.E
		biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p								
gi 6322136 ref NP_012211.1	YIL053W	isoform, osmotic stress; Rhr2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis; induced in response to both anaembic and along with the Hor2p/Gnp2r	2	3.9669	0.3871	2084.85	2085.302	1	361.8	50 Y.L1K2G1R4N2G1L1G1F1P111N2E1Q2D1P1S1K2S1.K
gi 6322136 ref NP_012211.1	YIL053W	isoform, osmolic stress; Rh/2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosvrthesis; induced in resonance to both anaerobic and, along with the Hor/20/Gop2r	2	4.2314	0.4163	2056.77	2058.302	1	723	63.88889 Y.LKGRNGLGFPINEQDPSKS.K
gi 6322136 ref NP_012211.1	YIL053W	isoform, osmotic stress; Rhr2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	2	4.4344	0.2855	1654.55	1656.891	1	1168.1	73.07692 N.D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2.G
gi 6322136 ref NP_012211.1	YIL053W	isoform, osmotic stress; RhZp Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	2	4.2492	0.2665	1830.43	1831.047	1	661.9	56.666668 A.N2D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2G1.R
gi 6322136 ref NP_012211.1	YIL053W	biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	2	3.2412	0.393	1712.35	1714.943	2	227.4	57.14286 N.D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2G1.R
gi 6322136 ref NP_012211.1	YIL053W	biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rh2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	2	5.4071	0.4017	1852.59	1851.017	1	1893.8	82.14286 E.T1D1E1V1E1L11F1D1D1Y1L1Y1A1K2.D
gi 6322136 ref NP_012211.1	YIL053W	biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rh2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	2	4.3728	0.3627	1837.81	1835.017	1	1986.8	82.14286 E.TDEVELIFDDYLYAK.D
gi 6322136 ref NP_012211.1	YIL053W	biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2r isoform, osmotic stress; Rhr2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	2	4.3948	0.2554	1845.75	1845.074	1	742.3	63.333332 T.A1N2D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2.G
gi 6322136 ref NP_012211.1	YIL053W	biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2r isoform, osmotic stress; Rhr2p Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol	2	4.0476	0.3628	1774.43	1772.995	1	794.7	67.85714 A.N2D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2.G
gi 6322136 ref NP_012211.1	YIL053W	biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	3.8569	0.274	1638.67	1636.891	1	685.1	69.230774 N.DVKQGKPHPEPYLK.G

		Acidic protein of the mitochondrial matrix involved in oxidative phosphorylation;								
gi 6322119 ref NP_012194.1	YIL070C	related to the human complement receptor gC1q-R; Mam33p Acidic protein of the mitochondrial matrix involved in oxidative phosphorylation:	2	4.3271	0.3787	1531.51	1529.739	1	1232.1	79.16667 T.RELVYHGPPFSNL.D
gi 6322119 ref NP_012194.1	YIL070C	related to the human complement receptor gC1q-R; Mam33p	2	3.8829	0.3281	2472.29	2473.701	1	605.8	40 T.RELVYHGPPFSNLDEELQESL.E
gi 6322119 ref NP_012194.1	YIL070C	Acidic protein of the mitochondrial matrix involved in oxidative phosphorylation; related to the human complement receptor gC1q-R; Mam33p	2	3.6083	0.2763	2504.65	2501.701	1	614	40 T.R4E1L1V1Y1H3G1P1P1F1S1N2L1D1E1E1L1Q2E1S1L1.E
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	3	3.8568	0.1747	2534.54	2535.604	1	553.9	32.142857 L.D1V1Y1P1H3E1P1A1K2N2G1E1G1S1F1N2D1E1L1N2S1W2.T
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	2	3.3852	0.2616	2534.15	2535.604	1	608.3	47.61905 L.D1V1Y1P1H3E1P1A1K2N2G1E1G1S1F1N2D1E1L1N2S1W2.T
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	2	2.9782	0.2733	2535.03	2535.604	2	261.3	35.714287 L.D1V1Y1P1H3E1P1A1K2N2G1E1G1S1F1N2D1E1L1N2S1W2.T
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	2	4.3858	0.289	2649.29	2649.763	2	463.2	38.636364 A.L1D1V1Y1P1H3E1P1A1K2N2G1E1G1S1F1N2D1E1L1N2S1W2.T
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	3	5.0832	0.3865	2720.57	2721.842	1	1545.4	39.130436 A.A1L1D1V1Y1P1H3E1P1A1K2N2G1E1G1S1F1N2D1E1L1N2S1W2.T
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	2	4.2943	0.3809	1783.89	1785.001	1	1186.7	67.85714 S.S1L1P1E1D1E1L111E1K2I1K2D1V1H3.A
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	2	4.1265	0.3511	2720.83	2721.842	1	649.2	43.47826 A.A1L1D1V1Y1P1H3E1P1A1K2N2G1E1G1S1F1N2D1E1L1N2S1W2.T
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	2	3.732	0.2962	2304.23	2303.638	1	708.7	50 S.S1L1P1E1D1E1L1I1E1K2I1K2D1V1H3A1I1G1I1R4.S
gi 6322116 ref NP_012191.1	YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	2	3.2582	0.2213	1974.13	1971.24	2	547.5	50 S.S1L1P1E1D1E1L1I1E1K2I1K2D1V1H3A1I1.G
gi 6322115 ref NP_012190.1	YIL075C	Subunit of the 26S proteasome, substrate of the N-acetyltransferase Nat1p; Rpn2p	2	3.4698	0.3287	2153.63	2153.418	1	487.8	44.444447 Q.S1A111D1V1L1D1P1L1T1K2D1P1V1D1F1V1R4Q2.A
gi 6322115 ref NP_012190.1	YIL075C	Subunit of the 26S proteasome, substrate of the N-acetyltransferase Nat1p; Rpn2p	3	4.079	0.2639	2282.87	2283.549	1	830	34.210526 L.Q2S1A1I1D1V1L1D1P1L1T1K2D1P1V1D1F1V1R4Q2.A
gi 6322115 ref NP_012190.1	YIL075C	Subunit of the 26S proteasome, substrate of the N-acetyltransferase Nat1p; Rpn2p	3	4.0741	0.3381	1993.13	1993.261	1	1736.7	48.4375 A.I1D1V1L1D1P1L1T1K2D1P1V1D1F1V1R4Q2.A
gi 6322115 ref NP_012190.1	YIL075C	Subunit of the 26S proteasome, substrate of the N-acetyltransferase Nat1p; Rpn2p	2	2.9043	0.2517	1992.25	1993.261	1	429.1	43.75 A.I1D1V1L1D1P1L1T1K2D1P1V1D1F1V1R4Q2.A
gi 6322115 ref NP_012190.1	YIL075C	Subunit of the 26S proteasome, substrate of the N-acetyltransferase Nat1p; Rpn2p	2	4.2441	0.4732	2064.51	2065.34	1	1181.6	67.64706 S.A1I1D1V1L1D1P1L1T1K2D1P1V1D1F1V1R4Q2.A
gi 6322115 ref NP_012190.1	YIL075C	Subunit of the 26S proteasome, substrate of the N-acetyltransferase Nat1p; Rpn2p	2	4.4563	0.3418	1934.51	1935.209	1	1074.4	65.625 S.A1I1D1V1L1D1P1L1T1K2D1P1V1D1F1V1R4.Q
gi 14318437 ref NP_116578.1	YIL078W	Threonyl-tRNA synthetase, essential cytoplasmic protein; Ths1p	2	3.8074	0.2541	2111.79	2110.251	1	1036.1	62.5 F.CTHDQIESEIENIFNFLQ
gi 14318437 ref NP_116578.1	YIL078W	Threonyl-tRNA synthetase, essential cytoplasmic protein; Ths1p Threonyl-tRNA synthetase, essential cytoplasmic protein; Ths1p	2	2.9681	0.229	1734.37	1735.811	6	213.6	50 F.CTHDQIESEIENIF.N
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p Homo-isocitrate debydrogenzes an NAD-linked mitochondrial enzyme required for	2	3.354	0.2195	1938.67	1940.108	1	641.6	44.444447 N.V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1.G
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p Homo-isocitrate debydrogenase, an NAD-linked mitochondrial enzyme required for	2	4.5973	0.4371	2288.45	2289.516	1	815.2	47.727272 S.ANVGPEIVIGEPCHGSAPDIAGK.G
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	2.9573	0.2401	2561.53	2561.984	2	211.7	31.25 L.T111G1L111P1G1D1G111G1K2E1V111P1A1G1K2Q2V1L1E1N2L1.N
gi 6322097 ref NP_012172.1	YIL094C	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.2754	0.3463	2242.83	2244.496	1	679.3	52.77778 F.R4E1P1Q2C1F1D1V1I1V1A1P1N2L1Y1G1D1I1L1.S
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	3.5101	0.2617	2222.73	2220.496	1	566.5	44.444447 F.REPQCFDVIVAPNLYGDIL.S
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ret NP_012172.1	YIL094C	decarboxylated to alpha-ketoadlpate; Lys12p Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	5.2742	0.3944	1908.73	1909.26	1	1424.2	71.875 V.K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1R4.E
	VII 004C	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively	0	4 4000	0 40 47	0400 57	0404 500	4	400.4	
gil6322097 [ref NP_012172.1]	YILU94C	decarboxylated to alpha-ketoadipate; Lys12p Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	4.1086	0.1947	2180.57	2181.533	1	486.4	50 F.A1N2V1R4P1V1R2S1V1E1G1E1R2G1R2P111D1M1V1.I
ail6322097/refINP 012172.1	YIL094C	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate: Lys12p	3	5.4545	0.4929	3780.41	3782.229	1	365.3	L.G1V1V1P1S1A1N2V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1G1K2G1I1A1 23.648647 N2P1I1A1T1I1R4.S
51		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	3	4.8009	0.3074	2178.83	2181.533	1	1757.1	46.05263 F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	4.0179	0.2992	2365.73	2366.825	1	415.1	42.857143 F.ANVRPVKSVEGEKGKPIDMVIV.R
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is ovidatively.								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.423	0.2246	1644.75	1646.863	1	667	67.85714 F.Q2E1T1G1K2A1L1P1D1E1T1V1K2V1L1.K
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is ovidatively.								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.686	0.3548	1742.95	1741.917	1	593	53.125 E.I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1G1K2.G
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	5.6162	0.4749	2129.07	2128.334	1	1384.9	60.000004 N.V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1G1K2.G
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.9697	0.4761	2103.49	2104.334	1	800.5	55 N.VGPEIVIGEPCHGSAPDIAGK.G
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	4.6526	0.4846	2243.19	2244.438	1	586.7	42.857143 A.N2V1G1P1E111V111G1E1P1C1H3G1S1A1P1D111A1G1K2.G
	VII 0040	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively	2	2 7440	0.4040	0017 74	0040 400	4	E20.0	
gilo322097[rei[NP_012172.1]	TILU94C	uecanooxyrated to alpha-кетоаdipate; Lys i ∠p Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	3.7443	0.4349	2217.71	2210.438	1	529.9	
ail6322097/refINP_012172_1	YIL094C	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate: Lys12p	2	5.3008	0.4231	2315 59	2316 516	1	737 1	45 454548 S.A1N2V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1G1K2 G
21		····· , ···· ·························	-					•		

		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p Homo-isocitrate debydrogenase, an NAD-linked mitochondrial enzyme required for	3	3.8665	0.3782	1885.73	1886.26	1	1119.6	42.1875 V.KSVEGEKGKPIDMVIVR.E
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	3	5.0447	0.2884	2181.14	2181.533	1	1723.4	46.05263 F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
		the fourth step in the biosynthesis of lysine. in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	4.3957	0.2179	2179.93	2181.533	1	424.9	47.368423 F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
gi 6322097 ref NP 012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.5496	0.2217	2107.79	2109.454	2	403.4	44.444447 A.N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
5100 00 101 <u>_</u> 0		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
-:::::::::::::::::::::::::::::::::::::	VII 0040	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively	0	4 4005	0.0404	0005 40	2205 225		557 A	
gilo322097 [rei]inP_012172.1]	TILU94C	Homo-isocitrate debydrogenase, an NAD-linked mitochondrial enzyme required for	2	4.4625	0.3164	2395.13	2395.825	1	557.4	47.01905 F.ATN2V IR4P IV IR2STV IETG IETRZG IR2PTITD IMTV ITV I.R
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.3189	0.2628	1554.17	1553.691	3	432.7	53.571426 E.I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1.G
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.3992	0.4258	2032.25	2033.212	1	675.5	47.368423 A.NVGPEIVIGEPCHGSAPDIA.G
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
ail6322097/refINP 012172.1	YIL094C	decarboxylated to alpha-ketoadipate: Lvs12p	2	4.2541	0.4656	2128.11	2128.29	1	849.2	50 S.A1N2V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1.G
51		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
ail6222007/rofIND_012172_1	VII 004C	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively	2	2 0165	0.2670	2102 57	2104 20	1	667	
gilo322097 [rei]inP_012172.1]	TILU94C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	3.9165	0.3679	2103.57	2104.29		667	45 S.ANVGPEIVIGEPCHGSAPDIA.G
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.9164	0.2817	1267.67	1268.513	1	691.7	70.83333 S.L1T111G1L111P1G1D1G111G1K2.E
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	1	3.5906	0.39	1268.65	1268.513	1	478.7	66.66667 S.L1T1I1G1L1I1P1G1D1G1I1G1K2.E
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
ail6322097/refINP 012172.1	YIL094C	decarboxylated to alpha-ketoadipate: Lvs12p	2	2.9776	0.3247	1652.11	1650.956	2	289.7	53.125 L.TIGLIPGDGIGKEVIPA.G
3.1		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
ail6222007/rofIND_012172_1	VII 004C	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively	2	2 2447	0.2507	1569.07	1560 679	1	710 /	
gilo322097 [rei]inF_012172.1]	1120940	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	3.2447	0.2597	1000.27	1509.078	1	/ 10.4	00.00007 L.3Q3DGEFREIGRE.V
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.6608	0.2719	1747.81	1749.073	3	250.3	50 V.K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1.R
		the fourth step in the biosynthesis of lysine. in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	3	4.4504	0.299	1909.31	1909.26	1	890.7	42.1875 V.K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1R4.E
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
gi 6322097 ref NP 012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.4739	0.2173	2079.99	2081.4	1	552.6	55.555557 F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1.V
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
ail6322007/rofIND_012172_1		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate: Lys12p	2	4 0302	0 2447	2170.95	2191 522	1	561.5	50 E A1N2\/1R4D1\/1K2S1\/1E1C1E1K2C1K2D1I1D1M1\/1
gil032203/[rei]i4r_0121/2.1]	1120340	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	2	4.0332	0.2447	2175.05	2101.555	'	501.5	
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	3	5.1202	0.3234	2178.68	2181.533	1	1331	46.05263 F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.1776	0.3274	2152.49	2154.533	1	630.7	52.63158 F.ANVRPVKSVEGEKGKPIDMV.I
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	3.0982	0.1909	1948.43	1949.208	1	313.8	47.058823 F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1.M
		Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for								
ail6322097/refINP_012172_1	YII 094C	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate: 1 vs12p	3	4 0195	0 2182	2109 56	2109 454	2	535.1	37.5 A N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1 I
910022001101111 _012112.11	1120010	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for	U		0.2102	2100.00	2100.101	-	000.1	
- 100000071 - (IND- 040470-4)	V/II 00 10	the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively		0.4405	0.0000	0000.04	0000 454		447.0	
gil6322097 [ref]NP_012172.1]	YIL094C	decarboxylated to alpha-ketoadlpate; Lys12p Homo-isocitrate debydrogenase, an NAD-linked mitochondrial enzyme required for	2	3.1195	0.3066	2083.01	2083.454	1	417.9	47.22222 A.NVKPVKSVEGEKGKPIDMV.I
		the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively								
gi 6322097 ref NP_012172.1	YIL094C	decarboxylated to alpha-ketoadipate; Lys12p	2	4.5248	0.3947	2554.77	2556.012	1	418.9	43.18182 F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1R4.E
		Phosphoinositide PI4.5P(2) binding protein, forms a complex with SIm2p; acts								
		downstream of Mss4p in a pathway regulating actin cytoskeleton organization in								
gi 6322086 ref NP_012161.1	YIL105C	response to stress; subunit of and phosphorylated by the TORC2 complex; SIm1p	3	4.632	0.385	3312.26	3310.754	1	959.1	36.53846 N.VDPQFEWDNFISRDPNFLLPNLPMRTF.K
		Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts								
		downstream of Mss4p in a pathway regulating actin cytoskeleton organization in								
gi 6322086 ref NP_012161.1	YIL105C	response to stress; subunit of and phosphorylated by the TORC2 complex; SIm1p	2	3.4895	0.176	2032.61	2032.411	7	396.6	53.125 F.ISRDPNFLLPNLPMRTF.K
		Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts								
		downstream of Mss4p in a pathway regulating actin cytoskeleton organization in								
gij6322086 ret NP_012161.1	YIL105C	response to stress; subunit of and phosphorylated by the TORC2 complex; SIm1p	2	3.8831	0.1579	1629.27	1627.942	1	1264.5	16.92308 F.ISRDPNFLLPNLPM.R
		Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts								
	VII 1050	downstream of Mss4p in a pathway regulating actin cytoskeleton organization in	2	E 6000	0.4400	2404 04	2400.050	4	700 5	
gilo322000[rei]NP_012161.1	TIL 105C	response to stress; subunit or and phosphorylated by the TOKG2 complex; SIm1p	3	5.689.0	0.4482	3461.01	3400.858	1	120.5	21.11113F.N2VIUTPIQZETETW2UTNZETI151K4U1P1N2F1L1L1P1N2L1P1M\$R411F1.K
		Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts								
ail6322086/refIND_012161_1	VII 105C	downstream of Mss4p in a pathway regulating actin cytoskeleton organization in	3	4 3104	0 3107	3443 36	3440 959	1	1073 5	
3/0022000/reiliar_012101.1	1121030	response to stress, subunit of and phosphorylated by the roncez complex, simplex	3	4.0104	0.5137	3443.30	3440.000		10/0.0	

gi 6322086 ref NP_012161.1	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; SIm1p	3	4.3328	0.2903	3464.45	3464.858	1	823.6	31.48148 F.N2V1D1P1Q2F1E1W2D1N2F1I1S1R4D1P1N2F1L1L1P1N2L1P1M1R4T1F1.K
gi 6322086 ref NP_012161.1	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; SIm1p	3	4.7194	0.3333	3349.37	3348.754	1	547.9	28.846153 N.V1D1P1Q2F1E1W2D1N2F111S1R4D1P1N2F1L1L1P1N2L1P1M1R4T1F1.K
gi 6322086 ref NP_012161.1	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; SIm1p	2	3.9853	0.2176	2055.53	2057.411	1	498.8	56.25 F.I1S1R4D1P1N2F1L1L1P1N2L1P1M1R4T1F1.K
gi 6322086 ref NP_012161.1	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; SIm1p	2	3.463	0.2161	2492.41	2493.816	1	343.6	42.105263 Q.F1E1W2D1N2F111S1R4D1P1N2F1L1L1P1N2L1P1M1.R
gi 6322086 ref NP_012161.1 gi 6322083]ref NP_012158.1	YIL105C YIL108W	Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; SIm1p Putative metalloprotease; Yil108wp	2 2	3.3337 3.0876	0.1855	2465.85 2218.15	2466.816 2216.414	1	435.7 417.2	47.368423 Q.FEWDNFISRDPNFLLPNLPM.R 50 N.S1T1G1A151P1P111F1P1K2E1E1C1T1W2N2R4L1.D
gi 6322083 ref NP_012158.1 gi 6322083 ref NP_012158.1	YIL108W	Putative metalloprotease; YiI108wp Putative metalloprotease; YiI108wp	3	4.5239	0.2807	2237.99	2239.528	1	781.3	38.88889 K.11V1Q2V1Q2H3P1Q2L1P1P1111Y1P111H3N2Q2.F
gil6322063[ref]NP_012158.1]	YIL 108W	Putative metalloprotease: Vil108wp	2	3 6205	0.4210	2230.47	2239.528	1	541 1	44 11765 O V1O2H3P1O2I 1P1P1I1T1Y1P1I1H3N2O2F1F1 K
gi 6322083 ref NP_012158.1	YIL108W	Putative metalloprotease, Y1108wp Putative metalloprotease; Y1108wp Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p;	2	3.1926	0.2552	1906.43	1907.16	1	521.5	50 Q.V1Q2H3P1Q2L1P1P1HTTY1P1HH3N2Q2.F
gi 6322082 ref NP_012157.1	YIL109C	Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the birding of the Sec13 complex to EP membranes; bonglogues to Lette and Letter;	2	3.605	0.219	2186.37	2187.376	1	425.6	50 Y.Q2H3L1Y1D1D1I1D1P1P1P1L1N2E1D1G1L1I1V1.R
gi 6322082 ref NP_012157.1	YIL109C	Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the	2	3.8209	0.3672	2326.59	2326.555	1	241.9	36.842106 Y.FKIPLDSENNEESADQINMM.D
gi 6322082 ref NP_012157.1	YIL109C	binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p; Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the	2	3.6807	0.3314	1830.37	1831.081	1	546.3	63.333332 H.FYPGFSGKNPNDIVKF.S
gi 6322082 ref NP_012157.1	YIL109C	binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p; Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the	2	3.8046	0.4023	2178.33	2179.378	1	424.4	47.22222 F.KIPLDSENNEESADQINMM.D
gi 6322082 ref NP_012157.1	YIL109C	binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p; Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the	2	3.1645	0.2089	2350.55	2351.555	1	362.2	39.473686 Y.F1K2I1P1L1D1S1E1N2N2E1E1S1A1D1Q2I1N2M1M1.D
gi 6322082 ref NP_012157.1	YIL109C	binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p; Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the	3	4.1436	0.3114	2323.04	2320.564	1	777.3	46.05263 Y.QHLYDDIDPPPLNEDGLIVR.C
gi 6322082 ref NP_012157.1	YIL109C	binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p; Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the	2	3.4252	0.351	2222.01	2223.458	1	397.4	50 G.Q2T1H3F1Y1P1G1F1S1G1K2N2P1N2D111V1K2F1.S
gi 6322082 ref NP_012157.1	YIL109C	binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p; Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the	2	3.161	0.3564	2197.69	2197.458	1	341	50 G.QTHFYPGFSGKNPNDIVKF.S
gi 6322082 ref NP_012157.1	YIL109C	Sec24p Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the birding of the Sec13 complex to ER membranes: homologous to Lating and Lasin;	2	4.61	0.4688	2201.33	2203.378	1	1142	61.11111 F.K2I1P1L1D1S1E1N2N2E1E1S1A1D1Q2I1N2M1M1.D
gi 6322082 ref NP_012157.1	YIL109C	Sec24p Sec24p Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the birding of the Sec32 complex to ER membranes: bonefocus to L tota and test and	2	3.0054	0.158	970.01	970.205	1	886.7	92.85714 L.L1T1K2I1P1Q2I1F1.Q
gi 6322082 ref NP_012157.1	YIL109C	Sec24p Putative mitochondrial porin (voltage-dependent anion channel), related to Por1p but not required for mitochondrial membrane permeability or mitochondrial osmotic	2	4.6898	0.511	1848.19	1851.081	1	528.9	63.333332 H.F1Y1P1G1F1S1G1K2N2P1N2D1I1V1K2F1.S
gi 6322077 ref NP_012152.1	YIL114C	stability; Por2p Putative mitochondrial porin (voltage-dependent anion channel), related to Por1p but not required for mitochondrial membrane permeability or mitochondrial osmotic	1	3.3795	0.2348	1408.54	1408.559	2	292	70 LFNRDFFHTNPL.S
gi 6322077 ref NP_012152.1	YIL114C	stability; Por2p Putative mitochondrial porin (voltage-dependent anion channel), related to Por1p but not required for mitochondrial membrane permeability or mitochondrial osmotic certability. Bordoni	2	3.0883	0.1853	1427.61	1426.559	3	491.7	70 LF1N2R4D1F1F1H3T1N2P1L1.S
gil6322070 ref NP_012152.1	YIL121W	Multidrug transporter required for resistance to quinidine, barban, cisplatin, and bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR): Odr2o	2	2.9071	0.2989	2006.47	2007,114	1	636.6	53.125 T.S1S1111R4E1N2D1F1E1D1E1L1A1F1S1M1.0
gi 6322070 ref NP_012145.1	YIL121W	Multidrug transporter required for resistance to quinidine, barban, cisplatin, and bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Odd2p	2	2.9133	0.2783	1880.39	1880.111	1	669.7	59.375 E.SVKPEPEITAPPHSRFS.R
gi 6322070 ref NP_012145.1	YIL121W	Multidrug transporter required for resistance to quinidine, barban, cisplatin, and bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr2p	1	2.809	0.2016	1473.91	1474.756	2	241.4	54.166668 K.S1Y1L1N2R4A1P111L1V1L1P1T1.V
gi 6322070 ref NP_012145.1	YIL121W	Multidrug transporter required for resistance to quinidine, barban, cisplatin, and bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr2p	1	2.9141	0.1936	1456.79	1457.756	2	286.1	58.333332 K.SYLNRAPILVLPT.V

		Multidrug transporter required for resistance to quinidine, barban, cisplatin, and								
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conterring multiple drug resistance (MFS-MDR); Qdr2p Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	2	3.3725	0.2066	1476.07	1474.756	2	555.5	70.83333 K.S1Y1L1N2R4A1P1I1L1V1L1P1T1.V
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Odr29 Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	2	4.3178	0.2347	1788.01	1788.933	3	333.5	60.714287 R.S1K2L1L1E1E1H3D1N2D1L1N2L1V1Q2.R
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Odr2y Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	3	3.8381	0.2991	2046.8	2047.253	7	402.6	29.411766 R.T1E1S1V1K2P1E1P1E1I1T1A1P1P1H3S1R4F1.S
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Odr29 Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	3	4.0847	0.2672	1900.34	1903.111	1	1073.4	43.75 E.S1V1K2P1E1P1E1I1T1A1P1P1H3S1R4F1S1.R
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Odr29 Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	2	3.9691	0.3944	1813.01	1815.032	1	1103	73.333336 E.S1V1K2P1E1P1E1I1T1A1P1P1H3S1R4F1.S
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr29 Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	2	4.0109	0.3573	1904.09	1903.111	1	1138.1	68.75 E.S1V1K2P1E1P1E1I1T1A1P1P1H3S1R4F1S1.R
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr2p Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	2	3.9547	0.3318	1734.11	1735.076	3	599.6	50 K.S1Y1L1N2R4A1P111L1V1L1P1T1V1R4.K
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr2p Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	3	4.3189	0.1618	1734.8	1735.076	4	1092.4	50 K.S1Y1L1N2R4A1P111L1V1L1P1T1V1R4.K
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr2p Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	1	2.7616	0.2513	1343.49	1344.437	4	393.5	55 S.L1H3L1D1N2P1D1Y1E1T1L1.E
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr2p Multidrug transporter required for resistance to quinidine, barban, cisplatin, and	2	4.0159	0.3386	1830.13	1830.958	1	1197.1	71.42857 S.I111R4E1N2D1F1E1D1E1L1A1E1S1M1.Q
gi 6322070 ref NP_012145.1	YIL121W	bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr2p	2	3.8584	0.3172	1917.25	1919.036	1	701.5	50 S.S1I111R4E1N2D1F1E1D1E1L1A1E1S1M1.Q
gi 6322067 ref NP_012142.1	YIL124W	NADPH-dependent 1-acyl dihydroxyacetone phosphate reductase found in lipid particles and ER; involved in phosphatidic acid biosynthesis and required for spore germination; capable of metabolizing mammalian steroid hormones; Ayr1p	1	3.6557	0.3656	1518.67	1519.778	1	859.2	62.5 Y.KLDISKPEEIVTF.S
gi 6322067 ref NP_012142.1	YIL124W	NADPH-dependent 1-acyl dihydroxyacetone phosphate reductase found in lipid particles and ER; involved in phosphatidic acid biosynthesis and required for spore germination; capable of metabolizing mammalian steroid hormones; Ayr1p	1	4.0553	0.3329	1535.64	1534.778	1	802.5	62.5 Y.K2L1D111S1K2P1E1E111V1T1F1.S
gi 6322067 ref NP_012142.1	YIL124W	NADPH-dependent 1-acyl dihydroxyacetone phosphate reductase found in lipid particles and ER; involved in phosphatidic acid biosynthesis and required for spore germination; capable of metabolizing mammalian steroid hormones; Ayr1p	2	3.704	0.3524	1618.47	1618.827	5	507.8	57.692307 T.DIADKRPLPETSIY.N
gi 6322067 ref NP_012142.1	YIL124W	NADPH-dependent 1-acyl dihydroxyacetone phosphate reductase found in lipid particles and ER; involved in phosphatidic acid biosynthesis and required for spore germination; capable of metabolizing mammalian steroid hormones; Ayr1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	4.3531	0.2196	1520.39	1519.778	1	1326.2	79.16667 Y.KLDISKPEEIVTF.S
gi 6322066 ref NP_012141.1	YIL125W	catalyzes a key step in the tricarboxylic acid (1CA) cycle, the oxidative decarboxyliation of alpha-ketoglutarate to form succinu/CAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	4.5465	0.3422	2125.65	2124.281	1	1654.8	71.875 L.RDSLNSYPNLEEIVWCQ.E
gi 6322066 ref NP_012141.1	YIL125W	catalyzes a key step in the thrcarboxylic acid (1 CA) cycle, the oxidative decarboxyliation of alpha-ketoglutarate to form succinity-ICAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	3.7302	0.3418	2236.23	2237.44	1	639.9	50 Q.LRDSLNSYPNLEEIVWCQ.E
gi 6322066 ref NP_012141.1	YIL125W	catalyzes a key step in the thrcarboxylic acid (1 CA) cycle, the oxidative decarboxyliation of alpha-ketoglutarate to form succinity-ICAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	5.0315	0.4001	1996.45	1996.15	1	1139.8	70 L.RDSLNSYPNLEEIVWC.Q
gi 6322066 ref NP_012141.1	YIL125W	catalyzes a key step in the thrcarboxylic acid (1 CA) cycle, the oxidative decarboxyliation of alpha-ketoglutarate to form succinity-ICAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	2.9816	0.186	1836.79	1836.011	1	532.7	57.14286 L.RDSLNSYPNLEEIVW.C
gi 6322066 ref NP_012141.1	YIL125W	catalyzes a key step in the tricarboxylic acid (1CA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinu/CAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	4.5339	0.4899	2436.45	2436.65	1	781.7	47.368423 F.AQLRDSLNSYPNLEEIVWCQ.E
gi 6322066 ref NP_012141.1	YIL125W	catalyzes a key step in the thrcarboxylic acid (1 CA) cycle, the oxidative decarboxyliation of alpha-ketoglutarate to form succinu/CAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	3.1592	0.2546	2260.61	2262.44	3	402.6	41.17647 Q.L1R4D1S1L1N2S1Y1P1N2L1E1E111V1W2C1Q2.E
gi 6322066 ref NP_012141.1	YIL125W	catalyzes a key step in the thrcarboxylic acid (1 CA) cycle, the oxidative decarboxyliation of alpha-ketoglutarate to form succinu/CAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	3.1764	0.4363	2023.45	2024.114	1	617.8	50 L.SLPHGYDGQGPEHSSGRLE.R
gi 6322066 ref NP_012141.1	YIL125W	catalyzes a key step in the thrcarboxylic acid (1 CA) cycle, the oxidative decarboxyliation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	5.0714	0.461	1728.71	1726.97	1	1723.7	82.14286 Q.WIIEDIEHGKSIGTK.E
gi 6322066 ref NP_012141.1	YIL125W	calaryzes a key step in the incarboxylic and (LCA) cycle, the oxidative decarboxylication of alpha-ketoglutarate to form succint/LCAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	3	4.1519	0.2605	1789.22	1788.057	1	1358.4	45 K.HDLDKEINLGPGILPR.F
gi 6322066 ref NP_012141.1	YIL125W	calaryzes a key step in the incarboxylic and (LCA) cycle, the oxidative decarboxylication of alpha-ketoglutarate to form succint/LCAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	4.5378	0.4275	1790.55	1788.057	1	963.8	63.333332 K.HDLDKEINLGPGILPR.F
gi 6322066 ref NP_012141.1	YIL125W	calaryzes a key step in the incarboxylic and (LCA) cycle, the oxidative decarboxylication of alpha-ketoglutarate to form succinity-ICAA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which	2	4.4313	0.3598	2659.49	2660.04	1	991.2	45.652176 F.KSPKELATEILPHEPTNVPESTLK.E
gi 6322066 ref NP_012141.1	YIL125W	cataryzes a key step in the incanoxytic actor (LCA) cycle, the Oxtdative decarboxytation of alpha-ketoglutarate to form succint)-COA; Kgd1p Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which cataryzes a low tation is the transherities and CCA) reside the activities	3	4.7847	0.3608	2659.49	2660.04	1	1033.8	32.608696 F.KSPKELATEILPHEPTNVPESTLK.E
gi 6322066 ref NP_012141.1	YIL125W	decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p ATPase component of the ATP-dependent RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; required for expression	2	5.4951	0.4317	2002.31	2003.309	1	2112.6	67.64706 F.SKHDLDKEINLGPGILPR.F
gi 6322065 ref NP_012140.1	YIL126W	of early meiotic genes; essential helicase-related protein homologous to Snf2p; Sth1p	2	3.9545	0.4405	2637.39	2638.761	1	615	47.61905 L.HGEEVQPITDEEREKTDYYEVA.H

		ATPase component of the ATP-dependent RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; required for expression of early meiotic genes; essential helicase-related protein homologous to SnI2p;								
gi 6322065 ref NP_012140.1	YIL126W	Shthp ATPase component of the ATP-dependent RSC chromatin remodeling complex required for kinetochore function in chromosome segregation, required for expression	2	4.5043	0.2797	2667.43	2667.761	1	369.8	40.476192 LH3G1E1E1V1Q2P1I1T1D1E1E1R4E1K2T1D1Y1Y1E1V1A1.H
ail6322065/refINP 012140.1	YIL126W	of early meiotic genes; essential helicase-related protein homologous to Snf2p; Sth1p	2	3.3067	0.2903	2720.13	2721.944	1	520.9	36.95652 C.N2H3P1F1V1F1D1E1V1E1G1V1V1N2P1S1R4G1N2S1D1L1L1F1.R
9-11		ATPase component of the ATP-dependent RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; required for expression of activ medic approx - secaratia being care random protein benefaceus to Scho-								
gi 6322065 ref NP_012140.1	YIL126W	Sth1p	3	4.0873	0.2092	2555.39	2556.836	2	463.9	34.090908 T.TVLENNDGKRAEEKPESKSPAKK.T
		ATPase component of the ATP-dependent RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; required for expression of early meiotic genes; essential helicase-related protein homologous to Sn/2p;								
gi 6322065 ref NP_012140.1	YIL126W	Sth1p	3	5.0873	0.4319	2666.45	2667.761	1	907.4	35.714287 L.H3G1E1E1V1Q2P1I1T1D1E1E1R4E1K2T1D1Y1Y1E1V1A1.H
		required for kinetochore function in chromosome segregation; required for expression								
		of early meiotic genes; essential helicase-related protein homologous to Snf2p;								
gil6322065[ref]NP_012140.1]	YIL126W	Stn1p ATPase component of the ATP-dependent RSC chromatin remodeling complex	2	4.1861	0.3368	2666.93	2667.761	1	328.8	38.095238 L.H3G1E1E1V1Q2P1111D1E1E1R4E1K211D1Y1Y1E1V1A1.H
aile22206EleafIND_012140_1	VII 126W/	required for kinetochore function in chromosome segregation; required for expression of early meiotic genes; essential helicase-related protein homologous to Snf2p;	2	4 1379	0.2051	1779 60	1770.00	4	1700.2	
gilo322065[rei]INP_012140.1]	TILIZOVV	ATPase component of the ATP-dependent RSC chromatin remodeling complex	2	4.1378	0.2951	1778.09	1779.99	1	1709.2	73.07092 N.SIIDFIKERQSEQW.S
		required for kinetochore function in chromosome segregation; required for expression								
ail6322065/refINP 012140.1	YIL126W	of early meiotic genes; essential helicase-related protein homologous to Sht2p; Sth1p	2	4.6602	0.3774	1802.35	1800.99	1	1763.5	76.92308 N.S1I1ID1F1I1K2E1R4Q2S1E1Q2W2.S
51		ATPase component of the ATP-dependent RSC chromatin remodeling complex								
		required for kinetochore function in chromosome segregation; required for expression								
gi 6322065 ref NP_012140.1	YIL126W	Sth1p	2	5.6612	0.4645	2209.59	2210.563	1	1171.8	67.64706 L.K2K2E1V1E1K2D1L1P1D1K2V1E1K2V1I1K2C1.K
		ATPase component of the ATP-dependent RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; required for expression of early meiotic genes; essential helicase-related protein homologous to Snf2p;								
gi 6322065 ref NP_012140.1	YIL126W	Sth1p	2	5.1896	0.4111	2186.27	2186.563	1	840.8	58.823532 L.KKEVEKDLPDKVEKVIKC.K
		ATPase component of the ATP-dependent RSC chromatin remodeling complex required for kinetochore function in chromosome segregation: required for expression								
		of early meiotic genes; essential helicase-related protein homologous to Snf2p;								
gi 6322065 ref NP_012140.1	YIL126W	Sth1p N-terminally acetylated protein component of the large (60S) ribosomal subunit	2	3.6107	0.3031	1739.61	1739.931	1	617.8	57.14286 Q.AHHNIPYLRDSPFTA.A
		binds to 5.8 S rRNA; has similarity to RpI16Bp, E. coli L13 and rat L13a ribosomal								
gi 6322058 ref NP_012133.1	YIL133C	proteins; transcriptionally regulated by Rap1p; Rpl16ap	2	3.6656	0.2879	1950.85	1951.319	1	516.8	53.125 F.EGIPPPYDKKKRVVVPQ.A
		binds to 5.8 S rRNA; has similarity to Rpl16Bp, E. coli L13 and rat L13a ribosomal								
gi 6322058 ref NP_012133.1	YIL133C	proteins; transcriptionally regulated by Rap1p; Rpl16ap	2	3.5485	0.2719	1974.69	1975.319	1	446.7	50 F.E1G111P1P1P1Y1D1K2K2K2R4V1V1V1P1Q2.A
		N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rol16Bo, E, coli L13 and rat L13a ribosomal								
gi 6322058 ref NP_012133.1	YIL133C	proteins; transcriptionally regulated by Rap1p; Rpl16ap	1	2.2041	0.2832	1104.4	1104.257	2	148.8	62.5 F.NKTRGPFHF.R
		N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rol16Bp. E. coli L13 and rat L13a ribosomal								
gi 6322058 ref NP_012133.1	YIL133C	proteins; transcriptionally regulated by Rap1p; Rpl16ap	1	2.3137	0.1647	1119.63	1120.257	1	174	62.5 F.N2K2T1R4G1P1F1H3F1.R
gi 6322054 ref NP_012129.1 gi 6322054 ref NP_012129.1	YIL137C	Putative metalloprotease; Tma108p	3	4.4084	0.1682	3080.06	3082.392	1	866	30.769232 L.S1T1E1E1K2D1Q2L1E1D1V1P1Y1Q2V1P1L1F1G1V1L1P1D1G1K2M1D1.T
gi 6322054 ref NP_012129.1	YIL137C	Putative metalloprotease; Tma100p	3	5.7339	0.2927	2964.86	2966.303	1	1643.5	36 L.S1T1E1E1K2D1Q2L1E1D1V1P1Y1Q2V1P1L1F1G1V1L1P1D1G1K2M1.C
gi 6322054 ref NP_012129.1	YIL137C	Putative metalloprotease; Tma108p	2	2.9892	0.1969	2152.93	2150.57	2	229.8	38.88889 I.DRASLTSSKLQSFLKKKIV.I
gi 6322054 ref NP_012129.1	YIL137C	Putative metalloprotease; Tma108p Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required	3	4.5742	0.3329	3312.98	3314.671	1	1021.9	29.464287 L.S1T1E1E1K2D1Q2L1E1D1V1P1Y1Q2V1P1L1F1G1V1L1P1D1G1K2M1D1T1K2.N
gi 6322049 ref NP_012124.1	YIL142W	for the assembly of actin and tubulins in vivo; Cct2p	2	3.1883	0.1861	1835.65	1836.904	1	649.2	56.666668 A.T1D1Q2T1L1D1E1A1E1R4S1L1H3D1A1L1.S
gi 6322049 ref NP_012124.1	YIL142W	for the assembly of actin and tubulins in vivo; Cct2p	2	3.867	0.2118	2222.43	2221.537	1	1083.2	52.77778 C.KLGECDVIEEIMLGEQPFL.K
ail6322049/refINP_012124_1	YII 142W/	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo: Cct2p	2	6 1689	0 3948	2519 27	2520 887	1	1571.9	52 499996 C K2I 1G1E1C1D1V1I1E1E1I1M1I 1G1E1O2D1E1I 1K2E1 S
giloozzo+oliciliti _012124.11	11214200	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required	2	0.1005	0.0040	2010.27	2020.007		10/1.0	
gi 6322049 ref NP_012124.1	YIL142W	for the assembly of actin and tubulins in vivo; Cct2p Suburit bata of the cutosolic chaparania Cct ring complex, related to Tcp1p, required	2	5.5037	0.3547	2499.45	2496.887	1	1807.1	55 C.KLGECDVIEEIMLGEQPFLKF.S
gi 6322049 ref NP_012124.1	YIL142W	for the assembly of actin and tubulins in vivo; Cct2p	2	5.1792	0.3652	2512.43	2512.887	1	755.7	52.499996 C.KLGECDVIEEIM@LGEQPFLKF.S
	VII 4 40W	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required	0	5 0500	0.0044	2520.00	2526 007		C00 5	
gi 6322049 ref NP_012124.1	YIL142W	for the assembly of actin and tubulins in vivo; Cct2p	2	5.2529	0.3211	2536.99	2536.887	1	688.5	52.499996 C.K2L1G1E1C1D1V11E1E111M\$L1G1E1Q2P1F1L1K2F1.S
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	5.1737	0.4745	2036.19	2037.097	1	1263.5	64.70589 Q.T1H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2.A
		Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa								
gi 6322225 ref NP_012300.1	YIR034C	pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	5.4625	0.4352	2109.51	2109.176	1	1373.2	61.11111 Q.T1H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1.L
		Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa								
gi 6322225 ref NP_012300.1	YIR034C	pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	4.4038	0.2943	2210.57	2211.396	1	775.9	57.894737 H.S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1L1V1K2.D
		Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa								
gi 6322225 ref NP_012300.1	YIR034C	pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	5.6023	0.3487	2453.63	2453.642	1	2238.4	61.904762 Q.T1H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1L1V1K2.D
		Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa								
gi 6322225 ref NP_012300.1	YIR034C	pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.0926	0.2327	1669.43	1668.8	1	487.9	64.28571 T.S1R4G1G1P1F1D1E1I1P1Q2A1D1I1F1.I
		Sa nine dehydrogenase (NAD+ 1-lysine-forming), catalyzes the conversion of so								
gi 6322225 ref NP_012300.1	YIR034C	pine to L-lysine, which is the first step in the lysine biosynthesis pathway; Lys1p	1	2.4565	0.2278	1377.57	1378.584	2	242.7	63.636364 S.I1D1H3L1P1S1L1L1P1R4E1A1.S
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	1	2.4908	0.3231	1263.53	1264.468	4	207.5	60.000004 I.S1I1D1H3L1P1S1L1L1P1R4.E

gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.307	0.2867	2578.47	2579.83	1	789	47.61905 L.K2W2D111K2E1T1S1R4G1G1P1F1D1E111P1Q2A1D111F1.J
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	1	2.4327	0.3088	1176.45	1177.389	1	526.8	65 L.HKVGIPDANIL.K
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.4896	0.2494	2539.97	2541.74	2	242.3	33.333336 K.G1H3G1T1L1Y1D1L1E1F1L1E1N2D1Q2G1R4R4V1A1A1F1.G
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.2254	0.2055	2208.55	2209.428	1	683.9	52.77778 I.S1I1D1H3L1P1S1L1L1P1R4E1A1S1E1F1F1S1H3.D
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	1	3.2124	0.2647	1513.53	1514.706	1	371.6	54.166668 D.H3L1P1S1L1L1P1R4E1A1S1E1F1.F
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.5754	0.2939	1663.53	1662.883	1	344	65.38461 D.H3L1P1S1L1L1P1R4E1A1S1E1F1F1.S
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.1735	0.3067	2305.63	2306.595	1	560.7	40.476192 L.G1R4C1G1S1G1A1I1D1L1L1H3K2V1G111P1D1A1N2I1L1.K
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	6.3851	0.4127	2223.47	2223.335	1	1721	65.789474 Q.T1H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1L1.V
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	4.8106	0.3719	2121.25	2121.23	1	1062.2	52.77778 T.H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1L1.V
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	3	5.4858	0.3895	2453.75	2453.642	1	1118	41.6666664 Q.T1H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1L1V1K2.D
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	5.3938	0.3377	2351.67	2351.537	1	1181.8	55 T.H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1L1V1K2.D
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.895	0.2292	1558.79	1560.763	1	1459	83.33333 L.K2E1M1P1E1T1D1T1F1P1L1V1H3.E
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	2.9445	0.255	1464.91	1466.662	1	590.9	70.83333 I.S1I1D1H3L1P1S1L1L1P1R4E1A1.S
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	1	3.6867	0.3973	1465.47	1466.662	1	431.9	75 I.S1I1D1H3L1P1S1L1L1P1R4E1A1.S
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.2345	0.2468	1895.47	1893.131	1	436.2	50 S.I1D1H3L1P1S1L1L1P1R4E1A1S1E1F1F1.S
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	2	3.6105	0.3178	2007.13	2007.071	1	596.9	50 T.H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1.L
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	3	4.8602	0.391	2348.96	2351.537	1	1708.3	41.25 T.H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1L1V1K2.D
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	1	2.9961	0.3147	1191.46	1192.389	5	504.2	55 L.H3K2V1G111P1D1A1N2I1L1.K
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	1	2.8308	0.1703	1148.69	1148.336	1	488.7	72.22222 D.H3L1P1S1L1L1P1R4E1A1.S
gi 6322225 ref NP_012300.1	YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	1	3.1848	0.2558	1306.56	1306.549	1	866.5	68.181816 L.L1H3K2V1G111P1D1A1N2I1L1.K
gi 6322228 ref NP_012303.1	YIR037W	Initial peroxidase that functions as a hydroperoxide receptor to sense intracellular hydroperoxide levels and transduce a redox signal to the Yap1 p transcription factor; Hyr1p	2	3.5374	0.3246	1690.79	1687.936	1	844.9	64.28571 LAPVDKKGQPFPFDQL.K
gi 6322228 ref NP_012303.1	YIR037W	hydroperoxide levels and transduce a redox signal to the Yap1p transcription factor; Hyr1p	2	3.033	0.1948	1705.97	1706.936	9	186.6	46.42857 LA1P1V1D1K2K2G1Q2P1F1P1F1D1Q2L1.K
gi 6322458 ref NP_012532.1	YJL002C	Alpha subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost1p	3	4.6026	0.2544	3574.22	3574.967	1	561.9	25.78125 T.TAPGDDGESEIRYGIIQFPNAISPQEEVSLVIK.S
gi 6322458 ref NP_012532.1	YJL002C	Alpha subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost1p	2	3.3898	0.2918	1752.43	1752.816	1	240.4	50 S.S1F1E1E1Y1H3P1P1N2D1E1S1L1L1G1.K
gi 6322458 ref NP_012532.1	YJL002C	Alpha subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost1p	2	4.1847	0.3683	1880.05	1882.99	1	519	53.333336 S.S1F1E1E1Y1H3P1P1N2D1E1S1L1L1G1K2.A
gi 6322458 ref NP_012532.1	YJL002C	Alpha subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost1p	2	4.062	0.3148	1865.09	1862.99	1	533.9	56.666668 S.SFEEYHPPNDESLLGK.A
gi 6322452 ref NP_012526.1	YJL008C	the assembly of actin and tubulins in vivo; Cct8p	2	3.3924	0.3027	1930.31	1931.023	2	336.1	41.17647 A.TQNNLDDIERAIDDGVAA.V
gi 6322452 ref NP 012526.1	YJL008C	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct8p	2	4.021	0.2141	2049.53	2049.21	1	439.8	53.125 E.S1D1E1G1V1K2D1I1R4E1E1N2I1Y1D1M1L1.A
gil6322452/refINP_012526_1	YJL008C	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo: Cct8p	2	5,1381	0.4473	2017 59	2018.318	1	691.4	57.894737 C.GATPLPRLGAPTPEELGLVE T
aile2224521rofNP_012020.1	VII 0000	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	<u>~</u>	E 4400	0.440	2017.00	2010.010	4	005.0	
91002240210114F_012020.1	I JLUUOU	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	2	1.000	0.449	2003.09	2041.310	-	000.0	
gijb322452 ret NP_012526.1	YJLU08C	the assembly of actin and tubulins in vivo; Cct8p Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	2	4.0067	0.3522	2026.45	2027.21	3	413.6	46.875 E.SDEGVKDIREENIYDMLA
gi 6322452 ref NP_012526.1	YJL008C	the assembly of actin and tubulins in vivo; Cct8p	2	4.0753	0.4722	1889.51	1890.187	1	955.5	61.764706 A.TPLPRLGAPTPEELGLVE.T

gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.7997	0.265	1633.87	1634.737	2	772.7	65.38461 Y.DDLKTELEDNLSKN.N
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.2151	0.1967	1796.59	1797.913	1	383.7	60.714287 S.YDDLKTELEDNLSKN.N
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.2623	0.2751	1468.35	1470.638	1	750.8	77.27273 Q.L1G1Q2E1P1P1E1W2V1R4E1L1.V
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.9717	0.4072	1684.43	1682.874	1	899.6	69.230774 Q.TQLGQEPPEWVREL.V
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.1153	0.1798	1946.67	1949.136	8	274.3	40.625 Q.T1Q2L1G1Q2E1P1P1E1W2V1R4E1L1V1G1S1.H
aji/42742256jrefINP 012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophaqic vacuolar fusion; Vtc4p	2	4.8625	0.2812	2348.53	2349.473	1	686.2	52.63158 Y.DDLKTELEDNLSKNNGQWTQ.E
oild2742256irefINP_012522.2IY.II_012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones: involved in pon-autophagic vacuolar fixion; Vicdo	2	4 8634	0 2853	2543 17	2541 649	1	703 5	50 S Y1D1D11 1K2T1E11 1E1D1N21 1S1K2N2N2G102W2T102 E
	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter	2	2 2244	0.4074	4044.72	4040.047		240.4	
gij42742256jretjNP_012522.2 YJL012C	cnaperones; involved in non-autopnagic vacuolar rusion; vtc4p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter	2	3.3241	0.1871	1914.73	1912.017	2	340.1	50 S.YDDLKTELEUNLSKNN.G
gi 42742256 ref NP_012522.2 YJL012C	chaperones; involved in non-autophagic vacuolar fusion; Vtc4p Vacuolar membrane protein involved in vacuolar polyphosphate accumulation;	2	3.0139	0.1569	2122.85	2121.2	2	342.3	47.058823 S.Y1D1D1L1K2T1E1L1E1D1N2L1S1K2N2N2G1Q2.W
gi 42742256 ref NP_012522.2 YJL012C	functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.9457	0.3183	2096.41	2097.2	1	659.2	58.823532 S.YDDLKTELEDNLSKNNGQ.W
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	5.557	0.3253	1814.69	1816.913	1	2518.3	82.14286 S.Y1D1D1L1K2T1E1L1E1D1N2L1S1K2N2.N
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	5.1821	0.36	2512.11	2512.649	1	524.9	55 S.YDDLKTELEDNLSKNNGQWTQ.E
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.9181	0.1905	2019.19	2019.151	1	564.2	59.375 Y.I1S1Y1D1D1L1K2T1E1L1E1D1N2L1S1K2N2.N
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	3	4.0347	0.2191	3525.92	3526.746	1	1159.3	30.172413 Y.DDLKTELEDNLSKNNGQWTQELETDFLESLE
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	1	2.4417	0.2918	1381.56	1382.661	1	399.6	68.181816 Q.MDVDIRKPPLPT.N
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	4.0794	0.333	1992.23	1991.176	1	1214.2	62.5 F.F1D1H3Y1F1N2G1D1Q2I1S1K2I1P1K2G1T1.T
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.4212	0.1972	2240.37	2241.458	1	444	44.444447 F.F1D1H3Y1F1N2G1D1Q2I1S1K2I1P1K2G1T1T1F1.D
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	4.9156	0.4006	2087.63	2089.277	1	1299.9	73.52941 Q.T1Q2L1G1Q2E1P1P1E1W2V1R4E1L1V1G1S1H3.L
gi 42742256 ref NP_012522.2 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	4.1246	0.3859	2065.63	2063.277	1	1247.5	67.64706 Q.TQLGQEPPEWVRELVGSH.L
ail42742256lrefINP 012522.21 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+ATPase activity and vacuolar transporter chaperones: involved in non-autophagic vacuolar fusion; Vtc4p	2	3.7406	0.1908	1990.47	1989.114	1	662.2	60.000004 M.VREDNEDGVDRTHKNW.R
aii/27/2256/ref/NP_012522.21_VII.0420	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaparonase involved in pon-autophatic vacuolar driver. Vicen	n	3 6649	0 1652	2147 27	2140 207	1	540 8	50 T M1\/1R4E1D1N2E1D1@1\/4D104T4U3K2N2M2 D
9172172200101111 _012022.21 1JL0120	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation	2	3.0040	0.1002	2141.31	2143.307	1	J+U.0	
gi 42742256 ref NP_012522.2 YJL012C	functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.6276	0.2421	2119.37	2120.307	1	791.8	59.375 T.MVREDNFDGVDRTHKNW.R
gi 42742256 ref NP_012522.2 YJL012C	vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	1	2.7131	0.2406	1458.78	1459.738	2	309.6	59.090908 T.ICVPVRVEPKVY.F

gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	2.9897	0.1819	1362.17	1362.528	1	281.4	75 K.E1R4H3V1N2D1F1L1K2G1K2.Y
gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	4.2973	0.1607	1688.61	1686.967	2	545.2	65.38461 M.RKEGKKPMNEIENL.E
gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.1015	0.281	1995.55	1998.151	1	510.3	53.125 Y.ISYDDLKTELEDNLSKN.N
gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	2.9947	0.2472	1934.51	1934.094	1	262.5	50 T.MVREDNFDGVDRTHKN.W
gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	1	3.322	0.2661	1317.75	1318.515	3	811.2	75 T.DIGVDWPFKQL.D
gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.8685	0.2816	1320.03	1318.515	4	1000.2	75 T.DIGVDWPFKQL.D
gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.4191	0.2307	1333.33	1332.515	1	1426.8	85 T.D111G1V1D1W2P1F1K2Q2L1.D
gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	2	3.1794	0.262	1581.29	1581.769	1	590.2	66.66667 T.QLGQEPPEWVREL.V
gi 42742256 ref NP_012522.2	YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtdp	2	4.5364	0.3938	1701.59	1702.874	1	784	65.38461 Q.T1Q2L1G1Q2E1P1P1E1W2V1R4E1L1.V
gi 27808709 ref NP_012515.2	YJL019W	for nuclear fusion, localizes to the spindle pole body half bridge, interacts with DnaJ- like chaperone Jem 1p and with centrin homolog Cdc3 1p; Mps3p Essential integral membrane protein required for spindle pole body duplication and	2	3.1928	0.3332	1916.47	1918.114	1	765.1	67.85714 N.KQEIWEEITNRLETQ.Q
gi 27808709 ref NP_012515.2	YJL019W	for nuclear fusion, localizes to the spindle pole body half bridge, interacts with DnaJ- like chaperone Jem1p and with centrin homolog Cdc31p; Mps3p Essential integral membrane protein required for spindle pole body duplication and for nuclear fusion. localizes to the spindle pole body half bridge, interacts with DnaJ-	2	3.8576	0.3228	2262.13	2263.52	1	315.2	39.473686 L.N2H3L1T1S1P1T1W2R4Q2G1S1G1V1Q2P111E1L1L1.T
gi 27808709 ref NP_012515.2	YJL019W	like chaperone Jem 1p and with centrin homolog Cdc31p; Mps3p Essential integral membrane protein required for spindle pole body duplication and	2	3.5865	0.3581	1891.71	1893.115	1	664.4	56.25 L.T1S1P1T1W2R4Q2G1S1G1V1Q2P111E1L1L1.T
gi 27808709 ref NP_012515.2	YJL019W	for nuclear rusion, localizes to the spinole pole body hair bridge, interacts with DhaJ- like chaperone Jem tp and with centrin homolog Cd21p; Mps3p Protein possibly involved in assembly of actin patches; interacts with an actin	2	4.0306	0.3598	2233.51	2234.52	1	325.2	42.105263 L.NHLTSPTWRQGSGVQPIELL.T
gi 14627173 ref NP_012514.2	YJL020C	assembly factor Las1/p and with the SH3 domains of 1 ype 1 myosins Myo3p and Myo5p; localized predominantly to cortical actin patches; Bbc1p Protein possibly involved in assembly of actin patches; interacts with an actin	2	3.6425	0.191	2968.77	2969.052	1	251.1	31.25 K.NEPYTETEEAEENEKTEPKPEFTPE.T
gi 14627173 ref NP_012514.2	YJL020C	assembly factor Las1/p and with the SH3 domains of 1 ype 1 myosins Myo3p and Myo5p; localized predominantly to cortical actin patches; Bbc1p Protein possibly involved in assembly of actin patches; interacts with an actin	2	3.9469	0.3442	1822.51	1823.081	1	591.5	60.000004 Q.I1V1S1E1F1K2D1E1V1I1Q2P1I1G1A1R4.T
gi 14627173 ref NP_012514.2	YJL020C	assembly factor Last7p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches; Bot1p Protein possibly involved in assembly of actin patches; interacts with an actin	3	5.3474	0.3751	4547.21	4548.797	1	913.1	24.324326 N.KNEPYTETEEAEENEKTEPKPEFTPETEHNEEPQMELL.A
gi 14627173 ref NP_012514.2	YJL020C	assembly factor Las1/p and with the SH3 domains of 1ype 1 myosins Myo3p and Myo5p; localized predominantly to cortical actin patches; Bbc1p Protein possibly involved in assembly of actin patches; interacts with an actin	3	3.8535	0.2028	2676.2	2673.798	1	527.2	30.681818 G.N2N2E1S1E1N2V1N2S1G1E1K2I1Y1P1Q2E1P1P1I1S1H3R4.T
gi 14627173 ref NP_012514.2	YJL020C	assembly factor Last7p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches; Bot1p Protein possibly involved in assembly of actin patches; interacts with an actin	2	3.5539	0.2601	1616.79	1617.802	1	652.6	57.692307 L.ALPKHNEVEEHVKS.S
gi 14627173 ref NP_012514.2	YJL020C	Assembly factor Last / p and winn the SH3 domains of 1 ype 1 myosins Myosp and MyoSp; localized predominantly to controlal actin patches; Bbc1p Protein possibly involved in assembly of actin patches; interacts with an actin	2	4.0004	0.2396	1789.35	1789.051	1	895.2	67.85714 L.K2E1N2E1K2K2I1V1P1E1P1I1N2R4A1.Q
gi 14627173 ref NP_012514.2	YJL020C	Assembly factor Last / p and win the SHS domains of type I myosins wyosp and MyoSp; localized predominantly to control a dcin patches; Bbc1p Protein possibly involved in assembly of actin patches; interacts with an actin	2	4.3284	0.3321	2905.53	2905.295	1	622	41.304348 Q.HKEKEEEEPEQLQELPRAIPVMPF.V
gi 14627173 ref NP_012514.2	YJL020C	Assembly factor Last / p and win the SHS domains of type I myosins wyosp and MyoSp; localized predominantly to control a dcin patches; Bbc1p Protein possibly involved in assembly of actin patches; interacts with an actin	2	3.875	0.329	1893.71	1894.181	1	683.5	56.666668 L.KENEKKIVPEPINRAQ.V
gi 14627173 ref NP_012514.2	YJL020C	assembly factor last // and with the Gris outname of year hypothypothypothypothypothypothypothypot	2	3.4545	0.3849	1639.23	1638.802	1	559.6	61.538464 L.A1L1P1K2H3N2E1V1E1E1H3V1K2S1.S
gi 14627173 ref NP_012514.2	YJL020C	absembly factor day to get a strain whith the Christ Outlines to tryper inflyosing mycop and Mycop; localized predominantly to cortical actin patches; Boctp Protein possibly involved in assembly of actin patches; interacts with an actin assembly forcer leaf or and with the SH2 domains of True Langeine Mycop and	3	4.112	0.2093	3020.96	3021.996	2	429.4	32.291664 H.EDREGDNDEEKEEEDSEENRRAALR.E
gi 14627173 ref NP_012514.2	YJL020C	assembly factor last the and with the of induction of the	3	4.4306	0.3171	3060.89	3061.996	2	408	31.25 H.E1D1R4E1G1D1N2D1E1E1K2E1E1E1D1S1E1E1N2R4R4A1A1L1R4.E
gi 14627173 ref NP_012514.2	YJL020C	Myo5p: localized predominantly to cortical actin patches; Bbc1p Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor I as17 and with the SH2 domains of True I myosine Myo3p and	3	4.6256	0.2588	4419.44	4420.623	1	612	21.527777 K.NEPYTETEEAEENEKTEPKPEFTPETEHNEEPQMELL.A
gi 14627173 ref NP_012514.2	YJL020C	MyoSp: localized predominantly to cortical actin patches; Bbc1p Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17o and with the SH3 domains of Two I myosins Myo3p and	2	4.6289	0.231	1766.19	1766.051	1	965.6	60.714287 L.KENEKKIVPEPINRA.Q
gi 14627173 ref NP_012514.2	YJL020C	Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	2.9256	0.2943	1704.47	1704.88	4	271.2	46.42857 L.ALPKHNEVEEHVKSS.A

gi 14627173 ref NP_012514.2	YJL020C	Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo3p; localized predominantly to cortical actin patches; Bbc1p	2	2.9307	0.338	1630.73	1629.943	3	515.6	56.666668 N.TAPPLPRAPPVPPATF.E
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	2	3.4968	0.3207	2758.43	2760.105	1	192.2	35.714287 M.E1K2E1E1P1L1L1N2E1D1K2E1R4T1V1L1F1P1I1K2Y1H3.E
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	2	3.4742	0.2762	2730.89	2729.105	1	179.2	40.476192 M.EKEEPLLNEDKERTVLFPIKYH.E
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	2	3.4539	0.2826	1468.19	1467.662	2	572.1	68.181816 Y.IKDPKESEFLFN.A
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	3	3.8739	0.2583	3021.29	3022.413	1	536.3	26.086956 K.E1M1E1K2E1E1P1L1L1N2E1D1K2E1R4T1V1L1F1P111K2Y1H3.E
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	2	3.714	0.2402	1700.67	1700.97	3	506.5	50 L.K2N2K2P1D1P1A111V1E1K2I1V1T1E1.A
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	3	5.5225	0.4104	3267.68	3266.747	1	1367	31 K.L1K2E1M1E1K2E1E1P1L1L1N2E1D1K2E1R4T1V1L1F1P111K2Y1H3.E
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	2	3.5085	0.2756	1797.63	1797.045	1	675.7	69.230774 N.E1D1K2E1R4T1V1L1F1P111K2Y1H3.E
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	3	3.8276	0.3054	2728.91	2729.105	2	456.7	30.952381 M.EKEEPLLNEDKERTVLFPIKYH.E
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	3	4.0577	0.3178	2893.01	2892.298	1	742.2	29.545454 E.M1E1K2E1E1P1L1L1N2E1D1K2E1R4T1V1L1F1P1I1K2Y1H3.E
gi 6322434 ref NP_012508.1	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunit; Rn2p	3	5.557	0.44	3231.47	3230.747	1	1759.6	35 K.LKEMEKEEPLLNEDKERTVLFPIKYH.E
gi 6322431 ref NP_012505.1	YJL029C	Component of the GARP (Golgi-associated retrograde protein) complex, Vps5rp- Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting; Vps53p	2	3.202	0.2394	1521.91	1522.739	1	590.4	58.333332 W.N2F1L1D1K2V11D11111T1TN2.F
gi 6322431 ref NP_012505.1	YJL029C	Component of the GARP (Solid-associated retrograde protein) complex, vps1p- Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting; Vps53p Component of the GARP (Golgi-associated attransphere) and a sorting of the solid sorting of the solid so	2	3.3671	0.2118	1505.89	1506.739	3	838.1	70.83333 W.NFLDKVIDIITTN.F
gi 6322431 ref NP_012505.1	YJL029C	Vps52p-Vps53p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting; Vps53p Component of the GABP (Golgi:securidate derivargate protein) complex, Vps51p-	2	3.0339	0.3833	1553.91	1552.9	1	682.8	65.38461 N.TIRLLOPVPPFSLA.G
gi 6322431 ref NP_012505.1	YJL029C	Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting; Vps53p	2	3.2965	0.2619	1569.65	1570.9	1	845.5	69.230774 N.T1I1R4L1L1Q2P1V1P1P1F1S1L1A1.G
gi 6322427 ref NP_012501.1	YJL033W	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis; Hca4p	2	3.5891	0.2235	1668.81	1666.971	2	526.5	57.692307 A.K2F1F1K2D1L1P111S1D1P1T1L1K2.G
gi 6322427 ref NP_012501.1	YJL033W	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis; Hca4p	2	3.8298	0.2671	2842.39	2843.889	1	812.2	39.583336 V.D1Y1S1H3G1H3N2P1S1N2S1V1D1D1D11111E1V1E1E1P1Q2T1L1.E
gi 6322427 ref NP_012501.1	YJL033W	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis; Hca4p	2	3.9477	0.2562	2811.99	2811.889	1	688.5	39.583336 V.DYSHGHNPSNSVDDDIIEVEEPQTL.E
gi 6322427 ref NP_012501.1	YJL033W	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis; Hca4p	3	4.0021	0.1629	3499.19	3498.606	1	716	24.166666 V.DYSHGHNPSNSVDDDIIEVEEPQTLEDLESL.T
gi 6322427 ref NP_012501.1	YJL033W	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis; Hca4p	3	7.6798	0.4251	3536.93	3536.606	1	1822	V.D1Y1S1H3G1H3N2P1S1N2S1V1D1D1D1I111E1V1E1E1P1Q2T1L1E1D1L1E1S1L 33.333336 1.T
gi 6322427 ref NP_012501.1	YJL033W	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 185 rRNA synthesis; Hca4p	2	4.4823	0.2633	1648.83	1649.971	1	1232.6	84.61539 A.KFFKDLPISDPTLK.G
gi 6322427 ref NP_012501.1	YJL033W	rutative inductional DEAD box have reincase, ingir-outy indinder suppression of a 01+ snoRNA processing mutant suggests an involvement in 185 rRNA synthesis; Hca4p Dead-box family ATP dependent helicase required for mRNA export from the nucleus: chatchar of the aversome commely renuired for 31 end formation of 5 PS	2	3.9832	0.3173	2309.51	2309.405	1	822.4	47.5 H.GHNPSNSVDDDIIEVEEPQTL.E
gi 6322411 ref NP_012485.1	YJL050W	RNA: Mr4p Dead-box family ATP dependent helicase required for mRNA export from the nucleus: co-factor of the exosome complex, required for 3' end formation of 8.8S	3	5.6442	0.4013	2554.01	2552.976	1	1165.5	39.772728 M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the nucleus; co-factor of the exosome complex, required for 3 end formation of 5.8S	2	4.0183	0.3311	2553.35	2552.976	1	461.1	43.18182 M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S	2	4.034	0.2948	2583.59	2581.976	1	453.7	43.18182 M.Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the nucleus; co-factor of the exosome complex, required for 3 end formation of 5.8S	3	7.3158	0.4058	2715.41	2714.169	1	1644.6	42.391304 T.M1Y111D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G111R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	rRNA; Mtr4p	2	3.296	0.1958	2186.49	2187.552	3	387	42.105263 D.S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
		Dead-box family ATP dependent helicase required for mRNA export from the nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S								
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gi 6322411 ref NP_012485.1	YJL050W	rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	3	4.9496	0.3964	2552.99	2552.976	4	611.8	30.681818 M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	3.5429	0.2624	2554.17	2552.976	1	554.2	45.454548 M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	3	5.8069	0.4133	2579.99	2581.976	1	1252.6	40.909092 M.Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G111R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	3	4.4368	0.3606	2684.15	2684.169	1	611.4	27.173912 T.MYIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	3.6063	0.2388	2684.75	2684.169	1	357.3	36.95652 T.MYIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	3	3.9316	0.2526	2784.5	2785.274	2	663.6	26.041666 N.TMYIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	3	4.9964	0.3846	3485.63	3485.925	1	1098.9	28.333334 M.YIDSPVNLLKPFNPTLPEGIRPAEEGEKSIC.A
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	3.1331	0.2885	1650.59	1650.962	1	815.7	60.714287 LLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	3.9082	0.3138	2161.27	2161.552	2	470.1	50 D.SPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	3	3.8139	0.2661	2159.78	2161.552	5	667.4	32.894737 D.SPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	3.9581	0.2966	1638.17	1637.854	1	1360.5	83.33333 Y.SRKHDLHEDMKQL.K
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	2.9479	0.2001	2078.65	2079.147	1	343.8	50 K.K2D1F1D1G1I1E1V1E1D1E1E1N2V1K2E1Y1.H
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3 end formation of 5.8S rRNs; Mr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	4.122	0.1835	1394.97	1394.627	2	1611.4	90 M.K2I1E1D1E1D1F1L1K2L1M1.K
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3 end formation of 5.8S rRNs; Mr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	4.092	0.2205	2417.45	2417.8	1	610.4	45.238094 Y.I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p Dead-box family ATP dependent helicase required for mRNA export from the	3	5.0878	0.331	2420	2417.8	1	1229.4	41.6666664 Y.I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus; co-factor of the exosome complex, required for 3 end formation of 5.8S rRNs; Mr4p Dead-box family ATP dependent helicase required for mRNA export from the	2	4.1226	0.3368	2580.23	2581.976	1	477.3	40.909092 M.Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	nucleus, co-factor or the exposition complex, required for send formation of 5.65 rRNA; Mrt4p Dead-box family ATP dependent helicase required for mRNA export from the surdewise in rate of the surgement employ, required for RNA export from the	2	3.6432	0.2699	2552.69	2552.976	1	405.5	40.909092 M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	RNA: Mirtap Dead-box family ATP dependent helicase required for a end winnetwork of 505 Dead-box family ATP dependent helicase required for RNA export from the suclaw: constort of the exposens complex, required for 3 and fermition of 5 PS	3	3.904	0.2321	2728.88	2730.169	1	622.8	26.086956 T.M\$Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G111R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	RNA: Mirtap Dead-box family ATP dependent helicase required for a end winnetwork of 505 Dead-box family ATP dependent helicase required for RNA export from the suclaw: constort of the exposens complex, required for 3 and fermition of 5 PS	3	6.4274	0.3679	2584.31	2581.976	1	1054.6	38.636364 M.Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G11R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	RNA: Mrt4p Dead-box family ATP dependent helicase required for mRNA export from the suclaus: concorrect manual expression and an another sector of the secto	3	4.864	0.3458	2552.3	2552.976	1	753.2	34.090908 M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	RNA; Mrt4p Dead-box family ATP dependent helicase required for RRNA export from the suclaw configured for the successory and the successory of the successory of the successory of the successory and the s	3	4.4956	0.3838	2681.63	2684.169	1	1208.8	32.608696 T.MYIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	RNA: Mirtap Dead-box family ATP dependent helicase required for RNA export from the nucleus: conjector of the exposure complex, required for RNA export from the	2	3.5725	0.2959	2712.25	2714.169	1	359.2	36.95652 T.M1Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G111R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	RNA: Mir4p Dead-box family ATP dependent helicase required for mRNA export from the nucleus: cractor of the exosome complex, required for 3' end formation of 5.85	2	2.9052	0.2229	2683.43	2684.169	1	300.7	32.608696 T.MYIDSPVNLLKPFNPTLPEGIRPA.E
gi 6322411 ref NP_012485.1	YJL050W	RNA: Mitration of the execution complex, required for Windows with the execution of the exe	2	4.013	0.3321	1673.51	1670.962	1	807.6	64.28571 L.L1K2P1F1N2P1T1L1P1E1G111R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	RNA; Mir4p Dead-box family ATP dependent helicase required for mRNA export from the	2	3.3956	0.3565	1783.69	1785.121	1	481.7	56.666668 N.L1L1K2P1F1N2P1T1L1P1E1G111R4P1A1.E
gi 6322411 ref NP_012485.1	YJL050W	rRNA; Mtr4p	3	4.7198	0.2381	2188.37	2187.552	1	885.4	40.789474 D.S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G111R4P1A1.E
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	3.817	0.3961	1769.27	1768.905	1	548.1	57.14286 A.T1Y1Q2E1R4D1P1A1N2L1P1W2G1S1L1.K
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	3.4521	0.3697	1710.25	1708.967	1	724.7	60.000004 L.AKVINDAFGIEEGLMT.T
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	3.9968	0.3271	2287.81	2286.62	1	625.8	50 N.C1L1A1P1L1A1K2V111N2D1A1F1G111E1E1G1L1M1T1.T

gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	4.586	0.4109	2142.59	2143.367	1	721.9	52.63158 D.S1T1G1V1F1K2E1L1D1T1A1Q2K2H3I1D1A1G1A1K2.K
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	4.6343	0.3774	1783.43	1783.031	1	1263.6	66.66667 T.V1S1H3D1D1K2H3I1I1I1D1G1V1K2I1A1.T
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	3.4159	0.3374	1878.63	1876.079	1	645.8	53.333336 A.TYQERDPANLPWGSLK.I
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	4.1489	0.3982	1762.73	1761.031	1	1192.4	63.333332 T.VSHDDKHIIIDGVKIA.T
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	2.9523	0.1556	1055.21	1054.275	1	746.1	83.33333 K.AVGKVLPELQ.G
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	3.1355	0.2645	1654.29	1654.745	1	547.8	65.38461 A.T1Y1Q2E1R4D1P1A1N2L1P1W2G1S1.S
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	2.9311	0.2297	1104.09	1104.252	3	197	66.66667 M.A1F1R4V1P1T1V1D1V1S1.V
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	2	3.0594	0.1756	2262.53	2263.62	3	291.8	32.5 N.CLAPLAKVINDAFGIEEGLMT.T
gi 6322409 ref NP_012483.1	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p Putative protein of unknown function, identified based on comparison to related yeast	2	3.6718	0.2825	2128.55	2129.286	1	398.3	47.22222 A.T1Q2K2T1V1D1G1P1S1H3K2D1W2R4G1G1R4T1A1.S
gi 13129172 ref NP_076894.1	YJL062W-A	species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Y[I062w-ap Putative protein of unknown function, identified based on comparison to related yeast	3	3.8405	0.3588	2614.91	2615.889	1	564	32.954548 F.L1H3K2D1N2D1F1A1D1V1P1I1P1P1I1D1P1Q2E1L1E1A1L1.K
gi 13129172 ref NP_076894.1	YJL062W-A	Species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Yjl062w-ap Putative protein of unknown function, identified based on comparison to related yeast	2	4.2957	0.2849	2615.51	2615.889	1	598.5	40.909092 F.L1H3K2D1N2D1F1A1D1V1P111P1P111D1P1Q2E1L1E1A1L1.K
gi 13129172 ref NP_076894.1	YJL062W-A	species; green fluorescent protein (GFP)-rusion protein localizes to the mitochondria; Yij062w-ap Putative protein of unknown function, identified based on comparison to related yeast	2	3.1558	0.3923	2472.71	2474.729	1	389	40.476192 L.HKDNDFADVPIPPIDPQELEAL.K
gi 13129172 ref NP_076894.1	YJL062W-A	species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; YjI062w-ap Putative protein of unknown function, identified based on comparison to related yeast	2	3.2083	0.1935	2763.57	2764.066	1	546.2	36.95652 H.F1L1H3K2D1N2D1F1A1D1V1P111P1P111D1P1Q2E1L1E1A1L1.K
gi 13129172 ref NP_076894.1	YJL062W-A	Species, green nuclescent protein (or -) rusion protein localizes to the mitocholdna, Y[lo62w-ap Putative protein of unknown function, identified based on comparison to related yeast	2	3.62	0.23	2616.03	2615.889	1	421.8	34.090908 F.L1H3K2D1N2D1F1A1D1V1P1I1P1P1I1D1P1Q2E1L1E1A1L1.K
gi 13129172 ref NP_076894.1	YJL062W-A	species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; YjI062w-ap Mitochondrial membrane protein of unknown function, contains no hydrophobic.	2	3.2252	0.1953	2587.77	2587.889	3	328.7	31.818182 F.LHKDNDFADVPIPPIDPQELEAL.K
gi 6322395 ref NP_012469.1	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic Mitochondrial membrane protein of unknown function, contains no hydrophobic	2	3.277	0.3627	1928.29	1931.196	1	702.7	70 K.LRDIDEYDNPLLPLPF.N
gi 6322395 ref NP_012469.1	YJL066C	stretches; Mpm1p Mitochondrial membrane protein of unknown function, contains no hydrophobic	2	4.1133	0.3542	1953.37	1951.196	1	605.7	63.333332 K.L1R4D1I1D1E1Y1D1N2P1L1L1P1L1P1F1.N
gi 6322395 ref NP_012469.1	YJL066C	stretches; Mpm1p Mitochandrial membrane protein of unknown function, contains no hydrophobic	2	2.9724	0.2437	1694.51	1693.095	2	313.3	53.571426 S.K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1.E
gi 6322395 ref NP_012469.1	YJL066C	stretches; Mpm1p	2	3.7173	0.3447	2376.71	2377.827	1	543	45 S.KAIPPLPQLDFLLPLEEIKSD.K
gi 6322395 ref NP_012469.1	YJL066C	stretches; Mpm1p	2	3.3041	0.1541	2800.33	2802.313	1	484.3	35.416664 C.L1V1P1S1K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1E1E1I1K2S1D1.K
gi 6322395 ref NP_012469.1	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	3	4.387	0.3749	2802.56	2802.313	1	720.6	30.208334 C.L1V1P1S1K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1E1E1I1K2S1D1.K
gi 6322395 ref NP_012469.1	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	2	2.9555	0.1707	2772.81	2774.314	4	317.5	29.166666 C.LVPSKAIPPLPQLDFLLPLEEIKSD.K
gi 6322395 ref NP_012469.1	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	2	3.1197	0.2418	2304.29	2303.663	2	268.9	38.88889 L.FPKLRDIDEYDNPLLPLPF.N
gi 6322395 ref NP_012469.1	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	2	4.1843	0.3614	2399.75	2401.827	1	403.3	45 S.K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1E1E1I1K2S1D1.K
gi 6322395 ref NP_012469.1	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	3	3.8476	0.2307	2399.15	2401.827	1	1404.2	38.75 S.K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1E1E1I1K2S1D1.K
gi 6322395 ref NP 012469.1	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	3	4.3923	0.191	2402.48	2401.827	1	779.3	38.75 S.K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1E1E1I1K2S1D1.K
ail6322395/refINP 012469.11	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches: Mom1p	2	4.3507	0.4445	2398.89	2401.827	1	640.5	55 S.K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1E1E1I1K2S1D1.K
gil6322381/refINP_012455.1	X II 080C	Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with translating ribosomes via multiple KH domains, similar to vertebrate vigilins;	2	3 275	0 2269	1484 49	1484 779	1	503.4	
91002200110114r_012400.1]		Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with translating ribosomes via multiple KH domains, similar to vertebrate vigilins;	۷	0.210	0.2203	1707.90			000.4	
gi 6322381 ref NP_012455.1	YJL080C	Scp160p Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with translating ribosomes via multiple KH domains, similar to vertebrate vigilins;	1	2.4848	0.1532	1483.67	1484.779	6	145.4	50 Q.LSITKPELSRIVQ.S
gi 6322381 ref NP_012455.1	YJL080C	Scp160p	2	3.4258	0.3793	2214.73	2215.555	1	328.4	42.105263 A.ATAEEHPQLEKKPTPLPSLK.D

gi 6322381 ref NP_012455.1	YJL080C	Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with translating ribosomes via multiple KH domains, similar to vertebrate vigilins; Scp160p	2	3.3102	0.3676	2825.87	2827.207	1	262.1	38 T.AEEHPQLEKKPTPLPSLKDLPSLGSN.A
		Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with translating thosomes via multiple KH domains, similar to vertebrate vigilins?								
gi 6322381 ref NP_012455.1	YJL080C	Scp160p Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with	2	3.6019	0.2759	2414.61	2414.811	1	608.5	45 A.ADVIINVPRKSDKVNDVVYIR.G
gi 6322381 ref NP_012455.1	YJL080C	translating ribosomes via multiple KH domains, similar to vertebrate vigilins; Scp160p Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with	3	3.8828	0.3187	2998.88	2999.391	1	579.1	28.703705 A.ATAEEHPQLEKKPTPLPSLKDLPSLGSN.A
gi 6322381 ref NP_012455.1	YJL080C	translating ribosomes via multiple KH domains, similar to vertebrate vigilins; Scp160p Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with	2	3.8092	0.3676	1788.23	1789.088	1	908.1	64.28571 N.VPRKSDKVNDVVYIR.G
gi 6322381 ref NP_012455.1	YJL080C	translating ribosomes via multiple KH domains, similar to vertebrate vigilins; Scp160p Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and EP, interacts in mRNA-dependent manner with	2	3.6336	0.2284	1586.75	1587.819	3	633.4	62.5 F.INFPRDNEIVTIR.G
gi 6322381 ref NP_012455.1	YJL080C	associated minimuoteal environe and Eris interacts in interversependent manifer wait translating fibosomes via multiple KH domains, similar to vertebrate vigilins; Scp160p	2	3.9863	0.3778	2042.83	2043.371	1	788.6	52.941177 T.AEEHPQLEKKPTPLPSLK.D
gi 6322368 ref NP_012442.1	YJL093C	Outward-rectifier potassium channel of the plasma membrane with two pore domains in tandem, each of which forms a functional channel permeable to potassium; carboxy tail functions to prevent inner gate closures; target of K1 toxin; Tok1p	3	4.1647	0.2578	2104.58	2102.441	2	534.8	38.235294 Y.TRGPEFWISPDTPLKFPL.N
gi 6322368 ref NP_012442.1	YJL093C	Outward-rectifier potassium channel of the plasma membrane with two pore domains in tandem, each of which forms a functional channel permeable to potassium; carboxy tail functions to prevent inner gate closures; target of K1 toxin; Tok1p	3	4.0619	0.4067	3109.85	3112.464	1	414.6	31 R.N2I1T1D111E1E1Y1T1R4G1P1E1F1W2I1S1P1D1T1P1L1K2F1P1L1.N
gi 6322368 ref NP_012442.1	YJL093C	Outward-rectifier potassium channel of the plasma membrane with two pore domains in tandem, each of which forms a functional channel permeable to potassium; carboxy tail functions to prevent inner gate closures; target of K1 toxin; Tok1p	2	3.3772	0.3577	2420.57	2419.732	2	424.8	39.473686 E.E1Y1T1R4G1P1E1F1W2I1S1P1D1T1P1L1K2F1P1L1.N
gi 6322368 ref NP_012442.1	YJL093C	Outward-rectifier potassium channel of the plasma membrane with two pore domains in tandem, each of which forms a functional channel permeable to potassium; carboxy tail functions to prevent inner gate closures; target of K1 toxin; Tok1p	2	3.1686	0.3439	2395.15	2394.732	1	379	36.842106 E.EYTRGPEFWISPDTPLKFPL.N
gi 6322368 ref NP_012442.1	YJL093C	Outward-rectifier potassium channel of the plasma membrane with two pore domains in tandem, each of which forms a functional channel permeable to potassium; carboxy tail functions to prevent inner gate closures; target of K1 toxin; Tok1p	2	4.2466	0.4001	2103.69	2102.441	1	807.6	61.764706 Y.TRGPEFWISPDTPLKFPL.N
gi 6322368 ref NP_012442.1	YJL093C	Outward-rectifier potassium channel of the plasma membrane with two pore domains in tandem, each of which forms a functional channel permeable to potassium; carboxy tail functions to prevent inner gate closures; target of K1 toxin; Tok1p Protein that forms a complex with the Sit4p protein phosphatase and is required for	2	3.2559	0.2819	2123.49	2125.441	1	704.2	52.941177 Y.T1R4G1P1E1F1W2I1S1P1D1T1P1L1K2F1P1L1.N
gi 6322363 ref NP_012437.1	YJL098W	its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p Protein that forms a complex with the Sit4p protein phosphatase and is required for	3	5.2136	0.4093	3354.38	3356.229	1	788.8	26.724138 N.DRSELKENEDDNTGDADDEVEDDTNQVESA.N
gi 6322363 ref NP_012437.1	YJL098W	its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p Protein that forms a complex with the Sit4p protein phosphatase and is required for	3	6.6721	0.5078	3394.79	3394.229	1	1766.1	N.D1R4S1E1L1K2E1N2E1D1D1N2T1G1D1A1D1D1E1V1E1D1D1T1N2Q2V1E1S1A1 36.206894 .N
gi 6322363 ref NP_012437.1	YJL098W	its function; member of a family of similar proteins including Sap4p, Sap15bp, and Sap190p; Sap185p Protein that forms a complex with the Sil4p protein phosphatase and is required for	2	4.3083	0.2123	1520.33	1520.812	1	885.9	81.818184 N.R4F1L1L1D1D1L1L111N2I1R4.L
gi 6322363 ref NP_012437.1	YJL098W	its function; memoer of a family or similar proteins including Sap4p, Sap1sp, and Sap190p; Sap185p Protein that forms a complex with the Sit4p protein phosphatase and is required for its functions memory of a family of privile proteins phosphatase and is required for	2	4.426	0.3099	1502.65	1501.812	2	913.2	81.818184 N.RFLLDDLLINIR.L
gi 6322363 ref NP_012437.1	YJL098W	is incluor, memory or a ranning or similar proteins including 3-ap44, 3-ap139, and Sap1390; Sap185p Protein that forms a complex with the Sil4p protein phosphatase and is required for the functions memory of a formula of air/fact proteins phosphatase and is required for	3	4.058	0.2456	3000.8	3002.236	5	386.3	28 T.R4L1N2F1N2P1D1S1D1A1T1E1Q2V1P1G1E1V1N2R4D1H3K2I1P1L1.K
gi 6322363 ref NP_012437.1	YJL098W	ns runcion; memoer or a ranning or similar proteins including Sap4p, Sap135p, and Sap130p; Sap185p Sap190p; Sap185p	3	4.1454	0.3047	3637.04	3638.721	1	472.9	31.034481 2.Y
gi 6322331 ref NP_012405.1	YJL130C	ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	3	4.8217	0.2415	2160.14	2160.452	1	1378.8	45.3125 V.PDMHLRDELVEELPRYF.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoyiphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.8546	0.2014	2342.29	2343.637	1	364.7	44.444447 Y.G1V1P1D1M1H3L1R4D1E1L1V1E1E1L1P1R4Y1F1.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoyiphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.7483	0.2717	2317.97	2316.637	1	496.6	47.22222 Y.GVPDMHLRDELVEELPRYF.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	3	4.3314	0.1754	2185.52	2185.452	1	820.7	37.5 V.P1D1M1H3L1R4D1E1L1V1E1E1L1P1R4Y1F1.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.5669	0.3371	2332.49	2333.624	1	478.2	44.736843 V.S1I1N2E1P1K2L1Y1V1P1P1A1D1N2K2H3I1E1L1Q2.T
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.414	0.4201	2305.75	2306.624	1	457.4	44.736843 V.SINEPKLYVPPADNKHIELQ.T

gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.3669	0.2291	2405.51	2405.756	1	567.3	42.5 K.VSINEPKLYVPPADNKHIELQ.T
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.8415	0.2788	2433.47	2433.756	1	1077.8	57.5 K.V1S1I1N2E1P1K2L1Y1V1P1P1A1D1N2K2H3I1E1L1Q2.T
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	3	4.0357	0.3946	2315.48	2316.637	1	986.3	37.5 Y.GVPDMHLRDELVEELPRYF.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	1	2.7909	0.2967	1256.71	1257.562	3	445.4	65 A.VKEIGFPVIVR.A
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.0845	0.247	1814.47	1815.06	1	584.7	53.333336 G.G1L1L1E1D1N2V1K2A1H3P1R4I1E1A1K2.K
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.1499	0.225	1746.27	1746.899	2	393.6	53.571426 E.S1T1P1G1P1R4D1T1E1F1L1F1D1V1F1.I
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	3	4.838	0.3864	2343.14	2343.637	1	1189.2	43.055553 Y.G1V1P1D1M1H3L1R4D1E1L1V1E1E1L1P1R4Y1F1.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	3	4.116	0.2254	2359.19	2359.637	1	1073.9	38.88889 Y.G1V1P1D1M\$H3L1R4D1E1L1V1E1E1L1P1R4Y1F1.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	2.9221	0.1713	1269.57	1272.562	9	709.7	70 A.V1K2E1I1G1F1P1V111V1R4.A
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.7339	0.2189	1762.25	1763.015	2	807.8	60.714287 R.M1L1D1Q2I1G1V1D1Q2P1A1W2K2E1L1.T
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.45	0.4038	2085.83	2087.42	1	404.6	41.666664 M.GLPLTPYPVEKLPDDYVAV.K
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.5113	0.4165	2106.11	2107.42	1	494.6	44.444447 M.G1L1P1L1T1P1Y1P1V1E1K2L1P1D1D1Y1V1A1V1.K
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.1785	0.3717	2332.61	2331.772	1	419.8	37.5 A.IMGLPLTPYPVEKLPDDYVAV.K
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.3589	0.2606	2353.89	2353.772	1	541.8	42.5 A.I1M1G1L1P1L1T1P1Y1P1V1E1K2L1P1D1D1Y1V1A1V1.K
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	1	3.1821	0.3226	1435.7	1436.692	1	724.3	62.5 N.L1V1S1P1P1E1L1R4L1P1E1G1L1.R
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines, both activities are subject to feedback inhibition by UTP; Ura2p	1	2.8436	0.3317	1420.5	1420.692	1	686.5	62.5 N.LVSPPELRLPEGL.R
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.177	0.2648	1439.61	1436.692	3	418.3	66.66667 N.L1V1S1P1P1E1L1R4L1P1E1G1L1.R
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	3	4.2461	0.33	2333.06	2333.624	1	623.8	39.473686 V.S1I1N2E1P1K2L1Y1V1P1P1A1D1N2K2H3I1E1L1Q2.T
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.6096	0.3596	2332.67	2333.624	1	341.5	39.473686 V.S1I1N2E1P1K2L1Y1V1P1P1A1D1N2K2H3I1E1L1Q2.T
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.3992	0.1552	2342.49	2343.637	6	286.8	36.11111 Y.G1V1P1D1M1H3L1R4D1E1L1V1E1E1L1P1R4Y1F1.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	3	5.0883	0.3054	2342.87	2343.637	1	798.7	37.5 Y.G1V1P1D1M1H3L1R4D1E1L1V1E1E1L1P1R4Y1F1.E
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.1758	0.3264	2445.19	2445.57	1	487.1	42.5 L.GFNETDLDIDIDYELNNPTDM.R
gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	1	2.3565	0.1505	1105.4	1106.327	1	391.8	66.66667 S.H3V111K2G1P1A1E1L1K2.E

gi 6322331 ref NP_012405.1	YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	2	3.25	0.2814	1251.73	1252.472	1	823.3	80 S.H3R4T111T1L1P1G1L111N2.I
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker, interacts with eIF4G; Tif2p	2	3.1451	0.2318	1059.47	1058.27	1	600.7	77.77778 Q.I1V1V1G1T1P1G1R4V1F1.D
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.1513	0.2557	1190.47	1188.401	1	456.4	75 A.Q2I1V1V1G1T1P1G1R4V1F1.D
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.0301	0.2074	1580.17	1580.75	3	235.5	54.1666668 Y.S1D1L1P1Q2Q2E1R4D1T1I1M1K2.E
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker, interacts with eIF4G; Tif2p	2	3.9611	0.3177	1838.37	1838.086	1	1058.6	71.42857 A.IYSDLPQQERDTIMK.E
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker, interacts with eIF4G; Tif2p	2	4.0995	0.2739	1859.35	1859.086	1	855.8	67.85714 A.I1Y1S1D1L1P1Q2Q2E1R4D1T111M1K2.E
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.8553	0.3053	2210.55	2209.457	1	762	52.941177 S.A1I1Y1S1D1L1P1Q2Q2E1R4D1T1I1M1K2E1F1.R
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	4.3615	0.3359	2183.65	2185.422	1	868.7	50 Y.K2F1D1D1M1E1L1D1E1N2L1L1R4G1V1F1G1Y1.G
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.6957	0.3379	2422.89	2424.73	1	1234	52.63158 V.VYKFDDMELDENLLRGVFGY.G
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.3594	0.2753	1536.55	1536.756	1	509	61.538464 L.R4D1A1Q2I1V1V1G1T1P1G1R4V1F1.D
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	4.2105	0.3975	1517.59	1515.756	1	861.5	76.92308 L.RDAQIVVGTPGRVF.D
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.6955	0.3493	1667.51	1666.94	1	783.8	69.230774 L.V1K2K2D1E1L1T1L1E1G111K2Q2F1.Y
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.5803	0.3424	1793.53	1792.106	1	197.7	53.333336 Q.QRAIMPIIEGHDVLAQ.A
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.967	0.3742	1684.69	1684.976	1	531.1	67.85714 Q.R4A111M1P11111E1G1H3D1V1L1A1Q2.A
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	1	2.6025	0.1658	1463.46	1464.766	1	513	62.5 Q.RAIMPIIEGHDVL.A
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.7123	0.3551	1665.57	1663.976	1	450.3	60.714287 Q.RAIMPIIEGHDVLAQ.A
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	4.2649	0.301	1908.95	1909.165	1	1061.4	66.66667 S.AIYSDLPQQERDTIMK.E
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	2.9154	0.1993	1838.85	1838.042	1	283.3	53.571426 Y.SDLPQQERDTIMKEF.R
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.3934	0.2845	1857.27	1859.042	5	267.9	50 Y.S1D1L1P1Q2Q2E1R4D1T111M1K2E1F1.R
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.1202	0.2651	1561.37	1561.75	1	431.3	75 Y.SDLPQQERDTIMK.E
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	5.0973	0.2157	1658.23	1656.833	1	2026.6	87.5 Y.K2F1D1D1M1E1L1D1E1N2L1L1R4.G
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.8876	0.2742	1640.75	1638.833	1	1687.4	79.16667 Y.KFDDMELDENLLR.G
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.4928	0.2782	2138.31	2137.378	2	425.8	46.875 A.I1Y1S1D1L1P1Q2Q2E1R4D1T1I1M1K2E1F1.R

gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.5995	0.333	2115.09	2114.378	1	684.9	53.125 A.IYSDLPQQERDTIMKEF.R
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	2	3.1028	0.1724	1151.67	1152.386	2	864.9	72.22222 Q.R4A111M1P11111E1G1H3.D
gi 6322323 ref NP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker, interacts with eIF4G; Tif2p	1	3.1841	0.2058	1377.57	1378.482	1	530.3	70 F.D1D1M1E1L1D1E1N2L1L1R4.G
ail6322323 refINP_012397.1	YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker: interacts with eIF4C; Tif2p	2	3.8484	0.2036	1377.87	1378,482	1	1519.6	80 F D1D1M1F1L1D1F1N2L1L1R4 G
gil6322280/rofINE_012363.1	V II 172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	1	3 1771	0.3838	1/37.62	1438 665	1	228.5	58 222222 T I 11 10/E11 1E101/1011 1210121 S
silc222209/ref/NP_012303.1	VII.470W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen		0.4544	0.0000	1407.02	1430.003	4	000.5	
gilo322289[rei]NP_012363.1]	TJL172VV	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	3.4511	0.2727	1438.45	1438.005		902.5	00.00007 1.LILIK4EILEIPIAIPILISIPISI.S
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	3.8099	0.3503	2168.47	2167.343	1	542.1	52.77778 S.K2N2G1D1D1Y1I1I1P1E1T1E1L1G1H3I1D1I1T1.L
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	3	4.2167	0.3294	2941.64	2939.214	1	894.3	32 L.SNAVRIPTVVQDKNPNPADDPDFYKH.F
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase vscS: expression is induced under low-nitrogen	1	3.1095	0.357	1437.84	1438.665	2	286.5	50 T.L1L1R4E1L1E1P1A1P1L1S1P1S1.S
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxynentidase vscS: expression is induced under low-nitrogen	2	5.0007	0.3986	2254.43	2255.421	1	643.5	52.63158 L.S1K2N2G1D1D1Y1111P1E1T1E1L1G1H3I1D111T1.L
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	2	3.3213	0.2556	2064.55	2064.346	1	760.2	50 L.RELEPAPLSPSSGPVWDIL.A
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	2	4.2436	0.4079	2316.05	2315.665	1	828.6	47.5 T.L1L1R4E1L1E1P1A1P1L1S1P1S1S1G1P1V1W2D1I1L1.A
gi 6322289 ref NP_012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	4.2929	0.3523	1794.07	1794.856	1	1082.4	67.85714 Q.D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3.F
gi 6322289 ref NP 012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	4.3299	0.3371	2039.51	2039.157	1	831.4	55.88235 L.S1K2N2G1D1D1Y1I11P1E1T1E1L1G1H3I1D1.I
gil6322289/refINP_012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions: Cps1p	2	4.9684	0.5141	2085.77	2087.346	1	1039.7	61.11111 L.R4E1L1E1P1A1P1L1S1P1S1S1G1P1V1W2D111L1.A
gil6322280/rofINE_012363.1	V II 172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	4 2847	0.4208	2280.65	2200.665	1	701.3	
31002220910114F_012000.1	13217200	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	4.2047	0.4200	2209.00	2230.003		500.0	
gi 6322289 ret NP_012363.1	YJL172W	Conditions; Cps1p Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	4.3405	0.3611	2230.81	2231.421	1	592.8	50 E.SKNGDDYIIPETELGHIDIT.L
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	3.4886	0.3129	2974.43	2976.214	1	396.5	34 L.S1N2A1V1R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3.F
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase vscS: expression is induced under low-nitrogen	3	5.5713	0.3883	3125.69	3124.39	1	561.9	26.923079 L.S1N2A1V1R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3F1.Y
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	3	5.1411	0.3511	2600.27	2599.82	1	760.1	33.333336 V.R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3.F
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	3	4.6907	0.2429	2918.48	2920.208	6	407.9	27.083334 N.A1V1R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3F1.Y
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	2	4.5663	0.4423	2308.85	2309.507	1	483.3	52.77778 W.K2F1P1P1F1S1G1H3Y1D1P1E1T1D1F1V1W2G1R4.G
gi 6322289 ref NP_012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	3	3.9006	0.3159	2311.4	2309.507	1	778.1	41.666664 W.K2F1P1P1F1S1G1H3Y1D1P1E1T1D1F1V1W2G1R4.G
gi 6322289 ref NP_012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	2.9566	0.2329	1368.25	1368.502	1	724.8	72.72727 A.T1P1I1N2A1E1K2G1Y1V1D1F1.E
gil6322289/refINP_012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions: Costp	2	4.1548	0.2594	1535.47	1536.667	1	990.6	79.16667 L.Y1T1W2E1G1S1D1P1D1L1K2P1L1.
gil6322289/refINP_012363.1	Y II 172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions: Cos1n	1	2 8141	0 2543	1209.5	1210 346	1	236.8	65 L R4E1I 1E1D141D1I 1S1D1S1 S
silc222200 ref NP_012000.1	VII.470W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen		2.0141	0.2040	1200.0	1210.040		100.0	
gilo322289/rei/INP_012363.1	TJL172VV	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen		2.0859	0.2028	1199.01	1200.381	4	162.9	55 L.STNZATVTR411PTTTVTQZ.D
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	1	2.8307	0.3024	1367.49	1368.502	1	567.4	63.636364 A.T1P1I1N2A1E1K2G1Y1V1D1F1.E
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	3.1658	0.3253	1423.27	1422.665	1	969.3	70.83333 T.LLRELEPAPLSPS.S
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase vscS; expression is induced under low-nitrogen	1	3.2567	0.374	1437.6	1438.665	1	378	54.166668 T.L1L1R4E1L1E1P1A1P1L1S1P1S1.S
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	2	4.9685	0.3673	2037.79	2039.157	1	1337.7	67.64706 L.S1K2N2G1D1D1Y1111P1E1T1E1L1G1H3I1D1.I
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	2	3.8825	0.2945	1953.71	1951.078	1	736.1	68.75 S.K2N2G1D1D1Y1111P1E1T1E1L1G1H3I1D1.I
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	2	3.0084	0.1886	1440.17	1438.665	4	681	62.5 T.L1L1R4E1L1E1P1A1P1L1S1P1S1.S
gi 6322289 ref NP_012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	2.7151	0.1969	1015.45	1016.103	3	276.1	68.75 N.E1H3V1D1V1P1G1H3L1.S
gi 6322289 ref NP_012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	2.3718	0.2358	1162.86	1164.392	1	411.2	61.11111 T.L1L1R4E1L1E1P1A1P1L1.S
gil6322289lrefINP_012363.1	Y.II 172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions: Costo	3	4 4153	0 2724	2036 48	2039 157	1	732.8	39 705883 S1K2N2G1D1D1Y1111P1E1T1E11 1G1H31D1
gil6322280/rofINE_012363.1	V II 172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	4 672	0.4207	2397 22	2287 742	1	771.0	52 380055 T I 11 404E11 1E10101011 1S101S1C10101010
31002220910114F_012000.1	10217200	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	4.072	0.4207	2307.33	2307.743		700	
gilo322269[rei]NP_012363.1]	TJL1/2VV	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	3.9813	0.3552	2444.53	2440.795	1	726	00 1.LILIK4EILIEIMIAIMILISIMISISIMIVIW2D111L1A1G1.I
gij6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	2	3.725	0.2914	2791.59	2792.191	1	388.5	34 I.L1L1R4E1L1E1P1A1P1L1S1P1S1S1G1P1V1W2D1I1L1A1G1T1I1Q2.D
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen	3	4.2046	0.287	2975.93	2976.214	1	690.9	28 L.S1N2A1V1R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3.F
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p Vacuolar carboxypeptidase vscS; expression is induced under low-nitrogen	2	3.9506	0.4024	2091.37	2091.268	1	348.8	56.25 W.K2F1P1P1F1S1G1H3Y1D1P1E1T1D1F1V1W2.G
gi 6322289 ref NP_012363.1	YJL172W	conditions; Cps1p	2	3.2446	0.349	2068.55	2070.268	1	334.2	46.875 W.KFPPFSGHYDPETDFVW.G

gi 6322289 ref NP_012363.1	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	3	4.1829	0.218	2847.68	2848.13	1	1448.6	36.95652 A.V1R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3F1.Y
gi 6322271 ref NP_012345.1	YJL190C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity to E. coli S8 and rat S15a ribosomal proteins; Rps22ap	2	3.9343	0.3054	1659.05	1659.839	1	411.5	69.230774 F.EYIDDHRSGKIVVQ.L
gi 6322271 ref NP_012345.1	YJL190C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity to E. coli S8 and rat S15a ribosomal proteins; Rps22ap	2	3.7519	0.3581	1679.67	1680.839	1	405.9	65.38461 F.E1Y111D1D1H3R4S1G1K2I1V1V1Q2.L
gi 6322271 ref NP_012345.1	YJL190C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity to E. coli S8 and rat S15a ribosomal proteins; Rps22ap Albha subunit of the translation initiation factor eIP2. involved in the identification of	2	3.6166	0.4364	1956.69	1959.131	1	388.8	63.333332 G.E1F1E1Y111D1D1H3R4S1G1K2I1V1V1Q2.L
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Aloha subunit of the translation initiation factor eIP2. involved in the identification of	1	2.9813	0.2799	1437.71	1436.663	1	464.7	59.090908 N.KYPEIDDIVMVN.V
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sul2p Aloha subunit of the translation initiation factor eIP2, involved in the identification of	2	3.7815	0.2304	1438.47	1436.663	1	772.8	77.27273 N.KYPEIDDIVMVN.V
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	3	4.6963	0.4135	2888.75	2891.201	1	1504.9	36.458336 L.SIIDETVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	2	3.6975	0.3146	2918.71	2920.201	1	275.4	33.333336 L.S1111D1E1T1V1W2E1G111E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	2	3.8781	0.3465	1424.51	1423.606	1	602.3	75 F.SYEGIDAIKDALK.S
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	3	4.1521	0.365	2233.85	2232.495	1	725.9	38.88889 T.VWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	3	5.5547	0.4216	2918.93	2920.201	1	1459.8	35.416664 L.S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	2	4.1395	0.4086	3132.03	3132.535	1	534.2	38.46154 F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Setb 1s required for regulation of translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor of IF2, involved in the identification of the translation initiation factor of F2 is an end of the setbility for an end of the identification of the setbility of the setbility of 60 for an end of the setbility for an end of the identification of the setbility of the setbility of 60 for an end of the setbility o	2	4.4806	0.4707	3163.05	3164.535	1	325.9	32.692307 F.K2L1S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon, prosphorylation of sero 1 set equired for regulation of translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the dott dealow be exchange of the for any elicit of the regulation by any end of the translation of the formation of the regulation of the translation by the dott dealow be exchanged and the formation of the regulation of the translation by the dott dealow be exchanged and the translation of the regulation of the regulation of the translation of the dott dealow be exchanged and the regulation of the regulation of the translation of the regulation of the regilation of the regula	3	4.8607	0.2238	3131.45	3132.535	2	895.5	25.961538 F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospectively and to see 1 a sequence to regulate to instantiation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the state codors benefactoralizing of SecTi is required for regulation of translation by	2	2.9756	0.2421	1510.89	1509.786	1	718.8	68.181816 E.KFQIPLEELYKT.I
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospectively and to see 1 a sequence to regulate to instantiation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the state codors benefactoralizing of SecTi is required for regulation of translation by	2	3.5798	0.3629	1437.99	1438.606	2	893.1	62.5 F.S1Y1E1G111D1A111K2D1A1L1K2.S
gi 6322466 ref NP_012540.1	YJR007W	The bian basis proposed with the constraints of the product of the	3	3.9277	0.2849	2833.97	2832.123	1	871.7	31.52174 S.I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	The bian basis proposed with the constraints of the product of the	2	3.7781	0.3888	2231.87	2232.495	1	559.5	44.444447 T.VWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospectively failed to effect the sequence of regulation of translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the state coder; becabendulation of SecTi is required for regulation of translation by	3	4.6483	0.4096	2230.13	2232.495	1	1173.8	48.61111 T.VWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospectively failed to effect the sequence of regulation of translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the state coder; becabendulation of SecTi is required for regulation of translation by	2	3.2126	0.2523	3131.29	3132.535	1	272.7	30.769232 F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospervise of OP for GTP; Su2p inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the state coder; benefactoralizing of SecTi is required for regulation of translation by	1	2.5694	0.2705	1510.87	1509.786	1	476.8	59.090908 E.KFQIPLEELYKT.I
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospectively and to set of the squared to regulate to its anisation of inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the state codor; becabenduation of Set and State is required for regulation of translation by	2	3.9123	0.3042	1523.93	1524.786	1	1731	90.909096 E.K2F1Q2I1P1L1E1E1L1Y1K2T1.I
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospectively and to set of the squared to regulate to its anisation of inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the state codor; becabenduation of Set and State is required for regulation of translation by	1	2.9131	0.2762	1523.67	1524.786	1	560.6	59.090908 E.K2F1Q2I1P1L1E1E1L1Y1K2T1.I
gi 6322466 ref NP_012540.1	YJR007W	The state count, prospectively and to see the squared for regulation of translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the state of the	2	3.0473	0.17	1638.07	1638.945	2	645.3	58.333332 E.K2F1Q2I1P1L1E1E1L1Y1K2T1I1.A
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospectively and to serve the squared to regulate to regulate the state state of the state	3	5.7707	0.3908	3131.78	3132.535	1	1599.3	33.653847 F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the start could, prosphoryration or seron required for regulation or translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start could access been been defined at a set of the start for a could be of translation by	3	4.7004	0.2534	3164.33	3164.535	1	1141.2	27.884615 F.K2L1S1111D1E1T1V1W2E1G111E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start could, prosphoryration or seron required for regulation or translation by inhibiting the exchange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start could access been been defined at a set of the start for a could be of translation by	2	3.6666	0.3799	2421.29	2421.669	1	487.6	45 S.I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1.K
gi 6322466 ref NP_012540.1	YJR007W	the state count, prospectively and to serve the squared to regulate to regulate the state state of the state	2	4.4003	0.3477	2508.51	2509.747	4	292.4	40.476192 L.S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1.K
gi 6322466 ref NP_012540.1	YJR007W	All other schange of GDP for GTP; Su2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the stat coding: biosphore/altion of SacF1 is required for regulation of translation by	2	3.9654	0.3196	1698.03	1696.882	1	899.9	65.38461 Y.E1N2K2Y1P1E1I1D1D111V1M1V1N2.V
gi 6322466 ref NP_012540.1	YJR007W	All other sectors and a sector of the sector	2	3.323	0.2102	1583.23	1580.779	1	1047.2	70.83333 Y.E1N2K2Y1P1E1I1D1D111V1M1V1.N
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p	2	3.7437	0.2452	1451.29	1450.663	2	844.4	81.818184 N.K2Y1P1E1I1D1D111V1M1V1N2.V

		Alpha subunit of the translation initiation factor eIF2, involved in the identification of								
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	2	3.6344	0.2751	1965.93	1967.149	1	796.8	62.5 W.E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	2	4.3844	0.2764	2255.29	2255.495	1	800.3	55.555557 T.V1W2E1G111E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	2	4.7541	0.3448	2230.89	2232.495	1	1358.4	69.44444 T.VWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of	2	4.4424	0.3652	2334.47	2333.6	1	737	55.263157 E.TVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Su22 Alpha subunit of the translation initiation factor eIF2, involved in the identification of	2	5.142	0.4512	2356.49	2357.6	1	1123.7	63.15789 E.T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphortylation of Set5 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the translation initiation factor eIF2.	2	4.0651	0.2446	2486.49	2487.715	1	538.3	47.5 D.E1T1V1W2E1G111E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphortylation of Set5 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the translation initiation factor eIF2.	3	4.8405	0.4525	2801.54	2804.123	1	905.7	33.695652 S.IIDETVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	the start codon; phosphortylation of Set5 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start of the translation initiation factor eIF2, involved in the identification of the start of the translation initiation factor eIF2.	2	4.6961	0.2823	2832.89	2832.123	1	383.9	39.130436 S.I111D1E1T1V1W2E1G111E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start cool in prospinorylation of series in equilited for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start of the translation initiation factor eIF2, involved in the identification of the start of the translation initiation factor eIF2.	2	4.1784	0.2739	2919.63	2920.201	4	220.7	29.1666666 L.S1111D1E1T1V1W2E1G111E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	the start couch prosphorylaution of series is required for regulation of infantsation by inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the active decise because addition of 6C4 is a contribute for scalable as it translations by	2	3.737	0.32	2888.91	2891.201	1	365.7	37.5 L.SIIDETVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	The start COUNT prospinorylation of series is required for required of regulation of rainstation by inibiting the exchange of GDP for GTP, Su/2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codes, sheependation of Secold is required for regulation of translation by	3	5.6156	0.4451	2917.67	2920.201	1	1172.4	32.291664 L.S11111D1E1T1V1W2E1G111E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon: obsorbiorylation of Sec51 is required for regulation of translation by	2	4.0176	0.3182	2726.45	2727.081	4	478.5	39.130436 F.KLSIIDETVWEGIEPPSKDVLDEL.K
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codor, phosphorylation of Ser51 is required for regulation of translation by	2	3.8089	0.2454	2751.89	2754.081	4	474.2	36.95652 F.K2L1S1III1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1.K
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by	3	5.4763	0.3031	3134.09	3132.535	1	1561.7	33.653847 F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by	3	4.3979	0.2367	3164.18	3164.535	1	768.3	25 F.K2L1S1111D1E1T1V1W2E1G111E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by	2	3.975	0.1515	1424.45	1422.681	1	1111.8	85 E.K2F1Q2I1P1L1E1E1L1Y1K2.T
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by	1	3.1056	0.2176	1408.5	1408.681	1	612.8	65 E.KFQIPLEELYK.T
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by	1	2.9102	0.2119	1524.55	1524.786	5	381	50 E.K2F1Q2I1P1L1E1E1L1Y1K2T1.I
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by	1	2.9754	0.2528	1510.66	1509.786	1	445.8	54.545456 E.KFQIPLEELYKT.I
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by	2	3.8944	0.2837	1525.49	1524.786	1	1360.3	86.36364 E.K2F1Q2I1P1L1E1E1L1Y1K2T1.I
gi 6322466 ref NP_012540.1	YJR007W	inhibiting the exchange of GDP for GTP; Sui2p Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and	2	3.6626	0.3631	2484.39	2485.747	1	398.3	42.857143 L.SIIDETVWEGIEPPSKDVLDEL.K
gi 6322468 ref NP_012542.1	YJR009C	gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; TdAp	2	3.3256	0.4149	1495.79	1497.651	1	884.2	75 F.QERDPANLPWASL.N
gi 6322468 ref NP_012542.1	YJR009C	Giyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	1	2.5591	0.2242	1385.48	1386.52	1	205.4	59.090908 Q.E1R4D1P1A1N2L1P1W2A1S1L1.N
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.4521	0.3697	1710.25	1708.967	1	724.7	60.000004 L.AKVINDAFGIEEGLMT.T
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.1076	0.2525	1388.31	1386.52	1	637.6	68.181816 Q.E1R4D1P1A1N2L1P1W2A1S1L1.N
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	1	2.7	0.2599	1368.52	1369.52	1	188.7	54.545456 Q.ERDPANLPWASL.N
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.0525	0.3598	1658.35	1658.768	1	736.6	64.28571 A.GEVSHDDKHIIVDGH.K
		Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate								
gi 6322468 ref NP_012542.1	YJR009C	to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.325	0.2093	1594.69	1595.79	1	899.2	69.230774 M.GVNEEKYTSDLKIV.S

gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.6141	0.3794	1682.41	1680.074	1	616.6	56.666668 K.KVVITAPSSTAPMFVM.G
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.392	0.2919	1695.59	1697.074	1	907.8	60.000004 K.K2V1V111T1A1P1S1S1T1A1P1M1F1V1M1.G
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.9968	0.3271	2287.81	2286.62	1	625.8	50 N.C1L1A1P1L1A1K2V111N2D1A1F1G111E1E1G1L1M1T1.T
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.076	0.458	1286.29	1286.39	1	959.5	85 S.HDDKHIIVDGH.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	3	4.9171	0.2588	1699.43	1698.939	1	2157.1	63.461536 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	1	4.1022	0.2868	1491.56	1492.6	1	658.7	62.5 E.V1S1H3D1D1K2H3I1I1V1D1G1H3.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.0798	0.3735	1374.27	1373.468	2	750.3	77.27273 V.SHDDKHIIVDGH.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.4686	0.3756	1392.39	1392.468	1	810.1	81.818184 V.S1H3D1D1K2H3I1I1V1D1G1H3.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.586	0.4109	2142.59	2143.367	1	721.9	52.63158 D.S1T1G1V1F1K2E1L1D1T1A1Q2K2H3I1D1A1G1A1K2.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.1777	0.3061	1354.19	1354.577	1	1036.2	72.72727 T.R4V1V1D1L1V1E1H3V1A1K2A1
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	5.867	0.4011	1807.89	1809.113	1	889.3	75 K.LNKETTYDEIKKVVK.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	3	4.4222	0.2814	1880.84	1880.192	1	1168.7	48.333332 K.LNKETTYDEIKKVVKA.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	5.2546	0.422	1880.63	1880.192	1	1017.3	70 K.LNKETTYDEIKKVVKA.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.5933	0.3128	1973.63	1973.271	1	920	65.625 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1K2A1A1.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.9223	0.3602	1785.33	1785.013	1	705.4	63.333332 E.VSHDDKHIIVDGHKIA.T
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.0846	0.3171	1195.39	1194.39	1	1039.1	80 R.V1V1D1L1V1E1H3V1A1K2A1
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.429	0.3304	1182.07	1180.39	1	1323.8	90 R.VVDLVEHVAKA
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.5144	0.1956	1611.77	1612.79	1	736.9	65.38461 M.G1V1N2E1E1K2Y1T1S1D1L1K2I1V1.S
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	3	3.8142	0.306	1491.47	1492.6	1	1282.7	50 E.V1S1H3D1D1K2H3I1I1V1D1G1H3.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.203	0.2982	1581.03	1581.806	1	1263.8	75 K.LNKETTYDEIKKV.V
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.848	0.3284	1493.27	1492.6	1	1021.5	75 E.V1S1H3D1D1K2H3I1I1V1D1G1H3.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	3	4.1333	0.3861	1806.44	1809.113	1	1083.7	51.785713 K.LNKETTYDEIKKVVK.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	5.3832	0.3862	1899.75	1901.192	1	926.5	66.66667 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1K2A1.A

gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.2393	0.2134	1278.35	1278.497	1	493.3	68.181816 M.V1R4V1A111N2G1F1G1R4I1G1.R
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	6.1302	0.3751	1828.55	1829.113	1	945.9	75 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1K2.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	3	4.4223	0.3725	1336.97	1336.577	1	1578.1	59.090908 T.RVVDLVEHVAKA
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	2.9523	0.1556	1055.21	1054.275	1	746.1	83.33333 K.AVGKVLPELQ.G
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	2.9311	0.2297	1104.09	1104.252	3	197	66.66667 M.A1F1R4V1P1T1V1D1V1S1.V
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.7284	0.3556	1767.27	1766.932	5	494.9	57.14286 A.T1F1Q2E1R4D1P1A1N2L1P1W2A1S1L1.N
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	1	2.7042	0.2044	1481.39	1482.575	1	484.4	58.333332 A.G1E1V1S1H3D1D1K2H3I1I1V1D1.G
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.3264	0.2189	1746.73	1745.932	4	449.5	53.571426 A.TFQERDPANLPWASLN
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.6167	0.4328	1302.63	1304.39	1	958.8	85 S.H3D1D1K2H3I1I1V1D1G1H3.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.2276	0.2071	1356.13	1354.543	9	738.5	80 N.KETTYDEIKKV.V
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.7102	0.3114	1698.35	1698.939	1	651.8	69.230774 K.L1N2K2E1T1T1Y1D1E1I1K2K2V1V1.K
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.0594	0.1756	2262.53	2263.62	3	291.8	32.5 N.CLAPLAKVINDAFGIEEGLMT.T
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	1	4.1317	0.1921	1598.94	1598.85	2	714.2	66.66667 N.K2E1T1T1Y1D1E1I1K2K2V1V1K2.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	4.4712	0.3171	1671.27	1670.929	1	854	76.92308 N.K2E1T1T1Y1D1E111K2K2V1V1K2A1.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.8658	0.378	1654.53	1652.929	1	699.9	61.538464 N.KETTYDEIKKVVKA.A
gi 6322468 ref NP_012542.1	YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	2	3.6718	0.2825	2128.55	2129.286	1	398.3	47.22222 A.T1Q2K2T1V1D1G1P1S1H3K2D1W2R4G1G1R4T1A1.S
gi 6322476 ref NP_012550.1	YJR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids; Ilv3p	2	3.7725	0.2946	1513.85	1514.775	1	541.7	75 M.E1L1G1I1L1P1R4D1I1L1T1K2E1.A
gi 6322476 ref NP_012550.1	YJR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids; Ilv3p	2	3.9018	0.2901	1382.35	1384.66	2	513.1	68.181816 M.E1L1G1I1L1P1R4D1I1L1T1K2.E
gi 6322476 ref NP 012550.1	YJR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids; Ilv3p	2	3.3738	0.234	1639.23	1638.93	9	518.6	57.14286 K.K2A1P1S1L1P1E1G1Q2E1I1I1K2P1L1.S
gil6322476lrefINP_012550.1	YJR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids: Ilv3p	2	3.5713	0.1893	1667.15	1666.695	2	232.5	66.66667 K.Q2F1T1F1F1F1F4F1D1V1V1F1H3.A
gi 6322476 refINP_012550.1	VIR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids: Ilv3n	2	5 2135	0.488	2330.39	2331 336	-	1395.8	57 894737 O E1T1E1E1E1E4E1D1V1V1/1E1H3A1C1P1G1P1G1S1C1 G
cilC2224701e114F_012550.11	VID0400	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to	2	0.2100	0.400	2350.53	2001.000	1	070	
gil6322476/rei/INP_012550.1	TJKUIGC	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to	2	3.2112	0.3511	2460.51	2401.407		376	
gi 6322476 ref NP_012550.1	YJR016C	biosynthesis of branched-chain amino acids; IIv3p Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to	2	3.7331	0.3674	2434.57	2434.467	1	682.9	50 K.QFTEEEREDVVEHACPGPGSC.G
gi 6322476 ref NP_012550.1	YJR016C	biosynthesis of branched-chain amino acids; Ilv3p Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to	2	3.5401	0.1727	1369.61	1368.66	4	410.4	63.636364 M.ELGILPRDILTK.E
gi 6322476 ref NP_012550.1	YJR016C	biosynthesis of branched-chain amino acids; Ilv3p Dibydroxyacid debydratase, catalyzes third step in the common pathway leading to	2	3.8024	0.2605	1501.85	1499.852	1	1203.1	75 T.MELGILPRDILTK.E
gi 6322476 ref NP_012550.1	YJR016C	biosynthesis of branched-chain amino acids; Ilv3p	2	4.4431	0.3368	1645.85	1646.968	1	2007.5	84.61539 T.M1E1L1G111L1P1R4D111L1T1K2E1.A
gi 6322476 ref NP_012550.1	YJR016C	biosynthesis of branched-chain amino acids; IIv3p	2	3.4999	0.199	1838.39	1839.116	2	690.6	53.125 R.Y1E1G1P1R4G1A1P1G1M1P1E1M1L1K2P1S1.S
gi 6322476 ref NP_012550.1	YJR016C	biosynthesis of branched-chain amino acids; IIv3p	2	4.6935	0.3106	1768.21	1769.104	1	703.7	66.66667 A.K2K2A1P1S1L1P1E1G1Q2E1I1I1K2P1L1.S
gi 6322476 ref NP_012550.1	YJR016C	Dinyuruxyacid denydratase, catalyzes tnird step in the common pathway leading to biosynthesis of branched-chain amino acids; Ilv3p	2	3.455	0.1946	1648.43	1647.695	1	413.4	75 K.QFTEEEREDVVEH.A
gi 6322476 ref NP_012550.1	YJR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids; Ilv3p	1	2.2313	0.2347	1161.75	1162.331	1	364.1	60.000004 E.DFKKPQVGVGS.C

gi 6322476 ref NP_012550.1	YJR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids; IV3p Mitochondrial matrix ATPase that is a subunit of the presequence translocase- associated protein import motor (PAM); involved in protein translocation into the	2	3.0367	0.3173	1459.87	1460.717	1	448.2	58.333332 F.KKEDFKKPQVGVG.S
gi 6322505 ref NP_012579.1	YJR045C	matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p Mitochondrial matrix ATPase that is a subunit of the presequence translocase- associated protein import matrix (PAM); involved in protein translocation into the	1	2.3161	0.2576	1503.71	1503.782	1	302.3	50 A.GIPPAPKGVPQIEVT.F
gi 6322505 ref NP_012579.1	YJR045C	matrix and protein folding; member of the heat shock protein translocation translocation time the startic stranslocation translocation translo	1	2.3896	0.2488	1285.65	1286.472	1	562.6	63.636364 F.T1K2E1G1E1R4L1V1G111P1A1.K
gi 6322505 ref NP_012579.1	YJR045C	associated protein import motor (PAW); Involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p Mitochondrial matrix ATPase that is a subunit of the presequence translocase-	3	4.0198	0.2876	1555.46	1554.833	9	689.2	50 F.TKEGERLVGIPAKR.Q
gi 6322505 ref NP_012579.1	YJR045C	associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p Mitochondrial matrix ATPase that is a subunit of the presequence translocase-	2	3.0987	0.2584	1682.01	1682.964	1	426.4	53.571426 F.TKEGERLVGIPAKRQ.A
gi 6322505 ref NP_012579.1	YJR045C	associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p Mitochondrial matrix ATPase that is a subunit of the presequence translocase-	2	3.1014	0.2489	1192.23	1190.385	4	256.1	65 A.EAYLGKPVKNA.V
gi 6322505 ref NP_012579.1	YJR045C	associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p	2	4.0544	0.3052	2211.59	2212.508	1	627.9	52.499996 M.EGKVPKIIENAEGSRTTPSVV.A
gi 6322505 ref NP_012579.1	YJR045C	Mitochondrial matrix AI Pase trait is a subunit of the presequence translocase- associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p	2	4.001	0.2113	2458.41	2459.764	2	361.7	38.636364 M.E1G1K2V1P1K2I1I1E1N2A1E1G1S1R4T1T1P1S1V1V1A1F1.T
	VIDAGO	Mitochondrial matrix ATPase that is a subunit of the presequence translocase- associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family;	2	2 0075	0.4004	2000 40	2008 402	7	205 7	
gil6322505 ref NP_012579.1	YJR045C	Scrip Mitochondrial matrix ATPase that is a subunit of the presequence translocase- associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family;	3	3.9075	0.1861	3896.18	3898.492	1	225.7	20.945946 A. IKDAGUIVGLNVLKVVNEPIAAALAYGLEKSDSKVVAV.F
gi 6322505 ref NP_012579.1	YJR045C	Ssc1p Mitochondrial matrix ATPase that is a subunit of the presequence translocase- associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding mapping of the host of head section 20 (HBCR) heading	2	3.9728	0.3772	1522.35	1522.67	1	1496.1	83.33333 F.KTETGIDLENDRM.A
gi 6322505 ref NP_012579.1	YJR045C	Matix and protein roomy, member of the near shock protein rooms, instruction of the resequence translocase- associated protein import motor (PAM); involved in protein translocation into the	2	3.4839	0.1671	1538.01	1540.67	1	1018.3	83.33333 F.K2T1E1T1G111D1L1E1N2D1R4M1.A
gi 6322505 ref NP_012579.1	YJR045C	matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p	2	2.9558	0.2366	1270.57	1270.472	1	463.3	68.181816 F.TKEGERLVGIPA.K
gil6322524/refINP_012598.1	YJR064W	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo: Cct5p	2	3.5102	0.2005	1838.37	1838.129	1	883.4	64.28571 N. VMDKDRKDVDFDLIK.M
gil6322524/refINP_012598.1	Y.IR064W	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo: Cct5n	2	3 7474	0.3986	2221.33	2221 549	6	277.8	32 5 T S1I 1G1P1R4G1I 1D1K2I1I 1IIS1P1D1G1E1I1T1IIT1 N
	V IDoc 4W/	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	-	0.0070	0.0007	2400.05	2400 540	ů,	2000 7	
gilo322524[rei]NP_012596.1]	TJKU64W	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for	2	3.2978	0.3087	2196.85	2190.549		386.7	37.5 T.SLGPRGLUNILISPUGETTT.N
gi 6322524 ref NP_012598.1	YJR064W	the assembly of actin and tubulins in vivo; Cct5p	3	3.8747	0.1832	1977.77	1980.249	4	808	43.333332 D.K2D1F1S1H3P1Q2M\$P1K2C1V1L1P1K2E1.G
gi 6322536 ref NP_012610.1	YJR076C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc11p	2	3.28	0.1758	1923.81	1922.061	1	707.4	56.666668 L.DNSPSFEIISDYIRHQ.Y
gi 6322536 ref NP_012610.1	YJR076C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc11p	2	2.9361	0.2099	1430.43	1429.619	6	248.4	70 Q.REKELREIEAR.L
gi 6322536 ref NP_012610.1	YJR076C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc11p Larce subunit of carbamovi phosphate svnthetase, which catalyzes a step in the	2	3.9768	0.2053	1448.29	1450.619	1	279.8	70 Q.R4E1K2E1L1R4E1I1E1A1R4.L
gi 6322569 ref NP_012643.1	YJR109C	synthesis of citrulline, an arginine precursor; Cpa2p	2	4.1304	0.3124	1968.19	1967.238	1	838.5	66.66667 L.A1D1K2I1Y1Y1L1P1V1T1P1E1Y1I1T1Y1.I
gi 6322569 ref NP_012643.1	YJR109C	synthesis of citrulline, an arginine precursor; Cpa2p	1	2.4692	0.1613	1453.36	1454.712	1	506.2	58.333332 M.N2F1H3V1P1L1P1P1S1G1I1L1F1.G
gi 6322569 ref NP_012643.1	YJR109C	synthesis of citrulline, an arginine precursor; Cpa2p	2	3.247	0.2057	1260.21	1260.421	6	402.2	68.181816 T.R4L1A1G1A1D1P1F1L1G1V1E1.M
gi 6322569 ref NP_012643.1	YJR109C	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; Cpa2p	3	4.0938	0.1502	3921.41	3920.432	1	341	21.212122 E.YDIKAVFNLASKRAESTDDVDYIMRRNAIDFAIP.L
gi 6322569 ref NP_012643.1	YJR109C	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; Cpa2p	2	4.0061	0.3384	1457.43	1456.711	1	689.7	61.538464 K.A1F1L1G1G1D1I1V1P1K2P1V1D1L1.M
ail6322569/refINP 012643.1	YJR109C	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor: Cpa2p	1	3.0618	0.2498	1409.64	1410.682	1	551	68.181816 Y.III1E1L1E1R4P1D1A1I1L1L1.T
gil6322569/refINP_012643.1	V IR109C	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the	1	2 9532	0 2741	1453.68	1454 712	1	585.2	58 333332 M N2E1H3V1P1I 1P1P1S1G1I1I 1E1 G
	VID400C	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the		2.0002	0.2741	4 004 00	4000.005		000.2	
gilo322569[rei]NP_012643.1]	TJR 109C	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the	2	2.9996	0.2805	1601.63	1602.905	0	339.6	50 1.M\$NZF1H3V1P1E1P1P151G11E1F1.G
gij6322569/ret/NP_012643.1	YJR109C	syntnesis or citrulline, an arginine precursor; Cpa2p Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the	2	2.9854	0.2419	1439.01	1438.712	5	323	58.333332 M.NEHVPLPPSGILE.G
gi 6322569 ref NP_012643.1	YJR109C	synthesis of citrulline, an arginine precursor; Cpa2p Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the	2	3.4751	0.3463	1454.21	1454.712	1	491.5	70.83333 M.N2F1H3V1P1L1P1P1S1G1I1L1F1.G
gi 6322569 ref NP_012643.1	YJR109C	synthesis of citrulline, an arginine precursor; Cpa2p Large subunit of carbamovl phosphate synthetase. which catalvzes a sten in the	2	4.1574	0.4037	1588.01	1586.905	1	1311.7	76.92308 T.M1N2F1H3V1P1L1P1P1S1G1I1L1F1.G
gi 6322569 ref NP_012643.1	YJR109C	synthesis of citrulline, an arginine precursor; Cpa2p	2	2.9731	0.1933	1568.85	1569.905	1	635.9	57.692307 T.MNFHVPLPPSGILF.G
gi 6322569 ref NP_012643.1	YJR109C	synthesis of citrulline, an arginine precursor; Cpa2p	2	3.6617	0.2789	1339.01	1338.608	1	841.7	77.27273 N.F1H3V1P1L1P1P1S1G1I1L1F1.G

gi 6322569 ref NP_012643.1	YJR109C	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; Cpa2p Highly conserved zinc metalloprotease that functions in two steps of a-factor	2	3.0402	0.164	1302.43	1302.56	4	685	75 S.K2V1N2Y1P1V1L111R4P1S1.Y
gi 6322577 ref NP_012651.1	YJR117W	maturation, U-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing; contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor	2	4.1973	0.358	2430.61	2430.628	1	798.2	57.5 L.SETKLPPVLEDEIDDETFHKS.R
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing; contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor maturation. Cutarminal CAX proteolysis and the first step of N-terminal proteolytic	2	4.575	0.3549	2455.21	2455.628	1	793.2	55 L.S1E1T1K2L1P1P1V1L1E1D1E111D1D1E1T1F1H3K2S1.R
gi 6322577 ref NP_012651.1	YJR117W	processing; contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor	1	3.3965	0.2074	1447.67	1447.72	1	814.9	68.181816 K.TILDHPNIPWKL.I
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing: contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor	1	3.8536	0.3668	1463.65	1464.72	1	921.1	68.181816 K.T111L1D1H3P1N2I1P1W2K2L1.I
gi 6322577 ref NP_012651.1	YJR117W	Institutation, C-terminal CAAR proteolysis and the first step of in-terminal proteolytic processing: contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor	2	3.4388	0.1812	1448.43	1447.72	1	1000.2	81.818184 K.TILDHPNIPWKL.I
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAX proteolysis and the tirst step of N-terminal proteolytic processing; contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor	1	3.0194	0.2994	1450.6	1450.693	1	470.2	54.545456 L.D1H3P1N2I1P1W2K2L1111S1.G
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing; contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor maturation. C-terminal CAAX proteolysis and the first step of N-terminal proteolytic.	1	3.2596	0.3405	1432.63	1433.693	1	705.9	63.636364 L.DHPNIPWKLIIS.G
gi 6322577 ref NP_012651.1	YJR117W	Processing: contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor matrix factor. C transmed CA AV protective in and the first data of M Jermion Lastracturities	2	3.092	0.228	1338.19	1336.621	1	1190.1	88.88889 F.I1K2Y1D1L1F1P1K2I1W2.H
gi 6322577 ref NP_012651.1	YJR117W	Initiatiation, Greenimia CARA proteotysis and the first size for Preterminal proteotysic processing; contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor maturation. C teramical CAV persteables and the first other of M teramical persteablish	2	2.9257	0.2027	1781.35	1781.117	1	399	50 K.T1I1L1D1H3P1N2I1P1W2K2L1I1I1S1.G
gi 6322577 ref NP_012651.1	YJR117W	Processing: contains multiple transmembrane spans; Ste24 Highly conserved zinc metalloprotease that functions in two steps of a-factor	3	4.167	0.3556	2429.21	2430.628	1	886	40 L.SETKLPPVLEDEIDDETFHKS.R
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAA proteolysis and the first step of N-terminal proteolytic processing: contains multiple transmerbrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor	2	4.8475	0.4935	2113.87	2113.329	1	561.8	61.764706 T.KLPPVLEDEIDDETFHKS.R
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing: contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor	2	3.7066	0.2959	2097.85	2097.234	2	412.3	44.11765 L.S1E1T1K2L1P1P1V1L1E1D1E111D1D1E1T1F1.H
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing; contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor maturation. C terminal CAX proteolscies and the first steps of N-terminal proteolytic	2	3.4501	0.2543	2078.53	2078.234	1	658.7	52.941177 L.SETKLPPVLEDEIDDETF.H
gi 6322577 ref NP_012651.1	YJR117W	Induation, Creminal Order processing and the mass specific processing processing and the processing an	2	5.3918	0.3749	2134.45	2135.329	1	496.3	64.70589 T.K2L1P1P1V1L1E1D1E111D1D1E1T1F1H3K2S1.R
gi 6322577 ref NP_012651.1	YJR117W	Processing: contains multiple transmembrane spans; Ste24 Highly conserved zinc metalloprotease that functions in two steps of a-factor	1	3.332	0.2911	1446.59	1447.72	1	1019.8	68.181816 K.TILDHPNIPWKL.I
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing: contains multiple transmembrane spans; Ste24p Highly conserved zinc metalloprotease that functions in two steps of a-factor	2	3.0103	0.1601	1448.91	1447.72	1	995.5	81.818184 K. TILDHPNIPWKL.I
gi 6322577 ref NP_012651.1	YJR117W	maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing; contains multiple transmembrane spans; Ste24p	2	3.2779	0.2157	1761.67	1761.117	1	342	46.42857 K.TILDHPNIPWKLIIS.G
gi 6322578 ref NP_012652.1	YJR118C	Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed DNA synthesis-induced filamentous growth; llm1p	3	5.6187	0.4017	4297.82	4299.251	1	514.2	22.297297 K.TETTEIIEIINDEENDDEDGKDNDDNNEKGNDDSDAKK
gi 6322578 ref NP_012652.1	YJR118C	Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed DNA synthesis-induced filamentous growth; Ilm1p	2	3.9084	0.2423	1682.25	1684.886	1	591.9	62.5 N.A111R4E1E1K2N2E1E1F1K2R4L1.N
gi 6322578 ref NP_012652.1	YJR118C	Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed DNA synthesis-induced filamentous growth; Ilm1p	3	4.9611	0.2689	4348.58	4347.251	1	391	K.T1E1T1T1E11111E11111N2D1E1E1N2D1D1E1D1G1K2D1N2D1D1N2N2E1K2G1N2 18.243242 D1D1S1D1A1K2K2
gi 6322578 ref NP_012652.1	YJR118C	required for slowed DNA synthesis-induced filamentous growth; IIm1p	2	2.9951	0.2443	1871.67	1872.174	8	373.7	43.333332 N.GVHDLIPLLENNVKYF.Q
gi 6322578 ref NP_012652.1	YJR118C	Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed DNA synthesis-induced filamentous growth; Ilm1p Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'- untranslated region contains a putative mRNA localization element common to genes	2	3.7261	0.2835	1662.15	1662.886	1	702.9	66.66667 N.AIREEKNEEFKRL.N
gi 6322582 ref NP_012656.1	YJR122W	encoding mitochondrial proteins; Caf17p Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'- untranelated region contains a putative mBNA localization element compone to dense	2	3.9682	0.3151	1959.25	1960.196	1	943.3	56.666668 Q.FPNLPKDIENPWFDNL.L
gi 6322582 ref NP_012656.1	YJR122W	encoding micchondria proteins; Caf17p Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta	2	4.8235	0.2365	1983.53	1981.196	1	1322.3	73.333336 Q.F1P1N2L1P1K2D111E1N2P1W2F1D1N2L1.L S.G1F1E1E1D1T1K2W2D1E1N2F1L1D1V1G1D1D1D1E1N2D1D1E1G1D1L1T1E1K
gi 6322592 ref NP_012666.1	YJR132W	homolog; Nmd5p Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta	3	5.1885	0.2279	4292.63	4295.397	1	512.8	19.285715 2Y1L1E1L111K2.N
gi 6322592 ref NP_012666.1	YJR132W	homolog; Nmd5p Karvopherin, a carrier protein involved in nuclear import of proteins: importin beta	1	2.5791	0.266	1457.67	1458.675	1	249.3	50 L.RHLTPADQELFM.G
gi 6322592 ref NP_012666.1	YJR132W	homolog; Nmd5p Karvonherin, a carrier protein involved in nuclear import of proteins: importin beta	3	4.4669	0.3699	4252.31	4253.397	1	761.8	21.428572 S.GFEEDTKWDENFLDVGDDDENDDEGDLTEKYLELIK.N
gi 6322592 ref NP_012666.1	YJR132W	homolog; Nmd5p	3	4.2736	0.2096	3491.66	3493.453	1	707.4	27.586206 S.GFEEDTKWDENFLDVGDDDENDDEGDLTEK.Y
gi 6322592 ref NP_012666.1	YJR132W	Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta homolog; Nmd5p	3	4.1376	0.1835	3655.91	3656.629	1	449.9	25 S.GFEEDTKWDENFLDVGDDDENDDEGDLTEKY.L
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	4.9864	0.3395	1911.43	1909.018	1	1007.1	78.57143 L.W2T1H3N2D1E1L1L1P1D1W2G1F1Q2Q2.Q
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.6333	0.3555	1889.87	1887.018	1	790.7	71.42857 L.WTHNDELLPDWGFQQ.Q

gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.8371	0.2819	2022.61	2023.177	1	491.3	56.666668 A.L1W2T1H3N2D1E1L1L1P1D1W2G1F1Q2Q2.Q
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	1	2.7934	0.3465	1572.47	1572.674	1	886.8	66.66667 W.THNDELLPDWGFQ.Q
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	1	3.0378	0.3677	1589.43	1590.674	1	792.7	66.66667 W.T1H3N2D1E1L1L1P1D1W2G1F1Q2.Q
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.5444	0.2485	1588.77	1590.674	1	686	70.83333 W.T1H3N2D1E1L1L1P1D1W2G1F1Q2.Q
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.8159	0.312	1758.21	1758.887	1	1099.3	84.61539 L.WTHNDELLPDWGFQ.Q
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.9545	0.324	2000.43	2000.177	1	503.8	60.000004 A.LWTHNDELLPDWGFQQ.Q
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	2.9052	0.2479	1866.23	1866.126	1	415.8	50 K.IWYPKEVVFDEVHFG.K
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.6214	0.3878	1501.31	1499.77	1	1426.4	81.818184 S.YFFDVHPPFAKM.M
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	1	3.0211	0.3606	1513.52	1514.77	1	491.3	59.090908 S.Y1F1F1D1V1H3P1P1F1A1K2M1.M
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	1	2.735	0.3027	1500.95	1499.77	1	539.3	59.090908 S.YFFDVHPPFAKM.M
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.2742	0.2414	1586.95	1586.848	1	502.2	58.333332 R.SYFFDVHPPFAKM.M
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	4.2046	0.2641	2105.73	2107.392	5	588.1	50 N.K2K2V1I1D1P1S1N2N2W2V1V1D1E1I1V1N2L1.D
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.0391	0.3392	1384.43	1382.577	1	907.2	70 S.Y1F1F1D1V1H3P1P1F1A1K2.M
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.7549	0.3584	1515.39	1514.77	1	1416.6	81.818184 S.Y1F1F1D1V1H3P1P1F1A1K2M1.M
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.6953	0.2737	1999.59	2000.264	1	864	60.000004 E.HWLLQPLPEPESRYSF.W
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.8294	0.1863	1955.33	1955.218	1	1139.1	56.25 K.KVIDPSNNWVVDEIVNL.D
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	3.5458	0.266	1777.77	1778.887	1	542.9	65.38461 L.W2T1H3N2D1E1L1L1P1D1W2G1F1Q2.Q
gi 6322603 ref NP_012677.1	YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate- D-mannose to protein serine/threonine residues; appears to form hornodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	2	2.9079	0.1688	1515.59	1514.77	1	493.4	59.090908 S.Y1F1F1D1V1H3P1P1F1A1K2M1.M
gi 6322604 ref NP_012678.1	YJR144W	Protein involved in mitochondrial genome maintenance; component of the mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p	2	5.4108	0.3436	2205.57	2206.541	1	1132.7	61.11111 K.VQKDLIEPLDPKDIEIKPD.G
gi 6322604 ref NP_012678.1	YJR144W	Protein involved in mitochondrial genome maintenance; component of the mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p	3	3.9925	0.2561	3005.21	3006.55	1	1701.9	35 Q.KDLIEPLDPKDIEIKPDGLIYLPEIK.Y
gi 6322604 ref NP_012678.1	YJR144W	mitochondral nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p Portain involved in mitochondrial genome maintenance; component of the	3	6.7996	0.444	3551.75	3553.177	1	1886.2	37.068966 K.VQKDLIEPLDPKDIEIKPDGLIYLPEIKYR.R
gi 6322604 ref NP_012678.1	YJR144W	mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p Portain involved in mitochondrial gapone mointenance, component of the	3	4.5955	0.2029	2229.23	2229.541	1	1422.1	47.22222 K.V1Q2K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1.G
gi 6322604 ref NP_012678.1	YJR144W	mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p Protein involved in mitochondrial genome maintenance; component of the	2	5.0894	0.1889	2228.99	2229.541	1	1099.2	61.11111 K.V1Q2K2D1L111E1P1L1D1P1K2D111E111K2P1D1.G
gi 6322604 ref NP_012678.1	YJR144W	mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p	2	3.3985	0.1664	2000.59	1999.278	1	673.8	59.375 Q.K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1.G

		Protein involved in mitochondrial genome maintenance; component of the								
ail6322604/refINP 012678.11	YJR144W	mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mom101p	3	4.2909	0.2779	3264.14	3266.813	1	574.1	25.925926 K.V1Q2K2D1L11E1P1L1D1P1K2D111E111K2P1D1G1L111Y1L1P1E111K2.Y
51		Protein involved in mitochondrial genome maintenance; component of the								
gi 6322604 ref NP 012678.1	YJR144W	mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p	3	6.5767	0.3103	3235.25	3233.813	1	2012.5	37.962963 K.VQKDLIEPLDPKDIEIKPDGLIYLPEIK.Y
		Protein involved in mitochondrial genome maintenance; component of the								
gi 6322604 ref NP_012678.1	YJR144W	mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p	3	5.3779	0.374	3006.92	3006.55	1	2600.7	40 Q.KDLIEPLDPKDIEIKPDGLIYLPEIK.Y
		Protein involved in mitochondrial genome maintenance; component of the								
gi 6322604 ref NP_012678.1	YJR144W	Mgm101p	2	3.3311	0.2594	3005.27	3006.55	1	266.8	30.000002 Q.KDLIEPLDPKDIEIKPDGLIYLPEIK.Y
		Protein involved in mitochondrial genome maintenance; component of the mitochondrial pucket required for the repair of ovidative mtDNA damage:								
gi 6322604 ref NP_012678.1	YJR144W	Mgm101p	3	6.6163	0.4206	3035.39	3036.55	1	2436.1	41 Q.K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1G1L1I1Y1L1P1E1I1K2.Y
		Protein involved in mitochondrial genome maintenance; component of the mitochondrial nucleoid, required for the repair of oxidative mtDNA damage;								
gi 6322604 ref NP_012678.1	YJR144W	Mgm101p	3	7.1167	0.4335	3589.88	3591.177	1	1932.6	37.931034 K.V1Q2K2D1L111E1P1L1D1P1K2D111E1I1K2P1D1G1L111Y1L1P1E1I1K2Y1R4.R
		Protein involved in mitochondrial genome maintenance; component of the mitochondrial nucleoid, required for the repair of oxidative mtDNA damage;								
gi 6322604 ref NP_012678.1	YJR144W	Mgm101p	3	3.8709	0.2334	3324.47	3325.913	1	517.3	23.148148 Q.KDLIEPLDPKDIEIKPDGLIYLPEIKYR.R
		highly expressed during stationary phase and repressed during logarithmic phase;								
gi 6322608 ref NP_012682.1	YJR148W	Bat2p Outosolic branched-chain amino acid aminotransferase, homolog of murine ECA39:	1	2.4314	0.2151	1383.62	1384.629	1	543.3	54.166668 K.K2E1L1V1T1A1P1L1D1G1T1I1L1.E
		highly expressed during stationary phase and repressed during logarithmic phase;								
gi 6322608 ref NP_012682.1	YJR148W	Bat2p Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39:	2	3.9975	0.2642	1384.29	1384.629	1	961	70.83333 K.K2E1L1V1T1A1P1L1D1G1T1I1L1.E
		highly expressed during stationary phase and repressed during logarithmic phase;								
gi 6322608 ref NP_012682.1	YJR148W	Bat2p Cvtosolic branched-chain amino acid aminotransferase, homolog of murine ECA39;	2	3.3479	0.2444	1903.25	1904.136	1	640.5	56.666668 S.AQRICLPTFDPEELIT.L
		highly expressed during stationary phase and repressed during logarithmic phase;								
gi 6322608 ref NP_012682.1	YJR148W	Bat2p Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39;	2	4.0931	0.2958	2038.35	2038.296	1	575.9	53.125 S.A1Q2R4I1C1L1P1T1F1D1P1E1E1L1I1T1L1.I
		highly expressed during stationary phase and repressed during logarithmic phase;		4 5007	0.0000	0017.07	0017 000		500	
gi 6322608 ret NP_012682.1	YJR148W	Bat2p Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine	2	4.5097	0.3999	2017.67	2017.296	1	532	53.125 S.AQRICLPTFDPEELITE.I
gi 6322852 ref NP_012925.1	YKL001C	metabolism; Met14p	2	3.0303	0.2261	1470.41	1469.614	1	601.3	68.181816 D.Q2K2T1V1E1E1C1A1T1I1I1Y1.E
gi 6322852 ref NP_012925.1	YKL001C	metabolism; Met14p	1	2.3994	0.236	1277.62	1278.467	5	110	50 Y.E1A1P1K2A1P1E1L1H3L1R4.T
gil63228521refINP_012925.11	YKL001C	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism: Met14p	2	3.1774	0.2862	1277.87	1278.467	1	411.7	85 Y.E1A1P1K2A1P1E1L1H3L1R4.T
3.1		Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine								
gi 6322852 ref NP_012925.1	YKL001C	metabolism; Met14p Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine	3	4.5746	0.3782	1541.51	1540.759	1	1440	60.416668 A.P1Y1E1A1P1K2A1P1E1L1H3L1R4.T
gi 6322852 ref NP_012925.1	YKL001C	metabolism; Met14p	1	2.3392	0.1899	1277.68	1278.467	1	149	60.000004 Y.E1A1P1K2A1P1E1L1H3L1R4.T
gi 6322852 ref NP_012925.1	YKL001C	Adenyiyisuirate kinase, required for suirate assimilation and involved in methionine metabolism; Met14p	2	4.1256	0.3982	1698.17	1700.916	1	592.8	60.714287 I.S1A1P1Y1E1A1P1K2A1P1E1L1H3L1R4.T
ail63228521rofIND_012025_11	VKI 001C	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine matchelism: Mat14p.	2	4 4208	0 3308	1611 70	1612 838	1	845.3	73.07602.5.0101V1E10101K20101E11.1H31.1D4.T
gilo3220321161141 _012323.11	TREOUTE	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine	2	4.4230	0.5550	1011.73	1012.000		040.0	75.01092 S.AIFTTTEIAITTIZAITTETETISEIK4.1
gi 6322852 ref NP_012925.1	YKL001C	metabolism; Met14p Negative regulator of transcription elongation, contains a TEIIS-like domain and a	2	3.1044	0.2568	1666.51	1664.842	1	524.9	66.66667 T.W2H3P1N2L1T1Y1D1E1R4K2A1L1.R
		PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably								
gi 6322848 ref NP_012921.1	YKL005C	binds RNA polymerase II large subunit; Bye1p Negative regulator of transcription elongation, contains a TFIIS-like domain and a	2	4.8211	0.2773	2457.41	2455.813	1	668.5	50 K.TRYEKDFYIVPSKGGEIPEIL.K
		PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably								
gi 6322848 ret NP_012921.1	YKL005C	binds RNA polymerase II large subunit; Bye1p Negative regulator of transcription elongation, contains a TFIIS-like domain and a	2	5.1814	0.3727	2480.55	2481.813	1	835.7	57.5 K. 11R4Y1E1K2D1F1Y111V1P1S1K2G1G1E111P1E111L1.K
-:::::::::::::::::::::::::::::::::::::	V/KI 0050	PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably	2	0 7400	0.4000	2024.02	2004 404		010.0	
gilo322848/rei/NP_012921.1/	TKLUUSC	Negative regulator of transcription elongation, contains a TFIIS-like domain and a	3	6.7108	0.4209	3224.03	3224.404	1	919.0	30 A.K25 IDTITATETNZETMTPTTTR4K2DTFTETSTETKZETH3K2LTR4TTNZ.A
ail6322848/refINP_012921_1	YKI 005C	PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably binds RNA polymerase II large subunit: Bye1p	3	4 6423	0 2816	3183 92	3184 464	1	415.6	27 000002 A KSDTAENEMPTRKDEESEKEHKI RYN A
310022010101111 _012021111	11120000	Ubiquitin-protein ligase (E3) that interacts with Rpt4p and Rpt6p, two subunits of the	0		0.2010	0100.02	01011101	·	110.0	
ail6322842/refINP 012915.11	YKL010C	19S particle of the 26S proteasome; cytoplasmic E3 involved in the degradation of ubiquitin fusion proteins; Ufd4p	1	2.8845	0.2764	1416.64	1417.651	1	491.7	62.5 L.GQHPVGRTLPEIL.S
51		Ubiquitin-protein ligase (E3) that interacts with Rpt4p and Rpt6p, two subunits of the								
gi 6322842 ref NP 012915.1	YKL010C	19S particle of the 26S proteasome; cytoplasmic E3 involved in the degradation of ubiquitin fusion proteins; Ufd4p	2	3.7503	0.1695	1965.35	1965.963	1	1291.7	63.333332 S.STEADREEEENCLDHM.R
		Ubiquitin-protein ligase (E3) that interacts with Rpt4p and Rpt6p, two subunits of the								
gi 6322842 ref NP_012915.1	YKL010C	ubiquitin fusion proteins; Ufd4p	2	3.3699	0.2551	2054.67	2055.158	2	465.6	46.875 L.E1N2P1S1T1P1D1K2T1E1E1D1W2K2G1I1W2.S
		Ubiquitin-protein ligase (E3) that interacts with Rpt4p and Rpt6p, two subunits of the								
gi 6322842 ref NP_012915.1	YKL010C	ubiquitin fusion proteins; Ufd4p	2	3.0254	0.1544	1479.61	1478.775	7	387.8	57.692307 Q.F1L1T1G1S1P1K2L1P1I1G1G1F1K2.S
		Ubiquitin-protein ligase (E3) that interacts with Rpt4p and Rpt6p, two subunits of the 19S particle of the 26S proteasome: cytoplasmic E3 involved in the degradation of								
gi 6322842 ref NP_012915.1	YKL010C	ubiquitin fusion proteins; Ufd4p	2	2.9633	0.2385	2032.33	2033.158	2	437.6	43.75 L.ENPSTPDKTEEDWKGIW.S
		Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs, associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the								
gi 6322838 ref NP_012911.1	YKL014C	biogenesis of the 60S ribosomal subunit; Urb1p	2	3.0485	0.1831	1690.45	1690.936	1	779.1	69.230774 N.E1F1H3T1R4I1P1D1L1P1I1F1V1S1.T
		associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the								
gi 6322838 ref NP_012911.1	YKL014C	biogenesis of the 60S ribosomal subunit; Urb1p Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs	2	2.979	0.3197	1950.55	1951.341	4	318.6	43.75 Y.F1D1F1S1L1P111L1P1R4L1L1V1P1S1K2S1.E
		associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the								
gi 6322838 ref NP_012911.1	YKL014C	biogenesis of the 60S ribosomal subunit; Urb1p Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs.	2	3.6618	0.4394	1495.93	1496.75	1	624.7	75 F.HTRIPDLPIFVST.L
		associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the	~	0.0400	0.0400	1050.00	4052 000	-		
gilo322838[ret]NP_012911.1]	TKLU14C	biogenesis of the 605 ribosomal subunit; Urb1p	2	2.9439	0.2408	1053.29	1053.333	5	664.4	15 Q.LTNPILKLL.K

		Nucleolar protoin required for the normal accumulation of 25S and 5.8S rPNAs								
ail63228381refINP_012911_1	YKI 014C	associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the biogenesis of the 60S ribosomal subunit. [161]	2	3 4034	0 2868	1690 59	1690 875	1	369.4	46 42857 K S1R4I 1P102D1D1111 1N2N2I1G1T11 1 R
gilo322030[rel[NF_012311.1]	TREOT40	Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs,	2	3.4034	0.2000	1030.33	1050.075		505.4	
gi 6322838 ref NP_012911.1	YKL014C	biogenesis of the 60S ribosomal subunit; Urb1p	2	5.2012	0.4154	2158.47	2159.305	1	2059.9	70.588234 W.E1F111K2D1E1E1E1E1I1L1E1A111G1D1T1R4.L
		Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs, associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the								
gi 6322838 ref NP_012911.1	YKL014C	biogenesis of the 60S ribosomal subunit; Urb1p Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs,	2	3.5009	0.353	1674.09	1671.936	1	456.9	61.538464 N.EFHTRIPDLPIFVS.T
gi 6322838 ref NP_012911.1	YKL014C	associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the biogenesis of the 60S ribosomal subunit; Urb1p	2	3.0381	0.3227	1514.85	1514.75	1	346.9	62.5 F.H3T1R4I1P1D1L1P1I1F1V1S1T1.L
		Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs, associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the								
gi 6322838 ref NP_012911.1	YKL014C	biogenesis of the 60S ribosomal subunit; Urb1p Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs.	2	2.9631	0.3498	1396.01	1395.644	1	370.7	72.72727 F.HTRIPDLPIFVS.T
ail63228381refINP_012911_1	VKI 014C	associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the biogenesis of the 60S ribosomal subunit.	2	3 1565	0 2368	1206.45	1205 442	1	497 3	
giloszzosoficiliti _012311.1	TRE0140	Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs, associated with the 27SA2 pre-incoment particles proposed to be involved in the	2	0.1000	0.2000	1200.40	1200.442		437.5	
gi 6322838 ref NP_012911.1	YKL014C	biogenesis of the 60S ribosomal subunit; Urb1p	2	5.6854	0.3223	2139.79	2137.305	1	1984.8	70.588234 W.EFIKDEEEEILEAIGDTR.L
-10000001{IND_040044_41	XKI 014C	associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the	2	0.4750	0 2027	4700.00	4722.000	2	050.4	
gilo322838[rel[NP_012911.1]	TKL014C	Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs,	2	3.1750	0.3037	1732.33	1733.069	3	258.1	42.007143 T.FIDIFISILIPIILIPIK4LILIVIPISI.K
gi 6322838 ref NP_012911.1	YKL014C	associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the biogenesis of the 60S ribosomal subunit; Urb1p	2	3.2554	0.2792	1414.03	1412.644	1	316.6	68.181816 F.H3T1R4I1P1D1L1P1I1F1V1S1.T
		Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase								
gi 6322833 ref NP_012906.1	YKL019W	that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor; Ram2p	2	5.0365	0.4303	2115.99	2115.313	1	1372.8	68.75 N.K2E1L1D1W2L1D1E1V1T1L1N2N2P1K2N2Y1.Q
		Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase								
ail63228331refINP 012906.11	YKL019W	that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor; Ram2p	2	3.2657	0.2139	1476.23	1475.638	4	862.6	63.636364 N.KELDWLDEVTLN.N
J		Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase								
ail63228331rofIND_012006_11		that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Pas proteins and a factor; Pam ² n	2	3 2255	0.2404	1363 71	1361 535	2	809.4	
giloszzosoficiliti _012500.1	INEOTOW	Alpha automit of both the foregoultransforege and tune I gerenulgerenultransforege	2	0.2200	0.2434	1000.71	1001.000	2	003.4	00 NALEBWEDE VIEW
		that catalyze prevalution of proteins containing a CAAX consensus motif; essential		0.0045	0.0055	1071.05	1071 505			
gi 6322833 ref NP_012906.1	YKLU19W	protein required for memorane localization of Kas proteins and a-factor; Kam2p	2	3.3245	0.2355	1374.85	1374.535	1	897.3	80 N.KZE1LID1WZLID1E1V111L1.N
		Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential								
gi 6322833 ref NP_012906.1	YKL019W	protein required for membrane localization of Ras proteins and a-factor; Ram2p	2	3.8365	0.309	2678.67	2678.955	1	401.6	42.857143 Y.D1Y1S1D1V1K2P1L1P111E1T1D1L1Q2D1E1L1C1R4I1M1.Y
		Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential								
gi 6322833 ref NP_012906.1	YKL019W	protein required for membrane localization of Ras proteins and a-factor; Ram2p Protein essential for cell growth and replication of M dsRNA virus; contains four beta-	2	3.1182	0.2838	2651.89	2651.955	1	531.9	45.238094 Y.DYSDVKPLPIETDLQDELCRIM.Y
gi 6322831 ref NP_012904.1	YKL021C	transducin repeats; Mak11p Protein essential for cell growth and replication of M dsRNA virus; contains four beta-	2	3.3686	0.3153	2542.55	2543.858	1	381.4	40.476192 L.S1L1D111P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1.H
gi 6322831 ref NP_012904.1	YKL021C	transducin repeats; Mak11p Protein essential for cell growth and replication of M dsRNA virus; contains four beta-	3	4.7875	0.1946	3009.08	3012.049	4	407.9	28.125 C.E1E1L1F1E1K2V1E1E1N2E1K2Q2E1D1D1D1D1K2E1D1I1S1P1A1.F
gi 6322831 ref NP_012904.1	YKL021C	transducin repeats; Mak11p Bratein expendition of M de DNA visuo; contains four both	3	4.9192	0.3785	3583.1	3583.657	1	758.8	26.785713 H.F1Y1P1C1E1E1L1F1E1K2V1E1E1N2E1K2Q2E1D1D1D1D1K2E1D1I1S1P1A1.F
gi 6322831 ref NP_012904.1	YKL021C	transducin repeats; Mak11p	3	5.0356	0.4695	2627.42	2629.938	1	903.2	40.476192 L.D111P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P111F1H3F1.Q
gi 6322831 ref NP_012904.1	YKL021C	transducin repeats; Mak11p	3	4.0514	0.2081	2543.3	2543.858	1	561.1	35.714287 L.S1L1D111P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1.H
gi 6322831 ref NP_012904.1	YKL021C	Protein essential for cell growth and replication of M dSRNA virus; contains four beta- transducin repeats; Mak11p	2	3.9585	0.4235	2542.65	2543.858	1	309	40.476192 L.S1L1D111P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P111F1.H
gi 6322831 ref NP_012904.1	YKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta- transducin repeats; Mak11p	2	4.0413	0.4295	2513.59	2514.858	1	341.9	40.476192 L.SLDIPNQKENDAAKTPHFMPIF.H
gi 6322831 ref NP_012904.1	YKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta- transducin repeats; Mak11p	2	5.2844	0.4464	2758.01	2760.069	1	740.4	45.454548 L.D111P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P111F1H3F1Q2.A
gi 6322831 ref NP_012904.1	YKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta- transducin repeats; Mak11p	2	4.6255	0.3492	2725.71	2727.069	1	642.3	45.454548 L.DIPNQKENDAAKTPHFMPIFHFQ.A
gi 6322831 ref NP 012904.1	YKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta- transducin repeats; Mak11p	2	3.5452	0.3746	2959.99	2962.307	1	350.3	37.5 L.S1L1D111P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1H3F1Q2.A
gi 6322831 ref NP 012904.1	YKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta- transducin repeats; Mak11p	3	5.429	0.3746	2929.58	2927.307	1	947	32.291664 L.SLDIPNQKENDAAKTPHFMPIFHFQ.A
gil6322831/refINP_012904.1	YKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta- transducin repeats: Mak11p	2	3.3805	0.3241	2629.43	2629.938	1	543.5	45.238094 L.D111P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P111F1H3F1.Q
gil6322831/ref/NP_012904_1	YKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta- transducin repeats: Mak11n	3	4 8339	0 3578	2960 3	2962 307	1	833.5	31 25 L S1I 1D11/P1N2O2K2E1N2D14141K2T1P1H3E1M1P1I/E1H3E1O2 4
gil6322831/ref/NP_012904.1	VKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta- transducin repeate: Mek11n	3	4.6074	0.4267	2508.74	2502.007	1	882.3	
gil0322831 refINE_012904.1	VKL 021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta-	2	2 4742	0.4207	2330.74	2330.330	1	416	
	INLUZIO	TFILE large subunit, involved in recruitment of RNA polymerase II to the promoter,	2	3.4/42	0.0420	2130.11	2199.110	1	410	L.N2K2E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1E
gijo322824jretjNP_012897.1	TKLU28W	activation of TFIIH, and promoter opening; 11a1p TFIIE large subunit, involved in recruitment of RNA polymerase II to the promoter,	3	4.6/74	0.3459	4507.49	4509.266	1	557.9	
gijb322824 ret NP_012897.1	YKLU28W	activation of IFIIH, and promoter opening; Ifa1p TFIIE large subunit, involved in recruitment of RNA polymerase II to the promoter,	3	7.6343	0.4992	4351.07	4352.162	1	2432.5	30.882303 N.KEEEEEEEEEEEEEEEEEEEEEEEEEEE
gi 6322824 ref NP_012897.1	YKL028W	activation of TFIIH, and promoter opening; Tfa1p TFIIE large subunit, involved in recruitment of RNA polymerase II to the promoter,	3	8.0651	0.5832	4464.89	4466.266	1	3761.2	32.857143 L.NKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
gi 6322824 ref NP_012897.1	YKL028W	activation of TFIIH, and promoter opening; Tfa1p TFIIE large subunit, involved in recruitment of RNA polymerase II to the promoter,	3	7.526	0.4655	4579.43	4579.425	1	1386.2	25 K.LNKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
ail6322824/refINP 012897.1	YKL028W	activation of TFIIH, and promoter opening: Tfa1p	3	6.7481	0.3484	4622.12	4623.425	1	1449.5	25.694445 D1E1T1A1R4E1N2.A

gi 6322824 ref NP_012897.1	YKL028W	TFIIE large subunit, involved in recruitment of RNA polymerase II to the promoter, activation of TFIIH, and promoter opening; Tfa1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to	3	8.6648	0.5778	4390.76	4393.162	1	2936.3	N.K2E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1E1
gi 6322823 ref NP_012896.1	YKL029C	pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to	3	5.6986	0.4112	2602.64	2601.791	1	1065.4	40.476192 T.R4E1N2T1F1Q2K2P1Y1S1D1E1E1V1T1K2T1P1V1G1S1R4.A
gi 6322823 ref NP_012896.1	YKL029C	pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to	2	3.2438	0.1537	2593.79	2593.905	2	573.7	42.857143 R.FRKPEGVFLDITEPDSIECRLA.T
gi 6322823 ref NP_012896.1	YKL029C	pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to	2	3.5254	0.2641	1657.39	1655.761	1	1713.5	80.769226 Y.RYELPSFNDDIQGT.G
gi 6322823 ref NP_012896.1	YKL029C	pyrtuvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to	2	3.1055	0.2551	1674.23	1674.761	2	699	57.692307 Y.R4Y1E1L1P1S1F1N2D1D111Q2G1T1.G
gi 6322823 ref NP_012896.1	YKL029C	pyrtuvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amin acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to meanter which is a key intermediate to uncare activations not a resource for the second secon	2	3.2447	0.3504	1387.35	1387.703	1	1011.5	77.27273 H.IKELVPIIYTPT.E
gi 6322823 ref NP_012896.1	YKL029C	pyruvate, wino'r so d key mien rickulate in sugar instauousan and a precursor for synthesis of several amine rickulate in sugar instauousan and a precursor for Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to ovrruvate which is a key intermediate in surgar metabolism and a precursor for	2	3.0245	0.3028	2010.53	2013.215	1	424.3	50 L.REGDSRPGLLPGLDTITNT.S
gi 6322823 ref NP_012896.1	YKL029C	synthesis of several amino acids: Mae 1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to ovruvate, which is a key intermediate in sugar metabolism and a precursor for	2	3.239	0.2714	2568.91	2569.791	3	207.5	35.714287 T.RENTFQKPYSDEEVTKTPVGSR.A
gi 6322823 ref NP_012896.1	YKL029C	synthesis of several amino acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for	2	4.4748	0.4312	2407.85	2409.667	1	554.8	50 R.FRKPEGVFLDITEPDSIECR.L
gi 6322823 ref NP_012896.1	YKL029C	synthesis of several amino acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for	2	2.9379	0.1615	1209.41	1209.466	1	847.9	87.5 Q.MWEPVYRPM.I
gi 6322823 ref NP_012896.1	YKL029C	synthesis of several amino acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for	2	2.9351	0.279	2656.49	2657.863	1	176.2	34.782608 E.QEQVPGGAPGETVKVPRDFDECLQ.W
gi 6322823 ref NP_012896.1	YKL029C	synthesis of several amino acids; Mae1p Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for	3	5.6625	0.329	2569.19	2569.791	1	1114.7	39.285713 T.RENTFQKPYSDEEVTKTPVGSR.A
gi 6322823 ref NP_012896.1	YKL029C	synthesis of several amino acids; Mae1p UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of	1	2.2171	0.1783	1101.8	1102.325	1	408.5	60.000004 C.GGIHPGRVLPV.C
gi 6322815 ref NP_012889.1	YKL035W	UDP-Gic trom glucose 1-phosphate and UTP, involved in a wide vanety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.4603	0.4378	2066.43	2067.269	1	1273.4	67.64706 Y.K2D1S1L1L1P1V1P1T1E1Y1D1S1P1L1D1A1W2.Y
gi 6322815 ref NP_012889.1	YKL035W	UDP-Git Chron glucose pylopinospinotypase (UOP ase), catanyses the reversible chromosomer uDP-Git Chron glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.1499	0.3856	2787.73	2788.085	1	783.2	41.6666664 D.SLLPVPTEYDSPLDAWYPPGHGDLF.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	1	2.5231	0.3157	1448.74	1450.604	1	327.1	59.090908 L.N2R4Q2Y1D1S1D1V1P1L1L1L1.M
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	3.4103	0.2237	1316.21	1314.438	1	383.4	75 F.NTDKDTEHLIK.K
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	1	3.6201	0.3015	1466.61	1466.634	1	551.7	57.692307 C.SDGHKIDIPNGSIL.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	3.0585	0.265	1468.51	1466.634	8	483.2	57.692307 C.SDGHKIDIPNGSIL.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	1	3.4705	0.2996	1483.52	1484.634	1	648.4	61.538464 C.S1D1G1H3K2I1D111P1N2G1S111L1.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	5.3016	0.466	3061.23	3062.348	1	761.7	42.307693 Y.K2D1S1L1L1P1V1P1T1E1Y1D1S1P1L1D1A1W2Y1P1P1G1H3G1D1L1F1.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	3	5.0139	0.3901	3061.88	3062.348	1	509.1	27.884615 Y.K2D1S1L1L1P1V1P1T1E1Y1D1S1P1L1D1A1W2Y1P1P1G1H3G1D1L1F1.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-GIc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	5.0338	0.4102	2082.41	2083.342	1	1155.9	59.375 T.L1E1W2D1K2I1K2S1P1N2P1D1E1V1V1K2Y1.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-GIc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.7333	0.3437	3031.71	3031.348	1	806	42.307693 Y.KDSLLPVPTEYDSPLDAWYPPGHGDLF.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	2.9152	0.2326	1545.81	1546.735	2	424.9	68.181816 V.P1K2E1H3I1D1E1F1K2N2I1R4.K
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.9136	0.4013	2052.71	2053.326	1	938.8	62.5 L.EVAQVPKEHIDEFKNIR.K

gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	3.2069	0.1954	2423.09	2422.743	3	157.4	39.473686 L.SVRQIEYLNRQYDSDVPLLL.M
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	3.4386	0.3075	1291.39	1291.455	1	978.9	81.818184 R.HFDGAHGVVVPR.S
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.1776	0.3776	1525.87	1526.735	1	1539	86.36364 V.PKEHIDEFKNIR.K
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.3869	0.4328	2537.59	2535.818	1	810.8	47.5 S.S1R4T1T1L1E1W2D1K2I1K2S1P1N2P1D1E1V1V1K2Y1.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.036	0.3875	2504.99	2506.818	1	1158.1	55 S.SRTTLEWDKIKSPNPDEVVKY.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	3	4.1716	0.3136	1527.08	1526.735	1	1192.7	52.272724 V.PKEHIDEFKNIR.K
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	2.932	0.1829	1752.97	1753.999	1	229.5	57.692307 A.QVPKEHIDEFKNIR.K
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	1	2.5665	0.2092	1432.63	1433.604	1	217.8	50 L.NRQYDSDVPLLL.M
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.5188	0.2756	1948.17	1948.183	1	804	60.000004 L.EWDKIKSPNPDEVVKY.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	3	3.8623	0.1656	1946.6	1948.183	1	791.1	40 L.EWDKIKSPNPDEVVKY.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.903	0.4393	3061.53	3062.348	1	858	44.230766 Y.K2D1S1L1L1P1V1P1T1E1Y1D1S1P1L1D1A1W2Y1P1P1G1H3G1D1L1F1.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	3	4.3229	0.5233	3028.76	3031.348	1	514.9	28.846153 Y.KDSLLPVPTEYDSPLDAWYPPGHGDLF.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	3	4.8391	0.4117	3060.5	3062.348	1	602.5	28.846153 Y.K2D1S1L1L1P1V1P1T1E1Y1D1S1P1L1D1A1W2Y1P1P1G1H3G1D1L1F1.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.9173	0.3529	2060.73	2061.342	1	1780	65.625 T.LEWDKIKSPNPDEVVKY.E
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.6155	0.4781	2078.35	2079.326	1	766.7	62.5 L.E1V1A1Q2V1P1K2E1H3I1D1E1F1K2N2I1R4.K
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	3.1564	0.2539	1877.13	1879.056	1	594.7	50 Y.K2D1S1L1L1P1V1P1T1E1Y1D1S1P1L1D1A1.W
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	2	4.6469	0.4098	2045.73	2047.269	1	1035.7	61.764706 Y.KDSLLPVPTEYDSPLDAW.Y
gi 6322815 ref NP_012889.1	YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and	2	4.1885	0.287	1969.53	1969.183	1	660.1	60.000004 L.E1W2D1K2I1K2S1P1N2P1D1E1V1V1K2Y1.E
gi 6322790 ref NP_012863.1	YKL060C	gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and	3	4.2592	0.3106	2928.32	2928.993	1	592.3	30.000002 T.GGEEDGVNNENADKEDLYTKPEQVYN.V
gi 6322790 ref NP_012863.1	YKL060C	gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and	3	4.4103	0.3289	2960.42	2961.993	1	918	33 T.G1G1E1E1D1G1V1N2N2E1N2A1D1K2E1D1L1Y1T1K2P1E1Q2V1Y1N2.V
gi 6322790 ref NP_012863.1	YKL060C	gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and	2	3.6422	0.2856	2959.83	2961.993	1	232.7	34 T.G1G1E1E1D1G1V1N2N2E1N2A1D1K2E1D1L1Y1T1K2P1E1Q2V1Y1N2.V
gi 6322790 ref NP_012863.1	YKL060C	gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for dlycolvsis and	2	3.7029	0.3743	2928.39	2928.993	1	196.1	32 T.GGEEDGVNNENADKEDLYTKPEQVYN.V
gi 6322790 ref NP_012863.1	YKL060C	gluconeogenesis; catalyzes the conversion of fructuse 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p	3	4.1609	0.1782	2814.26	2814.89	6	490.8	29.166666 T.GGEEDGVNNENADKEDLYTKPEQVY.N

	V/// 0000	Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate;		4 0500	0.0000	0400.00	0101 000	0	004.0	
gi 6322790 ref NP_012863.1	YKL060C	Fba1p Fructose 1.6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the conversion of fructose 1.6 bisphosphate into two 3-	3	4.0529	0.2982	3189.68	3191.302	2	331.2	23.148148 1.GGEEDGVNNENADKEDLY I KPEQVYNVY.K
gi 6322790 ref NP_012863.1	YKL060C	callobn products, grycerateringer-sprinsprate and univorsysteetine prosprate, Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and disconconcenesis: catalyzes the conversion of fructose 1.6 bisphosphate into two 3-	2	4.8257	0.3692	2056.37	2057.178	1	426.4	59.375 N.ENADKEDLYTKPEQVYN.V
gi 6322790 ref NP_012863.1	YKL060C	carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and	2	3.5129	0.1855	2342.55	2343.486	3	190.1	36.11111 N.E1N2A1D1K2E1D1L1Y1T1K2P1E1Q2V1Y1N2V1Y1.K
gi 6322790 ref NP_012863.1	YKL060C	gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Pba1p	2	4.9303	0.3624	2103.31	2101.382	1	763.6	47.22222 K.DYIMSPVGNPEGPEKPNKK.F
ail6322790/refINP_012863.11	YKL060C	Fructose 1,5-bisphosphate aldolase, a cytosolic enzyme required tor glycopisis and gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fhatn	1	2 7208	0 2333	989 44	990 151	1	291 9	88 75 V K2411 1H3P111S1P1N2 F
910022100101111 _012000.11	1120000	Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate;	·	2.1200	0.2000	000111	000.101		20110	
gi 6322790 ref NP_012863.1	YKL060C	Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3-	1	2.5443	0.2047	976.46	977.151	5	299.4	68.75 Y.KALHPISPN.F
gi 6322790 ref NP_012863.1	YKL060C	carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and clucopeonegae; and phosphate aldolase, a further of 6 bisphosphation to the 3-	2	4.4598	0.3627	2078.97	2079.178	3	216.6	46.875 N.E1N2A1D1K2E1D1L1Y1T1K2P1E1Q2V1Y1N2.V
gi 6322790 ref NP_012863.1	YKL060C	guconecyclinesis, caranyzes ind colineration of inductive no signification in two of carbon products: glyceratidehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1.6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and	2	4.0454	0.4631	1725.77	1725.942	1	730.7	63.333332 M.SPVGNPEGPEKPNKKF.F
gi 6322790 ref NP_012863.1	YKL060C	gluconeogenesis; catalyzes the conversion of fructose 1.6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p	2	4.3902	0.4862	1745.51	1746.942	1	1135.2	70 M.S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2F1.F
ail6322700/rofIND_012863_11	XKI 060C	Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyses the conversion of fructose 1,6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Ebath	2	4 6217	0.317	2254.07	2255 556	1	1008.2	55 263157 K K2D1Y11M151D11/161N2D15161D151K2D1N2K2K2 E
gilo322790[181]NF_012803.1]	TREUGUC	Fuctors 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and glyconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: olyceratleb/wed-3-biosphate and dih/droxyxaetome obosphate:	2	4.0217	0.317	2234.07	2233.330	I	1006.2	33.20313/ N.R.2011111110131F1V101192F1E101F1E102F102R2R2.F
gi 6322790 ref NP_012863.1	YKL060C	Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3-	2	2.9738	0.1511	2794.85	2796.128	3	182.6	28.260868 K.D1Y111M1S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2F1F1D1P1R4.V
gi 6322790 ref NP_012863.1	YKL060C	carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeonensis: catalyzes the conversion of fructose 1.6 bisphosphate into two 3-	2	3.1157	0.2806	2762.19	2764.128	1	366.3	36.95652 K.DYIMSPVGNPEGPEKPNKKFFDPR.V
gi 6322790 ref NP_012863.1	YKL060C	carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and	2	2.9106	0.2646	3085.01	3084.474	5	110.4	26 K.D1Y1I1M1S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2F1F1D1P1R4V1W2.V
gi 6322790 ref NP_012863.1	YKL060C	gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products; glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p Fba1p	2	3.7637	0.3785	1599.89	1598.765	1	433.9	57.14286 M.S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2.F
gi 6322790 ref NP_012863.1	YKL060C	I double the double of the second sec	2	3.9681	0.4153	1578.53	1578.765	1	830	71.42857 M.SPVGNPEGPEKPNKK.F
	V/// 0000	Fructose 1.6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the conversion of fructose 1.6 bisphosphate into two 3- carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate;		0.0000	0.0540	0010.15	0011 007		005.0	
gij6322790 ret NP_012863.1	YKL060C	Foatp Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3- carbon products: olverarighethwids-3-bhosphate and diffivitorxyaretone obosphate:	3	3.9808	0.2519	2012.15	2011.207	1	825.2	39./05883 M.STPTVTGTNZPTETGTPTETKZPTNZKZKZETFTUT.P
gi 6322790 ref NP_012863.1	YKL060C	Fba1p Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide	2	3.0918	0.3517	2242.77	2241.511	1	254.1	47.368423 M.SPVGNPEGPEKPNKKFFDPR.V
gi 6322777 ref NP_012850.1	YKL073W	translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	2	3.9391	0.3316	1643.89	1644.934	1	738	60.714287 D.S1L1L1D111V1K2P1I1N2D1A1V1T1K2.Q
gi 6322777 ref NP_012850.1	YKL073W	increased and considered on an emotopatistic detail and international of the power of the translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	2	4.151	0.3739	1628.57	1626.934	1	754.1	60.714287 D.SLLDIVKPINDAVTK.Q
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	3	4.6358	0.2683	2756.51	2757.072	1	715.6	28.40909 Q.FETEFADTIDNVREEFKKIKQPA.Y
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	2	3.7158	0.2664	2757.29	2757.072	1	231.1	36.363636 Q.FETEFADTIDNVREEFKKIKQPA.Y
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	3	4.9427	0.4066	2250.35	2250.56	1	1166.6	40.27778 E.FADTIDNVREEFKKIKQPA.Y
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	2	4.5588	0.3028	2250.21	2250.56	1	367.7	44.444447 E.FADTIDNVREEFKKIKQPA.Y

gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	2	3.5548	0.1789	1746.43	1747.004	1	876	65.38461 N.LFGEDLREHLFEIK.L
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	3	3.8344	0.2757	2609.57	2609.896	1	785.7	30.952381 F.ETEFADTIDNVREEFKKIKQPA.Y
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	3	5.8963	0.3987	2789.72	2788.072	1	1418.5	39.772728 Q.F1E1T1E1F1A1D1T111D1N2V1R4E1E1F1K2K2I1K2Q2P1A1.Y
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	2	3.0978	0.2942	2755.49	2757.072	1	244.8	34.090908 Q.FETEFADTIDNVREEFKKIKQPA.Y
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	2	3.5501	0.3009	2110.03	2108.318	1	421	50 K.RLPGYGKDDPNGIERIYGS.A
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	2	3.9364	0.3701	2276.95	2277.56	1	469.3	50 E.F1A1D1T1I1D1N2V1R4E1E1F1K2K2I1K2Q2P1A1.Y
gi 6322777 ref NP_012850.1	YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	3.1722	0.2733	1963.75	1964.188	1	334.7	50 K.RLPGYGKDDPNGIERIY.G
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	3.2357	0.1884	1893.61	1892.223	1	585.3	60.000004 N.AYRTLPINNMPVPEYL.E
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	3.6496	0.2935	1429.29	1426.612	1	673.5	72.72727 L.HDIVKPEDFVLN.S
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	5.4576	0.4521	2306.47	2307.619	1	1060.2	63.88889 N.A1Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1E1N2F1.Q
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	1	3.1055	0.1598	1561.61	1562.702	1	538.6	62.5 K.S1L1K2S1D1F1E1K2S1Y1E1T1L1.S
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	1	2.5778	0.3297	1546.63	1547.702	1	447.3	58.333332 K.SLKSDFEKSYETL.S
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	4.7052	0.2542	1646.29	1644.85	1	795.8	69.230774 R.S1L1H3D1I1V1K2P1E1D1F1V1L1N2.S
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	4.7488	0.3344	2086.37	2087.364	1	654.9	59.375 Y.R4T1L1P111N2N2M\$P1V1P1E1Y1L1E1N2F1.Q
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	5.2461	0.4698	2046.47	2048.364	1	986.3	68.75 Y.RTLPINNMPVPEYLENF.Q
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	3	4.6928	0.3721	3615.02	3617.015	1	425	N.D1F1I1L11IS1L1P1Q2N2A1Q2P1V1T1A1P1G1S1K2T1D1S1W2F1N2E1T1L1I1G1 25 G1R4.A
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	1	3.453	0.1861	1387.71	1387.703	6	605.5	63.636364 F.KLDKSIKDLITL.I
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	4.945	0.4356	2323.19	2323.619	1	919.2	58.333332 N.A1Y1R4T1L1P1I1N2N2M\$P1V1P1E1Y1L1E1N2F1.Q
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the	2	5.4989	0.3574	2071.23	2071.364	1	1194.3	68.75 Y.R4T1L1P111N2N2M1P1V1P1E1Y1L1E1N2F1.Q
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-	2	5.1886	0.4511	2284.97	2282.619	1	1764	75 N.AYRTLPINNMPVPEYLENF.Q
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-	2	4.3349	0.2607	1627.55	1626.85	1	838.1	73.07692 R.SLHDIVKPEDFVLN.S
gi 6322770 ref NP_012843.1	YKL080W	A r r ase (v-x1 r ase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-	2	3.8237	0.2429	2064.91	2064.364	1	658.5	56.25 Y.RTLPINNM@PVPEYLENF.Q
gi 6322770 ref NP_012843.1	YKL080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	4.2065	0.358	2237.03	2235.54	2	353.1	47.058823 A.Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1E1N2F1.Q

		Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
ail6322770/refINP 012843.1	YKL080W	membrane: Vma5p	2	2.9736	0.2517	2212.99	2211.54	1	537.3	47.058823 A.YRTLPINNMPVPEYLENF.Q
2/100-2010-01/01/01 2010-01/1		Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
ail6202770/rofIND 012942 1		endomembrane system; required for the V1 domain to assemble onto the vacuolar	2	2 060	0 2224	1207 57	1207 702	1	1021 6	
gilo322770[lei]NF_012643.1]	TREUGUW	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-	2	3.909	0.2224	1307.37	1367.703		1031.0	61.616164 F.REDKSIRDEITE.I
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6322770 ref NP_012843.1	YKL080W	membrane; Vma5p Subupit C of the eight-subupit V1 peripheral membrane domain of vacualar H+-	1	2.8572	0.1711	1205.44	1206.416	2	728.4	66.66667 S.D1F1K2I1P1E1F1K2I1G1.S
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6322770 ref NP_012843.1	YKL080W	membrane; Vma5p	1	2.5978	0.1774	1193.54	1194.416	6	574.2	61.11111 S.DFKIPEFKIG.S
		Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-								
		endomembrane system: required for the V1 domain to assemble onto the vacuolar								
gi 6322770 ref NP_012843.1	YKL080W	membrane; Vma5p	2	3.2529	0.2502	1913.71	1913.223	2	445	56.666668 N.A1Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1.E
		Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-								
		A I Pase (V-A I Pase), an electrogenic proton pump found throughout the and membrane system; required for the V1 domain to assemble onto the vacualar								
gil6322770/refINP 012843.1	YKL080W	membrane: Vma5p	2	4.6711	0.4999	2298.39	2298.619	1	1453.2	66.66667 N.AYRTLPINNM@PVPEYLENF.Q
		Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
gil6322770/rofINP_012843_1	VKI 080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar	2	4 7031	0 3710	2285 55	2282 610	1	1102.0	
gil0322770[tel[14F_012043.1]	TREODOW	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-	2	4.7031	0.3713	2200.00	2202.019		1132.3	
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6322770 ref NP_012843.1	YKL080W	membrane; Vma5p Subunit C of the eight subunit V/1 perioberal membrane demain of viscualer H i	3	4.6468	0.3248	2306.48	2307.619	1	696.6	37.5 N.A1Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1E1N2F1.Q
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6322770 ref NP_012843.1	YKL080W	membrane; Vma5p	3	4.6015	0.3174	2283.17	2282.619	1	1517.8	48.61111 N.AYRTLPINNMPVPEYLENF.Q
		Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6322770 ref NP_012843.1	YKL080W	membrane; Vma5p	2	5.5646	0.4129	2308.59	2307.619	1	1074.7	63.88889 N.A1Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1E1N2F1.Q
		Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-								
		A I Pase (V-A I Pase), an electrogenic proton pump found throughout the andomembrane system; required for the V1 domain to assemble onto the vacualar								
gil6322770/refINP 012843.1	YKL080W	membrane: Vma5p	1	3,1693	0.1957	1439.82	1440.685	1	283.9	65 A.A1R4E1K2K2F1I1P1R4E1F1.N
		Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
gil6322770/rofINP_012843_1	VKI 080W	endomembrane system; required for the V1 domain to assemble onto the vacuolar	1	2 0677	0 2223	1421 74	1/21 695	1	250.6	
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.2603	0.1662	1240.35	1240.288	1	617.7	72.22222 A.F1D1V1A1P1D1W2E1S1Y1.E
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.4748	0.2967	1696.23	1696.793	2	379.8	65.38461 K.L1D1P1T1K2E1E1D1K2E1F1V1N2N2.M
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.3349	0.2083	1806.53	1806.967	1	591.2	64.28571 T.KLDPTKEEDKEFVNN.M
gil6322769/refINP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.5258 5.0461	0.2472	2330.39	2331.556	3	276.3	52.77778 Y.EYTKLDPTKEEDKEEVNNM.W
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.4682	0.2357	1299.57	1300.501	5	126.2	65 Q.VADEKERARLL.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.24	0.3339	2862.83	2864.285	1	204.4	26 K.IIV1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi 6322769 ref NP_012842.1 gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.6392	0.2193	1317.5	1318.501 2864 285	3	135.2	65 Q.VTATDTETKZETK4ATK4LTLT.G 24 K IIIVIDTI 1E1O2S1S1E1E1A1S1I 1E1P1I 1K2O2A1P1A1E1I 1G1P1K2 G
gil6322769/refINP_012842.1	YKL081W	Translation elongation factor EF-1 gamma: Tef4p	3	4.3431	0.272	2834.03	2834.285	1	804.7	31 K.IVDLEQSSEFASLFPLKQAPAFLGPK.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	5.4104	0.416	3038.12	3036.496	1	913.3	30.555555 K.I1V1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2G1L1.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.5259	0.1784	1386.52	1386.594	1	570.6	66.66667 T.F1V1L1D1D1W2K2R4K2Y1.S
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	5.3444	0.4027	3177.41	3176.68	1	1367.6	33.035713 L.DVKIVDLEQSSEFASLFPLKQAPAFLGPK.G
gil6322769/refINP_012842.1	YKL081W	Translation elongation factor EF-1 gamma: Tef4p	2	3.3893	0.1700	1389.43	1386.594	1	1074.3	88.88889 T.F1V1L1D1D1W2K2R4K2Y1.S
5100 0101 =0 01										L.D1V1K2I1V1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2G1L1
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	4.7055	0.287	3383.42	3382.891	4	455.4	20.833332 .K
gi 6322769 ret NP_012842.1 gi 6322769 ref NP_012842.1	YKL081W	I ranslation elongation factor EF-1 gamma; Tef4p	3	4.0081	0.2396	3344.06 2244.37	3346.891	2	538.6 697.1	21.666666 L.DVKIVDLEQSSEFASLFPLKQAPAFLGPKGL.K 52.499996 S S1E1E141S1I 1E1P1I 1K2O241P141E1I 1C1P1K2C1I 1 K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	3.849	0.3163	2859.65	2858.168	1	471.4	31.818182 S.T1F1V1L1D1D1W2K2R4K2Y1S1N2D1D1T1R4P1V1A1L1P1W2.F
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	3.9212	0.2262	2242.4	2243.632	2	841.2	31.25 S.S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2G1L1.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.5932	0.2569	1116.67	1116.303	1	434.5	66.66667 Q.KAEKPKAEKS.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	5.1258	0.3316	2754.56	2756.063	1	520.8	34.523808 T.F1V1L1D1D1W2K2R4K2Y1S1N2D1D1T1R4P1V1A1L1P1W2.F
gil6322769/refINP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	5.4341	0.4594	2756.69	2756.063	1	298.5	78.125 W.D1K2P1V1V1V1V1V2G1E1D1K2E111V1D1G1K2.V
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	2.9996	0.1811	1554.41	1555.728	1	585.7	67.85714 E.KKKDEAKPADDAAPA.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.7453	0.4341	1937.49	1938.16	1	532	50 T.KLDPTKEEDKEFVNNM.W
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	5.5417	0.4129	2311.67	2311.561	1	1056.4	57.894737 M.W2A1W2D1K2P1V1V1V1N2G1E1D1K2E1I1V1D1G1K2.V
gil6322769/refINP_012842.1	YKL081W	Translation elongation factor EF-1 gamma: Tef4p	2	3.4274	0.3868	1475.37	1474.741	1	716.7	65.38461 V.A1A1S1P111V1K2T1P1F1A1E1V1K2.L
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.6123	0.3045	1460.39	1458.741	2	593.4	61.538464 V.AASPIVKTPFAEVK.L
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.8728	0.359	2861.85	2864.285	1	270.6	28 K.IIV1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gijo322769[ref]NP_012842.1	1KL081W YKL081W	rransiation elongation factor EF-1 gamma; Tef4p	3	4.6998	0.4029	3001.55	3004.496 1884 007	1	1093 668 9	33.333330 N.IVULEQSSEFASLFPLKQAPAFLGPKGL.K 58.823532 S.KAEKKKDEAKPADDAAPA K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.4619	0.195	1385.95	1386.594	1	954.7	77.77778 T.F1V1L1D1D1W2K2R4K2Y1.S
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.6219	0.267	1489.31	1488.699	1	846.4	80 S.T1F1V1L1D1D1W2K2R4K2Y1.S
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.4127	0.1716	1472.35	1471.699	3	574	70 S.TFVLDDWKRKY.S
gijo322769[ref]NP_012842.1 gi]6322769[ref]NP_012842.1	TKL081W YKL081W	rransiation elongation factor EF-1 gamma; Tef4p	2	4.6356	0.3392	1907.91	1386.594	1	395.4 486.2	06.666667 T.F1V1L1D1D1W2K2R4K2Y1.S
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.7952	0.2733	2069.69	2071.42	1	349.8	41.6666664 S.S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
			-						aa · -	
gi 6322769 ref NP_012842.1 gi 6322769 ref NP_012842.1	YKL081W	I ranslation elongation factor EF-1 gamma; Tef4p	3	5.0454	0.3956	3208.01	3210.68	1	881.7	29.464287 L.D1V1K2I1V1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2 1	3.185	0.2518	1069.58	1070.281	2	740.4	72.22222 L.K2Q2A1P1A1F1L1G1P1K2.G

gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	5.6761	0.3736	2610.86	2607.886	1	419.5	35 F.V1L1D1D1W2K2R4K2Y1S1N2D1D1T1R4P1V1A1L1P1W2.F
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.4505	0.2212	1704.39	1705.05	1	772.3	50 F.A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi 6322769 ref NP_012842.1 gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EE-1 gamma; Tef4p	2	4.0589	0.3001	2/24.77	2/23.003	1	870.1	35.7 14267 1.FVLDDWKKKTSNDDTKEVALEW.F 45.454548 K K2D1E141K2P141D1D14141P141K2K2P1K2H3P1L1E141L1 G
ail6322769/ref/NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.3094	0.2576	1635.61	1632.971	1	833.3	64.28571 A.S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.6047	0.1793	1101.44	1102.175	1	465.9	66.66667 N.G1E1D1K2E1I1V1D1G1K2.V
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.2522	0.304	1580.29	1582.634	1	326.8	62.5 L.D1P1T1K2E1E1D1K2E1F1V1N2N2.M
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.319	0.3263	1733.43	1732.882	2	373.9	46.666668 W.D1K2P1V1V1V1N2G1E1D1K2E1I1V1D1G1.K
gi 6322769 ref NP_012842.1	YKL081W	I ranslation elongation factor EF-1 gamma; Tet4p	1	2.7281	0.1813	1427.3	1428.473	1	404.5	61.11111 W.F1W2E1H3Y1N2P1E1E1Y1.S
gi[6322769]ref[NP_012842.1]	VKL081W	Translation elongation factor EE-1 gamma; Tel4p	2	3 505	0.2007	2222.13	2223.304	1	309.7	50.V EVTKI DDTKEEDKEEVNIN M
gil6322769/refINP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.7208	0.3049	2133.43	2147.373	1	733.4	53.125 T.K2L1D1P1T1K2E1E1D1K2E1E1V1N2N2M1W2.A
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.6707	0.2866	1414.53	1414.473	1	572.5	72.22222 W.FWEHYNPEEY.S
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	4.503	0.2716	2310.8	2311.561	1	1284.5	40.789474 M.W2A1W2D1K2P1V1V1V1N2G1E1D1K2E1I1V1D1G1K2.V
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.2977	0.1535	2286.53	2285.561	1	705.2	47.368423 M.WAWDKPVVVNGEDKEIVDGK.V
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	2.9154	0.1853	1563.21	1564.735	2	267.9	62.5 A.N2Q2V1A1D1E1K2E1R4A1R4L1L1.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.3106	0.1733	1710.39	1710.863	6	360.6	53.846157 T.K2L1D1P1T1K2E1E1D1K2E1F1V1N2.N
gi 6322769 ref NP_012842.1	YKL081W	I ranslation elongation factor EF-1 gamma; 1 ef4p	1	3.7008	0.3163	14/3.69	14/4./41	1	657.7	61.538464 V.A1A1S1P1I1V1K211P1F1A1E1V1K2.L
gi 6322769 ref NP_012842.1 gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	3.3573	0.3573	1457.57	1458.741	1	431 543.2	53.846157 V.AASPIVKTPFAEVK.L 44.44447 T.K2L1D1D1T1K2E1E1D1K2E1E1\/1N/2N1/M/2N1/M/2D
gil6322769/refINP_012842.1	YKL081W	Translation elongation factor EF-1 gamma, Tef4p	1	3 145	0.3107	1315.58	1316 583	1	481 7	63 636364 A SPIVKTPEAEVK I
ail6322769/ref/NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.2021	0.1755	1387.79	1386.594	2	455.2	61.11111 T.F1V1L1D1D1W2K2R4K2Y1.S
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.3668	0.2264	1387.39	1386.594	1	770.8	77.77778 T.F1V1L1D1D1W2K2R4K2Y1.S
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	4.2264	0.2407	2073.14	2071.42	1	1124	45.833336 S.S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.9506	0.4419	2047.57	2049.42	1	933.5	63.88889 S.SEFASLFPLKQAPAFLGPK.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.643	0.426	2073.07	2071.42	1	758.9	55.555557 S.S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.8745	0.3248	1056.6	1057.281	1	713.7	72.22222 L.KQAPAFLGPK.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.9555	0.3367	1343.33	1343.566	1	764.1	
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.8741	0.2701	1361.37	1360.566	1	1028.3	81.818184 S.KZATE1K2K2K2UTE1A1K2P1A1.U
gi 6322769 ref NP_012842.1 gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tel4p	2	3.9037	0.2929	2037.44	2037.271	4	473.9 520.5	50.5050505 S.NZATETNZNZNZUTETATNZPTATUTUTATATPTATNZ.N 50.4 D1D14141P141K2K2P1K2H3P11 1E1411 1 G
gil6322769/refINP_012842.1	YKL081W	Translation elongation factor EF-1 gamma, Tef4p	2	3 0203	0.2903	2242.67	2243 632	2	322.3	37.5.S.S1E1E1A1S1I 1E1P1I 1K202A1P1A1E1I 1G1P1K2G1I 1 K
gil6322769/ref/NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	4.1188	0.2367	2245.04	2243.632	2	885.7	31.25 S.S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2G1L1.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.1009	0.3329	1686.57	1686.05	1	1119	66.66667 F.ASLFPLKQAPAFLGPK.G
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.6085	0.3126	2084.57	2085.401	1	504.6	52.941177 L.T1Y1T1P1P1K2K2Q2K2A1E1K2P1K2A1E1K2S1.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.1125	0.294	2060.35	2060.401	1	449.6	50 L.TYTPPKKQKAEKPKAEKS.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.5036	0.2628	1980.07	1981.309	2	623.1	50 A.L1T1Y1T1P1P1K2K2Q2K2A1E1K2P1K2A1E1.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.6499	0.1849	1958.57	1958.309	1	604	53.125 A.LTYTPPKKQKAEKPKAE.K
gi 6322769 ref NP_012842.1	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	4.1271	0.355	1979.9	1981.309	1	946.4	40.625 A.L111Y111P1P1K2K2Q2K2A1E1K2P1K2A1E1.K 72.07603 S LEDLKOADAELODK C
gi[6322769]ref[NP_012842.1]	VKL081W	Translation elongation factor EE-1 gamma: Tef4p	2	3.5929	0.1909	1902 43	1905 193	1	706	56 25 A S1I 1E1D1I 1K202A1D1A1E1I 1C1D1K2C1I 1 K
gil0322703[tei]14F_012042.1]	INLOGIW	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and	2	3.0371	0.0000	1002.45	1005.105		700	30.23 A.31EIT IF IEIN202AIF IAIT IEIGIF IN201EI.N
ail6322765/refINP 012838.11	YKL085W	oxaloacetate: involved in the tricarboxylic acid (TCA) cycle: Mdh1p	2	3.6528	0.2656	2082.55	2082.191	1	705.9	58.333332 S.EVENTDPTQERVNVIGGHS.G
51		Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and								
gi 6322765 ref NP_012838.1	YKL085W	oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p	1	3.3448	0.3614	1475.46	1475.685	1	662.4	61.538464 L.GPDGIEKIHPIGEL.S
		Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and								
gi 6322765 ref NP_012838.1	YKL085W	oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p	2	3.9572	0.4974	2129.61	2131.434	1	504.1	40 F.ASPVTLGPDGIEKIHPIGELS.S
		Mitochondrial malate debudrogenase, catalyzes interconversion of malate and								
		wite nonunal malate denydrogenase, catalyzes miter conversion of malate and								
gi 6322765 ref NP_012838.1	YKL085W	oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p	2	4.1101	0.4274	2044.85	2044.356	1	528.7	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S
gi 6322765 ref NP_012838.1	YKL085W	microardinal material benchmodelinase, catalyzes matching and the material and oxaloacetate; involved in the tricarboxylic caid (TCA) cycle; Mdh1p Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic caid (TCA) cycle; Mdh1p Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic caid (TCA) cycle; Mdh1p	2	4.1101	0.4274	2044.85	2044.356	1	528.7	44.736843 F.ASPVTLGPDGIEKIHPIGELS
gi 6322765 ref NP_012838.1 gi 6322765 ref NP_012838.1	YKL085W YKL085W	Micotorolna interacte derplurgenase, catalyzes interconversion of manae and oxalaacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxalaacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Predicted phosphonantothenov/cystein decarboxylase, may be involved in	2 2	4.1101 3.1145	0.4274 0.3003	2044.85 1563.81	2044.356 1562.763	1 1	528.7 595.7	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S
gi 6322765 ref NP_012838.1 gi 6322765 ref NP_012838.1 ai 6322762 ref NP_012835.1	YKL085W YKL085W YKL088W	Micochordna manage derigingenase, catalyzes interconversion of manage and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzume A biosvnthesis; interacts with Sis2o and Vhs3p; Ykl088wp	2 2 2	4.1101 3.1145 2.9146	0.4274 0.3003 0.2067	2044.85 1563.81 1787.45	2044.356 1562.763 1787.139	1 1 1	528.7 595.7 402.5	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M
gi 6322765 ref NP_012838.1 gi 6322765 ref NP_012838.1 gi 6322762 ref NP_012835.1	YKL085W YKL085W YKL088W	Microtonana induced benchcologia. Set and the induced and the induced and oxalacectate; involved in the tricarboxylic caid (TCA) cycle; MdH1p Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxalacectate; involved in the tricarboxylic caid (TCA) cycle; MdH1p Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs2p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs2p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in the triangle of the triangle of triangle of the triangle of triangle of the triangle of triangl	2 2 2	4.1101 3.1145 2.9146	0.4274 0.3003 0.2067	2044.85 1563.81 1787.45	2044.356 1562.763 1787.139	1 1 1	528.7 595.7 402.5	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L111A1P1A1.M
gi 6322765 ref NP_012838.1 gi 6322765 ref NP_012838.1 gi 6322762 ref NP_012835.1 gi 6322762 ref NP_012835.1	YKL085W YKL085W YKL088W YKL088W	Microtordana materia benchurgenase, catalyzes materians of material and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Micochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2 2 2 2	4.1101 3.1145 2.9146 3.5387	0.4274 0.3003 0.2067 0.3747	2044.85 1563.81 1787.45 1782.65	2044.356 1562.763 1787.139 1785.067	1 1 1 1	528.7 595.7 402.5 559.4	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L111A1P1A1.M 64.28571 N.S111V1H3M1P1G1D1F1I1Y1F1N2P1K2.S
gi 6322765 ref NP_012838.1 gi 6322765 ref NP_012838.1 gi 6322762 ref NP_012835.1 gi 6322762 ref NP_012835.1	YKL085W YKL085W YKL088W YKL088W	Microtordan induce benytoreprise, catalyzes interconversion of manae and oxalaacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxalaacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in	2 2 2 2	4.1101 3.1145 2.9146 3.5387	0.4274 0.3003 0.2067 0.3747	2044.85 1563.81 1787.45 1782.65	2044.356 1562.763 1787.139 1785.067	1 1 1 1	528.7 595.7 402.5 559.4	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L111A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S
gi[6322765[ref]NP_012838.1] gi[6322765[ref]NP_012838.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W	Microtordia induct Berglangenase, catalyzes interconversion of manae and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; MdH1p Micochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; MdH1p Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507	0.4274 0.3003 0.2067 0.3747 0.3515	2044.85 1563.81 1787.45 1782.65 2056.43	2044.356 1562.763 1787.139 1785.067 2059.366	1 1 1 1	528.7 595.7 402.5 559.4 293.5	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q
gi[6322765]ref]NP_012838.1] gi[6322765]ref]NP_012838.1] gi[6322762]ref]NP_012835.1] gi[6322762]ref]NP_012835.1] gi[6322762]ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W	Micrototala involved in the tricarboxylic acid (TCA) cycle; Mdh1p Microtonaria involved in the tricarboxylic acid (TCA) cycle; Mdh1p Microtonarial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts With Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507	0.4274 0.3003 0.2067 0.3747 0.3515	2044.85 1563.81 1787.45 1782.65 2056.43	2044.356 1562.763 1787.139 1785.067 2059.366	1 1 1 1	528.7 595.7 402.5 559.4 293.5	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1IIV1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q
gi[6322765[ref]NP_012838.1] gi[6322765[ref]NP_012838.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W YKL088W	Microtordia in mate bench contracts, character and contract and contra	2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366	1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.VIM1R4D1W2S1P1L1T1P1V1L111A1P1A1.M 64.28571 N.S111V1H3M1P1G1D1F111Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q
gij6322765[ref]NP_012838.1] gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W YKL088W	Initiational and antice benchmodel and the control of the control	2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067	1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L111A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.86714 N.S1VLMPGCDEIVENEK S
gi[6322765[ref]NP_012838.1] gi[6322765[ref]NP_012838.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W YKL088W	Microfichal marke berglungenase, catalyzes markoniversion of marke and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Micochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69 1768.75	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067	1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1II1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V11IT1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S
gij6322765[ref]NP_012838.1] gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W	Mictoriolatian involved in the tricarboxylic acid (TCA) cycle; Mdh1p Mictorhondrian matter benydrogenase, catalyzes interconversion of matate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteline decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69 1768.75 1681.35	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885	1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.VIM1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S
gi[6322765[ref]NP_012838.1] gi[6322765[ref]NP_012838.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W	Initiation of the involved in the tricarboxylic acid (TCA) cycle; MdH p Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxalaacetate; involved in the tricarboxylic acid (TCA) cycle; MdH p Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69 1768.75 1681.35	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885	1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L111A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S
gi[6322765[ref]NP_012838.1] gi[6322765[ref]NP_012838.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W	Initiation of the involved in the tricarboxylic acid (TCA) cycle; MdH p Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxalacectate; involved in the tricarboxylic acid (TCA) cycle; MdH p Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69 1768.75 1681.35 2175.19	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47	1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q
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gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012838.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1]	YKL085W YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W	Initiation of the second secon	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977	1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1IIV1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V11IT1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.892307 L.D1V1V1Y1R4D1L1K2P1E1N211L1L1.D
gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012838.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W	Initiation of the interaction of	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977	1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D
gi[6322765[ref]NP_012838.1] gi[6322765[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012796.1] gi[6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W	Initiation of the interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977	1 1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1IIA1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1IIY1F1N2P1K2.S 41.17647 N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D
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gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012836.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W	Initiation of the intervent of the inter	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823	1 1 1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1	44.736843 F.ASPVTLGPDGIEKIHPIGELS. 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.33332 K.N2K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S
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gi[6322765[ref]NP_012838.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012796.1] gi]6322723[ref]NP_012796.1] gi]6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W	Initiational and the benchmarks of the second state of the second state of the second state is the second state of the second	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881	2044.85 1563.81 1787.45 1782.65 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2660.87	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823	1 1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.VIMIR4D1W2S1P1L1T1P1V1L1IIA1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1IIY1F1N2P1K2.S 41.17647 N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1IID1S1V1V1D1E1Y1L1S1E1.S
gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012838.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W YKL126W YKL126W	Initiation and an end of the second s	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997 3.0329	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881 0.4113 0.2087	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2660.87 2697.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823 2662.823	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3 378.1	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.33332 K.N2K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S 38.095238 S.NFDEEFTREKPIDSVVDEYLSE.S
gi[6322765[ref]NP_012838.1] gi[6322762[ref]NP_012838.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322723[ref]NP_012796.1] gi[6322723[ref]NP_012796.1] gi[6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W YKL126W YKL126W	Initiation and a method service of the service of t	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997 3.0329	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881 0.4113 0.2087	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2660.87 2697.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823 2662.823	1 1 1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3 378.1	44.736843 F.ASPVTLGPDGIEKIHPIGELS 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.33332 K.N2K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S 38.095238 S.NFDEEFTREKPIDSVVDEYLSE.S
gi[6322765[ref]NP_012838.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012796.1] gi]6322723[ref]NP_012796.1] gi]6322723[ref]NP_012796.1] gi]6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W YKL126W YKL126W	Initiational and the benchmarks of the second state of the second state of the second state is the second state of the second	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997 3.0329	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881 0.4113 0.2087	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2660.87 2697.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823 2662.823	1 1 1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3 378.1	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.VIMIR4D1W2S1P1L1T1P1V1L1IIA1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1IIY1F1N2P1K2.S 41.17647 N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V1IIT1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1IID1S1V1V1D1E1Y1L1S1E1.S 38.095238 S.NFDEEFTREKPIDSVVDEYLSE.S
gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012838.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012796.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W YKL126W YKL126W	Initiation and an analysis of the second sec	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997 3.0329	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881 0.4113	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2660.87 2697.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823 2662.823	1 1 1 1 1 1 1 1 1 1 1 1 1 1	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3 378.1	44.736843 F.ASPVTLGPDGIEKIHPIGELS 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.VIMIR4D1W2S1P1L1T1P1V1L1IIA1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S 38.095238 S.NFDEEFTREKPIDSVVDEYLSE.S
gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012838.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012796.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W YKL126W YKL126W	Initiation of the intervent of the inter	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997 3.0329 3.1419	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881 0.4113 0.2087	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2660.87 2697.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823 2662.823 2699.163	1 1 1 1 1 1 1 1 1 1 1 1 8	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3 378.1	44.736843 F.ASPVTLGPDGIEKIHPIGELS 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1IIA1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.33332 K.N2K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S 38.095238 S.NFDEEFTREKPIDSVVDEYLSE.S 30.434782 K.ILQEPLVFPDGFDRDAKDLLIGLLS
gi[6322765[ref]NP_012838.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012835.1] gi]6322762[ref]NP_012796.1] gi]6322723[ref]NP_012796.1] gi]6322723[ref]NP_012796.1] gi]6322723[ref]NP_012796.1] gi]6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W YKL126W YKL126W	Initiation and an end of the second s	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997 3.0329 3.1419	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881 0.2881 0.2087	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2660.87 2697.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823 2662.823 2699.163	1 1 1 1 1 1 1 1 1 1 1 1 8	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3 378.1 317.7	44.736843 F.ASPVTLGPDGIEKIHPIGELS 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V.1M1R4D1W2S1P1L1T1P1V1L111A1P1A1.M 64.28571 N.S111V1H3M1P1G1D1F111Y1F1N2P1K2.S 41.17647 N.K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N211L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P111D1S1V1V1D1E1Y1L1S1E1.S 38.095238 S.NFDEEFTREKPIDSVVDEYLSE.S 30.434782 K.ILQEPLVFPDGFDRDAKDLLIGLLS
gi[6322765[ref]NP_012838.1] gi[6322762[ref]NP_012838.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322762[ref]NP_012835.1] gi[6322723[ref]NP_012796.1] gi[6322723[ref]NP_012796.1] gi[6322723[ref]NP_012796.1] gi[6322723[ref]NP_012796.1] gi[6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W YKL126W YKL126W YKL126W	Initiation and an end of the second s	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997 3.0329 3.1419	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.4113 0.2087 0.1642	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2660.87 2697.69	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823 2662.823 2669.163 2239.597	1 1 1 1 1 1 1 1 1 1 1 1 8	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3 378.1 317.7	44.736843 F.ASPVTLGPDGIEKIHPIGEL.S 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1IIA1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1IIY1F1N2P1K2.S 41.17647 N.K2E1V1IIT1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.333332 K.N2K2E1V1IIT1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S 38.095238 S.NFDEEFTREKPIDSVVDEYLSE.S 30.434782 K.ILQEPLVFPDGFDRDAKDLLIGLLS
gij6322765[ref]NP_012838.1] gij6322762[ref]NP_012838.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322762[ref]NP_012835.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1] gij6322723[ref]NP_012796.1]	YKL085W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL088W YKL126W YKL126W YKL126W YKL126W	Initiation and an end of the second s	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4.1101 3.1145 2.9146 3.5387 3.507 4.3109 3.3226 2.9752 4.7176 3.7043 3.5963 3.8344 3.9997 3.0329 3.1419 3.8362	0.4274 0.3003 0.2067 0.3747 0.3515 0.3099 0.2884 0.1909 0.2681 0.3526 0.154 0.2881 0.2881 0.4113 0.2087 0.1642	2044.85 1563.81 1787.45 2056.43 2036.69 1768.75 1681.35 2175.19 2150.33 1708.31 2690.39 2690.39 2697.69 2240.59	2044.356 1562.763 1787.139 1785.067 2059.366 2037.366 1766.067 1680.885 2175.47 2151.47 1706.977 2689.823 2662.823 2669.163 2239.597	1 1 1 1 1 1 1 1 1 1 8 2	528.7 595.7 402.5 559.4 293.5 798.7 681.7 290 934.9 601.4 560.3 463.1 438.3 378.1 317.7 430.4	 44.736843 F.ASPVTLGPDGIEKIHPIGELS 53.571426 L.GPDGIEKIHPIGELS.S 43.333332 S.V1M1R4D1W2S1P1L1T1P1V1L1IIA1P1A1.M 64.28571 N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S 41.17647 N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 61.764706 N.KEVITAPTGPRVPFTEFF.Q 67.85714 N.SIVHMPGDFIYFNPK.S 45.833336 F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S 58.33332 K.N2K2E1V111T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q 47.22222 K.NKEVITAPTGPRVPFTEFF.Q 57.692307 L.D1V1V1Y1R4D1L1K2P1E1N2H1L1L1.D 38.095238 S.N2F1D1E1E1F1T1R4E1K2P1HD1S1V1V1D1E1Y1L1S1E1.S 38.095238 S.NFDEEFTREKPIDSVVDEYLSE.S 30.434782 K.ILQEPLVFPDGFDRDAKDLLIGLLS 30.434782 K.ILQEPLVFPDGFDRDAKDLLIGLLS

gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.6511	0.3028	2115.97	2117.372	2	477.7	53.125 L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1D1Y1Q2.G
gi 6322723 ref NP_012796.1	YKL126W	Serine/hreonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.7575	0.2049	2096.49	2094.372	1	1018.8	65.625 L.DVVYRDLKPENILLDYQ.G
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	3	4.2539	0.2766	2689.67	2689.823	1	716.4	34.523808 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.7508	0.2744	2675.97	2673.958	1	622.4	45.454548 N.MKDDDKTDTFCGTPEYLAPELLL.G
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.1924	0.2739	2004.85	2005.321	3	425.1	41.17647 L.VFPDGFDRDAKDLLIGLLS
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.6942	0.3432	2024.93	2027.321	1	629	47.058823 L.V1F1P1D1G1F1D1R4D1A1K2D1L1L111G1L1L1.S
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.8465	0.2109	2727.23	2728.163	1	326.1	32.608696 K.I1L1Q2E1P1L1V1F1P1D1G1F1D1R4D1A1K2D1L1L111G1L1L1.S
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	3	4.1585	0.2498	2731.13	2728.163	1	505.3	28.260868 K.I1L1Q2E1P1L1V1F1P1D1G1F1D1R4D1A1K2D1L1L111G1L1L1.S
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.5369	0.3354	1803.39	1805.009	1	359.5	57.14286 L.T1G1L1P1P1Y1Y1D1E1D1V1P1K2M1Y1.K
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.5794	0.4226	1787.49	1789.009	1	373.9	60.714287 L.TGLPPYYDEDVPKMY.K
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	2	3.2217	0.2552	2355.35	2357.47	5	265.6	36.11111 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1.L
gi 6322723 ref NP_012796.1	YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p Phosphoducomutase. minor isoform: catalvzes the conversion from dlucose-1-	3	4.26	0.3182	2692.19	2689.823	1	1026.2	35.714287 S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S
gi 6322722 ref NP_012795.1	YKL127W	phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p Phosphonlucomutase minor isoform: catalyzes the conversion from ducose-1-	2	3.7511	0.308	2288.33	2289.489	1	795.4	52.63158 Q.N2W2H3P1L1P1D1F1G1G1L1H3P1D1P1N2L1T1Y1A1.R
gi 6322722 ref NP_012795.1	YKL127W	phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p Phosphonlucomutase minor isoform: catalyzes the conversion from glucose-1-	2	2.9576	0.3419	2260.65	2262.489	1	668.3	44.736843 Q.NWHPLPDFGGLHPDPNLTYA.R
gi 6322722 ref NP_012795.1	YKL127W	phosphate to glucose-6-phosphate, which is a key strep in hexceme metabolism; Pgm1p Phosphate to glucose-6-phosphate, which is a key strep in hexcemetabolism; Pgm1p Phosphanelucomutase minor isoform: catalyzes the conversion from glucose-1-	2	3.0708	0.1724	2150.43	2148.385	3	296.5	36.11111 N.WHPLPDFGGLHPDPNLTYA.R
gi 6322722 ref NP_012795.1	YKL127W	phosphate to glucose-6-phosphate, which is a key streption or more glucose-1 phosphate to glucose-6-phosphate, which is a key streption hexces metabolism; Pgm1p Phosphonolucomutase minor isoform: catalyzes the conversion from glucose-1-	2	4.3697	0.4401	2217.61	2217.41	1	726.6	50 Q.N2W2H3P1L1P1D1F1G1G1L1H3P1D1P1N2L1T1Y1.A
gi 6322722 ref NP_012795.1	YKL127W	Phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-	2	3.6606	0.3126	2172.33	2173.385	1	437.1	41.6666664 N.W2H3P1L1P1D1F1G1G1L1H3P1D1P1N2L1T1Y1A1.R
gi 6322722 ref NP_012795.1	YKL127W	Prosphale to glucose-o-prosphale, which is a key step in nexose metabolism; Pgm1p Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-	2	4.396	0.3221	2100.39	2101.306	1	594.6	52.941177 N.W2H3P1L1P1D1F1G1G1L1H3P1D1P1N2L1T1Y1.A
gi 6322722 ref NP_012795.1	YKL127W	phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-	2	3.2985	0.304	2191.49	2191.41	1	628.3	47.22222 Q.NWHPLPDFGGLHPDPNLTY.A
gi 6322722 ref NP_012795.1	YKL127W	phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has	2	4.2	0.4248	2075.91	2077.306	1	581.1	55.88235 N.WHPLPDFGGLHPDPNLTY.A
gi 6322720 ref NP_012793.1	YKL129C	little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has	2	3.6159	0.2427	2268.79	2269.563	5	164.7	34.210526 N.G1I1T1D1K2N2K2D1Q2L1Q2K2D1L1I1E1L1I1G1T1.T
gi 6322720 ref NP_012793.1	YKL129C	little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has	2	3.6085	0.2053	1830.43	1830.089	1	821	63.333332 K.NKDQLQKDLIELIGTT.T
gi 6322720 ref NP_012793.1	YKL129C	little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has	1	3.4674	0.427	1207.54	1208.406	1	299.5	72.22222 K.NRLEVPPHVF.A
gi 6322720 ref NP_012793.1	YKL129C	little etfect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has	1	3.688	0.2438	1223.61	1224.406	1	346.4	77.77778 K.N2R4L1E1V1P1P1H3V1F1.A
gi 6322720 ref NP_012793.1	YKL129C	little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has	1	2.718	0.1886	1317.56	1318.521	1	289.9	66.66667 Q.IKNERNFHIF.Y
gi 6322720 ref NP_012793.1	YKL129C	intre errect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p	1	2.8677	0.2384	1335.62	1336.521	3	170	55.555557 Q.I1K2N2E1R4N2F1H3I1F1.Y

gi 6322720 ref NP_012793.1	YKL129C	little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytosketen or ganization; Myo39 One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has	2	3.6641	0.3224	2343.75	2344.668	1	335.5	37.5 N.GITDKNKDQLQKDLIELIGTT.T
ail6322720/refINP_012793.11	YKL129C	little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization: Myo3p	2	2.9024	0.2463	1162.53	1163.362	7	1074.9	87.5 N.I. FDWIVDRV N
gi 6322706 ref NP_012779.1	YKL143W	Protein required for growth at low temperature; Ltv1p	2	3.8116	0.2694	1597.67	1598.824	2	662.5	69.230774 Q.H3L1K2P1I1G1L1D1P1E1N2S1I1F1.I
gi 6322706 ref NP_012779.1	YKL143W	Protein required for growth at low temperature; Ltv1p	1	3.715	0.239	1597.62	1598.824	1	562.2	61.538464 Q.H3L1K2P1I1G1L1D1P1E1N2S1I1F1.I
gi 6322706 ref NP_012779.1 gi 6322706 ref NP_012779.1	YKL143W YKL143W	Protein required for growth at low temperature; Ltv1p	2	3.4427	0.3	1983.87	1985.158	2	498.3 567.1	57.692307 Q.HLKPIGLDPENSIF.I 50 M.LDDFLDNYELESGGRKL.A
								_		E.A1K2D1E1D1E1F1E1D1E1F1D1E1W2D1I1D1N2V1E1N2F1E1D1E1N2Y1V1K2E1
gi 6322706 ret NP_012779.1 gi 6322706 ref NP_012779.1	YKL143W YKI 143W	Protein required for growth at low temperature; Ltv1p Protein required for growth at low temperature; Ltv1p	3	4.4343	0.2207	3793.25	3794.765	1	467.3 661.3	20.689655 M 65.38461 Q H3I 1K2P1I1G1I 1D1P1E1N2S1I1E1 I
gi 6322706 ref NP_012779.1	YKL143W	Protein required for growth at low temperature; Ltv1p	2	2.9538	0.1632	1581.61	1580.824	5	304.9	50 Q.HLKPIGLDPENSIF.I
gi 6322704 ref NP_012777.1	YKL145W	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for optimal CDC20 transcription; interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p; Rpt1p	2	4.3163	0.2338	2152.63	2152.406	1	587.1	52.77778 Y.KAPLEDDDKKPDDDKIVPL.T
gi 6322704 ref NP_012777.1	YKL145W	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for optimal CDC20 transcription; interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p; Rpt1p	2	2.9002	0.1681	1580.21	1580.704	2	217.6	62.5 L.K2Q2T1E1N2D1L1K2D111E1A1R4.I
gi 6322704 ref NP_012777.1	YKL145W	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for optimal CDC20 transcription; interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p; Rpt1p	2	3.7174	0.3191	1776.89	1777.055	1	936.5	67.85714 L.R4E1V1V1E1L1P1L1L1S1P1E1R4F1A1.T
gi 6322704 ref NP_012777.1	YKL145W	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for optimal CDC20 transcription; interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p; Rpt1p	2	3.4732	0.1832	1977.49	1975.289	1	953.3	65.625 S.K2Y1N2I1E1L1P1L1P1R4I1D1P1S1V1T1.M
		One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in								
ail6322704/refINP_012777.1	YKL145W	the degradation of ubiquitinated substrates; required for optimal CDC20 transcription; interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p; Rpt1p	2	4.6378	0.3893	1705.21	1704.976	1	813.5	73.07692 L R4E1V1V1E1L1P1L1L1S1P1E1R4E1.A
51										
		One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiguitinated substrates; required for optimal CDC20 transcription;								
gi 6322704 ref NP_012777.1	YKL145W	interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p; Rpt1p	2	4.4046	0.4428	1685.27	1684.976	1	860.7	69.230774 L.REVVELPLLSPERF.A
gil6322699/refINP_012772.1	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.3148	0.1874	1272.33	1270.469	1	1054.1	77.27273 K SPKDQGELIGILN
	141 45014	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis;		0.0504	0.050.4	1571.00	1570 700		1001.0	
gi 6322699 ret NP_012772.1	YKL150W	Mcr1p Mitochondrial NADH-cvtochrome b5 reductase, involved in ergosterol biosvnthesis:	2	3.8534	0.2524	1571.83	1572.798	1	1331.3	75 G.DDKWIDLPISKIE.E
gi 6322699 ref NP_012772.1	YKL150W	Mcr1p	2	3.5214	0.2629	1832.69	1831.029	2	490.2	53.571426 G.DDKWIDLPISKIEEE.S
gi 6322699 ref NP_012772.1	YKL150W	Michonana wabr-cytochronie bo reductase, involved in ergosteror biosynthesis, Mcr1p	2	3.548	0.2235	1452.21	1452.579	1	965.3	86.36364 A.H3H3I1V1E1N2P1N2D1K2T1K2.V
ail63226991refINP 012772.11	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.1215	0.1599	1668.17	1668.815	3	235.3	53.846157 A.H3H3I1V1E1N2P1N2D1K2T1K2V1N2.L
ail6322699/refINP_012772_1	YKI 150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis;	2	3 6439	0 2135	1645 27	1645 815	з	492.2	
giloo22000101141_012172.11	111210000	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis;	-	0.0400	0.2100	1040.21	1040.010		452.2	
gi 6322699 ref NP_012772.1	YKL150W	Mcr1p Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis;	2	3.4602	0.1725	1761.95	1758.975	2	397.7	60.714287 A.HHIVENPNDKTKVNLL
gi 6322699 ref NP_012772.1	YKL150W	Mortp Mitochandrial NADH-cutochrome b5 reductase, involved in errosteral biosynthesis:	2	3.0582	0.3729	2075.67	2077.388	1	499.4	47.22222 K.FVTPKGSNVVRPYTPVSDL.S
gi 6322699 ref NP_012772.1	YKL150W	Mcchondhai NADH-Cytochronie bo reductase, involved in ergosteror biosynthesis, Mcr1p	2	4.0669	0.2952	2133.89	2132.508	1	473.5	47.058823 N.KVFKGDDKWIDLPISKIE.E
gi 6322699 ref NP_012772.1	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.8162	0.2139	1473.63	1472.71	1	1654.8	81.818184 D.D1K2W2I1D1L1P1I1S1K2I1E1.E
ail6322600/rofIND_012772_1		Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis;	2	3 303	0 2017	1599.67	1588 708	1	027.0	66 66667 C D1D1K2W2I1D11 1D111S1K2I1E1 E
gilo322033[tel[Nr_012772.1]	TREISOW	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	3.505	0.2017	1300.07	1500.790		321.5	
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3- ohosphoglycerate to 2-ohosphoglycerate during glycolysis and the reverse reaction	2	3.6647	0.3365	1620.19	1620.797	1	643.1	61.538464 Y.K2Y1V1D1P1N2V1L1P1E1T1E1S1L1.A
gi 6322697 ref NP_012770.1	YKL152C	during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3- phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction	2	3.6501	0.3613	1947.73	1949.164	1	516.5	53.333336 L.V1F1E1L1D1E1N2L1K2P1S1K2P1S1Y1Y1.L
gi 6322697 ref NP_012770.1	YKL152C	during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3- phosphoglycerate to 2-phosphoglycerate during qlycolysis and the reverse reaction	2	3.6675	0.1644	1929.33	1930.164	1	646.4	60.000004 L.VFELDENLKPSKPSYY.L
gi 6322697 ref NP_012770.1	YKL152C	during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutaes, mediates the conversion of 3- phosphoglycerate to 2-phosphoglycerate during qlycolysis and the reverse reaction	2	3.8875	0.3349	2226.37	2225.417	1	636.5	58.333332 K.GDERYKYVDPNVLPETESL.A
gi 6322697 ref NP_012770.1	YKL152C	during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3- phosphoglycerate to 2-besphoglycerate during glucohisis and the reverse reaction	2	4.9447	0.3632	2596.47	2597.8	1	465.4	42.857143 F.S1Q2K2G1D1E1R4Y1K2Y1V1D1P1N2V1L1P1E1T1E1S1L1.A
gi 6322697 ref NP_012770.1	YKL152C	during gluconeogenesis; Gpm1g during gluconeogenesis; Gpm1g Tetrameric phosphoglycerate mutase, mediates the conversion of 3- beocheolic prost to 2-beocheolic works of during site of the conversion of 3- beocheolic prost to 2-beocheolic works of during site of the conversion of 3- beocheolic prost to 2-beocheolic works of during site of the conversion of 3- beocheolic prost to 2-beocheolic works of during site of the conversion of 3- beocheolic prost to 2-beocheolic works of during site of the conversion of 3- beocheolic prost to 2-beocheolic works of during site of the conversion of 3- beocheolic prost to 2-beocheolic works of during site of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 2-beocheolic works of the conversion of 3- beocheolic prost to 3-beocheolic works of the conversion of 3- beocheolic prost to 3-beocheolic works of the conversion of 3- beocheolic prost to 3-beocheolic works of the conversion of 3- beocheolic prost to 3-beocheolic works of the conversion of 3- beocheolic prost to 3-beocheolic works of the conversion of 3- beocheolic prost to 3-beocheolic works of the conversion of 3- beocheolic prost to 3-beocheolic works of 3- beocheolic prost to 3-beocheolic works of 3- beocheolic prost to 3-beocheolic works of 3-beocheolic works of 3- beocheolic works of	2	4.8872	0.3913	2035.67	2037.418	1	725.3	56.25 L.A1L1V1I1D1R4L1L1P1Y1W2Q2D1V1I1A1K2.D
gi 6322697 ref NP_012770.1	YKL152C	phospholycenet to 2-phospholycerate outing groups and the reverse reaction during gluconeogenesis; Gpm1p Tetrameric phospholycerate mutase, mediates the conversion of 3-	2	3.0333	0.2055	2013.69	2014.418	1	517.2	40.625 L.ALVIDRLLPYWQDVIAK.D
gi 6322697 ref NP_012770.1	YKL152C	An spin-ogrycerate to 2-pinospinogrycerate during givcorysis and the reverse reaction during gluconeogenesis; Cpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	1	2.9042	0.2521	1573.64	1574.746	1	192.8	53.846157 Y.R4R4S1F1D1V1P1P1P1P111D1A1S1.S
gi 6322697 ref NP_012770.1	YKL152C	prosprogrycerate to 2-prosprogrycerate during glycorysis and the reverse reaction during glyconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3- beambendynerate (32-beambendynerate) during a during glycorysis of 3-	2	4.2658	0.4094	1605.39	1604.797	1	677.5	61.538464 Y.KYVDPNVLPETESLA
gi 6322697 ref NP_012770.1	YKL152C	during gluconeogenesis; Gpm1p	2	3.2925	0.1597	1699.71	1700.855	1	327.5	57.692307 F.E1L1D1E1N2L1K2P1S1K2P1S1Y1Y1.L

One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has

		Tetrameric phosphoglycerate mutase, mediates the conversion of 3-								
gi 6322697 ref NP_012770.1	YKL152C	during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	4.033	0.2992	2282.51	2280.493	1	677	52.63158 F.ELDENLKPSKPSYYLDPEAA.A
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpmip Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	3.4412	0.2805	2305.49	2303.493	1	533.2	44.736843 F.E1L1D1E1N2L1K2P1S1K2P1S1Y1Y1L1D1P1E1A1A1.A
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpmip Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	2.9227	0.2086	1922.71	1923.13	1	528.7	53.125 D.ENLKPSKPSYYLDPEAA.A
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpmip Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	3.3999	0.2341	1621.55	1620.813	1	923.3	65.38461 L.V1F1E1L1D1E1N2L1K2P1S1K2P1S1.Y
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpmi 7 Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	3.7737	0.3254	2248.37	2249.417	1	423.6	50 K.G1D1E1R4Y1K2Y1V1D1P1N2V1L1P1E1T1E1S1L1.A
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	3.2206	0.2333	2525.69	2526.802	1	223.4	38.095238 L.VFELDENLKPSKPSYYLDPEAA.A
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	3.6672	0.3536	2549.73	2551.802	2	209.3	38.095238 L.V1F1E1L1D1E1N2L1K2P1S1K2P1S1Y1Y1L1D1P1E1A1A1.A
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpmip ps, Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	3.5904	0.2919	2567.87	2568.8	1	395.6	42.857143 F.SQKGDERYKYVDPNVLPETESLA
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	4.1921	0.3795	1858.03	1856.957	1	791.1	64.28571 R.H3G1Q2S1E1W2N2E1K2N2L1F1T1G1W2.V
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p Tetrameric phosphoglycerate mutase, mediates the conversion of 3-	2	4.1742	0.4246	1698.27	1696.816	1	1474.1	80.769226 H.GQSEWNEKNLFTGW.V
gi 6322697 ref NP_012770.1	YKL152C	phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeotide substrates: sequence coordinates have changed since RT-PCR analysis	1	2.6185	0.2278	1309.47	1310.44	1	356.3	61.11111 E.W2N2E1K2N2L1F1T1G1W2.V
gi 9755335 ref NP_012765.2	YKL157W	showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis	2	3.2899	0.2542	1430.03	1427.594	1	1087.1	72.72727 R.SKTIELEDPTFF.K
gi 9755335 ref NP_012765.2	YKL157W	showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis	2	3.0454	0.3827	1612.63	1612.779	1	509.1	62.5 L.HYDLTVEPDFKTF.K
gi 9755335 ref NP_012765.2	YKL157W	showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis	2	3.0655	0.1766	1801.43	1799.975	3	331.6	53.571426 L.SERSKTIELEDPTFF.K
gi 9755335 ref NP_012765.2	YKL157W	showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dinentide substrates: sequence coordinates have changed since RT-PCR analysis	1	2.4398	0.2498	1163.59	1164.396	2	111	68.75 K.NFRIPVRVY.A
gi 9755335 ref NP_012765.2	YKL157W	showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p	2	2.9783	0.3363	1448.47	1448.709	1	761.9	70.83333 L.RSSHPIEVPVKKA.D
gi 6322682 ref NP_012755.1	YKL166C	Subunit of cytoplasmic cAMP-dependent protein kinase, which contains redundant catalytic subunits Tpk1p, Tpk2p, and Tpk3p and regulatory subunit Bcy1p; promotes vegetative growth in response to nutrients; inhibits filamentous growth; Tpk3p	3	4.0812	0.2426	2230.7	2228.555	2	1055.9	38.88889 L.NAELKFPPFFHPDAQDLLK.K
gi 6322682 ref NP_012755.1	YKL166C	Subunit of cytoplasmic cAMP-dependent protein kinase, which contains redundant catalytic subunits Tpk1p, Tpk2p, and Tpk3p and regulatory subunit Bcy1p; promotes vegetative growth in response to nutrients; inhibits filamentous growth; Tpk3p	3	5.1131	0.3372	2254.28	2253.555	1	1035.2	43.055553 L.N2A1E1L1K2F1P1P1F1F1H3P1D1A1Q2D1L1L1K2.K
gi 6322682 ref NP_012755.1	YKL166C	Subunit of cytoplasmic cAMP-dependent protein kinase, which contains redundant catalytic subunits Tpk1p, Tpk2p, and Tpk3p and regulatory subunit Bcy1p; promotes vegetative growth in response to nutrients; inhibits filamentous growth; Tpk3p Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit	2	5.0984	0.3271	1955.31	1957.044	1	1565.4	75 S.Q2F1D1R4Y1P1E1E1E1F1N2Y1G1I1Q2.G
gi 6322676 ref NP_012749.1	YKL172W	assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit	2	4.2728	0.3706	2642.41	2642.749	1	822.8	45.238094 T.SETNTDEHIKDIYDDTERELAF.Y
gi 6322676 ref NP_012749.1	YKL172W	assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit	2	3.7956	0.3321	2590.35	2589.731	1	620.8	42.5 E.TNTDEHIKDIYDDTERELAFY.K
gi 6322676 ref NP_012749.1	YKL172W	assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit	2	4.1249	0.3215	2805.83	2805.925	1	687.6	36.363636 T.SETNTDEHIKDIYDDTERELAFY.K
gi 6322676 ref NP_012749.1	YKL172W	assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p Receptor for a factor receptor, transcribed in alpha cells and required for mating by alpha cells, countes to MAP kinase cascade to mediate oberomone response; linand	2	3.2537	0.2383	2426.09	2426.555	1	460.9	44.736843 E. TNTDEHIKDIYDDTERELAF.Y
gi 6322671 ref NP_012743.1	YKL178C	bound receptors are endocytosed and recycled to the plasma membrane; GPCR; Ste3p Receptor for a factor receptor, transcribed in alpha cells and required for mating by	2	4.21	0.315	1994.69	1994.203	1	1330.5	71.875 Y.LFADKETDDILDEIDLK.E
gi 6322671 ref NP_012743.1	YKL178C	aipna cells, couples to MAP kinase cascade to mediate pheromone response; ligand bound receptors are endocytosed and recycled to the plasma membrane; GPCR; Ste3p Receptor for a factor receptor, transcribed in alpha cells and required for mating by	2	4.2537	0.2754	1735.65	1733.867	1	1743.9	75 F.ADKETDDILDEIDLK.E
gi 6322671 ref NP_012743.1	YKL178C	alpha cells, couples to MAP kinase cascade to mediate pheromone response; ligand bound receptors are endocytosed and recycled to the plasma membrane; GPCR; Ste3p	2	5.0806	0.2985	1562.07	1562.7	1	1766.5	87.5 D.K2E1T1D1D111L1D1E111D1L1K2.E

		Receptor for a factor receptor, transcribed in alpha cells and required for mating by alpha cells, couples to MAP kinase cascade to mediate pheromone response; ligand bound receptors are endocytosed and recycled to the plasma membrane; GPCR;								
gi 6322671 ref NP_012743.1	YKL178C	Ste3p Receptor for a factor receptor, transcribed in alpha cells and required for mating by alpha cells, couples to MAP kinase cascade to mediate pheromone response; ligand	1	4.1188	0.2617	1546.79	1547.7	1	990.1	70.83333 D.KETDDILDEIDLK.E
ail63226711refINP_012743_11	YKI 178C	bound receptors are endocytosed and recycled to the plasma membrane; GPCR; Ste3n	2	5 1856	0 2751	1749 77	1750 867	1	2106.5	78 57143 E A1D1K2E1T1D1D1111 1D1E111D11 1K2 E
giloozzon (holiwi _012140.1)	INE I/ 00	Receptor for a factor receptor, transcribed in alpha cells and required for mating by alpha cells, couples to MAP kinase cascade to mediate pheromone response; ligand	2	0.1000	0.2701	1145.11	1100.001		2100.0	
ail63226711refINP_012743_11	VKI 178C	bound receptors are endocytosed and recycled to the plasma membrane; GPCR;	2	4 089	0 298	1547 73	1547 7	1	1446.8	
giloszzor fileifti _012140.11	INEITOO	Receptor for a factor receptor, transcribed in alpha cells and required for mating by	-	4.005	0.200	1041.10	1047.1		1440.0	00.00000 BINE I BBIEBEIDENLE
		alpha cells, couples to MAP kinase cascade to mediate pheromone response; ligand								
		bound receptors are endocytosed and recycled to the plasma membrane; GPCR;								
gi 6322671 ret NP_012743.1	YKL178C	STE3p Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	5.4155	0.2872	2012.49	2013.203	1	2287.9	75 Y.L1F1A1D1K2E111D1D111L1D1E111D1L1K2.E
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.0686	0.1783	1918.51	1919.036	2	446.6	50 R.S1K2E1W2F1Q2L1D1D1E1D1F1D1L1L1.N
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
gil6322666/refINP_012739_1	YKI 182W	saturated fatty acids; contains acetyltransacylase, denydratase, enoyi reductase, malonyl transacylase, and nalmitoyl transacylase activities; Eas1n	2	4 1805	0 3337	2141 87	2143 369	1	678	62.51 W2I1D1E1P1E1N2I 1D1E1D1P1R4D1V1I1K2 G
gil0322000/rei/W _012733.1	TRETOZVV	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.1005	0.5557	2141.07	2143.303		0/0	
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.5782	0.2574	2119.65	2120.369	1	456.7	53.125 L.WIDEPFNLDFDPRDVIK.G
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids: contains acetyltransacylase, debydratase, enoyl reductase								
gi 6322666 ref NP 012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	3	4.0778	0.165	2333.3	2331.595	1	594.8	40.27778 L.W2I1D1E1P1F1N2L1D1F1D1P1R4D1V1I1K2G1K2.D
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
	V/// 1001//	saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,		0.0000	0.0000	0000 50	0004 505		000.0	
gil6322666[ref]NP_012739.1]	YKL182W	maionyl transacylase, and palmitoyl transacylase activities; Fas1p Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.3209	0.3209	2329.59	2331.595	2	336.6	44.444447 L.W2IID1E1P1F1N2L1D1F1D1P1R4D1V111R2G1R2.D
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	4.6435	0.3173	2076.49	2079.224	1	974.3	63.333332 L.R4S1K2E1W2F1Q2L1D1D1E1D1F1D1L1L1.N
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
gil6322666/refINP_012739_1	YKI 182W	saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Eas1p	1	3 1707	0 3441	1526.61	1525 829	4	222.1	50 L 11G1R4P1P1L1L1V1P1G1M1T1P1C1 T
giloszzooolicii i _012103.11	THE TOZAN	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain		0.1707	0.0441	1020.01	1020.020	-	222.1	
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.2578	0.3739	1923.23	1923.301	1	429	50 F.GPIKVELPTKETVEIGIV.D
		saturated fatty acids: contains acetyltransacylase, dehydratase, enoyl reductase.								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.8595	0.3507	2252.39	2252.616	1	474.2	44.736843 K.C1F1G1P1I1K2V1E1L1P1T1K2E1T1V1E1I1G1I1V1.D
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,	0	2 4044	0.0500	2045 45	20.45 220		700.4	
gil6322666[ref]NP_012739.1]	YKL182W	maionyl transacylase, and palmitoyl transacylase activities; Fas1p Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.1811	0.2523	2045.15	2045.339	1	763.1	60.000004 M.L1W2K2E1F1D1E11111F1N2L1P1K2N2K2.L
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.8263	0.3631	2248.47	2247.64	1	407.9	52.77778 W.KEFDETIFNLPKNKLVPTL.E
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
gil6322666/refINP_012739_1	YKI 182W	saturated fatty acids; contains acetyltransacylase, denydratase, enoyi reductase, malonyl transacylase, and nalmitoyl transacylase activities; Eas1n	2	4 5227	0 4317	2270.69	2271 64	1	359.4	52 77778 W K2E1E1D1E1T111E1N2I 1P1K2N2K2I 1V1P1T1I 1 E
giloszzooolicii i _012103.11	THE TOZAN	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	-	4.0221	0.4017	2210.00	2271.04		000.4	
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	3	4.5389	0.3007	2459.12	2459.853	1	533	36.842106 L.W2K2E1F1D1E1T1I1F1N2L1P1K2N2K2L1V1P1T1L1.E
		saturated fatty acids: contains acetyltransacylase, debydratase, enoyl reductase								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.521	0.3147	2432.59	2433.853	1	495.5	50 L.WKEFDETIFNLPKNKLVPTL.E
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,	0	0 4004	0.0504	4000.07	4000.005		4070.0	
gilb322666[rei]NP_012739.1]	TKL 18200	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.4224	0.2501	1623.87	1822.025	1	1270.2	64.2657111.GSEPIKEIIDINWERT.E
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.3676	0.3493	2303.89	2305.595	1	500.6	55.555557 L.WIDEPFNLDFDPRDVIKGK.D
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltrapsacylase, debydratase, epoyl reductase								
gi 6322666 ref NP 012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.473	0.2969	2055.23	2057.224	1	881.9	60.000004 L.RSKEWFQLDDEDFDLL.N
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
	V/// 1001//	saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,		0.040	0.0004	0454.40	0454 474		0047	
gi 6322666 ret NP_012739.1	YKL182W	maionyl transacylase, and palmitoyl transacylase activities; Fas1p Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	2.919	0.2031	2154.43	2154.474	8	234.7	43.75 S.E1R4I1V1D1C1111R4L1P1V1K2W2E11111.1
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	3	4.0396	0.2419	2434.97	2433.853	1	527.6	34.210526 L.WKEFDETIFNLPKNKLVPTL.E
		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
gil6322666/refINP_012739_11	YKI 182W	saturated raity actos; contains acetyliransacylase, denydratase, enoyi reductase, malonyl transacylase, and nalmitoyl transacylase activities: Fas1n	2	2 964	0 1857	1356 29	1356 651	1	695.3	70 C JIRI PVKWETT T
310022000101111 _012100111		Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	-	2.001	0.1001	1000.20	1000.001	·	000.0	
		saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase,								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.5513	0.1811	1957.97	1955.097	4	370.8	50 L.E1W2L1E1N2P1S1N2T1P1D1K2D1Y1L1L1.S
		saturated fatty acids: contains acetyltransacylase, dehydratase, enoyl reductase.								
gi 6322666 ref NP_012739.1	YKL182W	malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.0164	0.2375	1372.21	1372.651	3	343.6	60.000004 C.IIIIR4L1P1V1K2W2E1T1T1.T
		Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and								
gij6322639 ret NP_012712.1	YKL210W	essential for viability; Uba1p Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and	2	4.1202	0.3408	2613.55	2614.828	1	587.2	45.238094 F.KLEPVDFEKDDD I NHHIEFITA.C
gi 6322639 ref NP 012712.1	YKL210W	essential for viability; Uba1p	2	3.0933	0.1865	2150.29	2149.299	1	403.1	41.17647 D.K2V1G1P1E1T1E1E1I1F1N2D1S1F1W2E1S1L1.D
		Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and								· · ·
gi 6322639 ref NP_012712.1	YKL210W	essential for viability; Uba1p Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and	2	3.1185	0.2941	2007.31	2005.083	1	269.2	35.294117 F.T1P1N2A1N2L1K2I1Q2V1N2D1D1D1P1D1P1N2.A
gi 6322639 ref NP 012712.1	YKL210W	essential for viability; Uba1p	2	3.0215	0.2243	1432.71	1432.749	2	340.6	72.72727 F.TEVKVPRKISFK.S
	-	Lipid phosphoinositide phosphatase of the ER and Golgi, involved in protein								
gi 6322637 ref NP_012710.1	YKL212W	trafficking and secretion; Sac1p	2	3.5806	0.4717	1831.11	1833.183	1	822.2	60.000004 N.GIQFVNWPKLVDVGFL.V

gi 6322637 ref NP_012710.1	YKL212W	Lipid phosphoinositide phosphatase of the ER and Golgi, involved in protein trafficking and secretion; Sac1p	2	4.5287	0.3754	1854.81	1853.183	1	887.5	66.66667 N.G1I1Q2F1V1N2W2P1K2L1V1D1V1G1F1L1.V
gi 6322637 ref NP_012710.1	YKL212W	Lipid phosphoinositide phosphatase of the ER and Golgi, involved in protein trafficking and secretion; Sac1p	2	2.933	0.2654	1511.29	1512.619	1	248.1	62.5 N.T1V1E1E1T1G1R4F1N2G1H3V1F1.Y
gi 6322637 ref NP_012710.1	YKL212W	Lipid phosphoinositide phosphatase of the ER and Golgi, involved in protein trafficking and secretion; Sac1p	3	5.2658	0.3412	2512.73	2511.673	1	1354.4	43.75 N.N2W2T1D1G1P1R4Q2D1S1Y1D1L1F1L1G1G1F1R4P1H3.T
gi 6322637 ref NP_012710.1	YKL212W	Lipid phosphoinositide phosphatase of the ER and Golgi, involved in protein trafficking and secretion; Sac1p	3	5.3051	0.2362	2478.74	2479.673	1	757.5	35 N.NWTDGPRQDSYDLFLGGFRPH.T
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.8349	0.342	1920.37	1921.071	1	1019.6	65.625 N.GVDSLDPFDQIKDSDIR.T
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sta1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	2.9038	0.1891	1648.75	1649.798	1	744.2	73.07692 D.SLDPFDQIKDSDIR.T
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	4.8662	0.3858	1940.53	1943.071	1	900.4	65.625 N.G1V1D1S1L1D1P1F1D1Q2I1K2D1S1D111R4.T
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	4.3634	0.3259	2160.33	2159.335	1	750.6	52.77778 N.G1V1D1S1L1D1P1F1D1Q2I1K2D1S1D1I1R4T1I1.M
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.7054	0.1633	2136.63	2135.335	1	1094.8	61.11111 N.GVDSLDPFDQIKDSDIRTI.M
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.2068	0.2241	1567.55	1566.736	2	755.1	66.66667 D.P1F1D1Q2I1K2D1S1D111R4T111.M
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.4913	0.1708	2266.49	2266.528	1	493.1	42.105263 N.GVDSLDPFDQIKDSDIRTIM.Y
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.2814	0.3671	1936.81	1938.188	1	449.6	52.77778 R.QVAVDPKTGKPLPTQPSSS.K
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.49	0.2304	1960.55	1961.188	1	261.1	44.444447 R.Q2V1A1V1D1P1K2T1G1K2P1L1P1T1Q2P1S1S1S1.K
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.8683	0.4213	1581.27	1578.765	1	1859.7	84.61539 T.KVPVGDQPPDIERQ.I
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	1	2.9705	0.3979	1577.65	1578.765	1	454.5	61.538464 T.KVPVGDQPPDIERQ.I
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	4.2007	0.3591	2188.23	2189.349	1	456	47.22222 F.K2N2G1V1D1S1L1D1P1F1D1Q2I1K2D1S1D111R4.T
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.8728	0.3177	2005.51	2004.288	1	524.1	52.941177 L.KDATIPTNEFVVDIIKAE.Q
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.7281	0.3227	2122.53	2123.236	1	416.3	46.875 R.E1A1L1E1N2E1R4K2F1F1E1N2H3P1S1Y1S1.S
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	4.771	0.3573	2311.71	2310.525	1	760.1	60.526318 T.FKNGVDSLDPFDQIKDSDIR.T
gi 6322853 ref NP_012926.1	YKR001C	G1 Pase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.3053	0.241	2116.47	2117.447	1	415.9	47.22222 F.LKDATIPTNEFVVDIIKAE.Q
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.4875	0.1521	2097.87	2098.236	2	224.4	40.625 R.EALENERKFFENHPSYS.S
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	3	3.9103	0.3102	2340.62	2341.488	4	317.8	30.555555 R.E1A1L1E1N2E1R4K2F1F1E1N2H3P1S1Y1S1S1K2.A
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	4.2049	0.3121	2314.81	2313.488	1	224.4	44.444447 R.EALENERKFFENHPSYSSK.A
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.0606	0.3342	2177.67	2179.54	5	181.8	36.11111 T.KVPVGDQPPDIERQIKDMLL
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	3	4.1386	0.2218	2524.04	2524.79	1	965.1	34.523808 T.FKNGVDSLDPFDQIKDSDIRTI.M

gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.7175	0.2703	2064.87	2066.38	1	605.5	52.941177 T.KVPVGDQPPDIERQIKDM.L
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	4.6435	0.3839	2112.47	2113.294	1	1053.1	62.5 A.LENERKFFENHPSYSSK.A
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	3	5.3262	0.4662	2312.24	2313.488	1	842.2	45.833336 R.EALENERKFFENHPSYSSK.A
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	1	2.7434	0.2103	1267.45	1267.337	1	481.2	66.66667 E.DNKEEWGEFL.H
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	2.906	0.3563	1536.25	1536.768	2	329.3	57.14286 V.AVDPKTGKPLPTQPS.S
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	2.9681	0.2279	1553.31	1554.768	7	262.8	50 V.A1V1D1P1K2T1G1K2P1L1P1T1Q2P1S1.S
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	1	2.7599	0.3199	1577.75	1578.765	1	364	53.846157 T.KVPVGDQPPDIERQ.I
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.2785	0.2857	1666.83	1668.798	1	686.5	65.38461 D.S1L1D1P1F1D1Q2I1K2D1S1D1I1R4.T
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.5727	0.3911	1580.23	1578.765	1	867.4	73.07692 T.KVPVGDQPPDIERQ.I
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.6411	0.2854	1598.21	1598.765	1	737.6	65.38461 T.K2V1P1V1G1D1Q2P1P1D111E1R4Q2.I
gi 6322853 ref NP_012926.1	YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	2	3.2453	0.3873	1896.77	1898.042	1	899.1	67.85714 A.LENERKFFENHPSYS.S
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	2	3.8732	0.2877	2632.07	2633.996	1	875.4	52.380955 L.S1E1W2N2W2P1Q2P1V1I1L1K2P1I1E1D1G1P1L1Q2V1R4.V
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	2	3.3275	0.3267	2864.83	2865.343	1	292.7	39.583336 F.DSLLRERKELDEIAPVPDAFVPIIK.I
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	3	4.652	0.3308	2900.09	2898.343	1	1057.3	33.333336 F.D1S1L1L1R4E1R4K2E1L1D1E1I1A1P1V1P1D1A1F1V1P1I1I1K2.I
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	3	4.533	0.2991	2863.82	2865.343	1	1397.5	38.541664 F.DSLLRERKELDEIAPVPDAFVPIIK.I
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	2	3.4804	0.3043	2602.47	2602.996	1	760.9	50 L.SEWNWPQPVILKPIEDGPLQVR.V
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	2	4.4988	0.3346	2243.31	2243.545	1	519.9	44.444447 L.S1E1W2N2W2P1Q2P1V1I1L1K2P1I1E1D1G1P1L1.Q
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	2	4.4173	0.3814	2221.49	2219.545	1	793.7	52.77778 L.SEWNWPQPVILKPIEDGPL.Q
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	2	3.9197	0.2625	2304.05	2305.67	1	638.1	44.736843 R.E1R4K2E1L1D1E1I1A1P1V1P1D1A1F1V1P1I111K2.I
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	2	3.9983	0.2779	2602.69	2602.996	1	653.2	50 L.SEWNWPQPVILKPIEDGPLQVR.V
gi 6322854 ref NP_012927.1	YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	3	4.4416	0.2972	2601.23	2602.996	1	1100.5	44.04762 L.SEWNWPQPVILKPIEDGPLQVR.V
		Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for								
gi 6322854 ref NP_012927.1	YKR002W	mRNA nuclear export; may also polyadenylate rRNAs; Pap1p Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	3.5659	0.4108	2175.03	2175.554	1	386.1	41.6666664 E.R4K2E1L1D1E1I1A1P1V1P1D1A1F1V1P1I1I1K2.I
gi 6322870 ref NP_012943.1	YKR018C	localizes to the cytoplasm and nucleus; Ykr018cp Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	3.3946	0.2995	1871.91	1870.081	1	1139.5	70 Q.AMEDLPEEEITDHKVL.S
gi 6322870 ref NP_012943.1	YKR018C	localizes to the cytoplasm and nucleus; Ykr018cp	2	3.229	0.1687	1888.45	1889.082	1	737.2	60.000004 Q.A1M1E1D1L1P1E1E1E1I1T1D1H3K2V1L1.S

		Putative protein of unknown function: green fluorescent protein (GEP)-fusion protein								
gi 6322870 ref NP_012943.1	YKR018C	localizes to the cytoplasm and nucleus; Ykr018cp	2	3.5908	0.2782	2094.49	2094.326	1	657.2	53.125 I.PYELTPEEQKDKDLLQF.A
gi 6322870 ref NP_012943.1	YKR018C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; Ykr018cp	2	3.5615	0.1871	1533.27	1531.698	1	613.9	83.33333 Q.E1G1C1D111L1D1E1K2V1L1P1K2.F
ail6322870/refINP_012943.1	YKR018C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	3 5747	0 2398	2649 65	2649 888	2	370.8	35 714287 E N2S1V1D111P1Y1E11 1T1P1E1E1Q2K2D1K2D11 1L1Q2E1 A
silcopop70i==fND_042042.41	VKD040C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	-	0.0040	0.5400	0040.00	0045 574	-	4404.0	
gilo322870[rei]NP_012943.1]	TKRUIBC	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	6.0616	0.5499	2343.89	2345.574	I	1124.9	59.523808 N.NZETETETETETINZPTETDTGTTATTTSTPTVTH5ETTAT. Y
gi 6322870 ref NP_012943.1	YKR018C	localizes to the cytoplasm and nucleus; Ykr018cp Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein	2	3.0102	0.2234	1845.33	1846.149	1	770.8	56.666668 W.KLEGMDGLPESKEWLL.R
gi 6322870 ref NP_012943.1	YKR018C	localizes to the cytoplasm and nucleus; Ykr018cp Putative ATP-dependent RNA helicase of the DEAD-box family involved in	2	3.4268	0.3037	2621.63	2622.888	1	436.2	35.714287 F.NSVDIPYELTPEEQKDKDLLQF.A
gi 6322876 ref NP_012949.1	YKR024C	ribosomal biogenesis; Dbp7p	2	3.4185	0.1935	2147.91	2149.379	1	685.4	50 L.P1G1E1E1E1K2Y1M1D1Y111Q2P1Y1H3P1M1.G
gi 6322876 ref NP_012949.1	YKR024C	ribosomal biogenesis; Dbp7p	2	4.4049	0.3324	2615.59	2615.033	1	795.1	42.5 L.LFLLPGEEEKYMDYIQPYHPM.G
gi 6322876 ref NP_012949.1	YKR024C	Putative A I P-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp7p	3	4.8029	0.158	2617.88	2615.033	1	934.7	38.75 L.LFLLPGEEEKYMDYIQPYHPM.G
gi 6322876 ref NP_012949.1	YKR024C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp7p	3	4.606	0.2003	2639.69	2640.033	1	837.6	36.25 L.L1F1L1L1P1G1E1E1E1K2Y1M1D1Y1I1Q2P1Y1H3P1M1.G
ail6322876/refINP_012949_1	YKR024C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis: DbnZp	2	4 1061	0.3159	2637 77	2640 033	1	908.2	45 151 1 1P1G1E1E1E1K2Y1M1D1Y111Q2P1Y1H3P1M1 G
silcopopoli-sfND_042005_4	VKD020W	General amino acid permease; localization to the plasma membrane is regulated by	-	5 9570	0.4400	20070 47	2010.000		704.0	
gilo322892[rei]NP_012965.1]	TKRU39W	General amino acid permease; localization to the plasma membrane is regulated by	2	5.3579	0.4123	2076.47	2011.319	I	781.9	70.566234 F.K2R4V IK2P IIIE IV ID IP INZEISTE IATE IK2V I.A
gi 6322892 ref NP_012965.1	YKR039W	nitrogen source; Gap1p General amino acid permease; localization to the plasma membrane is regulated by	1	2.7348	0.1696	1264.56	1264.44	8	324.8	61.11111 L.A1E1Q2R4F1L1P1E1I1F1.S
gi 6322892 ref NP_012965.1	YKR039W	nitrogen source; Gap1p General amino acid permease: localization to the plasma membrane is regulated by	2	3.0001	0.241	2098.65	2099.227	1	227.7	41.17647 S.S1Y1E1K2N2N2P1D1N2L1K2H3N2G1I1T1I1D1.S
gi 6322892 ref NP_012965.1	YKR039W	nitrogen source; Gap1p	2	3.1804	0.2264	1592.49	1594.662	5	239.6	50 S.S1Y1E1K2N2N2P1D1N2L1K2H3N2.G
gi 6322892 ref NP_012965.1	YKR039W	nitrogen source; Gap1p	2	3.876	0.2721	2305.59	2303.582	1	571.1	55.555557 A.E1K2M1D111D1T1G1R4R4E1V1D1L1D1L1L1K2Q2.E
gi 6322892 ref NP_012965.1	YKR039W	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source; Gap1p	3	4.0116	0.181	1948.73	1947.205	1	1066.9	43.75 K.R4V1K2P1I1E1V1D1P1N2L1S1E1A1E1K2V1.A
gil6322892/refINP_012965.11	YKR039W	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source; Gap1p	2	4.0506	0.3363	1845.47	1847.072	1	501.3	66.66667 F.K2R4V1K2P11F1V1D1P1N2L1S1F1A1F1.K
gil6322802/rofINB_012065_1	VKP030W	General amino acid permease; localization to the plasma membrane is regulated by	2	3 1/18	0 1015	1003.60	1005 240	1	857.4	65 625 S E1K2D4V4K2D414E1V4D1D1D1021 S4E104E1 K
gilo322092 101 14F_012905.1	TKR039W	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of	2	3.1410	0.1915	1993.09	1993.249	I	657.4	03.020 3.F IN2R4V IN2F ITTE I VID IF IN2LIGIETATET.K
gi 6322901 ref NP_012974.1	YKR048C	microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	2	5.5165	0.339	2735.61	2735.788	1	1185.2	50 L.N2E1T1E1L1L1V1D1E1E1E1K2A1Q2N2D1S1E1E1E1Q2V1K2.G
		Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the								
gi 6322901 ref NP_012974.1	YKR048C	transport of H2A and H2B histones to the nucleus; Nap1p Protein that interacts with mitotic cyclin CIb2p; required for the regulation of	2	3.5629	0.2377	2467.55	2467.786	3	255.3	40 L.E1Y1L1Q2D111G1L1E1Y1L1T1D1G1R4P1G1F1K2L1L1.F
		microtubule dynamics during mitosis; controls bud morphogenesis; involved in the								
gi 6322901 ref NP_012974.1	YKR048C	transport of H2A and H2B histones to the nucleus; Nap1p Protein that interacts with mitotic cyclin Clb2p; required for the regulation of	2	5.0735	0.3023	3093.95	3094.194	1	668.6	36.53846 L.N2E1T1E1L1L1V1D1E1E1E1K2A1Q2N2D1S1E1E1E1Q2V1K2G111P1S1.F
gi 6322901 ref NP 012974.1	YKR048C	microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	2	4.8557	0.412	3059.95	3061.194	1	897.6	44.230766 L.NETELLVDEEEKAQNDSEEEQVKGIPS.F
		Protein that interacts with mitotic cyclin Clb2p; required for the regulation of								
gi 6322901 ref NP_012974.1	YKR048C	transport of H2A and H2B histories to the nucleus; Nap1p	3	4.0718	0.3494	3393.2	3394.584	1	312.4	25 L.NETELLVDEEEKAQNDSEEEQVKGIPSFW.L
		microtubule dynamics during mitosis; controls bud morphogenesis; involved in the								L.N2E1T1E1L1L1V1D1E1E1E1K2A1Q2N2D1S1E1E1E1Q2V1K2G1I1P1S1F1W2L1T
gi 6322901 ref NP_012974.1	YKR048C	transport of H2A and H2B histones to the nucleus; Nap1p Protein that interacts with mitotic cyclin Clb2p; required for the regulation of	3	4.4133	0.4403	3645.53	3646.848	1	281.2	21.666666 1.A
ail6322901/refINP_012974.1	YKR048C	microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histories to the nucleus; Nap1p	2	2.9174	0.1848	1279.19	1278.488	1	944	80 B. TIEKITPIESE F
244442444444444444444444444444444444444		Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubula duramica during mitodic controls was approximately and the managements involved in the								
gi 6322901 ref NP_012974.1	YKR048C	transport of H2A and H2B histones to the nucleus; Nap1p	2	3.4509	0.2353	1291.27	1290.488	1	954.8	80 R.T1I1E1K2I1T1P1I1E1S1F1.F
		Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the								
gi 6322901 ref NP_012974.1	YKR048C	transport of H2A and H2B histones to the nucleus; Nap1p Protein that interacts with mitotic cvclin Clb2p; required for the regulation of	2	5.9949	0.2827	2191.29	2190.236	1	1259.1	64.70589 Q.NEDQDEELEEDLEERLAL.D
ail63229011refINP_012974_1	VKR048C	microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histories to the nucleus; Nan1p	3	4 0651	0 2319	2708 48	2706 788	1	1084 3	
giloo22301 itelini _012374.1	11110400	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of	0	4.0001	0.2010	2100.40	2100.100		1004.0	04.00000 EINETEEVDEEEN ANDOELEAVICO
gi 6322901 ref NP_012974.1	YKR048C	transport of H2A and H2B histones to the nucleus; Nap1p	2	5.0898	0.1798	2214.53	2213.236	1	1768.8	64.70589 Q.N2E1D1Q2D1E1E1L1E1E1D1L1E1E1R4L1A1L1.D
		Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the								
gi 6322901 ref NP_012974.1	YKR048C	transport of H2A and H2B histones to the nucleus; Nap1p	2	3.3866	0.3452	1550.19	1550.808	1	765.5	66.66667 Q.V1R4T1I1E1K2I1T1P1I1E1S1F1.F
	VICEADONN	S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in sulfate		0.0000	0.040		1510 700	0	100.0	
gilo322922[rei]NP_012995.1]	TKRU09W	assimilation, methionine metabolism, and sironeme biosynthesis, weirp		3.0696	0.218	1511.44	1512.762	2	422.9	53.846157 F.K2DIR3GTT IIIPTVIVILIPIGIII51.5
gi 6322922 ref NP_012995.1	YKR069W	S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in sulfate assimilation, methionine metabolism, and siroheme biosynthesis; Met1p	2	3.1144	0.2103	1886.27	1885.152	3	376.3	50 K.W2V1P1E1V1V1E1E1I1G1S1R4P1P1G1V1L1.V
		S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in sulfate								
gi 6322922 ref NP_012995.1	YKR069W	assimilation, methionine metabolism, and siroheme biosynthesis; Met1p	2	4.1483	0.3937	2127.83	2129.485	1	1000.1	58.333332 L.L1K2W2V1P1E1V1V1E1E1I1G1S1R4P1P1G1V1L1.V
gi 6322923 ref NP_012996.1	YKR070W	localizes to the mitochondrion; Ykr070wp	2	2.9046	0.2781	1636.37	1636.891	1	542.2	61.538464 L.RNEKSGKPSIPIYF.S
gi 6322923 ref NP_012996.1	YKR070W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion; Ykr070wp	2	4.1668	0.3467	2166.51	2165.371	1	475.7	47.22222 T.GVYNEGDDLKECKPTLIVN.D
gi 6322923 ref NP_012996.1	YKR070W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion; Ykr070wp	2	4.1587	0.358	1503.43	1502.795	1	1431.2	76.92308 Q.K2L1P1L1L1G1T1K2P1S1T1S1P1F1.H
		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytrolasmic.								
gi 6322935 ref NP 013008.1	YKR082W	concentration gradient of the GTPase Gsp1p; Nup133p	2	3.0627	0.1842	1540.99	1541.698	7	441	58.333332 S.LDQESIEHDLKLT.S

		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to								
dile20202ElrofINID_012009_1	VKD092W	both sides of the NPC, required to establish a normal nucleocytoplasmic	2	2 2227	0 1055	1700 65	1709 962	1	740.1	
gil6322935[ref]NP_013008.1]	YKR082W	concentration gradient of the G Pase Gsp1p; Nup133p Subunit of the Nun84p subcomplex of the nuclear pore complex (NPC), localizes to	2	3.3327	0.1955	1709.65	1708.863	1	749.1	69.230774 N.AIREEIYEEISQVE.I
		both sides of the NPC, required to establish a normal nucleocytoplasmic								
gi 6322935 ref NP_013008.1	YKR082W	concentration gradient of the GTPase Gsp1p; Nup133p	2	3.5809	0.3721	1767.55	1768.883	1	564.1	57.692307 N.NLYDDNHLDWNHVL.C
		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to								
gil6322935/refINP_013008_1	YKR082W	concentration gradient of the GTPase Gsp1p: Nup133p	2	4 5774	0 3441	2486 71	2485 773	1	909.6	50 K R4V1E1D1E1E1I 1P1K2N2N2D1E1P1I 1P1S1V1D1I 1I 1 C
310022000101111 _010000111		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to	-		0.0111	2100.71	2100.110		000.0	
		both sides of the NPC, required to establish a normal nucleocytoplasmic								
gi 6322935 ref NP_013008.1	YKR082W	concentration gradient of the GTPase Gsp1p; Nup133p	2	2.9105	0.2329	1924.39	1923.127	1	1185	63.333332 N.AIREEIYEEISQVETL.N
		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleosite plasmic.								
gil6322935/refINP_013008_1	YKR082W	concentration gradient of the GTPase Gsp1p: Nup133p	2	3 7871	0 4004	1707 87	1707 835	3	259.9	53 571426 K ENEETNSKPEVGEVK S
310022000101111 _010000111		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to	-	0.1011	0.1001			0	200.0	
		both sides of the NPC, required to establish a normal nucleocytoplasmic								
gi 6322935 ref NP_013008.1	YKR082W	concentration gradient of the GTPase Gsp1p; Nup133p	2	3.5945	0.2234	1962.19	1963.151	1	1323.5	73.333336 C.FYDGILEEGEKTIRYE.L
		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic								
gil6322935/ref/NP 013008.1	YKR082W	concentration gradient of the GTPase Gsp1p: Nup133p	2	4.3501	0.2677	2458.09	2458.773	1	1075.2	50 K.RVFDEELPKNNDFPLPSVDLL.C
51		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to								
		both sides of the NPC, required to establish a normal nucleocytoplasmic								
gi 6322935 ref NP_013008.1	YKR082W	concentration gradient of the GTPase Gsp1p; Nup133p	2	3.7065	0.1803	1759.45	1760.951	1	387	63.333332 A.L1N2P1N2D1Q2D1E1T1G1G1L1I1I1IK2.G
		both sides of the NPC, required to establish a normal nucleocytoplasmic								
gi 6322935 ref NP_013008.1	YKR082W	concentration gradient of the GTPase Gsp1p; Nup133p	2	3.5966	0.2074	1811.73	1812.03	1	489.2	50 L.ALNPNDQDETGGLIIIK.G
		Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to								
		both sides of the NPC, required to establish a normal nucleocytoplasmic								
gi 6322935 ref NP_013008.1	YKR082W	concentration gradient of the GTPase Gsp1p; Nup133p	2	4.0435	0.2177	1981.23	1983.151	1	1561.8	76.6666664 C.F1Y1D1G111L1E1E1G1E1K21111R4Y1E1.L
gil6322939/refINP_013012.1	YKR086W	splicing, exhibits ATP-dependent RNA unwinding activity: Prp16p	2	3.8562	0.2659	1901.39	1901.141	6	279.1	43.75 E.E1G1N2A1P1Q2E1T1I1P1G1R4T1E1P1V1Q2.T
240000000000000000000000000000000000000		RNA helicase in the DEAH-box family involved in the second catalytic step of	_					-		
gi 6322939 ref NP_013012.1	YKR086W	splicing, exhibits ATP-dependent RNA unwinding activity; Prp16p	2	3.463	0.2806	1878.37	1878.141	1	512	53.125 F.FGNAPQFTIPGRTFPVQ.T
	MICDOOD	RNA helicase in the DEAH-box family involved in the second catalytic step of	0	0.0000	0.0745	0050.00	0050 4		404.0	
gil6322939[ref]NP_013012.1]	YKR086W	splicing, exhibits ATP-dependent RNA unwinding activity; Prp16p RNA belicase in the DEAH-box family involved in the second catalytic step of	2	3.2938	0.2715	2052.93	2053.4	1	461.6	44.11765 V.P1E1P1L1S1E1L1P1E1E1A1K2L1L1P1V1I1R4.N
gi 6322939 ref NP 013012.1	YKR086W	splicing, exhibits ATP-dependent RNA unwinding activity; Prp16p	2	4.2353	0.1896	1796.51	1797.132	1	934.4	64.28571 E.L1S1K2F1P1F1I1D1K2P1P1L1Q2T1F1.L
		Integral membrane peptide transporter, mediates transport of di- and tri-peptides;								
gil6322046/rofINP_013010_1	VKP003W	conserved protein that contains 12 transmembrane domains; PTR2 expression is regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	1 116	0 4208	2046 60	2044.063	1	675	
gil0322340[tel[14]_013013.1]	11(10351)	regulated by the re-end rule pathway via repression by Cupsp, r trzp	2	4.440	0.4230	2340.03	2344.003	'	0/5	ST.ST.EKTNESPOPEDEDFEGPTELEMIQTE.K
		Integral membrane peptide transporter, mediates transport of di- and tri-peptides;								
		conserved protein that contains 12 transmembrane domains; PTR2 expression is								
gi 6322946 ref NP_013019.1	YKR093W	regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	3.2472	0.288	1606.35	1605.919	1	1070.4	72.72727 C.KVFIFYPIYWTQ.Y
		Integral membrane peptide transporter, mediates transport of di- and tri-peptides;								
		conserved protein that contains 12 transmembrane domains; PTR2 expression is								
gi 6322946 ref NP_013019.1	YKR093W	regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	3.7428	0.3774	1887.35	1889.003	1	846.3	66.66667 W.YNEPLGHNTPNHVHVC.W
		The sector of the sector of the two sectors are the two sectors of the sector of the s								
		conserved protein that contains 12 transmembrane domains: PTR2 expression is								
gi 6322946 ref NP_013019.1	YKR093W	regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	3.2655	0.4406	1277.47	1277.463	1	984.8	75 L.SPVTVDPKFTW.L
		• • • • • • • • •								
		Integral membrane peptide transporter, mediates transport of di- and tri-peptides;								
aile222046trofIND_012010_1	VKB002W	conserved protein that contains 12 transmembrane domains; PTR2 expression is	2	2 4907	0 2272	1069.01	1067 507	1	067 5	
gilo322940[lei]INF_013019.1]	TKK095W	regulated by the N-end fulle pathway via repression by Cupsp, Pli2p	2	3.4007	0.2373	1200.31	1207.597		907.5	00.00009 L.IIFIFIFERF.V
		Integral membrane peptide transporter, mediates transport of di- and tri-peptides;								
		conserved protein that contains 12 transmembrane domains; PTR2 expression is								
gi 6322946 ref NP_013019.1	YKR093W	regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	3.3607	0.24	2012.11	2012.091	1	588.4	50 M.DYEEEDEFDLNPISAPK.A
		Integral membrane pentide transporter, mediates transport of di- and tri-pentides:								
		conserved protein that contains 12 transmembrane domains; PTR2 expression is								
gi 6322946 ref NP_013019.1	YKR093W	regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	3.789	0.3748	2197.33	2197.273	1	1068.2	52.77778 M.DYEEEDEFDLNPISAPKAN.D
		Integral membrane peptide transporter, mediates transport of di- and tri-peptides;								
gil6322046/rofINP_013010_1		conserved protein that contains 12 transmembrane domains; PTR2 expression is	2	4 4502	0 2065	2485.60	2486 702	1	717 7	
gil0322340[tel[14] _013013.1]	11(10351)	regulated by the re-end rule pathway via repression by Cupsp, 1 tizp	2	4.4332	0.3003	2403.03	2400.732	'	111.1	33.203137 S. WIREKWIT WINDKI VDEIKKALE
		Dynamin-related GTPase required for mitochondrial fission and the maintenance of								
		mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial								
gi 6323028 ref NP_013100.1	YLL001W	tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	2	5.3853	0.5393	2338.55	2339.475	1	833.6	57.5 N.SPLIEEDDNSVNPHDEVTKIS.G
		Dynamin-related GTPase required for mitochondrial fission and the maintenance of								
		mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial								
gi 6323028 ref NP_013100.1	YLL001W	tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	2	6.5495	0.4779	2364.51	2365.475	1	1033.8	60.000004 N.S1P1L1I1E1E1D1D1N2S1V1N2P1H3D1E1V1T1K2I1S1.G
		Dynamin-related G I Pase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial								
gil6323028/ref/NP 013100.1	YLL001W	tubules at sites at which division will occur: also participates in endocytosis: Dnm1p	3	5.1638	0.3614	2338.97	2339.475	1	1181.6	38.75 N.SPLIEEDDNSVNPHDEVTKIS.G
and a state of the factor should		······································	-							
		Dynamin-related GTPase required for mitochondrial fission and the maintenance of								
dil6323028/rofIND_042400.41	VI.1.0041M	mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial	2	4 5064	0 2747	2805 65	2808 027	4	533.3	
9/0020020/10/14F_010100.1	ILLOUIW	toouros at ones at which division will occur, also participates in endocytosis; Dhimip	2	4.0901	0.3747	2030.00	2030.037	1	000.Z	
		Dynamin-related GTPase required for mitochondrial fission and the maintenance of								
	14100000	mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial	-		0.000-	0405	0404		057 -	
gij6323028 ret NP_013100.1	YLLU01W	tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	3	5.9093	0.2939	3162.77	3161.365	1	957.7	37.5 F.S1L1G1D111D1D1L1E1N2A1E1P1P1L1T1E1R4E1E1L1E1C1E1L111K2.R

gi 6323028 ref NP_013100.1	YLL001W	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	3	4.993	0.3384	3131.63	3129.365	1	876.4	35.576923 F.SLGDIDDLENAEPPLTEREELECELIK.R
gi 6323028 ref NP_013100.1	YLL001W	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	1	2.5775	0.1662	1521.46	1522.571	5	140	45.454548 K.E1R4N2H3A1D1E1W2G1E1F1L1.H
gi 6323028 ref NP_013100.1	YLL001W	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	2	3.2909	0.1834	2916.47	2918.218	2	268.9	31.818182 N.K2T1V1E1E1S1L1D1K2E1E1D1Y1F1R4K2H3P1V1Y1R4T1I1.S
gi 6323028 ref NP_013100.1	YLL001W	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	1	2.4695	0.2871	1503.35	1503.571	1	171.1	50 K.ERNHADEWGEFL.H
gi 6323028 ref NP_013100.1	YLL001W	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	2	3.2696	0.3227	2026.23	2027.133	1	732.6	53.333336 R.F1Y1D1F1D1D111K2R4E111E1N2E1T1A1.R
gi 6323028 ref NP_013100.1	YLL001W	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	2	3.803	0.294	1596.23	1596.806	2	573.5	61.538464 T.K2V1P1I1G1E1Q2P1P1D1I1E1K2Q2.I
gi 6323028 ref NP_013100.1	YLL001W	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial tubules at sites at which division will occur; also participates in endocytosis; Dnm1p Nucleolar DEAD-box protein required for ribosome assembly and function, including	3	4.5814	0.2499	2919.08	2918.218	1	1179.2	35.227272 N.K2T1V1E1E1S1L1D1K2E1E1D1Y1F1R4K2H3P1V1Y1R4T111.S
gi 6323021 ref NP_013093.1	YLL008W	synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p Nucleolar DEAD-box protein required for ribosome assembly and function, including	2	3.3261	0.1704	2518.53	2515.784	1	529.7	47.5 L.VMDEADRMLEEGFQDELNEIM.G
gi 6323021 ref NP_013093.1	YLL008W	synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p Nucleolar DEAD-box protein required for ribosome assembly and function, including	1	2.462	0.3074	1196.51	1197.416	3	406.4	66.666667 F.K2N2L1E1V1P1V1L1I1C1.T
gi 6323021 ref NP_013093.1	YLL008W	synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p Nucleolar DEAD-box protein required for ribosome assembly and function, including	2	3.7396	0.3698	1632.03	1630.721	1	991.3	73.07692 D.F1Y1A1P1E1T1E1G1D1E1A1K2K2Q2.M
gi 6323021 ref NP_013093.1	YLL008W	synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p Nucleolar DEAD-box protein required for ribosome assembly and function, including	2	4.0446	0.2472	2163.01	2160.38	1	898.3	55.88235 M.NDTIEDILVEEKEEKEIL.R
gi 6323021 ref NP_013093.1	YLL008W	synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p Nucleolar DEAD-box protein required for ribosome assembly and function, including	2	4.3576	0.3837	2022.71	2023.025	1	810.1	58.823532 K.K2V1S1E1G1D1N2L1D1E1D1V1H3E1D1L1D1A1.G
gi 6323021 ref NP_013093.1	YLL008W	synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p Nucleolar DEAD-box protein required for ribosome assembly and function, including	2	4.8226	0.2086	2180.27	2181.38	1	863.3	55.88235 M.N2D1T111E1D111L1V1E1E1K2E1E1K2E111L1.R
gi 6323021 ref NP_013093.1	YLL008W	synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p	1	2.9876	0.1907	1111.44	1112.359	1	561.4	72.22222 A.S1T1R4V1I1V1L1L1P1T1.R
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	2	3.3075	0.2909	1828.81	1831.231	1	481.8	53.333336 Q.K2A111E1T111P111E1K2L1P1F111L1S1.S
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	2	3.4187	0.1893	1811.75	1813.231	1	538.4	53.333336 Q.KAIETIPIEKLPFILS.S
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	3	4.5648	0.1861	3039.92	3042.462	1	663.5	31.25 Q.Q2E1N2P1Y111Y1Y1P1T1P1N2P111P1V1K2M1P1K2D1E1K2T1F1.K
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	3	3.858	0.2935	3009.32	3011.462	1	507	31.25 Q.QENPYIYYPTPNPIPVKMPKDEKTF.K
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	2	2.9115	0.1647	1376.49	1374.552	5	660.5	70 Q.T1Y1H3R4S1P1L1L1E1Q2L1.R
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	2	3.2813	0.2859	1743.59	1743.153	7	542.8	53.571426 Q.K2A111E1T111P111E1K2L1P1F111L1.S
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	2	3.7131	0.3188	1728.83	1726.153	3	571.8	57.14286 Q.KAIETIPIEKLPFIL.S
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	3	3.8632	0.3605	3138.68	3139.593	1	571.8	26 Q.QQENPYIYYPTPNPIPVKMPKDEKTF.K
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	3	4.2645	0.358	3264.74	3267.724	1	589.3	25.961538 Q.QQQENPYIYYPTPNPIPVKMPKDEKTF.K
gi 6323016 ref NP_013088.1	YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	2	4.286	0.2007	2379.11	2379.819	1	1145.5	55.263157 Y.IYYPTPNPIPVKMPKDEKTF.K

		Heat shock protein that cooperates with Yd1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses including; heat, ethanol, and sodium arsenite; involved in [PSI+] propagation;								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses	2	4.4621	0.3493	1867.63	1869.137	1	755.7	56.25 N.L1V1R4I1P1Q2Q2Q2P1A1P1A1E1I1T1P1S1.Y
ail6323002/refINP_013074_1	YI I 026W	including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation;	2	4 9039	0 4133	1083.80	1985 241	1	945.6	61 764706 R N2I 1//1R4I1P1020202P141P141E1I1T1P1S1 V
giloo20002[ici]iii _010074.1]	TELOZOW	Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses including: thet, shock and and im graphic interview in IREU is reconstitute;	2	4.0000	0.4100	1000.00	1300.241	ľ	343.0	
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Hsp104p Hot above protein that apparented with Vdi1p (Hop40) and Soc1p (Hop70) to refeld	2	4.1678	0.4821	1845.55	1846.137	1	981.8	65.625 N.LVRIPQQQPAPAEITPS.Y
		and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation;								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold	2	4.1026	0.351	1515.59	1512.703	1	685.3	75 L.LFDEVEKAHPDVL.T
		and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation;								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses	1	3.3089	0.4321	1511.45	1512.703	1	750.2	70.83333 LLFDEVEKAHPDVL.T
gi 6323002 ref NP_013074.1	YLL026W	including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation; Hsp104p	2	3.4214	0.2782	2416.47	2415.539	9	224.9	40 K.GKSRDENVPEEAEECLEVLPN.H
		Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat ethanol, and sodium graspite; involved in [PSL4] propagation;								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Hsp104p	3	4.4327	0.2901	2156.12	2157.335	2	851.8	41.17647 A.V1A1R4D1S1K2P1E1E1L1D1S1K2E1R4Q2L1Q2.L
		and reactivate previously denatured, aggregated proteins; responsive to stresses								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p	1	2.6952	0.2749	1589.28	1590.786	1	173.8	50 Y.R4R4L1P1D1S1A1L1D1L1V1D1I1S1.C
		Heat shock protein that cooperates with Yd1p (Hsp40) and Ssa1p (Hsp70) to rebid and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat ethanol and softium arsenite; involved in IPSI+I propagation;								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Hsp104p	2	3.3975	0.3826	2182.89	2185.419	1	354.9	50 Q.A1R4Q2G1K2L1D1P1V1I1G1R4E1E1E1I1R4S1T1.I
		and reactivate previously denatured, aggregated proteins; responsive to stresses								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p	2	3.2312	0.257	2055.95	2055.174	1	317.9	56.666668 L.RQRYNEEKHGHEELTQ.A
		and reactivate previously denatured, aggregated proteins; responsive to stresses								
gi 6323002 ref NP_013074.1	YLL026W	Hispholp in the second state of the second state with Vd14 (Les 40) and Sector (Les 70) to an and so the second state of the s	2	3.3573	0.2273	2084.39	2085.174	1	182.8	43.333332 L.R4Q2R4Y1N2E1E1K2H3G1H3E1E1L1T1Q2.A
		and reactivate previously denatured, aggregated proteins; responsive to stresses								
gi 6323002 ref NP_013074.1	YLL026W	including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation; Hsp104p	2	3.6266	0.1709	2158.11	2157.335	1	340.8	47.058823 A.V1A1R4D1S1K2P1E1E1L1D1S1K2E1R4Q2L1Q2.L
		Heat shock protein that cooperates with Yd1p (Hsp40) and Ssa1p (Hsp/0) to retold and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation;								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold	2	3.1795	0.2592	2154.65	2155.419	1	310.6	44.444447 Q.ARQGKLDPVIGREEEIRST.I
	V/1 L 00014/	and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation;		0.750	0.0405	0407.07	0400.005		740.0	
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold	2	3.759	0.3105	2127.67	2129.335	1	710.6	58.823532 A. VARDSKPEELDSKERQLQ.L
		and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation;								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold	2	3.1782	0.3935	1475.29	1475.644	1	704.2	68.181816 K.YKGDFEERFKGV.L
		and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation;								
gi 6323002 ref NP_013074.1	YLL026W	Hsp104p	2	3.5622	0.2983	1575.75	1576.798	1	774.9	62.5 S.DHQHPQLQPIHIL.A
		Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH;								
gi 6323000 ref NP_013072.1	YLL028W	phosphorylation enhances activity and sorting to the plasma membrane; Tpo1p	2	3.7862	0.4147	1227.41	1226.345	1	688.6	80 H.A1A1H3E1D1V1E1L1S111K2.D
		Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH;								
gi 6323000 ref NP_013072.1	YLL028W	phosphorylation enhances activity and sorting to the plasma membrane; Tpo1p	3	4.676	0.3954	2610.68	2608.853	1	374.3	31.818182 N.C1A1P1M1G1G1D1R4P1Y1P1P1S1L1P1S1R4D1L1Y1E1V1T1.F
		Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH:								
gi 6323000 ref NP_013072.1	YLL028W	phosphorylation enhances activity and sorting to the plasma membrane; Tpo1p	1	3.0144	0.1903	1081.51	1082.188	1	638.8	75 A.H3E1D1V1E1L1S111K2.D
		Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes untake of polyamines at alkaline pH and excretion at acidic pH:								
gi 6323000 ref NP_013072.1 gi 6322999 ref NP_013071.1	YLL028W YLL029W	phosphorylation enhances activity and sorting to the plasma membrane; Tpo1p hypothetical protein; YII029wp	1 3	2.6814 3.9798	0.2239 0.3255	1069.52 3723.11	1070.188 3725.153	1 1	610.3 533	75 A.HEDVELSIK.D 21.774193 K.GKVELVPVEENLVDSIWPDFETLPERPCNDLLL K.GK2VELVPVEENLVDSIWPDFETLPERPCNDLLL
gi 6322999 ref NP_013071.1 gi 6322999 ref NP_013071.1	YLL029W YLL029W	hypothetical protein; YII029wp hypothetical protein; YII029wp	3 3	5.3011 4.6367	0.3874	3761.75 3841.19	3764.153 3838.312	1 1	720.5 928.4	25.78125 K.GKVELVPVEENLVDSWPDFETLPERPCNDLLLL
ail6322999/ref/NP 013071 1	YLL029W	hypothetical protein: YII029wp	3	5,2977	0,2251	3993.68	3992,472	1	799	K.G1K2V1E1L1V1P1V1E1E1N2L1V1D1S1I1W2P1D1F1E1T1L1P1E1R4P1C1N2D1L 24.242424 1L1L1L1.K
gi 6322999 ref NP_013071.1	YLL029W	hypothetical protein; YII029wp	3	4.9794	0.2468	3948.89	3951.472	1	1136.3	26.51515 K.GKVELVPVEENLVDSIWPDFETLPERPCNDLLLL.K K.G1K2V1E1L1V1P1V1E1E1N2L1V1D1S1I1W2P1D1F1E1T1L1P1E1R4P1C1N2D1L
gi 6322999 ref NP_013071.1 gi 6322999 ref NP_013071_1	YLL029W YLL029W	hypothetical protein; YII029wp hypothetical protein: YII029wp	3 2	5.6803 3,186	0.451	3875.36 1245.99	3878.312 1245.548	1 1	825.5 729.2	25.78125 1L1L1.L 70 L.KIGIDPKLITF.N
gi 6322999 ref NP_013071.1 gi 6322999 ref NP_013071.1	YLL029W YLL029W	hypothetical protein; YII029wp hypothetical protein; YII029wp	2	4.3861 3.2518	0.3778	1718.83	1719.95	1	906.4 446.1	69.230774 T.IHLTKPTKEEMDNY.T 57.692307 K.G1K2V1E1L1V1P1V1E1E1N2L1V1D1.S
			-					-		

gi 6322999 ref NP_013071.1 gi 6322999 ref NP_013071.1	YLL029W YLL029W	hypothetical protein; YII029wp hypothetical protein; YII029wp Putative ATPase of the AAA family, required for export of pre-ribosomal large	2 2	3.4398 4.5272	0.2988 0.2686	2429.99 2454.51	2429.741 2454.741	4 1	210.7 457	31.578945 D.SIWPDFETLPERPCNDLLLL.K 44.736843 D.S111W2P1D1F1E1T1L1P1E1R4P1C1N2D1L1L1L1L1.k
gi 6322994 ref NP_013066.1	YLL034C	suburns from the nucleus, distinction between the nucleous, nucleophasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	4.3776	0.2308	1917.91	1916.265	1	1330.8	80 S.LFIELPNTEEKLDIIK.T
gi 6322994 ref NP_013066.1	YLL034C	subarnis from the nucleus, distinction between the nucleous, nucleophastin, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	4.6181	0.2449	2131.65	2130.53	1	841.9	58.823532 S.LFIELPNTEEKLDIIKTL.T
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distinuted between the nucleous, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.9108	0.2826	2204.33	2204.419	1	329.5	55.88235 A.G1R4F1D1R4E1I1C1L1N2V1P1N2E1V1S1R4L1.H
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleouis, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	3	3.8686	0.2445	2202.95	2204.419	1	593.4	36.764706 A.G1R4F1D1R4E1I1C1L1N2V1P1N2E1V1S1R4L1.H
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.208	0.404	1713.75	1713.073	1	493.6	61.538464 A.IVQPIKRPELYEKV.G
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	2.9643	0.2549	2015.79	2017.37	1	338.4	46.875 L.FIELPNTEEKLDIIKTL.T
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleoulus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	4.3293	0.2624	2150.41	2151.53	1	993.3	64.70589 S.L1F1I1E1L1P1N2T1E1E1K2L1D1I1I1K2T1L1.T
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleous, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.0797	0.2046	1650.23	1648.859	2	624.2	57.14286 T.AKREGFATVPDVTWA.N
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleous, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.8877	0.2699	1493.25	1490.83	1	1221.7	75 Q.L1M1E1L1I1G1L1P1I1L1H3P1E1.I
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleous, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.3079	0.3061	1505.49	1506.814	1	924.1	75 M.E1L111G1L1P111L1H3P1E111F1.L
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleous, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.8491	0.2802	1464.37	1464.613	1	1197.6	77.27273 M.L1K2D1V1I1E1S1E1L1E1E1F1.G
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.7584	0.363	1492.35	1491.814	1	539.4	62.5 M.ELIGLPILHPEIF.L
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.9104	0.2805	1766.73	1769.166	1	1135.6	64.28571 Q.L1M\$E1L1I1G1L1P1I1L1H3P1E1I1F1.L
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.2977	0.2343	1639.75	1639.006	1	954.2	69.230774 L.M1E1L1I1G1L1P111L1H3P1E1I1F1.L
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	4.5077	0.3142	1750.73	1753.166	1	830.2	67.85714 Q.L1M1E1L1I1G1L1P1I1L1H3P1E1I1F1.L
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	2.9678	0.2195	1377.39	1376.698	1	599.3	72.72727 E.L111G1L1P111L1H3P1E111F1.L
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleous, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p Putative ATPase of the AAA family, required for export of pre-ribosomal large	2	3.4561	0.2993	1736.53	1736.166	1	640.3	57.14286 Q.LMELIGLPILHPEIF.L
gi 6322994 ref NP_013066.1	YLL034C	subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.2683	0.1597	1577.09	1576.923	1	448.4	58.333332 N.M1A1I1V1Q2P1I1K2R4P1E1L1Y1.E
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	3.4807	0.2915	1412.67	1412.715	1	1081	70.83333 K.APIIQFPKLVGTQ.E
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	4.218	0.3208	1755.93	1756.802	1	1484.4	75 F.N2I1T1D1E1N2S1G1E1S1G1G1K2G1E111K2.S
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	4.6117	0.3831	2160.39	2159.292	1	714.5	58.823532 K.E1L1S1P1E1E1Y1D1K2I1D1G1N2E1I1N2R4L1.M
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	3.9178	0.1977	2338.53	2339.452	1	772.8	47.22222 M.D1S1R4D1Y1K2Y1D1E1E1I1Q2L1P1D1V1S1E1L1.K
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	1	3.3809	0.2682	1153.84	1152.484	1	248.8	66.66667 D.NVRVPLPILM.D
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	3.632	0.2698	1429.23	1428.715	1	1021.1	70.83333 K.A1P1111Q2F1P1K2L1V1G1T1Q2.E
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	3	4.6393	0.3521	2069.18	2067.26	1	1190.6	42.647057 F.NIDRDPLPQDDTPELKVT.S
		Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in								
gi 6322988 ref NP_013060.1	YLL040C	sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p Protein of unknown function; heterooligomeric or homooligomeric complex;	2	3.3952	0.2026	1570.99	1569.92	1	1131.6	75 M.MDFIKFPGSPWIM.D
gi 6322988 ref NP_013060.1	YLL040C	peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	1	3.6097	0.2406	1584.71	1584.92	1	784.2	58.333332 M.M1D1F1I1K2F1P1G1S1P1W2I1M1.D

gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	1	2.8152	0.2526	1568.5	1569.92	1	600.4	54.166668 M.MDFIKFPGSPWIM.D
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	2.9945	0.2428	1700.31	1701.112	1	646.6	53.846157 A.MMDFIKFPGSPWIM.D
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	2.9245	0.164	2514.69	2514.847	1	385.8	38.095238 L.QAPLIILPLDPHDWDTPCAIID.A
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	4.249	0.2502	2611.47	2612.926	1	381.1	36.363636 L.Q2A1P1L1111L1P1L1D1P1H3D1W2D1T1P1C1A1111D1A1.G
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	3.3819	0.2224	2480.63	2482.795	1	493	38.095238 Q.A1P1L1111L1P1L1D1P1H3D1W2D1T1P1C1A1111D1A1.G
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	2	3.6723	0.3483	2459.57	2457.795	1	797.3	47.61905 Q.APLIILPLDPHDWDTPCAIIDA.G
gi 6322988 ref NP_013060.1	YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacualar protein sorting and protein-Golgi retention; Vps13p	2	3.9002	0.2931	2585.45	2585.926	1	581.3	43.18182 L.QAPLIILPLDPHDWDTPCAIIDA.G
gi 6322980 ref NP_013052.1	YLL048C	similar to mammalian bile transporters; Ybt1p	2	3.4395	0.275	2580.19	2580.811	1	547.8	35 F.SWEENFEKDINTIRENELSLL.L
gi 6322980 ref NP_013052.1	YLL048C	Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport; similar to mammalian bile transporters; Ybt1p	2	3.808	0.3071	1473.95	1474.703	1	1440.3	86.36364 L.FRFLEPETGHIK.I
gil6322080/rofINE_013052.1	VI 1 0/8C	Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport;	1	3 1736	0 3630	1473 47	1474 703	1	337.6	
gilo322300[rei]14r_013032.1]	1220400	Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport;		5.1750	0.3033	1473.47	1474.705		337.0	
gi 6322980 ref NP_013052.1	YLL048C	similar to mammalian bile transporters; Ybt1p Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport;	1	3.4957	0.1524	1491.59	1492.703	2	363.3	68.181816 L.F1R4F1L1E1P1E1T1G1H3I1K2.I
gi 6322980 ref NP_013052.1	YLL048C	similar to mammalian bile transporters; Ybt1p Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport:	2	3.2256	0.2212	2280.99	2281.527	1	508.5	41.666664 M.NRFSKDIEAIDQELTPYIQ.G
gi 6322980 ref NP_013052.1	YLL048C	similar to mammalian bile transporters; Ybt1p	2	3.4331	0.2425	1491.87	1492.703	1	928	77.27273 L.F1R4F1L1E1P1E1T1G1H3I1K2.I
gi 6322980 ref NP_013052.1	YLL048C	similar to mammalian bile transporters; Ybt1p	1	2.6585	0.3094	1473.68	1474.703	6	247.6	54.545456 L.FRFLEPETGHIK.I
gi 6323048 ref NP 013120.1	YLR020C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; involved in sterol metabolism; Yeh2p	3	4.0453	0.2176	2095.04	2096.435	1	781.3	42.647057 F.KSRLNDGVEEVKREPILL.L
gil6323048/rofINE_013120.1	VI PO20C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane;	3	1 21 13	0 2228	2122.85	2122 /25	1	803.3	
gilo323046[rei]ivF_013120.1]	TLR020C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane;	3	4.2143	0.2220	2122.00	2123.433	'	803.3	44.11/03 F.R23 IK4LIN2D IGTVTETETVTR2K4ETFTTLTLTL
gi 6323048 ref NP_013120.1	YLR020C	involved in sterol metabolism; Yeh2p Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane;	2	4.1627	0.4132	1559.11	1558.808	1	1282.1	79.16667 L.W2A1H3D1V1I1D1R4I1G1K2P1M1.I
gi 6323048 ref NP_013120.1	YLR020C	involved in sterol metabolism; Yeh2p Stervi ester bydrolase, catalyzes stervi ester bydrolysis at the plasma membrane.	2	3.8681	0.2581	1870.65	1869.183	1	696.9	53.333336 K.G1A1E1K2I1F1P1D1K2K2T1W2F1P1I1A1.K
gi 6323048 ref NP_013120.1	YLR020C	involved in sterol metabolism; Yeh2p	2	3.7068	0.3613	1808.77	1811.131	1	638.1	53.571426 G.A1E1K2I1F1P1D1K2K2T1W2F1P1I1A1.K
gi 6323048 ref NP_013120.1	YLR020C	involved in sterol metabolism; Yeh2p	2	3.8402	0.3076	1851.87	1849.183	2	472.6	46.666668 K.GAEKIFPDKKTWFPIA.K
ail6323048/refINP 013120.1	YLR020C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; involved in sterol metabolism; Yeh2p	2	3.2432	0.2629	1538.17	1538.808	1	864.9	70.83333 L.WAHDVIDRIGKPM.I
51		Protein involved in retrograde transport to the cis-Golgi network; forms heterodimer								
gi 6323068 ref NP_013140.1	YLR039C	With Kgp1p that acts as a G1P exchange factor for Yptop; involved in transcription of rRNA and holosomal protein genes; Rc1p Protein involved in retrograde transport to the cis-Golgi network; forms heterodimer with Rndh that ards as a G1P exchance factor for Yotfkr involved in transcription of	3	4.2696	0.2994	1921.34	1921.18	4	1090	43.333332 L.T1L1L1D1N2I1E1K2I1I1D1V1I1R4D1E1.I
gi 6323068 ref NP_013140.1	YLR039C	rRNA and ribosomal protein genes; Ric1p Protein involved in retrograde transport to the cis-Golgi network; forms heterodimer with Rgp1p that acts as a GTP exchange factor for Ypt6p; involved in transcription of	3	3.9805	0.181	1900.97	1900.18	1	1155.9	43.333332 L.TLLDNIEKIIDVIRDE.I
gi 6323068 ref NP_013140.1	YLR039C	rRNA and ribosomal protein genes; Ric1p Protein involved in retrograde transport to the cis-Golgi network; forms heterodimer	2	3.1551	0.2853	1902.75	1900.18	1	577.4	46.666668 L.TLLDNIEKIIDVIRDE.I
gi 6323068 ref NP_013140.1	YLR039C	with Rgp1p that acts as a GTP exchange factor for Ypt6p; involved in transcription of rRNA and ribosomal protein genes; Ric1p Protein involved in retrograde transport to the cis-Golgi network; forms heterodimer	2	3.3555	0.3332	1920.65	1921.18	1	574.6	50 L.T1L1L1D1N2I1E1K2I1I1D1V1I1R4D1E1.I
gi 6323068 ref NP_013140.1	YLR039C	with kgp ip that acts as a G iP exchange factor for Yptop; involved in transcription of rRNA and flosomal protein genes; Rtc1p Protein involved in retrograde transport to the cis-Golgi network; forms heterodimer with Ronfo that acts as a GTP exchance factor for Yoffic; involved in transcription of	2	3.2187	0.3374	1418.31	1418.74	1	877.6	77.27273 K.MHLWPVSPPQLL.R
gi 6323068 ref NP_013140.1	YLR039C	rRNA and ribosomal protein genes; Ric1p Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,	2	3.9437	0.2313	1435.13	1434.74	1	996.5	77.27273 K.M1H3L1W2P1V1S1P1P1Q2L1L1.R
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdct p Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,	2	3.5853	0.3377	2097.67	2099.386	1	411.3	44.44447 S.LKPNDAESEKEVIDTILAL.V
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic	2	4.0872	0.2744	2120.21	2121.386	1	617.8	50 S.L1K2P1N2D1A1E1S1E1K2E1V1I1D1T111L1A1L1.V
gi 6323073 ref NP_013145.1	YLR044C	fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic	3	3.8832	0.2236	2901.2	2902.257	1	678.4	29 L.Q2T1P1I1D1M1S1L1K2P1N2D1A1E1S1E1K2E1V1I1D1T1I1L1A1L1.V
gi 6323073 ref NP_013145.1	YLR044C	termentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1 p Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic formaticities decarboxylates pyruvate to acetaldehyde whilet to glucose atteact	3	3.8818	0.1932	3462.86	3464.976	3	556.6	23.275862 Q.DKSFNDNSKIRMIEIMLPVFDAPQNLVEQA.K
gi 6323073 ref NP_013145.1	YLR044C	rementation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to diucose-, ethanol-	2	5.0955	0.2497	2800.07	2800.315	1	714.7	45.833336 T.Y1V1T1Q2R4P1V1Y1L1G1L1P1A1N2L1V1D1L1N2V1P1A1K2L1L1.Q
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	3	4.4336	0.3012	3506.78	3504.976	1	660.9	22.413794 Q.D1K2S1F1N2D1N2S1K2I1R4M1I1E1I1M1L1P1V1F1D1A1P1Q2N2L1V1E1Q2A1.K

		Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic								
ail62020721rofIND_01214E_11	VI BOAAC	fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,	2	3 2227	0.2059	1402 70	1404 797	1	026 5	65 28461 L D1A1N2L1\/1D1L1N2\/1D1A1K2L1L1 0
gilo323073[tel[INF_013145.1]	TLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic	2	3.2221	0.2956	1493.79	1494.707	1	930.5	05.56401 E.FTATNZETVIDTETNZVIFTATKZETET.Q
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,								
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p Major of these purjunte deserbendese jestimese, key estima is electrolis	2	4.7443	0.4561	2766.15	2768.315	1	896.3	52.083332 T.YVTQRPVYLGLPANLVDLNVPAKLL.Q
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol								
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	2	3.3691	0.407	1476.25	1477.787	1	805.6	61.538464 L.PANLVDLNVPAKLL.Q
		Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic								
gil6323073lrefINP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	3	3.9658	0.1611	3542.36	3541.186	1	711.5	24 193548 T.YVTORPVYLGLPANLVDLNVPAKLLQTPIDMS.L
giloszesi elisititi _e te tiette	12:101:10	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic	0	0.0000	0.1011	0012.00	0011100		711.0	
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,								
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p Major of these purjuete deserbendese jestimese, key settime in electrolis	2	3.3538	0.1506	1664.03	1662.832	1	550.3	60.714287 N.D1A1E1S1E1K2E1V1I1D1T1I1L1A1L1.V
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,								
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	2	3.8717	0.2722	1786.31	1786.907	1	951.4	56.666668 M.G1K2G1S1I1D1E1Q2H3P1R4Y1G1G1V1Y1.V
		Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic								
gil6323073/refINP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	2	3.2122	0.3173	1624.39	1622,731	1	657.2	64.28571 M.G1K2G1S1I1D1E1Q2H3P1R4Y1G1G1V1.Y
		Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic								
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,								
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic	2	3.5986	0.2871	1764.35	1763.907	1	1158.1	60.000004 M.GKGSIDEQHPRYGGVY.V
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,								
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	1	2.5186	0.2325	1054.48	1054.208	4	262.2	68.75 W.D1H3L1S1L1L1P1T1F1.G
		Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic								
gil6323073/refINP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	1	2.8047	0.2093	1323.33	1324.592	4	391	63.636364 A.N2L1V1D1L1N2V1P1A1K2L1L1.Q
3.1		Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic	-							
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,						_		
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p Major of three pyruwate decarboxylase isozymes, key enzyme in alcoholic	1	2.5481	0.1989	1308.55	1309.592	5	459.7	68.181816 A.NLVDLNVPAKLL.Q
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,								
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	1	3.4253	0.3624	1298.66	1299.513	1	799.2	72.72727 W.DHLSLLPTFGAK.D
		Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic								
ail6323073 ref NP 013145.1	YLR044C	and autoregulation: involved in amino acid catabolism: Pdc1p	1	3.9409	0.3209	1313.53	1314.513	2	657.1	63.636364 W.D1H3L1S1L1L1P1T1F1G1A1K2.D
51		Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic								
- 100000701 (INID- 040445-4)	14 59449	fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,		0.0540	0.4000	4005 40	4000.000		500.0	
gij6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic	1	2.9512	0.1902	1005.49	1006.209	1	583.6	75 E.K2L111H3G1P1K2A1Q2.Y
		fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-,								
gi 6323073 ref NP_013145.1	YLR044C	and autoregulation; involved in amino acid catabolism; Pdc1p	1	2.6835	0.3279	991.55	992.209	1	585.4	75 E.KLIHGPKAQ.Y
		Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates								
ail6323074 ref NP 013146.1	YLR045C	alignment: interacts with spindle pole body component Spc72p; Stu2p	2	4.0808	0.4044	2503.55	2504.901	1	821	50 S.MLPEETILDKLPKDFQERITS.S
3-1		Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates								
- 100000741 (INID- 040440-41	V4 D0450	microtubule dynamics during spindle orientation and metaphase chromosome	•	0.0077	0.0014	0500.07	0504.004		407.0	
gij6323074 ret NP_013146.1	YLR045C	alignment; interacts with spindle pole body component Spc/2p; Stu2p Microtubule-associated protein (MAP) of the XMAP215/Dis1 family: regulates	2	3.2277	0.2611	2503.97	2504.901	1	427.8	37.5 F.SMLPEETILDKLPKDFQERIT.5
		microtubule dynamics during spindle orientation and metaphase chromosome								
gi 6323074 ref NP_013146.1	YLR045C	alignment; interacts with spindle pole body component Spc72p; Stu2p	2	3.9703	0.3078	2708.97	2708.058	1	585.5	38.636364 F.S1M1L1P1E1E1T111L1D1K2L1P1K2D1F1Q2E1R4I1T1S1S1.K
		Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates								
gi 6323074 ref NP 013146.1	YLR045C	alignment; interacts with spindle pole body component Spc72p; Stu2p	2	3.3717	0.2764	2680.01	2679.058	1	290.6	40.909092 F.SMLPEETILDKLPKDFQERITSS.K
		Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates								
-100000741{IND_040440_41	VI DO450	microtubule dynamics during spindle orientation and metaphase chromosome	2	2 0502	0.0000	4 400 00	4 400 000		4007.0	
gil6323074 ret NP_013146.1	YLR045C	alignment; Interacts with spindle pole body component Spc72p; Stu2p Microtubule-associated protein (MAP) of the XMAP215/Dis1 family: regulates	2	3.8563	0.2236	1493.29	1492.669	1	1037.8	70.83333 T.GNNSDLLEEILFK.K
		microtubule dynamics during spindle orientation and metaphase chromosome								
gi 6323074 ref NP_013146.1	YLR045C	alignment; interacts with spindle pole body component Spc72p; Stu2p	3	3.9035	0.2773	2531.3	2531.901	3	309.5	30.000002 F.S1M1L1P1E1E1T1I1L1D1K2L1P1K2D1F1Q2E1R4I1T1.S
		Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap;								
gil6323077/refINP 013149.11	YLR048W	gene reduces growth rate, deletion of both genes is lethal: Rps0bp	1	2,4805	0.2608	1499.51	1500.562	5	209.5	45.833336 Y.RNPEEVEQVAEEA.A
51		Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap;								
-:::::::::::::::::::::::::::::::::::::	VI DO40W	required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0	2	4 0004	0.400	4000 55	4940.045		4.405.0	
gil6323077 [rei]NP_013149.1]	TLR048VV	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap;	2	4.0294	0.432	1809.55	1810.915	1	1405.0	78.57143 T.FTRNPEEVEQVAEEA.A
		required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0								
gi 6323077 ref NP_013149.1	YLR048W	gene reduces growth rate, deletion of both genes is lethal; Rps0bp	2	4.5992	0.3123	1832.39	1830.915	1	1216.3	71.42857 Y.F1Y1R4N2P1E1E1V1E1Q2V1A1E1E1A1.A
		Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rBNA along with Rps0Ap; deletion of either RPS0.								
gi 6323077 ref NP_013149.1	YLR048W	gene reduces growth rate, deletion of both genes is lethal; Rps0bp	1	2.7908	0.2959	1095.61	1096.234	1	137.6	61.11111 C.NNRGKHSIGL.I
		C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into								
ail63230851rofIND_013157_11	VI POS6W	episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow	1	2 5273	0 2774	1160 58	1160 276	1	453.8	61 11111 H S1E1H3P1V1D1G1E1I 102 S
gil0323003[tel]14F_013137.1]	TEROSOW	C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into		2.5215	0.2774	1100.00	1100.270		400.0	
		episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow								
gi 6323085 ref NP_013157.1	YLR056W	on non-fermentable carbon sources; Erg3p	3	4.2364	0.1549	2721.65	2721.854	1	505.4	31.818182 F.IKEVEGDDNDRIYENDPNTKKNN
		episterol a precursor in ergosterol biosynthesis: mutants are viable, but cannot grow								
gi 6323085 ref NP_013157.1	YLR056W	on non-fermentable carbon sources; Erg3p	2	3.6815	0.3602	2754.47	2755.854	5	162.5	34.090908 F.I1K2E1V1E1G1D1D1N2D1R4I1Y1E1N2D1P1N2T1K2K2N2N2
		C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into								
ail6323085/ref/NP 013157 1	YLR056W	episteroi, a precursor in ergosteroi biosynthesis; mutants are viable, but cannot grow on non-fermentable carbon sources: Erg3p	2	3,4622	0.2126	2721.21	2721.854	1	273	38.636364 F.IKEVEGDDNDRIYENDPNTKKNN
51		C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into	-					•		
		episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow	~	4 0000	0 4470	0000.05	0000 470	,	400 7	
gilo323065[rei]NP_013157.1]	I LKUS6W	on non-remientable carbon sources; Ergap	2	4.0983	0.4176	2392.35	2393.472	1	430.7	50 P.HKZETVTETGTDTDTNZD1K4H1Y1E1NZD1P1NZ11K2.K

		C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into								
gi 6323085 ref NP_013157.1	YLR056W	on non-fermentable carbon sources; Erg3p	2	3.3848	0.2049	1990.33	1991.176	3	290.4	46.6666668 S.Y1R4R4P1D1D1S1L1F1D1P1K2L1R4D1A1.K
		C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow								
gi 6323085 ref NP_013157.1	YLR056W	on non-fermentable carbon sources; Erg3p	2	3.2433	0.2198	2720.77	2721.854	9	175.9	31.818182 F.IKEVEGDDNDRIYENDPNTKKNN
		episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow								
gi 6323085 ref NP_013157.1	YLR056W	on non-fermentable carbon sources; Erg3p C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into	3	4.1832	0.1913	2758.31	2755.854	1	446.6	30.681818 F.I1K2E1V1E1G1D1D1N2D1R4I1Y1E1N2D1P1N2T1K2K2N2N2
gil6323085/refINP_013157_1	YI R056W	episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow	2	3 1224	0 2724	1964 53	1965 176	1	454 4	53 333336 S YRRPDDSI EDPKI RDA K
910020000101111 _01010111	121000011	C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into	-	0.1221	0.2721	100 1.00	1000.110	·	10111	
gi 6323085 ref NP_013157.1	YLR056W	on non-fermentable carbon sources; Erg3p	2	3.3494	0.2211	1616.61	1615.833	1	560.8	66.666667 Y.RRPDDSLFDPKLR.D
gi 6323087 ref NP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.4998	0.4213	1670.13	1670.801	1	1179.9	69.230774 F.P1Y1R4V1N2P1E1T1G1I1I1D1Y1D1.T
gil6323087lrefINP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.0306	0.2237	1194.39	1194.42	2	543.5	70.83333 S.A1L1V1P1G1G1V1R4I1G1A1P1A1.M
gil6323087/rofINP_013150_1	VI POSSC	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	3 2771	0.3357	008 13	908.049	1	575 1	77 77778 \/ D1G1G1\/1D4/1G1A1D1A1 M
gilos23007 [rel[NF_013133.1]	TEROSOC	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	5.2771	0.3337	300.13	300.043		575.1	
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	1	2.6265	0.3114	1178.65	1178.42	1	444.9	54.166668 S.ALVPGGVRIGAPA.M
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	1	2.5914	0.2516	1281.65	1282.498	1	380	53.846157 K.S1A1L1V1P1G1G1V1R4I1G1A1P1A1.M
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cutosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	3.9623	0.2872	1606.33	1606.773	1	1382.1	80.769226 Y.RVNPETGIIDYDTL.E
gi 6323087 ref NP_013159.1	YLR058C	Shm2p	2	3.8498	0.4338	1864.71	1867.065	1	863.3	60.000004 F.PYRVNPETGIIDYDTL.E
gi 6323087 ref NP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.6933	0.4487	1839.25	1840.04	1	1245.9	63.333332 K.TGKEVLYDLENPINFS.V
ail6323087lrefINP 013159.11	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.9907	0.3219	1754.83	1752.962	1	1543.7	71.42857 K.TGKEVLYDLENPINF.S
gil6323087/refINP_013159.1	YI R058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	4 6474	0 3846	1689 77	1690 845	1	2033.9	80 760226 D P1E1//1D1S11111K2D1E111E1R4O2 K
gilos23007 iteliNF_013133.1	VI Docoo	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	4.0474	0.0040	1009.77	1030.045		2033.9	
gi 6323087 ret NP_013159.1	YLR058C	Snm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	4.4299	0.2482	2003.33	2003.127	1	570.9	68.75 V.DTDPEVDSIIKDEIERQ.K
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	4.5983	0.375	2026.61	2025.127	1	613.1	68.75 V.D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	4.0318	0.3129	1910.67	1909.039	1	453.8	66.66667 D.T1D1P1E1V1D1S11111K2D1E111E1R4Q2.K
gi 6323087 ref NP_013159.1	YLR058C	Sharen Shar	2	4.1387	0.3773	1809.55	1806.933	1	431.2	71.42857 T.D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi 6323087 ref NP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.1652	0.361	2126.43	2125.26	1	344.1	52.941177 L.V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi 6323087 ref NP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.5317	0.4564	2212.61	2215.419	1	1177.9	69.44444 H.LVDTDPEVDSIIKDEIERQ.K
ail6323087lrefINP 013159.11	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.4094	0.2385	1888.55	1888.039	7	288.7	56.666668 D.TDPEVDSIIKDEIERQ.K
gil6323087/rofINP_013150_1	VI PO58C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	1	2 6691	0.2058	1305 47	1206 426	3	134.4	60 000004 P G1M1G1E1E1D1E1H3P4I1\/1 Q
gilos23007 ellive_013133.1	TEROSOC	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;		2.0031	0.2050	1303.47	1300.430	5	434.4	
gi 6323087 ret NP_013159.1	YLR058C	Snm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	1	2.5209	0.2183	1290.51	1290.436	2	331	55 R.GMGEEDFHRIV.Q
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	5.7792	0.4595	2466.63	2467.638	1	798.5	60.000004 T.S1H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cutosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	3	6.3412	0.4441	2467.37	2467.638	1	1883.9	51.25 T.S1H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi 6323087 ref NP_013159.1	YLR058C	Shozp	3	4.1934	0.2164	1671.89	1671.845	1	830.6	44.230766 D.PEVDSIIKDEIERQ.K
gi 6323087 ref NP_013159.1	YLR058C	Shm2p	2	4.8878	0.4151	2441.53	2439.638	1	667.1	57.5 T.SHLVDTDPEVDSIIKDEIERQ.K
gi 6323087 ref NP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.9004	0.4758	2352.67	2352.56	1	786.9	63.15789 S.HLVDTDPEVDSIIKDEIERQ.K
gil6323087lrefINP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	3	5.1161	0.4786	2351.06	2352.56	1	949.3	43 421055 S.HI.VDTDPEVDSIIKDEIERO K
ail6222007/rofIND_012150_1	VI DOE9C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	2 5002	0.0249	2280.25	2270 672	1	727.0	
gilosz3007 iteline _013133.1	TEROSOC	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	5.5665	0.2340	2300.23	2313.012		121.5	
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	3.9287	0.3174	2403.05	2405.672	1	526	40 R.S1I1N2P1K2T1G1K2E1V1L1Y1D1L1E1N2P1I1N2F1S1.V
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	3.4578	0.2295	2292.55	2292.594	1	517.9	39.473686 R.SINPKTGKEVLYDLENPINF.S
gi 6323087 ref NP_013159.1	YLR058C	Shm2p	2	3.456	0.262	2316.69	2317.594	1	620.1	42.105263 R.S1I1N2P1K2T1G1K2E1V1L1Y1D1L1E1N2P1I1N2F1.S
gi 6323087 ref NP_013159.1	YLR058C	Shapp	2	4.0475	0.2952	1889.55	1890.19	1	604.8	56.25 R.GVRSINPKTGKEVLYDL.E
gi 6323087 ref NP_013159.1	YLR058C	Shm2p	2	3.5245	0.2892	2692.73	2692.044	1	525.6	43.47826 R.GVRSINPKTGKEVLYDLENPINFS.V
gi 6323087 ref NP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	1	2.3005	0.1833	1193.65	1194.42	7	323.2	45.833336 S.A1L1V1P1G1G1V1R4I1G1A1P1A1.M
gil6323087lrefINP_013159.1	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	5.1565	0.4287	2240.43	2239.419	1	697.8	61.11111 H.I.1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2 K
gil6223087/rofIND_013450.41	VI ROFOC	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	-	4 8004	0 3757	1626.15	1624 772	•	1107.2	
yijuszsuorireijNP_013159.1	I LRUSOL	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	4.0094	0.3/5/	1020.10	1024.//3		1107.3	
gijb323087[ret]NP_013159.1]	YLR058C	snmzp Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	5.1332	0.3531	2466.17	2467.638	1	886.1	62.5 I.S1H3L1V1U111U1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism:	3	5.1252	0.5211	2436.92	2439.638	1	1405.7	47.5 T.SHLVDTDPEVDSIIKDEIERQ.K
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism	2	5.2882	0.4617	2379.01	2379.56	1	742.8	57.894737 S.H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi 6323087 ref NP_013159.1	YLR058C	Shm2p	2	3.1275	0.1909	2351.31	2352.56	1	524.2	50 S.HLVDTDPEVDSIIKDEIERQ.K

		Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;								
gi 6323087 ref NP_013159.1	YLR058C	Shm2p	3	4.363	0.3845	2465.72	2467.638	1	690.2	36.25 T.S1H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
ail6323087/refINP_013159_1	YI R058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2n	1	2 7425	0 2619	1576 53	1577 818	1	463	50 R SINPKTGKEVLYDL E
3.1		Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;								
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cutosolic soring budroxymethyltransferase, involved in one-carbon metabolism:	3	5.9027	0.4021	2381.63	2379.56	1	1017.9	42.105263 S.H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi 6323087 ref NP 013159.1	YLR058C	Shm2p	2	3.7923	0.4455	1864.27	1863.167	1	722.5	60.526318 N.SIPGDKSALVPGGVRIGAPA.M
		Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;								
gi 6323087 ref NP_013159.1	YLR058C	Shm2p Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism:	2	3.5271	0.3454	1886.29	1887.167	1	684.2	57.894737 N.S1I1P1G1D1K2S1A1L1V1P1G1G1V1R4I1G1A1P1A1.M
gi 6323087 ref NP_013159.1	YLR058C	Shm2p	2	3.9939	0.325	1912.47	1913.19	1	461.6	56.25 R.G1V1R4S1I1N2P1K2T1G1K2E1V1L1Y1D1L1.E
-:::02020071(IND_042450.4)		Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	2	4.40	0.0040	0004.00	0000.044		000.0	
gilo323067 [rei]NP_013159.1]	TLR058C	Srinzp Cvtosolic serine hvdroxymethyltransferase, involved in one-carbon metabolism:	3	4.43	0.3842	2091.32	2092.044	'	002.3	31.52174 R.GVRSINPRIGREVLIDLENPINFS.V
gi 6323087 ref NP_013159.1	YLR058C	Shm2p	2	3.7049	0.3378	1909.49	1907.056	1	724.8	60.000004 E.S1F1P1Y1R4V1N2P1E1T1G1I1I1D1Y1D1.T
gil6323097/rofIND_013150_1	VI POSSC	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism;	1	2 2152	0 2073	806 42	807.062	4	343.0	
gilo22007[felfin _013138.1]	TEROSOC	Beta subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with Frs2p to generate the active enzyme; evolutionarily distant from mitochondrial phenylalanyl-tRNA synthetase based on protein sequence, but substrate binding is	·	2.3133	0.2075	030.42	037.002	4	545.5	
gi 6323089 ref NP_013161.1	YLR060W	similar; Frs1p Beta subunit of outoplasmic phenylalanyl-tPNA synthetase, forms a tetramor with	2	3.3967	0.4401	1968.25	1971.133	1	426.8	50 Y.WIEEDDSVKTYFPGRGA.K
		Frs2p to generate the active enzyme; evolutionarily distant from mitochondrial								
		phenylalanyl-tRNA synthetase based on protein sequence, but substrate binding is								
gi 6323089 ref NP_013161.1	YLR060W	similar; Frs1p Beta subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with	3	4.2917	0.2432	2306.24	2304.649	1	1397.1	44.736843 Q.SKEDKDILHVDIPVTRPDIL.H
		Frs2p to generate the active enzyme; evolutionarily distant from mitochondrial								
		phenylalanyl-tRNA synthetase based on protein sequence, but substrate binding is								
gi 6323089 ref NP_013161.1	YLR060W	similar; Frs1p Beta subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with	2	4.9325	0.4017	2304.09	2304.649	1	1267.7	55.263157 Q.SKEDKDILHVDIPVTRPDIL.H
		Frs2p to generate the active enzyme; evolutionarily distant from mitochondrial								
-:::02020001#ND_042404_4		phenylalanyl-tRNA synthetase based on protein sequence, but substrate binding is	0	0.0047	0.0040	4050 70	4054 070	0	050.4	
gil6323089[ref]NP_013161.1]	YLR060W	similar; Frs1p Beta subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with	2	3.3847	0.2219	1353.79	1354.679	2	859.4	68.181816 A.NFIAKPLPINKV.5
		Frs2p to generate the active enzyme; evolutionarily distant from mitochondrial								
-:::02020001#ND_042404_4		phenylalanyl-tRNA synthetase based on protein sequence, but substrate binding is		2 0000	0.4405	4505.0	4500.005		c00	
gil6323089[ref]NP_013161.1]	YLR060W	similar; Frs1p Protein component of the large (60S) ribosomal subunit, responsible for joining the	1	3.6602	0.4435	1595.6	1596.925	1	628	65.38461 Y.VHIIEDSPVFPVIM.D
		40S and 60S subunits; regulates translation initiation; has similarity to rat L10								
gi 6323104 ref NP_013176.1	YLR075W	ribosomal protein and to members of the QM gene family; RpI10p	1	3.1498	0.2347	1457.47	1458.57	1	196.9	65 L.ENNIREFPEYF.A
		40S and 60S subunits; regulates translation initiation; has similarity to rat L10								
gi 6323104 ref NP_013176.1	YLR075W	ribosomal protein and to members of the QM gene family; Rpl10p	2	3.2948	0.1918	1618.45	1618.728	1	646.9	62.5 L.E1N2N2I1R4E1F1P1E1Y1F1A1A1.Q
		Protein component of the large (60S) ribosomal subunit, responsible for joining the								
gi 6323104 ref NP 013176.1	YLR075W	ribosomal protein and to members of the QM gene family; RpI10p	2	2.9729	0.3164	1716.31	1715.86	2	314.8	50 K.GSLENNIREFPEYF.A
		Protein component of the large (60S) ribosomal subunit, responsible for joining the								
ail6323104/refINP_013176_1	YI R075W	40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the OM gene family: Rpl10p	2	3 8475	0 2312	1734 33	1734.86	1	588 7	69 230774 K G1S1I 1E1N2N2I1R4E1E1P1E1Y1E1 A
giloszoro ilisifiti _oronio.il	Litteren	Protein component of the large (60S) ribosomal subunit, responsible for joining the	-	0.0110	0.2012		1101.00	·	000.1	
		40S and 60S subunits; regulates translation initiation; has similarity to rat L10		0.0000	0.0700	4000 74	1050 017		500 5	
gil6323104 ref NP_013176.1	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the	2	2.9388	0.2768	1860.71	1858.017	1	502.5	50 K.GSLENNIKEFPEYFAA.Q
		40S and 60S subunits; regulates translation initiation; has similarity to rat L10								
gi 6323104 ref NP_013176.1	YLR075W	ribosomal protein and to members of the QM gene family; RpI10p	1	2.5206	0.1688	1214.6	1215.351	5	204.2	62.5 N.NIREFPEYF.A
		40S and 60S subunits: regulates translation initiation: has similarity to rat L10								
gi 6323104 ref NP_013176.1	YLR075W	ribosomal protein and to members of the QM gene family; Rpl10p	1	2.3291	0.163	1243.66	1243.404	1	380.4	55.555557 N.IREFPEYFAA.Q
		Protein component of the large (60S) ribosomal subunit, responsible for joining the								
gi 6323104 ref NP 013176.1	YLR075W	ribosomal protein and to members of the QM gene family; RpI10p	2	3.1513	0.2343	1865.49	1865.034	1	617.8	60.714287 K.K2G1S1L1E1N2N2I1R4E1F1P1E1Y1F1.A
		Protein component of the large (60S) ribosomal subunit, responsible for joining the								
ail6323104/refINP_013176_1	YI R075W	40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the OM gene family: Rpl10p	2	3 0003	0 288	1058 33	1058 227	2	380.4	75 N R441V1P1D1S1K2I1R4 I
giloszoro ilisifiti _oronio.il	Litteren	Protein component of the large (60S) ribosomal subunit, responsible for joining the	-	0.0000	0.200	1000.00	1000.221	-	000.1	
		40S and 60S subunits; regulates translation initiation; has similarity to rat L10		0.5500	0.0004	1010 11	10.10.007		400.4	
gi 6323104 ref NP_013176.1	YLR075W	ribosomal protein and to members of the QM gene family; Kpl10p Protein component of the large (60S) ribosomal subunit responsible for joining the	2	3.5533	0.2231	1043.41	1042.227	1	483.4	81.25 N.RAVPDSKIR.I
		40S and 60S subunits; regulates translation initiation; has similarity to rat L10								
gi 6323104 ref NP_013176.1	YLR075W	ribosomal protein and to members of the QM gene family; Rpl10p	2	3.457	0.2152	1475.09	1474.57	1	687.8	75 L.E1N2N2I1R4E1F1P1E1Y1F1.A
		40S and 60S subunits; regulates translation initiation; has similarity to rat L10								
gi 6323104 ref NP_013176.1	YLR075W	ribosomal protein and to members of the QM gene family; Rpl10p	2	4.3646	0.4207	2083.21	2083.286	1	801.4	59.375 L.S1K2K2G1S1L1E1N2N2I1R4E1F1P1E1Y1F1.A
		Protein component of the large (60S) ribosomal subunit, responsible for joining the								
gi 6323104 ref NP 013176.1	YLR075W	ribosomal protein and to members of the QM gene family; RpI10p	2	3.9889	0.4509	2056.81	2059.286	1	693	53.125 L.SKKGSLENNIREFPEYF.A
		Protein whose 24kDa cleavage product is found in endosome-enriched membrane								
gi 6323112 ref NP_013184.1	YLR083C	fractions, predicted to be a transmembrane protein; Emp70p Protein whose 24/Da cleavage product is found in endosome enriched membrane	2	4.743	0.3494	2024.91	2026.216	1	958	63.333332 R.F1H3F1C1Q2P1E1K2V1E1K2Q2P1E1S1L1.G
gi 6323112 ref NP_013184.1	YLR083C	fractions, predicted to be a transmembrane protein; Emp70p	2	3.4388	0.1879	2006.09	2004.216	1	948.5	63.333332 R.FHFCQPEKVEKQPESL.G
		Protein whose 24kDa cleavage product is found in endosome-enriched membrane								
gi 6323112 ref NP_013184.1 gi 6323118 ref NP_013190_1	YLR083C	fractions, predicted to be a transmembrane protein; Emp70p Putative alapine transaminase (dutamic pyruvic transaminase); Alt1p	2	3.7031	0.2864	1924.65 1786 21	1925.015	1	621.5 518.1	50 N.ELNLDDDFQEDSGWKL.N 57 14286 K RDEGEISYPEDIELT A
gi 6323118 ref NP_013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Altip	2	3.4516	0.2528	1854.81	1855.996	1	346	46.666668 K.RDEGEISYPEDIFLTA.G
gi 6323118 ref NP 013190.11	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	2.9832	0.1873	1913.57	1911.218	1	525.3	56.25 F.CRGPETGVLIPIPQYPL.Y
gi 6323118 ref NP_013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.9268	0.4734	2176.43	2175.499	1	824.8	58.333332 F.CRGPETGVLIPIPQYPLYT.A
gi 6323118 ref NP_013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.0968	0.2294	1029.91	1029.268	2	977	81.25 F.PKIDLPFKA.V
gi 6323118 ref NP_013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.0515	0.2442	1255.77	1256.531	1	1059.2	80 F.PKIDLPFKAVQ.E
gi 6323118 ref NP_013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	1	2.5318	0.2623	1387.85	1388.736	1	693.4	59.090908 Y.LFPKIDLPFKAV.Q
gi 6323118 ref NP_013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.5063	0.2746	1518.39	1516.867	2	675.4	75 Y.LFPKIDLPFKAVQ.E
gi 6323118 ref NP 013190.11	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.9824	0.393	1708.13	1708.837	1	980.2	64.285/1 L.MVRPPVEGEESFESD.Q
gi 6323118 ref NP_013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	4.4805	0.4436	2247.37	2246.577	1	745.9	55.263157 F.CRGPETGVLIPIPQYPLYTA.T
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gi 6323118 ref NP 013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	1	2.7587	0.256	1291.16	1289.604	1	719.7	70 Y.LFPKIDLPFKA.V
gil6323118/refINP_013190.1	YLR089C	Putative alanine transaminase (olutamic pyruvic transaminase): Alt1p	2	3.5879	0.3652	1576.79	1577.645	1	795.7	69.230774 M.VRPPVEGEESFESD.Q
gi[6222118]rof[ND_012100.1]	VI R080C	Putative glamine transaminase (glatamic pyravie transaminase), Att p	2	2 0055	0.0002	2075 50	2074 204	1	200.4	
gilo323116[rei]iNP_013190.1]	TLR089C	Putative alanine transaminase (glutarnic pyruvic transaminase); Attrp	2	2.9955	0.2071	2075.59	2074.394		322.4	41.17047 F.CKGPETGVLIPIPQTPLT.1
gi 6323118 ref NP_013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.7286	0.2909	2170.57	2171.554	1	614.2	58.333332 S.IFCRGPETGVLIPIPQYPL.Y
gi 6323118 ref NP 013190.1	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.4712	0.3248	1681.87	1680.043	1	1154.8	73.07692 M.YLFPKIDLPFKAVQ.E
gil6323118/refINP_013190_1	YI R089C	Putative alanine transaminase (glutamic pyruvic transaminase): Alt1p	2	3 4981	0 2974	1453 53	1452 78	1	1027.8	72 72727 M YI EPKIDI PEKA V
gil6222119[rofIND_012100_1]	VI DOROC	Putative algories transportinges (aluternic putavis transportinges); Altap	-	2 2200	0.1029	1524 52	1522.967	4	ECC 0	70 92222 V I 1E1D1K2I1D1I 1D1E1K2A1\/1O2 E
gilo323110[rei]ivF_013190.1]	ILK009C	Putative ataline transaminase (gutarine pyrovic transaminase), Attrp	2	3.3209	0.1920	1554.55	1552.007		500.0	10.03333 T.LIFIFIKZIIDILIFIFIKZAIVIQZ.E
		v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion;								
		inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar								
gil9755337/refINP_013194.2	YLR093C	membrane: Nvv1p	3	4.2564	0.2214	1640.69	1641.094	2	879.4	51.923077 F.T1L1V1D1M1P1K2I1L1P1I1R4I1L1.S
3.10.0000.1.0.1.00.00.0=1		v-SNARE component of the vacualar SNARE complex involved in vesicle fusion:	-					-		
		V-SIVARE component of the vacuoial Sivare complex involved in vesicle fusion,								
		inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar								
gi 9755337 ref NP_013194.2	YLR093C	membrane; Nyv1p	2	3.0872	0.2342	1521.61	1521.988	2	608.5	62.5 T.LVDMPKILPIRIL.S
		v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion:								
		inhibite ATP-dependent Ca(2+) transport activity of Pmc1p in the vacualar								
	V/I D0000	infinitions A re-dependent Ca(2+) transport activity of Find tp in the vacuolar		0.0007	0.0000	4500.00	4504 000		000.0	
gi 9755337 ret NP_013194.2	YLR093C	membrane; Nyv1p	1	2.9067	0.2993	1520.68	1521.988	3	229.8	54.166668 I.LVDMPKILPIRILS
		v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion;								
		inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar								
gil0755337/rofIND_013104_2	VI PO03C	membrane: Nuvin	2	3 8044	0.282	16/1 21	16/1 00/	1	760 7	65 38461 E T1I 1\/1D1M1D1K2I1I 1D1I1D4I1I 1 S
gij9/33337 [rei]14/_013134.2]	TER0350	nenibrane, Nyvip	2	3.0344	0.202	1041.21	1041.034		100.1	03.304011.11E1V1D1WITFINZITETF111R4ITET.3
		v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion;								
		inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar								
ail9755337/refINP 013194.2	YLR093C	membrane: Nvv1p	2	3.6467	0.2559	1625.87	1623.094	1	906.4	69.230774 F.TLVDMPKILPIRIL.S
510 000 101 =0 000 1		v-SNARE component of the vacualar SNARE complex involved in vesicle fusion:								
		individual dependent $C_{2}(2)$ transport activity of Product in the vacual r								
		initions ATP-dependent Ca(2+) transport activity of Filterp in the vacuolar								
gi 9755337 ref NP_013194.2	YLR093C	membrane; Nyv1p	3	4.3045	0.1648	1789.73	1789.27	2	735	41.07143 C.F1T1L1V1D1M1P1K2I1L1P1I1R4I1L1.S
		v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion;								
		inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacualar								
-::07552271{IND_042404.01	VI DODDO		2	2 0507	0.0077	4700.00	4770.07	4	4400.0	
gij9755337 [rei]NP_013194.2]	TLR093C	membrane, Nyv Ip	3	3.9507	0.2077	1769.93	1770.27		1130.2	50 C.FTLVDWPKILPIRIL.5
		v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion;								
		inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar								
ail9755337/refINP_013194_2	VI R093C	membrane: Nw(1)	2	3 7618	0 2738	1642.65	1641 094	2	545 1	57 692307 F T1I 1V1D1M1P1K2I1I 1P1I1R4I1I 1 S
gija/3333/[rei]i4/_013134.2]	TER035C		2	3.7010	0.2750	1042.00	1041.034	2	343.1	37.0323071.11ETV1D1W1F1K2HEIF1HK4HEI.3
		v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion;								
		inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar								
ail9755337/refINP 013194.2	YLR093C	membrane: Nvv1p	3	3.8477	0.23	1640.03	1641.094	2	548.2	44.230766 F.T1L1V1D1M1P1K2I1L1P1I1R4I1L1.S
510 000 101 =0 000 1		v-SNARE component of the vacualar SNARE complex involved in vesicle fusion:								
		is bis to Appendix of the vacuular strain to the provide investigation of the vacuular								
		inhibits ATP-dependent Ca(2+) transport activity of Princip in the vacuolar								
gi 9755337 ref NP_013194.2	YLR093C	membrane; Nyv1p	2	2.935	0.202	1538.55	1538.988	1	632.4	58.333332 T.L1V1D1M1P1K2I1L1P1I1R4I1L1.S
		Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle								
		with the Rivi complex (Rivin-Inita-Inita) may mediate ATP-dependent remodeling								
	V/I D 4000	with the Kikr complex (Kikr IP-Ip) (P-Ip)(P), may mediate Arr-dependent remodeling	•	0 700 4	0.0044	0400.07	0101 005		755 4	
gi 6323135 ref NP_013207.1	YLR106C	of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.7634	0.3941	2100.97	2101.225	1	755.1	52.77778 Q.K2V1I1G1D1G1I1E1S1I1S1E111D1D1N2W2L1S1.A
		Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle								
		with the Pix1 complex (Pix1p-Inita-Inita) may mediate ATP-dependent remodeling								
		with the Rikt complex (Riktp-Iphp-Ipisp), may mediate ATF-dependent temodeling								
gi 6323135 ref NP_013207.1	YLR106C	of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	4.9974	0.4269	2078.27	2079.225	1	879.8	58.333332 Q.KVIGDGIESISETDDNWLS.A
		Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle								
		with the Rivi complex (Rivin-Inita-Inita) may mediate ATP-dependent remodeling								
-: 102024251 FIND 042207 41	VI DAOCO	with the KixT complex (KixTp-tp)Tp-tp)39), may include ATF-dependent remodeling	0	2 0005	0 4024	04 40 74	0450 004	2	075 4	
gi 6323135 ret NP_013207.1	YLR106C	of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.0885	0.1834	2149.71	2150.304	3	275.4	42.105263 Q.KVIGDGIESISETDDNWLSA.S
		Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle								
		with the Pix1 complex (Pix1p-Inita-Inita) may mediate ATP-dependent remodeling								
	V/I D 4000	with the fixer complex (fix rp-ip) p-ip)(p), may mediate Arr-dependent remotening	•	5 5004	0 4004	0444.45	04.44.000		4 405 5	
gi 6323135 ref NP_013207.1	YLR106C	of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	5.5294	0.4391	2141.45	2141.339	1	1405.5	67.64706 T.NEKDISSPENLDDIYFKL.A
		Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle								
		with the Pirit complex (Pirite Inite Inite Inite Area and the Area de the Area de the								
		with the RixT complex (RixTP-IpTP-IpISP), may mediate ATP-dependent remodeling								
gi 6323135 ref NP_013207.1	YLR106C	of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	2.9777	0.1776	1972.79	1974.181	3	374.9	43.333332 L.NRLLDDNRELFIPETQ.E
		Huge dynein-related AAA-type ATPase (midasin) forms extended pre-60S particle								
		with the Pirit complex (Pirite Inite Inite Inite Area and the Area de the Area de the								
		with the RixT complex (RixTp-IpTp-IpISp), may mediate ATP-dependent remodeling								
gi 6323135 ref NP_013207.1	YLR106C	of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.4477	0.3475	1466.39	1466.68	1	408.8	72.72727 Q.E1V1V1H3P1H3P1D1F1L1L1F1.A
		Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle								
		with the Pirit complex (Pirite Inite Inite Inite Area and the Area de the Area de the								
		with the RixT complex (RixTP-IpTP-IpISP), may mediate ATP-dependent remodeling								
gi 6323135 ref NP_013207.1	YLR106C	of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	3	4.0955	0.207	2165.36	2165.373	2	719.8	37.5 L.H3F1D1D1I1P1Q2D1E1L1E1I1I1L1R4E1R4.C
		Huge dynein-related AAA-type ATPase (midasin) forms extended pre-60S particle								
		Tuge dy Bit Hein-telated AAA-type ATF ase (Initiaasin), torins extended pre-ous particle								
		with the Rix1 complex (Rix1p-IpI1p-IpI3p), may mediate ATP-dependent remodeling								
gi 6323135 ref NP_013207.1	YLR106C	of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	1	3.3318	0.3553	1467.54	1466.68	1	236	59.090908 Q.E1V1V1H3P1H3P1D1F1L1L1F1.A
		Huge dynain-related AAA-type ATPase (midacin) forms extended pre-60S particle								
		Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle								
		Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling								
gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ip1p1p3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.3128	0.2489	2139.45	2139.373	1	476.2	53.125 L.HFDDIPQDELEIILRER.C
gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lpi1p-lpi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.3128	0.2489	2139.45	2139.373	1	476.2	53.125 L.HFDDIPQDELEIILRER.C
gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.3128	0.2489	2139.45	2139.373	1	476.2	53.125 L.HFDDIPQDELEIILRER.C
gi 6323135 ret NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle	2	3.3128	0.2489	2139.45	2139.373	1	476.2	53.125 L.HFDDIPQDELEIILRER.C
gij6323135/ret/NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p)pi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling	2	3.3128	0.2489	2139.45	2139.373	1	476.2	53.125 L.HFDDIPQDELEIILRER.C
gi 6323135 ref NP_013207.1 gi 6323135 ref NP_013207.1	YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-IpiTp-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.3128 3.4947	0.2489 0.3876	2139.45 1853.39	2139.373 1853.008	1	476.2 814.2	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K
gi 6323135 ref NP_013207.1 gi 6323135 ref NP_013207.1	YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.3128 3.4947	0.2489 0.3876	2139.45 1853.39	2139.373 1853.008	1	476.2 814.2	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K
gi 6323135 ref NP_013207.1 gi 6323135 ref NP_013207.1	YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-IpiTp-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle and the result of the temperature of temperature of temperature of temperature of the temperature of tempe	2	3.3128 3.4947	0.2489 0.3876	2139.45 1853.39	2139.373 1853.008	1	476.2 814.2	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K
gi 6323135 ref NP_013207.1 gi 6323135 ref NP_013207.1	YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle	2	3.3128 3.4947	0.2489 0.3876	2139.45 1853.39	2139.373 1853.008	1	476.2 814.2	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K
gi[6323135]ref[NP_013207.1] gi[6323135]ref[NP_013207.1]	YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lpi1p-lpi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lpi1p-lpi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lpi1p-lpi3p), may mediate ATP-dependent remodeling	2	3.3128 3.4947	0.2489 0.3876	2139.45 1853.39	2139.373 1853.008	1	476.2 814.2	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K
gi[6323135]ref]NP_013207.1] gi[6323135]ref]NP_013207.1] gi[6323135]ref]NP_013207.1]	YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent from nucleoplasm to cytoplasm; Mdn1p	2 2 3	3.3128 3.4947 4.0379	0.2489 0.3876 0.3434	2139.45 1853.39 1907.27	2139.373 1853.008 1907.257	1 1 1	476.2 814.2 997.8	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1IIV1K2F1.S
gij6323135/ref/NP_013207.1 gij6323135/ref/NP_013207.1 gij6323135/ref/NP_013207.1	YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-IpiTp-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2 2 3	3.3128 3.4947 4.0379	0.2489 0.3876 0.3434	2139.45 1853.39 1907.27	2139.373 1853.008 1907.257	1 1 1	476.2 814.2 997.8	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1I1V1K2F1.S
gi 6323135 ref NP_013207.1 gi 6323135 ref NP_013207.1 gi 6323135 ref NP_013207.1	YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin) forms extended pre-60S particle	2 2 3	3.3128 3.4947 4.0379	0.2489 0.3876 0.3434	2139.45 1853.39 1907.27	2139.373 1853.008 1907.257	1 1 1	476.2 814.2 997.8	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1II1V1K2F1.S
gij6323135/ref NP_013207.1 gij6323135/ref NP_013207.1 gij6323135/ref NP_013207.1	YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p), may mediate ATP dependent tremodeling the second se	2 2 3	3.3128 3.4947 4.0379	0.2489 0.3876 0.3434	2139.45 1853.39 1907.27	2139.373 1853.008 1907.257	1 1 1	476.2 814.2 997.8	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1I1V1K2F1.S
gi[6323135]ref]NP_013207.1] gi[6323135]ref]NP_013207.1] gi[6323135]ref]NP_013207.1]	YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling	2 2 3	3.3128 3.4947 4.0379	0.2489 0.3876 0.3434	2139.45 1853.39 1907.27	2139.373 1853.008 1907.257	1 1 1	476.2 814.2 997.8	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1I1V1K2F1.S
gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1]	YLR106C YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2 2 3 2	3.31283.49474.03793.1506	0.2489 0.3876 0.3434 0.2066	2139.45 1853.39 1907.27 1451.33	2139.373 1853.008 1907.257 1450.68	1 1 1	476.2 814.2 997.8 480	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1II1V1K2F1.S 72.72727 Q.EVVHPHPDFLLF.A
gi[6323135]ref]NP_013207.1] gi[6323135]ref]NP_013207.1] gi[6323135]ref]NP_013207.1] gi[6323135]ref]NP_013207.1]	YLR106C YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2 2 3 2	3.3128 3.4947 4.0379 3.1506	0.2489 0.3876 0.3434 0.2066	2139.45 1853.39 1907.27 1451.33	2139.373 1853.008 1907.257 1450.68	1 1 1	476.2 814.2 997.8 480	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1I1V1K2F1.S 72.72727 Q.EVVHPHPDFLLF.A
gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1]	YLR106C YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ip1p-Ip3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lp1p-lp3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lp1p-lp3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lp1p-lp3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lp1p-lp3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin) forms extended pre-60S particle with the Rix1 complex (Rix1p-lp1p-lp3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin) forms extended pre-60S particle subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin) forms extended pre-60S particle subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin) forms extended pre-60S particle	2 2 3 2	3.3128 3.4947 4.0379 3.1506	0.2489 0.3876 0.3434 0.2066	2139.45 1853.39 1907.27 1451.33	2139.373 1853.008 1907.257 1450.68	1 1 1 1	476.2 814.2 997.8 480	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1II1V1K2F1.S 72.72727 Q.EVVHPHPDFLLF.A
gij6323135[ref]NP_013207.1] gij6323135[ref]NP_013207.1] gij6323135[ref]NP_013207.1] gij6323135[ref]NP_013207.1]	YLR106C YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2 2 3 2	3.3128 3.4947 4.0379 3.1506	0.2489 0.3876 0.3434 0.2066	2139.45 1853.39 1907.27 1451.33	2139.373 1853.008 1907.257 1450.68	1 1 1	476.2 814.2 997.8 480	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1I1V1K2F1.S 72.72727 Q.EVVHPHPDFLLF.A
gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1] gij6323135/ref/NP_013207.1]	YLR106C YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-ip1p-Ip3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-bip1p-Ip3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-bip1p-Ip3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-bip1p-1p3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-bip1p-1p3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-bip1p-1p3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-pip1p-1p3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2 2 3 2	3.3128 3.4947 4.0379 3.1506	0.2489 0.3876 0.3434 0.2066	2139.45 1853.39 1907.27 1451.33	2139.373 1853.008 1907.257 1450.68	1 1 1	476.2 814.2 997.8 480	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1I1V1K2F1.S 72.72727 Q.EVVHPHPDFLLF.A
gi[6323135]ref]NP_013207.1] gi]6323135]ref]NP_013207.1] gi]6323135]ref]NP_013207.1] gi]6323135]ref]NP_013207.1] gi]6323135[ref]NP_013207.1]	YLR106C YLR106C YLR106C YLR106C YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2 2 3 2 1	3.3128 3.4947 4.0379 3.1506 3.4613	0.2489 0.3876 0.3434 0.2066 0.3336	2139.45 1853.39 1907.27 1451.33 1450.54	2139.373 1853.008 1907.257 1450.68 1450.68	1 1 1 1	476.2 814.2 997.8 480 310.5	53.125 L.HFDDIPQDELEIILRER.C 64.28571 L.ITVRHPLSEFTNDYC.K 40 S.R4L1L1E1D1L1K2D1L1A1N2P1I1V1K2F1.S 72.72727 Q.EVVHPHPDFLLF.A 68.181816 Q.EVVHPHPDFLLF.A

gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-lpi1p-lpi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.3359	0.2374	1625.67	1624.921	2	612.7	57.692307 A.KHLYPSIEPDIIAK.M
gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.7529	0.168	1691.47	1692.846	1	1091.2	67.85714 L.S1K2L1E1D1G1I1N2E1L1E1L1I1S1N2.K
gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.4843	0.1672	1674.17	1674.846	2	1185	67.85714 L.SKLEDGINELELISN.K
gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	3.2219	0.1805	1206.31	1206.444	1	1152	83.33333 Q.L1L111E1D111F1G1K2F1.S
gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	4.5134	0.4007	2081.99	2083.301	1	983.2	58.823532 L.S1E1K2G1D1A1E1P1I1K2A1H3P1D1F1R4I1F1.A
gi 6323135 ref NP_013207.1	YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	2	4.4243	0.4668	2057.13	2058.301	1	1074.4	61.764706 L.SEKGDAEPIKAHPDFRIF.A
gi 6323138 ref NP_013210.1	YLR109W	Thiol-specific peroxiredoxin, reduces hydroperoxides to protect against oxidative damage; function in vivo requires covalent conjugation to Urm1p; Ahp1p	2	3.7969	0.2855	2019.53	2019.343	2	504	50 N.YLDELVKEKEVDQVIVV.T
gi 6323138 ref NP_013210.1	YLR109W	Thiol-specific peroxiredoxin, reduces hydroperoxides to protect against oxidative damage; function in vivo requires covalent conjugation to Urm1p; Ahp1p	2	4.1801	0.2656	2037.69	2039.343	4	476.7	50 N.Y1L1D1E1L1V1K2E1K2E1V1D1Q2V1I1V1V1.T
gi 6323138 ref NP_013210.1	YLR109W	Thiol-specific peroxiredoxin, reduces hydroperoxides to protect against oxidative damage; function in vivo requires covalent conjugation to Urm1p; Ahp1p	2	3.0363	0.2418	2119.33	2120.448	2	305.1	44.11765 N.YLDELVKEKEVDQVIVVT.V
gi 6323142 ref NP_013214.1	YLR113W	Mitogen-activated protein kinase involved in osmoregulation via three independent osmosensors; mediates the recruitment and activation of RNA Pol II at Hot1p- dependent promoters; localization regulated by Ptp2p and Ptp3p; Hog1p	2	3.9483	0.4167	1716.39	1713.798	1	812.7	63.333332 Y.SAPYHDPTDEPVADAK.F
gi 6323142 ref NP_013214.1	YLR113W	Mitogen-activated protein kinase involved in osmoregulation via three independent osmosensors; mediates the recruitment and activation of RNA Pol II at Hot1p- dependent promoters; localization regulated by Ptp2p and Ptp3p; Hog1p	2	4.1527	0.4283	1731.27	1732.798	1	1146.3	70 Y.S1A1P1Y1H3D1P1T1D1E1P1V1A1D1A1K2.F
gi 6323142 ref NP_013214.1	YLR113W	Mitogen-activated protein kinase involved in osmoregulation via three independent osmosensors; mediates the recruitment and activation of RNA Pol II at Hot1p- dependent promoters; localization regulated by Ptp2p and Ptp3p; Hog1p	2	3.5961	0.3213	1878.35	1878.995	1	848.5	71.42857 K.FDWHFNDADLPVDTW.R
gi 6323142 ref NP_013214.1	YLR113W	Mitogen-activated protein kinase involved in osmoregulation via three independent osmosensors; mediates the recruitment and activation of RNA Pol II at Hot1p- dependent promoters; localization regulated by Ptp2p and Ptp3p; Hog1p	2	3.3755	0.2393	1900.17	1898.995	1	634.6	64.28571 K.F1D1W2H3F1N2D1A1D1L1P1V1D1T1W2.R
gi 6323142 ref NP_013214.1	YLR113W	Mitogen-activated protein kinase involved in osmoregulation via three independent osmosensors; mediates the recruitment and activation of RNA Pol II at Hot1p- dependent promoters; localization regulated by Ptp2p and Ptp3p; Hog1p	1	2.3191	0.1745	1193.55	1194.364	9	259.5	55.555557 T.S1L1P1H3R4D1P111P1F1.S
gi 6323177 ref NP_013249.1	YLR148W	Vacuolar peripheral membrane protein that promotes vesicular docking/fusion reactions in conjunction with SNARE proteins, required for vacuolar biogenesis, forms complex with Pep5p that mediates protein transport to the vacuole; Pep3p	2	3.5619	0.2175	1551.49	1549.764	2	758.1	66.66667 M.KFPLVLPDESEQF.E
gi 6323177 ref NP_013249.1	YLR148W	Vacuolar peripheral membrane protein that promotes vesicular docking/fusion reactions in conjunction with SNARE proteins, required for vacuolar biogenesis, forms complex with Pep5p that mediates protein transport to the vacuole; Pep3p	2	4.4658	0.2977	1947.09	1948.226	1	1114.2	70 M.KFPLVLPDESEQFERL.K
gi 6323177 ref NP_013249.1	YLR148W	Vacuolar peripheral membrane protein that promotes vesicular docking/fusion reactions in conjunction with SNARE proteins, required for vacuolar biogenesis, forms complex with Pep5p that mediates protein transport to the vacuole; Pep3p	2	4.1184	0.3419	1966.69	1969.226	1	1149	70 M.K2F1P1L1V1L1P1D1E1S1E1Q2F1E1R4L1.K
gi 6323177 ref NP_013249.1	YLR148W	Vacuolar peripheral membrane protein that promotes vesicular docking/fusion reactions in conjunction with SNARE proteins, required for vacuolar biogenesis, forms complex with Pep5p that mediates protein transport to the vacuole; Pep3p	3	3.9616	0.3493	1947.77	1948.226	1	1923.7	48.333332 M.KFPLVLPDESEQFERL.K
gi 6323177 ref NP_013249.1	YLR148W	Vacuolar peripheral membrane protein that promotes vesicular docking/fusion reactions in conjunction with SNARE proteins, required for vacuolar biogenesis, forms complex with PepSp that mediates protein transport to the vacuole; Pep3p	2	4.1757	0.3039	1947.79	1948.226	1	1302	73.333336 M.KFPLVLPDESEQFERL.K
gi 6323182 ref NP 013254.1	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	1	2.6842	0.3347	1474.58	1474.652	9	209.4	42.307693 K.K2I1V1D1E1G1L1N2G1V1D1L1V1S1.R
ail6323182lrefINP 013254 1	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions: Acs2o	2	4.0417	0.2515	1617.53	1614.839	1	2075.8	85.71429 K.KIVDEGLNGVDLVSR.I
gil6323182/refINP_013254.1	VLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerotic conditions; Acs20	2	2 977/	0.2080	1515.85	1516 638	5	359.6	58 333332 O H3E1Y1N2S1O2P1G1K/G1Y1V1T1 D
gij0525102jreijNF_015254.1	VI P1520	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	4	2.3114	0.2009	1010.00	1296 444	7	519.0	
	1LR 1030	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	1	2.20/0	0.213	1200.72	1200.441		010.1	
gijo323182jret[NP_013254.1]	YLK153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	2	4.2132	0.387	1632.55	1634.839	1	0.800	(1.42007 K.KZITVTUTETGTLTNZGTVTUTLTVTSTK4.I
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p Acetyl-ccA synthetase isoform, required for growth on glucose; expressed under	3	3.994	0.4134	2291.66	2293.5	1	1042.8	34.210526 N.A1T1E1G1D1A1E1H3I1T1P1D1N2L1R4R4E1L1I1L1.Q
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	2	3.408	0.3239	2152.31	2153.321	1	560	47.058823 L.G1S1V1G1E1P1I1S1P1D1L1W2E1W2Y1H3E1K2.V
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	2	3.4333	0.1943	1865.37	1863.158	2	578.9	53.125 K.K2I1V1D1E1G1L1N2G1V1D1L1V1S1R4I1L1.V
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p	2	3.2468	0.2871	1919.59	1921.3	1	651.6	55.88235 K.K2G1D1T1V1A1I1Y1L1P1M1I1P1E1A1V1I1A1.M

		Acetyl-coA synthetase isoform, required for growth on glucose; expressed under								
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p AcetylecoA synthetase isoform, required for growth on glucose; expressed under	3	4.1353	0.3379	1588.55	1588.676	1	1517.9	50 D.G1A1G1R4D1H3D1G1Y1Y1W2I1R4.G
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p	2	4.4319	0.3695	2675.11	2673.887	1	242.4	38.636364 L.G1S1V1G1E1P1I1S1P1D1L1W2E1W2Y1H3E1K2V1G1N2K2N2.C
ail6323182/rofIND_013254_1	VI P153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	2	3 0254	0.256	2222.65	2225 658	1	721.6	45 W G1V1K2K2G1D1T1V1A111V111P1M\$1P1E1A1V111A1 M
gilo3231821eilinF_013234.1	ILK 1550	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	2	3.0234	0.230	2223.05	2223.000		721.0	
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p	2	3.3359	0.2856	2212.39	2209.658	1	676.1	47.5 W.G1V1K2K2G1D1T1V1A1I1Y1L1P1M1I1P1E1A1V1I1A1.M
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p	2	3.3072	0.2278	2187.53	2186.658	4	331.6	35 W.GVKKGDTVAIYLPMIPEAVIA.M
	VI D4500	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	0	2 52 40	0 4007	4057.07	4050 700		500.4	
gi 6323182 ret NP_013254.1	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under	2	3.5349	0.4267	1657.87	1658.769	1	569.4	68.181816 S.V1W2N2H3H3D1R4Y1M1D111Y1.L
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p	2	3.0822	0.4091	1604.99	1605.703	1	642.6	70.83333 F.ESTPAYPDYGRYW.R
ail6323182/refINP_013254.1	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions: Acs2p	1	2,7533	0.3291	1587.37	1588.714	1	447.2	50 L.G1S1V1G1E1P1I1S1P1D1L1W2E1W2.Y
3.1		Acetyl-coA synthetase isoform, required for growth on glucose; expressed under								
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p AcetylecoA synthetase isoform, required for growth on glucose; expressed under	2	3.3682	0.2889	1493.19	1492.588	1	421.7	68.181816 E.S1T1P1A1Y1P1D1Y1G1R4Y1W2.R
gi 6323182 ref NP_013254.1	YLR153C	anaerobic conditions; Acs2p	2	3.6943	0.2097	1500.95	1500.695	1	1258.4	81.818184 Q.S1I1N2E1P1E1K2F1F1D1K2M1.A
		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.2988	0.1672	1479.45	1478.627	1	1187.5	70.83333 H.D1A1L1K2D1E1K2D1L1G1R4S1L1.E
		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.2515	0.2524	1461.43	1460.627	1	1238.3	70.83333 H.DALKDEKDLGRSL.E
		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),								
ail6323204/refINP 013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	3	4.6562	0.3802	2447.81	2448.687	1	1109.6	40 S.SQETKETEEEPKKAKEDSLIK.E
51		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),								
ail6323204/refINP_013276_1	YLR175W	probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	3 1814	0.3377	1896 51	1897 141	1	871 9	58 823532 R SGHYTPIPAGSSPI KRDI K
91002020 1101111 _010210.11	121111011	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),	-	0.1011	0.0011	1000.01	1001111	·	01.110	
ail6323204/refINP_013276_1	VI R175W	probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	1	2 6065	0 2256	1535 68	1535 807	1	193.5	
giloszozo4irciliti _010210.11	LICHOW	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),		2.0000	0.2200	1000.00	1000.001		100.0	0.00000 CIMERDEN RRW.0
ail6222204/rofIND_012276_11		probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts	2	2 4024	0 0000	1901 05	1902 115	1	752 5	
gil0323204[rei]INF_013270.1]	ILK175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),	2	3.4021	0.2332	1091.95	1893.115		755.5	03.333332 V.R4LIN3DIAILIK2DIEIK2DIEIK10IR43ILI.E
- 1000000 41- (IND- 040070 41	VI D47514	probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts	•	0.0050	0.0004	1010 07	1010.000	•	500.0	
gi 6323204 ret NP_013276.1	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),	2	3.2359	0.2891	1810.07	1810.063	6	596.2	53.125 S.GHYTPIPAGSSPLKRDL.K
		probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs).	3	4.1632	0.4011	1775	1775.011	1	915.5	45 G.H3Y111P111P1A1G1S1S1P1L1K2R4D1L1.K
		probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p Component of box H/ACA small nucleolar ribonucleoprotein particles (spoRNPs)	1	2.724	0.2049	1459.48	1460.627	1	735.5	70.83333 H.DALKDEKDLGRSL.E
		probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.3906	0.2055	1460.01	1460.627	1	1111.6	66.66667 H.DALKDEKDLGRSL.E
		probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	2	4.6948	0.2071	2256.83	2257.478	1	580.2	55.555557 Q.E1T1K2E1T1E1E1E1P1K2K2A1K2E1D1S1L111K2.E
		probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	2	4.5961	0.2733	2449.85	2448.687	1	896.7	60.000004 S.SQETKETEEEPKKAKEDSLIK.E
		component of box H/ACA small nucleolar ribonucleoprotein particles (snorkNPs), probable rRNA pseudouridine synthase, binds to snorkNP Nop10p and also interacts								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.7188	0.3198	1530.07	1530.69	1	442.7	70.83333 R.L1H3D1A1L1K2D1E1K2D1L1G1R4.S
		component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	1	2.803	0.151	1183.52	1184.28	1	321.3	62.5 L.R4Y1E1E1G1I1E1L1Y1.D
		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Non10p and also interacts								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.3888	0.3591	1732.61	1732.928	1	1595.6	71.42857 R.L1H3D1A1L1K2D1E1K2D1L1G1R4S1L1.E
		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	1	2.7602	0.3409	1583.76	1584.812	1	355.2	54.166668 N.L1I1E1F1D1N2K2R4N2L1G1V1F1.W
		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),								
gi 6323204 ref NP_013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	2	4.4217	0.388	1710.61	1710.928	1	1834.7	75 R.LHDALKDEKDLGRSL.E
		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),								
ail6323204/refINP 013276.1	YLR175W	with ribosomal biogenesis protein Nop53p; Cbf5p	1	2.3669	0.2252	1367.54	1368.545	1	294.4	59.090908 A.G1S1S1P1L1K2R4D1L1K2S1Y1.I
51		Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs),								
gil6323204/refINP_013276_1	YLR175W	probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	4 6719	0 4232	2157 49	2157 439	1	907.5	55 555557 G H3Y1T1P1I1P1A1G1S1S1P1I 1K2R4D1I 1K2S1Y1 I
giloszozo4iciliti _010210.11	I EIKI I OW	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	-	4.0715	0.4202	2107.40	2101.400		507.5	
ail6323200/rofIND_013281_1		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p	2	3 71/19	0 4241	1676 31	1677 695	1	480	53 571426 T S1E1S1V1C1E1C1H3P1D1K311C1D1O3 V
gil0323203[tel[14]_013201.1]	LICIOUW	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	2	5.7140	0.4241	10/0.51	1077.005		400	
-:::::::::::::::::::::::::::::::::::::	VI D400W	the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p	0	4 7045	0 0000	4700 40	4700 707		4400 7	
gilo323209[rei]inP_013281.1]	TLR 160W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	2	4.7015	0.3229	1733.49	1732.767		1160.7	76.6666664 Q.GTVTH3ETETK2DTETETDTTGTATGTDTQ2.G
	VI D4COM	the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p	~	4.000	0.400	0007.05	0007 405		700.0	
gijo323209[ret]NP_013281.1]	1LK180W	and sam2p); sam1p S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	2	4.089	0.462	2387.35	∠387.495	1	780.2	47.0 1900 E.SVGEGMPDKICDQVSDAILDAC.L
	VIDACOW	the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p	~	4.0470	0.0440	004.0.00	0044 400		505.0	
gij6323209[ret]NP_013281.1]	YLK180W	and Sam2p); Sam1p S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl droup of ATP to	2	4.0473	0.3412	2210.39	2211.498	1	505.2	41.000004 S.U1E1E11111D11111S1K2N2F1D1L1R4P1G1V1L1.V
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p	-							
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	2	3.1969	0.286	2155.81	2155.467	1	431.1	41.666664 K.R4V1Q2V1Q2F1S1Y1A1I1G111A1E1P1L1S1L1H3.V

		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to								
ail6323209/refINP_013281.1	YLR180W	the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p): Sam1p	2	2.9404	0.2199	1850.89	1853.01	1	412.9	50 Q.V1T1V1E1Y1K2D1D1H3G1R4W2V1P1Q2 R
giloozozoolioiliti _01020111	121110011	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	-	2.0101	0.2100	1000.00	1000.01		112.0	
-:::02020001#ND_042204_41	VI D400W	the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p	0	0 7575	0.0700	4740 75	4740.004		502.2	
gilo323209[rei]NP_013281.1]	TLR 160W	Sadenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	2	3./5/5	0.2798	1/19./5	1719.031		592.Z	57.14200 L.VIKZETETDTETATR4PTITYTETPTTTAT.5
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	2	3.2309	0.2371	2678.67	2680.093	2	317.5	33.333336 E.III1E1K2V1I1P1R4D1M1L1D1E1N2T1K2Y1F1I1Q2P1S1.G
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	2	4.3797	0.2976	1506.35	1506.679	1	1768.2	87.5 A.T1K2S1D1E1E11111D11111S1K2.N
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	3	4.3148	0.302	2316.23	2317.655	1	1067.2	36.842106 L.V1K2E1L1D1L1A1R4P1I1Y1L1P1T1A1S1Y1G1H3F1.T
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1).								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	2	3.6649	0.3785	1711.95	1712.767	1	663.3	60.000004 Q.GVHEEKDLEDIGAGDQ.G
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	2	5.1172	0.3848	2544.57	2543.61	1	471.3	40.909092 S.E1S1V1G1E1G1H3P1D1K2I1C1D1Q2V1S1D1A1I1L1D1A1C1.L
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to								
ail6323209/refINP 013281.1	YLR180W	and Sam2p): Sam1p	2	4.4564	0.46	2411.65	2413.495	1	708.3	42.857143 E.S1V1G1E1G1H3P1D1K2I1C1D1Q2V1S1D1A1I1L1D1A1C1.L
3.1		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to								
ail6323209/refINP_013281_1	YI R180W	the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3 4714	0 1618	1647 39	1646 952	1	731 1	65 38461 V1K2E1 1D1 1A1R4P1 1V1 1P1T1 A
giloozozoolioiliti _01020111	121110011	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	-	0.1111	0.1010	1011.00	1010.002			
ail62022001rofIND_012281_1		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p	2	2 5 1 9 4	0.2701	1629 50	1639.053	1	1022.2	
gilo323209[ter]INF_013261.1]	ILKIOUW	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	2	3.3104	0.2701	1020.39	1028.952		1023.3	73.07092 L.VRELDLARFITEFT.A
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gil6323209[ref]NP_013281.1]	YLR180W	and Sam2p); Sam1p S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	2	4.2286	0.4543	2189.83	2191.485	1	764.2	50 K.V111P1R4D1M1L1D1E1N211K2Y1F111Q2P151.G
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to	3	3.8801	0.1943	3250.73	3251.684	1	726.3	24.107143 K.VIPRDMLDENTKYFIQPSGRFVIGGPQGD.A
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p S-adonocylmethioning synthetase, catalyzes transfer of the adonocyl group of ATP to	2	4.276	0.3588	2168.33	2167.485	1	765.4	52.941177 K.VIPRDMLDENTKYFIQPS.G
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p S adapage/methicsing synthetics, path/zee transfer of the adapage/ group of ATP to	2	4.2502	0.4477	2050.31	2051.328	1	586.8	58.823532 K.I1V1R4D1T111K2K2I1G1Y1D1D1S1A1K2G1F1.D
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								K.V1I1P1R4D1M1L1D1E1N2T1K2Y1F1I1Q2P1S1G1R4F1V1I1G1G1P1Q2G1D1A1G
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	3	4.7725	0.3571	3634.97	3637.08	1	639.2	24.21875 1L1T1.G
		the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	3	3.8741	0.2723	3082.43	3079.544	1	521.2	26.923079 K.VIPRDMLDENTKYFIQPSGRFVIGGPQ.G
		5-adenosylmetrionine synthetase, catalyzes transfer of the adenosyl group of A I P to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	3	5.0862	0.3191	3116.03	3116.544	2	667.5	26.923079 K.V1I1P1R4D1M1L1D1E1N2T1K2Y1F1I1Q2P1S1G1R4F1V1I1G1G1P1Q2.G
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine: one of two differentially regulated isozymes (Sam1p								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	2	4.4042	0.2048	1404.01	1404.574	1	1574.3	86.36364 T.K2S1D1E1E1111D11111S1K2.N
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine: one of two differentially regulated isozymes (Sam1)								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	2	3.6097	0.2416	1490.57	1491.679	2	774.6	62.5 A.TKSDEEIIDIISK.N
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	2	3.734	0.2533	1762.73	1761	1	790.8	61.538464 K.V1I1P1R4D1M1L1D1E1N2T1K2Y1F1.I
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to								
gi 6323209 ref NP_013281.1	YLR180W	and Sam2p); Sam1p	3	4.764	0.3407	2380.16	2379.723	1	900.5	38.88889 S.E1I111E1K2V1I1P1R4D1M1L1D1E1N2T1K2Y1F1.I
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to								
gi 6323209 ref NP 013281.1	YLR180W	and Sam2p); Sam1p	2	3.2648	0.1882	2378.43	2379.723	1	357.6	47.22222 S.E1I1I1E1K2V1I1P1R4D1M1L1D1E1N2T1K2Y1F1.I
		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to								
ail6323209/refINP_013281.1	YLR180W	the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p): Sam1p	3	4.2543	0.265	2249.78	2249.608	1	646.4	36.764706 E.III1E1K2V1I1P1R4D1M1L1D1E1N2T1K2Y1E1.I
3.1		Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	-							
ail6323216/rofIND_013288.11	VI D197W	to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate;	3	5 4594	0 4034	3563 24	3560.030	1	610.4	27 586206 E D1K2S1E1E1D102E1T1N2L1E111M1D1E1K2H302C1\/1D1C1V1D1T11111D4E1
giloszoz rojiciji i _010200.1	LICION	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	0	0.4004	0.4004	0000.24	0000.000		013.4	
ail6323216/rofIND_013288.11	VI D197W	to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate;	3	4 0020	0 3183	3520.4	3520.030	1	602.5	
gil0323210[rei]NF_013200.1]	I LIX IO/W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	5	4.0323	0.5105	3320.4	3320.333	'	002.5	
ail6202016IrofIND_012299_1		to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate;	2	4 9207	0.240	2126.27	2127 450	1	616.0	
gilo323210[10]10F_013200.1]	ILK IO/W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	2	4.0307	0.349	2120.37	2127.439	'	010.9	52.941177 F.HWIFTETK2H3Q201VTF10111DT11111K4F1.L
-:::::::::::::::::::::::::::::::::::::		to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate;	0	4 000	0.0044	0400 40	2402.450		4007.0	
gilo323210[rei]INP_013288.1]	1LK 167 W	UDP-glucose:sterol glucosyltransferase, conserved enzyme involved in synthesis of	2	4.066	0.3641	2102.43	2102.459	I.	1207.2	67.64706 F.IMPEKHQGVPGTDTIIKF.L
gi 6323218 ref NP_013290.1	YLR189C	sterol glucoside membrane lipids, involved in autophagy; Atg26p	2	3.4329	0.2519	1954.59	1953.268	1	568.5	50 L.K2I1P1L1P1N2I1I1E1I1D1D1Q2P1I1V1N2.K
gi 6323218 ref NP 013290.1	YLR189C	sterol glucoside membrane lipids, involved in autophagy; Atg26p	2	3.5537	0.259	2083.79	2083.442	1	592	47.058823 L.K2I1P1L1P1N2I1I1E1I1D1D1Q2P1I1V1N2K2.A
	VI D4000	UDP-glucose:sterol glucosyltransferase, conserved enzyme involved in synthesis of	~	0.0001	0.0040	4504 47	4504.000	~	405 7	
gij6323218 ret NP_013290.1	YLR189C	steroi giucoside membrane lipids, involved in autophagy; Atg26p UDP-glucose:sterol glucosyltransferase, conserved enzyme involved in synthesis of	2	2.9621	0.2346	1524.47	1524.668	9	405.7	57.692307 K.EDGIKTAISAIYNE.L
gi 6323218 ref NP_013290.1	YLR189C	sterol glucoside membrane lipids, involved in autophagy; Atg26p	2	3.1098	0.2706	1931.69	1932.268	2	455.5	43.75 L.KIPLPNIIEIDDQPIVN.K
gi 6323218 ref NP 013290.1	YLR189C	sterol glucoside membrane lipids, involved in autophagy; Atg26p	2	4.5396	0.3971	2059.53	2060.442	1	1120.4	58.823532 L.KIPLPNIIEIDDQPIVNK.A

gi 6323218 ref NP_013290.1	YLR189C	UDP-glucose:sterol glucosyltransferase, conserved enzyme involved in synthesis of sterol glucoside membrane lipids, involved in autophagy; Atg26p	3	3.8445	0.343	2059.79	2060.442	2	991	38.235294 L.KIPLPNIIEIDDQPIVNK.A
gil6323218lrefINP_013290_1	YI R189C	UDP-glucose:sterol glucosyltransferase, conserved enzyme involved in synthesis of sterol glucoside membrane linids, involved in autophagy: Ata26p	3	4 9463	0 2787	2083 37	2083 442	1	1014.5	44 11765 L K2I1P1I 1P1N2I1I1F1I1D1D102P1I1V1N2K2 A
giloszoz toliciji i _015250.11	TERTOSO	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of	0	4.0400	0.2707	2000.07	2000.442		1014.0	
gi 6323224 ref NP_013296.1	YLR195C	myrstic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nm1p N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of	3	6.7971	0.4947	3902.99	3905.369	1	1752.8	W.R411022111182D1F1D1E1R2V1V1E1E1G1P1HD1R2P1R211P1E1D1HS1D1R2P 31.060606 1L1P1L1.L
gi 6323224 ref NP_013296.1	YLR195C	myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of	3	5.279	0.3854	3863.12	3862.369	1	1423.1	28.030304 W.RTQPVKDFDEKVVEEGPIDKPKTPEDISDKPLPL.L
gi 6323224 ref NP_013296.1	YLR195C	myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of	2	3.3689	0.3255	1512.63	1511.715	1	610.5	72.72727 L.KKEDIDQVFELF.K
gi 6323224 ref NP_013296.1	YLR195C	myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p N-myristoy! transferase, catalyzes the cotranslational, covalent attachment of	3	6.6519	0.4636	4105.49	4107.607	1	1245.1	W.R4T1Q2P1V1K2D1F1D1E1K2V1V1E1E1G1P1I1D1K2P1K2T1P1E1D1IIS1D1K2P 26.428572 1L1P1L1L1S1.S
gi 6323224 ref NP_013296.1	YLR195C	myristic acid to the N-terminal dycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of	3	6.1029	0.526	4061.15	4062.607	1	1416.6	27.857143 W.RTQPVKDFDEKVVEEGPIDKPKTPEDISDKPLPLLS.S
gi 6323224 ref NP_013296.1	YLR195C	myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of	2	3.5016	0.2056	1655.77	1655.847	2	619.4	53.571428 L.FLDDLKFGPGDGFLN.F
gi 6323224 ref NP_013296.1	YLR195C	myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p	2	3.9486	0.1787	1527.17	1526.715	1	828.8	81.818184 L.K2K2E1D111D1Q2V1F1E1L1F1.K
gi 6323225 ref NP_013297.1	YLR196W	Protein with WD-40 repeats involved in rRNA processing; associates with trans- acting ribosome biogenesis factors; similar to beta-transducin superfamily; Pwp1p	2	5.2901	0.2649	1986.71	1987.094	1	1872	73.333336 L.K2D1Q2L1D111D1D1D1L1K2E1Y1N2L1E1.E
gi 6323225 ref NP_013297.1	YLR196W	Protein with WD-40 repeats involved in rRNA processing; associates with trans- acting ribosome biogenesis factors; similar to beta-transducin superfamily; Pwp1p	1	2.2993	0.1841	1166.52	1166.413	2	352.5	66.66667 H.H3D1L1M1L1P1A1F1P1L1.C
gi 6323225 ref NP_013297.1	YLR196W	Protein with WD-40 repeats involved in rRNA processing; associates with trans- acting ribosome biogenesis factors; similar to beta-transducin superfamily; Pwp1p Essential evolutionarily-conserved nucleolar protein component of the box C/D	3	5.349	0.2683	3305.96	3305.449	1	1625.1	34.25926 K.FHEGEKGEDPYISLPNQEDSQEEKQELQ.V
gi 6323226 ref NP_013298.1	YLR197W	snoRNP complexes that direct 2-O-methylation of pre-rKNA during its maturation; overexpression causes spindle orientation defects; SiK1p Essential evolutionarily-conserved nucleolar protein component of the box C/D	2	4.4102	0.3197	1557.97	1558.772	1	1336.1	71.42857 V.A1P1N2L1S1E1L1I1G1E1V111G1A1R4.L
gi 6323226 ref NP_013298.1	YLR197W	siteXine complexes that direct 2-Ometrylation on pre-rived during its maturation, overexpression causes spinled orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D sonRNP complexes that direct 2-Ometrylation of rex-RNA during its maturation;	2	3.549	0.2638	1857.59	1857.033	1	1010.3	64.28571 S.IKEEFPYVDCISNEL.A
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle or industrial of por https://doi.org/10.1007/ Essential evolutionarily-conserved nucleolar protein component of the box C/D sonRNP complexes that direct 2:-One-thylation of new-RNA during its maturation:	2	4.007	0.3894	1540.07	1539.772	1	890.4	64.28571 V.APNLSELIGEVIGAR.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D sonRNP complexes that direct 2'-Omethylation of one-rRNA during its maturation:	2	3.8065	0.2418	1659.69	1658.905	1	782.7	63.333332 T.V1A1P1N2L1S1E1L11G1E1V111G1A1R4.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2°-Omethylation of pre-rRNA during its maturation;	2	3.4457	0.3229	1528.15	1528.733	1	759.6	65.38461 K.M1H3T1V1A1P1N2L1S1E1L1I1G1E1.V
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-Omethylation of ore-rRNA during its maturation;	2	4.3461	0.1539	1722.57	1720.963	1	521.6	56.25 M.HTVAPNLSELIGEVIGA.R
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'Omethylation of pre-rRNA during its maturation;	2	4.6586	0.4514	1739.83	1740.963	1	848.2	62.5 M.H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1.R
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2-O-methylation of pre-rRNA during its maturation;	2	4.1607	0.3969	1871.53	1873.156	1	724.1	52.941177 K.M1H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1.R
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	2	5.6579	0.4963	1875.95	1877.151	1	1847.7	82.35294 M.HTVAPNLSELIGEVIGAR.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	2	3.3152	0.3521	1885.29	1883.123	1	334.1	46.6666668 W.H3F1P1E1L1A1K2L1V1P1D1N2Y1T1F1A1.K
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	3	3.8942	0.1867	1877.75	1877.151	2	997.4	39.705883 M.HTVAPNLSELIGEVIGAR.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	3	3.9198	0.3021	2033.03	2033.343	1	817.3	37.5 K.M1H3T1V1A1P1N2L1S1E1L111G1E1V111G1A1R4.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	2	4.12	0.3938	2022.61	2024.343	1	806	58.333332 K.M@HTVAPNLSELIGEVIGAR.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	2	4.1871	0.3867	2008.55	2008.343	1	949.8	61.11111 K.MHTVAPNLSELIGEVIGAR.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	1	2.7953	0.2011	1206.65	1207.415	1	383.3	70 L.KTKGNTPKYGLI
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	2	3.1763	0.2777	1207.33	1207.415	1	444.3	75 L.KTKGNTPKYGLI
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	2	2.9346	0.214	1258.45	1257.473	1	1072.9	77.27273 N.LSELIGEVIGAR.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	3	3.8655	0.2773	2556.23	2553.838	2	621.2	33.75 S.IKEEFPYVDCISNELAQDLIR.G
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p	3	4.4535	0.3539	2680.52	2681.957	3	325	29.545454 M.ELYNKDKPAAEVEETKEKESSKK.R

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gi 6323226 ref NP_013298.1	YLR197W	Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p	1	3.1265	0.2912	1282.84	1283.554	2	440.3	59.090908 L.KAILDLNLPKAS.S
nil6323226/refINP_013298.11	YI R197W	Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects: Sik1n	3	5 0588	0 3363	3536.66	3536 927	3	648.8	24 166666 LAISDKNI GPSIKEEEPYVDCISNELAODI IR G
gilo20220iciliti _010230.1	TERTOT	Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	0	0.0000	0.0000	0000.00	0000.021	0	040.0	
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2:-O-methylation of pre-rRNA during its maturation:	2	4.3911	0.2214	2275.93	2276.506	1	547.4	55.263157 Y.NKDKPAAEVEETKEKESSKK.R
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D	3	4.508	0.2317	2278.25	2276.506	1	857.6	39.473686 Y.NKDKPAAEVEETKEKESSKK.R
gi 6323226 ref NP_013298.1	YLR197W	snoRNP complexes that direct 2-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D	3	4.8885	0.2761	2303.45	2303.506	1	929.6	40.789474 Y.N2K2D1K2P1A1A1E1V1E1E1T1K2E1K2E1S1S1K2K2.R
gi 6323226 ref NP_013298.1	YLR197W	snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p	2	5.3285	0.4803	1898.79	1901.151	1	1680.3	79.411766 M.H3T1V1A1P1N2L1S1E1L111G1E1V111G1A1R4.L
gi 6323226 ref NP_013298.1	YLR197W	sonRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p	3	3.8784	0.2861	2847.68	2849.196	1	356.1	23.958332 Y.D1Y1L1C1E1K2M1H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1R4.L
gi 6323226 ref NP_013298.1	YLR197W	Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p	2	3.808	0.4017	1878.55	1877.151	1	440.7	52.941177 M.HTVAPNLSELIGEVIGAR.L
		Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	2	4 4406	0.0766	2021 22	2022 242	2	708.4	27.5 K M4L0T4/464D4N91404E41414C4E4/414C4644D41
gijo323220jreijiNP_013296. Ij	TLRI97W	Essential evolutionally-conserved nucleolar protein component of the box C/D noRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation;	3	4.4496	0.2766	2031.32	2033.343	2	798.4	37.5 K.MIRSTIVIAIPINZLISTEILIIIGTEIVIIIGTAIK4.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2cometivation of nor-rRNA during its maturation;	2	3.2884	0.2887	2035.27	2033.343	1	666.5	50 K.M1H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1R4.L
gi 6323226 ref NP_013298.1	YLR197W	overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D	3	4.8389	0.3747	2432.36	2432.693	1	972.4	41.25 Y.NKDKPAAEVEETKEKESSKKR.K
gi 6323226 ref NP_013298.1	YLR197W	snorkNP complexes that direct 2-U-methylation or pre-rkNA during its maturation; overexpression causes spindle orientation defects; Sik1p Essential evolutionarily-conserved nucleolar protein component of the box C/D	3	4.5541	0.3973	2462.18	2463.693	1	798.2	40 Y.N2K2D1K2P1A1A1E1V1E1E1T1K2E1K2E1S1S1K2K2R4.K
gi 6323226 ref NP_013298.1	YLR197W	snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p Essential evolutionarity-conserved nucleolar protein component of the box C/D	1	2.6482	0.3336	1207.84	1207.415	1	347.4	65 L.KTKGNTPKYGLI
gi 6323226 ref NP_013298.1	YLR197W	snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p Essential evolutionarit/conserved nucleolar protein component of the box C/D	2	4.4094	0.2594	1273.43	1272.473	1	1575.7	90.909096 N.L1S1E1L1I1G1E1V1I1G1A1R4.L
gi 6323226 ref NP_013298.1	YLR197W	snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p	1	2.8954	0.2436	1337.49	1336.458	2	476.7	60.000004 L.L1D1Q2L1D1K2D1I1N2T1F1.A
gi 6323244 ref NP 013316.1	YLR215C	Protein involved in nutritional control of the cell cycle; regulates abundance of the translation initiation factor eIF2; ortholog of human D123 protein; Cdc123p	2	4.2577	0.2571	1663.57	1664.779	1	1207.3	69.230774 L.S1D1T1F1K2D1L1I1D1E1I1V1H3D1.V
gi 6323244 ref NP_013316.1	YLR215C	Protein involved in nutritional control of the cell cycle; regulates abundance of the translation initiation factor eIF2; ortholog of human D123 protein; Cdc123p Protein involved in nutritional control of the cell uncles regulates abundance of the	2	4.0761	0.247	2192.97	2193.281	1	615.9	53.125 T.Q2R4D1L1N2Y1Y1D1Y1L1D1E1L1S1D1T1F1.K
gi 6323244 ref NP_013316.1	YLR215C	translation initiation factor eIF2; ortholog of human D123 protein; Cdc123p	3	4.6907	0.2984	2336.18	2335.726	1	1838.9	44.736843 L.I1D1E1I1V1H3D1V1V1L1P1K2F1P1D1K2S1F1V1L1.D
gi 6323244 ref NP_013316.1	YLR215C	Protein involved in nutritional control of the cell cycle; regulates abundance of the translation initiation factor eIF2; ortholog of human D123 protein; Cdc123p Protein involved in nutritional control of the cell cycle; regulates abundance of the	2	4.211	0.2837	2334.75	2335.726	1	833	50 L.I1D1E1I1V1H3D1V1V1L1P1K2F1P1D1K2S1F1V1L1.D
gi 6323244 ref NP_013316.1	YLR215C	translation initiation factor eIF2; ortholog of human D123 protein; Cdc123p	1	2.7829	0.2029	1503.65	1504.841	1	586.2	54.166668 D.V1V1L1P1K2F1P1D1K2S1F1V1L1.D
gi 6323244 ref NP_013316.1	YLR215C	Protein involved in nutritional control of the cell cycle; regulates abundance of the translation initiation factor eIF2; ortholog of human D123 protein; Cdc123p	3	4.5144	0.2356	1666.64	1664.779	1	1497.8	51.923077 L.S1D1T1F1K2D1L1I1D1E1I1V1H3D1.V
gi 6323244 ref NP_013316.1	YLR215C	Protein involved in nutritional control of the cell cycle; regulates abundance of the translation initiation factor eIF2; ortholog of human D123 protein; Cdc123p	2	3.3028	0.2535	2332.89	2335.726	1	605.5	44.736843 L.I1D1E1I1V1H3D1V1V1L1P1K2F1P1D1K2S1F1V1L1.D
nil6323244/refINP_013316_1	YLR215C	Protein involved in nutritional control of the cell cycle; regulates abundance of the translation initiation factor eIE2: ortholog of human D123 protein: Cdc123p	2	3 2085	0 2214	1738.39	1738 833	3	616.1	54 166668 T Q2R4D1I 1N2Y1Y1D1Y1I 1D1E1I 1 S
	VI DODOW	Putative vacuolar Fe2+Mn2+ transporter, suppresses respiratory deficit of yfn1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial	2	0.2000	0.2214	0110.00	0110.000		010.1	
gij6323249 ret NP_013321.1	YLR220W	Iron accumulation; Ucc1p Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial	2	3.8907	0.1973	2112.73	2110.372	1	942.6	52.9411// N.SNLINKEIEUILLEINPN.F
gi 6323249 ref NP_013321.1	YLR220W	iron accumulation; Ccc1p Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants which lack the ortholog of mammalian frataxin, by preventing mitochoodrial	3	4.579	0.1534	2046.86	2047.294	4	1273.3	43.75 S.N2L111N2R4E111E1D111L1L1E111N2P1N2.F
gi 6323249 ref NP_013321.1	YLR220W	iron accumulation; Ccc1p Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1	2	3.2088	0.2364	2615.51	2617.831	1	479.9	40.476192 N.S1N2L111N2R4E111E1D111L1L1E111N2P1N2F1S1D1E1.T
gi 6323249 ref NP_013321.1	YLR220W	mutants, which lack the ortholog of mammalian trataxin, by preventing mitochondrial iron accumulation; Ccc1p Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1	3	4.0315	0.211	2135.78	2135.372	2	774.8	41.17647 N.S1N2L111N2R4E111E1D111L1L1E111N2P1N2.F
gi 6323249 ref NP_013321.1	YLR220W	mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1	3	4.8156	0.1702	2109.89	2110.372	3	1406.5	44.11765 N.SNLINREIEDILLEINPN.F
gi 6323249 ref NP_013321.1	YLR220W	mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1	2	4.2026	0.213	2021.65	2023.294	1	1394	68.75 S.NLINREIEDILLEINPN.F
gi 6323249 ref NP_013321.1	YLR220W	mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p	2	3.2562	0.1808	2135.63	2135.372	1	734.9	47.058823 N.S1N2L111N2R4E111E1D111L1L1E111N2P1N2.F
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	4.1856	0.2537	2644.33	2645.971	1	484.5	37.5 T.N2S1P1S1L1R4I1I1P1V1P1D1L1S1G1P1E1A1S1L1P1L1D1V1E1.I
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	4.2018	0.3776	2615.75	2616.971	1	638.3	41.6666664 T.NSPSLRIIPVPDLSGPEASLPLDVE.I
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	4.4011	0.3038	2298.47	2299.635	1	501.5	45.238094 T.N2S1P1S1L1R4I1I1P1V1P1D1L1S1G1P1E1A1S1L1P1L1.D

gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	3.2772	0.3399	3064.05	3065.491	1	592.6	32.142857 LATNSPSLRIIPVPDLSGPEASLPLDVEIY.E
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	4.4659	0.3457	2923.27	2924.307	1	694.4	36.53846 T.N2S1P1S1L1R4I1I1P1V1P1D1L1S1G1P1E1A1S1L1P1L1D1V1E1I1Y1.E
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	3.7674	0.2397	2778.85	2779.203	1	680.3	38 N.SPSLRIIPVPDLSGPEASLPLDVEIY.E
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	3.8005	0.3528	2892.65	2893.307	1	1232.8	46.153847 T.NSPSLRIIPVPDLSGPEASLPLDVEIY.E
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	3.4703	0.2715	2532.99	2533.93	1	598	40.909092 S.L1R4I1I1P1V1P1D1L1S1G1P1E1A1S1L1P1L1D1V1E1I1Y1.E
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	4.6628	0.4318	2807.77	2808.203	1	801.8	40 N.S1P1S1L1R4I1I1P1V1P1D1L1S1G1P1E1A1S1L1P1L1D1V1E1I1Y1.E
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	4.705	0.3927	1924.09	1925.189	1	1622.3	70.588234 L.ATPVLDEINIIDLTPGSR.K
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	3.2558	0.2047	1811.15	1813.042	1	535	53.125 T.N2S1P1S1L1R4I1I1P1V1P1D1L1S1G1P1E1.A
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	4.4058	0.3814	1792.49	1792.042	1	1092.6	65.625 T.NSPSLRIIPVPDLSGPE.A
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	3.2255	0.238	1861.93	1863.121	2	541.7	41.17647 T.NSPSLRIIPVPDLSGPEA.S
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	4.1664	0.344	2275.65	2273.635	1	515.6	45.238094 T.NSPSLRIIPVPDLSGPEASLPL.D
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	2	3.1573	0.278	2402.47	2401.74	1	465.5	40.909092 A.T1N2S1P1S1L1R4I1I1P1V1P1D1L1S1G1P1E1A1S1L1P1L1.D
gi 6323251 ref NP_013323.1	YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-185 rRNA; Utp13p Small tho-Like GTPace essential for establishment and maintenance of cell polarity:	2	3.413	0.3069	2158.63	2159.531	1	448.2	45 N.SPSLRIIPVPDLSGPEASLPL.D
gi 6323259 ref NP_013330.1	YLR229C	mutants have defects in the organization of actin and septins; Cdc2p	2	3.2789	0.1545	1727.61	1726.952	1	517.6	64.28571 C.F1S1V1I1S1P1P1S1F1E1N2V1K2E1K2.W
gi 6323259 ref NP_013330.1	YLR229C	mutants have defects in the organization of actin and septins; Cdc42p	2	4.4471	0.2854	2383.43	2383.671	1	1324.1	60.526318 F.S1V111S1P1P1S1F1E1N2V1K2E1K2W2F1P1E1V1H3.H
gi 6323259 ref NP_013330.1	YLR229C	Small rho-like GTPase, essential for establishment and maintenance of cell polarity; mutants have defects in the organization of actin and septins; Cdc42p	1	2.2252	0.2245	1201.34	1200.382	1	440.5	68.75 V.KEKWFPEVH.H
gi 6323259 ref NP_013330.1	YLR229C	Small rho-like GTPase, essential for establishment and maintenance of cell polarity; mutants have defects in the organization of actin and septins; Cdc42p	2	3.4201	0.2781	2530.37	2531.847	1	796	47.5 C.F1S1V1I1S1P1P1S1F1E1N2V1K2E1K2W2F1P1E1V1H3.H
ail6323259/refINP 013330.1/	YLR229C	Small rho-like GTPase, essential for establishment and maintenance of cell polarity; mutants have defects in the organization of actin and septins; Cdc42p	2	3,1903	0.2862	2056.07	2058.301	1	389.9	46.875 I.SPPSFENVKEKWFPEVH.H
gil6323259/refINP_013330.1	VI R229C	Small rho-like GTPase, essential for establishment and maintenance of cell polarity;	1	2 4771	0.4293	1432.45	1433 582	1	523	
sil0222200 refinit _010000.11	VI D2200	Small rho-like GTPase, essential for establishment and maintenance of cell polarity;		4.0000	0.9570	0500.07	0504.047		044.0	
gilo3232391ei1ivF_013330.1	TLK2290	Small rho-like GTPase, essential for establishment and maintenance of cell polarity;	2	4.0230	0.3379	2502.97	2304.047		044.3	50 C.F5VISFFSEINVRENWFFEVN.H
gi 6323259 ref NP_013330.1	YLR229C	mutants have defects in the organization of actin and septins; Cdc42p Small rho-like GTPase, essential for establishment and maintenance of cell polarity;	2	3.417	0.3358	2270.73	2270.593	2	391.9	38.88889 S.VISPPSFENVKEKWFPEVH.H
gi 6323259 ref NP_013330.1	YLR229C	mutants have defects in the organization of actin and septins; Cdc42p Small rho-like GTPase, essential for establishment and maintenance of cell polarity;	2	3.0455	0.2897	2268.61	2268.574	1	461.3	50 C.FSVISPPSFENVKEKWFPE.V
gi 6323259 ref NP_013330.1	YLR229C	mutants have defects in the organization of actin and septins; Cdc42p	2	4.4305	0.3521	2357.31	2357.671	1	1099.2	55.263157 F.SVISPPSFENVKEKWFPEVH.H
		Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-								
gi 6323269 ref NP_013341.1	YLR240W	regulate protein sorting; similar to p110 subunit of mammalian PI 3-kinase; Vps34p	2	3.2832	0.3551	1918.65	1919.325	2	339	50 L.VKVRPIALPLDPDVLIC.D
		Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-								
gi 6323269 ref NP_013341.1	YLR240W	phosphate; forms membrane-associated signal transduction complex with Vps15p to regulate protein sorting; similar to p110 subunit of mammalian PI 3-kinase; Vps34p	2	4.0178	0.293	1938.81	1940.325	1	795.4	71.875 L.V1K2V1R4P1I1A1L1P1L1D1P1D1V1L1I1C1.D
		Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-								
gi 6323269 ref NP_013341.1	YLR240W	phosphate; forms membrane-associated signal transduction complex with Vps15p to regulate protein sorting; similar to p110 subunit of mammalian PI 3-kinase; Vps34p Methionine aminopeotidase, catalyzes the cotranslational removal of N-terminal	3	3.8565	0.4456	2362.64	2364.851	1	594.7	35 L.GQDPKPFPPLMKLPPQIIEAF.G
gi 6323273 ref NP_013345.1	YLR244C	methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal	3	4.9388	0.3926	3335.09	3336.695	1	817.9	29.464287 A.S1Y1P1L1T1P1R4R4Y1V1P1E1D111P1K2P1D1W2A1A1N2G1L1P1V1S1E1Q2.R
gi 6323273 ref NP_013345.1	YLR244C	methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal	2	3.0305	0.2651	2286.27	2285.521	1	627.2	50 L.HNAKDGLEGAYDPFPKFKYS.G
gi 6323273 ref NP_013345.1	YLR244C	methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal	3	4.0103	0.2717	3298.49	3297.695	1	693.5	28.57143 A.SYPLTPRRYVPEDIPKPDWAANGLPVSEQ.R
gi 6323273 ref NP_013345.1	YLR244C	methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal	3	3.9816	0.2253	3368.84	3368.773	1	536	25.862068 K.ASYPLTPRRYVPEDIPKPDWAANGLPVSEQ.R
ail62222721rofNP_042245_41		methionine from nascent polypeptides; function is partially redundant with that of	•	5 1151	0 4240	3409 77	3409 773	4	934 6	K.A1S1Y1P1L1T1P1R4R4Y1V1P1E1D1I1P1K2P1D1W2A1A1N2G1L1P1V1S1E1Q2.
gil6323278/rofIND_043350.4	TLK2440	mapup, map (p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC consorter: bindr and burghurse, ATPL Volta-	3	5.4451	0.324	3408.77	2751 604	1	031.0	
9100202101101111F_010000.1	1 L1124911	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.3022	0.321	2131.21	2131.034	I	1044.0	
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	3.2674	0.2591	2578.55	2579.482	1	563	40.476192 V.D1N2I1P1V1G1P1N2F1D1D1E1E1D1E1G1E1D1L1C1N2C1.E

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gil6323278/rofINP_013350_1	VI P240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 6414	0.3660	2725 60	2724 694	1	1444 1	
gil0323276/10/10/10/3330.1/	1LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.0414	0.3009	2725.09	2724.094		1444.1	34.347624 R.AVDINIF VGFNFDDEEDEGEDLGING.E
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl.tRNA (AA-tRNA)	3	4.1627	0.3214	2751.65	2751.694	1	656	28.260868 R.A1V1D1N2I1P1V1G1P1N2F1D1D1E1E1D1E1G1E1D1L1C1N2C1.E
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	2.9428	0.2104	1413.93	1413.657	1	848.1	62.5 L.VEDPQVIAPFLGK.L
		I ranslational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.1005	0.1627	1528.23	1526.702	3	407.1	58.333332 L.E1F1K2F1P1E1P1G1Y1L1E1G1V1.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	1	2 707	0 1831	1526 54	1526 702	2	186.3	50 L E1E1K2E1P1E1P1G1Y1L1E1G1V1 K
giloszozi oliciliti _010000.1]	TEN245W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)		2.707	0.1001	1020.04	1020.702	2	100.0	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyl.tRNA (AA-tRNA)	1	2.6248	0.4071	1511.8	1512.702	1	217.7	54.166668 L.EFKFPEPGYLEGV.K
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.5495	0.2238	1154.6	1155.342	2	202	61.11111 D.NAWIPRGELV.E
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.3814	0.1552	1533.52	1531.744	6	211.5	45.833336 M.C1K2L1V1E1D1P1Q2V1I1A1P1F1.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP 013350.1	YLR249W	cassettes: binds and hydrolyses ATP: Yef3p	2	3.4562	0.2689	1588.09	1588.627	1	390.6	61.538464 T.VYVEHDIDGTHSDT.S
giloszozi olisiliti _s issesili	121121011	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-	0.1002	0.2000	1000.00	1000.021		000.0	
- 100000701 - (INID: 040050 4)	10 00 000	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		0.04.40	0.0055	4070.00	4074 000		000.0	
gil6323278/ret/NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	2.9149	0.2055	1972.33	1974.008	1	260.3	46.666668 1.Q2E1E1C1R411V1Y1V1E1H3D111D1G111.H
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.343	0.2872	2393.43	2394.457	1	235.5	42.105263 N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3D1.I
		to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	2.9994	0.2209	2752.69	2753.862	1	262.7	32.608696 N.GQVDGFPTQEECRTVYVEHDIDGT.H
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP 013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3p	2	4,4384	0.2661	1783.63	1784.93	1	653.5	67.85714 A.T1E1T1V1D1N2K2D1I1E1R4E1I1P1S1.L
3.1		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	_					-		
-:::02020701#ND_042250.41	VI DO40W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	0	2 0220	0.0005	4000 45	1901 012		774.0	
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.6326	0.2925	1890.45	1891.043	1	774.9	60.000004 A.STF1L1N2G1N2I1I1E1H3D1V1P1E1H3F1.F
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	5.3876	0.2997	1991.69	1991.133	1	992.5	45.3125 F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
		to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	2.9907	0.221	1702.71	1703.955	1	1038.3	64.28571 M.C1K2L1V1E1D1P1Q2V1I1A1P1F1L1G1.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP 013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3p	2	3.7488	0.2104	2566.59	2567.802	1	507.5	40.476192 Y.E1E1L1S1N2T1D1L1E1F1K2E1P1E1P1G1Y1L1E1G1V1K2.T
3.1		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6202078/rofINID_012250_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	2 0096	0 2777	2542.62	2542 802	1	100.0	
gilo323276/rei/NP_013350.1/	1LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.9966	0.3777	2042.03	2542.802		433.3	42.837143 f.EELSNIDLEFRFPEPGTLEGVK.1
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.5763	0.3222	1972.27	1970.229	1	709.7	56.25 T.DLEFKFPEPGYLEGVKT.K
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	4.0707	0.2652	2671.28	2669.907	1	614.8	28.40909 Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.2697	0.3456	2668.65	2669.907	1	607.3	38.636364 Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1.K
31		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
-:::02020701{IND_042250_4]	VI DO40W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 4 4 7 0	0 2022	0040.05	0040.007	4	4000.0	
gilo323276/rei/NP_013350.1/	TLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.1479	0.3933	2642.05	2643.907	1	1220.8	52.272724 F.EELSNIDLEFRFPEPGTLEGVKI.K
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.9068	0.3909	1645.41	1645.903	1	579.7	61.538464 M.C1K2L1V1E1D1P1Q2V1I1A1P1F1L1.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	5.1533	0.2577	2440.41	2437.628	1	787.1	47.5 Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.2218	0.1875	1040.63	1042.181	5	679.3	87.5 L.L1K2D1E1T1V1A1P1R4.F
31		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6202078/rofINID_012250_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	2 1507	0 2029	1159 62	1156 241	1	1007.2	
gilo323276/10/10/10/3330.1/	12824900	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.1597	0.3020	1150.05	1150.541		1097.5	94.44444 E.E.I.E.IKZDTETTTVTATETR4.F
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational algoration factor, stimulates the binding of aminocasul tPNIA (AA tPNIA)	1	3.0821	0.2765	1155.55	1156.341	1	455.9	72.22222 E.L1L1K2D1E1T1V1A1P1R4.F
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.9122	0.2011	1499.35	1500.606	1	783.9	68.181816 E.K2K2E1D1E1E1D1K2F1D1A1M1.G
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to thosomes by releasing EE-1 alpha from the thosomel complex contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.7413	0.3133	1484.44	1485.606	1	907.8	72.72727 E.KKEDEEDKFDAM.G
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gil6323278 refINP_013350_1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3p	3	4,8424	0.2028	2255.9	2253.452	1	998 9	39.473686 E.K2K2E1D1E1E1D1K2E1D1A1M\$G1N2K2I1A1G1G1K2 K
5-1-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-			0		0.2020	2200.0			000.0	

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	VI R249W/	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and budrolyces ATP: Yef3n	2	2 9805	0 2562	2441 39	2442 587	1	374 1	42.5 M R4411141N2G1O2V1D1G1E1P1T1O2E1E1C1R4T1V1V1 V
gil0525270[rel[Nr_015550.1]	121124311	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	2.3005	0.2302	2441.33	2442.307		574.1	
ail6323278/refINP 013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3p	2	3.1925	0.2383	2672.17	2672.835	1	360.4	36.363636 M.R4A1I1A1N2G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1.H
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.5123	0.3095	1572.33	1569.714	1	1258.6	75 N.IIEHDVPEHFFGE.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	5.0977	0.358	1992.23	1991.133	1	801.7	62.5 F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	2.9449	0.237	1401.55	1400.662	1	501.1	68.181816 L.R4M1P1E1L1I1P1V1L1S1E1T1.M
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.2635	0.3374	1399.62	1400.662	8	171.1	50 L.R4M1P1E1L1I1P1V1L1S1E1T1.M
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.9244	0.2498	1384.65	1385.662	2	189.8	54.545456 L.RMPELIPVLSET.M
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.1349	0.2494	1386.47	1385.662	1	635.6	72.72727 L.RMPELIPVLSET.M
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyLtRNA (AA.tRNA)	2	3.5608	0.1993	1899.59	1899.089	3	439.6	50 A.T1E1T1V1D1N2K2D1I1E1R4F1I1P1S1L1.I
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.0039	0.3009	2190.07	2190.458	1	514.4	47.22222 K.ATETVDNKDIERFIPSLIQ.C
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.9743	0.2502	2120.61	2119.379	1	612.9	58.823532 A.TETVDNKDIERFIPSLIQ.C
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.9502	0.2058	2039.81	2041.274	1	796.2	59.375 T.E1T1V1D1N2K2D111E1R4F111P1S1L111Q2.C
ail62022781rofIND_012250_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	2 0626	0.2024	1515 67	1516 954	1	E2E 4	
gil0323270[ter]INF_013330.1]	ILR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.0030	0.2034	1515.07	1510.054		525.4	00.00007 L.RWFELFVLSETW.W
ail6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	1	2 0032	0 2347	1515 55	1516 854	2	165.9	50 L RMPELIPVI SETM W
giloo20270101111 _010000.11	12124511	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)		2.0002	0.2047	1010.00	1010.004	-	100.0	
ail6323278/refINP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3p	2	2.932	0.3078	1534.81	1532.854	1	486.7	62.5 L.R4M1P1E1L1I1P1V1L1S1E1T1M1.W
giloozozi oli oli ili _01000011	12112 1011	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-	LIUGE	0.007.0	100 1.01	1002.001		100.1	
gil6323278/refINP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3p	2	4.3622	0.3101	2175.77	2177.371	1	659.9	50 F.L1N2G1N2I1I1E1H3D1V1P1E1H3E1E1G1E1L1A1.K
3.1		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.1671	0.2133	2202.53	2202.387	1	854.8	52.77778 A.SFLNGNIIEHDVPEHFFGE.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	5.0813	0.3928	2226.41	2227.387	1	1126.1	58.333332 A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.9984	0.4284	2341.31	2341.547	1	1185.3	60.526318 A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.3367	0.2136	1553.31	1551.706	3	692.9	72.72727 L.T1R4K2E1I1E1E1H3C1S1M1L1.G
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	2.968	0.2418	1534.29	1533.706	1	645.3	68.181816 L.TRKEIEEHCSML.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	2.9924	0.1889	1076.91	1077.309	1	900.2	87.5 E.AIKDKLIEF.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	3.4394	0.2793	1570.71	1569.714	2	732.9	58.333332 N.IIEHDVPEHFFGE.L
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	3.0196	0.2206	1571.57	1569.714	1	530.8	58.333332 I.IEHDVPEHFFGEL.A
	N/1 D0 40144	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		0.4050	0.0455	0450.04	0450 074		540	
gi 6323278 ret NP_013350.1	YLR249W	Cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.4052	0.2155	2152.61	2152.371	1	519	44.444447 F.LNGNIIEHDVPEHFFGELA.K
ail6323278/rofIND_013350_1	VI P240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	3 2000	0.286	1597 40	1586 714	1	711 7	66 66667 I I1E1H3D1V/1D1E1H3E1E1C1E1I 1 A
gil0525270[rei]rei	111124311	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	5.2555	0.200	1307.43	1300.714	'	711.7	
gil6323278/refINP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3p	2	4.6923	0.4244	1873.75	1875.029	1	1514.1	73.333336 N.G1N2I1I1E1H3D1V1P1E1H3E1E1G1E1L1.A
giloozozi oli oli ili _01000011	12112 1011	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-		0.1211	1010.10	10101020			
gi 6323278 ref NP 013350.11	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	1	2.5996	0.2569	1589.42	1586.714	1	211.6	50 I.I1E1H3D1V1P1E1H3F1F1G1E1L1.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.195	0.4202	1856.33	1854.029	1	1309.9	70 N.GNIIEHDVPEHFFGEL.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to tibosomes by releasing EF-1 alpha from the tibosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.3789	0.2616	2575.01	2572.044	2	437.3	36.363636 S.AVIIDNMCKLVEDPQVIAPFLGK.L

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/rafIND_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	3 6007	0 3083	218/ 27	2192 367	1	405.0	
gil0323276/10/10/10/10/01/01/01/01/01/01/01/01/01/	1LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.0007	0.3062	2104.27	2102.307	'	405.9	41.22222 Q.GAGERIERREDEEDREDAMI®.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacy. LtRNA (AA-tRNA)	3	5.1136	0.2807	2189.09	2191.367	1	955.9	38.88889 Q.G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.3458	0.3348	2192.41	2191.367	1	864.8	55.555557 Q.G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350.1	YLR249W	cassettes: binds and hydrolyses ATP: Yef3p	2	3,7979	0.2591	2378.39	2379.55	2	421.7	42.5 S.G1Q2G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2E1D1A1M1.G
3.1		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	_					-		
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacy. LtRNA (AA-tRNA)	2	3.2667	0.1894	1413.87	1412.573	1	1078.6	72.72727 N.A1W2I1P1R4G1E1L1V1E1S1H3.S
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.1869	0.17	1357.57	1358.566	2	591.5	63.636364 L.K2E1F1E1G1G1V111111T1H3.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.3292	0.1658	1516.56	1517.681	2	333.5	50 S.HLDKTPSEYIQW.R
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
	VI DO40W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	0.0077	0.0455	0040 50	2245 622		740.0	
gil0323276[10]10F_013330.1]	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.0077	0.3155	2340.39	2345.032	'	749.5	50 T.KZATITETTIVIDINZKZDITETR4FITIF151ETTQ2.C
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.6718	0.1867	1358.41	1358.566	1	1256.1	77.27273 L.K2E1F1E1G1G1V111111T1H3.S
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.9027	0.311	2057.43	2057.478	1	597.9	50 L.V1E1D1P1Q2V1I1A1P1F1L1G1K2L1L1P1G1L1K2.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/rafIND_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	5 2222	0 4288	10/7 /3	10/0 065	1	825.8	67 64706 L P4P4\/1G1N2\/1G1E1D1D1A1I1D1E1\/1S1H3A1 G
gilo323276/10/10/10/01/01/01/01/01/01/01/01/01/01/	124910	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	5.2232	0.4200	1947.43	1949.005	'	020.0	07.04700 E.R4R4V101N2V101E1D1D1A111F1E1V131H5A1.0
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.7367	0.3718	1544.39	1544.804	1	2112.3	76.92308 K.A1L1K2E1F1E1G1G1V1I1I11T1H3.S
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.0962	0.25	1543.57	1544.804	2	516.5	53.846157 K.A1L1K2E1F1E1G1G1V1I1I11T1H3.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gil6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	1	2 656	0 1847	1532 55	1533 706	2	501.4	68 181816 L TRKEIEEHCSML G
giloszozi eli eli ti _ e i e e e e e e e e e e e e e e e e	121121011	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	·	2.000	0.1011	1002.00	1000.100	-	00111	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl.tRNA (AA.tRNA)	1	2.7098	0.2134	1342.55	1343.566	1	613	68.181816 L.KEFEGGVIIITH.S
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.2964	0.2932	1527.66	1527.804	1	192.1	61.538464 K.ALKEFEGGVIIITH.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.8715	0.4189	2224.59	2225.599	1	701.6	55.555557 L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/rafIND_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	3 7/1	0 302	2200.61	2100 500	1	760.2	
gil0323270[rei]in _013330.1]	161/24311	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	5.741	0.552	2200.01	2133.333	'	103.2	55.55557 E.QVINELENDETVALINI NIV.V
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	4.4982	0.3895	2222.87	2225.599	1	1430.3	45.833336 L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.5073	0.2166	2324.69	2325.731	1	545.4	44.736843 L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1V1.E
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350.1	YLR249W	cassettes: binds and hydrolyses ATP: Yef3p	2	4.5435	0.4283	2311.77	2312.758	1	1147.8	57.894737 T.LQVVNELLKDETVAPREKIV.V
giloszozi eli eli ti _ e i e e e e e e e e e e e e e e e e	121121011	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-	1.0 100	0.1200	2011111	2012.100			
- 100000701 (INID: 040050 41	V/I DO 1014/	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		4 005	0.0004	0044.04	0040 750		1010	
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	3	4.265	0.2891	2314.91	2312.758	1	1318	42.105263 T.LQVVNELLKDE I VAPREKIV.V
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	5.2032	0.3986	3440.12	3439.931	1	814.7	27.586206 Y.EELSNTDLEFKFPEPGYLEGVKTKQKAIVK.V
		I ranslational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	5.3439	0.3477	3685.88	3685.332	1	619.7	23.4375 M.VDAAKDQVALRMPELIPVLSETMWDTKKEVKAA.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	YI R249W/	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and bydrolyses ATP: Yef3p	3	5 0462	0 303	3475 73	3476 931	1	663	25 862068 Y E1E1I 1S1N2T1D1I 1E1E1K2E1P1E1P1G1Y1I 1E1G1V1K2T1K2O2K2A1I1V1K2 V
giloszozrolicitu _010000.1	TER245W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	0	0.0402	0.000	0470.70	0470.001		000	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyLtRNA (AA-tRNA)	2	4.0849	0.3077	2060.33	2061.254	1	842.5	60.000004 E.S1H3L1D1K211P1S1E1Y111Q2W2R4F1Q2.1
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.0137	0.2215	2063.73	2065.286	1	583.4	53.125 A.G1T1W2Q2R4P1H3L1I1V1L1D1E1P1T1N2Y1.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	6.1023	0.3919	2705.06	2704.189	1	1654.6	44.31818 L.R4M1P1E1L1I1P1V1L1S1E1T1M1W2D1T1K2K2E1V1K2A1A1.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refIND 013350 41	YI R240M	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 177	0.2045	2204 72	2295 503	1	677 1	47.5 K2T1 1R4R4\/1G1N2\/1G1E1D1D1A1!/P1E1\/1S1H2A1.G
9100202101101017_010000.1	1 21124911	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.477	0.2940	2204.13	2230.000		077.1	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.9428	0.2781	2263.89	2264.503	1	560.3	45 L.KTLRRVGNVGEDDAIPEVSHA.G

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
	N/1 DO 4014/	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		4 755	0.0404	1700.04	1700.050		4445.0	
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.755	0.3484	1762.21	1763.056	1	1445.8	73.333336 L.STKZATLTKZETFTETGTGTV11111111143.5
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.6176	0.4018	1743.85	1743.056	1	1478	73.333336 L.SKALKEFEGGVIIITH.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3n	1	2 8636	0 2224	1310 73	1320 58	8	321.2	
gil0323270[rei]14r_013330.1]	161(245)	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)		2.0030	0.2224	1313.75	1320.30	0	521.2	00.000004 A.GTWQRTHEIVE.D
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.6013	0.306	2675.89	2674.189	1	465.2	43.18182 L.RMPELIPVLSETMWDTKKEVKAA.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	VI R249W	consettes: binds and bydrolyses ATP: Yef3n	2	3 7724	0 2696	3016.49	3018 338	1	360.2	38 & G1T1W2O2R4P1H3I 111V1I 1D1E1P1T1N2V1I 1D1R4D1S1I 1G1&1I 1 S
gil0323270[rei]14r_013330.1]	161(245)	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.7724	0.2030	3010.43	3010.330		300.2	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	4.4345	0.2377	2924.27	2924.286	3	533.8	28.125 G.TWQRPHLIVLDEPTNYLDRDSLGAL.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	VI R249W	consettes: binds and bydrolyses ATP: Yef3n	з	6 5806	0 2702	3017 15	3018 338	3	831.6	33 & G1T1W2O2R4P1H3I 111V1I 1D1E1P1T1N2V1I 1D1R4D1S1I 1G141I 1 S
giloszozroliciliti _010000.1	121124511	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	0	0.0000	0.2702	5017.15	0010.000	0	001.0	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.4611	0.2628	1678.55	1679.781	1	429.9	53.571426 L.DEPTNYLDRDSLGAL.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	VI R249W	consettes: binds and bydrolyses ATP: Yef3n	2	4 626	0 4225	1695 61	1694 888	1	1343.4	
giloszozroliciliti _010000.1	121124511	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-	4.020	0.4220	1000.01	1004.000		1040.4	70.01140 Q.01/D11EV1E1V11EE.0
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.5478	0.4389	1714.33	1711.888	1	1326.9	78.57143 Q.C1I1A1D1P1T1E1V1P1E1T1V1H3L1L1.G
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail62222781rofIND 012250 11	VI P240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 2402	0 2224	1400 07	1409 657	1	1557.0	70 166671 \/1E1D1D100\/11141D1E11101K21
gil0323276[fei]IVF_013350.1]	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.3493	0.2221	1420.07	1420.037		1557.9	79.10007 E.VIEIDIFIQZVIIIAIFIFIEIGIKZE
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.3028	0.3442	1512.47	1512.702	1	535.5	66.66667 L.EFKFPEPGYLEGV.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gil6323278/rofINP_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	1	3 0562	0.2676	1525 73	1526 702	1	254 5	58 3333331 E1E1K2E1D1E1D1C1V1I 1E1C1V1 K
gil0323270[rei]14F_013330.1]	161(245)	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)		3.0302	0.2070	1020.70	1520.702		204.0	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.8018	0.2051	1987.07	1989.229	1	629.2	53.125 T.D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail62222781rofIND 012250 11	VI P240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	E 0202	0.2004	2062 52	2062 227	1	1270 7	
gil0323276[fei]IVF_013350.1]	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	5.0302	0.2994	2002.55	2003.237		13/0.7	04.70309 L3 INZTIDIETETETRZETETETETETETETETETETETETETETET
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.0748	0.4661	1886.57	1887.998	1	1047.5	68.75 T.VYVEHDIDGTHSDTSVL.D
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
-: 102020701 (IND 042250 4)	VI DO40W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	4	0.04.44	0.0400	4000 55	4000 450	2	404.5	
gij6323278/rei/NP_013350.1/	1LR249W	Casselles; binds and hydrolyses ATP; felsp Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	'	2.8141	0.2168	1299.55	1300.458	2	191.5	55 D.NZATWZITPTR4GTETLTVTET.5
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.7311	0.2645	1283.69	1284.458	1	193.8	60.000004 D.NAWIPRGELVE.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail62222781rofIND 012250 11	VI P240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	2 2602	0 1622	2506.05	2506 670	1	2477	40 476102 0 \/4D101E1B1T402E1E401B4T4\/4X4\/4E1H2D4HD10101T4 H
gil0323276[fei]IVF_013350.1]	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.3002	0.1023	2090.00	2590.079		347.7	40.476192 Q.VIDIGIFIFITIQ2EIEICIK411VITIVIEIH3DIIIDIGITI.H
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.5503	0.2884	2783.45	2784.862	1	324.3	34.782608 N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3D111D1G1T1.H
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail62222781rofIND 012250 11	VI B240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	2 7001	0 2205	1240.01	1049 41	1	000.2	85 E K2E1D1E1D1C1V111E1C1V11K
gil0323276[fei]IVF_013350.1]	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.7901	0.3365	1249.01	1240.41		909.3	65 F.NZFIFIEIFIGITILIEIGIVI.N
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.4913	0.264	1247.54	1248.41	1	653.5	65 F.K2F1P1E1P1G1Y1L1E1G1V1.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
-: 102020701 (IND 042250 4)	VI DO40W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	0	2 01 10	0.004.0	4500.05	4504 744		000.0	
gij6323278/rei/NP_013350.1/	1LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.9119	0.3016	1533.25	1531.744	1	030.9	79.10007 M.CTK2LTVTETDTPTQ2VTTATPTFT.L
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.5558	0.3503	1515.81	1516.744	1	728.9	75 M.CKLVEDPQVIAPF.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail62222781rofIND 012250 11	VI B240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 5066	0.2409	2106 29	2105 202	1	659 4	41 17647 EL 1NOC1NOI114E1H2D1\/1D1E1H2E1E1C1E1L 1 A
gil0323276[fei]IVF_013350.1]	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	3	4.5900	0.3490	2100.30	2105.292		000.4	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.7151	0.2189	1285.59	1286.456	1	131	55 N.E1L1L1K2D1E1T1V1A1P1R4.F
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3n	2	3 1132	0 3676	1841 35	1843 877	1	644.8	57 14286 O E1E1C1R4T1\/1Y1\/1E1H3D1I1D1G1T1 H
gil0525270[rei]11 _010550.1]	121124511	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-	0.1102	0.0070	1041.00	1040.011		044.0	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.539	0.4547	2276.69	2278.368	1	647.9	55.555557 N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3.D
		I ranstational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP 013350 11	YLR249W	consostes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	4,0564	0,3781	2250.77	2252.368	1	755.8	55,555557 N.GQVDGFPTQEECRTVYVEH.D
3,		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-		2.5.01					
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gij6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.0483	0.221	1684.19	1682.825	1	225.5	57.692307 F.E1T1V1D1N2K2D111E1R4F111P1S1.L

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/rafIND_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 1854	0.267	1765 47	1764.03	1	631	
gil0323270[rei]inF_013330.1]	ILR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.1004	0.207	1705.47	1704.93		031	07.00714 A.TETVDINDIERFIFS.L
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.6365	0.3691	1988.27	1991.133	1	779	59.375 F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	4.7213	0.2239	1989.5	1991.133	1	956.4	43.75 F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350.1	YLR249W	cassettes: binds and hydrolyses ATP: Yef3p	2	2.9748	0.1829	1398.55	1400.662	3	455.4	63.636364 L.R4M1P1E1L1I1P1V1L1S1E1T1.M
3.1		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elegention factor, stimulates the binding of aminoacyl-tPNA (AA-tPNA)	1	3.2987	0.2581	1399.62	1400.662	1	173.2	50 L.R4M1P1E1L111P1V1L1S1E111.M
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.487	0.3281	2273.27	2272.516	1	1110	55.263157 L.SNTDLEFKFPEPGYLEGVKT.K
		I ranslational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	5.2464	0.3379	2274.02	2272.516	1	2987.3	50 L.SNTDLEFKFPEPGYLEGVKT.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6222270/rofIND_012250_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 1007	0.2707	2141 65	21 42 270	1	720.2	61 764706 A T1E1T1\/1D1N0K2D114E1D4E114D1811 11402 C
gil0323270[rei]inF_013330.1]	12024900	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.1227	0.2707	2141.00	2143.379	'	730.2	01.704700 A.TTETTWIDINZR2DITETR4FITF131ETTQ2.C
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.1993	0.1739	2214.47	2215.458	1	423.5	44.444447 K.A1T1E1T1V1D1N2K2D1I1E1R4F1I1P1S1L1I1Q2.C
		to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.4459	0.3757	1855.57	1857.978	1	393.4	57.14286 S.H3D1S1V1F1L1D1N2V1C1E1Y1111N2.Y
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/rofIND_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	3 76/1	0 3516	1937 57	1838 078	1	450.0	
gil0323270[rei]inF_013330.1]	12624900	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.7041	0.3510	1037.37	1030.970	'	400.9	57.14200 S.HDSVFLDINVCETIIN.1
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.2403	0.2163	1167.56	1168.441	3	249.2	66.66667 L.R4M1P1E1L1I1P1V1L1S1.E
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.3243	0.2986	2038.29	2039.215	1	553.2	46.875 T.ISHDSVFLDNVCEYIIN.Y
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef3p	2	5.631	0.4255	2104.47	2105.292	1	534.1	50 EL1N2G1N2I1I1E1H3D1V1P1E1H3E1E1G1E1L1.A
3.1		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
-100000701 (IND-040050-4)	V/I D0 40144	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		4 0007	0.0007	0074.00	0070 000		000.4	
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.6867	0.3097	2674.83	2673.882	1	668.1	40.909092 K.A1Y1E1E1L1S1N211D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.K
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.7183	0.3757	2647.27	2648.882	1	697.6	43.18182 K.AYEELSNTDLEFKFPEPGYLEGV.K
		I ranslational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.0065	0.2887	1155.76	1156.341	1	459.7	72.22222 E.L1L1K2D1E1T1V1A1P1R4.F
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	VI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and bydrolyses ATP; Vef3p	1	2 9913	0 3435	1141 59	1142 341	2	388.1	66 66667 E LI KDETVAPR E
giloo20270/10/10/10/10/0000.1	TEN245W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)		2.0010	0.0400	1141.00	1142.041	2	000.1	00.00007 E.EEKBETYWI K.I
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyLtRNA (AA-tRNA)	2	3.6412	0.2763	1743.57	1744.881	3	/15	61.538464 R.I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	4.8287	0.4009	3041.93	3043.092	7	368.5	24 Q.V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3D1I1D1G1T1H3S1D1T1.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.3161	0.3823	1568.54	1569.714	1	760.2	58.333332 N.IIEHDVPEHFFGE.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	VI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and bydrolyses ATP; Vef3p	з	4 8303	0 3875	3531.86	3533 645	1	576.4	N.G1Q2V1D1G1F1P111Q2E1E1C1R411V1Y1V1E1H3D111D1G111H3S1D111S1V1
giloo20270/10/10/10/10/0000.1	TEN245W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	0	4.0000	0.0070	0001.00	0000.040		070.4	20.00002 21.0
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.749	0.4003	1685.77	1682.873	1	857.9	65.38461 N.IIEHDVPEHFFGEL.A
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.6004	0.3744	1815.83	1816.977	1	883.7	60.714287 G.N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.3208	0.3996	1967.35	1968.133	1	1187.5	62.5 L.NGNIIEHDVPEHFFGEL.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/rofIND_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	3 402	0 2531	2171 25	2171 /11	7	377.9	
gil0323270[rei]i4r_013330.1]	111124310	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.402	0.2001	2171.25	2171.411	'	577.0	30.00009 E.SNIDELINITEL GILLGWAT
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacul-tRNA (AA-tRNA)	3	3.8321	0.2523	2171.78	2171.411	1	2421.7	44.444447 L.SNTDLEFKFPEPGYLEGVK.T
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.2141	0.2594	2296.21	2295.516	1	637.2	42.105263 L.S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1.K
		I ranslational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	5.3788	0.399	2612.6	2615.044	1	1282.9	35.227272 S.A1V1I1I1D1N2M\$C1K2L1V1E1D1P1Q2V1I1A1P1F1L1G1K2.L
=		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	YI R249M	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	3 4571	0 2893	2613.87	2615 044	1	417.6	38 636364 S & 1//11/1/D1N2M\$C1K2I 1//1E1D1P1O2//11/&1P1E1I 1G1K2 I
8-100202101101101-010000.1	1	ouccouco, onico ana nyaronyoco mini, recop	2	0.4071	0.2000	2010.07	2010.044		-11.0	

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	3.6544	0.2574	2207.51	2207.367	1	508	50 Q.G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M\$.G
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	2.7286	0.162	1435.37	1434.546	1	212.8	59.090908 E.S1H3L1D1K2T1P1S1E1Y111Q2.W
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-tRNA)	2	4.117	0.3045	1921.35	1922.065	1	786.4	61.764706 L.RRVGNVGEDDAIPEVSHA.G
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elonqation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	2.9837	0.252	1323.41	1323.494	5	824.5	75 A.WIPRGELVESH.S
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef9a Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA)	1	2.4705	0.2023	1341.59	1340.494	1	209.9	65 A.W2I1P1R4G1E1L1V1E1S1H3.S
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational eloncation factor, stimulates the binding of aminoacvI-tRNA (AA-tRNA)	2	3.1263	0.2396	1395.99	1394.573	1	1082.8	77.27273 N.AWIPRGELVESH.S
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA)	1	3.2311	0.2185	1530.57	1528.677	1	289.7	58.333332 D.N2A1W2I1P1R4G1E1L1V1E1S1H3.S
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex, contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyLtRNA (AA-tRNA)	2	3.6325	0.2055	1964.55	1964.183	3	299.5	53.125 T.KATETVDNKDIERFIPS.L
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex, which wo ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor: stimulates the binding of amingacyLIRNA (AA-IRNA)	2	4.3709	0.3546	1623.95	1622.759	1	1128.5	79.16667 E.S1H3L1D1K2T1P1S1E1Y111Q2W2.R
gi 6323278 ref NP_013350.1	YLR249W	to ribosares by releasing EF-1 shipts from the ribos and complex, contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyLIRNA (AALRNA)	2	5.9538	0.3204	1835.53	1834.129	1	905.6	56.666668 M.C1K2L1V1E1D1P1Q2V11A1P1F1L1G1K2.L
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yel3p Translational elegandin factor: stimulates the binding of amingacy.tRNA (AA+RNA)	3	4.3175	0.2369	1816.88	1815.129	1	2521.9	61.666668 M.CKLVEDPQVIAPFLGK.L
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex, contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elonaction factor. stimulates the binding of amingacvI-IRNA (AA-IRNA)	2	3.6682	0.3298	2167.19	2166.367	1	645.9	52.77778 Q.GAGPRIEKKEDEEDKFDAM.G
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3) Translational elonqation factor, stimulates the binding of aminoacyl-IRNA (AA-tRNA)	2	4.0392	0.3364	2193.39	2191.367	1	669.6	52.77778 Q.G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3) Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA)	1	2.2047	0.3196	1322.58	1323.494	8	136	50 A.WIPRGELVESH.S
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef9 Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.9129	0.3337	2011.01	2011.307	1	418.6	50 L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2.I
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yd3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA)	2	2.9008	0.2703	1533.69	1534.681	1	738.5	72.72727 S.H3L1D1K2T1P1S1E1Y111Q2W2.R
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yd3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA)	2	4.332	0.2047	1359.81	1358.566	1	1881.9	90.909096 L.K2E1F1E1G1G1V1111111183.S
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Ver3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA)	2	4.1052	0.1653	1345.83	1343.566	1	1709.8	86.36364 L.KEFEGGVIIITH.S
gi 6323278 ref NP_013350.1	YLR249W	to nbosomes by releasing L+-1 alpha from the nbosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Vel3p Translational elongation factor, stimulates the binding of aminoacyLtRNA (AA-tRNA)	1	2.6013	0.1563	1532.59	1533.706	1	501.2	68.181816 L.TRKEIEEHCSML.G
gi 6323278 ref NP_013350.1	YLR249W	to noosomes by eleasing L+ 1 alpha from ten noosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyI-IRNA (AA-IRNA)	1	2.7011	0.2539	1357.97	1358.566	1	688.9	63.636364 L.K2E1F1E1G1G1V111111T1H3.S
gi 6323278 ref NP_013350.1	YLR249W	to incosome by releasing Er-1 alpha norm in moscinal complex, contains two ABC cassettes; binds and hydrolyses ATP; Y63p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-tRNA) to choosene burglescince E1 a clube from the choosened complex groups on the APC	3	4.1881	0.3091	2225.51	2225.599	2	847.1	36.11111 L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
gi 6323278 ref NP_013350.1	YLR249W	to incosines by releasing EFF1 appra norm in modernal complex, contains two ABC cassettes; binds and hydrolyses ATP; Y63p Translational elongation factor, stimulates the binding of aminoacyI-IRNA (AA-IRNA) to chocomes by reflection EFF1 albeb from the chocome and complex; contains two ABC	2	3.7598	0.3919	2224.85	2225.599	1	585.7	47.22222 L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
gi 6323278 ref NP_013350.1	YLR249W	to inconness of preasing L1 - apprentime incorporation complex, contains two ADC cassettes; birds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA) to checkness burglescies EE-1 albeit form the checkness contains two APC	2	4.3525	0.2916	1459.39	1456.725	1	1274.4	70.83333 A.LKEFEGGVIIITH.S
gi 6323278 ref NP_013350.1	YLR249W	to inconness of predaming L1 - approximation in nonservice complex, contains two ADC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA) to rithosomes by relassion EF-1 albeb from the rithosomal complex; contains two APC	2	4.0431	0.2432	1472.33	1472.725	1	1993.7	83.33333 A.L1K2E1F1E1G1G1V111111T1H3.S
gi 6323278 ref NP_013350.1	YLR249W	consolutes of producing LP - update Norther Indodenial complex, contains two rEC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA) to ribecomes by relaesion EF-1 albeb from the ribecome according contains; two APC	2	3.9192	0.2302	1528.45	1527.804	1	1544.4	65.38461 K.ALKEFEGGVIIITH.S
gi 6323278 ref NP_013350.1	YLR249W	to incontes by predaing L1 - aptra horin ten horizontal complex, contains two ADC cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-tRNA) to chocomes by reflection EE-1 albeb from the chocome and complex; contains two APC	2	4.1406	0.3421	2034.01	2035.224	1	777.7	58.333332 T.LRRVGNVGEDDAIPEVSHA.G
gi 6323278 ref NP_013350.1	YLR249W	to incontes by predaing L1 - aptra horin ten horizontal complex, contains two ADC cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-tRNA) to chocomes by reflection EE-1 albeb from the chocome and complex; contains two APC	3	5.9733	0.5677	3199.94	3202.243	1	1145.8	30.769232 F.R4K2R4A1V1D1N2I1P1V1G1P1N2F1D1D1E1E1D1E1G1E1D1L1C1N2C1.E
gi 6323278 ref NP_013350.1	YLR249W	consistence by determined and the partial form the observal complex, contains two ABC cassettes; binds and hydrolyses ATP; Yrd3p Translational elongation factor, stimulates the binding of aminoacyl-IRNA (AA-IRNA) to ribosomes by relaasion EF-1 albeb from the observal complex, contains two APC	3	5.3395	0.476	3165.95	3165.243	1	1299.8	30.769232 F.RKRAVDNIPVGPNFDDEEDEGEDLCNC.E
gi 6323278 ref NP_013350.1	YLR249W	consistence by determining the second	2	3.2633	0.2839	3165.71	3165.243	1	406	32.692307 F.RKRAVDNIPVGPNFDDEEDEGEDLCNC.E
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	4.349	0.3001	2338.22	2339.758	1	684.4	36.842106 T.L1Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail6202078/rofIND_012250_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	1	2 212	0.1564	1207.02	1206 425	7	245
gil6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yet 3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	2.312	0.1564	1207.93	1206.425	/	345
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.0513	0.2936	1519.69	1519.787	1	469.7
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail6323278/refINP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.7315	0.3843	1741.31	1741.956	1	1100.9
34		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	5.1054	0.2756	1758.53	1760.956	1	909.1
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.6783	0.4515	2114.31	2115.227	1	606.8
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail62222781-ofIND 012250 1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 2240	0 5456	2126.22	2129 227	1	702.6
giloszsz/olieiline_013550.1	1LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.2349	0.5450	2130.33	2130.227		703.0
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.5449	0.1644	1600.45	1599.781	7	567.5
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail6323278/refINP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.7761	0.1718	1597.42	1598,766	2	1128.4
5100 0101		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl.tRNA (AA-tRNA)	2	5.1753	0.4054	1974.99	1975.159	1	1431.5
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.8041	0.2464	1467.54	1468.65	5	843.3
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail62222781-ofIND 012250 1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	E 11E0	0.2575	1750.01	1756.05	1	1210.2
gij6323278[rei]NP_013350.1]	1LK249VV	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	5.1159	0.2575	1759.01	1756.95	1	1210.2
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.5059	0.3429	1494.29	1494.616	1	866.6
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail6323278/refINP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.3462	0.276	1363.79	1364.486	1	357.6
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
	N/L DO 1011/	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		0.0504	0.0500	1000.00	100151		4500
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl.tRNA (AA-tRNA)	2	3.6501	0.2522	1396.29	1394.54	1	1593
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.129	0.2255	1617.83	1618.781	1	932.9
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
gil6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and bydrolyses ATP; Vef3p	1	3 1833	0 1563	1367 59	1368 518	2	323 5
giloo20210101111 _010000111	12121011	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	·	0.1000	0.1000	1001.00	1000.010	-	020.0
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	2.9395	0.1818	1370.47	1368.518	2	845.2
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.4145	0.3491	1527.54	1526.702	1	219.1
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail62222781-ofIND 012250 1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	2 7605	0 2220	1510.01	1512 702	1	045.0
giloszsz/olieiline_013550.1	1LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.7005	0.3336	1012.01	1512.702		940.9
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.0686	0.1929	2239.15	2240.58	1	451.9
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail6323278/refINP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.1077	0.1701	2217.57	2218.58	2	449.8
34		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl.tRNA (AA-tRNA)	2	5.1821	0.3471	1815.89	1816.975	1	1580.1
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.9338	0.2927	1758.01	1757.937	1	840.2
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail62222781-ofIND 012250 1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 2026	0.164	1607 53	1696 950	1	1010 0
giloszsz/olieiline_013550.1	1LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.2030	0.104	1007.55	1000.039		1213.0
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.2179	0.176	1569.67	1570.755	1	880.2
		I ranslational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
gi 6323278 ref NP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.6292	0.2908	1584.71	1584.766	1	966.5
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl.tRNA (AA-tRNA)	2	5.07	0.2938	2043.35	2043.237	1	1273.8
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.7483	0.3332	1957.83	1956.159	1	1090.7
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)							
ail6323278/refINP_013350_1	YI R249/M	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and bydrolyses ATP; Yef3p	2	3 3801	0 2426	1382.00	1380 54	1	1272.8
9-100202101010114F_010000.1	12124311	Translational elongation factor, stimulates the binding of aminoacvl-tRNA (AA-tRNA)	2	0.0091	0.2420	1002.03	1000.04		1212.0
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC							
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.2159	0.1618	1298.53	1300.458	4	752.6

1	2.312	0.1564	1207.93	1206.425	7	345	60.000004 L.KEFEGGVIIIT.H
2	3.0513	0.2936	1519.69	1519.787	1	469.7	63.636364 K.KAKDILDEFRKR.A
2	4.7315	0.3843	1741.31	1741.956	1	1100.9	71.42857 T.NMEFQYPGTSKPQIT.D
2	5.1054	0.2756	1758.53	1760.956	1	909.1	67.85714 T.N2M1E1F1Q2Y1P1G1T1S1K2P1Q2I1T1.D
2	3.6783	0.4515	2114.31	2115.227	1	606.8	52.941177 N.GQVDGFPTQEECRTVYVE.H
2	4.2349	0.5456	2136.33	2138.227	1	703.6	55.88235 N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1.H
2	3.5449	0.1644	1600.45	1599.781	7	567.5	57.692307 A.IGADLIDERIIDQQ.A
1	3.7761	0.1718	1597.42	1598.766	2	1128.4	70.83333 T.D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
2	5.1753	0.4054	1974.99	1975.159	1	1431.5	65.625 S.N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.K
1	3.8041	0.2464	1467.54	1468.65	5	843.3	63.636364 T.D1L1E1F1K2F1P1E1P1G1Y1L1.E
2	5.1159	0.2575	1759.01	1756.95	1	1210.2	71.42857 T.D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.K
2	3.5059	0.3429	1494.29	1494.616	1	866.6	73.07692 M.R4A1I1A1N2G1Q2V1D1G1F1P1T1Q2.E
2	3.3462	0.276	1363.79	1364.486	1	357.6	62.5 M.R4A1I1A1N2G1Q2V1D1G1F1P1T1.Q
2	3.6501	0.2522	1396.29	1394.54	1	1593	90 H.L1D1K2T1P1S1E1Y1I1Q2W2.R
2	4.129	0.2255	1617.83	1618.781	1	932.9	69.230774 A.I1G1A1D1L1I1D1E1R4I1I1D1Q2Q2.A
1	3.1833	0.1563	1367.59	1368.518	2	323.5	70 L.E1F1K2F1P1E1P1G1Y1L1E1.G
2	2.9395	0.1818	1370.47	1368.518	2	845.2	80 L.E1F1K2F1P1E1P1G1Y1L1E1.G
1	3.4145	0.3491	1527.54	1526.702	1	219.1	54.166668 L.E1F1K2F1P1E1P1G1Y1L1E1G1V1.K
2	3.7605	0.3338	1512.31	1512.702	1	945.9	79.16667 L.EFKFPEPGYLEGV.K
2	3.0686	0.1929	2239.15	2240.58	1	451.9	47.22222 A.V1I1I1D1N2M\$C1K2L1V1E1D1P1Q2V1I1A1P1F1.L
2	3.1077	0.1701	2217.57	2218.58	2	449.8	44.444447 A.VIIDNM@CKLVEDPQVIAPF.L
2	5.1821	0.3471	1815.89	1816.975	1	1580.1	75 S.N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
2	3.9338	0.2927	1758.01	1757.937	1	840.2	64.28571 L.SNTDLEFKFPEPGYL.E
2	4.2836	0.164	1687.53	1686.859	1	1213.8	73.07692 S.N2T1D1L1E1F1K2F1P1E1P1G1Y1L1.E
2	3.2179	0.176	1569.67	1570.755	1	880.2	70.83333 N.T1D1L1E1F1K2F1P1E1P1G1Y1L1.E
1	3.6292	0.2908	1584.71	1584.766	1	966.5	66.66667 T.DLEFKFPEPGYLE.G
2	5.07	0.2938	2043.35	2043.237	1	1273.8	61.764706 L.SNTDLEFKFPEPGYLEGV.K
2	4.7483	0.3332	1957.83	1956.159	1	1090.7	62.5 S.NTDLEFKFPEPGYLEGV.K
2	3.3891	0.2426	1382.09	1380.54	1	1272.8	80 H.LDKTPSEYIQW.R

70 D.N2A1W2I1P1R4G1E1L1V1E1.S

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail63232781rofIND_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	1	2 0/08	0 2760	1355 50	1356 519	1	203.8	
gilo323276/10/10/10/3330.1	1LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	'	2.9490	0.2709	1333.39	1330.318	'	293.0	05 LEFRFEFGILE.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elegantics factor, atimulates the hinding of aminopaul (RNA (AA +RNA)	1	3.1632	0.2715	1237.61	1238.402	1	412.9	77.77778 L.E1F1K2F1P1E1P1G1Y1L1.E
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.8915	0.2469	1227.5	1227.402	1	310.2	66.66667 L.EFKFPEPGYL.E
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	2 9214	0 2123	1240.39	1238 402	6	555.6	83 33333 E1E1K2E1P1E1P1G1Y1L1 E
giloszozi oliciliti _010000.11	12124311	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-	2.5214	0.2120	1240.00	1200.402	0	000.0	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tPNA (AA-tPNA)	2	4.6107	0.3792	1992.25	1991.133	1	827.7	59.375 L.N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.2062	0.2066	1738.41	1740.95	3	551.4	50 T.DLEFKFPEPGYLEGV.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP 013350.1	YLR249W	cassettes: binds and hydrolyses ATP: Yef3p	2	3.4421	0.3418	1518.13	1516.606	1	732.9	81.818184 E.K2K2E1D1E1E1D1K2F1D1A1M\$.G
31		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
	N/1 DO 1011/	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		4.0700	0.0004	4504.04	1500.000		1007 5	
gil6323278/rei/NP_013350.1/	TLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.2730	0.2081	1501.91	1500.000	1	1307.5	80.30304 E.K2K2ETDTETETDTK2FTDTATMT.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	4.0822	0.2279	1499.47	1500.606	1	924.4	72.72727 E.K2K2E1D1E1E1D1K2F1D1A1M1.G
		I ranslational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.8048	0.1594	1487.52	1485.606	1	866	72.72727 E.KKEDEEDKFDAM.G
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6202070/rofIND_012250_1	VI B240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 11 00	0 220	1407.05	1495 606	1	902 7	
gilo323276[rei]inF_013330.1]	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.1100	0.336	1407.20	1465.000	'	093.7	11.21213 E.RREDEEDRFDAM.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.1474	0.3256	1419.37	1418.546	1	959.2	77.27273 E.SHLDKTPSEYIQ.W
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.7655	0.3606	1418.65	1418.546	1	405	59.090908 E.SHLDKTPSEYIQ.W
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and bydrolyses ATP; Vef3p	1	2 3969	0 1601	1235 42	1236 37	1	490.9	61 11111 N JEHDVPEHE E
giloszozi oliciliti _010000.11	12124311	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)		2.0000	0.1001	1200.42	1200.07		400.0	on the management of the state
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tPNA (AA-tPNA)	1	2.817	0.2495	1249.52	1250.37	1	569.1	66.66667 N.I1I1E1H3D1V1P1E1H3F1.F
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.8339	0.1756	1299.43	1300.458	3	234	60.000004 D.N2A1W2I1P1R4G1E1L1V1E1.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.404	0.3889	1568.58	1569.714	1	1171.1	70.83333 N.IIEHDVPEHFFGE.L
3.1		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
	N/1 DO 1011/	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		0.0040	0 4707	4550.40	1550 700		070 4	
gil6323278/ret/NP_013350.1/	YLR249W	cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	3.0048	0.1787	1552.48	1552.709	2	373.1	45.833336 E.11V1D1N2K2D111E1R4F111P1S1.L
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.6213	0.1685	1534.64	1534.709	1	448.7	50 E.TVDNKDIERFIPS.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.8067	0.2613	1248.43	1248.41	1	971.6	85 F.K2F1P1E1P1G1Y1L1E1G1V1.K
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6202070/rofIND_012250_1	VI B240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	1	2 6706	0.2102	1247.40	1049 41	1	E76 E	65 E K2E1D1E1D1C1V1L1E1C1V1 K
gilo323276[rei]inF_013330.1]	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	'	2.0700	0.2103	1247.49	1240.41	'	576.5	65 F.K2FTFTETFTGTTTETGTVT.K
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.9343	0.3574	1471.48	1472.554	1	248.9	59.090908 I.E1H3D1V1P1E1H3F1F1G1E1L1.A
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.3859	0.213	1455.48	1456.554	2	182	50 I.EHDVPEHFFGEL.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and bydrolyses ATP; Vef3p	2	4 9798	0.4358	1875 37	1876 973	1	793.8	60 000004 L N2G1N2I1I1E1H3D1V1P1E1H3E1E1G1E1 L
giloszozi oliciliti _010000.11	12124311	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-	4.57 50	0.4000	10/0.07	10/0.5/0		100.0	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyLtRNA (AA-tRNA)	2	4.5318	0.4088	1758.57	1760.869	1	1291.7	67.85714 N.G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.3028	0.3415	1854.31	1854.973	1	638.5	53.333336 L.NGNIIEHDVPEHFFGE.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.8096	0.3937	1530.63	1531.744	1	818.2	79.16667 M.C1K2L1V1E1D1P1Q2V1I1A1P1F1.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
-:::02020701{IND_042250_4	VI DO40W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	0	4 00 40	0.4450	4000.04	4004 433		755.0	
gilo3232101181/INP_013350.1	1 LR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.9049	0.4450	10.0001	1991.133	1	105.2	33.373 F.L INZO INZITI E IN3D I V IP IE IN3F IF IG 1E 1.L
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	4.3082	0.2989	1991.27	1991.133	1	1168.2	45.3125 F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.0937	0.3427	1798.21	1796.977	1	877.2	60.714287 G.NIIEHDVPEHFFGEL.A

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	3.2812	0.2407	1803.57	1802.965	1	530	53.571426 F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1.G
	V/ D0 4014/	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	0	0.404		1000 57	1000 000		0447	
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex; contains two ABC	2	3.101	0.2963	1628.57	1629.903	1	614.7	61.538464 M.CKLVEDPQVIAPFL.G
gi 6323278 ref NP_013350.1	YLR249W	cassettes; bind and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	2.5721	0.2341	1339.44	1340.561	1	848.9	65 D.LEFKFPEPGYL.E
gi 6323278 ref NP_013350.1	YLR249W	to hosome by hereasing Er-1 appart from the hosomal complex, contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.8588	0.4288	2136.81	2139.309	1	813.7	55.88235 S.F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.7699	0.1691	1639.39	1640.861	2	963.5	65.38461 D.L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.K
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor. stimulates the binding of aminoacvI-tRNA (AA-tRNA)	2	3.5572	0.374	1624.41	1625.861	4	591.8	50 D.LEFKFPEPGYLEGV.K
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyL-IRNA (AA-IRNA)	2	4.5896	0.4083	2298.33	2299.466	1	485	42.105263 V.A1S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
gi 6323278 ref NP_013350.1	YLR249W	to ribosome by releasing EF-1 alpha from the inbosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Transletional cleanating frogs entimication binding of minaged (BMA) (AA (BNA))	2	4.1713	0.2754	2040.59	2039.22	1	603.2	50 A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1.G
gi 6323278 ref NP_013350.1	YLR249W	translational elongation factor, sumbares the binding of animology environment of the second se	2	5.0291	0.4293	2228.49	2227.387	1	930.7	55.555557 A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
gi 6323278 ref NP_013350.1	YLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	3	4.0577	0.2062	2229.05	2227.387	1	848.1	43.055553 A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.L
ail6323278 refINP_013350.1	YLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef30	2	3,1622	0.235	2230.33	2228.469	1	675.5	47.22222 S.FL NGNIJEHDVPEHFEGEL A
gil6323278/rofIND_013350_1	VI P240W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC constants; binds and hydrolyces ATE: Vef2o	2	4 105	0.4478	2250.65	2253 460	1	601.0	
	TER249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4.105	0.4478	2230.05	2203.409		091.9	
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses AI P; Yet3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4.2874	0.2942	1938.79	1939.261	1	817.5	70 L.R4M1P1E1L111P1V1L1S1E111M1W2D111.K
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Ye(3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 albha from the ribosomal comolex; contains two ABC	2	3.6091	0.2617	1918.13	1919.261	1	619.7	60.000004 L.RMPELIPVLSETMWDT.K
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to discompete by relacting EE1 alpha from the discomplex contains two ABC	2	4.2356	0.3802	2411.77	2413.626	1	479.4	40 V.A1S1F1L1N2G1N2l1l1E1H3D1V1P1E1H3F1F1G1E1L1.A
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.7906	0.4817	2340.61	2341.547	1	692.1	50 A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
gi 6323278 ref NP_013350.1	YLR249W	to noosomes by releasing Er-1 aipna from the noosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.2585	0.1909	1434.17	1434.546	1	1143.4	77.27273 E.S1H3L1D1K2T1P1S1E1Y1I1Q2.W
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	3.3171	0.158	1434.38	1434.546	1	422	59.090908 E.S1H3L1D1K2T1P1S1E1Y1I1Q2.W
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyL-IRNA (AA-IRNA)	2	3.0237	0.1933	939.27	939.23	1	1103.9	93.75 F.LGKLLPGLK.S
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yet3p Translational elegantics frater, crimitates the binding of aminoacul (PNA (AA+PNA))	2	3.4925	0.1697	1530.25	1528.677	1	1363.7	75 D.N2A1W2I1P1R4G1E1L1V1E1S1H3.S
gi 6323278 ref NP_013350.1	YLR249W	Translational Europauti racion; satindare une ontaing of animology during (Accurct) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Ye(3p Taesoletical depending of participant (ACCURC)	1	3.0227	0.184	1527.53	1528.677	1	394.3	70.83333 D.N2A1W2I1P1R4G1E1L1V1E1S1H3.S
gi 6323278 ref NP_013350.1	YLR249W	translational elongation factor, sumbates the binoing of anniholdsyl-trivia (AA-trivia) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	1	2.4331	0.3083	1507.61	1508.677	1	305.3	58.333332 D.NAWIPRGELVESH.S
gi 6323278 ref NP_013350.1	YLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	3.8707	0.3328	1603.91	1604.759	1	1280	79.16667 E.SHLDKTPSEYIQW.R
ail6323278 refINP_013350.1	YLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and hydrolyses ATP: Yef30	1	3.9981	0.3949	1585.51	1586.714	1	917.7	62.5 N.IIIIEIH3DIV1P1E1H3E1E1G1E1.L
cil6222278/rof/ND_012250_1	VI P240W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC execution: bindp and hypothesis and TPC Vertice	2	4 0579	0.4177	1914 40	1915 120	1	1027.0	
gilo323278[rei]NP_013350.1]	TLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex, contains two ABC	2	4.9578	0.4177	1614.49	1815.129	1	1937.9	80 MICKLYEDPQVIAPPLGK.L
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyI-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	3.7275	0.3353	1781.53	1781.965	2	411.8	50 F.LNGNIIEHDVPEHFF.G
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to discompete by relacting EE1 alpha from the discomplex contains two ABC	2	4.9474	0.4352	2080.55	2081.292	1	725.9	55.88235 F.LNGNIIEHDVPEHFFGEL.A
gi 6323278 ref NP_013350.1	YLR249W	cassettes; bio releasing Let - i apria nom the hossonia complex, contains two ABC cassettes; bios and hydrolyses ATF; Yef3p Translational elongation factor, stimulates the binding of aminoacyI-tRNA (AA-tRNA)	2	3.9546	0.3473	2317.45	2315.547	1	663.9	47.368423 A.SFLNGNIIEHDVPEHFFGEL.A
gi 6323278 ref NP_013350.1	YLR249W	to nousonies by releasing t=1 appa from the hbosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyI-tRNA (AA-tRNA)	3	4.5539	0.3043	2343.38	2341.547	1	808.3	40.789474 A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	3.3544	0.2247	1321.55	1322.551	7	494.5	65 T.M1W2D1T1K2K2E1V1K2A1A1.A

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350.11	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP: Vef3p	2	3 1353	0 2659	1532 57	1533 706	1	669 5	68 181816 TRKEIEEHCSMI G
gil0323276/10/10/10/10/01/01/01/01/01/01/01/01/01/	1LR24911	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.1333	0.2039	1552.57	1555.700		009.5	60. 10 10 10 L. TRREIEERCSWIL.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyLtRNA (AA-tRNA)	1	2.6195	0.189	1550.53	1551.706	1	368.9	59.090908 L.T1R4K2E1I1E1E1H3C1S1M1L1.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.4272	0.2449	1345.63	1343.566	1	1109.6	77.27273 L.KEFEGGVIIITH.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	5.0531	0.4664	2069.09	2069.435	1	1266.4	65.625 L.R4M1P1E1L1I1P1V1L1S1E1T1M1W2D1T1K2.K
31		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
	V/I D0 4014	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC			0.404.0	0045 57	00.47.405		1000 7	
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.4948	0.4918	2045.57	2047.435	1	1326.7	68.75 L.RMPELIPVLSETMWDTK.K
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	3.9736	0.2619	2261.06	2261.66	1	681.7	32.5 L.V1E1D1P1Q2V1I1A1P1F1L1G1K2L1L1P1G1L1K2S1N2.F
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	3.8517	0.2126	2035.55	2035.478	4	535.6	36.11111 L.VEDPQVIAPFLGKLLPGLK.S
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6202078/rofINID_012250_1	VI P240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	1	2 5762	0 1677	1522.62	1522 706	1	407	62 626264 TRKEIEEHCSMI C
gilo323276/rei/iNP_013350.1	TLR249VV	Translational elongation factor, stimulates the binding of aminoacvl-tRNA (AA-tRNA)		2.5763	0.1677	1532.63	1533.706	1	427	03.030304 L. I KKEIEERCSINE.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.8028	0.2544	1411.53	1410.613	1	776.1	75 K.A1K2D1I1L1D1E1F1R4K2R4.A
		to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	3	3.8459	0.2512	2224.58	2225.599	1	789.1	37.5 L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6202078/rofINID_012250_1	VI P240W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	2 7609	0 174	1250 55	1259 566	1	1494 5	96 26264 L K2E1E1E1C1C1\/111111111111111
gilo323276/10/10/10/01/01/01/01/01/01/01/01/01/01/	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.7090	0.174	1339.55	1336.300	'	1404.0	00.30304 L.NZE IFTETGTGTV1111111113.3
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.3795	0.2241	1529.81	1527.804	1	640.5	53.846157 K.ALKEFEGGVIIITH.S
		to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.2245	0.2344	1190.65	1191.383	1	235	77.77778 T.E1F1V1K2K2C1P1A1A1K2.A
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350_1	VI R249W/	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes: binds and bydrolyses ATP: Vef3p	2	3 3532	0 1721	1545 85	1544 804	2	543.9	53 846157 K A1I 1K2E1E1E1G1G1V1IIII1T1H3 S
gil0323270[rei]in _013330.1]	111/24311	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.3332	0.1721	1343.03	1344.004	2	545.5	33.04013/ N.ATEINZETTETOTOTOTITITITITI.3
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elemention factor, stimulates the binding of emissional tRNA (AA tRNA)	1	3.0776	0.2195	1357.69	1358.566	1	738.6	68.181816 L.K2E1F1E1G1G1V1I1I11T1H3.S
		to ribosomes by releasing EF-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.5699	0.2149	1598.21	1598.766	1	1433.4	83.33333 T.D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/refINP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP: Yef3p	2	3.3489	0.1741	1406.71	1404.663	1	681.9	66.66667 K.A1L1K2E1F1E1G1G1V1I1I11T1 H
giloszozi eli eli ti _ e i e e e e e e e e e e e e e e e e		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	-	0.0100	0	1100.11	11011000	·	001.0	
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC						_		
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yet3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	2.4833	0.2033	1141./1	1141.359	1	120	61.11111 F.KIEGTPRRIA.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.2336	0.3267	1025.87	1026.308	1	521.1	61.11111 F.LGKLLPGLKS.N
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP 013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.7682	0.154	940.65	939.23	1	753.7	75 F.LGKLLPGLK.S
31		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
	VI DO40W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	2.0000	0.0540	4700 75	4700.075		4504.0	
gilo323276/10/10/10/01/01/01/01/01/01/01/01/01/01/	1LK249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.9009	0.3349	1790.75	1799.975	'	1001.0	11.42657 S.NIDLEFRFFEFGILE.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.579	0.2556	2278.15	2279.443	1	1040.9	50 Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	4.0902	0.2279	2148.09	2149.328	1	1176.4	58.823532 Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1.E
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gil6323278/refINP_013350_1	YI R249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and bydrolyses ATP; Yef3n	2	3 5214	0.3059	1840 57	1842 055	1	1013 5	60 000004 N TOLEEKEPEPGYLEGV K
3.1		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	_							
- 100000701 (INID: 040050 41	V/I DO (0)//	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC		4 4000		4005 40	4004.000			
gi 6323278 ret NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yer3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.4222	0.2906	1605.49	1604.828	1	1143	75 F.L1H3E1K2K2A1K2D111L1D1E1F1.R
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	3.2122	0.2032	1585.69	1586.828	1	819.1	66.66667 F.LHEKKAKDILDEF.R
		I ranslational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EE-1 alpha from the ribosomal complex: contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.2851	0.3733	1569.19	1569.714	1	1024.5	70.83333 N.IIEHDVPEHFFGE.L
		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
ail6323278/rafIND_013350_1		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	4 1031	0 3404	1702 50	1700 873	1	850.2	65 38461 N 1111E1H3D1\/1D1E1H3E1E1G1E1L1 A
9100202101101017_010000.1	1 LIX24911	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.1031	0.3404	1102.09	1100.013		000.2	00.00 TO INTITLE HOD IV IT LET OF IF IOTE ILLA
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	1	2.7034	0.2352	1201.48	1202.298	1	487.3	61.11111 H.D1V1P1E1H3F1F1G1E1L1.A
		to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC								
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p	2	3.8663	0.1665	1525.73	1526.702	1	785.2	75 L.E1F1K2F1P1E1P1G1Y1L1E1G1V1.K

		Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)								
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	3.7536	0.3001	1904.39	1905.053	1	601.7	50 L.S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
-102020701#ND_042250.41	VI DO40W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	0	2 0000	0.0074	4000 70	4070 050	4	000.0	
gij6323276jreijNP_013350.1j	TLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to rihosomes by releasing FF-1 alpha from the rihosomal complex; contains two ABC	2	2.9980	0.3371	1009.79	1670.859	1	823.3	01.336404 S.NIDLERRPEPGILE
gi 6323278 ref NP_013350.1	YLR249W	cassettes; Johd and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	3.821	0.3621	1455.25	1455.65	1	1303.9	86.36364 T.DLEFKFPEPGYL.E
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminacc/LtRNA (AAJRNA)	2	4.0937	0.3325	2129.07	2129.328	1	876.2	52.941177 Y.EELSNTDLEFKFPEPGYL.E
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	4.9843	0.469	1966.75	1968.133	1	961.7	62.5 F.LNGNIIEHDVPEHFFGE.L
gi 6323278 ref NP_013350.1	YLR249W	ransiauona elongauon ractor, sumulates ne ononing or animotocy-erviva (AA-RIVA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	1	2.9632	0.385	1512.7	1512.702	1	244	54.166668 L.EFKFPEPGYLEGV.K
gi 6323278 ref NP_013350.1	YLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	3.3676	0.1571	1700.57	1700.871	3	585	50 N.T1D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
ail62222781-ofIND_012250_11	VI P240W/	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC execution; binde and hydrole use ATE: V=720.	2	2 00 2 7	0.2408	1774 27	1774 097	2	700.2	
gijo323276[rei]NP_013350.1]	TLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC	2	3.9927	0.2408	1774.37	1774.937	2	790.2	00./ 1420/ LS INZ1 IUTLIETETRZETPTETPTGTTTLL.E
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to chosemes by releasing EE-1 along from the chosemel complex; contains two ABC	2	3.9008	0.2863	1583.63	1584.766	1	1346.2	79.16667 T.DLEFKFPEPGYLE.G
gi 6323278 ref NP_013350.1	YLR249W	cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	1	3.368	0.2715	1455.54	1455.65	1	1073.7	72.72727 T.DLEFKFPEPGYL.E
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	2	4.4699	0.3792	2416.27	2414.628	1	622.8	42.5 Y.EELSNTDLEFKFPEPGYLEGV.K
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA)	3	5.3332	0.2629	2980.7	2981.338	1	1035.9	33 A.GTWQRPHLIVLDEPTNYLDRDSLGAL.S
gi 6323278 ref NP_013350.1	YLR249W	to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yel3p	3	6.6071	0.2612	3020.12	3018.338	1	1255.3	35 A.G1T1W2Q2R4P1H3L1I1V1L1D1E1P1T1N2Y1L1D1R4D1S1L1G1A1L1.S
gi 6323279 ref NP_013351.1	YLR250W	to the cytoplasm in a punctate pattern; Ssp120p	2	4.8932	0.4288	1723.37	1724.836	1	1603.3	84.61539 Q.H3D1E1S1E1K2I1D1N2E1M1A1K2R4.V
gi 6323279 ref NP_013351.1	YLR250W	to the cytoplasm in a punctate pattern; Ssp120p	2	4.7952	0.4365	1911.99	1913.019	1	1020.7	76.666664 M.G1Q2H3D1E1S1E1K2I1D1N2E1M1A1K2R4.V
gi 6323279 ref NP_013351.1	YLR250W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ssp120p	2	3.149	0.1767	1842.17	1843.907	1	411.9	57.14286 H.HEHEIEHEEEIQRGA.S
gi 6323279 ref NP_013351.1	YLR250W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ssp120p	2	3.4719	0.1777	1620.05	1619.751	1	375.5	68.181816 W.EEWHMDHEHQLK.D
gi 6323279 ref NP_013351.1	YLR250W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ssp120p	2	3.1151	0.1894	2472.35	2473.635	1	225.1	44.444447 W.EEWHMDHEHQLKDYTPETF.F
gi 6323279 ref NP 013351.1	YLR250W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ssp120p	2	4.8772	0.4174	2006.57	2009.048	1	966.4	66.66667 L.H3H3E1H3E1I1E1H3E1E1E1I1Q2R4G1A1.S
gil6323279/refINP_013351.1	YLR250W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern: Ssp120p	2	5,2893	0.453	2236.61	2237.367	1	977.5	61 764706 E L1L1H3H3E1H3E1H3E1H3E1E1E1H1Q2R4G1A1 S
nil6323279/refINP_013351_1	YI R250W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the ovtoplasm in a punctate pattern: Sen120n	2	3 1783	0 2036	2777 31	2777 926	2	175.9	35 S1W2E1E1W2H3M1D1H3E1H3O2I 1K2D1Y1T1P1E1T1E1 E
	N/L DOCOM	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	2	0.0000	0.2030	2111.51	2111.520	2	005.4	
gi 6323279 ref NP_013351.1	YLR250W	to the cytoplasm in a punctate pattern; Ssp120p Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	2	3.9082	0.3497	1980.29	1981.048	1	895.1	66.66667 L.HHEHEIEHEEEIQRGA.S
gi 6323279 ref NP_013351.1	YLR250W	to the cytoplasm in a punctate pattern; Ssp120p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates	2	3.9509	0.3037	1868.05	1868.907	1	392.5	53.571426 H.H3E1H3E111E1H3E1E1E111Q2R4G1A1.S
gi 6323288 ref NP_013360.1	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	1	3.0636	0.4005	1435.3	1436.778	1	869.3	56.666668 A.GAGGMPGGMPGMPGMM
		Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolion after heat shock: role in mDNA transmission; similarity to groEL:								
gi 6323288 ref NP_013360.1	YLR259C	Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of	2	4.1727	0.453	1511.53	1511.718	1	1003.2	76.666664 T.RAAVEEGILPGGGTAL.V
gi 6323288 ref NP_013360.1	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	1	3.7207	0.4287	1510.64	1511.718	1	296.3	56.666668 T.RAAVEEGILPGGGTAL.V
		Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after beat shock: role in mtDNA transmission: similarity to grow for a similarity to grow for the similarity to the similar								
gi 6323288 ref NP_013360.1	YLR259C	HSp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of	2	3.0843	0.3306	1538.61	1539.642	2	260.4	62.5 G.EKKDRYDDALNAT.R
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	1	3.248	0.3442	1538.53	1539.642	1	168.2	50 G.EKKDRYDDALNAT.R
		Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refinition after heat shock; role in mTNA transmission; similarity to proFL								
gi 6323288 ref NP_013360.1	YLR259C	Prosterior containing and most most most in the main required for ATP-dependent folding of recursors exchange in a complex second by required for ATP-dependent folding of	2	3.1078	0.2783	1418.45	1418.636	1	424.2	77.27273 D.NFDQKLGVDIIR.K
gi 6323288 ref NP 013360.11	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	1	2.4349	0.2208	1546.7	1546.81	2	245.7	62.5 D.NFDQKLGVDIIRK.A
		Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolion after heat shock: role in mIDNA transmission: similarity to norE1.								
gi 6323288 ref NP_013360.1	YLR259C	Hsp60p	3	3.8531	0.3218	1617.65	1617.889	1	833.1	51.923077 D.NFDQKLGVDIIRKA.I

	VI 00500	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL;	2	2 7442	0.4700	1220.04	1220.000	2	4507.4	
gij6323288 ret NP_013360.1	YLR259C	Hspoup Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refiding after beact scale, in atDNA transmission; ginalitative to grade L	2	3.7412	0.1703	1329.81	1329.666	Z	1597.1	85 S.KVEFEKPLLLL.S
gi 6323288 ref NP_013360.1	YLR259C	Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates	2	4.6693	0.4063	2040.93	2042.257	1	454.9	52.77778 L.NGSGPKEAIQERIEQIKGS.I
gi 6323288 ref NP_013360.1	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of procures polyaphides and complex assembly: prevents aggregating and mediates	2	4.0679	0.2428	1617.07	1617.889	1	1159.6	73.07692 D.NFDQKLGVDIIRKA.I
gi 6323288 ref NP_013360.1	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of	2	3.4778	0.1585	1637.73	1638.889	1	704.2	65.38461 D.N2F1D1Q2K2L1G1V1D1I1I1R4K2A1.I
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of	3	5.1285	0.4033	2640.62	2643.059	1	1677	37.5 S.RVLDEVVVDNFDQKLGVDIIRKA.I
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.0454	0.2498	2204.73	2205.643	1	375.8	47.22222 Y.FITDPKSSKVEFEKPLLLLS
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.1047	0.1765	2227.41	2227.643	2	285	41.6666664 Y.F111T1D1P1K2S1S1K2V1E1F1E1K2P1L1L1L1L1.S
	14 00500	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL;	0	1 0001	0.0040	1000.01	1007 000		170.0	
gi 6323288 ret NP_013360.1	YLR259C	Hspoup Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL;	2	4.2231	0.3243	1806.61	1807.023	1	478.6	36.666668 S.GIP1K2E1ATHQ2E1K4HE1Q21K2G1S1.I
gi 6323288 ref NP_013360.1	YLR259C	Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates	2	4.762	0.4283	1786.75	1789.081	1	1656.6	76.666664 K.G1R4N2V1L111E1Q2P1F1G1P1P1K2I1T1.K
gi 6323288 ref NP_013360.1	YLR259C	Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates	2	3.0118	0.2521	1506.35	1506.609	1	899.2	70.83333 K.LIDEYGDDFAKGY.D
gi 6323288 ref NP_013360.1	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypaptides and complex assembly: prevents anyregation and mediates	1	2.982	0.3021	1510.69	1511.718	2	224.9	46.666668 T.RAAVEEGILPGGGTAL.V
gi 6323288 ref NP_013360.1	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of	2	3.7702	0.2435	1617.55	1617.889	1	832.1	73.07692 D.NFDQKLGVDIIRKA.I
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of	2	3.9007	0.1878	1953.27	1953.153	1	375.6	50 N.G1S1G1P1K2E1A1I1Q2E1R4I1E1Q2I1K2G1S1.I
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	4.2939	0.4471	1925.23	1928.153	1	495.8	52.941177 N.GSGPKEAIQERIEQIKGS.I
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	4.9384	0.3599	1766.17	1767.081	1	1251.4	70 K.GRNVLIEQPFGPPKIT.K
ail63232881rafIND_013360.11	VI R250C	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL;	3	5.0625	0 1843	1766 72	1767 091	1	2220.5	
910323200101141 _0 13300.11	TER209C	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL;	5	5.0025	0.1043	1700.72	1707.001		2320.3	
gi 6323288 ref NP_013360.1	YLR259C	Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to group	2	3.9429	0.3838	2324.67	2324.683	1	426.5	40.476192 A.ITRPAKQIIENAGEEGSVIIGK.L
gi 6323288 ref NP_013360.1	YLR259C	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates	3	4.0346	0.2748	2324.39	2324.683	1	532.5	35.714287 A.ITRPAKQIIENAGEEGSVIIGK.L
gi 6323288 ref NP_013360.1	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly: prevents aggregation and mediates	1	2.57	0.2037	1214.48	1215.302	2	607.1	72.22222 G.KLIDEYGDDF.A
gi 6323288 ref NP_013360.1	YLR259C	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of	2	3.9149	0.3923	1552.61	1553.842	1	1107.4	65.38461 R.NVLIEQPFGPPKIT.K
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of	2	3.1348	0.2038	1342.49	1340.605	4	788.3	68.181816 V.LIEQPFGPPKIT.K
gi 6323288 ref NP_013360.1	YLR259C	precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	1	3.0932	0.3886	1552.86	1553.842	1	630.9	61.538464 R.NVLIEQPFGPPKIT.K
gi 6323288 ref NP_013360.1	YLR259C	retradecarriefic mitocnondria cnaperonin required for A IP-dependent tolding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	1	3.4636	0.1831	1216.5	1216.506	1	749.6	77.77778 S.KVEFEKPLLLL

		Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of								
		precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL;								
gi 6323288 ref NP_013360.1	YLR259C	Hsp60p	2	3.4244	0.1943	1565.37	1566.81	1	1034.4	70.83333 D.N2F1D1Q2K2L1G1V1D1111R4K2.A
		Percursor polypeptides and complex assembly; prevents aggregation and mediates								
	V/I D0500	protein refolding after heat shock; role in mtDNA transmission; similarity to groEL;			0 40 45	101150	10.15 100		100.0	
gi 6323288 ref NP_013360.1	YLR259C	Hsp60p Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp	2	3.1418	0.1945	1944.53	1945.186	2	460.9	44.444447 C.AVKAPGFGDNRKNTIGDIA.V
gi 6323294 ref NP_013366.1	YLR264W	and has similarity to rat S28 ribosomal protein; Rps28bp	1	2.7159	0.1674	1585.63	1586.841	7	237.9	50 R.N2V1K2G1P1V1R4E1N2D111L1V1L1.M
gi 6323294 ref NP_013366.1	YLR264W	and has similarity to rat S28 ribosomal protein; Rps28bp	1	3.0656	0.3249	1565.74	1566.841	1	243.1	50 R.NVKGPVRENDILVL.M
ail6202204/rofIND_012266_1	VI DOG AWA	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp	1	2 2064	0.2406	1500 50	1592.02	6	276.0	
gilo323294[rei]NF_013300.1]	ILK204W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp		3.2904	0.3400	1002.00	1565.95	0	270.9	40.133647 N.VKGF VKENDILVLIM.E
gi 6323294 ref NP_013366.1	YLR264W	and has similarity to rat S28 ribosomal protein; Rps28bp Brotein component of the small (40S) ribosomal subunit: nearly identical to Rps28Bp	2	3.0256	0.2271	1602.51	1602.93	6	270.6	57.692307 N.V1K2G1P1V1R4E1N2D111L1V1L1M1.E
gi 6323294 ref NP_013366.1	YLR264W	and has similarity to rat S28 ribosomal protein; Rps28bp	2	3.2864	0.2538	1565.93	1566.841	6	434	61.538464 R.NVKGPVRENDILVL.M
ail6323294/refINP_013366_1	YI R264W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp	1	2 7506	0 2088	1565.85	1566 841	2	236.3	
91002020 1101111 _010000.11	121120111	Putative nicotinamide N-methyltransferase, has a role in rDNA silencing and in	·	2.7000	0.2000	1000.00	1000.011	-	200.0	
gi 6323315 ref NP_013387.1	YLR285W	lifespan determination; Nnt1p Beta subunit of the translation initiation factor eIE2B, the quanine-nucleotide	2	3.501	0.3449	1966.33	1967.197	1	564.1	46.875 A.G1L1F1E1E1P1E1D1F1L1P1P1P1P1K2P1H3.F
		exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2;								
gi 6323322 ref NP_013394.1	YLR291C	first identified as a negative regulator of GCN4 expression; Gcd7p Beta subunit of the translation initiation factor eIE2B, the guanine-nucleotide	2	5.815	0.4779	2043.19	2042.294	1	2027.2	73.52941 Q.GIKDLIDEIKNIDEGIQQ.I
		exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2;								
gi 6323322 ref NP_013394.1	YLR291C	tirst identified as a negative regulator of GCN4 expression; Gcd7p Beta subunit of the translation initiation factor eIF2B, the guanine-nucleotide	2	2.9273	0.2775	1947.75	1949.154	1	335.4	46.42857 A.R4W2N2H3V1N2D1L111E1Q2I1R4D1L1.G
	V/I D0040	exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2;		0.000	0.0400	101100	1011100			
gi 6323322 ret NP_013394.1	YLR291C	Beta subunit of the translation initiation factor eIF2B, the guanine-nucleotide	2	3.992	0.3192	1914.93	1914.163	1	1044.1	65.625 Q.GIKDLIDEIKNIDEGIQ.Q
	VI DO04C	exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2;	0	5 7045	0 2020	0000 45	2005 204		4075.0	
gilo323322[rei]NP_013394.1]	TLR291C	Instituentined as a negative regulator of GCN4 expression, Gcd7p	2	5.7045	0.3029	2062.45	2065.294	1	1975.0	73.52941 Q.G ITK2DTETTDTETTK2N2TDTETGTTQ2Q2.1
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	1	2.2593	0.1698	1080.59	1081.259	7	334.1	64.28571 Y.NFEKPFLW.L
		GTP binding protein (mammalian Pann bomolog) involved in the maintenance of								
		nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p,								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	2	3.7679	0.1912	1445.51	1445.617	1	1025.5	75 K.SNYNFEKPFLW.L
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of								
ail6323324/refINP_013396_1	YI R293C	nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p,	1	2 6546	0 1984	1459 53	1460 617	1	494.2	60 000004 K S1N2Y1N2E1E1K2P1E1I 1W2 I
giloszosz4itelitű _010000.11	TER2000			2.0040	0.1504	1400.00	1400.017		404.2	
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport: regulated by Pro20p, Rna1p								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	1	2.7099	0.2092	1444.64	1445.617	1	608.3	65 K.SNYNFEKPFLW.L
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of								
	V/I D0000	nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p,		4 5054	0.0400	1 100 00	4 400 047		1000.0	
gi 6323324 ret NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb3up, Cse1p and Kap95p; yeast Gsp2p nomolog; Gsp1p	2	4.5251	0.2422	1463.29	1460.617	1	1320.6	85 K.S1N2Y1N2F1E1K2P1F1L1W2.L
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	2	2.9734	0.2461	1245.47	1244.435	1	757.1	81.25 N.YNFEKPFLW.L
		CTP binding protein (mammalian Pann bamalag) involved in the maintenance of								
		nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p,								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	2	3.2695	0.2912	1828.89	1829.108	1	680.2	57.14286 S.AKSNYNFEKPFLWLA.R
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of								
ail6323324/refINP_013396_1	YI R293C	nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p,	2	3 8095	0 2523	1422 51	1420 665	2	193.4	68 181816 C G1N2K2V1D1V1K2E1R4K2V1K2 A
giloszosz4itelitű _010000.11	TER2000		2	0.0000	0.2020	1422.01	1420.000	-	100.4	
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization. RNA processing and transport: regulated by Pro20p. Rna1p.								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	2	3.4696	0.1926	1661.85	1662.87	1	835.6	62.5 S.A1K2S1N2Y1N2F1E1K2P1F1L1W2.L
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of								
		nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p,								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	2	3.5358	0.2521	1775.63	1777.029	1	709.4	57.692307 S.A1K2S1N2Y1N2F1E1K2P1F1L1W2L1.A
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	2	4.1846	0.273	1719.73	1720.963	2	401.2	60.000004 A.R4K2L1A1G1N2P1Q2L1E1F1V1A1S1P1A1.L
		CTP hinding protein (mammalian Page hamalag) involved in the maintenance of								
		nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p,								
gi 6323324 ref NP_013396.1	YLR293C	Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	2	4.117	0.1828	1448.23	1445.617	1	1355	85 K.SNYNFEKPFLW.L
		GTP binding protein (mammalian Ranp homolog) involved in the maintenance of								
ail6323324lrefINP 013396 11	YLR293C	nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p, Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kan95p; veast Gsp2p homolog; Gsp1p	1	2,6073	0.1544	1459.44	1460.617	1	581.1	65 K.S1N2Y1N2F1E1K2P1F1L1W2.L
Street dealer for the second										
		G I P binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; regulated by Prp20p. Rna1p.								

gi 6323324 ref NP_013396.1	YLR293C	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p, Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	1	2.8908	0.2567	1444.61	1445.617	1	630.5	65 K.SNYNFEKPFLW.L
gi 6323324 ref NP_013396.1	YLR293C	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p, Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	2	3.6627	0.2914	1371.87	1372.539	1	880.4	77.77778 S.N2Y1N2F1E1K2P1F1L1W2.L
gi 6323324 ref NP_013396.1	YLR293C	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p, Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	1	2.6858	0.1829	1245.56	1244.435	1	356.7	68.75 N.YNFEKPFLW.L
gi 6323324 ref NP_013396.1	YLR293C	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p, Yrb1p, Yrb2p, Yrb4p, Yrb30p, Cse1p and Kap35p; yeast Csp2p homolog; Csp1p	1	2.3143	0.1824	1255.63	1256.435	4	309.3	62.5 N.Y1N2F1E1K2P1F1L1W2.L
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p	2	3.0733	0.2209	1824.51	1825.025	2	714.9	60.000004 R.F1Q2N2P1T1S1N2V1L1E1E1R4I1A1A1L1.E
gi 6323333 ref NP_013406.1	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	4.3369	0.2939	2343.07	2341.486	1	413.8	52.77778 R.F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2.A
gi 6323333 ref NP_013406.1	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	4.1438	0.3651	2342.27	2341.473	1	702.2	52.77778 E.A1R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4.T
gi 6323333 ref NP_013406.1	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	5.3975	0.2568	2575.4	2573.752	1	1444.9	43.75 E.A1R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2.A
ail63233331refINP_013406.11	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis: Met17p	2	4.9518	0.3894	2574.51	2573.752	1	1154.8	60.000004 E.A1R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2 A
gil63233331refINP_013406.1	YI R303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	2	3 0554	0 1527	1612.03	1610 789	1	876.1	57 692307 S V/1G11/E1E11/D1D11/11/1D1E102 0
	VI Docow	O-acetyl horroserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	2	0.0004	0.1027	0000.07	0010.700		4707.0	T.T1IIG1G1IIIIV1D1S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met1/p O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	3	6.7599	0.5014	3839.87	3841.233	1	1767.2	30.303032 1H3G111.1
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	2	4.2051	0.4314	2975.79	2976.247	1	595.7	39.583336 S.G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1H3G1T1.I
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	3	4.9241	0.4446	2676.65	2675.949	1	704.4	35.714287 S.G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1.H
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p	2	4.6629	0.3162	2673.73	2675.949	1	790	45.238094 S.G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1.H
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p	2	3.2785	0.2109	2412.05	2413.565	2	579.1	42.105263 R.F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2A1.V
gi 6323333 ref NP_013406.1	YLR303W	o-acetyl nomoserine-o-acetyl serine suimydrylase, required for sulfur amino acid synthesis; Met17p	2	3.694	0.3492	2514.15	2513.697	1	653.9	45 R.F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2A1V1.Y
gi 6323333 ref NP_013406.1	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	3.8136	0.2836	2572.67	2573.752	2	426.7	42.5 E.A1R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2.A
gi 6323333 ref NP 013406.1	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	4.312	0.3552	2644.25	2645.831	1	536.8	42.857143 E.A1R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2A1.V
ail63233331refINP_013406.11	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis: Met17p	3	5,1979	0.4015	2745.71	2745.963	1	966.9	34.090908 E.A1R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2A1V1.Y
gil63233331rofIND_013406_1	VI P303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	3	5 3034	0 3226	2000.00	2010 130	1	1022.1	25 860564 E M104E1/4E1C1D1N2D1E1E1E1E1E4K2/4E1D1E1D4T1K2M1/4V1 I
sil022222231ref[ND_012400.1]	VI D202W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	2	5.0070	0.0220	2000.00	2010.100		647.0	
gij6323333jreijNP_013406.1	YLR202W	Synthesis; Metr7p O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	3	5.3078	0.4331	3209.27	3200.019	1	017.0	T.T111G1G11111V1D1S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y
	VI Docow	O-acetyl homosrine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	5	0.0330	0.0012	0100.00	0400.000		370.4	
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met1 /p O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	3	3.9685	0.1821	3182.06	3180.414	1	702.5	28.846153 V.D151G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1H3G111.I
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	3	4.0049	0.2164	3190.7	3188.592	1	582	26.85185 T.T1I1G1G1I1I1V1D1S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1.E
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	1	2.9366	0.262	1341.59	1342.538	4	401.1	54.545456 H.K2H3G111P1V1V1V1D1N2T1F1.G
gi 6323333 ref NP_013406.1	YLR303W	Synthesis; Met17p	3	5.2667	0.3599	3062.69	3064.325	1	857.3	30.000002 D.S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1H3G1T1.I
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p	2	4.4336	0.2763	2322.29	2323.605	1	385.5	44.44447 S.G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1.E
gi 6323333 ref NP_013406.1	YLR303W	synthesis; Met17p	3	4.2973	0.3282	2620.25	2617.897	1	1254.2	38.75 G.K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1.H
gi 6323333 ref NP_013406.1	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	3.5702	0.297	1879.17	1877.149	1	862.2	61.538464 G.K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1.S
gi 6323333 ref NP_013406.1	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	3.6799	0.2882	1949.79	1949.019	1	790.9	56.666668 R.F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1.R
gi 6323333 ref NP_013406.1	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	3.4619	0.2845	2108.05	2109.207	1	526	46.875 A.R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1.R
ail63233331refINP 013406.11	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis: Met17p	2	4.9649	0.3564	2182.99	2181.285	1	718.2	58.823532 E.A1R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1.R
ail63233331refINP_013406.11	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis: Met17p	2	3.8141	0.2777	1996.55	1997.206	1	730	58.823532 E.G1V1K2D1L1P1N2A1D1K2E1T1D1P1F1K2L1S1.G
gile222222010[NIT_012406_1]	VI B202W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	-	4.0752	0.1560	2574.52	2572 752		729 5	22 75 E A4D4E4V4E4C4D4N9D1E4E1E1E4E4V2V4E4D4E4D4T4V2 A
gilossossiteitti _013400.1	VI Docow	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid	5	4.0733	0.1303	2014.00	4707.005		130.5	
gij6323333 ret NP_013406.1	YLR303W	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	2	4.2919	0.2421	1786.35	1787.025	2	1113.7	69.230/74 S.GIK2F1P1W2K2D1Y1P1E1K2F1P1Q2.F
gi 6323335 ref NP_013407.1	YLR304C	required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p Aconitase, required for the tricarboxvlic acid (TCA) cvcle and also independently	2	4.1605	0.2808	1704.69	1705.862	1	1183.4	73.07692 A.DYDKINPDDRIDIL.G
ail6323335/refINP_013407_1	YLR304C	required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Acoto	2	4,0098	0.1878	1724.35	1724,862	1	1590.6	76.92308 A.D1Y1D1K2I1N2P1D1D1R4I1D111L1 G
2-1-1-2-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	210040	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	2		0070					
gi 6323335 ref NP_013407.1	YLR304C	required for infloctional genome manentarice, component or the mitocholdinal nucleoid; mutation leads to glutamate auxotrophy; Aco1p Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial anone maintenance: component of the mitochondrial	2	3.8194	0.1839	1458.81	1460.73	3	622.8	66.66667 W.D1G1K2D1A1K2D1M1P1I1L11K2.A
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	3	4.3116	0.3004	4041.26	4041.47	1	576.6	20 A.DKDAEYDEVVEIDLNTLEPYINGPFTPDLATPVSKM.K

		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail6323335/refINP_013407.1	YLR304C	required for mitochondrial genome maintenance; component of the mitochondrial nucleoid: mutation leads to glutamate auxotrophy: Aco1p	3	5.4514
34		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
-1022222511ND 042407 41	VI D2040	required for mitochondrial genome maintenance; component of the mitochondrial	2	4 0000
gip32335[rei]NP_013407.1]	TLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	2	4.8206
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.4049
		Aconitase, required for the tricarboxylic acid (ICA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.2108
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail622222EtrofIND 012407 11	VI B204C	required for mitochondrial genome maintenance; component of the mitochondrial	2	4 1022
gip32335[rei]NP_013407.1]	TLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	2	4.1022
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	2.9592
		Aconitase, required for the tricarboxylic acid (ICA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP 013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.1972
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
	V/I D0040	required for mitochondrial genome maintenance; component of the mitochondrial		0.4007
gi 6323335 ref NP_013407.1	YLR304C	Aconitase required for the tricarboxylic acid (TCA) cycle and also independently	1	2.4367
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.8249
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail6323335/refINP_013407_1	YI R304C	nucleoid: mutation leads to dutamate auxotrophy: Aco1p	2	4 2845
giloszocoliciini _010401.1]	TEROOTO	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	2	4.2040
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.509
		required for mitochondrial genome maintenance: component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.2666
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail622222EtrofIND 012407 11	VI B204C	required for mitochondrial genome maintenance; component of the mitochondrial	2	2 079
gil0323335110110F_013407.11	TLK304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	3	3.970
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.4736
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail63233351refINP 013407.11	YLR304C	nucleoid: mutation leads to olutamate auxotrophy: Aco1p	2	4.8588
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ret NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.06
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	2.9479
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail6323335/refINP_013407_1	YI R304C	nucleoid: mutation leads to dutamate auxotrophy: Aco1p	2	4 1919
24		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	_	
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.7497
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.2981
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail622222EtrofIND 012407 11	VI B204C	required for mitochondrial genome maintenance; component of the mitochondrial	2	4 04 50
gil0323333[rei]NF_013407.1]	TER3040	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	5	4.2130
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.5928
		Aconitase, required for the tricarboxylic acid (ICA) cycle and also independently		
gi 6323335 ref NP 013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.5356
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
	V/I D0040	required for mitochondrial genome maintenance; component of the mitochondrial		0 7000
gip323335[rei]NP_013407.1]	TLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		2.7229
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.2548
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail63233351refINP 013407.11	YLR304C	nucleoid: mutation leads to olutamate auxotrophy: Aco1p	1	2.6022
51		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
		required for mitochondrial genome maintenance; component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.2807
		required for mitochondrial genome maintenance: component of the mitochondrial		
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.2883
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
ail6323335/refINP 013407 11	YLR304C	required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy: Aco1p	1	2,9035
21		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently		
	V/I D05 12	required for mitochondrial genome maintenance; component of the mitochondrial	_	0.0505
gilb32335[ref NP_013407.1]	TLK304C	nucleoio; mutation leads to glutamate auxotrophy; Aco1p	2	3.2529

3	5.4514	0.2541	2405.99	2405.616	5	760.3	34.210526 L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D11L1.G
2	4.8206	0.4117	2402.89	2405.616	2	719	44.736843 L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
2	3.4049	0.2852	1873.35	1874.058	1	651.7	56.666668 N.PADYDKINPDDRIDIL.G
2	4.2108	0.2351	1807.69	1809.038	1	583.6	60.000004 Q.V1G1G1E1K2D1L1K2R4A1I1D1L1N2K2E1.V
2	4.1022	0.3007	2682.67	2682.023	1	417.3	43.47826 L.TDKLKDKDGNEFMLKPPHGDGLPQ.R
2	2.9592	0.2466	1737.91	1736.001	8	264.7	46.42857 K.YNMGFWKPGSGIIHQ.I
2	3.1972	0.2894	1609.61	1607.87	1	485.7	57.692307 K.YNMGFWKPGSGIIH.Q
1	2.4367	0.1615	1343.55	1344.528	1	336.2	54.545456 M.G1F1W2K2P1G1S1G1I1I1H3Q2.I
2	3.8249	0.2455	1926.47	1925.998	1	940.8	56.25 L.SADKDAEYDEVVEIDLN.T
2	4.2845	0.2647	1653.21	1652.752	3	882.1	65.38461 D.KDAEYDEVVEIDLN.T
2	3.509	0.2589	1681.71	1682.84	1	688.7	60.714287 N.T1Y1Q2A1P1P1A1D1R4S1T1V1E1V1K2.V
2	3.2666	0.2546	1662.23	1662.84	1	800.4	64.28571 N.TYQAPPADRSTVEVK.V
3	3.978	0.2719	1444.43	1444.73	5	737	50 W.DGKDAKDMPILIK.A
1	2.4736	0.2072	1183.22	1183.352	1	402.9	72.22222 R.EHAALEPRFL.G
2	4.8588	0.3771	2405.81	2405.616	1	653.9	44.736843 L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
2	3.06	0.2208	1441.79	1440.744	1	372.6	57.692307 L.GLAELAPGKPVTMR.V
2	2.9479	0.1739	1247.47	1246.495	1	523.7	72.72727 A.GLPQVAKPVTVH.C
2	4.1919	0.1861	1786.37	1786.038	1	685.1	60.000004 Q.VGGEKDLKRAIDLNKE.V
2	3.7497	0.257	2049.01	2048.347	2	431.9	47.058823 Q.VGGEKDLKRAIDLNKEVY.D
1	2.2981	0.2473	1213.53	1214.398	4	248.9	50 M.G1F1W2K2P1G1S1G1I1I1H3.Q
3	4.2158	0.1751	3059.63	3058.439	1	1215.8	33.653847 L.TDKLKDKDGNEFMLKPPHGDGLPQRGY.D
2	3.5928	0.3249	1857.25	1856.234	1	926.3	66.66667 F.KPWDGKDAKDMPILIK.A
1	2.5356	0.1875	1326.78	1327.528	1	455.1	63.636364 M.GFWKPGSGIIHQ.I
1	2.7229	0.3275	1330.65	1330.59	1	831.4	68.181816 N.MGFWKPGSGIIH.Q
2	3.2548	0.387	1344.69	1346.59	1	1140.9	77.27273 N.M1G1F1W2K2P1G1S1G11111H3.Q
1	2.6022	0.2549	1345.33	1346.59	1	775.9	68.181816 N.M1G1F1W2K2P1G1S1G11111H3.Q
2	3.2807	0.225	1610.85	1611.656	1	722.7	61.538464 S.ADKDAEYDEVVEID.L
1	2.2883	0.2685	1207.42	1208.313	1	345.3	61.11111 T.IERDGQLETF.K
1	2.9035	0.2995	1283.76	1284.557	1	716.4	66.66667 L.GLAELAPGKPVTM.R
2	3.2529	0.3557	1286.33	1284.557	1	776.1	70.83333 L.GLAELAPGKPVTM.R

		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently								
ail6323335/refINP_013407_1	VI R304C	required for mitochondrial genome maintenance; component of the mitochondrial	2	3 7617	0.369	1690 33	1688 979	1	562.9	
gilo5255551eilini _015407.11	1610040	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	2	5.7017	0.303	1030.55	1000.373	1	302.9	33.333330 F.INGET IT DEATE VORWIN
	10 000 10	required for mitochondrial genome maintenance; component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	1	2.6616	0.3863	1413.45	1414.514	1	177.5	59.090908 G.EYKGVPDTARDY.R
		required for mitochondrial genome maintenance; component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.6936	0.2419	2117.35	2116.335	1	689.4	50 F.KNPADYDKINPDDRIDIL.G
		required for mitochondrial genome maintenance; component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.5424	0.3618	2377.81	2377.616	1	777.6	47.368423 L.NFKNPADYDKINPDDRIDIL.G
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently								
gi 6323335 ref NP 013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.6127	0.3804	2404.45	2405.616	1	623.4	42.105263 L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently								
ail62022251rofIND_012407.11	VI B204C	required for mitochondrial genome maintenance; component of the mitochondrial	2	E 2206	0.2056	2406.20	2405 616	1	11/2 /	20.4726061 N2E4K2N2D144D1V1D1K2HN2D1D1D1D4D4HD1H14.4 C
gilo5255551eilini _015407.11	1210040	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	5	3.2300	0.2330	2400.23	2403.010	1	1145.4	
	10 000 10	required for mitochondrial genome maintenance; component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	1	2.2281	0.275	1141.49	1142.346	1	581.9	72.22222 G.FWKPGSGIIH.Q
		required for mitochondrial genome maintenance; component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.0872	0.2509	1327.49	1327.528	1	566.5	68.181816 M.GFWKPGSGIIHQ.I
		required for mitochondrial genome maintenance: component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.6153	0.2022	1425.66	1426.618	1	389.9	68.181816 S.SREHAALEPRFL.G
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently								
ail6323335/refINP_013407.1	YLR304C	required for mitochondrial genome maintenance; component of the mitochondrial nucleoid: mutation leads to glutamate auxotrophy: Aco1p	2	3.1054	0.3101	1459.49	1458.721	1	754.2	62.5 N.MGEWKPGSGIIHOJ
310020000101111 _01010111	1210010	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	-	0.1001	0.0101	1100.10	1100.121		101.2	
-100000051 (IND-040407-4)	V/I D0040	required for mitochondrial genome maintenance; component of the mitochondrial		0.0400	0.0540	4 470 00	1170 701		707.0	
gil632335[ret[NP_013407.1]	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	2	3.6499	0.3516	1476.03	14/6./21	1	707.6	66.66667 N.M1G1F1W2K2P1G1S1G1111H3Q2.1
		required for mitochondrial genome maintenance; component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.6884	0.3351	1457.48	1458.721	1	481.9	58.333332 N.MGFWKPGSGIIHQ.I
		required for mitochondrial genome maintenance: component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.3416	0.4651	1330.29	1330.59	1	1167.4	81.818184 N.MGFWKPGSGIIH.Q
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.1771	0.348	1344.63	1346.59	1	848.3	72.72727 N.M1G1F1W2K2P1G1S1G1I1I1H3.Q
		Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently								
ail6323335/refINP_013407_1	VI R304C	required for mitochondrial genome maintenance; component of the mitochondrial	2	3 0049	0 3975	1444 17	1444 694	1	574 7	62.5 X NINGEWKPGSGIIH O
giloo20000101141_010401.11	TER0040	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	2	0.0040	0.0070	1444.17	1444.004		014.1	
	10 000 10	required for mitochondrial genome maintenance; component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently	1	2.8093	0.2294	1535.68	1535.746	1	291.2	53.846157 M.LKPPHGDGLPQRGY.D
		required for mitochondrial genome maintenance; component of the mitochondrial								
gi 6323335 ref NP_013407.1	YLR304C	nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.8158	0.2559	1690.35	1688.938	1	542.2	60.714287 F.M1L1K2P1P1H3G1D1G1L1P1Q2R4G1Y1.D
		Subunit of the RSC chromatin remodeling complex required for kinetochore function								
		in chromosome segregation; essential gene required for cell cycle progression;								
gi 6323354 ref NP_013425.1	YLR321C	phosphorylated in the G1 phase of the cell cycle; Snf5p paralog; Sfh1p	2	3.8794	0.1721	2012.35	2011.138	1	717.1	60.714287 C.N2L1Q2D1R4F1F1E1D1N2F1Q2W2N2L1.N
		Subunit of the RSC chromatin remodeling complex required for kinetochore function								
		in chromosome segregation; essential gene required for cell cycle progression;								
gi 6323354 ref NP_013425.1	YLR321C	phosphorylated in the G1 phase of the cell cycle; Shf5p paralog; Sth1p	2	3.7127	0.2529	1986.39	1987.138	1	811.3	64.28571 C.NLQDRFFEDNFQWNL.N
		Subunit of the RSC chromatin remodeling complex required for kinetochore function								
		in chromosome segregation; essential gene required for cell cycle progression;								
gi 6323354 ref NP_013425.1	YLR321C	phosphorylated in the G1 phase of the cell cycle; Sht5p paralog; Sth1p Perovisional integral membrane protein, involved in negative regulation of	2	3.0745	0.2469	1759.15	1759.875	1	946.3	79.16667 C.NLQDRFFEDNFQW.N
		peroxisome number; partially functionally redundant with Pex31p; genetic								
-100000501 (IND-040400-4)		interactions suggest action at a step downstream of steps mediated by Pex28p and		0.4000	0.4000	0500.00	0500.000		774 5	
gi 6323356 ref NP_013428.1	YLR324W	Percylsomal integral membrane protein, involved in penative regulation of	2	3.1323	0.1933	2530.63	2530.666	1	771.5	52.499996 L.SYERTPWIDEFLNEAPSPENF.H
		peroxisome number; partially functionally redundant with Pex31p; genetic								
-100000501 (IND-040400-4)		interactions suggest action at a step downstream of steps mediated by Pex28p and		4 4000	0 40 40	0000.0	0500.004		000 0	
gi 6323356 ref NP_013428.1	YLR324W	Percylsomal integral membrane protein, involved in penative regulation of	3	4.1962	0.1643	3602.3	3599.821	1	633.9	25.862068 L.SYERTPWIDEFLNEAPSPENFHLPEETNTM@.V
		peroxisome number; partially functionally redundant with Pex31p; genetic								
-:::02022501fND_042420_4		interactions suggest action at a step downstream of steps mediated by Pex28p and	2	5 0440	0.0700	2502.0	2502.004		0000 4	
gil0323330 101 NF_013420.1]	11432411	Peroxisomal integral membrane protein, involved in negative regulation of	3	5.0115	0.3792	3302.0	3363.621	'	2332.4	37.000900 L.STERTFWIDEFLNEAFSFENFHLFEETNIM.V
		peroxisome number; partially functionally redundant with Pex31p; genetic								
aile2022E6IrofIND_012429_1		interactions suggest action at a step downstream of steps mediated by Pex28p and	2	2.06	0 2012	1620 50	1620 944	1	207 5	ER 222222 T WIKKREKERSEEKV T
gil0323330 rei INF_013420.1]	11432411	Peroxisomal integral membrane protein, involved in negative regulation of	2	2.90	0.2013	1029.39	1030.041	'	307.5	30.333332 1.WKKF3KED3F3K1.1
		peroxisome number; partially functionally redundant with Pex31p; genetic								
aile2022E6IrofIND_012429_1		interactions suggest action at a step downstream of steps mediated by Pex28p and	2	4 1000	0.2065	2557 25	2557 666	1	506.0	
giju323330[rei]NP_013428.1]	1 LR32411	Peroxisomal integral membrane protein, involved in negative regulation of	2	4.1230	0.2900	2007.35	2007.000	1	090.9	JUL STITE IN 41 IF IWZ I DIE IF IL INZEIAIP IS IPIE INZFI.H
		peroxisome number; partially functionally redundant with Pex31p; genetic								
ail6323356 refINP_013428_1	YLR324W	Interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p: Pex30p	2	3,4595	0.3335	2279 51	2280 412	1	519 1	47.22222 Y.ERTPWTDEFLNEAPSPENF H
5-1		Nicotinic acid mononucleotide adenylyltransferase, involved in NAD(+) salvage	2	0000	0.0000		2200.712		515.1	
gi 6323360 ref NP_013432.1	YLR328W	pathway; Nma1p	2	3.0832	0.2309	2871.71	2872.247	1	385.8	36 T.RAPDFKPPSADEELIPPPDPESKIPK.S
gi 6323360 ref NP 013432.1	YLR328W	pathway; Nma1p	3	4.3015	0.1913	2906.93	2904.247	2	532.1	28 T.R4A1P1D1F1K2P1P1S1A1D1E1E1L1I1P1P1P1D1P1E1S1K2I1P1K2.S
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additional biolestication of the strategy of the strate	gi 6323362 ref NP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	3	4.3996	0.4627	2931.35	2934.009	1	380.7	25.961538 S.V1A1V1E1P1S1N2E1D1V1K2P1E1E1K2G1S1E1A1E1D1D1I1N2N2V1S1.K
Second Particle Second	gi 6323362 ref NP 013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	3	4.0884	0.2557	2899.97	2902.009	1	450.7	28.846153 S.VAVEPSNEDVKPEEKGSEAEDDINNVS.K
Material	ail6323362lrefINP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating: Chs5p	2	3.3455	0.2191	2813.69	2814.931	1	470.2	34 S. VAVEPSNEDVKPEEKGSEAEDDINNV.S
Jack Jack Jack Jack Jack Jack Jack Jack	=:::::::::::::::::::::::::::::::::::::	VI Dooow	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	-	2.04.00	0.2101	2400.00	2011001		470.0	
Subscher 1 1 1 1 </td <td>gilo323362 rei NP_013434.1 </td> <td>TLR330W</td> <td>Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p</td> <td>2</td> <td>3.8106</td> <td>0.369</td> <td>2122.09</td> <td>2123.111</td> <td>1</td> <td>476.3</td> <td>52.11118 Q.KSEDIDIHSNEQADINGFVQ.1</td>	gilo323362 rei NP_013434.1	TLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	3.8106	0.369	2122.09	2123.111	1	476.3	52.11118 Q.KSEDIDIHSNEQADINGFVQ.1
pick 2000/pick 1000 (Vision (gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	3.2078	0.237	2371.95	2373.66	1	393.2	37.5 T.T1Q2D1H3H3V1I1E1F1P1T1V1L1L1P1E1N2V1K2A1G1.S
generalized sector vector	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	4.0856	0.3825	1902.45	1903.01	1	1060.7	58.823532 L.KSEPVGTPNIEENKADSS.A
package value <	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p	3	3.942	0.1871	3094.55	3094.166	1	546.8	27.777779 V.A1V1E1P1S1N2E1D1V1K2P1E1E1K2G1S1E1A1E1D1D1I1N2N2V1S1K2E1.A
pp:2002-09 0.1000 main all all all all all all all all all al	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p	3	4.093	0.2284	3032.72	3030.183	1	480.5	28.703705 S.VAVEPSNEDVKPEEKGSEAEDDINNVSK.E
PART of about housing of a	gi 6323362 ref NP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	2	3.5641	0.3533	3030.75	3030.183	2	320.9	29.62963 S.VAVEPSNEDVKPEEKGSEAEDDINNVSK.E
Description Description Description Constrain	gi 6323362 ref NP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	3	3.8549	0.3211	3193.73	3194.298	1	1441.9	33.92857 S.V1A1V1E1P1S1N2E1D1V1K2P1E1E1K2G1S1E1A1E1D1D1I1N2N2V1S1K2E1.A
Appendix and any set of a single sector is notice in order to explore the part of any set of a single sector is not any set of any set of a single sector is not any set of a single sector	ail6323362lrefINP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating: Chs5p	2	4.2041	0.3357	3159.37	3159.298	1	464.1	30.357143 S.VAVEPSNEDVKPEEKGSEAEDDINNVSKE A
Mathematical John M Number M </td <td>ail62222621rofIND_012424.1</td> <td>VI P220W/</td> <td>Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p</td> <td>-</td> <td>4 2905</td> <td>0.2067</td> <td>2104.17</td> <td>2104 209</td> <td>4</td> <td>221.4</td> <td>20 574 42 S 1/4 & 41/4 54 B4 S4 N 254 D 41/4 K 2 D 4 54 54 54 54 54 54 54 54 54 54 54 54 5</td>	ail62222621rofIND_012424.1	VI P220W/	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	-	4 2905	0.2067	2104.17	2104 209	4	221.4	20 574 42 S 1/4 & 41/4 54 B4 S4 N 254 D 41/4 K 2 D 4 54 54 54 54 54 54 54 54 54 54 54 54 5
Hit 2002 Height 2019 All V1308 Percent as an intermal in the darge matrix 260 members 000000000000000000000000000000000000	gilo323362 rei ivr_013434.1	TERSSOW	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	4.2095	0.3007	3194.17	3194.290		331.1	
Index 2000 MP - 014441 VEX.000 Index 2000 MP - 014444 Index 20	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	3.017	0.1661	1645.85	1646.883	9	530.5	65.38461 Q.DHHVIEFPTVLLPE.N
updet updet <td< td=""><td>gi 6323362 ref NP_013434.1 </td><td>YLR330W</td><td>localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p</td><td>2</td><td>3.6665</td><td>0.262</td><td>1664.27</td><td>1664.883</td><td>2</td><td>506.1</td><td>69.230774 Q.D1H3H3V1I1E1F1P1T1V1L1L1P1E1.N</td></td<>	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	3.6665	0.262	1664.27	1664.883	2	506.1	69.230774 Q.D1H3H3V1I1E1F1P1T1V1L1L1P1E1.N
Bit	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p	1	2.8253	0.2887	1188.92	1189.36	3	237.8	66.66667 K.HNNIPIVRPE.W
gas222 gas22 gas22 <t< td=""><td>gi 6323362 ref NP_013434.1 </td><td>YLR330W</td><td>localization, also involved in cell fusion during mating; Chs5p</td><td>2</td><td>4.0974</td><td>0.3199</td><td>2115.57</td><td>2116.425</td><td>1</td><td>1408.6</td><td>63.88889 Q.DHHVIEFPTVLLPENVKAG.S</td></t<>	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p	2	4.0974	0.3199	2115.57	2116.425	1	1408.6	63.88889 Q.DHHVIEFPTVLLPENVKAG.S
pipeling Detail of universe find the interments by space of universe find the optimise by space	gi 6323362 ref NP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	2	4.771	0.401	2138.85	2141.425	1	1283.8	58.333332 Q.D1H3H3V1I1E1F1P1T1V1L1L1P1E1N2V1K2A1G1.S
Partial of all stand and match lines and an	gi 6323362 ref NP 013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	2	2.955	0.3057	2060.87	2059.373	1	693.3	50 Q.DHHVIEFPTVLLPENVKA.G
Name Name <th< td=""><td>gil6323362lrefINP_013434_1</td><td>YI R330W/</td><td>Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p</td><td>1</td><td>2 5469</td><td>0 1892</td><td>1404 68</td><td>1405 681</td><td>2</td><td>387 3</td><td></td></th<>	gil6323362lrefINP_013434_1	YI R330W/	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	1	2 5469	0 1892	1404 68	1405 681	2	387 3	
Biologram Biologram Biologram Control Contro Control Contr Control Control		VI DODDW	Protein of unknown function, involved in ching mating, onsop Protein of unknown function, involved in ching mating, onsop		2.0400	0.1032	1704.00	1704.005	-	404.0	
glig23236/pi4/pi-013441 V1830W backardsmin date module and migrating Chick 2 4468 0.368 641.31 20.238 4 210.11 50.015102XLETEETERX222X440PF1423 glig23236Pr14/P_013441 V1830W backardsmin date module and migrating Chick 2 4468 0.369 647.66 1 12 2 668.25 1 110 71.27 66.86872 CLICPT110101111 (EXETINSTID111.0 glig23236714/P_013441 V1830W backardsmin date module and migrating Chick 3 44.44 0.369 647.66 168.52 1 148.3 32.8.V1AINTEETERTS202344240PF142 glig23236714/P_013441 V1830W backardsmin date module and migrating Chick 3 344 0.369 647.66 1 5 45.3 35.0 CLGPLDPLKEEND glig23236714/P_013441 V1830W backardsmin date module and migrating Chick 1 2.4456 0.267 468.83 1 6.85 2.453 50.0 CLGPLDPLKEENDLQ glig23326714/P_013441 V1830W backardsmin date module and migrating Chick 1 2.4456 0.277 1.488.44 1	gi 6323362 ret NP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	3.8516	0.2379	1724.87	1724.895	1	401.8	70.833333 Q.NZL1E1E1E1K2K2Q2R4N2H3F1K2.S
JIE323252[HP]-01344.1 VR3200 Decilization, also involved in cylication datageneric plasming Chap 2 3.00 2102 4.225 1 125 66.8687 CL16 ¹ PL1DPL1K2E ¹¹¹⁵ DDL1.0 JIE323252[HP]-01344.1 VR3200 Decilization a lab involved in cylication datageneric plasming Chap 3 4.444 0.200 1267.2 1 152 74.28657 CL16 ¹ PL1DPL1K2E ¹¹¹⁵ DDL1.0 JIE323252[HP]-01344.1 VR3200 Decilization a lab involved in cylication datageneric plasming Chap 3 4.444 0.2013 1 4.443 2 2 4.445 2 4.445 2 4.445 2 4.445 2 4.446 4.445 2 4.446 4.445 2 4.446 4.445 2 4.446 4.445 4.446 5 4.462 4.445 4.445 4.446 5 4.462 4.446 4.446 1 1.462.46 4.446 1 1.462.46 4.462 4.462 4.462.46 4.462.46 4.462.46 1.462.46 1 4.466.46 4.462.46 4.462.46 1.462.46 1.462.46 <td>gi 6323362 ref NP_013434.1 </td> <td>YLR330W</td> <td>localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p</td> <td>2</td> <td>4.0329</td> <td>0.3465</td> <td>2041.31</td> <td>2043.236</td> <td>4</td> <td>291.1</td> <td>50 Q.V1S1Q2N2L1E1E1E1K2K2Q2R4N2H3F1K2.S</td>	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	4.0329	0.3465	2041.31	2043.236	4	291.1	50 Q.V1S1Q2N2L1E1E1E1K2K2Q2R4N2H3F1K2.S
git233232[hpp] 0142.01 0200000000000000000000000000000000000	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	3.2693	0.2103	1422.93	1424.651	1	752.7	66.66667 C.L1G1P1L1D1P1L1K2E1I1S1D1L1.Q
pick232320/pikP_0144.1 UK300 result number in number in number in number in the bargenesity in pickang Casty in the bargenesis in the contresplate Casty in the bargenesity in the bargenesit	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; ChS5p	2	4.4643	0.3697	1687.69	1685.922	1	1182	71.42857 T.V1C1L1G1P1L1D1P1L1K2E1I1S1D1L1.Q
Bit State Sta	gi 6323362 ref NP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	3	4.4541	0.374	2845.82	2845.931	1	528.9	34 S.V1A1V1E1P1S1N2E1D1V1K2P1E1E1K2G1S1E1A1E1D1D1I1N2N2V1.S
Protect in diversion Protect i	gi 6323362 ref NP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	3	3.9104	0.2091	2813.81	2814.931	1	416.3	32 S.VAVEPSNEDVKPEEKGSEAEDDINNV.S
Bit wilds Protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 VLR3W Disatistication, allow onlyme name; Chosp protein of unknown hunchin, involved in cliff biosprimes by regulating Orks p (Bis233382)rel/PIP_0144.41 <t< td=""><td>ail6323362 refINP_013434.1 </td><td>YLR330W</td><td>Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating: Chs5p</td><td>1</td><td>2.6348</td><td>0.2616</td><td>1424.75</td><td>1424.651</td><td>2</td><td>499.2</td><td>54.166668 C.I.1G1P1I.1D1P1I.1K2E1I1S1D1I.1.Q</td></t<>	ail6323362 refINP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating: Chs5p	1	2.6348	0.2616	1424.75	1424.651	2	499.2	54.166668 C.I.1G1P1I.1D1P1I.1K2E1I1S1D1I.1.Q
unication (1) close (1) Lice (1)	gil6323362lrefINP_013434_1	YI R330W/	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	1	2 4435	0.267	1409.83	1410 651	5	426.3	
glig2.32.362/glig1NP_0.33.4.1 VLR33W Pointable in able model in fell able of uning manual class provides in cell able of uning manual class p	vil00200021101141 _010404.11	NL DOGOW	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	1	2.4400	0.207	1409.00	1410.001	5	420.5	
glig232382[e]th[NP_01343.1] YLR3300 backation, also involved in cell fusion during maing: ChsSp 2 4.480 0.321 fisk.4 1 fisk.388 87.5 RH302E1E1011E1LE141E101EX2D glig232382[e]th[NP_01343.1] YLR3300 backation, also involved in cell fusion during maing: ChsSp 3 4.327 0.316 27.57.23 1 648.6 31.52174 SN2E1D1Y1R2P1E1EX2E1D1111R12X2Y1SN2E1A1.A glig232382[e]th[NP_01343.1] YLR3300 backation: also involved in cell fusion during maing: ChsSp 2 3.486 0.1729 1207.41 1206.36 3 267.7 66.66677.K H30221E111111111111141E1E141E1011111112121111111111	gi 6323362 ret NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	4.0037	0.3207	1671.19	1669.922	1	1000.4	75 T.VCLGPLDPLKEISDL.Q
glig232382[ell[NP_01344.1]VR.830WDeclaration, also involved in cell fusion during mating: Ch5p34.3270.3152675.62677.7231648.631.52174SN2ETO1V1K2P1E1E1K2G1S1E1A1E1D10111N2N2V1S1K2E1A1.Aglig232382[ell[NP_01344.1]VR.930Wvolknown function, involved in line biosynthesis by regulating Ch3p23.14860.1721207.411208.361871.183.3333 K H3N2N21P11V1K2P1E1E1K2G1S1E1A1E1D1011N2N2V1S1K2E1A1.Aglig232382[ell[NP_01344.1]VR.930Wvolknown function, involved in cell fusion during mating: Ch5p23.44560.22681632.431632.451147773.07692 LE1K2Y1G1TH3K2P1E1S1P11V1K4P1E1.Wglig232382[ell[NP_01344.1]VR.930Wlocalization, also involved in cell fusion during mating: Ch5p23.4860.22681632.431632.451147773.07692 LE1K2Y1G1TH3K2P1E1S1P11V1K4P1E1.Wglig232382[ell[NP_01344.1]VR.830Wlocalization, also involved in cell fusion during mating: Ch5p23.4860.22681632.431632.451147773.07692 LE1K2Y1G1TH3K2P1E1S1P11V1K4P1E1.Wglig232382[ell[NP_01344.1]VR.830Wlocalization, also involved in cell fusion during mating: Ch5p23.4860.26161614.211613.65423.0750.LEKYGTHKFESPVLKIglig233382[ell[NP_01344.1]VR.830Wlocalization, also involved in cell fusion during mating: Ch5p24.2740.3962.66.112.07.750.LEKYGTHKFESPVLKIglig233382[ell[NP_01344.1]VR.830Wlocalization, also involved in cell fusion during mating: Ch5p </td <td>gi 6323362 ref NP_013434.1 </td> <td>YLR330W</td> <td>localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p</td> <td>2</td> <td>4.4808</td> <td>0.3217</td> <td>1583.41</td> <td>1584.649</td> <td>1</td> <td>1589.3</td> <td>87.5 R.H3Q2E1E1D111E1L1E1A1E1P1K2.D</td>	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	4.4808	0.3217	1583.41	1584.649	1	1589.3	87.5 R.H3Q2E1E1D111E1L1E1A1E1P1K2.D
gi[323328[re][NP_01343.1] YLR300V resizuation and molecular andin and molecular and molecular and molecular a	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Brotein of unknown function, involved in chilin biopurthosis by regulating Chs2p	3	4.3237	0.3515	2675.96	2677.723	1	648.6	31.52174 S.N2E1D1V1K2P1E1E1K2G1S1E1A1E1D1D111N2N2V1S1K2E1A1.A
Problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem of unknown function, mixed in child biosynthesis by regulating Cksby problem in clsbw problem ino	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Ch55p	2	3.1486	0.1729	1207.41	1206.36	1	871.1	83.33333 K.H3N2N2I1P1I1V1R4P1E1.W
Protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein of unknown function, involved in chilts hosynthesis by regulating Chs5p protein durater protein with a possible role in the canoregulatory giverol response, interacts with phospholpase C (Pic1); putative honolog of human NOM1 which is implicated in acute myeloid teakemis. SgdTp gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls23368/refINP_013440.1 gls2	gi 6323362 ref NP_013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	1	2.826	0.2408	1205.58	1206.36	3	267.7	66.66667 K.H3N2N2I1P1I1V1R4P1E1.W
Protein of unknown function, involved in chilin biosynthesis by regulating ChS3p gil6323362[rel[NP_013434.1] VLR3000 [calization, also involved in aclitin biosynthesis by regulating ChS3p gil6323362[rel[NP_013434.1] VLR3000 [calization, also involved in chilin biosynthesis by regulating ChS3p gil6323362[rel[NP_013434.1] VLR3000 [calization, also involved in chilin biosynthesis by regulating ChS3p gil6323362[rel[NP_013434.1] VLR3000 [calization, also involved in chilin biosynthesis by regulating ChS3p gil6323362[rel[NP_013434.1] VLR3000 [calization, also involved in chilin biosynthesis by regulating ChS3p gil6323362[rel[NP_013434.1] VLR3000 [calization, also involved in cell fusion during mating: ChS5p gil6323362[rel[NP_013440.1] VLR3060 [the is simplicated in acute myeloid leukemia; Sgd1p gil6323368[rel[NP_013440.1] VLR3060 [the is simplicated in acute myeloid leukemia; Sgd1p gil6323368[rel[NP_013440.1] VLR3060 [the is simplicated in acute myeloid leukemia; Sgd1p gil6323368[rel[NP_013440.1] VLR3060 [the is and metrication is the comoregulatory glycerol response; Interacts with phospholipase C [P(c1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p gil6323368[rel[NP_013440.1] VLR3060 [the is and metrication is complex equation glycerol response; Interacts with phospholipase C [P(c1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p gil6323368[rel[NP_013440.1] VLR3060 [the is and metrication is complex equation glycerol response; Interacts with phospholipase C [P(c1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p gil6323368[rel[NP_013440.1] VLR3060 [the is anglex equation is complex equation glycerol response; Interacts with phospholipase C [P(c1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p gil6323368[rel[NP_013440.1] VLR3060 [the kemia; Sgd1p which is implicated in acute myeloid leukemia; Sgd1p gil6323368[rel[NP_013440.1] VLR3060 [the kemia; Sgd1p which is impl	gi 6323362 ref NP 013434.1	YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	2	4.4558	0.2836	1632.43	1632.854	1	487	73.07692 L.E1K2Y1G1T1H3K2P1E1S1P1V1L1K2.I
gliadProtein of unknown function, involved in cell fusion during mating: Chs5p23.51960.16611827.631826.1462320.750 LEKYGTHKPESPVLKIV.Ngli6323362[rel[NP_013434.1]YLR330Wlocalization, also involved in cell fusion during mating: Chs5p23.51960.16611827.631826.1462320.750 LEKYGTHKPESPVLKIV.Ngli6323362[rel[NP_013434.1]YLR30Wlocalization, also involved in cell fusion during mating: Chs5p24.27740.39582056.312057.2631439.260.000004 Q.N2L1E1E1E1KX2Q2R4N2H3F1K2S11IQ2.Agli6323368[rel[NP_013440.1]YLR336Cwithich is implicated in acute myeloid leukemis; Sgd1p33.890.20722384.092381.651775.140.789474 S.K2I1S111E1D1D1L1L1D1D11P1D1W2N2I1I1A1R4.Qgli6323368[rel[NP_013440.1]YLR336Cwithich is implicated in acute myeloid leukemis; Sgd1p26.59440.3954237.9.612381.6511677.963.15789 S.K2I1S111E1D1D1L1L1D1D11P1D1W2N2I1I1A1R4.Qgli6323368[rel[NP_013440.1]YLR336Cwithich is implicated in acute myeloid leukemis; Sgd1p26.01980.4559235.3912356.651212.9.871.05263 S.KISIEDDLLDDIPDWNIIAR.Qgli6323368[rel[NP_013440.1]YLR336Cwithich is implicated in acute myeloid leukemis; Sgd1p223.28680.1881658.571658.9331676.660.714287 Q.KZTID1G11R41P1G1V11L1D1E1L1.Kgli6323368[rel[NP_013440.1]YLR336Cwithich is implicated in acute myeloid leukemis; Sgd1p22.91380.2132	gil6323362lrefINP_013434_1	YI R330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating: Chs5p	2	3 4388	0 2616	1614 21	1613 854	2	239.8	57 692307 EKYGTHKPESPVI K
yii:0323308/ref[NP_01340.1] YLR330W localization, also involved in cell fusion during mating: Classp 2 3.198 0.1001 1627.83 1620.146 2 3.01.7 30 LEK/GTIRKEGFVCNUV gi[6323368]ref[NP_013440.1] YLR330W localization, also involved in cell fusion during mating: Classp 2 4.2774 0.3958 2056.31 2057.263 1 439.2 60.000004 Q.N2L1E1E1E1K2K2Q2R4N2H3F1K2S1I1Q2.A gi[6323368]ref[NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 6.5944 0.3954 2381.65 1 775.1 40.789474 S.K2I1S111E1D1D1L1L1D1D111P1D1W2N2I11A1R4.Q gi[6323368]ref[NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 6.0188 0.4559 235.91 235.65 1 1677.9 63.15789 S.K211S111E1D1D1L1L1D1D111P1D1W2N2I11A1R4.Q gi[6323368]ref[NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 6.0188 0.4559 235.91 235.65 1 2129.8 71.05263 S.KISIEDDLLDDIPDWNIAR.Q gi[6323368]ref[NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.2868 0.188 1658.57 1658.933	gil6222262[rof[ND_012424.1]	VI P220W/	Protein of unknown function, involved in chilin biosynthesis by regulating Chs3p	-	2 5106	0.1661	1927.62	1926 146	-	200.0	
gil6323362/reflNP_01343.1]YLR330Vlocalization, also involved in cell tusion during mating: Chsp Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p24.27740.39582056.312057.2631439.260.000004 Q.N2L1E1E1E1K2K2Q2R4N2H3F1K2S1I1Q2.Agil6323368/reflNP_013440.1]YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p33.890.20722384.092381.651775.140.789474 S.K2IIS1IE1D1D1L1L1D1D11H1P1D1W2N2IIIA1R4.Qgil6323368/reflNP_013440.1]YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p26.59440.39542379.612381.65111677.963.15789 S.K2IIS1IE1D1D1L1L1D1D11H1P1D1W2N2IIIA1R4.Qgil6323368/reflNP_013440.1]YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p26.01980.45592353.912355.6512129.871.05263 S.KISIEDDLLDDIPDWNIIAR.Qgil6323368/reflNP_013440.1]YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p23.28680.1881658.571658.9331676.660.714287 Q.K2T1D1G11R411P1G1V111L1D1E1L1.Kgil6323368/reflNP_013440.1]YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p23.28680.1881658.571658.9331676.660.714287 Q.K2T1D1G11R411P1G1V111L1D1E1L1.Kgil6323368/reflNP_013440.1]YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p23.19880.21321	giloszssozireiline_013454.1	TERSSOW	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p	2	3.5190	0.1001	1027.03	1820.140	2	320.7	JUL.ENTOTHNESEVENIV.IN
gil6323368/ref NP_01340.1 YLR38CYLR38Cresponse; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gil6323368/ref NP_01340.1 YLR38CYLR38CVLR38CVLR38CNomice interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 respon	gi 6323362 ref NP_013434.1	YLR330W	localization, also involved in cell fusion during mating; Chs5p Essential nuclear protein with a possible role in the osmoregulatory glycerol	2	4.2774	0.3958	2056.31	2057.263	1	439.2	60.000004 Q.N2L1E1E1E1K2K2Q2R4N2H3F1K2S1I1Q2.A
Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p gil6323368/ref NP_013440.1] YLR336C which is implicate	ail6323368 refINP 013440.1	YLR336C	response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia: Sod1p	3	3.89	0.2072	2384.09	2381.65	1	775.1	40.789474 S.K2I1S1I1E1D1D1L1L1D1D1I1P1D1W2N2I1I1A1R4.Q
and points, interacts with phospholipase (Plo1p), putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p26.59440.39542379.612381.6511677.963.15789 S.K2I1S111E1D1D1L1L1D1D111P1D1W2N2I111A1R4.Qgil6323368/ref NP_013440.1 YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p26.59440.39542379.612381.6511677.963.15789 S.K2I1S111E1D1D1L1L1D1D111P1D1W2N2I111A1R4.Qgil6323368/ref NP_013440.1 YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p26.01980.45592353.912355.6512129.871.05263 S.KISIEDDLLDDIPDWNIIAR.Qgil6323368/ref NP_013440.1 YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p23.28680.1881658.571658.9331676.660.714287 Q.K2T1D1G111R411P1G1V111L1D1E1L1.Kgil6323368/ref NP_013440.1 YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p22.91320.30482444.752442.7281464.147.5 K.SKISIEDDLLDDIPDWNIIAR.Qgil6323368/ref NP_013440.1 YLR336Cwhich is implicated in acute myeloid leukemia; Sgd1p23.19880.21321930.291929.1111293.860.714287 F.LHHYEEMENILKDQ.Q	51		Essential nuclear protein with a possible role in the osmoregulatory glycerol								
gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 6.0198 0.4559 2353.91 2355.65 1 2129.8 71.05263 S.KISIEDDLLDDIPDWNIIAR.Q gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.2868 0.188 1658.57 1658.933 1 676.6 60.714287 Q.K2T1D1G111R411P1G1V111L1D1E1L1.K gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.2868 0.188 1658.57 1658.933 1 676.6 60.714287 Q.K2T1D1G111R411P1G1V111L1D1E1L1.K gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 2.9132 0.3048 2444.75 2442.728 1 464.1 47.5 K.SKISIEDDLLDDIPDWNIIAR.Q gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.1988 0.2132 1930.29 1929.111 1 293.8 60.714287 F.LHHYEEMENILKDQ.Q	gi 6323368 ref NP_013440.1	YLR336C	which is implicated in acute myeloid leukemia; Sgd1p	2	6.5944	0.3954	2379.61	2381.65	1	1677.9	63.15789 S.K2I1S1I1E1D1D1L1L1D1D111P1D1W2N2I1I1A1R4.Q
gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 6.0198 0.4559 235.91 235.65 1 219.8 71.05263 S.KISIEDDLLDDIPDWNIIAR.Q gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.2868 0.188 1658.57 1658.933 1 676.6 60.714287 Q.K2T1D1G111R411P1G1V111L1D1E1L1.K gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.2868 0.188 1658.57 1658.933 1 676.6 60.714287 Q.K2T1D1G111R411P1G1V111L1D1E1L1.K gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 2.9132 0.3048 2444.75 2442.728 1 464.1 47.5 K.SKISIEDDLLDDIPDWNIIAR.Q gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.1988 0.2132 1930.29 1929.111 1 293.8 60.714287 F.LHHYEEMENILKDQ.Q			Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1								
gil6323368/ref/NP_013440.1] YLR336C response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gil6323368/ref/NP_013440.1] YLR336C victor with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gil6323368/ref/NP_013440.1] YLR336C victor with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gil6323368/ref/NP_013440.1] YLR336C victor with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gil6323368/ref/NP_013440.1] YLR336C victor with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gil6323368/ref/NP_013440.1] YLR336C victor with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gil6323368/ref/NP_013440.1] YLR336C victor with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gil6323368/ref/NP_013440.1] YLR336C victor methods with a spossible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gilfo323368/ref/NP_013440.1] YLR336C victor methods with a spossible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p 2 3.1988 0.2132 1930.29 1929.111 1 293.8 60.714287 F.LHHYEEEMENILKDQ.Q	gi 6323368 ref NP_013440.1	YLR336C	which is implicated in acute myeloid leukemia; Sgd1p Essential nuclear protein with a possible role in the osmoregulatory glycerol	2	6.0198	0.4559	2353.91	2355.65	1	2129.8	71.05263 S.KISIEDDLLDDIPDWNIIAR.Q
gi[6323368]ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.1988 0.2132 1930.29 1929.111 1 293.8 60.714267 F.LHHYEEEMENILKDQ.Q	ail63233681rofINP_013440.11	VI P336C	response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid laukamia; Sod1p	2	3 2868	0 199	1659 57	1658 033	1	676.6	60 71/287 O K2T4D1G111D/14D1G1\/111 1D1E11 1 K
response; interacts with phospholipase C (Pic1p); putative homolog of human NUM1 gi[6323368/ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 2.9132 0.3048 2444.75 2442.728 1 464.1 47.5 K.SKISIEDDLLDDIPDWNIIAR.Q Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Pic1p); putative homolog of human NOM1 gi[6323368/ref]NP_013440.1] YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.1988 0.2132 1930.29 1929.111 1 293.8 60.714287 F.LHHYEEEMENILKDQ.Q	9-19920000110114r _010440.1	. 110000	Essential nuclear protein with a possible role in the osmoregulatory glycerol	2	0.2000	0.100	1000.07	1000.000	,	010.0	
Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 gi[6323368 ref]NP_013440.1 YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.1988 0.2132 1930.29 1929.111 1 293.8 60.714287 F.LHHYEEEMENILKDQ.Q	gi 6323368 ref NP_013440.1	YLR336C	response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p	2	2.9132	0.3048	2444.75	2442.728	1	464.1	47.5 K.SKISIEDDLLDDIPDWNIIAR.Q
gij6323368/ref/NP_013440.1 YLR336C which is implicated in acute myeloid leukemia; Sgd1p 2 3.1988 0.2132 1930.29 1929.111 1 293.8 60.714287 F.LHHYEEEMENILKDQ.Q			Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1								
	gi 6323368 ref NP_013440.1	YLR336C	which is implicated in acute myeloid leukemia; Sgd1p	2	3.1988	0.2132	1930.29	1929.111	1	293.8	60.714287 F.LHHYEEEMENILKDQ.Q

		Essential nuclear protein with a possible role in the osmoregulatory glycerol								
gi 6323368 ref NP_013440.1	YLR336C	response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p Essential unclear protein with a possible role in the osmoregulatory dynarol	2	4.5844	0.32	2026.37	2027.238	1	1313.2	78.125 S.IEDDLLDDIPDWNIIAR.Q
gi 6323368 ref NP_013440.1	YLR336C	response; interacts with phospholipase C (Pic(rp); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p	2	3.7356	0.2964	2201.41	2199.463	1	765.8	55.555557 S.KISIEDDLLDDIPDWNIIA.R
qi 6323368 ref NP 013440.1	YLR336C	Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sqd1p	2	2.9818	0.1631	2220.63	2221.463	3	468	44.444447 S.K2I1S1I1E1D1D1L1L1D1D111P1D1W2N2I1I1A1.R
	V// D0000	Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1		0.0040	0.4470	0000 70	0004.05		0100.0	
gij6323368 ret NP_013440.1	YLR336C	which is implicated in acute myeloid leukemia; Sga1p Essential nuclear protein with a possible role in the osmoregulatory glycerol response: interacts with phospholipase C (Plc1p): putative homolog of human NOM1	2	6.6846	0.4178	2382.73	2381.65	1	2100.3	/1.05263 S.K2HS1HETU101L1L10101HP101W2N2HHA1K4.Q
gi 6323368 ref NP_013440.1	YLR336C	which is implicated in acute myeloid leukemia; Sgd1p Essential nuclear protein with a possible role in the osmoregulatory glycerol	3	3.9588	0.2122	2381.21	2381.65	1	963.8	43.421055 S.K2I1S1I1E1D1D1L1L1D1D1I1P1D1W2N2I1I1A1R4.Q
gi 6323368 ref NP_013440.1	YLR336C	which is implicated in acute myeloid leukemia; Sgd1p Essential nuclear protein with a possible role in the osmoregulatory glycerol	2	3.6339	0.2092	1950.71	1951.111	1	1280.6	71.42857 F.L1H3H3Y1E1E1E1M1E1N2I1L1K2D1Q2.Q
gi 6323368 ref NP_013440.1	YLR336C	response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p	2	5.3393	0.3772	2049.23	2049.238	1	1129.3	75 S.I1E1D1D1L1L1D1D111P1D1W2N2I111A1R4.Q
gi 6323371 ref NP 013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	4.2583	0.377	1635.91	1634.781	1	1189.3	73.07692 S.S1I1L1D1I1T1D1E1E1L1V1S1H3F1.V
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	1	2.5615	0.172	1277.45	1278.393	1	422.7	66.66667 L.V1D1R4I1E1N2P1E1K2Y1.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	1	2.5144	0.2428	1263.51	1263.393	1	314.3	66.66667 L.VDRIENPEKY.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	1	3.1584	0.3725	1457.58	1458.64	1	352.6	50 K.L1R4E1Y1L1E1E1Y1K2S1L1.F
ail6323371/refINP 013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rop0p	2	5.1054	0.4507	2283.79	2285.465	1	1425.6	70.588234 Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
qi 6323371 ref NP 013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	4.3076	0.3478	2608.35	2609.798	1	1008.8	52.499996 A.A1S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	3	4.1923	0.3749	2579.99	2581.798	1	697.6	35 A.ASYHYPEIEDLVDRIENPEKY.A
ail6323371 refINP 013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rop0p	3	4.0152	0.3694	2536.61	2537.719	1	1118.3	44.736843 A.S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1 A
gil6323371/refINP_013444.1	VI R340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	3 5401	0 3953	2579.91	2581 798	1	390.1	
ail62222271/refIND_012444.1	VI P240W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	4 0224	0.0000	2010.01	2600 709	1	404.9	
vil00200741(ND_010444.1]	1004000	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	3	4.0231	0.3306	2010.00	2009.790	1	494.0	
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	5.2698	0.3906	2513.53	2510.719	1	2032.3	65.789474 A.SYHYPEIEDLVDRIENPEKY.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	3.5866	0.3936	2564.73	2565.799	1	913.7	50 S.YHYPEIEDLVDRIENPEKYAA.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E, coli L10e:	2	3.6725	0.3404	2752.41	2753.956	1	608.5	43.18182 A.S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1A1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	3	4.3005	0.362	2287.46	2285.465	1	498.8	41.17647 Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorplated on serine 302; Rp0p	1	3.5393	0.3606	1440.73	1440.645	1	325.3	66.66667 A.RAGAVAPEDIWVR.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	2	3.8236	0.2182	1547.75	1548.792	1	469.7	75 F.L1S1D1L1P1D1F1E1K2L1L1P1F1.V
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	2	3.6238	0.4404	1617.55	1618.781	1	860.7	65.38461 S.SILDITDEELVSHF.V
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	2	3.0723	0.4276	1460.33	1460.645	1	479.1	58.333332 A.R4A1G1A1V1A1P1E1D111W2V1R4.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	1	2.9145	0.2756	1442.74	1443.64	1	449	60.000004 K.LREYLEEYKSL.F
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	4.3458	0.4581	2259.47	2260.465	1	1002	58.823532 Y.HYPEIEDLVDRIENPEKY.A
ail6323371 refINP 013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rop0p	2	4.4419	0.3945	2282.97	2285.465	1	1198.6	61.764706 Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
gil6323371/refINP_013444_1	YI R340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	4 9649	0 3102	2448 41	2449 641	1	1441 5	58 333332 S Y1H3Y1P1E111E1D11 1\/1D1R4I1E1N2P1E1K2Y1 A
gil6222271 rofIND_012444.1	VI P240W	Conserved ribosomal protein PO similar to rat PO, human PO, and E. coli L10e;	2	4 1255	0.2002	2590.24	2591 709		014.9	
vil00200741(ND_010444.1]	1004000	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	4.1200	0.3992	2000.21	2001.790		914.0	
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	5.1613	0.3448	2608.87	2609.798	1	829.7	50 A.A1S1Y1H3Y1P1E111E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	3.5254	0.3157	2402.01	2402.623	1	800.3	44.736843 Y.HYPEIEDLVDRIENPEKYAA.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	3.0643	0.3266	2499.65	2501.701	1	497.2	40 Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1A1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	5.5721	0.4462	2535.69	2537.719	1	2207.6	68.42105 A.S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	3	4.2352	0.3047	2446.82	2449.641	1	840.8	47.22222 S.Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	2	3.3519	0.3049	2357.73	2357.544	1	698.2	47.22222 Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	2	3.9644	0.2729	2473.75	2473.701	5	390.1	37.5 Y.HYPEIEDLVDRIENPEKYAAA.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	3	5.179	0.4408	2612.03	2609.798	1	810.3	33.75 A.A1S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	3	4.2276	0.3895	2536.22	2537.719	1	1136.4	44.736843 A.S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	3.5407	0.3398	2332.69	2331.544	1	658	47.22222 Y.HYPEIEDLVDRIENPEKYA.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	4.4176	0.34	2424.85	2423.641	1	1540.4	63.88889 S.YHYPEIEDLVDRIENPEKY.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein PU similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	3.7461	0.2489	2653.27	2652.877	1	718.3	45.238094 A.SYHYPEIEDLVDRIENPEKYAA.A

		Conserved ribosomal protein P0 similar to rat P0, human P0, and E, coli L10e:								
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p Conserved ribosomal protein P0 similar to rat P0, human P0, and E, coli I 10e;	2	4.4958	0.4081	2592.49	2593.799	1	918.5	52.499996 S.Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; RPDPD	2	4.9545	0.2194	2682.47	2681.877	1	1352.1	52.380955 A.S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; Rpp0p	2	4.3093	0.2956	2636.87	2636.877	1	1071	47.61905 S.YHYPEIEDLVDRIENPEKYAAA.A
gi 6323371 ref NP_013444.1	YLR340W	shown to be phosphorylated on serine 302; RppOp	2	3.2467	0.2475	2493.79	2494.72	1	531.9	39.473686 S.YHYPEIEDLVDRIENPEKYA.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	4.333	0.3313	2664.81	2665.877	1	1154.1	50 S.Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1A1.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	3.6759	0.2393	2721.73	2723.956	2	511.6	36.363636 A.SYHYPEIEDLVDRIENPEKYAAA.A
gi 6323371 ref NP_013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	3	3.8939	0.2541	2824.88	2826.034	1	737.3	29.347824 A.A1S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1A1.A
gi 6323371 ref NP 013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	4.0115	0.2754	2520.01	2521.72	1	867.5	47.368423 S.Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1.A
gi 6323371 ref NP 013444.1	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	2	4.2396	0.427	2580.69	2581.798	1	942	50 A.SYHYPEIEDLVDRIENPEKYA.A
gil6323371/refINP_013444.11	YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpo0p	3	4.3397	0.2543	3677.81	3679.084	1	871.7	N.Y1K2D1L1L1A1V1A1I1A1A1S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1 25.833332 A
gil6323371/refINP_013444_1	YI R340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302. Rpp0n	1	2 7419	0.3156	1265 48	1266.35	1	614.5	61 11111 A SYHYPEIEDI V
gil6323371/refINP_013444_1	VI R340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	3 1435	0.2156	1559 35	1556 815	1	785.2	67 85714 S I 1411/G1V1P1T11 1P1S1\/1G1H3T11 1 I
gil6323371/rofINP_013444.1	VI P340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e;	2	3 3375	0.2403	1537 31	1534 702	2	532.4	
gilo3233711eiline_013444.1	TER340W	Catch tie suburit of 4.2 bate D churce surthers for ationally reducted with elements	2	3.3375	0.2493	1557.51	1554.792	2	552.4	19.1000/ F.LSDLFDFEKLLFF.V
		catalytic subunit of 1,3-beta-b-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall								
gi 6323374 ref NP_013446.1	YLR342W	synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.1083	0.1963	1493.41	1491.745	1	1012.9	72.72727 L.LYRVENPEIVQM.F
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.0015	0.3834	1768.27	1766.865	1	766.3	62.5 Q.LSGNPILGDGKSDNQNH.A
oil6323374/refINP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance: localizes to sites of cell wall remodelino: Fks1p	2	2.9656	0.2172	1563.73	1564.698	2	451.7	68 181816 L REIREDDOESR V
3.1		Catalytic subunit of 1.3-beta-D-olucan synthese, functionally redundant with alternate								
gi 6323374 ref NP_013446.1	YLR342W	catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.1263	0.2111	2328.07	2327.688	1	428.8	52.77778 V.L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.5668	0.2521	2277.85	2276.615	1	462.3	47.22222 Q.RQEPMPEGDFLNRVITPIY.H
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	2.9348	0.1986	2598.83	2600.032	1	135.9	30.952381 K.I1V1L1E1D1G1T1K2L111E1L1P1L1E1E1R4Y1L1R4L1G1.D
ail6323374lrefINP 013446.11	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance: localizes to sites of cell wall remodelino: Fks1p	3	4.3288	0.2286	2427.29	2427.821	1	1213.4	38.157894 I.V1L1E1D1G1T1K2L111E1L1P1L1E1E1R4Y1L1R4L1.G
3.1		Catalytic subunit of 1.3-beta-D-olucan synthese, functionally redundant with alternate								
gi 6323374 ref NP_013446.1	YLR342W	catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.6272	0.2875	1170.4	1171.257	1	505.4	66.66667 L.HYGHPDFINA.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.2252	0.1984	1447.51	1444.639	1	574.5	80 Q.LHPVEWECFVK.D
		Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate								
gi 6323374 ref NP_013446.1	YLR342W	catalytic subunit Csc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.6935	0.3255	2302.37	2301.688	1	1368.1	43.055553 V.LEDGTKLIELPLEERYLRL.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.9796	0.2176	2329.04	2327.688	1	1670.7	47.22222 V.L1E1D1G1T1K2L11E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.3429	0.2088	1212.63	1213.422	2	207.5	66.66667 L.TPHYAERILL.S
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.8241	0.4587	1877.61	1876.129	1	1411.2	80 Y.DRNKPKTDVLVPIGCY.N
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Csc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.0343	0.3362	1876.94	1876.129	1	659	45 Y.DRNKPKTDVLVPIGCY.N
nil6323374/refINP_013446-11	YI R342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance: localizes to sites of cell wall remodeling. Ex1n	1	2 6203	0 2324	1537 69	1538 957	2	154 3	62.5 C. OL PLIJIPKIDKE H
5-1-5-2001 (holini _010++0.1)	. 2.107211	Catalytic subunit of 1 3-beta-D-olucan synthese functionally redundant with alternate		2.0200	0.2024		1000.001	2	101.0	
gi 6323374 ref NP_013446.1	YLR342W	catalytic subunit Gsc2p; binds to regulary subunit Rhoftp; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.3769	0.2213	1553.69	1554.957	1	184.9	62.5 C.Q2L1P1L11111P1K2I1D1K2F1.H

gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.54	0.2523	1555.69	1554.957	1	631.8	83.33333 C.Q2L1P1L111111P1K2I1D1K2F1.H
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.9182	0.4105	1472.53	1473.637	1	553.6	65 L.KQLHPVEWECF.V
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.2802	0.2503	1946.09	1944.325	1	828.7	63.333332 D.GTKLIELPLEERYLRLG
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	2.9297	0.2833	1942.67	1941.19	1	549.2	50 M.P1E1G1D1F1L1N2R4V1I1T1P1I1Y1H3F1.I
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.6285	0.2579	1159.62	1160.378	1	249.9	75 N.R4V1I1T1P1I1Y1H3F1.I
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.9398	0.5206	2150.83	2152.464	1	512.9	55.88235 C.IYDRNKPKTDVLVPIGCY.N
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.9202	0.458	2558.69	2560.933	1	487.8	45 Q.RQEPMPEGDFLNRVITPIYHF.I
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.5924	0.373	1526.69	1527.723	1	457.4	53.846157 K.IHKHIGDSLDGVVH.N
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.61	0.2306	1450.13	1450.579	1	589.2	68.181816 Q.R4Q2E1P1M1P1E1G1D1F1L1N2.R
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.8608	0.2275	1377.63	1378.586	1	503	60.000004 L.YRVENPEIVQM.F
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.8873	0.2571	1393.45	1394.586	3	470.9	60.000004 L.Y1R4V1E1N2P1E1I1V1Q2M1.F
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.8002	0.4815	2243.47	2244.634	1	1471.1	58.333332 K.IVLEDGTKLIELPLEERYL.R
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.7008	0.2066	1590.57	1589.766	1	524.4	62.5 Q.RQEPMPEGDFLNR.V
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.9481	0.2048	1543.66	1544.834	1	306.3	59.090908 L.IELPLEERYLRL.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.3774	0.3382	2301.79	2303.615	2	280	36.11111 Q.R4Q2E1P1M1P1E1G1D1F1L1N2R4V1I1T1P1I1Y1.H
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.4286	0.2593	1614.13	1614.826	1	1042.1	66.66667 L.R4L1G1D1V1V1W2D1D1V1F1F1K2.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.84	0.2201	2325.65	2327.688	1	326	44.444447 V.L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.4112	0.224	2513.07	2513.981	6	235	35 K.IVLEDGTKLIELPLEERYLRL.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.1876	0.1992	2539.85	2541.981	1	254.8	42.5 K.I1V1L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.2278	0.4539	2511.41	2513.981	1	700.2	33.75 K.IVLEDGTKLIELPLEERYLRL.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	3.1069	0.2189	1577.52	1575.728	4	339.7	59.090908 Q.L1H3P1V1E1W2E1C1F1V1K2D1.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	3.1238	0.3199	1560.48	1559.728	1	476	59.090908 Q.LHPVEWECFVKD.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	3.9086	0.1585	2597.99	2600.032	1	771.9	30.952381 K.I1V1L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1G1.D

gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	3.0987	0.3196	1299.85	1300.417	1	560.5	65 K.L1H3Y1G1H3P1D1F1I1N2A1.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	3.0455	0.2457	1444.57	1444.639	1	499.4	65 Q.LHPVEWECFVK.D
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.0173	0.3858	1446.29	1444.639	1	594.3	80 Q.LHPVEWECFVK.D
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.2002	0.2345	1458.59	1459.639	1	521.6	75 Q.L1H3P1V1E1W2E1C1F1V1K2.D
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	3.5637	0.2957	1401.5	1402.522	1	617.7	68.181816 K.L1H3Y1G1H3P1D1F111N2A1T1.F
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.8802	0.3853	1284.67	1284.417	1	767.1	70 K.LHYGHPDFINA.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.2651	0.3298	2541.11	2541.981	1	1002.9	35 K.I1V1L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.3929	0.2274	1785.43	1784.93	1	273.8	46.875 F.K2R4K2L1V1G1D1E1S1E1K2A1A1G1D1A1S1.R
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	2.9212	0.219	2011.71	2012.288	4	277.6	43.75 C.11Y1D1R4N2K2P1K2T1D1V1L1V1P111G1C1.Y
qi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.1491	0.334	2589.89	2591.933	1	426.5	42.5 Q.R4Q2E1P1M1P1E1G1D1F1L1N2R4V111T1P111Y1H3F1.I
qi 6323374 ref NP 013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.255	0.3802	1875.95	1876.129	1	793.2	63.333332 Y.DRNKPKTDVLVPIGCY.N
ail6323374/ref/NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance: localizes to sites of cell wall remodeling: Fks1p	2	4.198	0.3797	2174.97	2176.464	1	403.6	50 C.11Y1D1R4N2K2P1K2T1D1V1L1V1P111G1C1Y1.N
9,002007 (10,1,1, _0,0,1,0,1)		Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall	-			2				
gi 6323374 ret NP_013446.1	YLR342W	synthesis and maintenance; localizes to sites of cell wall remodeling; FKs1p Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit GS-27; blinds to regulatory subunit BRo1p; involved in cell wall	2	3.9069	0.2296	2340.51	2337.603	1	662.6	55.555557 M.C111Y1D1R4N2K2P1K211D1V1L1V1P111G1C1Y1.N
gi 6323374 ref NP_013446.1	YLR342W	curd/pro-backing to book and the program of the product of the pro	2	3.4865	0.2789	2310.83	2312.603	1	828	58.333332 M.CIYDRNKPKTDVLVPIGCY.N
gi 6323374 ref NP_013446.1	YLR342W	catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	3.8688	0.2056	2719.37	2722.064	1	536.9	30.952381 Q.Q2R4Q2E1P1M1P1E1G1D1F1L1N2R4V1I1T1P1I1Y1H3F1.
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-U-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.3046	0.4468	1528.41	1527.723	1	1277.8	76.92308 K.IHKHIGDSLDGVVH.N
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.5005	0.3381	2050.39	2051.214	1	982.8	68.75 A.YLDEEPPLTEGEEPRIY.S
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.7317	0.4029	1327.67	1327.479	1	593.1	65 L.GDVVWDDVFFK.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.8936	0.3826	1339.48	1340.479	1	752	70 L.G1D1V1V1W2D1D1V1F1F1K2.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.5605	0.3061	1326.57	1327.479	1	788.2	75 L.GDVVWDDVFFK.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.7602	0.2237	1275.44	1276.607	1	223.7	70 C.Q2L1P1L111111P1K211D1.K
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	3.0497	0.154	1264.97	1263.607	1	197.1	70 C.QLPLIIIPKID.K
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.7026	0.2429	1265.85	1263.607	1	813.7	85 C.QLPLIIIPKID.K

gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.5338	0.2406	1403.55	1402.647	1	830.6	80 K.L1I1E1L1P1L1E1E1R4Y1L1.R
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.2164	0.1809	1274.79	1276.607	1	1149.4	85 C.Q2L1P1L111111P1K211D1.K
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	5.188	0.3948	2052.73	2053.342	1	1174.7	62.5 V.L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1.R
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.1967	0.2183	2034.44	2032.342	1	1355.8	43.75 V.LEDGTKLIELPLEERYL.R
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.0581	0.3739	2031.55	2032.342	1	1176	59.375 V.LEDGTKLIELPLEERYL.R
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	5.6611	0.3942	2268.81	2267.634	1	1807.8	66.66667 K.I1V1L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1.R
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.2833	0.2581	1585.79	1586.698	1	513.8	72.72727 L.R4E11111R4E1D1D1Q2F1S1R4.V
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.672	0.38	2383.73	2385.74	1	324.3	44.736843 V.L1E1D1G1T1K2L111E1L1P1L1E1E1R4Y1L1R4L1G1.D
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.586	0.2556	1596.35	1596.826	1	2059.4	83.33333 L.RLGDVVWDDVFFK.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.2595	0.264	2325.14	2327.688	1	1095.3	41.6666664 V.L1E1D1G1T1K2L111E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.1787	0.2103	2326.11	2327.688	1	399.4	52.77778 V.L1E1D1G1T1K2L111E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.7368	0.3732	2300.57	2301.688	1	408.6	52.77778 V.LEDGTKLIELPLEERYLRLG
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	3.2686	0.3673	1458.6	1459.639	1	510.7	65 Q.L1H3P1V1E1W2E1C1F1V1K2.D
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	3.2627	0.2461	1444.59	1444.639	1	543.2	65 Q.LHPVEWECFVK.D
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.2789	0.2659	1063.52	1064.236	1	434.8	78.57143 A.H3W2Q2A1P1L1L1W2.F
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.7054	0.2599	2541.74	2541.981	1	1546.5	42.5 K.I1V1L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	3	4.0583	0.3914	2514.2	2513.981	1	774.1	32.5 K.IVLEDGTKLIELPLEERYLRLG
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.5161	0.3856	1897.21	1898.129	1	606.1	66.666667 Y.D1R4N2K2P1K2T1D1V1L1V1P1I1G1C1Y1.N
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.8356	0.2272	1555.51	1554.957	1	533.4	79.16667 C.Q2L1P1L111111P1K2I1D1K2F1.H
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.1395	0.1813	1968.05	1967.325	1	569.9	56.666668 D.G1T1K2L111E1L1P1L1E1E1R4Y1L1R4L1.G
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	3.0754	0.1945	1339.51	1340.479	1	711.6	70 L.G1D1V1V1W2D1D1V1F1F1K2.T
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.5459	0.1618	1033.42	1034.176	1	787.9	75 K.I1H3K2H3I1G1D1S1L1.D
gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	1	2.3434	0.2036	1019.51	1020.177	2	339.9	56.25 K.IHKHIGDSL.D

gi 6323374 ref NP_013446.1	YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	2	4.9168	0.3971	2070.19	2071.214	1	930.3	68.75 A.Y1L1D1E1E1P1P1L1T1E1G1E1E1P1R4I1Y1.S
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	3.6306	0.1572	1453.47	1453.678	1	1425.1	81.818184 N.HILEPVLEFVEQ.N
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	4.2563	0.3371	1625.31	1624.834	1	1684	76.92308 C.GNHILEPVLEFVEQ.N
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	4.5522	0.2538	1642.51	1642.834	1	1938.8	80.769226 C.G1N2H3I1L1E1P1V1L1E1F1V1E1Q2.N
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	4.5255	0.3918	1897.77	1899.077	1	1791.5	73.333336 Q.NCGNHILEPVLEFVEQ.N
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	4.203	0.282	2038.11	2036.18	1	904.9	59.375 Q.N2C1G1N2H3I1L1E1P1V1L1E1F1V1E1Q2N2.I
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	1	2.325	0.3098	1386.53	1387.578	2	307.4	54.545456 A.GLHDKPEALFPY.V
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	3.3756	0.2302	1509.77	1508.732	3	617.7	62.5 A. DIELPHGAWPELM.K
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	3.7636	0.4215	1691.77	1692.97	1	687.8	67.85714 A.IADIELPHGAWPELM.K
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	3.8735	0.2703	1712.09	1710.97	1	625.1	64.28571 A.I1A1D1I1E1L1P1H3G1A1W2P1E1L1M1.K
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	1	2.3802	0.2081	1453.67	1453.678	8	316.1	45.454548 N.HILEPVLEFVEQ.N
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	2	4.9519	0.2674	1921.57	1920.077	1	1362.8	70 Q.N2C1G1N2H3I1L1E1P1V1L1E1F1V1E1Q2.N
gi 6323379 ref NP_013451.1	YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p Acetohydroxyacid reductiosmerase mitochondrial notation invanched.	2	3.3409	0.2301	1526.31	1524.732	2	647.3	66.66667 A.D111E1L1P1H3G1A1W2P1E1L1M1.K
gi 6323387 ref NP_013459.1	YLR355C	chain aming acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; IVSp Acatobutrouncid reductoremance, mitochondrial protein involved in branched	2	3.9575	0.3173	1526.79	1526.715	1	721	75 N.A1L1K2P1V1F1Q2D1L1Y1E1S1T1.K
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; IIV5p	2	3.5649	0.4046	1513.29	1511.715	1	516.8	62.5 N.ALKPVFQDLYEST.K
gi 6323387 ref NP_013459.1	YLR355C	Acetonydroxyacid reductoisomerase, mitochondnai protein involved in branched- chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; IIV5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	1	2.3951	0.1954	1454.47	1454.636	1	405.5	50 A.L1K2P1V1F1Q2D1L1Y1E1S1T1.K
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	1	2.8807	0.2498	1377.54	1378.584	3	425.9	65 K.L1E1K2E1L1D1T111R4N2M1.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; IIv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	3.9832	0.3282	2118.45	2117.448	2	568.5	50 L.D1W2Y1P1I1F1K2N2A1L1K2P1V1F1Q2D1L1.Y
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	2.9939	0.1813	1479.49	1476.713	1	649.4	75 L.THVEPPKDLDVIL.V
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; IIv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	3.5989	0.2916	2754.95	2757.047	1	363.7	42.857143 L.EFNSQPDYREKLEKELDTIRNM.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	4.1793	0.3222	2303.57	2303.687	1	1052.9	55.555557 G.A1L1D1W2Y1P1I1F1K2N2A1L1K2P1V1F1Q2D1L1.Y
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	3	6.3486	0.4266	2788.88	2790.047	1	1548.2	41.6666664 L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T111R4N2M1.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	3	5.3748	0.2824	2756.9	2757.047	3	711.7	33.333336 LEFNSQPDYREKLEKELDTIRNM.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	3.3043	0.2584	2789.39	2790.047	1	223.7	33.333336 L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T111R4N2M1.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	3	4.3185	0.2872	2397.44	2395.651	1	970.8	38.88889 N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T111R4N2M1.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.7233	0.2073	2369.53	2366.651	1	635.5	55.555557 N.SQPDYREKLEKELDTIRNM.E

		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
ail6323387/rofIND_013450_1	VI P355C	chain amino acid biosynthesis, also required for maintenance of wild-type	2	3 0315	0 1821	2202 73	2205 651	1	640	55 555557 N \$102P1D1V1P4E1K2I 1E1K2E1I 1D1T111P4N2M1 E
gilo323367 [rei]NF_013439.1]	TER355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	3.9315	0.1021	2392.73	2393.031		040	55.555557 N.5TQ2FTDTTTR4ETR2ETETR2ETETDTTTTR4N2MT.E
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; IIv5p	2	3.4115	0.3112	1247.99	1248.397	1	892	80 F.S1H3G1F1S1P1V1F1K2D1L1.T
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	3.0447	0.3076	1773.95	1771.11	6	291.5	50 T.HVEPPKDLDVILVAPK.G
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
ail6323387/refINP_013459.11	VI R355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA: IIv5n	2	3 3014	0.2896	1327.83	1326 542	1	608.4	77 27273 L RDNGLNV/IIGVR K
giloszoco ireini _010403.1]	TEROSOO	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	-	0.0014	0.2000	1027.00	1020.042		000.4	
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	4.0892	0.3124	1553.05	1553.805	1	553.9	65.38461 L.NLRDNGLNVIIGVR.K
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	4.0599	0.1916	1576.53	1576.805	1	601.2	65.38461 L.N2L1R4D1N2G1L1N2V1I1I1G1V1R4.K
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
qi 6323387 ref NP 013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	5.5681	0.4716	2257.35	2257.585	1	1282.8	60.000004 L.T1H3V1E1P1P1K2D1L1D1V1I1L1V1A1P1K2G1S1G1R4.T
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
ail6222227/rofIND 012450 1	VI DOFFC	chain amino acid biosynthesis, also required for maintenance of wild-type	2	2 0740	0 1020	040.27	041 162	1	1422.1	
gilo323367 [rei]NF_013439.1]	TER355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	3.0749	0.1030	940.37	941.102		1433.1	87.5 N.GENVIIGVR.K
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; IIv5p	2	3.7619	0.2832	1364.37	1362.584	1	1390.4	85 K.LEKELDTIRNM.E
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	3	4.9956	0.3019	2303.27	2303.687	1	1064.7	44.444447 G.A1L1D1W2Y1P1I1F1K2N2A1L1K2P1V1F1Q2D1L1.Y
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
ail6323387/refINP_013459.11	YLR355C	mitochondrial DNA: Ilv5p	2	3.5059	0.2187	2756.63	2757.047	1	354.4	40.476192 L.EENSQPDYREKLEKELDTIRNM.E
910020001 [101] H _010 10011]	LINGOOD	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	-	0.0000	0.2101	2100.00	2.01.011		00111	
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ret NP_013459.1	YLR355C	Mitochondrial DINA; IIV5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	3.681	0.3181	2788.49	2790.047	1	231.3	35.714287 L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D11111R4N2M1.E
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; IIv5p	3	6.0797	0.3371	2790.23	2790.047	1	1802.6	44.04762 L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T111R4N2M1.E
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	4.5229	0.4567	1894.47	1893.215	1	837.1	65.625 L.T1H3V1E1P1P1K2D1L1D1V1I1L1V1A1P1K2.G
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; IIv5p	2	4.8854	0.4037	2014.89	2016.345	1	1195.5	63.88889 L.THVEPPKDLDVILVAPKGS.G
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
ail6323387/refINP_013459_1	YI R355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA: IIv5n	2	4 271	0 3385	1871 69	1872 215	1	972 3	68 75 L THVEPPKDLDVILVAPK G
gilos2000/ [rel[14] _010403.1]	TEROSOO	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	4.271	0.0000	107 1.05	1072.210		512.0	00.70 ETHVEFT REEDVIEWARKO
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ret NP_013459.1	YLR355C	MITOCNONDRIAL DINA; IIV5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	3.6334	0.172	2394.47	2395.651	1	571.3	55.555557 N.STQ2P1D1Y1R4E1K2L1E1K2E1L1D11111R4N2M1.E
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	3	4.1271	0.3421	2398.25	2395.651	1	1568.3	43.055553 N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T111R4N2M1.E
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	3	4.6146	0.4578	1872.53	1872.215	1	1262.1	46.875 L.THVEPPKDLDVILVAPK.G
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
gi 6323387 ref NP 013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	5.4879	0.409	2231.05	2229.585	1	1627.8	67.5 L.THVEPPKDLDVILVAPKGSGR.T
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
ail6323387/refINP_013459_1	YI R355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA: Ilv5n	1	2 7328	0 2649	1445 62	1446 646	1	350.9	
gilos2000/ [rel[14] _010403.1]	TEROSOO	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-		2.7020	0.2045	1440.02	1440.040		000.0	of house with online in
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ret NP_013459.1	YLR355C	Mitochondrial DINA; IIV5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	3.4716	0.2939	1446.33	1446.646	1	866.1	75 A.AIEDGWVPGKNLF. I
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; IIv5p	2	3.6256	0.2796	1463.89	1462.646	1	639.8	66.66667 A.A1I1E1D1G1W2V1P1G1K2N2L1F1.T
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	1	2.8829	0.2048	1267.55	1267.47	8	433.5	66.66667 G.ALDWYPIFKN.A
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
gi 6323387 ref NP 013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	3.7655	0.3744	1267.31	1267.47	1	1449.2	83.33333 G.ALDWYPIFKN.A
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
ail6323387/rofIND_013450_1	VI P355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA: Ily5p	2	3 3063	0 151	1282.05	1280 47	3	1175 /	77 77778 C A11 1D1/W2V1D111E1K2N2 A
gilos2000/ [rel[14] _010403.1]	TEROSOO	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	2	0.0000	0.101	1202.00	1200.47	0	1170.4	
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ret NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p Acetobydroxyacid reductoisomerase, mitochondrial protein involved in branched-	1	2.8313	0.2523	1361.51	1362.584	3	436	65 K.LEKELDTIRNM.E
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	3.3258	0.1956	1197.07	1194.416	1	1234.7	88.88889 N.ALKPVFQDLY.E
		chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	2	3.0872	0.2388	2510.71	2511.751	1	340	50 L.EFNSQPDYREKLEKELDTIR.N
		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p	3	4.632	0.408	2770.85	2773.047	1	1005.3	39.285713 L.EFNSQPDYREKLEKELDTIRNM@.E

		Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched- chain amino acid biosynthesis, also required for maintenance of wild-type								
gi 6323387 ref NP_013459.1	YLR355C	mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	3	5.0863	0.2338	2805.11	2806.047	1	2056.6	40.476192 L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T111R4N2M\$.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; IIv5p Acatebratemundit acidesiamanace, mitochondrial protein involved in bronchod	2	3.7058	0.3275	2756.03	2757.047	1	326.8	40.476192 L.EFNSQPDYREKLEKELDTIRNM.E
gi 6323387 ref NP_013459.1	YLR355C	Acetowinyotoxyadul reductosomerase, mitochonara potem involved in oranomer- chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-	3	5.4844	0.2584	2759.15	2757.047	1	1096.3	36.904762 L.EFNSQPDYREKLEKELDTIRNM.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acatebudenuoid to during process mitochondrial protein in wherd in branchod	2	4.2042	0.3435	2364.91	2366.651	1	728.5	58.333332 N.SQPDYREKLEKELDTIRNM.E
gi 6323387 ref NP_013459.1	YLR355C	Actionydioxyadul reductiosonieriase, mitochondra plotein involved in pranched chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p Acetholydroxyacid reductoisomerase mitochondrial protein involved in branched-	3	5.0797	0.4186	2478.65	2480.755	1	1916.2	42.105263 F.NSQPDYREKLEKELDTIRNM.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; INSp Acatholyticywardi reductrisomerase, mitochondrial protein involved in branched.	1	3.0202	0.3233	1233.65	1234.397	3	749	70 F.SHGFSPVFKDL.T
gi 6323387 ref NP_013459.1	YLR355C	Actionydioxyddd feduddiadontaac, mitochanan, procin mydrod in ordanado chain amino acid biosynthesis, also required for maintenance of wildtype mitochondrial DNA; llv5p Acetobutrouccid radiuchicomarces, mitochondrial protein involved in branchad.	1	3.3236	0.261	1247.48	1248.397	2	871.6	70 F.S1H3G1F1S1P1V1F1K2D1L1.T
gi 6323387 ref NP_013459.1	YLR355C	Activity of second seco	2	3.8571	0.214	2394.39	2395.651	1	736.5	58.333332 N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T111R4N2M1.E
gi 6323387 ref NP_013459.1	YLR355C	chain amino acid biosynthesis, also required for mainter provide the divergence of the second acid biosynthesis, also required for mainter provide the divergence of the second acid biosynthesis, also required for mainter and the second acid biosynthesis and the second acid biosynthesis acid biosynth	3	4.1548	0.1871	2395.55	2395.651	1	1099.1	38.88889 N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T111R4N2M1.E
gi 6323387 ref NP_013459.1	YLR355C	Activity of a scholar teaucidation and a scholar and a sch	3	3.8477	0.2289	2366.81	2366.651	1	1195.5	38.88889 N.SQPDYREKLEKELDTIRNM.E
gi 6323387 ref NP_013459.1	YLR355C	Actionly to system reduction interesting in the interesting in the interesting of the interesting in the int	2	2.9842	0.2091	2359.21	2356.725	3	314.6	33.333336 L.SDAAQSETWPAIKPLLTKGKTL.Y
gi 6323389 ref NP_013461.1	YLR357W	Che on to subulities on the Kenicoler the Structure of Childrane (KCC) complex, required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	3	4.7111	0.1766	2559.02	2556.893	1	1240.4	40.476192 T.DMDIDNPKDADFPDLIRKPLIN.I
gi 6323389 ref NP_013461.1	YLR357W	One of its subulities on the Kernober the Structure of Chromatian (KSC) complex, required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 16 culturation is the "Demodel" the Structure of Chromatia" (ASC) appendix:	2	3.9519	0.3428	2966.59	2966.303	1	632.3	37.5 N.L1K2E1K2Y1P1Q2L1V1Y1P1D1L1G1P1L1P1D1E1P1G1Y1E1E1F1.Q
gi 6323389 ref NP_013461.1	YLR357W	Chief of a subject to the restriction of the restriction of the complex, required for expression of mid-late sportilation-specific genes; involved in telomere maintenance; Rsc2p One of 16: eubunite of the reproduct the Structure of Chromatia' (RSC) complex;	2	4.0257	0.2989	2936.79	2938.303	1	991.6	45.833336 N.LKEKYPQLVYPDLGPLPDEPGYEEF.Q
gi 6323389 ref NP_013461.1	YLR357W	one of 16 address of net refinition and solutions or official solutions of the solution of	2	3.9167	0.3247	1649.99	1649.841	1	2083.5	80.769226 S.RYNIPTIIDDLTSQ.A
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex:	2	4.4729	0.2804	1668.99	1668.841	1	1348.2	69.230774 S.R4Y1N2I1P1T1I1I1D1D1L1T1S1Q2.A
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	2	3.6365	0.4237	1907.17	1907.149	1	688.4	55.555557 H.DRVPEPTMGSPDAPPLVGA.V
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	2	3.0589	0.3882	1929.49	1929.149	1	436.6	50 H.D1R4V1P1E1P1T1M1G1S1P1D1A1P1P1L1V1G1A1.V
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	2	4.0537	0.2684	2446.61	2446.54	1	851.7	50 K.DKDDDGLEPDVENEKESLPGPF.V
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	3	4.5953	0.2782	2585.57	2585.893	1	891.2	35.714287 T.D1M1D111D1N2P1K2D1A1D1F1P1D1L111R4K2P1L11N2.I
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	2	3.7811	0.3359	2555.71	2556.893	2	384.8	40.476192 T.DMDIDNPKDADFPDLIRKPLIN.I
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	3	5.1274	0.2767	4215.53	4216.391	1	543.3	22.222223 LEYEEVEETMEDVTGKDKDDDGLEPDVENEKESLPGPF.V
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	3	4.9931	0.3881	2966.57	2966.303	1	960	30.208334 N.L1K2E1K2Y1P1Q2L1V1Y1P1D1L1G1P1L1P1D1E1P1G1Y1E1E1F1.Q
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	3	5.3038	0.2963	2938.52	2938.303	1	1743.2	38.541664 N.LKEKYPQLVYPDLGPLPDEPGYEEF.Q
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	2	4.2956	0.3335	2938.39	2938.303	1	615.1	37.5 N.LKEKYPQLVYPDLGPLPDEPGYEEF.Q
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex;	3	4.3134	0.231	3434.48	3435.898	1	743.3	28.57143 N.LKEKYPQLVYPDLGPLPDEPGYEEFQQKL.R
gi 6323389 ref NP_013461.1	YLR357W	required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	3	4.3106	0.2007	2672.69	2673.007	1	1063.5	35.227272 W.KACLPEEIRDLDEATIPVNGRKF.F
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphinoglipid biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	1	2.9639	0.2908	1454.56	1454.623	1	455.7	58.333332 K.V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi 6323404 ref NP_013476.1	YLR372W	chain 20-25-carbon fatty acids from C18-CoA primers; involved in regulation of sphinogloipt biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	1	2.9483	0.2555	1440.53	1438.623	1	511.7	62.5 K.VHVPSIENPFGIE.L
gi 6323404 ref NP_013476.1	YLR372W	criain 20-20-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p	2	3.5491	0.3061	1439.91	1438.623	1	635	75 K.VHVPSIENPFGIE.L

		Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long								
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon tatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes year long	2	3.6658	0.3283	1453.79	1454.623	1	754.3	79.16667 K.V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p	2	3.7882	0.3543	2378.49	2377.595	1	239.6	38.88889 K.V1F1E1Y1F1S1G1Y1P1A1E1Q2F1E1F111H3N2K2.T
		Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of								
gi 6323404 ref NP_013476.1	YLR372W	sphingolipid biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	1	3.3691	0.2717	1566.64	1566.797	1	919.4	65.38461 L.KVHVPSIENPFGIE.L
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon tatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p Flongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	2	4.0967	0.3799	1586.65	1584.797	1	986.4	76.92308 L.K2V1H3V1P1S1I1E1N2P1F1G111E1.L
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p	1	3.8731	0.3317	1583.62	1584.797	1	924.9	65.38461 L.K2V1H3V1P1S1I1E1N2P1F1G1I1E1.L
		Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of								
gi 6323404 ret NP_013476.1	YLR372W	sphingolipid biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers: involved in regulation of	2	2.9393	0.1898	1698.65	1698.957	1	841	64.28571 F.L1K2V1H3V1P1S111E1N2P1F1G111E1.L
gi 6323404 ref NP_013476.1	YLR372W	sphingolipid biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	2	3.0485	0.2347	2334.91	2335.701	1	597.1	47.368423 K.V1H3V1P1S1I1E1N2P1F1G1I1E1L1W2P1I1F1S1K2.V
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p	2	3.8706	0.3891	1439.19	1438.623	1	619.3	75 K.VHVPSIENPFGIE.L
oil6323404/refINP_013476_1	YI R372W	Elongase, involved in ratty acid and spiningolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphinonlinid biosynthesis; Surdn	1	2 6237	0.336	1438 64	1438 623	1	416.5	
9100204041c1141_010410.11	TEROTEN	Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of		2.0201	0.000	1400.04	1400.020		410.5	
gi 6323404 ref NP_013476.1	YLR372W	sphingolipid biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	1	2.4897	0.2193	1453.71	1454.623	2	475.9	58.333332 K.V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon tatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p Flongase involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	2	3.7832	0.2925	1568.59	1566.797	1	909.6	76.92308 L.KVHVPSIENPFGIE.L
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon faity acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p	2	3.5937	0.4348	1677.97	1679.957	1	879.5	67.85714 F.LKVHVPSIENPFGIE.L
	V/ D070W/	Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of		0.4544	0.0447	1500.15	4500 707		005	
gi 6323404 ret NP_013476.1	YLR372W	sphingolipid biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-Secarbon fatty acids from C18-CoA primers: involved in regulation of	2	3.1544	0.2447	1569.15	1566.797	1	965	76.92308 L.KVHVPSIENPFGIE.L
gi 6323404 ref NP_013476.1	YLR372W	sphingolipid biosynthesis; Sur4p Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long	1	3.4195	0.3496	1583.49	1584.797	1	736.6	57.692307 L.K2V1H3V1P1S111E1N2P1F1G111E1.L
gi 6323404 ref NP_013476.1	YLR372W	chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p	1	3.2788	0.2713	1566.72	1566.797	1	763	57.692307 L.KVHVPSIENPFGIE.L
oil6323404/refINP_013476.1	YI R372W	Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Surdo	2	3 7826	0 4055	1587 39	1584 797	1	832.4	76 92308 K2V1H3V1P1S1I1E1N2P1E1G111E1
		Essential subunit of Sec61 complex (Sec61p, Sbh1p, and Sss1p); forms a channel for SRP-dependent protein import and retrograde transport of misfolded proteins out								
gi 6323411 ref NP_013482.1	YLR378C	of the ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61 p	2	3.3718	0.2379	1881.71	1882.213	1	591.4	56.666668 L.PEVIAPERKVPYNQKL.I
		for SRP-dependent protein import and retrograde transport of misfolded proteins out of the ER; with Sec63 complex allows SRP-independent protein import into ER;								
gi 6323411 ref NP_013482.1	YLR378C	Sec61p Essential subunit of Sec61 complex (Sec61p, Sbh1p, and Sss1p); forms a channel	2	4.0589	0.3613	1905.81	1905.213	3	529.5	53.333336 L.P1E1V11A1P1E1R4K2V1P1Y1N2Q2K2L1.I
ail62024441rofIND_04249241	VI B279C	for SRP-dependent protein import and retrograde transport of misfolded proteins out of the ER; with Sec63 complex allows SRP-independent protein import into ER;	2	4 2706	0 2025	0005 74	2295 742	1	640 7	
91032341111e11NF_013462.11	TERSTOC	Essential subunit of Sec61 complex (Sec61p, Sbh1p, and Sss1p); forms a channel for SRP-dependent protein import and retrograde transport of misfolded proteins out	2	4.3790	0.3925	2303.71	2363.743	I	042.7	30 F.E.ISTFTETFTETVTTATFTETR4K2VTFTTTIK2Q2A2EL1
gi 6323411 ref NP_013482.1	YLR378C	of the ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	2	3.5056	0.2632	1073.85	1074.356	1	1107.1	93.75 Q.I1G1I1Y1P1I1K2L1F1.Y
		Essential subunit of Secon complex (Seconp, Sonip, and Sssip); forms a channel for SRP-dependent protein import and retrograde transport of misfolded proteins out of the ER with Sec63 complex allows SRP-independent protein import into ER:								
gi 6323411 ref NP_013482.1	YLR378C	Sec61p Essential subunit of Sec61 complex (Sec61p, Sbh1p, and Sss1p); forms a channel	2	3.0675	0.298	1063.93	1064.356	1	1209.2	93.75 Q.IGIYPIKLF.Y
ail62024441rofIND_04249241	VI DOZOC	for SRP-dependent protein import and retrograde transport of misfolded proteins out of the ER; with Sec63 complex allows SRP-independent protein import into ER;	2	2 9054	0 2077	2244.02	2245 592	1	455.2	
91032341111e11NF_013462.11	TERS/6C	Essential subunit of Sec61 complex (Sec61p, Sbh1p, and Sss1p); forms a channel for SRP-dependent protein import and retrograde transport of misfolded proteins out	2	3.0904	0.3077	2244.93	2243.363	I	400.5	41.22222 F.ESFLFEVIAFERRYFINGR.L
gi 6323411 ref NP_013482.1	YLR378C	of the ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	2	4.6942	0.3897	2271.37	2271.583	1	736.2	52.77778 F.E1S1F1L1P1E1V1I1A1P1E1R4K2V1P1Y1N2Q2K2.L
		Essential subunit of Sec61 complex (Sec61p, Sbh1p, and Sss1p); forms a channel for SRP-dependent protein import and retrograde transport of misfolded proteins out of the Ex with Sec63 complex allows SRP-independent protein import into EP.								
gi 6323411 ref NP_013482.1	YLR378C	Sec61p Shosphatidylinositol transfer protein with a potential role in lipid turnover; interacts	2	3.5355	0.3784	2357.39	2358.743	1	377.3	39.473686 F.ESFLPEVIAPERKVPYNQKL.I
gi 6323412 ref NP_013484.1	YLR380W	specifically with thioredoxin peroxidase (Tsa2p) and may have a role in oxidative stress resistance; Csr1p	2	3.5475	0.3137	1925.45	1924.123	1	682.7	63.333332 T.AQWIEHQPLNDPAYIQ.L
gi 6323412 ref NP 013484.11	YLR380W	specifically with thioredoxin peroxidase (Tsa2p) and may have a role in oxidative stress resistance; (Sr1p	3	3.8743	0.2633	3109.25	3110.246	1	693.4	28.846153 Q.Y111P1R4Y1L1G1G1E1N2D1N2D1L1D1H3Y1T1P1P1D1G1S1L1D1V1H3.L
		Phosphatidylinositol transfer protein with a potential role in lipid turnover; interacts specifically with thioredoxin peroxidase (Tsa2p) and may have a role in oxidative	-					-		· · · · · · · · · · · · · · · · · · ·
gi 6323412 ref NP_013484.1	YLR380W	stress resistance; Csr1p Phosphatidylinositol transfer protein with a potential role in lipid turnover; interacts specifically with thipropring pergvidese (Tea?s) and may have a role in ordering	2	3.0802	0.2545	1655.35	1655.983	8	324.6	54.166668 A.PWIFNPIWNIIKN.W
gi 6323412 ref NP_013484.1	YLR380W	specificary with thioreduxin peroxidase (15a2p) and may have a role in oxidative stress resistance; Csr1p	2	3.4127	0.1802	1614.55	1612.958	1	985.8	70.83333 K.APWIFNPIWNIIK.N

gi 6323412 ref NP_013484.1	YLR380W	Phosphatidylinositol transfer protein with a potential role in lipid turnover; interacts specifically with thioredoxin peroxidase (Tsa2p) and may have a role in oxidative stress resistance; Csr1p	2	2.939	0.3215	1273.73	1272.535	1	884.6	88.88889 H.KAPWIFNPIW.N
ail62224121cafIND_012494.11		Phosphatidylinositol transfer protein with a potential role in lipid turnover; interacts specifically with thioredoxin peroxidase (Tsa2p) and may have a role in oxidative drage registrance: (crtip)	2	2 0 2 8	0 2172	1046 52	1047 122	1	650.2	
gilo323412[rei]i4r_013404.1]	TERSOOW	Phosphatidylinositol transfer protein with a potential role in lipid turnover; interacts	2	3.320	0.5172	1940.00	1947.125		030.5	30.000000 1.A.QZWZITE II JQZF TE II ZDTF TATT TT QZ.E
gi 6323412 ref NP_013484.1	YLR380W	specifically with thioredoxin peroxidase (1sa2p) and may have a role in oxidative stress resistance; Csr1p Phosphatidylinositol transfer protein with a potential role in lipid turnover; interacts	2	3.02	0.181	1550.23	1549.721	1	830.9	77.27273 M.IEKEREELVEQF.L
gi 6323412 ref NP_013484.1	YLR380W	specifically with thioredoxin peroxidase (Tsa2p) and may have a role in oxidative stress resistance; Csr1p	2	3.0852	0.1853	1258.45	1258.549	3	1136.7	83.3333 W.IFNPIWNIK.N
gi 42742289 ref NP_013493.2	YLR389C	Metalloprotease involved, with homolog Ax11p, in N-terminal processing of pro-a- factor to the mature form; member of the insulin-degrading enzyme family; Ste23p	2	3.177	0.3618	2138.51	2139.459	1	361	36.842106 M.KSPGLNPALTLPRPNEFVST.N
gi 42742289 ref NP_013493.2	YLR389C	Metalloprotease involved, with homolog Ax11p, in N-terminal processing of pro-a- factor to the mature form; member of the insulin-degrading enzyme family; Ste23p	2	3.6136	0.3282	2064.69	2065.351	1	837.9	56.25 F.TVPDMEEHWESKPPRIL.S
gi 42742289 ref NP_013493.2	YLR389C	Metalloprotease involved, with homolog Ax11p, in N-terminal processing of pro-a- factor to the mature form; member of the insulin-degrading enzyme family; Ste23p	2	3.0081	0.1619	1526.47	1526.745	4	433.1	63.636364 N.S1F1E1P1K2K2D1R4F1E1I1L1.K
gi 42742289 ref NP_013493.2	YLR389C	Metalloprotease involved, with homolog Ax11p, in N-terminal processing of pro-a- factor to the mature form; member of the insulin-degrading enzyme family; Ste23p	2	4.2496	0.3735	2212.31	2212.528	1	867.7	55.88235 S.FTVPDMEEHWESKPPRIL.S
gi 42742289 ref NP_013493.2	YLR389C	Metalloprotease involved, with homolog Ax11p, in N-terminal processing of pro-a- factor to the mature form; member of the insulin-degrading enzyme family; Ste23p	2	4.4964	0.4899	2236.13	2237.528	1	866.6	50 S.F1T1V1P1D1M1E1E1H3W2E1S1K2P1P1R4I1L1.S
gi 42742289 ref NP_013493.2	YLR389C	Metalloprotease involved, with homolog Ax11p, in N-terminal processing of pro-a- factor to the mature form; member of the insulin-degrading enzyme family; Ste23p ATPase of the CDC4RPAS1/SFC18 (AAA) tamik forms a hexameric complex; may	2	3.3212	0.2842	1565.29	1566.886	1	708.8	62.5 T.L1F1V1A1P1V1R4Q2P1M1K2D1F1.E
gi 6323429 ref NP_013501.1	YLR397C	be involved in degradation of aberrant mRNAs; Afg2p	1	3.0127	0.334	1593.67	1594.894	1	538.6	57.692307 L.KSAIEIPLHQPTLF.S
gi 6323429 ref NP_013501.1	YLR397C	be involved in degradation of aberrant mRNAs; Afg2p	2	3.54	0.3675	1610.49	1612.894	1	801.7	65.38461 L.K2S1A1I1E1I1P1L1H3Q2P1T1L1F1.S
gi 6323429 ref NP_013501.1	YLR397C	ATPase of the CDC48/PAS1/SEC18 (AAA) family, forms a hexameric complex; may be involved in degradation of aberrant mRNAs; Afg2p	2	3.0191	0.2585	1595.11	1594.894	1	949.9	65.38461 L.KSAIEIPLHQPTLF.S
gi 6323429 ref NP_013501.1	YLR397C	ATPase of the CDC48/PAS1/SEC18 (AAA) family, forms a hexameric complex; may be involved in degradation of aberrant mRNAs; Afg2p	2	3.0446	0.2459	1646.15	1645	1	718.8	70.83333 S.A1M1R4E1I1F1L1E1M1P1K2V1Y1.W
gi 6323442 ref NP_013514.1	YLR410W	Protein of unknown function probably involved in the function of the cortical actin cytoskeleton; putative ortholog of S. pombe asp1+; Vip1p	3	3.891	0.3846	2688.47	2685.911	3	350.9	25 L.H3N2R4Q2F1L1E1N2l1F1D1P1G1L1P1N2E1A1I1A1D1E1L1.G
gi 6323442 ref NP_013514.1	YLR410W	Protein of unknown function probably involved in the function of the cortical actin cytoskeleton; putative ortholog of S. pombe asp1+; Vip1p	3	3.8591	0.2197	2654.84	2653.911	1	510.6	28.40909 L.HNRQFLENIFDPGLPNEAIADEL.G
ail6323442/refINP 013514.1	YLR410W	Protein of unknown function probably involved in the function of the cortical actin cvtoskeleton; putative ortholog of S, pombe asp1+; Vip1p	2	4.0266	0.3363	1734.77	1734.933	1	320.7	60.714287 L.L1R4E1G1K2E1A1P1P1Q2F1A1W2P1S1.K
gil6323442lrefINP_013514_1	YI R410W	Protein of unknown function probably involved in the function of the cortical actin	2	3 4592	0.3902	1715 71	1713 933	1	716.9	64 285711 L REGKEAPPOFAWPS K
gil6323445/rofINP_013517_1	VI P413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periobent XIr41awn	-	3 3803	0.315	1/30 77	1438 707		285.2	
gil6323445[ref]NP_013517.1]	VLP412W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	2	3.3033	0.313	1439.77	1430.707	- 1	440.6	
	TER413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	2	3.332	0.2762	1440.39	1436.707		449.0	
gi 6323445 ret NP_013517.1	YLR413W	to the cell periphery; YIr413wp Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	2	3.3359	0.3651	1780.47	1780.932	1	427.2	53.5/1426 S.RIIEEHESPIDAEKN.F
gi 6323445 ref NP_013517.1	YLR413W	to the cell periphery; YIr413wp Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	2	3.5733	0.284	2698.21	2699.94	1	233.3	34.090908 L.N2I1G1K2D1D1L1H3L1D1G1E1L1Q2D1R4Q2H3M1Y1V1P1A1.V
gi 6323445 ref NP_013517.1	YLR413W	to the cell periphery; YIr413wp Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes	2	3.7881	0.3927	2664.11	2665.94	1	520.4	45.454548 L.NIGKDDLHLDGELQDRQHMYVPA.V
gi 6323445 ref NP_013517.1	YLR413W	to the cell periphery; YIr413wp Protein of unknown function; green fluorescent protein (GEP)-fusion protein localizes	2	3.0873	0.36	1438.35	1438.707	1	443	72.72727 E.EKTKLSPVFELF.A
gi 6323445 ref NP_013517.1	YLR413W	to the cell periphery; YIr413wp Protein drugscour functions group functionation (CER) function protein localized	1	3.7358	0.2998	1452.7	1452.707	1	317.1	68.181816 E.E1K2T1K2L1S1P1V1F1E1L1F1.A
gi 6323445 ref NP_013517.1	YLR413W	to the cell periphery; YIr413wp	1	2.967	0.2054	1440.01	1438.707	1	230.4	59.090908 E.EKTKLSPVFELF.A
gi 6323445 ref NP_013517.1	YLR413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; YIr413wp	1	2.9611	0.2945	1437.68	1438.707	1	331	68.181816 E.EKTKLSPVFELF.A
gi 6323445 ref NP_013517.1	YLR413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; Ylr413wp	2	2.9698	0.1951	1441.45	1438.707	1	396.2	72.72727 E.EKTKLSPVFELF.A
gi 6323453 ref NP_013525.1 ai 6323453 ref NP_013525.1	YLR421C YLR421C	Subunit of the 19S regulatory particle of the 26S proteasome lid; Rpn13p Subunit of the 19S regulatory particle of the 26S proteasome lid; Rpn13p	3	4.2784 5.3685	0.2715 0.4354	2733.41 4025	2732.944 4026.272	1	615.1 859.1	29.545454 C.E1Y1NZE1D151R4L1C1T1P1I1P1V1Q2C1E1I1E11IKZP1N2.E C.E1Y1NZE1D151R4L1C1T1P1I1P1V1Q2G1E1I1E1I1KZP1N2E1E1E1E1L1G1F1W 27.34375 2D1F1.E
gi 6323453 ref NP_013525.1	YLR421C	Subunit of the 19S regulatory particle of the 26S proteasome lid; Rpn13p	3	5.3582	0.3669	3985.07	3985.272	1	855.2	25 C.EYNEDSRLCTPIPVQGEIEIKPNEEEELGFWDF.E
gi 6323453 ref NP_013525.1 gi 6323453 ref NP_013525.1	YLR421C YLR421C	Subunit of the 19S regulatory particle of the 26S proteasome lid; Rph13p Subunit of the 19S regulatory particle of the 26S proteasome lid; Rph13p	2	3.7928	0.2768	1770.15	1770.905	6	482.6	50 E.IIK2P1N2E1E1E1E1L1G1F1W2D1F1.E
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	3.0303	0.3127	1704.27	1701.914	1	655.1	57.14286 H.VDEDGEPIDIKPVKF.L
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Cm1p	2	4.2349	0.4636	1951.73	1954.144	1	1791.3	68.75 H.DHVDEDGEPIDIKPVKF.L
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	3	4.8448	0.3612	3541.91	3542.745	2	318.7	22.580645 A.EDPSRDTSGWEEADDEPAPIKIETPVTPTETK.K
ail6323460/refINP 013533.11	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Crn1p	2	3.5907	0.3651	2103.73	2103.447	1	499.6	47.22222 F.A1V111P111E1E1V1G1K2A1P1D1Q2V1P1L1F1R4.G
gil6323460/refINP_013533.1	YI R429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Cm1n	2	4 8361	0.3606	2081 33	2079 447	1	1069	58 333332 E AVIPIEEVGKAPDOVPI ER G
gil6323460/refIND_013533_1	VI R420W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity. Cm1p	2	4 8730	0.4074	2526 51	2527 921	, 1	107 9	40 L E1E1K2K2E102P1K2V/1E1K2P1/194E194E142E1V/4K2 O
9100204001010110F_010003.1	11142311	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.0738	0.4074	2020.01	2027.021		131.0	
gijo323460[ret[NP_013533.1]	YLK429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.4423	0.3773	2628.71	2627.952	1	390	47.01900 L.EEKKEUPKVEKPISESEKEVKU.E A.TIDIR4K202E102S1L1P102E1E1K2S1S1E1K2T1K2S1P1E102E1K2S1A1T1P1
gij6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	5.3018	0.3776	3964.16	3965.218	1	564.9	26.470589 P1S1S111T1.A
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.477	0.2263	2912.95	2914.28	1	252.6	37.5 Q.ETALEEKKEQPKVEKPISESEKEVK.Q
ail6323460/refINP 013533.11	YLR429W	complex to regulate its activity: Cm1p	3	4.7362	0.3281	3143.72	3144.391	1	669.8	28.846153 F.F1V1P1R4R4S1E1E1F1Q2E1D1I1Y1P1D1A1P1S1N2K2P1A1L1T1A1E1.E

		Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p								
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.0665	0.3054	3107.67	3108.391	1	437.8	36.53846 F.FVPRRSEEFQEDIYPDAPSNKPALTAE.E
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	3	3.9588	0.215	2103.29	2103.429	1	1373	45.833336 V.IPIEEVGKAPDQVPLFRGH.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	3	4.303	0.2268	2129.09	2129.429	1	1182.7	44.444447 V.I1P111E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	3	4.5836	0.1841	2013.89	2015.269	1	1583.1	50 I.P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.T
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	3.2902	0.282	1425.05	1422.63	1	1424.3	79.16667 V.GKAPDQVPLFRGH.T
ail6323460/refINP 013533.11	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Crn1p	2	5.5688	0.4281	2274.57	2273.64	1	1419.8	60.000004 F.AVIPIEEVGKAPDQVPLFRGH.T
gil6323460/refINP_013533.1	VI R429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity. Crn1p	3	6 2348	0.4031	3949 76	3949 445	1	1000 7	
210020400101111_010000.1	121(425W	Coronin, cortical actin cycloskeletal component that associates with the Arp2p/Arp3p	0	0.2040	0.4001	0000 54	0004.005		1000.7	
gilb323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	3.968	0.3794	2090.51	2091.285	2	494.8	50 Y.KFHDHVDEDGEPIDIKPV.K
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.1514	0.2967	2694.65	2693.932	1	709.6	45.454548 F.FVPRRSEEFQEDIYPDAPSNKPA.L
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cvtoskeletal component that associates with the Arp2o/Arp3p	3	4.3072	0.1515	2908.55	2908.197	1	746.5	32.291664 F.FVPRRSEEFQEDIYPDAPSNKPALT.A
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p Coronin, cortical actin cytoskeletal component that associates with the Am2n/Am3n	2	4.4044	0.2268	2943.61	2942.197	1	486	37.5 F.F1V1P1R4R4S1E1E1F1Q2E1D111Y1P1D1A1P1S1N2K2P1A1L1T1.A
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	2	3.7651	0.1667	2910.69	2908.197	1	508	37.5 F.FVPRRSEEFQEDIYPDAPSNKPALT.A
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	2	4.1983	0.2866	3011.99	3014.276	1	547.2	40 F.F1V1P1R4R4S1E1E1F1Q2E1D1I1Y1P1D1A1P1S1N2K2P1A1L1T1A1.E
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	3.9317	0.3494	2838.97	2840.092	1	289.7	34.782608 F.F1V1P1R4R4S1E1E1F1Q2E1D1I1Y1P1D1A1P1S1N2K2P1A1L1.T
gi 6323460 ref NP 013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	5.8941	0.52	2302.53	2301.64	1	1333.2	55 F.A1V111P111E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.T
gil6323460/refINP_013533.1	YI R429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	3 6892	0.3718	2104.03	2103 429	1	564	
gil6323460/rofINP_013533.1	VI P420W/	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4 257	0.4052	1779 73	1770 003	1	1088.2	
gilo323400 rei r4r_013333.1	121042300	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.237	0.4032	1110.15	1119.995		1000.2	
gij6323460 ret NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	5.7241	0.3159	1989.02	1990.269	1	1894.6	52.9411/7 I.PIEEVGKAPDQVPLFRGH. I
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	5.9677	0.4496	3534.71	3534.986	1	819.9	26.666668 L.EEKKEQPKVEKPISESEKEVKQEAPKSPSPL.K
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.35	0.4044	1990.83	1990.269	1	1752.1	67.64706 I.PIEEVGKAPDQVPLFRGH.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.1793	0.3614	2012.59	2015.269	1	523.1	58.823532 I.P111E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	2	3.6648	0.1757	2420.99	2420.817	1	880.9	45.238094 A.FAVIPIEEVGKAPDQVPLFRGH.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p	2	5.3382	0.4549	2392.53	2393.635	1	1280.1	60.526318 Y.K2F1H3D1H3V1D1E1D1G1E1P1I1D1I1K2P1V1K2F1.L
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	3.346	0.2984	2436.03	2436.811	1	336.7	47.5 T.ETKKDRTPKVEPSKELKPEPV.S
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	3	4.8706	0.2552	2740.7	2740.128	1	468.9	28.260868 T.E1T1K2K2D1R4T1P1K2V1E1P1S1K2E1L1K2P1E1P1V1S1I1A1.T
gi 6323460 ref NP 013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	4.2601	0.2913	2706.97	2708.128	1	557.7	52.173912 T.ETKKDRTPKVEPSKELKPEPVSIA.T
ail6323460/refINP 013533.11	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Crn1p	2	4.4241	0.4024	2739.77	2740.128	1	284.2	45.652176 T.E1T1K2K2D1R4T1P1K2V1E1P1S1K2E1L1K2P1E1P1V1S1I1A1.T
gil6323460/refINP_013533.1	YI R429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Cm1p	2	4 5916	0 2876	2349.65	2349 733	1	774 7	52 499996 K KDRTPKVEPSKELKPEPVSIA T
gil6323460/rofIND_013533.1	VI R420W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	-	4.0160	0.2146	2010.00	2010.100		E92.6	
gijo323460jreijivr_013535.1j	11.142900	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.9109	0.3140	2377.13	2311.133	'	562.0	
gi 6323460 ret NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	3.6564	0.3044	2105.31	2106.47	3	433.4	47.22222 D.RTPKVEPSKELKPEPVSIA.1
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	3.6411	0.3789	2582.35	2580.9	1	545.8	45.238094 Y.KFHDHVDEDGEPIDIKPVKFLT.G
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	6.5359	0.4151	2507.84	2507.795	1	2459	45 Y.K2F1H3D1H3V1D1E1D1G1E1P1I1D1I1K2P1V1K2F1L1.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p Coronin, cortical actin cytoskeletal component that associates with the Am2n/Am3n	2	5.1781	0.3992	2481.81	2479.795	1	991.9	52.499996 Y.KFHDHVDEDGEPIDIKPVKFL.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	3	4.3901	0.3864	2068.43	2067.303	1	1290.2	44.11765 H.DHVDEDGEPIDIKPVKFL.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	2	3.0638	0.2132	2068.13	2067.303	1	306.3	44.11765 H.DHVDEDGEPIDIKPVKFL.T
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	3	5.8015	0.3658	2913.2	2914.28	1	1090.5	33.333336 Q.ETALEEKKEQPKVEKPISESEKEVK.Q
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	2.9463	0.2077	1360.37	1357.593	7	573.6	75 A.NLDKDERLLKL.E
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	4.4808	0.3317	2500.51	2499.821	1	318.8	47.5 L.EEKKEQPKVEKPISESEKEVK.Q
gil6323460/refINP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Crn1p	2	3.2168	0.406	1736.83	1737.91	1	1042.5	73.333336 W NIREEKIVSEGPAHTG A
gil6323460/rofINB_013533_1	VI P420W/	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4 3608	0.2603	211/ 27	2115 285	1	862.2	55 98225 V K251H2D1H2V/ID151D1/C151D1/I1K2D1//1 K
sil0223400/ref[NP_013533.1]	VL D 420W	Complex to regulate its activity, Cm1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.0050	0.2003	2007.74	2113.203	,	002.2	
gij6323460/rei/iNP_013533.1	1LR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	4.247	0.2467	2907.74	2908.197	1	647.3	
gijo323460jretjNP_013533.1	1LR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	3.6586	0.1741	2908.47	2908.197	3	300.6	
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	4.0005	0.4264	2270.66	2273.64	1	803.8	41.25 F.AVIPIEEVGKAPDQVPLFRGH.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	4.7906	0.2806	2942.27	2942.197	1	598.2	28.125 F.F1V1P1R4R4S1E1E1F1Q2E1D111Y1P1D1A1P1S1N2K2P1A1L1T1.A
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Aro2n/Aro3n	3	3.8933	0.1729	2980.7	2979.276	1	837.8	30.000002 F.FVPRRSEEFQEDIYPDAPSNKPALTA.E
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p	2	3.9494	0.3052	2981.19	2979.276	1	438.1	36 F.FVPRRSEEFQEDIYPDAPSNKPALTA.E

gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	3.2159	0.2413	2806.03	2807.092	3	103.4	30.434782 F.FVPRRSEEFQEDIYPDAPSNKPAL.T
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	4.7938	0.4252	2365.95	2366.635	1	1341.8	60.526318 Y.KFHDHVDEDGEPIDIKPVKF.L
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	3	5.6446	0.4869	2363.9	2366.635	1	1872.3	46.05263 Y.KFHDHVDEDGEPIDIKPVKF.L
gi 6323460 ref NP 013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	3	6.0778	0.4291	3661.58	3663.16	1	936.6	27.419355 L.EEKKEQPKVEKPISESEKEVKQEAPKSPSPLK.S
gil6323460lrefINP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Crn1p	3	4.9724	0.3958	3820.22	3821.317	1	622.4	25.757576 LEEKKEQPKVEKPISESEKEVKOEAPKSPSPLKSA S
gil6323460/rofINP_013533.1	VI P420W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	5 6072	0.4541	3147.08	31/9 591	1	010.3	
gilo323400 rel NF_013535.1	11.42900	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	5.0072	0.4541	3147.90	3140.301		910.3	
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	5.3324	0.2596	2481.02	2479.795	1	755	35 Y.KFHDHVDEDGEPIDIKPVKFL.I
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	4.8756	0.2776	2709.59	2708.128	4	437.2	29.347824 T.ETKKDRTPKVEPSKELKPEPVSIA.T
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p Coronin, cortical actin cytoskeletal component that associates with the Am2n/Am3n	2	3.8104	0.2837	1774.85	1776.083	1	622.8	56.25 F.AVIPIEEVGKAPDQVPL.F
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	3	4.2065	0.2308	2626.58	2627.952	1	696.8	34.523808 L.EEKKEQPKVEKPISESEKEVKQ.E
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p	2	2.9572	0.2787	2626.59	2627.952	1	186.9	35.714287 L.EEKKEQPKVEKPISESEKEVKQ.E
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	3	5.3143	0.3977	2758.43	2757.067	3	559.9	31.818182 L.EEKKEQPKVEKPISESEKEVKQE.A
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	2.988	0.265	2032.59	2031.368	1	356	41.17647 A.V111P111E1E1V1G1K2A1P1D1Q2V1P1L1F1R4.G
gil6323460lrefINP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Crn1p	3	4.687	0.359	2276.42	2273.64	1	806.1	41.25 F.AVIPIEEVGKAPDQVPI FRGH.T
gil6222460/rofIND_012522.1	VI P420W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4 7256	0.4254	2209 74	2201 64	1	720.7	
gilo323400 rel NF_013535.1	11.42900	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	4.7250	0.4354	2290.71	2301.04		120.1	
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	5.5369	0.5164	2301.29	2301.64	1	1344.8	55 F.A1V111P111E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.T I.A1V1N2W2N2A1S1G1G1G1A1F1A1V111P111E1E1V1G1K2A1P1D1Q2V1P1L1F1F
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	3	3.9415	0.2885	3451.43	3448.841	2	429.8	17.96875 4G1H3.T L.E1E1K2K2E1Q2P1K2V1E1K2P1I1S1E1S1E1K2E1V1K2Q2E1A1P1K2S1P1S1P1L
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p Coronin, cortical actin cytoskeletal component that associates with the Am2n/Am3n	3	6.0876	0.4549	3572.81	3574.986	1	804.2	28.333334 1.K
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Cm1p	3	4.3002	0.3414	3016.43	3014.276	1	558.6	26 F.F1V1P1R4R4S1E1E1F1Q2E1D1I1Y1P1D1A1P1S1N2K2P1A1L1T1A1.E
gi 6323460 ref NP_013533.1	YLR429W	complex to regulate its activity; Crn1p	3	4.1164	0.3004	2806.25	2807.092	1	761.2	32.608696 F.FVPRRSEEFQEDIYPDAPSNKPAL.T
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	5.3546	0.5277	2229.41	2229.561	1	1195.4	57.894737 A.V111P111E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.T
gi 6323460 ref NP_013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	2	4.7273	0.4509	2200.87	2202.561	1	1139.2	57.894737 A.VIPIEEVGKAPDQVPLFRGH.T
ail6323460/refINP 013533.1	YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity: Crn1p	2	5.3626	0.4649	2272.65	2273.64	1	1568.4	60.000004 F.AVIPIEEVGKAPDQVPLFRGH.T
gil6323460/refINP_013533.1	VI R429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity. Cro1p	2	4 7625	0 4447	2478 55	2479 795	1	823	
sil0223400 ref NP_012523.1	VL D 400W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p	2	4.0004	0.0074	2470.00	2470.705		202.0	
gi 6323460 ref NP_013533.1	YLR429W	Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase	3	4.0094	0.2274	2480.12	2479.795	9	392.9	28.75 Y.KFHDHVDEDGEPIDIKPVKFL.I
		(V-ATPase), an electrogenic proton pump found in the endomembrane system; stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane;								
gi 6323480 ref NP_013552.1	YLR447C	Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase	2	4.5867	0.4008	1773.71	1772.99	1	784.7	70 S.D111D1P1D1L1K2S1D1L1L1P1N2I1G1K2.L
		(V-ATPase), an electrogenic proton pump found in the endomembrane system; stabilizes VQ subunits; required for V1 domain assembly on the vacualar membrane;								
gi 6323480 ref NP_013552.1	YLR447C	Vma6p Subjuit D of the five subjuit V/0 integral membrane demain of vegueler H L ATRese	2	3.4591	0.2121	1948.13	1949.147	2	431.4	47.058823 Q.S1S1D111D1P1D1L1K2S1D1L1L1P1N2I1G1K2.L
		(V-ATPase), an electrogenic proton pump found in the endomembrane system;								
gi 6323480 ref NP_013552.1	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p	2	4.1856	0.3252	2241.65	2240.602	1	481.1	52.63158 S.DIDPDLKSDLLPNIGKLYPL.A
		Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system;								
ail63234801refINP_013552.11	VI R447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane;	2	4 5247	0 3089	1754 49	1752 946	1	481	73 07692 & E1E1I 1D1D1M1N2I1E1I1I1R4N2K2 I
giloozo400101141 _010002.11	TEI(4470	Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase	2	4.0247	0.0000	1704.45	1102.040		401	
		stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane;								
gi 6323480 ref NP_013552.1	YLR447C	Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase	1	2.2306	0.1502	1310.68	1310.449	2	400.4	66.66667 Y.KAYLEDFYNF.V
		(V-ATPase), an electrogenic proton pump found in the endomembrane system; stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane;								
gi 6323480 ref NP_013552.1	YLR447C	Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase	2	4.7855	0.3582	2439.53	2439.758	1	451.5	45.238094 Q.S1S1D111D1P1D1L1K2S1D1L1L1P1N2I1G1K2L1Y1P1L1.A
		(V-ATPase), an electrogenic proton pump found in the endomembrane system;								
gi 6323480 ref NP_013552.1	YLR447C	Vma6p	2	3.9169	0.3029	2417.67	2414.758	1	478.3	45.238094 Q.SSDIDPDLKSDLLPNIGKLYPL.A
		(V-ATPase), an electrogenic proton pump found in the endomembrane system;								
gi 6323480 ref NP_013552.1	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p	2	4.6652	0.4014	2328.73	2327.68	1	544.6	52.499996 S.SDIDPDLKSDLLPNIGKLYPL.A
		Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system:								
ail6323480/refINP_013552.11	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane;	2	4 0464	0 2432	2262 33	2263 602	1	396.6	47 368423 S D11D1P1D11 1K2S1D11 11 1P1N21G1K21 1V1P11 1 A
9-10020-00110114r_010002.1	1	Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase	2	0404	0.2402	2202.00	2200.002		000.0	
	V// D / / = 0	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane;	-			1015	1017	_	055 5	
gi 6323480 ref NP_013552.1	YLR447C	Vma6p	2	3.3276	0.337	1916.37	1917.265	5	353.9	46.875 D.P1D1L1K2S1D1L1L1P1N2I1G1K2L1Y1P1L1.A
ail6223480[rafIND_013552.1]	VI P447C	Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system; stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vms6v	1	2,652	0 2675	1195 5	1106 340	1	499	
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gilosza400fielfiar_013332.11	TEINHAI	Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system; tabilitize V0 subunits; varying for VL domain assembly on the vacuolar membrane;	1	2.052	0.2075	1193.5	1130.343		435	
gi 6323480 ref NP_013552.1	YLR447C	Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system;	1	3.2882	0.352	1353.64	1354.506	4	367.2	59.090908 T.GTIHDRDKGEIL.Q
gi 6323480 ref NP_013552.1	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+ATPase	1	2.7826	0.1783	1211.59	1212.349	1	502.7	66.66667 T.I1H3D1R4D1K2G1E1I1L1.Q
gi 6323480 ref NP_013552.1	YLR447C	(V-A1 Pase), an electrogenic proton pump round in the endomembrane system; stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p Subunit 0 of the fitue-subunit V0 intercal membrane domain of vacuolar H=+ATDase	2	3.7532	0.244	1732.47	1732.946	1	369	57.692307 A.EELDDMNIEIIRNK.L
ail63234801refINP 013552.11	YLR447C	Subdim b of une sound in your meganine from the endomembrane system; (V-ATPase), an electrogenic proton pump found in the endomembrane system; stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6o	2	3.7522	0.3673	1578.61	1579.706	1	637.2	70.83333 F.LETGNLEDHFYQL.E
31111111111111		Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system; stabilizes V0 subunits; required for V1 domain assembly on the vacuolar membrane;								
gi 6323480 ref NP_013552.1	YLR447C	Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system;	2	3.1568	0.284	1442.55	1443.726	5	346.6	58.333332 K.SDLLPNIGKLYPL.A
gi 6323480 ref NP_013552.1	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system;	2	3.7036	0.2614	1458.31	1458.726	2	359.6	62.5 K.S1D1L1L1P1N2I1G1K2L1Y1P1L1.A
gi 6323480 ref NP_013552.1	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system;	1	2.2274	0.2689	1442.55	1443.726	1	365.6	50 K.SDLLPNIGKLYPL.A
gi 6323480 ref NP_013552.1	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system;	1	2.3342	0.2526	1372.59	1372.506	4	293.8	54.545456 T.G1T111H3D1R4D1K2G1E1I1L1.Q
gi 6323480 ref NP_013552.1	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system;	1	2.3192	0.1707	1253.66	1254.56	2	376.7	65 D.L1L1P1N2I1G1K2L1Y1P1L1.A
gi 6323480 ref NP_013552.1	YLR447C	stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity	1	2.5827	0.2154	1241.77	1241.56	1	432.4	65 D.LLPNIGKLYPL.A
gi 6323482 ref NP_013554.1	YLR449W	to Prop. overproduction suppresses the growth defect resulting from the absence of E3 ubiquith-protein ligase Tom1p; ProP Nuclear protein, putative peptidy-prolyl cis-trans isomerase (PPIase) with similarity to Erroday overproducting expensioned the growth defect exception from the obsence of	2	3.2203	0.156	2011.37	2011.22	1	446.1	50 T.M1A1A1I1D1P1E1P1F1D1D1D1K2K2P1S1T1L1.R
gi 6323482 ref NP_013554.1	YLR449W	to rp1sp, overproduction suppresses and grown concernest resoning monitor absence of E3 ubiquith-protein ligase Tom1p; Fpr4p Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPlase) with similarity to For3p: overproduction suppresses the growth defect resultion from the absence of	2	2.9496	0.2798	1642.67	1643.88	1	803.4	66.66667 Y.GKQALPGIPANSELTF.D
gi 6323482 ref NP_013554.1	YLR449W	E3 ubiquitin-protein ligase Tom1p; Fpr4p Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of	2	3.8804	0.3464	1904.49	1905.205	1	1117.1	55.88235 K.LLEGGIIIEDRVTGKGPH.A
gi 6323482 ref NP_013554.1	YLR449W	E3 ubiquitin-protein ligase Tom1p; Fpr4p Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPlase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of	2	3.4264	0.3659	2671.73	2672.14	1	618.2	41.304348 Y.SLNVEPYSPTPALNFKIPVTIRIT.M
gi 6323482 ref NP_013554.1	YLR449W	E3 ubiquitin-protein ligase TomTp; Fpr4p Nuclear protein, putative peptidyl-protyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquity pertokin largest TomAps Exerct	1	2.2842	0.2425	1497.7	1498.768	3	100.2	46.153847 M.AVGGERRIVIPAPY.A
gil6323462[ref NP_013554.1]	YLR449W	E3 ubiquitry potenting as a form (j), primp Nuclear protein, putative peptidyl-prot() (c-trans isomerase (PPIase) with similarity to Ppr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitrip-rortein ligase Tom1p; Por4p	2	4.619	0.2456	1876.91	1878.139	1	527.4	55.88235 LEGGIIEDRVTGKGPHAK.K
gi 6323482 ref NP_013554.1	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPlase) with similarity to Fpr3p, overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	4.3616	0.3941	2102.81	2104.457	1	748.3	52.63158 K.LLEGGIIIEDRVTGKGPHAK.K
gi 6323482 ref NP_013554.1	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPlase) with similarity to Fpr3p: overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom fp: Fpr4p Nuclear entries, authors are onticid, and kids trans isomerane (PDIane) with similarity	2	3.3613	0.2972	1990.37	1991.22	1	605.1	55.88235 T.MAAIDPEPFDDDKKPSTL.R
gi 6323482 ref NP_013554.1	YLR449W	Nuclear protein, putative pepuly-provi castrals isofinetase (Fridae) with similarity to Fpr3p, overproduction suppresses the growth defact resulting from the absence of E3 ubiquitin-protein jutative peptidy-provid castrans isomerase (PPlase) with similarity	2	3.8128	0.2754	1729.49	1730.015	1	1180.2	75 E.KVKDSEESKPKPKTK.L
gi 6323482 ref NP_013554.1	YLR449W	to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Torn1p; Fpr4p Nuclear protein, putative peptidyl-protyl (cis-trans isomerase (PPlase) with similarity	2	3.9626	0.3553	1990.65	1991.298	1	664.8	52.77778 L.LEGGIIIEDRVTGKGPHAK.K
gi 6323482 ref NP_013554.1	YLR449W	to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquith-protein ligase Tom1p; Fpr4p Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity	2	4.3532	0.4252	1876.75	1878.139	1	622.5	58.823532 L.EGGIIIEDRVTGKGPHAK.K
gi 6323482 ref NP_013554.1	YLR449W	to rprop, overproduction suppresses the growth detect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPlase) with similarity to En3p; overproduction suppresses the growth defect resulting from the absence of	3	4.5996	0.4533	1877.48	1878.139	1	955.9	42.647057 L.EGGIIIEDRVTGKGPHAK.K
gi 6323482 ref NP_013554.1	YLR449W	E3 ubiquitin-protein ligase Tom1p; Fpr4p Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the	2	3.5076	0.2522	1903.53	1903.139	1	486.9	58.823532 L.E1G1G111111E1D1R4V1T1G1K2G1P1H3A1K2.K
gi 6323635 ref NP_013706.1	YML008C	ergosterol biosynthetic pathway by methylating position C-24; Erg6p Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the	2	3.1809	0.2139	1916.17	1917.023	1	426.1	57.14286 T.D1K2Y1D1E1N2N2P1E1H3R4K2I1A1Y1.E
gi 6323635 ref NP_013706.1	YML008C	ergosterol biosynthetic pathway by methylating position C-24; Erg6p Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the	2	3.4251	0.2238	1887.51	1888.969	4	226.5	57.14286 Y.L1R4N2W2D1G1R4T1D1K2D1A1E1E1R4.R
gi 6323635 ref NP_013706.1	YML008C	ergosterol biosynthetic pathway by methylating position C-24; Erg6p	2	3.5166	0.2113	1892.27	1893.023	1	832.9	60.714287 T.DKYDENNPEHRKIAY.E

gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	2	3.2915	0.3808	1856.43	1858.021	1	456.7	50 E.A1T1C1H3A1P1K2L1E1G1V1Y1S1E1I1Y1.K
gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	2	4.8432	0.4563	2199.55	2198.575	1	928.2	61.764706 K.KYNLSDQMDFVKGDFMKM.D
gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	2	4.4108	0.3071	1802.09	1800.934	1	1032.8	69.230774 D.K2Y1D1E1N2N2P1E1H3R4K2I1A1Y1.E
gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransterase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	2	3.1766	0.2073	1683.03	1683.837	1	384.2	61.538464 T.C1H3A1P1K2L1E1G1V1Y1S1E1I1Y1.K
gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransterase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	2	3.8369	0.3102	1775.47	1777.934	1	1204.7	73.07692 D.KYDENNPEHRKIAY.E
gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	1	2.9318	0.1709	958.56	958.166	1	497.8	75 Y.K2V1L1K2P1G1G1T1F1.A
gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	2	3.8866	0.3644	1993.37	1994.128	1	729.7	60.000004 M.TDKYDENNPEHRKIAY.E
gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransterase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	2	4.1987	0.3126	2017.47	2019.128	1	709.6	60.000004 M.T1D1K2Y1D1E1N2N2P1E1H3R4K2I1A1Y1.E
gi 6323635 ref NP_013706.1	YML008C	Delta(24)-sterol C-methyltransterase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	3	4.7625	0.3086	2891.42	2891.994	1	359.1	34.090908 Y.L1R4N2W2D1G1R4T1D1K2D1A1E1E1R4R4L1E1D1Y1N2E1A1.T
gi 6323635 ref NP_013706.1	YML008C	Delta[24]-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p Protein that forms a complex with Spt4p and mediates both activation and inhibition	1	2.7693	0.2001	947.58	947.166	1	500	75 Y.KVLKPGGTF.A
gi 6323632 ref NP_013703.1	YML010W	of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p Protein that forms a complex with Spt4p and mediates both activation and inhibition	3	4.4013	0.2826	2738.87	2738.03	1	692.5	34.375 L.R4K2I1F1E1P1G1D1H3V1T1V1I1N2G1E1H3Q2G1D1A1G1L1V1L1.M
gi 6323632 ref NP_013703.1	YML010W	of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p Protein that forms a complex with Spt4p and mediates both activation and inhibition	2	5.0943	0.2563	1848.65	1849.32	1	1351.4	66.66667 Q.K2L1L111P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi 6323632 ref NP_013703.1	YML010W	of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p Protein that forms a complex with Spt4p and mediates both activation and inhibition	2	3.7691	0.2972	1977.93	1979.451	1	423.8	56.25 S.Q2K2L1L11P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi 6323632 ref NP_013703.1	YML010W	of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p Protein that forms a complex with Spt4p and mediates both activation and inhibition	3	4.6269	0.1846	1955.15	1957.451	1	2283.9	50 S.QKLLIPVQELPLLLKPN.K
gi 6323632 ref NP_013703.1	YML010W	of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p Protein that forms a complex with Spt4p and mediates both activation and inhibition	3	4.7496	0.2051	1982.12	1979.451	1	1605.7	45.3125 S.Q2K2L1L111P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi 6323632 ref NP_013703.1	YML010W	or transcription elongation; spr4p-sptpp complex also plays a role in pre-mKNA processing; Spt5p Protein that forms a complex with Spt4p and mediates both activation and inhibition	3	4.6226	0.1739	1831.04	1829.32	1	2792.9	58.333332 Q.KLLIPVQELPLLLKPN.K
gi 6323632 ref NP_013703.1	YML010W	or transcription elongation; spr4p-sptpp complex also plays a role in pre-mKNA processing; Spt5p Protein that forms a complex with Spt4p and mediates both activation and inhibition	2	3.6054	0.317	1958.75	1957.451	1	418.2	53.125 S.QKLLIPVQELPLLLKPN.K
gi 6323632 ref NP_013703.1	YML010W	or transcription elongation, spray-spray complex also prays a fole in pre-mixtva processing; Spf5p Protein that forms a complex with Spf4p and mediates both activation and inhibition of the protein that forms a complex with Spf4p and mediates both activation and inhibition	2	4.5295	0.4244	2106.47	2105.307	1	891.2	58.823532 LR4K2I1F1E1P1G1D1H3V1T1V1I1N2G1E1H3Q2.G
gi 6323632 ref NP_013703.1	YML010W	or transcription elongation; spray-spray complex also prays a role in pre-mixiva processing; Spf5p Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription eleventing; Set4p Spt4p complex elevendure a set6 in set spBM.	2	2.9261	0.3205	1627.33	1625.868	1	497.7	73.07692 L.RKIFEPGDHVTVIN.G
gi 6323632 ref NP_013703.1	YML010W	or transcription enorgation, sprep-sprop complex also plays a role in pre-mixive processing; Sp5p Protein that forms a complex with Sp14p and mediates both activation and inhibition of transcription closenting; Sc14p, Sp14p, see provide class of sc1ap.	3	4.9526	0.1555	1978.1	1979.451	1	2439	50 S.Q2K2L1L111P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi 6323632 ref NP_013703.1	YML010W	or transcription enorgation, sprep-sprop complex also plays a role in pre-mixive processing; Sp5p Protein that forms a complex with Sp14p and mediates both activation and inhibition of transcription closenting; Sc14p, Sp14p, see provide class of sc1ap.	2	3.5099	0.2905	1976.87	1979.451	1	402.2	53.125 S.Q2K2L1L111P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi 6323632 ref NP_013703.1	YML010W	or transcription elongation; spray-spray complex also prays a role in pre-mixtva processing; Spfsp Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elevanting; Set4p Spt4p complex elevance such as new in the set SPLA.	2	3.5648	0.3553	1955.85	1957.451	1	792.9	68.75 S.QKLLIPVQELPLLLKPN.K
gi 6323632 ref NP_013703.1	YML010W	or transcription elongation; spray-spray complex also prays a role in pre-mixtva processing; Spfsp Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elevanting; Set4p Spt4p complex elevance such as new in the set SPLA.	3	4.9955	0.3042	1960.37	1957.451	2	1493.3	43.75 S.QKLLIPVQELPLLLKPN.K
gi 6323632 ref NP_013703.1	YML010W	processing; Spt5p	2	4.7298	0.3141	1828.67	1829.32	1	1419.5	70 Q.KLLIPVQELPLLLKPN.K
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimenc complex with Erp1, Erp2, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	4.4521	0.1853	1576.21	1576.698	1	1743.3	87.5 R.R4V1E1E111T1D1E111V1D1E1L1.T
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	1	3.147	0.1735	1577.68	1576.698	5	347.6	50 R.R4V1E1E111T1D1E111V1D1E1L1.T
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	3.8031	0.2943	1827.63	1824.979	1	1161.6	71.42857 R.RVEEITDEIVDELTY.L
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport, Erv25p	2	5.084	0.4505	2064.97	2066.313	1	1979.4	78.125 R.RVEEITDEIVDELTYLK.N
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport, Erv25p	2	4.1587	0.3293	1940.61	1938.139	1	640.9	60.000004 R.RVEEITDEIVDELTYL.K
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	3.7542	0.2989	1616.63	1617.756	1	1382.8	82.14286 L.SRAIELDIESGAEAR.D
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	3.4637	0.3305	1638.91	1638.756	1	1081.7	67.85714 L.S1R4A111E1L1D111E1S1G1A1E1A1R4.D
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	4.8984	0.3549	1955.49	1957.139	1	1246.5	63.333332 R.R4V1E1E1I1T1D1E1I1V1D1E1L1T1Y1L1.K
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	3.7315	0.3289	1356.39	1354.633	4	385.9	75 N.EKLKPIEVELR.R
gi 6323630 ref NP_013701.1	YML012W	of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	3.3168	0.2069	1559.43	1558.815	1	775.8	66.66667 S.A1N2E1K2L1K2P1I1E1V1E1L1R4.R

gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	1	3.3395	0.1659	1370.72	1370.633	1	232.3	70 N.E1K2L1K2P1I1E1V1E1L1R4.R
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	1	2.4322	0.1591	1575.76	1576.698	9	355.4	50 R.R4V1E1E1I1T1D1E1I1V1D1E1L1.T
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	4.1313	0.3408	2086.97	2087.313	1	1015.5	56.25 R.R4V1E1E111T1D1E111V1D1E1L1T1Y1L1K2.N
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	3.1576	0.1739	1356.59	1354.633	1	413.6	75 N.EKLKPIEVELR.R
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	1	3.1224	0.3392	1353.75	1354.633	1	213.3	65 N.EKLKPIEVELR.R
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	3.9305	0.1799	1562.23	1560.698	1	1474.4	83.33333 R.RVEEITDEIVDEL.T
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	2	4.0591	0.1804	1578.87	1576.698	1	1379	83.33333 R.R4V1E1E111T1D1E111V1D1E1L1.T
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	1	3.4548	0.2791	1354.72	1354.633	1	228.8	70 N.EKLKPIEVELR.R
gi 6323630 ref NP_013701.1	YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of group II intron-splicing defects of a mutation in MRS2 and of a conditional mutation	2	3.41	0.2009	1371.17	1370.633	3	376.1	70 N.E1K2L1K2P1I1E1V1E1L1R4.R
gi 41629688 ref NP_013695.2	YML017W	in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of	2	2.909	0.1782	2440.75	2441.766	6	258.1	36.842106 D.L1P1P1R4F1S1N2F1D1I1E1D1L1F1Q2A1K2F1T1K2.F
gi 41629688 ref NP_013695.2	YML017W	group II intron-splicing defects of a mutation in MRS2 and of a conditional mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of	3	4.1461	0.2844	2207.6	2207.445	1	919.1	44.736843 L.KKQTPTEEESHSATPTPKPL.S
gi 41629688 ref NP_013695.2	YML017W	group II intron-splicing detects or a mutation in MRS2 and or a conditional mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of	2	5.396	0.484	2206.47	2207.445	1	833.5	57.894737 L.KKQTPTEEESHSATPTPKPL.S
gi 41629688 ref NP_013695.2	YML017W	group in introl-splicing detects of a mutation in MRS2 and of a conductinal mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of group II intro-splicing detects of a mutation in MRS2 and of a conditional mutation	2	4.9283	0.4457	2232.81	2233.445	1	695.2	57.894737 L.K2K2Q2T1P1T1E1E1E1S1H3S1A1T1P1T1P1K2P1L1.S
gi 41629688 ref NP_013695.2	YML017W	in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine	2	5.1355	0.4498	2206.41	2207.445	1	1113.4	60.526318 L.KKQTPTEEESHSATPTPKPL.S
gi 6323619 ref NP_013690.1	YML022W	and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine	2	3.069	0.194	1203.33	1203.467	3	638.1	70 R.SKLNAPVFTLL.N
gi 6323619 ref NP_013690.1	YML022W	and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine	2	3.7439	0.25	1663.95	1662.885	1	615.2	61.538464 A.LHQYPNFPSEGILF.E
gi 6323619 ref NP_013690.1	YML022W	and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine	2	3.4548	0.3337	1693.33	1693.943	1	769.4	65.38461 F.EDFLPIFRNPGLFQ.K
gi 6323619 ref NP_013690.1	YML022W	and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine	2	3.4283	0.2353	1584.25	1582.812	1	691	70.83333 F.E1D1F1L1P111F1R4N2P1G1L1F1.Q
gi 6323619 ref NP_013690.1	YML022W	and 5-phosphoribosy/pyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p	2	3.6918	0.3766	1679.71	1680.885	1	852.4	73.07692 A.L1H3Q2Y1P1N2F1P1S1E1G1I1L1F1.E
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	4.1576	0.2706	2003.65	2001.329	1	458.5	58.823532 A.W2T1N2I1P1R4K2E1G1G1L1G1P1I1N2I1P1L1.L
gi 6323613 ref NP_013684.1	YML028W	Ubiquitious housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	4.6422	0.2816	2074.55	2073.408	1	523.3	55.555557 L.A1W2T1N2I1P1R4K2E1G1G1L1G1P1I1N2I1P1L1.L
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	3.1592	0.2856	2162.73	2160.567	1	715.6	52.63158 A.WTNIPRKEGGLGPINIPLLA.D
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	3.4624	0.282	2189.65	2187.567	1	460.7	44.736843 A.W2T1N2I1P1R4K2E1G1G1L1G1P1I1N2I1P1L1L1A1.D
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	4.0881	0.2637	2162.79	2160.567	1	955.5	57.894737 L.AWTNIPRKEGGLGPINIPLLA
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	3.7566	0.2211	1979.23	1976.329	1	570.5	58.823532 A.WTNIPRKEGGLGPINIPL.L
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	2.9231	0.2545	1902.11	1903.275	6	583.7	47.058823 W.TNIPRKEGGLGPINIPLL.A

gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	3.1858	0.2345	2115.67	2115.489	1	346.6	38.88889 A.W2T1N2I1P1R4K2E1G1G1L1G1P1I1N2I1P1L1L1.A
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	3.3385	0.3129	2256.99	2259.646	2	346	35 L.A1W2T1N2I1P1R4K2E1G1G1L1G1P1I1N2I1P1L1L1A1.D
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	3.3579	0.2376	2188.27	2187.567	1	366.3	42.105263 L.A1W2T1N2I1P1R4K2E1G1G1L1G1P1I1N2I1P1L1L1.A
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	3.54	0.3898	1609.91	1609.869	1	606.5	60.714287 L.AWTNIPRKEGGLGPI.N
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	4.2908	0.3024	2046.71	2047.408	1	960.2	63.88889 L.AWTNIPRKEGGLGPINIPL.L
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	3.3762	0.29	1973.95	1974.354	1	439.7	44.444447 W.TNIPRKEGGLGPINIPLLA.D
gi 6323613 ref NP_013684.1	YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	2	2.9949	0.1547	2231.11	2231.646	1	599.7	42.5 L.AWTNIPRKEGGLGPINIPLLA.D
gi 27808713 ref NP_013680.2	YML032C	Protein that stimulates strand exchange by facilitating Rad51p binding to single- stranded DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during vegetative growth and meiosis; Rad52p	2	4.1871	0.3608	2204.03	2205.425	1	600.3	64.70589 D.K2V1K2F1D1P1P1D1F1D1E1N2N2L1F1R4P1T1.D
		Protein that stimulates strand exchange by facilitating Rad51p binding to single-								
gi 27808713 ref NP_013680.2	YML032C	of double-strand breaks in DNA during vegetative growth and meiosis; Rad52p Protein with a putative role in sister chromatid segregation, potentially	2	4.3149	0.4242	2178.75	2180.425	1	722.3	67.64706 D.KVKFDPPDFDENNLFRPT.D
gi 6323607 ref NP_013679.1	YML034W	phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p Protein with a putative role in sister chromatid segregation, potentially	2	3.8139	0.3358	2503.51	2503.595	1	459	47.5 Q.ELQEEVNEQLEHENGSEFDVK.Q
gi 6323607 ref NP_013679.1	YML034W	hosphorylated by Cdc28p; green fluorescent protein (GFP)-fluor protein localizes to the nuclear periphery; Src1p Protein with a putative role in sister chromatid segregation, potentially	2	4.5016	0.4668	1945.67	1944.158	1	621.9	60.000004 T.RIETPOLPTEKDVEKC.E
gi 6323607 ref NP_013679.1	YML034W	hosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery: Src1p	3	5.847	0.4551	3523.19	3522.978	1	961.7	27.5 D.KLPQKEVPSTILVPEVEQQEPSQSERTPSLF.S
gi 6323607 ref NP_013679.1	YML034W	Protein with a potative fore in sister Command eeglegator, potentiary phosphorylated by Cdc2g; green flucescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p Protein with a putative role in sister chromatid segregation, potentially	3	4.2277	0.2876	3091.7	3090.397	1	615.7	28.846153 Q.K2E1V1P1S1T111L1V1P1E1V1E1Q2Q2E1P1S1Q2S1E1R4T1P1S1L1F1.S
gi 6323607 ref NP_013679.1	YML034W	phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p	3	5.5887	0.1799	3856.34	3856.321	1	1119.7	27.272728 S.FADKLPQKEVPSTILVPEVEQQEPSQSERTPSLF.S
ail6323607/refINP_013679_1	YMI 034W	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear perinbery: Src1n	3	4 4983	0 2713	3897 98	3899 321	1	853.2	S.F1A1D1K2L1P1Q2K2E1V1P1S1T1I1L1V1P1E1V1E1Q2Q2E1P1S1Q2S1E1R4T1P 25.1S1I.1E1.S
910020001101111 _010010111	111200111	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes	0		0.2110	0001.00	0000.021		000.2	
gi 6323607 ref NP_013679.1	YML034W	to the nuclear periphery; Src1p Protein with a putative role in sister chromatid segregation, potentially	2	3.12	0.2167	2186.05	2187.519	1	336.6	44.444447 D.K2L1P1Q2K2E1V1P1S1T111L1V1P1E1V1E1Q2Q2.E
gi 6323607 ref NP_013679.1	YML034W	phosphorylated by Cdc2bp; green fluorescent protein (GFP)-tusion protein localizes to the nuclear periphery; Src1p AMP deaminase, tetrameric enzyme that catalyzes the deamination of AMP to form	3	6.5766	0.3919	3561.44	3562.978	1	1097.1	D.K2L1P1Q2K2E1V1P1S11111L1V1P1E1V1E1Q2Q2E1P1S1Q2S1E1K411P1S1L1F 30.000002 1.S
gi 6323606 ref NP_013677.1	YML035C	IMP and ammonia; may be involved in regulation of intracellular adenine nucleotide pools; Amd1p AMP deaminase, tetrameric enzyme that catalyzes the deamination of AMP to form	3	4.7377	0.3016	2989.61	2990.213	2	503.9	28 Q.N2D1D1Q2N2P1K2N2K2P1G1W2V1V1Y1P1P1P1P1K2P1S1Y1N2S1D1.T
gi 6323606 ref NP_013677.1	YML035C	IMP and ammonia; may be involved in regulation of intracellular adenine nucleotide pools; Amd1p AMP deaminase, tetrameric enzyme that catalyzes the deamination of AMP to form	3	5.2039	0.3361	2954.12	2955.213	1	1019.8	36 Q.NDDQNPKNKPGWVVYPPPPKPSYNSD.T
gi 6323606 ref NP_013677.1	YML035C	IMP and ammonia; may be involved in regulation of intracellular adenine nucleotide pools; Amd1p AMP despinance, totrameric anyways that catalyzes the despinations of AMP to form	3	4.0908	0.2269	2506.22	2505.766	1	1135.3	36.904762 Q.N2D1D1Q2N2P1K2N2K2P1G1W2V1V1Y1P1P1P1P1K2P1S1.Y
gi 6323606 ref NP_013677.1	YML035C	IMP and ammonia; may be involved in regulation of intracellular adenine nucleotide pools; Amd1p	2	3.3822	0.3311	2474.31	2475.766	1	346.1	40.476192 Q.NDDQNPKNKPGWVVYPPPPKPS.Y
gi 6323606 ref NP_013677.1	YML035C	AMP deaminase, tetrameric enzyme that catalyzes the deamination of AMP to form IMP and ammonia; may be involved in regulation of intracellular adenine nucleotide pools; Amd1p	3	3.9895	0.2945	2751.89	2753.046	1	625.3	32.608696 Q.NDDQNPKNKPGWVVYPPPPKPSYN.S
ail63235931refINP_013664.11	YMI 048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression;	2	4 0177	0 3256	2792.65	2793 888	1	452 5	43 18182 M E1H3V1E1&1D1N2E1E1N2I 1E1E1I 1N2D1S1K2P1I 1IID1O2 I
gilo20000101111 _010004.11	TWILDHOW	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression;	2	4.0177	0.0200	2132.00	2733.000		402.0	
gi 6323593 ref NP_013664.1	YML048W	Gst2p ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression;	1	2.2845	0.1971	1191.45	1190.345	2	412.8	62.5 F.H3E1K2E1P1V1K2F1Y1.K
gi 6323593 ref NP_013664.1	YML048W	Gsf2p ER localized integral membrane protein that may promote secretion of certain	1	2.8985	0.2946	1436.68	1437.681	1	637.1	65 S.IFHEKEPVKFY.K
gi 6323593 ref NP_013664.1	YML048W	nexces transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p ER localized integral membrane protein that may promote secretion of certain between transporter, including Gal2m; involved in a transport representation	1	3.1982	0.2311	1451.58	1452.681	1	651.7	70 S.I1F1H3E1K2E1P1V1K2F1Y1.K
gi 6323593 ref NP_013664.1	YML048W	Gsf2p	2	2.967	0.2281	1436.77	1437.681	1	925.1	75 S.IFHEKEPVKFY.K

		ER localized integral membrane protein that may promote secretion of certain								
gi 6323593 ref NP_013664.1	YML048W	nexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	2	3.0294	0.1925	1901.65	1902.118	1	231.3	50 V.KLRREIADEKEKASNN.D
		ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression;		0 1015	0.0004		1511 70			
gil6323593[rei]NP_013664.1]	TIVIL048VV	GSI2p ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression;	2	3.4215	0.2901	1511.15	1511.73	1	1154.2	75 N.NILEET DGUIGHMI.N
gi 6323593 ref NP_013664.1	YML048W	Gsf2p ER localized integral membrane protein that may promote secretion of certain	2	3.5603	0.1959	1453.27	1452.681	1	966.7	75 S.I1F1H3E1K2E1P1V1K2F1Y1.K
gi 6323593 ref NP_013664.1	YML048W	hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p EP localized integral membrane protein that may promote secretion of certain	1	2.8736	0.3288	1436.79	1437.681	1	674.1	70 S.IFHEKEPVKFY.K
ail62225021rofIND_012664_1	VMI 049W/	hexose transporters, including Gal2p; involved in glucose-dependent repression;	2	2 2505	0.2055	1426 75	1427 691	1	076 7	
gil0323335[rei]Nr _013004.1]	1101204000	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression;	2	5.2505	0.2933	1430.75	1437.001	1	570.7	
gi 6323593 ref NP_013664.1	YML048W	Gsf2p ER localized integral membrane protein that may promote secretion of certain	3	3.8798	0.1973	1437.95	1437.681	1	1937	67.5 S.IFHEKEPVKFY.K
gi 6323593 ref NP_013664.1	YML048W	Record anisponens, including Gal2p; involved in glucose-dependent repression, Gsf2p ER localized integral membrane protein that may promote secretion of certain	2	3.0494	0.2429	1436.69	1437.681	1	1020.9	75 S.IFHEKEPVKFY.K
gi 6323593 ref NP_013664.1	YML048W	hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	1	2.8232	0.3119	1436.64	1437.681	1	680.5	70 S.IFHEKEPVKFY.K
ail6323593/refINP_013664.1	YML048W	EX localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2n	2	3.5903	0.176	1452.25	1452.681	1	1131	80 S.11F1H3F1K2F1P1V1K2F1Y1 K
3.1		\sim								
gi 6323583 ref NP_013655.1	YML057W	Calcarregular A, one isotorm (include a construction of the calcargular solution of calcaretini, a Ca++/calmodulin-regulated protein phosphatase which regulates Cr21p (a stress- response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	3	6.9626	0.4202	2998.76	2996.166	1	1046.7	40.625 L.W2A1D1P111E1E1Y1D1E1V1L1D1K2D1L1T1E1E1D111V1N2S1K2.T
		Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin,								
gi 6323583 ref NP_013655.1	YML057W	a Ca++/calmodulin-regulated protein phosphatase which regulates Crz1p (a stress- response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	2	2.9561	0.2543	3079.13	3080.326	5	256.7	28 L.LWADPIEEYDEVLDKDLTEEDIVNSK.T
		Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin,								
gi 6323583 ref NP_013655.1	YML057W	response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	2	4.3672	0.4553	3109.79	3110.326	1	903.9	44 L.L1W2A1D1P111E1E1Y1D1E1V1L1D1K2D1L1T1E1E1D111V1N2S1K2.T
		Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin, a Ca++/calmodulin-regulated protein phosphatase which regulates Crz1p (a stress-								
gi 6323583 ref NP_013655.1	YML057W	response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	3	6.072	0.5007	3110.33	3110.326	1	746.6	37 L.L1W2A1D1P111E1E1Y1D1E1V1L1D1K2D1L1T1E1E1D111V1N2S1K2.T
		Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin, a Ca++/calmodulin-regulated protein phosphatase which regulates Crz1p (a stress-								
gi 6323583 ref NP_013655.1	YML057W	response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	2	2.9757	0.2391	1447.53	1447.679	5	309.8	70 L.KLNFNDHFWLL.R
		Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin, a Ca++/calmodulin-regulated protein phosphatase which regulates Crz1p (a stress-								
gi 6323583 ref NP_013655.1	YML057W	response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	2	4.2368	0.386	1725.57	1725.989	1	638.7	56.666668 F.SKEPNLISVPAPITVC.G
		a Ca++/calmodulin-regulated protein phosphatase which regulates Cr21p (a stress-								
gi 6323583 ref NP_013655.1	YML057W	response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	2	5.6163	0.426	2995.09	2996.166	1	690.5	50 L.W2A1D1P111E1E1Y1D1E1V1L1D1K2D1L111E1E1D111V1N2S1K2.1
	VMI 05714/	Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin, a Ca++/calmodulin-regulated protein phosphatase which regulates Crz1p (a stress-	2	E 0702	0.4500	2005 00	2007 400		770.0	
giloszssesitetine_013055.1	TWE057W	Contains three calcium and lipid binding domains; localized to the bud; green fluoreacent particip (CED) finish and in a particip localized to the call participant; mBNA is	2	5.0705	0.4326	2903.99	2907.100	1	110.5	32.003332 L.WADFIELTDEVLUKDLTEEDIVINSK.T
ail63235681rofIND_013630_11	VMI 072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal	2	3 5206	0 1596	1744 41	17/2 005	1	453 5	60 74/297 K T41 1D4D4\/4\//2N/2E4D4A1K2H2H141 4 S
gil0323300[rei]Nr _013039.1]	TWEOTZC	Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	3.3230	0.1390	1/44.41	1742.333	1	433.3	
qi 6323568 ref NP 013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p,	3	4.0786	0.2806	3070.07	3071.998	1	373.2	25.961538 K.KEDENEDTTEKEEDENEESSQTDVGIA.K
		Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is								
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p,	2	3.8633	0.4072	1931.71	1933.122	1	473.4	50 D.K2N2G1Q2V1P1P1V1P1E1V1P1Q2E1Y1T1Q2
		Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is								
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p,	2	3.2597	0.2973	1909.89	1911.122	1	444	50 D.KNGQVPPVPEVPQEYTQ
		Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is								
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p,	2	4.0427	0.3357	2630.27	2631.875	1	621.5	40.909092 K.I1N2Y1G1K2D1K2N2G1Q2V1P1P1V1P1E1V1P1Q2E1Y1T1Q2
		Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is transled to the bud view of the pRNA to conserve the translet of the protein to the								
gi 6323568 ref NP_013639.1	YML072C	portion of Tcb1p, Contains three showing and linid hinding densities the state that have	2	5.3691	0.459	2072.49	2073.291	1	778.9	68.75 H.W2F1P1V1K2E1D1K2S1E1E1K2A1V1E1R4A1.E
		fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is								
gi 6323568 ref NP_013639.1	YML072C	argeneu to the bud via the mixink transport system involving She/p; C-terminal portion of Tcb1p,	2	4.342	0.4135	2601.61	2601.875	1	503.1	40.909092 K.INYGKDKNGQVPPVPEVPQEYTQ
		fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is transfer to the budy is the mPNA transport protein localizes (Green Company).								
gi 6323568 ref NP_013639.1	YML072C	portion of Tcb1p,	2	4.0527	0.3536	1613.75	1614.78	1	431	61.538464 F.H3E1E1E1K2K2K2V1G1G1N2L1P1Q2.K

gi 6323568 ref NP_013639.1	YML072C	Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green	2	4.5047	0.3827	1595.79	1593.78	1	1046.3	84.61539 F.HEEEKKKVGGNLPQ.K
gi 6323568 ref NP_013639.1	YML072C	fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tob1p, Contains three calcium and lipid binding domains; localized to the bud; green functions three calcium and lipid binding domains; localized to the bud; green	3	4.3454	0.437	2784.47	2785.216	8	266	26.086956 K.TLDPVWNEDAKIPILSRSKNQVIF.N
gi 6323568 ref NP_013639.1	YML072C	Tuprescent protein (GFP)-rusion protein localizes to the cell periphery; mKNA is targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green functionation to the protein for the authoritication of the authoritication of the trans-	2	3.5254	0.2207	1854.51	1854.116	1	924.4	70 T.LFHEEEKKKVGGNLPQ.K
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green	2	5.5545	0.4118	2212.49	2213.432	1	2053.3	76.47059 L.H3W2F1P1V1K2E1D1K2S1E1E1K2A1V1E1R4A1.E
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green functionation to the protein (CCB) function to the protein system of the protein (CCB) with the protein to the protein (CCB) with the protein to the protein to the protein (CCB) with the protein to the protein (CCB) with the protein to the protein t	3	4.4069	0.3384	2215.94	2213.432	1	1055.4	44.11765 L.H3W2F1P1V1K2E1D1K2S1E1E1K2A1V1E1R4A1.E
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (CEP)/fusion protein localized to the cell periphery; mRNA is	3	5.1041	0.3311	2952.23	2954.454	1	1436.9	35.576923 Q.GSFNPEYIKPSFDIVKGGITDKPMKIA.S
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (CEP)/fusion protein localized to the cell periphery; mRNA is	2	3.2298	0.1958	1712.37	1712.103	1	736.5	53.846157 F.LSKFWVIYMPVLSQ.Q
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (CEPV/tision protein localizes) to the cell periphery; mRNA is	2	4.0107	0.2839	1384.47	1382.544	1	507.5	85 L.K2L1K2D1H3E1H3K2V1T1E1.S
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (CEP)/fusion protein localized to the cell periphery; mRNA is	3	5.11	0.3836	2329.64	2327.591	1	933.6	43.055553 S.L1H3W2F1P1V1K2E1D1K2S1E1E1K2A1V1E1R4A1.E
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GPP)-fusion protein localizes to the cell periphery: mRNA is	2	4.9026	0.4036	2048.87	2049.291	1	1360.5	68.75 H.WFPVKEDKSEEKAVERA.E
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery: mRNA is	2	3	0.2815	1178.99	1179.448	1	1041.6	85 S.VKLGDGHLIVK.I
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	3.1545	0.252	1364.53	1364.544	1	296.2	80 L.KLKDHEHKVTE.S
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	3.6235	0.1908	1548.47	1548.785	1	498.4	63.636364 N.VKNPRWNETKYL.L
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	4.3911	0.3861	1740.33	1740.957	1	616.9	67.85714 L.FHEEEKKKVGGNLPQ.K
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	4.4776	0.4061	1793.43	1792.998	1	1070.3	73.07692 S.L1H3W2F1P1V1K2E1D1K2S1E1E1K2.A
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	4.1069	0.3602	1773.27	1772.998	1	1331.7	73.07692 S.LHWFPVKEDKSEEK.A
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	3.6755	0.2513	2075.35	2075.35	1	216.7	44.11765 F.H3E1E1E1K2K2K2V1G1G1N2L1P1Q2K2V111N2.Q
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	5.3171	0.4063	2204.55	2205.481	1	742.7	58.333332 F.H3E1E1E1K2K2K2V1G1G1N2L1P1Q2K2V111N2Q2.Q
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is	2	4.8371	0.4291	2174.83	2176.481	1	1017.2	58.333332 F.HEEEKKKVGGNLPQKVINQ.Q
gi 6323568 ref NP_013639.1	YML072C	targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, N-terminally acetylated protein component of the large (60S) ribosomal subunit has	2	3.5786	0.3068	1569.47	1568.785	1	437.3	59.090908 N.V1K2N2P1R4W2N2E1T1K2Y1L1.L
gi 6323567 ref NP_013638.1	YML073C	similarity to RpI6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; RpI6ap N-terminally acetylated protein component of the large (60S) ribosomal subunit, has	2	3.5448	0.2331	1593.39	1592.805	3	515.7	65.38461 Q.K2A1P1K2W2Y1P1S1E1D1V1A1A1L1.K
gi 6323567 ref NP_013638.1	YML073C	similarity to RpI6Bp and to rat L6 ribosomal protein; binds to 5.85 rRNA; RpI6ap N-terminally acetylated protein component of the large (605) ribosomal subunit has	2	4.1516	0.4013	1722.41	1722.979	1	1156.4	64.28571 Q.K2A1P1K2W2Y1P1S1E1D1V1A1A1L1K2.K
gi 6323567 ref NP_013638.1	YML073C	Similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.85 (RNA; Rpl6ap N-terminally acetylated protein component of the large (60%) ribosomal suburit, bec	1	3.6274	0.1922	1591.58	1592.805	1	870.9	57.692307 Q.K2A1P1K2W2Y1P1S1E1D1V1A1A1L1.K
gi 6323567 ref NP_013638.1	YML073C	similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	1	3.3246	0.3059	1574.65	1575.805	1	874.1	61.538464 Q.KAPKWYPSEDVAAL.K

gi 6323567 ref NP_013638.1	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to RpI6Bp and to rat L6 ribosomal protein; binds to 5.85 rRNA; RpI6ap	2	4.3615	0.4019	1704.73	1703.979	1	1207.7	75 Q.KAPKWYPSEDVAALK.K
gi 6323567 ref NP_013638.1	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to RpI6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; RpI6ap	2	3.7152	0.3107	1592.29	1592.805	1	375	57.692307 Q.K2A1P1K2W2Y1P1S1E1D1V1A1A1L1.K
gi 6323567 ref NP_013638.1	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to RpI6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; RpI6ap	1	3.3501	0.1713	1591.85	1592.805	4	620	50 Q.K2A1P1K2W2Y1P1S1E1D1V1A1A1L1.K
gi 6323567 ref NP_013638.1	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to RpI6Bp and to rat L6 ribosomal protein, binds to 5.8S rRNA; RpI6ap	2	2.9917	0.1896	1404.01	1404.64	1	571	72.72727 S.F1S1L1K2N2G1D1K2P1H3M1L1.K
gi 6323567 ref NP_013638.1	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	2	3.6863	0.2625	1592.59	1592.805	1	418.9	61.538464 Q.K2A1P1K2W2Y1P1S1E1D1V1A1A1L1.K
gi 6323567 ref NP_013638.1	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	1	3.6299	0.2269	1592.68	1592.805	1	841.2	57.692307 Q.K2A1P1K2W2Y1P1S1E1D1V1A1A1L1.K
gi 6323567 ref NP_013638.1	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to RpI6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; RpI6ap	2	3.4616	0.3798	1574.87	1575.805	1	503.8	65.38461 Q.KAPKWYPSEDVAAL.K
gi 6323567 ref NP_013638.1	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.85 (RNA; Rpl6ap Nucleolar peptidyl-protyl cis-trans isomerase (PPIase); FK506 binding protein;	1	3.3788	0.3715	1574.62	1575.805	1	862.1	57.692307 Q.KAPKWYPSEDVAAL.K
gi 6323566 ref NP_013637.1	YML074C	phosphorylated by casein kinase II (Cka1p-cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1; Fpr3p Nucleolar peptidy-prolyl cis-trans isomerase (PPIase); FK506 binding protein;	2	3.0516	0.2038	1610.73	1610.952	1	488.9	53.571426 Y.TPVPAIDVTMPITVR.I
gi 6323566 ref NP_013637.1	YML074C	prosphorylated by caselin kinase in (ckatp-ckatp-ckotp-ckotp-ckotp) dephosphorylated by Ptp1p: Fp2p Nucleolar peptidy-prolyl cis-trans isomerase (PPIase); FK506 binding protein;	2	4.3143	0.4035	1627.63	1628.952	1	833.3	67.85714 Y.T1P1V1P1A111D1V1T1M1P111T1V1R4.I
gi 6323566 ref NP_013637.1	YML074C	prosphorylated by caselin kinase iii (ckai p-cka2p-ckoi p-cko2p) and dephosphorylated by Ptp1p: Fp7a Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; obserbendylated by caselin (ckase iii (ckato Cka2o Ckato Cka	3	6.7076	0.2002	4060.28	4060.936	1	1166.2	28.125 1E1P1K2.K
gi 6323566 ref NP_013637.1	YML074C	photophotyfacted of y outsoframidiation (charp outspond) and dephotophotyfacted by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorytated by casein kinase III (Cka1p-Cka2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1p-Ckb2p-Ckb1	2	2.9496	0.2798	1642.67	1643.88	1	803.4	66.66667 Y.GKQALPGIPANSELTF.D
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein; phosphorylated by casein kinase III (Cka1p-Cka2p-Ckb1p-Ckb2p) and	3	6.4861	0.2626	4364.09	4364.363	1	367.8	20 E.EVQEEDEEDNDGEEEQEEEEEQKEEVKPEPKKSK.K
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein; phosphorylated by casein kinase III (Cka1p-Cka2p-Ckb1p-Ckb2p) and	3	6.1679	0.4177	4235.21	4236.189	1	599.8	23.529411 E.EVQEEDEEDNDGEEEQEEEEEEQKEEVKPEPKKS.K E.E1V102E1E1D1E1E1D1N2D1G1E1E1E102E1E1E1E1E1E1E1E102K2E1E1V1K2P
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and	3	5.5149	0.3531	4277.81	4279.189	1	516.7	22.058825 1E1P1K2K2S1.K
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein;	3	6.0563	0.3041	4491.2	4492.537	1	340.5	
gi 6323566 ref NP_013637.1	YML074C	pnospnorylated by caselin kinase III (Uka1p-Uka2p-Uko1p-Uko2p) and dephosphorylated by Ptp: Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; bearbearted by recyclic kinase III (Ukata Cledan Clefan Chan and	3	5.1321	0.2586	4538.09	4539.537	7	210.5	18.055555 1E1P1K2K2S1K2K2.E
gi 6323566 ref NP_013637.1	YML074C	pinospinolytated by caseni kinase in (ckarp-ckar	3	6.4377	0.2121	4021.67	4020.936	1	828.1	25.78125 E.EVQEEDEEDNDGEEEQEEEEEQKEEVKPEPK.K
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p: Fpr3p Vucleolar peptidy-prolyl cis-trans isomerase (PPlase); FK506 binding protein; phoephontiated by zeroing kinase II (Victo_Ck2o); Ck10, Ck120, and	2	4.4448	0.2816	1879.41	1879.043	1	443.6	52.941177 L.E1G1G111V111E1D1R4T111G1D1G1P1Q2A1K2.R
gi 6323566 ref NP_013637.1	YML074C	pinospinolytated by Ptp1p: Fp2p dephosphorekated by Ptp1p: Fp2p Nucleolar peptidyl-prolyt cis-trans isomerase (PPIase); FK506 binding protein; phosphorytated by case in (cisase III (cisato_Cle2po_Clotho_Cle2po_Clance))	3	5.7356	0.2733	4668.08	4669.652	1	406.5	18.918919 1E1P1K2K2E1K12K2E1K
gi 6323566 ref NP_013637.1	YML074C	pinospinol jialed u dealin killiage in (ckarp-ckarp-ckarp-ckarp-ckarp-ckarp-ckarp- dephosphorylated by Pip1p: Fp/2p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein (inase III (ckarp-cka2p-ck1p-ckb1p-ck1p-ck1p-ck1p-ck1p-ck1p-ck1p-ck1p-ck	3	6.6331	0.2901	4407.95	4409.363	1	531.1	22.142857 1E1P1K2K2S1K2.K
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein; phosphorylated by casein kinase III (Cka1p-Cka2p-Ckb1p-Ckb2p) and	2	3.7285	0.3114	2094.69	2093.335	3	319.3	42.105263 K.V1L1E1G1G111V111E1D1R4T111G1D1G1P1Q2A1K2.R
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and	2	4.4263	0.455	2067.15	2068.335	1	619.7	55.263157 K.VLEGGIVIEDRTIGDGPQAK.R
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and	3	6.0867	0.2815	4620.02	4621.652	1	451.5	20.27027 E.EVQEEDEEDNDGEEEQEEEEEEQKEEVKPEPKKSKKE.K
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and	2	4.3805	0.3293	2311.13	2311.587	1	954.4	52.380955 K.S1K2V1L1E1G1G1I1V1I1E1D1R4T1I1G1D1G1P1Q2A1K2.R
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1; Fp73p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and	2	3.2636	0.1637	1458.27	1457.667	1	317.8	66.66667 K.KDLEEGPTKPKSK.K
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fp73p Nucleolar peptidyl-prolytic is-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and	2	4.2233	0.322	1884.43	1883.133	1	355.9	56.666668 V.E1F1K2K2D1L1E1E1G1P1T1K2P1K2S1K2.K
gijo323566/ref/NP_013637.1	YML074C	ueprospring/ated by Ptp 1; Ptrdp Nucleolar petidyl-prol() is-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase III (Cka1p-Cka2p-Ckb1p-Ckb2p) and despectbourdated by Pthrite: Epr3n	1	2.357	0.1619	1285.78	1285.532	5	126.1	
gij6323566/refINP_013637.1	YML074C	Nucleolar perildy-provide is-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dehoershouldard by PInto: Epr3n	2	2.0149	0.3035	1861.81	1862 133	3	211.8	
9-10020000 i cilitir _010007.1]	111120740	soprioprior juico by t ip (p, t prop	4	0.0010	0.0000	1001.01	1002.100	-	211.0	

		Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein;								
gil6323566/rofIND_013637.11	VMI 074C	phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Epr3p	2	2 0055	0.2	2110 21	2110 /23	1	256 7	44 11765 V EEKKDI EEGPTKPKSKKE O
giloszssoolieilini _015057.1]	TIME074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein;	2	2.3033	0.2	2113.21	2113.425	'	230.7	44.1705 V.EI KIDELEGF IKI KOKKE.Q
-102025001{IND_042027_41	VAL 0740	phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and	2	4 0075	0.4455	0040 57	0040 507	4	004.0	
gi 6323566 ret NP_013637.1	YML074C	depnosphorylated by Ptp1p; Pp3p Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase): FK506 binding protein:	2	4.0075	0.4155	2212.57	2213.597	1	824.6	57.894737 LINVEPT IPVPAIDVIMPITVR.I
		phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and								
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p Nucleolar pentidyl-prolyl cis-trans isomerase (PPlase): EK506 binding protein:	2	3.7806	0.2268	2325.35	2326.756	1	1248.1	52.499996 S.LNVEPYTPVPAIDVTMPITVR.I
		phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and								
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p	2	4.2609	0.4312	2412.49	2413.835	1	907.1	50 Y.SLNVEPYTPVPAIDVTMPITVR.I
		phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and								
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p	2	3.2194	0.3258	2237.41	2237.597	5	346.9	36.842106 L.N2V1E1P1Y1T1P1V1P1A1I1D1V1T1M1P1I1T1V1R4.I
		Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and								
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p	2	4.1114	0.3825	2350.47	2351.756	1	566	40 S.L1N2V1E1P1Y1T1P1V1P1A1I1D1V1T1M1P1I1T1V1R4.I
		Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and								
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p	2	4.492	0.4841	2438.65	2439.835	1	1026.1	52.380955 Y.S1L1N2V1E1P1Y1T1P1V1P1A1I1D1V1T1M1P1I1T1V1R4.I
		Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein;								
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p	2	3.5648	0.3402	2246.13	2248.191	1	400.4	41.666664 K.RNPDFEDDDFLGGDFDEDE.I
		Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein;								
gi 6323566 ref NP_013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p	2	3.8743	0.3484	1778.05	1778.783	1	603	57.14286 K.R4N2P1D1F1E1D1D1D1F1L1G1G1D1F1.D
		Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein;								
gi 6323566 ref NP 013637.1	YML074C	dephosphorylated by Ptp1p; Fpr3p	2	4.1569	0.421	1855.19	1856.043	1	846	64.70589 L.EGGIVIEDRTIGDGPQAK.R
		Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein;								
gil6323566/refINP_013637.1	YML074C	phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p: Fpr3p	2	3.86	0.3285	1646.05	1646.881	1	389.5	65.38461 V.EEKKDLEEGPTKPK.S
9.1111		Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein;								
gil6323566/refINP_013637_1	YML074C	phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Epr3p	2	3 3479	0 245	1667 55	1664 881	1	404 7	65 38461 V E1E1K2K2D1I 1E1E1G1P1T1K2P1K2 S
giloszosobiellel _010001.1	111120740	Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein;	2	0.0475	0.240	1007.00	1004.001		404.7	
gil6323566/refINP_013637_1	YML074C	phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Epr3p	з	4 2519	0 2544	1874 66	1874 188	1	1352 7	
gilos25500[rei]rar_015057.1]	TIME074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPlase); FK506 binding protein;	5	4.2313	0.2344	10/4.00	1074.100	'	1552.7	
dile202566 rofIND 012627 1	VMI 074C	phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and	2	2 6010	0.2400	2270.05	2270 462	0	169.7	
gilo323300[rei]INF_013037.1]	TIME074C	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans	2	3.0919	0.3499	2270.95	2270.403	0	100.7	30.00009 L.NIIKKNPDPEDDDPE00DP.D
	VAL 070W	isomerization of peptide bonds N-terminal to proline residues; involved in protein		2 500	0.4055	4005 50	4000 505	0	244.2	
gi 6323562 ret NP_013633.1	YML078W	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans	1	2.598	0.1955	1285.56	1286.535	2	341.3	66.66667 F.H3R4111P1D1F1M11Q2.G
	100000	isomerization of peptide bonds N-terminal to proline residues; involved in protein		0 5407	0.0000	1000 71	1071 010			
gi 6323562 ret NP_013633.1	YML078W	rerolding after import into mitochondria; Cpr3p Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans	2	3.5197	0.3988	1668.71	1671.013	1	893.9	73.07692 K.GVPFHRIIPDFMIQ.G
		isomerization of peptide bonds N-terminal to proline residues; involved in protein								
gi 6323562 ref NP_013633.1	YML078W	refolding after import into mitochondria; Cpr3p Mitochondrial pentidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans	2	3.0847	0.2129	1269.93	1270.535	1	1194	88.88889 F.HRIIPDFMIQ.G
		isomerization of peptide bonds N-terminal to proline residues; involved in protein								
gi 6323562 ref NP_013633.1	YML078W	refolding after import into mitochondria; Cpr3p Alpha-tubulin: associates with beta-tubulin (Tub2n) to form tubulin dimer, which	2	3.3188	0.2866	1288.37	1286.535	1	1146.3	83.33333 F.H3R4I1I1P1D1F1M1I1Q2.G
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p	3	4.7671	0.3302	2755.76	2755.928	4	314.6	27.000002 L.E1H3G1I1K2P1D1G1H3L1E1D1G1L1S1K2P1K2G1G1E1E1G1F1S1T1.F
gil6323554/refINP_013625_1	YMI 085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules: Tub1p	2	3 4382	0 3874	2754 43	2755 928	1	571.6	38 E1H3G111K2P1D1G1H31 1E1D1G11 1S1K2P1K2G1G1E1E1G1E1S1T1 E
giloo20004[ici]i4i _010020.1]	TWILDOOD	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	0.4002	0.0014	2104.40	2100.020		071.0	
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p Alpha-tubulin; associates with bata-tubulin (Tub2p) to form tubulin dimor, which	3	4.2862	0.2608	1900.37	1901.166	1	604.9	40 H.Y1T1V1G1R4E1I1L1G1D1V1L1D1R4I1R4.K
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p	3	4.2392	0.3872	1874.48	1876.166	1	678.2	41.666664 H.YTVGREILGDVLDRIR.K
gil6323554/rofIND_013625_1	VMI 085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	3 5807	0 3424	2860 55	2870 105	1	313 /	
giloo20004[ici]i4i _010020.1]	TWILDOOD	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	0.0007	0.0424	2003.00	2070.100		010.4	0.40104 ELENOIRI DONEEDOLORI ROBEDI OTT.
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p	3	6.7045	0.4629	3104.78	3106.342	1	1630.7	33.035713 Y.S1L1E1H3G1I1K2P1D1G1H3L1E1D1G1L1S1K2P1K2G1G1E1E1G1F1S1T1F1.F
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p	3	6.3242	0.3575	3069.02	3070.342	1	1665.9	34.82143 Y.SLEHGIKPDGHLEDGLSKPKGGEEGFSTF.F
dile202554/rofIND_012625_1	VMI 095C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	4 0 2 7 9	0.4510	2014 50	2015 222	1	417.0	
gilo323534[rei]ivF_013025.1]	TIMEU03C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	4.0270	0.4319	2014.59	2015.235	1	417.9	36.333332 L.ENGIKFUGHLEDGLSKFKG.G
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p	2	4.3254	0.4399	2159.73	2158.419	1	584.2	47.368423 Y.SLEHGIKPDGHLEDGLSKPK.G
gi 6323554 ref NP 013625.1	YML085C	Alpha-tubulin; associates with beta-tubulin (1ub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	3	4.5815	0.3484	3077.24	3078.39	1	653.7	30.000002 R.A1I1Y1V1D1L1E1P1N2V1I1D1E1V1R4N2G1P1Y1K2D1L1F1H3P1E1.Q
		Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which								
gi 6323554 ret NP_013625.1	YML085C	polymerizes to form microtubules; I ub1p Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	3.6707	0.2361	2903.73	2904.105	1	140.8	30.769232 L.E1H3G111K2P1D1G1H3L1E1D1G1L1S1K2P1K2G1G1E1E1G1F1S111F1.F
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p	2	4.1558	0.3235	1981.87	1983.181	1	315.6	50 L.E1H3G111K2P1D1G1H3L1E1D1G1L1S1K2P1K2.G
gil6323554lrefINP_013625.1	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules: Tub1p	1	2.3216	0.1951	1351.68	1352.665	2	596.8	65 N.LVPYPRIHEPL.V
51		Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which								
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p Alpha-tubulin: associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	3.302	0.424	1182.53	1181.334	1	714.5	75 D.GHLEDGLSKPK.G
gi 6323554 ref NP_013625.1	YML085C	polymerizes to form microtubules; Tub1p	2	4.0415	0.3597	1957.55	1958.181	2	265.7	52.941177 L.EHGIKPDGHLEDGLSKPK.G
ail6323553 ref NP 013624 1	YML086C	D-Arabinono-1,4-lactone oxidase, catalyzes the final step in biosynthesis of D- erythroascorbic acid, which is protective against oxidative stress: Alo1p	1	2,3745	0,2405	1268.55	1268,365	1	440.9	61.11111 L.KVEEWYGEDL.K
		D-Arabinono-1,4-lactone oxidase, catalyzes the final step in biosynthesis of D-								
gi 6323553 ref NP_013624.1	YML086C	erythroascorbic acid, which is protective against oxidative stress; Alo1p D-Arabinono-1,4-lactone oxidase, catalyzes the final step in biosvnthesis of D-	2	3.5121	0.304	1657.85	1654.99	1	748.3	61.538464 S. IKIYAPLTPFVEKF.V
gi 6323553 ref NP_013624.1	YML086C	erythroascorbic acid, which is protective against oxidative stress; Alo1p	2	3.6599	0.1778	1258.81	1260.523	7	1025.3	75 A.T1I1R4V1V1P1G1F1N2I1K2.S
ail6323553/ref/NP 013624 1	YML086C	D-Arabinono-1,4-lactone oxidase, catalyzes the final step in biosynthesis of D- erythroascorbic acid, which is protective against oxidative stress: Alo1p	2	3,7458	0.3432	1670.41	1670.99	1	1064.7	69.230774 S.T1K2I1Y1A1P1L1T1P1F1V1E1K2F1.V

		Subunit of the signal recognition particle (SRP), involved in protein targeting to the								
gi 6323531 ref NP_013602.1	YML105C	ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	4.5393	0.2871	2193.49	2195.316	1	1036	58.823532 M.PRLEEIDDFNDIDDLDME.L
gil6323531/refINP_013602_1	YMI 105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER: interacts with Srp54p; homolog of mammalian SRP19; Sec65p.	2	5 2903	0.3986	2401 69	2403 554	1	1314.3	50 M P1R4I 1E1E1I1D1D1E1N2D1I1D1D1I 1D1M1E1I 1A1 E
gijoo2000 (Foljini _010002.1)	11121000	Subunit of the signal recognition particle (SRP), involved in protein targeting to the	-	0.2000	0.0000	2101.00	2100.001	•	101110	
gi 6323531 ref NP_013602.1	YML105C	ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p Subunit of the signal recognition particle (SPP) involved in protein targeting to the	2	4.5142	0.3463	2062.65	2063.268	1	1165.9	62.5 E.S1L1R4E111P1Y1G1P1D1F1D1N2I1E1F1K2.K
gi 6323531 ref NP_013602.1	YML105C	ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	5.1486	0.5055	2215.17	2217.316	1	1934.2	64.70589 M.P1R4L1E1E1I1D1D1F1N2D1I1D1D1L1D1M1E1.L
-:::::::::::::::::::::::::::::::::::::	VMI 4050	Subunit of the signal recognition particle (SRP), involved in protein targeting to the	2	4 0047	0.057	0000.04	0070 554		000.4	
gilo323531[rei]NP_013602.1]	TIVIL TUSC	Subunit of the signal recognition particle (SRP), involved in protein targeting to the	2	4.2217	0.257	2360.31	2379.554	I	632.1	42.105263 M.PRLEEIDDFNDIDDLDMELA.E
gi 6323531 ref NP_013602.1	YML105C	ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	3	4.3624	0.278	3569.96	3572.92	1	858.9	21.6666666 M.PRLEEIDDFNDIDDLDMELAELDPSLRTPIA.P
ail6323531/refINP 013602.1/	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER: interacts with Sro54p; homolog of mammalian SRP19; Sec65p	2	4.6153	0.3624	1840.35	1841.03	1	1739.4	82.14286 L.REIPYGPDFDNIEFK.K
51		Subunit of the signal recognition particle (SRP), involved in protein targeting to the								
gi 6323531 ref NP_013602.1	YML105C	ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p Subunit of the signal recognition particle (SRP), involved in protein targeting to the	3	4.2658	0.3825	1841.18	1841.03	1	1546.1	48.214287 L.REIPYGPDFDNIEFK.K
gi 6323531 ref NP_013602.1	YML105C	ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	5.2034	0.3443	1861.37	1861.03	1	2102.9	82.14286 L.R4E111P1Y1G1P1D1F1D1N2I1E1F1K2.K
ail63235311refINP_013602_11	YMI 105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER: interacts with Srp54p; homolog of mammalian SRP19; Sec65p.	3	5 0975	0.3885	2062 55	2063 268	1	1758 1	50 E S1I 184E111P1Y1G1P1D1E1D1N2I1E1E1K2 K
giloo2000 (jioijini _010002.1)	11121000	Subunit of the signal recognition particle (SRP), involved in protein targeting to the	0	0.0010	0.0000	2002.00	2000.200	•		
gi 6323531 ref NP_013602.1	YML105C	ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p Subunit of the signal recognition particle (SRP) involved in protein targeting to the	2	5.1458	0.3386	2062.13	2063.268	1	1657.1	68.75 E.S1L1R4E111P1Y1G1P1D1F1D1N2I1E1F1K2.K
gi 6323531 ref NP_013602.1	YML105C	ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	4.5405	0.3574	2040.81	2041.268	1	1647.7	68.75 E.SLREIPYGPDFDNIEFK.K
ail6323526/rofIND_013507_1	VMI 110C	2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase, involved in	2	3 02	0 3834	2062.20	2063 161	1	771.0	58 823532 I V/S1N2G1E1K2I 1E1E1I1D1S1D1S1K2D1I1V1 T
giloszoszofielliti _015557.1]	TWETTOO	2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase, involved in	2	5.52	0.0004	2002.23	2003.101	'	111.5	36.023332 E.VISIN261E IN2ETETETIDISTO ISTN201111.1
gi 6323526 ref NP_013597.1	YML110C	ubiquinone (Coenzyme Q) biosynthesis; located in mitochondria; Coq5p	2	4.9884	0.4255	1740.75	1741.846	1	675.7	67.85714 N.GEKLEEIDSDSKDIY.T
gi 6323526 ref NP 013597.1	YML110C	2-nexaprenyi-b-metnoxy-1,4-benzoquinone metnyitransrerase, invoived in ubiquinone (Coenzyme Q) biosynthesis; located in mitochondria; Coq5p	1	2.9434	0.2643	1470.43	1470.68	1	285.4	63.636364 L.EFSKIENPLMDF.A
		Component of the mannan polymerase I; forms a complex with Mnn9p, which is								
gi 6323521 ref NP_013592.1	YML115C	involved in in mannan synthesis; mutants are vanadate-resistant; Van1p Component of the mannan polymerase I; forms a complex with Mnn9p, which is	2	4.5477	0.3855	3084.57	3085.255	1	983.2	41.6666664 Y.KTIDLEDEEYYDYDFEDIDPEVISK.F
gi 6323521 ref NP_013592.1	YML115C	involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	2	4.0987	0.3969	1843.53	1843.002	1	916.2	64.28571 F.S1P1P1F1H3E1N2Y1D1K2P1F1R4S1V1.Q
ail63235211refINP_013592_11	YMI 115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is involved in in mannan synthesis: mutants are vanadate-resistant: Van1p	3	4 7919	0.3625	3664.88	3665 807	1	665.7	22 413794 K SSENYKTIDI EDEEYYDYDEEDIDPEVISK E
giloszosz (i cilitii _010002.1)	TWETTOO	Component of the mannan polymerase I; forms a complex with Mnn9p, which is	0	4.7515	0.0020	0004.00	0000.007		000.7	
gi 6323521 ref NP_013592.1	YML115C	involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	2	3.5178	0.3143	1647.79	1645.763	1	659	61.538464 W.HIYEPSDDDLKEIA.S
gi 6323521 ref NP_013592.1	YML115C	involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	3	4.0478	0.2257	3259.13	3260.432	3	452	24 Y.K2T1I1D1L1E1D1E1E1Y1Y1D1Y1D1F1E1D1I1D1P1E1V1I1S1K2F1.D
gil6323521/rofIND_013502_1	VMI 115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is	3	4 8047	0 340	3234 38	3030 430	1	1010	
gilo323321[tel[14]_013332.1]	TWETTOO	Component of the mannan polymerase I; forms a complex with Mnn9p, which is	5	4.0047	0.343	3234.30	3232.432	'	1010	
gi 6323521 ref NP_013592.1	YML115C	involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	2	3.0708	0.2225	2092.67	2093.403	1	694.2	56.25 E.VLTPKDDEKYQRELNML.F
gi 6323521 ref NP_013592.1	YML115C	involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	2	3.9313	0.455	1820.41	1821.002	1	1011.4	64.28571 F.SPPFHENYDKPFRSV.Q
	100 4450	Component of the mannan polymerase I; forms a complex with Mnn9p, which is	~	0.0507	0.0000	0055 45	0057.004		045.0	
gij6323521 [ref NP_013592.1]	YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is	2	3.9507	0.3639	2955.45	2957.081	1	915.6	43.47826 Y.KTIDLEDEEYYDYDFEDIDPEVIS.K
gi 6323521 ref NP_013592.1	YML115C	involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	2	4.3258	0.3775	2981.01	2982.081	1	513.5	43.47826 Y.K2T1I1D1L1E1D1E1E1Y1Y1D1Y1D1F1E1D1I1D1P1E1V1I1S1.K
		High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter: regulated by Pho4p and Spt7p: mutation confers resistance to arsenate:								
gi 6323512 ref NP_013583.1	YML123C	exit from the ER during maturation requires Pho86p; Pho84p	2	3.0378	0.2778	1424.17	1424.727	1	793	66.66667 F.TVDIIGRKPIQLA.G
		High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter: regulated by Pho4p and Spt7p; mutation confers resistance to arsenate;								
gi 6323512 ref NP_013583.1	YML123C	exit from the ER during maturation requires Pho86p; Pho84p	2	3.3604	0.2693	1809.43	1809.995	1	305.9	56.666668 A.ERSLHKEHLTEGGNMA.F
		High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter: regulated by Pho4p and Spt7p; mutation confers resistance to assenate;								
gi 6323512 ref NP_013583.1	YML123C	exit from the ER during maturation requires Pho86p; Pho84p	2	3.4186	0.3077	1737.79	1738.916	1	224	46.42857 A.ERSLHKEHLTEGGNM.A
		High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese								
gi 6323512 ref NP_013583.1	YML123C	exit from the ER during maturation requires Pho86p; Pho84p	2	2.9021	0.1829	1953.77	1952.224	4	410.7	50 N.DFAHIEDPLERRRLAL.E
		High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese								
gi 6323512 ref NP_013583.1	YML123C	exit from the ER during maturation requires Pho86p; Pho84p	1	2.9604	0.2146	1423.76	1424.727	1	392	58.333332 F.TVDIIGRKPIQLA.G
		High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese								
gi 6323512 ref NP 013583.1	YML123C	exit from the ER during maturation requires Pho86p; Pho84p	2	3.0728	0.2528	1352.97	1353.648	1	1135	72.72727 F.TVDIIGRKPIQL.A
51		High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese								
gil6323512lrefINP_013583_1	YMI 123C	transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; evit from the ER during maturation requires Pho86p; Pho84p	2	3 2785	0.3385	1792 43	1792 985	7	319.4	50 N D1E1A1H3I1E1D1P1I 1E1R4R4R4I 1 A
9.1II		Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	_					-		
gi 6323511 ref NP_013582.1	YML124C	polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p Alpha-tubulin: associates with beta-tubulin (Tub2n) to form tubulin dimer, which	3	4.4121	0.1741	1991.18	1989.186	1	1584.1	51.666664 H.Y1T1V1G1R4E1I1V1D1E1V1E1E1R4I1R4.K
gi 6323511 ref NP_013582.1	YML124C	polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	2	4.2201	0.4014	2016.23	2015.18	1	439.2	58.823532 L.E1H3G111K2E1D1G1H3L1E1D1G1L1S1K2P1K2.G
gil6323511/refINP_013582_1	YMI 124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	2	3 2633	0 2847	2225 75	2223 552	6	242 5	
giloszos i ficiliti _010002.11	10121240	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	0.2000	0.2047	2220.10	2220.002	0	242.0	
gi 6323511 ref NP_013582.1	YML124C	polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p Alpha-tubulin; associates with beta-tubulin (Tub2n) to form tubulin dimer, which	2	3.9058	0.4332	1989.79	1990.18	1	479	50 L.EHGIKEDGHLEDGLSKPK.G
gi 6323511 ref NP_013582.1	YML124C	polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	1	2.3216	0.1951	1351.68	1352.665	2	596.8	65 N.LVPYPRIHFPL.V
ail6323511/refIND_013583.41	YMI 124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	3 303	0 424	1182 53	1181 334	1	714 5	75 D GHI EDGI SKPK G
9100200111reiline_010002.1	1 WIL 1240	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which	2	0.002	0.424	1102.00	1101.334	I	7 14.0	10 D.OHELDGEONI N.G
gi 6323511 ref NP_013582.1	YML124C	polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimor, which	3	4.3135	0.3244	2786.69	2787.927	5	376.1	27.000002 L.E1H3G1I1K2E1D1G1H3L1E1D1G1L1S1K2P1K2G1G1E1E1G1F1S1T1.F
gi 6323511 ref NP_013582.1	YML124C	polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	2	2.9851	0.1911	1826.69	1827.087	1	269.1	57.692307 G.R4E1I1V1D1E1V1E1E1R4I1R4K2M1.A
		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; pull mutants have a cell separation defect:								
gi 6323510 ref NP_013581.1	YML125C	Pga3p	3	4.8013	0.3104	3023.87	3026.256	1	1922.5	38.541664 Y.A1N2E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2.V

		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein								
gi 6323510 ref NP_013581.1	YML125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	5.0472	0.3074	2811.17	2809.074	1	1048	35.227272 N.ETENDILLKDELDEMAEKYPHFQ.V
		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein	2	3.3508	0.301	2837.57	2838.074	1	372.2	38.636364 N.E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2.V
ail6323510 ref NP 013581.1	YML125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Poa3o	2	4.2522	0.3439	3189.73	3190.432	1	534	36 L.Y1A1N2E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2.V
51		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum: null mutants have a cell separation defect:								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Essential protein required for meturation of Costa and Photo: CED fusion protein	2	4.1676	0.3115	2682.37	2680.943	1	393.1	45.238094 N.ETENDILLKDELDEMAEKYPHF.Q
		localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ret NP_013581.1	YML125C	Pga3p Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein	3	5.8048	0.3815	3031.04	3029.302	1	2254.8	39.583336 L.YANETENDILLKDELDEMAEKYPHF.Q
gi 6323510 ref NP_013581.1	YML125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	3.116	0.2181	1773.25	1772.896	2	534.9	57.14286 H.Y1V1V1H3Y1P1S1D1R4W2T1G1D1V1G1.Y
		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Essential protein required for maturation of Gas1p and Pho8p: GEP-fusion protein	3	6.0108	0.2203	3431.51	3430.706	1	1403.6	32.407406 L.Y1A1N2E1T1E1N2D111L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2V1H3.Y
ail6323510/refINP_013581_1	YMI 125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pna3n	2	3 657	0.3453	2311 55	2313 537	1	504.5	50 T K2D102M1N2R4Y1I 1P1E1Y1S1E1D1N2R4I 1I 1
giloszos telteltett _etebettin	11121200	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein	-	0.001	0.0100	2011.00	2010.001		001.0	
gi 6323510 ref NP_013581.1	YML125C	Pga3p Escential protein required for maturation of Costa and Bha?a: CEB funion protein	2	2.9595	0.2651	1298.43	1297.5	1	577.5	70 V.RVPIDGKQEVR.Y
		localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein	2	3.1171	0.3019	1395.83	1396.633	2	356.2	59.090908 A.VRVPIDGKQEVR.Y
gi 6323510 ref NP_013581.1	YML125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	3.7558	0.3226	1654.25	1654.804	1	490.9	66.66667 D.E1L1D1E1M1A1E1K2Y1P1H3F1Q2.V
		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Essential protein required for maturation of Gas1p and Pho8p: GEP-fusion protein	2	3.634	0.4361	2807.67	2809.074	1	397.8	38.636364 N.ETENDILLKDELDEMAEKYPHFQ.V
ail6323510/refINP_013581_1	YMI 125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect;	3	4 5705	0 2802	2840 24	2838 074	1	917 5	32 954548 N E1T1E1N2D1111 11 1K2D1E11 1D1E1M1&1E1K2V1P1H3E1O2 V
	11021200	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein	0	4.0700	0.2002	2040.24	2000.014		517.5	
gi 6323510 ref NP_013581.1	YML125C	Pga3p	2	4.4931	0.2969	3156.97	3157.432	1	784.4	40 L.YANETENDILLKDELDEMAEKYPHFQ.V
		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein	3	4.0828	0.1547	2683.82	2680.943	7	639.3	28.57143 N.ETENDILLKDELDEMAEKYPHF.Q
gi 6323510 ref NP_013581.1	YML125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	4.1287	0.2109	3077	3078.347	1	1421.7	35.416664 N.E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2V1H3.Y
		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein	3	5.0186	0.3222	3392.69	3393.706	1	734.4	26.85185 L.YANETENDILLKDELDEMAEKYPHFQVH.Y
ail6323510 ref NP_013581.1	YML125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Poa3p	3	3.8057	0.3653	3042.98	3045.347	1	1249.9	35 416664 N.ETENDILLKDELDEMAEKYPHEOVH Y
giloszos telteltett _orosos i	11121200	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum null mutants have a cell separation defact.	0	0.0001	0.0000	0012.00	00101011	•	121010	
gi 6323510 ref NP_013581.1	YML125C	Pga3p	1	3.2297	0.2832	1567.54	1568.783	1	397.9	61.538464 T.N2I1L1D1E1P1V1H3G1I1Y1I1P1A1.A
		localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein	1	2.8204	0.321	1550.48	1551.783	2	266	50 T.NILDEPVHGIYIPA.A
gi 6323510 ref NP_013581.1	YML125C	localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	4.0426	0.1772	2198.99	2199.377	3	895.4	40.625 T.K2D1Q2M1N2R4Y1L1P1E1Y1S1E1D1N2R4L1.L
		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect;								
gi 6323510 ref NP_013581.1	YML125C	Pga3p Glycoprotein required for oxidative protein folding in the endoplasmic reticulum;	2	2.9049	0.1946	1566.19	1566.844	1	510.2	61.538464 H.VAVRVPIDGKQEVR.Y
gi 6323505 ref NP_013576.1	YML130C	Ero1p Givcoprotein required for exidative protein folding in the endoplasmic reticulum	1	3.1592	0.2749	1577.61	1578.688	1	299	57.692307 L.N2A111N2E1N2I1R4D1D1L1S1A1L1.L
gi 6323505 ref NP_013576.1	YML130C	Ero1p Givenprotein required for exidative protein folding in the endoplasmic reticulum:	1	3.0515	0.2945	1557.65	1558.688	1	246.8	53.846157 L.NAINENIRDDLSAL.L
gi 6323505 ref NP_013576.1	YML130C	Erolp Glycoprotein required for evidative protein folding in the endoplasmic reticulum:	2	4.1982	0.275	1561.51	1558.688	1	709.9	65.38461 L.NAINENIRDDLSAL.L
gi 6323505 ref NP_013576.1	YML130C	Erolp Chapteristic required for evidetive protein folding in the endeplasmic reticulum:	1	2.3045	0.2428	1320.57	1320.488	1	611.6	65 K.TGKWEPNLDLF.M
gi 6323505 ref NP_013576.1	YML130C	Erolp	1	2.5467	0.2535	1528.44	1529.742	3	367.6	54.545456 W.KIQPYLPEFSFC.D
gi 6323505 ref NP_013576.1	YML130C	Giycoprotein required for oxidative protein rolding in the endoplasmic reticulum; Ero1p	2	4.298	0.3465	1830.53	1829.114	1	1012.7	73.07692 A.LWKIQPYLPEFSFC.D
gi 6323505 ref NP_013576.1	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	4.1797	0.2955	1848.01	1846.114	2	1073.7	73.07692 A.L1W2K2I1Q2P1Y1L1P1E1F1S1F1C1.D
gi 6323505 ref NP_013576.1	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	3.7316	0.2647	1946.19	1944.203	1	949.4	67.85714 L.WKIQPYLPEFSFCDL.V
gi 6323505 ref NP_013576.1	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	4.5033	0.3395	2073.73	2076.363	1	1159.4	76.666664 A.L1W2K2I1Q2P1Y1L1P1E1F1S1F1C1D1L1.V
gi 6323505 ref NP 013576.1	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	4.5534	0.3771	2149.63	2148.441	1	982.2	65.625 K.A1L1W2K2I1Q2P1Y1L1P1E1F1S1F1C1D1L1.V
ail6323505/ref/NP_013576_1	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	3,2751	0,153	1450.13	1448.662	1	438.1	63.636364 T.KTGKWEPNLDLF.M
gil6323505lrefINP_013576_1	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Erotip	2	4.3081	0.3204	1899 41	1900 193	1	1119.8	75 K ALWKIQPYLPEFSEC D
gil6323505lrefIND_013576_1	YMI 1300	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum;	2	4 2007	0.3492	1017 12	1018 102	1	636.6	
9-1002000010114r _010070.1	10121300	E.o.p	4	7.2007	0.0402	1017.10	1010.100		0.00.0	

gi 6323505 ref NP_013576.1	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	3.2948	0.2216	1965.13	1962.203	1	887.5	64.28571 L.W2K2I1Q2P1Y1L1P1E1F1S1F1C1D1L1.V
ail6323505/rofIND_013576_1	VMI 130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum;	1	2 0731	0 2312	1450.67	1448 662	2	466.4	
silossosium (NP_015570.1)	1WE 1300	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum;		2.3731	0.2012	1430.07	1440.002	2	400.4	
gi 6323505 ret NP_013576.1	YML130C	Ero1p Glycoprotein required for oxidative protein folding in the endoplasmic reticulum;	2	4.4681	0.3987	1734.67	1731.955	1	1433.3	83.33333 L.W2K2I1Q2P1Y1L1P1E1F1S1F1C1.D
gi 6323505 ref NP_013576.1	YML130C	Ero1p Givcoprotein required for oxidative protein folding in the endoplasmic reticulum:	2	4.2979	0.234	1717.51	1715.955	1	1403.8	83.33333 L.WKIQPYLPEFSFC.D
gi 6323505 ref NP_013576.1	YML130C	Ero1p	1	2.8144	0.3273	1447.46	1448.662	1	543.5	63.636364 T.KTGKWEPNLDLF.M
gi 6323505 ref NP_013576.1	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	1	3.411	0.2088	1466.12	1464.662	1	428.2	63.636364 T.K2T1G1K2W2E1P1N2L1D1L1F1.M
		eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	4.0419	0.4439	2275.17	2275.39	1	1568.9	61.764706 K.AVEQDNKEYEDWEKSYLQ.K
		organization but not in growth or translation initiation, can rescue cytokinesis and								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p eIF3 component of unknown function; deletion causes defects in mitochondrial	2	3.5419	0.2792	2336.73	2338.536	1	845.1	52.63158 A.ALDTTPERNFNDEFQAIKDL.T
ail6323654/refINP_013725_1	YMR012W	organization but not in growth or translation initiation, can rescue cytokinesis and	2	2 9951	0 2076	1658.09	1657 991	6	A1A A	57 142861 KDI SKDVPVELVPSLV
gil0323034[rel[Nr_013723.1]	1101101200	elF3 component of unknown function; deletion causes defects in mitochondrial	2	2.3331	0.2070	1030.03	1037.331	U	414.4	57.14200 E.KDESKD VI VI EVI SE.V
gi 6323654 ref NP_013725.1	YMR012W	organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.4753	0.2617	1773.13	1771.028	1	625	64.28571 L.SFAPYNPVPPFYRSK.G
		eIF3 component of unknown function; deletion causes defects in mitochondrial								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.123	0.2813	1828.43	1828.08	2	347.5	50 L.SFAPYNPVPPFYRSKG.H
		eIF3 component of unknown function; deletion causes detects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	3	5	0.4282	3474.83	3475.835	1	692.3	31.034481 F.SSLPLGPIKERSKQEEKDEKSDPEEKKNTF.K
		organization but not in growth or translation initiation, can rescue cytokinesis and								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p eIF3 component of unknown function; deletion causes defects in mitochondrial	2	3.5804	0.28	2151.99	2154.298	1	739.4	52.941177 L.DTTPERNFNDEFQAIKDL.T
ail62026E4lrofIND_01272E_1	VMP012W/	organization but not in growth or translation initiation, can rescue cytokinesis and	2	2 4000	0 2226	2177.61	2170 209	2	429.4	
gil0323034[rei]NF_013723.1]	TIVINUTZW	eIF3 component of unknown function; deletion causes defects in mitochondrial	2	3.4220	0.2320	2177.01	2179.290	3	430.1	
gi 6323654 ref NP_013725.1	YMR012W	organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	4.9377	0.3803	2298.85	2299.39	1	1189.2	55.88235 K.A1V1E1Q2D1N2K2E1Y1E1D1W2E1K2S1Y1L1Q2.K
		eIF3 component of unknown function; deletion causes defects in mitochondrial								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	3	3.8127	0.3018	2276.87	2275.39	1	527.6	41.17647 K.AVEQDNKEYEDWEKSYLQ.K
		organization but not in growth or translation initiation, can rescue cytokinesis and								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p eIE3 component of unknown function: deletion causes defects in mitochondrial	3	4.089	0.2601	3747.05	3745.045	6	236.4	20.833332 R.SKQEEKDEKSDPEEKKNTFKDVTDEEKLKFN.E
-1020205411ND 04272541	VMD040W/	organization but not in growth or translation initiation, can rescue cytokinesis and	2	2 0005	0.0450	4700 50	4704 000		074.0	
gilo323654[rei]NP_013725.1]	TIVIRUTZVV	elF3 component of unknown function; deletion causes defects in mitochondrial	2	3.0000	0.2459	1792.53	1791.028	I	674.3	67.69714 L.STETATETTINZETVTETETTIK4STK2.G
gi 6323654 ref NP 013725.1	YMR012W	organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	4.3894	0.3214	1670.31	1670.831	1	612.4	69.230774 T.V1K2L1P1K2E1D1N2H3S1H3N2T1K2.H
		elF3 component of unknown function; deletion causes defects in mitochondrial								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.7202	0.3315	1650.57	1647.831	1	420.3	61.538464 T.VKLPKEDNHSHNTK.H
		eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	3	6.1252	0.3603	3516.11	3516.835	1	840.2	32.75862 F.S1S1L1P1L1G1P111K2E1R4S1K2Q2E1E1K2D1E1K2S1D1P1E1E1K2K2N2T1F1.K
		organization but not in growth or translation initiation, can rescue cytokinesis and								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p eIF3 component of unknown function; deletion causes defects in mitochondrial	2	3.2282	0.2648	1882.19	1881.048	1	488.1	56.666668 N.YNADPKPEPVDEFYPV.N
ail6323654/refINP 013725.1	YMR012W	organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictvostelium cluA- mutant: Clu1p	2	3.1417	0.2869	1897.29	1899.048	4	415.2	53.333336 N.Y1N2A1D1P1K2P1E1P1V1D1E1E1Y1P1V1 N
9·1······		elF3 component of unknown function; deletion causes defects in mitochondrial								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.0765	0.1999	1136.33	1134.34	2	1046.9	93.75 Y.M1E1N2P1F1T1L1I1R4.S
		eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and								R.S1K2Q2E1E1K2D1E1K2S1D1P1E1E1K2K2N2T1F1K2D1V1T1D1E1E1K2L1K2F1
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	3	4.8699	0.2465	3784.64	3787.045	1	423	25 N2.E
		organization but not in growth or translation initiation, can rescue cytokinesis and								
gi 6323654 ref NP_013725.1	YMR012W	mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of	3	4.5306	0.3837	2307.86	2309.405	1	735	39.705883 A.R4Q2N2F1D1N2I1E1E1T1G1N2R4Y1P1H3R4Q2.T
ail6323657/refINP_013728_1	YMR015C	the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a target of acole antifungal drugs: Erg5p	2	2 9912	0 1982	1942 37	1944 061	1	348.3	
giloo2000/ficiliti _010/20.1	TMILLOTOO	C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of	2	2.5512	0.1302	1042.07	1344.001		040.0	
gi 6323657 ref NP_013728.1	YMR015C	the G-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a target of azole antifungal drugs; Erg5p	2	3.4773	0.1964	1962.27	1963.061	6	252.9	50 A.L1H3D1P1E1V1Y1E1N2P1D1E1F1I1P1E1.R
		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	2	3.3001	0.2094	1902.75	1901.123	1	572.3	50 R.N2N2D1M1S1T1E1L1N2L1D1L111E1K2M1.K
		the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of	2	3.9419	0.2958	2286.29	2286.462	1	948.8	55.88235 A.LHDPEVYENPDEFIPERW.V
ail6323657/refINP_013729_1	YMR015C	the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a target of acole antifungal drugs; Erg5p	2	3 8131	0 2227	2309 83	2311 462	1	767.6	52 941177 A 1H3D1P1E1V1Y1E1N2P1D1E1E1I1P1E1R4W2 V
9-1-1-2000 10-101 _0101 20-1		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of	2	0.0101	U.LLL1	2000.00	2011.702			
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	2	3.1136	0.29	2517.57	2514.71	1	571.3	44.736843 A.LHDPEVYENPDEFIPERWVE.G

		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of								
ail6323657/refINP_013728.1	YMR015C	the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a target of azole antifungal drugs; Erg5p	2	3.0799	0.4186	2657.47	2658.84	1	589.8	45.238094 A LHDPEVYENPDEFIPERWVEGS K
3/10000001/00/100020001		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of	-					-		
gi 6323657 ref NP_013728.1	YMR015C	the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a target of azole antifungal drugs; Erg5p	2	4.5935	0.3401	2686.83	2687.84	1	830.3	47.61905 A.L1H3D1P1E1V1Y1E1N2P1D1E1F1I1P1E1R4W2V1E1G1S1.K
		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	2	3.495	0.3509	1252.11	1252.544	1	1085.6	88.88889 K.FKFWPIIGPF.L
		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(22) double hand in the sterol side abain in accepteral bisourthesis, may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	1	2.4852	0.2367	1253.62	1252.544	1	518.7	66.66667 K.FKFWPIIGPF.L
		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(23) double bond in the starol side chain in errorsterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	2	2.9137	0.2412	1508.45	1508.819	4	691	54.545456 K.F1K2F1W2P1I1I1G1P1F1L1E1.S
		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(23) double bond in the sterol side chain in errorsterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	1	2.6734	0.1599	1263.44	1264.544	4	470.1	61.11111 K.F1K2F1W2P1I1I1G1P1F1.L
		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis: may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	2	3.8377	0.2265	1262.79	1264.544	1	1048.2	88.88889 K.F1K2F1W2P1I1I1G1P1F1.L
		C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	3	4.5862	0.3266	2686.37	2687.84	1	551.5	32.142857 A.L1H3D1P1E1V1Y1E1N2P1D1E1F1I1P1E1R4W2V1E1G1S1.K
		the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	2	2.9245	0.3124	1254.31	1252.544	1	1200.2	88.88889 K.FKFWPIIGPF.L
		the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p	1	2.2159	0.2293	1251.7	1252.544	1	526	66.66667 K.FKFWPIIGPF.L
		the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p C-22 starol desaturase, a cytochrome P450 enzyme that catalyzes the formation of	2	3.7743	0.272	1263.69	1264.544	1	1032.6	88.88889 K.F1K2F1W2P1111G1P1F1.L
		the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of	1	2.2341	0.1628	1263.6	1264.544	4	406.4	55.555557 K.F1K2F1W2P1I1I1G1P1F1.L
		the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a								
gi 6323657 ref NP_013728.1	YMR015C	target of azole antifungal drugs; Erg5p Protein required for maturation of the 25S and 5.8S ribosomal RNAs: constituent of	2	3.4092	0.3031	1252.47	1252.544	1	1049.3	88.88889 K.FKFWPIIGPF.L
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	2	3.0268	0.3049	2353.49	2353.507	1	449.6	47.22222 Q.RNEQTDDSINPYEPLIDWF.T
gi 6323693 ref NP 013764.1	YMR049C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of 66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	2	3.9908	0.3419	2454.25	2454.612	1	912.4	52.63158 Q.RNEQTDDSINPYEPLIDWFT.R
	VMD040C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	0	0 7044	0.2402	2400.07	0404 040		505.4	
gilo323693[rei]NP_013764.1]	TIMR049C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	2	3.7311	0.3483	2460.27	2401.012	1	595.4	41.306423 Q.R4N2E IQ21101015111N2P111E IP1E11101W2F111.R
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	3	4.2314	0.2258	2989.34	2989.23	1	835.1	30.434782 K.IQRNEQTDDSINPYEPLIDWFTRH.E
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	2	3.53	0.3376	2780.53	2781.94	2	352.8	33.333336 Q.R4N2E1Q2T1D1D1S1I1N2P1Y1E1P1L1I1D1W2F1T1R4H3.E
ail6323693/refINP_013764_1	YMR049C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of 66S pre-ribosomal particles; bomologous to mammalian Bop1; Erb1p	2	3 1464	0 1933	2746 43	2747 94	1	319.7	30 952381 O RNEOTDDSINPYEPI IDWETRH E
		Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	-		0.1000	21.10.10	2			
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	2	3.0784	0.2323	1400.51	1398.676	1	695.4	68.181816 E.N2I1H3L1I1V1P1P1I1F1G1Y1.D
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	1	2.7002	0.2129	1398.58	1398.676	1	554.1	63.636364 E.N2I1H3L1I1V1P1P1I1F1G1Y1.D
gi 6323693 ref NP 013764.1	YMR049C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of 66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	3	6.976	0.4769	3898.58	3899.179	1	1277.9	L.R4A1P1K2L1P1P1P1P1P1P1E1ES1Y1N2P1P1E1E1Y1L1L1S1P1E1E1K2E1A1W2E 32.03125 1N2T1.E
	VMD040C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	2	5 0700	0.0000	2705 50	2707.074		000.0	L.R4A1P1K2L1P1P1P1T1N2E1E1S1Y1N2P1P1E1E1Y1L1L1S1P1E1E1K2E1A1W2E
gilo323693[rei]NP_013764.1]	TWR049C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	3	5.9763	0.3608	3795.50	3797.074	1	902.0	20.012900 1112.1
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	2	3.0439	0.2349	1988.73	1989.245	1	284.6	46.666668 Q.WNKPSQKQLEKDICIT.I
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	3	6.1667	0.3813	3754.61	3756.074	1	1522.4	30.645163 L.RAPKLPPPTNEESYNPPEEYLLSPEEKEAWEN.T
ail63236931refINP_013764_1	YMR049C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	3	6 6708	0 4708	3855.08	3857 179	1	1453.9	32 8125 I RADKI DODTNEESYNDDEEYI I SDEEKEAWENT E
giloszosoliciliti _010704.11	111110400	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of	0	0.0700	0.4700	0000.00	0001.110		1400.0	LR4A1P1K2L1P1P1P1T1N2E1E1S1Y1N2P1P1E1E1Y1L1L1S1P1E1E1K2E1A1W2
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p Protein required for maturation of the 25S and 5.8S ribosomal RNAs: constituent of	3	6.0181	0.3689	3548	3550.854	1	1927.1	35.344826 E
gi 6323693 ref NP_013764.1	YMR049C	66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	3	5.1298	0.2794	3513.32	3512.854	1	1377.8	32.75862 L.RAPKLPPPTNEESYNPPEEYLLSPEEKEAW.E
		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane								
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p	2	3.2484	0.201	1537.63	1535.709	1	778.4	70.83333 M.DMEDATEKVIRDL.H
		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane								T.A1A1L1P1T1Q2N2Y1V1D1S1I1D1N2F1L1D1D1F1Y1L1Q2P1Y1E1K2E1A1I1Y1G1
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p	3	4.4439	0.3927	4666.52	4668.024	1	470	19.871796 E1P1D1H3V1I1T1V1D1.V
		mediating resistance to copper ion toxicity, belongs to class of integral membrane								A.A1L1P1T1Q2N2Y1V1D1S1I1D1N2F1L1D1D1F1Y1L1Q2P1Y1E1K2E1A1I1Y1G1E1
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p	3	4.1289	0.2937	4594.64	4595.945	1	466.7	19.078947 P1D1H3V1I1T1V1D1.V
		mediating resistance to copper ion toxicity, belongs to class of integral membrane								
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron untake and involved in	2	3.1923	0.2501	2868.83	2869.978	1	234.2	40.909092 N.EVDENEERQVNEDRHSTEKHQFL.T
		mediating resistance to copper ion toxicity, belongs to class of integral membrane								
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	2	3.1927	0.1892	2018.29	2019.084	6	487.9	53.125 Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1.P
	MIDATO	mediating resistance to copper ion toxicity, belongs to class of integral membrane	-	0.45.15		1001	1001	-	100/-	
gijb323703 ret NP_013774.1	YMRU58W	multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	2	3.4548	0.2044	1301.63	1301.48	8	1204.3	/5 L.EKDEIVEIVLN.N
	VMDocowy	mediating resistance to copper ion toxicity, belongs to class of integral membrane	2	4 2405	0.0707	4092 47	1002 250	4	472.0	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R
gilo323/03[rei]NP_013//4.1]	I IVINUDOVV	municopper oxidases, recop	3	4.2490	0.2121	4003.17	4003.352		413.0	

		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane								
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	2	3.0668	0.2795	1210.31	1210.277	3	837	77.77778 T.G1W2D1Y1R4N2V1D1G1L1.K
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediotics encietance to encode is encietive, belonger to the order and membrane	2	3.466	0.1842	1552.73	1552.709	1	787.9	70.83333 M.D1M1E1D1A1T1E1K2V1I1R4D1L1.H
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class on integral memorane multicopper oxidases; Fel3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to comper ion toxicity, belonger to class of integral memorane mediation resistance to comper ion toxicity, belonger to class of integral memorane mediation resistance to comper ion toxicity, belonger to class of integral memorane mediation resistance to comper ion toxicity, belonger to class of integral memorane mediation resistance to comper ion toxicity, belonger to class of integral memorane mediation resistance to compering toxicity.	2	5.3407	0.3613	1767.35	1766.902	1	757	69.230774 D.S1I1D1N2F1L1D1D1F1Y1L1Q2P1Y1.E
gi 6323703 ref NP_013774.1	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	2	4.207	0.3469	1816.05	1815.974	1	613	56.666668 Y.EKEAIYGEPDHVITVD.V
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in medicities resistance to compare ion trivity. belongs to class of integral membrane	2	4.2244	0.2398	1683.65	1684.902	1	1181.8	76.92308 M.M1D1M1E1D1A1T1E1K2V1I1R4D1L1.H
gi 6323703 ref NP_013774.1	YMR058W	meticiang resistance to copper non toxicity, belongs to class of integral memorane multicopper oxidases; Fe13p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in medicibles encietance tax-senger is tervicibly. Indegra to class of integral memorane	2	4.2938	0.3834	1877.23	1875.146	1	1343.9	66.66667 Y.G1M1M1D1M1E1D1A1T1E1K2V1I1R4D1L1.H
gi 6323703 ref NP_013774.1	YMR058W	meticianing resistance to Copper ion toxicity, belongs to class of integral memorane multicopper oxidases; Fel3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to comper ion toxicity. belongs to class of integral membrane	2	3.7246	0.358	1854.61	1855.146	1	1114.9	60.000004 Y.GMMDMEDATEKVIRDL.H
gi 6323703 ref NP_013774.1	YMR058W	meticiang residence of corport on toxicity, belongs of class of integral memorane multicopper oxidases; Fe13p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to comparing notivity. Jelonger to class of integral membrane	2	3.0721	0.2241	1543.45	1542.798	4	346	58.333332 F.I1L1E1K2D1E111V1E111V1L1N2.N
gi 6323703 ref NP_013774.1	YMR058W	meticiang residence of Copper ion toxicity, belongs of class of integral memorane multicopper oxidases; Fe13p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to concer ion toxicity. belongs to class of integral membrane	3	4.8857	0.3864	3023.03	3024.082	1	507.5	29.347824 LL1N2E1V1D1E1N2E1E1R4Q2V1N2E1D1R4H3S1T1E1K2H3Q2F1.L
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fef3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to concer ion toxicity. Jelonos to class of interval membrane	3	5.428	0.3963	3379.46	3380.607	1	825	30.357143 Y.D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1L1.Y
gi 6323703 ref NP_013774.1	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	3	4.6012	0.4145	3138.41	3140.257	1	436.5	27.083334 N.E1V1D1E1N2E1E1R4Q2V1N2E1D1R4H3S1T1E1K2H3Q2F1L1T1K2.A
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane	3	5.552	0.4187	3589.79	3590.811	1	869.4	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R 33.62069 4.R
gi 6323703 ref NP_013774.1	YMR058W	meticiang residence of Copper on toxicity, beings to class of integral memorane multicopper oxidases; Forba Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in modificities requirement to energie is the tright. Is hear of integral memorane modificities requirements are nergie is the tright.	2	6.1514	0.5324	2323.73	2325.499	1	1134.2	63.15789 LE1K2D1E111V1E111V1L1N2N2Q2D1T1G1T1H3P1F1.H
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class or integral memorane multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	2	3.2509	0.1521	1313.09	1314.48	1	1263.6	75 LE1K2D1E111V1E111V1L1N2.N
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class or integral memorane multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	3	4.7012	0.2034	3589.76	3590.811	1	382.4	
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class or integral memorane multicopper xidases; Fet3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in	3	4.3323	0.3581	3805.73	3807.076	1	342.7	23.387096 T1L1.Y
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class or integral memorane multicopper xidases; Fet3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediotase ancientone tax-energy is territy; belong to the open of integral memorane	3	4.7485	0.309	3968.72	3969.193	5	298.9	Q.R4D1R411110101A1L1G1E1V1P1H3S1F1D1P101N2H3P1A1F1P1E111P1M1R 19.53125 4R4D1T1.L
gi 6323703 ref NP_013774.1	YMR058W	meticiang residence of corport to totally, belongs to class of integral memorane multicopper oxidases; Fel3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to comperion to vicin. In January to class of integral membrane	3	4.0738	0.1806	3815.21	3818.088	1	513.1	25 Q.RDRTYDDALGEVPHSFDPDNHPAFPEYPMRRD.T
gi 6323703 ref NP_013774.1	YMR058W	metitiating residence of opport in toking, exercise a large integral metiticapper oxidases; Fef2 multicopper oxidases; Fef2 Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to comperion toxicity. belongs to class of integral membrane	3	4.8835	0.3331	3145.88	3148.43	1	826.1	33.653847 D.A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1L1.Y
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fef3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to cooper ion toxicity. belongs to class of interral membrane	3	4.8896	0.3737	4297.25	4299.632	1	303.6	20.714287 L1Y1V1R4P1Q2.S
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to cooper ion toxicity, belonas to class of integral membrane	3	4.0756	0.3006	4247.03	4248.632	9	185.7	17.857143 R.TYDDALGEVPHSFDPDNHPAFPEYPMRRDTLYVRPQ.S
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to cooper ion toxicity, belonas to class of integral membrane	2	4.2065	0.3518	2359.59	2358.615	1	454.8	44.736843 LK2S1R4P1V1I1T1C1N2G1Q2F1P1W2P1D1I1T1V1N2.K
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	3	4.3181	0.1589	2934.65	2932.166	1	623.3	32.291664 D.A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class or integral memorane multicopper xidases; Fet3p Ferro-02-xidoreductase required for high-affinity iron uptake and involved in modificities required to thigh-affinity is hold to class of integral memorane	3	3.9023	0.2235	4097.21	4099.352	1	652.2	Q.R4D1R411710101A1L1G1E1V1P1H3S1F1D1P1D1R2H3P1A1F1P1E171P1M5K 25 4R4D171L1.Y
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper non toxicity, belongs to class on integral memorane multicopper oxidases; Fet3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in modificities required as to senger is the tright. Is hold as the hold of integral memorane modificities required as to senger is the tright. Is hold as the hold of integral memorane modificities required as the senger is the tright.	3	4.5891	0.3134	3752.3	3750.999	2	453.4	26.666668 4R4.D
gi 6323703 ref NP_013774.1	YMR058W	meticating resistance of copper ion toxicity, belongs to class of integral memorane multicopper oxidases; Fe13p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in modificities requirements are negotic to trivingly, belongs of the class of integral memorane	2	3.2948	0.2736	1952.11	1949.121	1	316.2	50 D.E1I1V1E1I1V1L1N2N2Q2D1T1G1T1H3P1F1.H
gi 6323703 ref NP_013774.1	YMR058W	multicopper voldases; Fel3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to comper ion toxicity. Jelanes to class of interare membrane	2	2.9882	0.1787	2699.67	2698.879	2	259.5	30.434782 Y.DDALGEVPHSFDPDNHPAFPEYPM.R
gi 6323703 ref NP_013774.1	YMR058W	multicopper voldases; Fel3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to comper ion toxicity. Jelanes to class of interare membrane	3	5.2863	0.4374	3163.04	3164.343	1	1059.5	36.53846 Y.D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fel3p multicopper oxidases; Fel3p Ferro-02-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to coopper ion toxicity. Jelanors to class of interral membrane	3	4.6542	0.3121	3125.99	3126.343	1	661.5	31.730768 Y.DDALGEVPHSFDPDNHPAFPEYPMRRD.T
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p	3	4.1922	0.3717	3445.01	3446.624	1	790.3	26.785713 Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M\$.R

		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to conner ion toxicity, belongs to class of integral membrane								
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-Q2-oxidoreductase required for high-affinity iron uptake and involved in	3	4.1679	0.268	3389.96	3390.624	1	500.1	25.892857 R.TYDDALGEVPHSFDPDNHPAFPEYPMRRD.T
gil6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases: Fet3p	3	5.8854	0.4652	3427.88	3430.624	1	853.6	33 92857 Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1 R
910020100101111 _01011 111		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediation resistance to conner ion toxicity, belongs to class of integral membrane	0	0.0001	0.1002	0127.00	01001021		000.0	
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p	3	4.7153	0.3653	2748.32	2745.927	4	499.9	29.545454 L.G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
ail6323703/refINP_013774_1	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multiconper ovidase: Fata	з	5 6082	0 3808	2858.6	2860.087	1	671 7	35 860564 & L1G1E1V1P1H3S1E1D1P1D1N2H3P1&1E1P1E1Y1P1M1R4R4D1 T
gilo323703 tellini _013774.1	1111100000	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediciting registrance to connect ion toxicity, belongs to class of integral membrane	5	5.0002	0.3000	2050.0	2000.007		0/1./	
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p	3	4.6334	0.2834	2825.45	2825.087	5	376.8	32.608696 A.LGEVPHSFDPDNHPAFPEYPMRRD.T
		remo-02-oxidoreductase required for high-attinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane								
gi 6323703 ret NP_013774.1	YMR058W	multicopper oxidases; Fetsp Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	3	3.8891	0.3329	2962.55	2962.192	1	378.9	
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class or integral membrane multicopper oxidases; Fet3p	3	5.837	0.3961	4030.88	4033.351	1	337.1	21.212122 V1R4P1Q2.S
		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane								
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	3	5.4201	0.247	3984.68	3984.351	1	305.4	21.212122 Y.DDALGEVPHSFDPDNHPAFPEYPMRRDTLYVRPQ.S
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.3975	0.2315	2893.76	2896.166	1	716.3	35.416664 D.ALGEVPHSFDPDNHPAFPEYPMRRD.T
		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane								
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	3	4.4657	0.3124	3032.09	3034.271	2	584.4	31 D.A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1.L
gi 6323703 ref NP_013774.1	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	5.3487	0.2532	3865.61	3867.088	3	555.4	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R 25.80645 4R4D1.T
		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane								
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in	3	4.1188	0.2451	3111.68	3110.43	4	441.9	28.846153 D.ALGEVPHSFDPDNHPAFPEYPMRRDTL.Y
ail6323703lrefINP 013774.11	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases: Fet3p	3	3.8438	0.1823	3311.12	3312.606	1	760.8	25.925926 D.A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1L1Y1.V
5100 - 101 - 10 - 11		Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane								T.I102R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1
gi 6323703 ref NP_013774.1	YMR058W	multicopper oxidases; Fet3p	3	4.8246	0.22	4111.88	4111.378	2	581.3	23.484848 M1R4R4D1.T
ail6323703/refINP_013774_1	YMR058W	mediating resistance to copper ion toxicity, belongs to class of integral membrane multiconper ovidase: Eatan	з	3 9443	0 2158	4056 53	4059 378	3	458.6	
gil6323713/rof/ND_013793.1	VMP067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p;	2	2 6120	0.2075	1670 46	1590 906	1	1029	20.46671 D4/204/404/404/404/404/404/404/404/404/40
gil6323712 ref NP_013783.1	VMP067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p;	2	3 5475	0.2373	1605 73	1695.055	1	661.0	61 539464 H I 101K201V1011 1011 1011 011 10 10
gil6323712 ref NP_013783.1	VMP067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p;	2	1 13/0	0.202	2727 32	2728 152	1	700.6	24.782608 D E40214D1G4D4D151V4/4K2E4M4D151D402D414A4D11114D4 0
gil6323712 ref NP_013763.1	VMP067C	UBX4p UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p;	3	2.0465	0.2494	2000.05	2000 476	1	199.0	26. D E402HD4C4D4D451V1V1K2E1M1F151D1Q2F1HAF1HE1K4.Q
silc222712 rel NP_012782.1	VMD007C	UBX4p UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p;	2	5.0405	0.1022	2990.95	2990.470	4	100.5	
gij6323712 rei NP_013783.1	TMR067C	UBX4p UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p;	3	5.4442	0.3589	2954.93	2954.476	1	832	
gij6323712 rei NP_013783.1	TMR067C	UBX4p UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p;	3	5.4451	0.2969	2993.03	2990.475	1	011.1	
gi 6323712 ret NP_013783.1	YMR067C	UBX4p UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p;	3	4.3269	0.3554	1613.87	1616.861	1	803.9	45.83336 I.NREDIPHNIKIK.F
gi 6323712 ref NP_013783.1	YMR067C	Ubx4p	3	5.2611	0.3511	2858.48	2858.283	1	1148.5	34.375 R.F1Q2I1P1G1R4D1S1V1V1K2E1M1P1S1D1Q2P111A1P111L1R4Q2.M
		Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent								
gi 6323722 ref NP_013793.1	YMR076C	manner, may function as a protein-protein interaction scaffold; Pds5p	2	3.1625	0.1895	2283.21	2283.582	1	298.4	47.058823 F.E1Y1L1L1P1F1E1P1D1N2D1K2R4V1H3R4L1L1.T
		Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent								
gi 6323722 ref NP_013793.1	YMR076C	manner, may function as a protein-protein interaction scaffold; Pds5p	3	5.3304	0.4306	3275.72	3276.492	1	516.7	24.038462 Y.Q2D1K2L1V1E1D1E1I1D1E1E1E1G1P1Q2K2E1E1A1P1K2K2H3R4P1Y1.G
		Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent								
gi 6323722 ref NP_013793.1	YMR076C	manner, may function as a protein-protein interaction scaffold; Pds5p	3	4.8863	0.3394	3238.49	3238.492	1	931.1	28.846153 Y.QDKLVEDEIDEEEGPQKEEAPKKHRPY.G
		Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent								
gi 6323722 ref NP_013793.1	YMR076C	manner, may function as a protein-protein interaction scaffold; Pds5p ATP-dependent RNA helicase of the SFI superfamily, required for nonsense	2	2.9731	0.1903	1559.63	1559.716	1	305	61.538464 S.IAPDVPRDELAESF.T
gi 6323726 ref NP_013797.1	YMR080C	mediated mRNA decay and for efficient translation termination at nonsense codons; involved in telomere maintenance; Nam7p	2	3.8197	0.279	1955.81	1955.258	1	1318.6	62.5 K.L1F1R4D1G1V1K2P1E1Q2I1G1V1I1T1P1Y1.E
		ATP-dependent RNA helicase of the SFI superfamily, required for nonsense mediated mRNA decay and for efficient translation termination at nonsense codons;								
gi 6323726 ref NP_013797.1	YMR080C	involved in telomere maintenance; Nam7p ATP-dependent RNA helicase of the SFI superfamily, required for nonsense	2	3.1561	0.3682	1929.15	1928.195	1	1394.5	62.5 L.GHQVVDISFDVPLPKEF.S
gi 6323726 ref NP_013797.1	YMR080C	mediated mRNA decay and for efficient translation termination at nonsense codons; involved in telomere maintenance; Nam7p	2	3.5195	0.2327	1842.03	1839.901	2	774.6	56.666668 V.S1L1H3P1D1S1D1L1G1D1T1V1L1E1C1Y1.N
o		ATP-dependent RNA helicase of the SFI superfamily, required for nonsense mediated mRNA decay and for efficient translation termination at nonsense codons:	-					-		
gi 6323726 ref NP_013797.1	YMR080C	involved in telomere maintenance; Nam7p Mitochondrial alcohol dehvdrogenase isozyme III: involved in the shuttling of	2	3.5829	0.2518	2388.25	2385.557	1	547.7	47.22222 K.N2A1N2W2D1T1D1Q2W2Q2P1L111E1D1R4Q2L1L1.S
ail6323729/refINP 013800 1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production: Adh3p	1	3,2203	0.2745	1463.71	1464.659	1	565.7	58.333332 L.GIDAGEEKEKLFK.K
and the state of the state of the										

		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	Production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	1	3.4447	0.1639	1479.63	1480.659	1	603.6	58.333332 L.G1I1D1A1G1E1E1K2E1K2L1F1K2.K
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenese isograme III: involved in the chuttling of	2	3.8603	0.3771	1463.87	1464.659	1	984.1	75 L.GIDAGEEKEKLFK.K
gi 6323729 ref NP_013800.1	YMR083W	mitochondinal alcohol deliyorugenase loszyme int, involved in the anduting bi mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	3.5246	0.2947	1482.33	1480.659	1	490.8	62.5 L.G1I1D1A1G1E1E1K2E1K2L1F1K2.K
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenese isogyme III: involved in the shuttling of	2	4.5577	0.2175	1723.77	1724.992	1	800	64.28571 L.G1I1D1A1G1E1E1K2E1K2L1F1K2K2L1.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to be cytosol under anaerobic conditions and ethanol production; Adh3p	1	2.7292	0.3167	1387.61	1388.653	2	365.1	54.545456 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6323729 ref NP_013800.1	YMR083W	Mitochondrial alcohol denydrogenase isozyme III; involved in the shutting or mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	1	2.5824	0.3201	1371.66	1372.653	1	428.5	59.090908 W.HGDWPLPVKLPL.V
gi 6323729 ref NP_013800.1	YMR083W	Mitochondrial Alcohol denyarogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	4.0013	0.3503	1908.71	1911.189	1	908.4	60.000004 L.H3Y1K2D1I1P1V1P1E1P1K2P1N2E1I1L1.I
gi 6323729 ref NP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	4.1527	0.2364	2141.41	2141.453	1	367.9	50 L.H3Y1K2D1I1P1V1P1E1P1K2P1N2E1I1L1I1N2.V
gil6323720/rofIND_013800.11	VMP083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; AdBa	2	4 0213	0 17/3	1272 51	1372 653	2	003.2	
giloszszzalielike_013600.1	TINKU03W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	4.0213	0.1743	1373.51	1372.033	2	903.2	11.21213 W.HGDWFLF VKLFL.V
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	3.9028	0.3171	1389.17	1388.653	1	913.2	77.27273 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and athanol	2	3.3747	0.5021	1526.81	1528.838	1	977.8	61.538464 W.HGDWPLPVKLPLVG.G
gi 6323729 ref NP_013800.1	YMR083W	Microhodral alcohol dehydrogenase isozyme III; involved in the shatting of	2	3.6008	0.3031	2116.01	2117.453	1	447.5	50 L.HYKDIPVPEPKPNEILIN.V
gi 6323729 ref NP_013800.1	YMR083W	micononal NADA to the cycloso under anaerobic conducts and emanor production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	3.8372	0.2218	2240.43	2241.585	1	437	41.666664 L.H3Y1K2D111P1V1P1E1P1K2P1N2E1I1L111N2V1.K
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	1	3.6275	0.5242	1584.61	1585.889	1	711.5	60.714287 W.HGDWPLPVKLPLVGG.H
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	1	3.9187	0.3257	1548.73	1546.838	1	763.7	65.38461 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NAUH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	1	4.2403	0.196	1530.76	1528.838	1	669.9	61.538464 W.HGDWPLPVKLPLVG.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	4.0285	0.3654	1544.83	1546.838	1	1584	73.07692 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial INAUH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	4.1809	0.3378	1807.53	1807.084	1	757.9	59.375 G.D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	4.213	0.3331	2061.67	2063.329	1	950.3	52.63158 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	3.393	0.1672	2035.93	2037.329	1	929.2	52.63158 W.HGDWPLPVKLPLVGGHEGAG.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	1	3.1869	0.2966	1502.89	1502.782	2	347.7	50 W.P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	4.0856	0.2109	1911.37	1909.198	2	635.3	50 W.HGDWPLPVKLPLVGGHEG.A
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	5.3908	0.5128	1872.75	1875.146	1	2720.6	78.125 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	3.9274	0.3104	1933.63	1933.198	1	968.1	55.88235 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1.A
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	5.3715	0.1849	2164.61	2163.461	1	1184.9	57.5 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III: involved in the shuttling of	3	6.2355	0.4098	1872.29	1875.146	1	2287.5	59.375 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	4.9812	0.2428	2135.53	2136.461	1	1256.1	57.5 W.HGDWPLPVKLPLVGGHEGAGV.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	3	4.4151	0.2057	2163.32	2163.461	1	925.3	36.25 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	3	4.5296	0.2323	2136.11	2136.461	1	1171.9	40 W.HGDWPLPVKLPLVGGHEGAGV.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.2336	0.3097	2260.61	2263.594	1	339.1	35.714287 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1V1.V

		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	4.3629	0.2311	2334.91	2334.726	1	606.5	45.454548 W.HGDWPLPVKLPLVGGHEGAGVVV.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	3.1129	0.3085	1336.49	1336.485	1	404.1	63.636364 L.GIDAGEEKEKLF.K
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehvdrogenase isozvme III: involved in the shuttling of	1	3.0921	0.1723	1349.55	1350.485	1	551.2	63.636364 L.G1I1D1A1G1E1E1K2E1K2L1F1.K
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehvdrogenase isozyme III: involved in the shuttling of	1	2.7404	0.2092	1335.65	1336.485	2	399.4	54.545456 L.GIDAGEEKEKLF.K
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol (dehydrogenase isozyme III: involved in the shuttling of	1	3.5165	0.2173	1480.68	1480.659	1	562.1	58.333332 L.G1I1D1A1G1E1E1K2E1K2L1F1K2.K
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaeronic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogogogo iscaure III: involved in the shuttling of	2	3.6894	0.2253	1814.61	1817.136	7	295.9	50 Y.KDIPVPEPKPNEILIN.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial babbi octivausgenae taozime mi, mondria mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dobudopenage jezame III: jevolved in the shuttling of	2	4.2176	0.189	1980.75	1980.312	1	934.9	65.625 H.YKDIPVPEPKPNEILIN.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to be cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial INADH dehvergeneses iscaume III: involved in the shuttling of	2	3.6992	0.4357	1534.33	1534.755	1	859.1	79.16667 L.HYKDIPVPEPKPN.E
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	1	2.5284	0.2438	1371.68	1372.653	1	491.7	63.636364 W.HGDWPLPVKLPL.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial alcohol denydrogenase isozyme in, involved in the shutting of mitochondrial NDH to the cytosol under anaerobic conditions and ethanol production; Adh3p.	1	2.8215	0.2997	1387.71	1388.653	1	473.3	63.636364 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial AICHO to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	4.1543	0.2945	1389.27	1388.653	1	794.6	72.72727 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.2467	0.4238	1584.61	1585.889	1	754.8	53.571426 W.HGDWPLPVKLPLVGG.H
gi 6323729 ref NP_013800.1	YMR083W	Milconondrial alconol denydrogenase isozyme III; involved in the snutling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	4.5673	0.3791	1602.57	1604.889	1	1399.2	67.85714 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1.H
gi 6323729 ref NP_013800.1	YMR083W	Milconondrial alconol denydrogenase isozyme III; involved in the snutling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	1	3.8202	0.4412	1527.82	1528.838	1	830.4	65.38461 W.HGDWPLPVKLPLVG.G
gi 6323729 ref NP_013800.1	YMR083W	Milconondrial alconol denydrogenase isozyme III; involved in the snutling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	1	4.0913	0.34	1547.81	1546.838	1	934.5	69.230774 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6323729 ref NP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.7892	0.311	1546.45	1546.838	2	1584	73.07692 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6323729 ref NP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; AdhSp	2	3.7319	0.3079	1888.95	1890.189	1	707.7	53.333336 L.HYKDIPVPEPKPNEIL.I
gi 6323729 ref NP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.6967	0.1943	1528.03	1528.838	2	1105.1	65.38461 W.HGDWPLPVKLPLVG.G
gi 6323729 ref NP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.4802	0.3343	2214.89	2216.585	3	401.4	41.666664 L.HYKDIPVPEPKPNEILINV.K
gi 6323729 ref NP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.69	0.2842	1371.73	1372.653	4	575.6	63.636364 W.HGDWPLPVKLPL.V
qi 6323729 ref NP 013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; ddh3p	2	4.1868	0.3424	2024.49	2025.349	1	802.7	53.125 K.L1H3Y1K2D1I1P1V1P1E1P1K2P1N2E1I1L1.I
ail6323729lrefINP 013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; ddh3o	2	4.1358	0.3584	2004.39	2003.349	1	949.9	56.25 K.LHYKDIPVPEPKPNEIL.I
ail6323729irefINP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production: ddh3n	2	3.7659	0.2226	2254.53	2255.612	1	418.8	44 444447 K I 1H3Y1K2D1I1P1V1P1E1P1K2P1N2E1I1I 1I1N2 V
gil6323729/refINP_013800.1	YMR083W	Micochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; dth30.	2	3.0099	0.2501	1788 35	1786.084	1	417.7	
ail6323720/rofINP_013800.1	VMP083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol productions; ddba	2	3 7217	0.2301	2220.05	2220.612	1	404.2	
ail6323720/rofINP_013800.1	VMP083W	Mitochondrial acohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol conduction; dh 3a.	2	4 7241	0.4506	1979.05	1080.277	1	1216.4	
oil6223729161NP_013800.1	VMD093W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	6.0769	0.4300	2005.28	2005 277	1	1405.5	47 22222 W H2C4D4W2D41 4D41/4K21 4D41 41/4C4C4H2E4C4A4 C
-:::0222729[fei[NP_012800.1]	VMD000W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	3	0.2708	0.1657	2005.28	4702.024	1	1495.5	
gilo323729[rel[NP_013800.1]	I WIKU83W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	3	4.4812	0.1015	1/22.65	1723.037	3	1100.0	
gijo323729 ret NP_013800.1	YMRU83W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	5.0083	0.4635	18/2.73	18/5.146	1	2044.3	71.875 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p	2	4.8911	0.4199	1743.59	1745.031	1	1408.3	66.66667 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E

		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	5.0732	0.4569	1850.97	1852.146	1	2194.1	75 W.HGDWPLPVKLPLVGGHE.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	4.851	0.2868	1722.53	1723.031	1	2158.6	76.666664 W.HGDWPLPVKLPLVGGH.E
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	3	6.3864	0.463	1872.47	1875.146	1	1846.9	53.125 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	4.8889	0.4433	2160.73	2163.461	1	1124.1	57.5 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	5.0006	0.1972	2136.17	2136.461	1	1036.8	55 W.HGDWPLPVKLPLVGGHEGAGV.V
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	3	5.9524	0.4437	1849.85	1852.146	1	2719.1	62.5 W.HGDWPLPVKLPLVGGHE.G
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	3	5.2536	0.3403	1742.9	1745.031	1	1579.1	51.666664 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E
gi 6323729 ref NP_013800.1	YMR083W	mitochondrial INAUH to the cytosol under anaerobic conditions and emanol production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitechondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitechondrial INAUH to the outper which even grave philic preditions and otherspl.	2	3.1536	0.2337	1560.89	1560.864	1	834.4	65.38461 D.W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6323729 ref NP_013800.1	YMR083W	microindrata include the cytosol under anaerobic conditions and emanoi production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	3	4.8128	0.1633	1982	1980.277	1	962.6	41.6666664 W.HGDWPLPVKLPLVGGHEGA.G
gi 6323729 ref NP_013800.1	YMR083W	microbindial NAPA in the ergoson under an electronic conductions and emandi production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NAPA to the cutors(under gragerbic conditions and ethanol	2	4.8422	0.3295	2004.39	2005.277	1	1530.1	63.88889 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.G
gi 6323729 ref NP_013800.1	YMR083W	microbindial NDH to the dytogenase isozyme III; involved in the shuttling of microbindial alcohol dehydrogenase isozyme III; involved in the shuttling of microbindial NDH to the cutosol under anaerobic conditions and ethanol	3	4.9838	0.2384	2262.86	2263.594	1	939.3	38.095238 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1V1.V
gi 6323729 ref NP_013800.1	YMR083W	microbindia Arban to the system and a microbind and statistical and statistic production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NDH to the cvtosol under anaerobic conditions and ethanol	3	4.124	0.1777	2237.69	2235.594	2	669.2	33.333336 W.HGDWPLPVKLPLVGGHEGAGVV.V
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	4.0559	0.342	1755.61	1753.048	1	1136.4	64.28571 H.YKDIPVPEPKPNEIL.I
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	4.2588	0.2705	1769.89	1771.048	1	1251.9	67.85714 H.Y1K2D111P1V1P1E1P1K2P1N2E1I1L1.I
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	3.9075	0.1784	2003.37	2001.312	1	874.6	65.625 H.Y1K2D11P1V1P1E1P1K2P1N2E1I1L111N2.V
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	2.9069	0.2938	1715.17	1715.005	5	354.1	50 H.GDWPLPVKLPLVGGHE.G
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	1	2.7936	0.2432	1387.78	1388.653	1	406.1	59.090908 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	3.6585	0.2005	1552.65	1552.755	1	521.6	66.66667 LH3Y1K2D111P1V1P1E1P1K2P1N2.E
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	1	2.5366	0.3597	1371.62	1372.653	2	457.9	59.090908 W.HGDWPLPVKLPL.V
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	4.3253	0.3016	1389.25	1388.653	1	964.5	77.27273 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	1	4.0372	0.2692	1529.96	1528.838	1	702.8	61.538464 W.HGDWPLPVKLPLVG.G
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	1	3.2679	0.2435	1586.92	1585.889	1	406.5	46.42857 W.HGDWPLPVKLPLVGG.H
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	3.4332	0.2331	1487.81	1488.786	1	1007.8	66.66667 W.H3G1D1W2P1L1P1V1K2L1P1L1V1.G
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	1	4.0023	0.3302	1547.6	1546.838	1	985.2	69.230774 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	4.1249	0.3893	1584.69	1585.889	1	1560.6	
gil6323729/ref/NP_013800.1	YMR083W	production; Adnap Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	3.931	0.2191	1547.31	1546.838	2	1279.6	
gil6323729/ref/NP_013800.1	VMP083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol moduration; dh3a	2	2.7133	0.1778	1079.03	1272 653	1	554.4	
ail6323729/refINP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol moduction; 4dh3n	2	2 9968	0.1778	1667.29	1666 915	4	413.5	61 538464 K I 1H3Y1K2D1IIP1V1P1F1P1K2D1N2 E
gil6323729/refINP_013800.1	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol moduction; 4dh3n	2	4.0178	0.2713	1528.61	1528.838	2	1290.1	
5-1-1-201-201-01-01-00-00-11			2		001		.020.000	-	.200.1	

		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of								
ail62227201rofIND_012800_1	VMD092W/	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	2 2267	0 2242	1022 72	1000 144	1	406.4	
gilo323729[rei]NP_013800.1]	TIVIRU63W	Mitochondrial alcohol dehydrogenase isozyme III: involved in the shuttling of	2	3.3267	0.2343	1033.73	1633.141	1	490.4	30.000000 K.GKLHTKDIPVPEPKPN.E
		mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p	2	5.166	0.5049	1873.97	1875.146	1	1755.5	65.625 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of								
gil6323729/refINP_013800_1	YMR083W	mitochondrial NADH to the cytosol under anaeropic conditions and ethanol production: Adb3p	2	5 2552	0 4408	2002 81	2005 277	1	1189.3	61 11111 W H3G1D1W2P1I 1P1V1K2I 1P1I 1V1G1G1H3E1G1A1 G
gil0020120[101141 _010000.1]	1111100011	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	-	0.2002	0.4400	2002.01	2000.211		1100.0	
		mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p	2	4.8338	0.4932	1721.59	1723.031	1	2181.5	76.666664 W.HGDWPLPVKLPLVGGH.E
		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cutocol under anaerobic conditions and ethanol								
gil6323729/refINP_013800.1	YMR083W	production: Adh3p	3	6.6669	0.4155	1850.69	1852,146	1	1951.9	56.25 W.HGDWPLPVKLPLVGGHE.G
giloozor zeli oli ili _o receci il		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	Ū	0.0000	0.1100	1000.00	1002.1110		1001.0	
		mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p	3	5.1465	0.1981	1981.67	1980.277	1	1548.3	50 W.HGDWPLPVKLPLVGGHEGA.G
		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cutosol under anaerobic conditions and ethanol								
ail6323729/refINP 013800.11	YMR083W	production: Adh3p	2	5.0269	0.5071	1849.89	1852,146	1	3140.9	84.375 W.HGDWPLPVKLPLVGGHE.G
5100 101 2000		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of								
		mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p Mitochondrial alcohol debydrogenase isozyme III: involved in the shuttling of	3	6.0883	0.3685	1743.38	1745.031	1	1820.2	56.666668 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E
		mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p	2	4.5257	0.435	1978.47	1980.277	1	1250.1	61.11111 W.HGDWPLPVKLPLVGGHEGA.G
		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of								
-: 102222201 (IND_042800.4)	VMD000W	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	F 0570	0.0407	2000 42	2005 077		1000 0	
gilb323729[rei]NP_013800.1]	TIVIRU63VV	Mitochondrial alcohol dehydrogenase isozyme III: involved in the shuttling of	3	5.9576	0.2427	2006.42	2005.277	1	1006.6	41.000004 W.H3GIDIW2PILIPIVIK2LIPILIVIGIGIH3EIGIAI.G
		mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p	3	5.3805	0.2526	1723.46	1723.031	1	2156.4	60.000004 W.HGDWPLPVKLPLVGGH.E
		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of								
gil6323720/rofINP_013800.11	VMP083W/	mitochondrial NADH to the cytosol under anaerobic conditions and ethanol	2	5 1551	0.2685	1746 20	1745 031	1	1501 1	66 66667 W H3C1D1W2D1I 1D1V1K2I 1D1I 1V1C1C1H3 E
gil0525725[rei]14 _015000.1]	1101100500	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of	2	5.1551	0.2005	1740.23	1745.051		1301.1	
		mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p	3	5.867	0.3839	1872.68	1875.146	1	1782.6	53.125 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of								
ail6323729/refINP 013800.11	YMR083W	production: Adh3p	2	4.015	0.3807	2135.43	2136.461	1	640.2	45 W.HGDWPLPVKLPLVGGHEGAGV.V
5100 101 = 0001		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of								
		mitochondrial NADH to the cytosol under anaerobic conditions and ethanol								
gi 6323729 ref NP_013800.1	YMR083W	production; Adh3p	3	4.3842	0.1753	2137.7	2136.461	1	916.9	35 W.HGDWPLPVKLPLVGGHEGAGV.V
gi[6323735]ref[NP_013806.1]	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	2	3.1476	0.1939	1265.71	1286.604	1	485.5 639.2	64 28571 S S1Y1I 1R4G1P1N2F1P1T1D111F1V1R4 I
gi 6323735 ref NP_013806.1	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	2	3.4507	0.33331	1849.67	1850.213	1	802.5	67.85714 K.FHEYNLALPKFPILF.S
gi 6323735 ref NP_013806.1	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	2	2.9592	0.3057	1782.85	1783.04	6	388.1	50 S.SYLRGPNFPTDIFVR.I
gi 6323735 ref NP_013806.1	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	1	3.0159	0.1664	1286.49	1286.604	1	516.5	60.000004 Y.N2L1A1L1P1K2F1P1I1L1F1.S
gi[6323735 ref NP_013806.1]	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	2	2.909	0.2464	1374.09	1374.682	2	555.5 861.2	68.181816 Y.N2L1A1L1P1K2F1P111L1F1S1.L
gil6323735/refINP_013806.1	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	2	3.2851	0.2376	1273.42	1273.604	2	507.7	65 Y.NLALPKEPILE.S
		Nuclear protein that may have a role in nuclear protein import and maintenance of								
gi 6323738 ref NP_013809.1	YMR091C	proper telomere length; Npl6p	2	4.4503	0.3784	2171.55	2171.359	1	1128.7	61.764706 L.S1E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4.A
ail62227281cofIND 012800 1	VMP001C	Nuclear protein that may have a role in nuclear protein import and maintenance of	2	2 2406	0.2105	2244.62	2246 510	1	265	
gilo323736[rei]NF_013609.1]	TWIKU91C	Nuclear protein that may have a role in nuclear protein import and maintenance of	2	3.3400	0.3195	2244.03	2240.319	1	205	30.00009 S.EIFREITEDV VDEDVERALT
gi 6323738 ref NP_013809.1	YMR091C	proper telomere length; Npl6p	2	4.8035	0.385	2355.81	2357.598	1	1320.6	55.263157 L.S1E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4A1I1.T
		Nuclear protein that may have a role in nuclear protein import and maintenance of								
gi 6323738 ref NP_013809.1	YMR091C	proper telomere length; Npl6p	2	3.432	0.2508	2458.49	2459.703	1	1050.4	50 L.S1E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4A1I1T1.E
gil6323738/rofIND_013800_1	VMP001C	Nuclear protein that may have a role in nuclear protein import and maintenance of	2	3 0/25	0 3803	2422 43	2434 703	1	021.4	
gil0525750[rei]14r_015005.1]	TWINGSTO	Nuclear protein that may have a role in nuclear protein import and maintenance of	2	3.3423	0.3002	2432.43	2434.703	,	321.4	JULISEIR KEITED VUDED VERKIT.E
gi 6323738 ref NP_013809.1	YMR091C	proper telomere length; Npl6p	2	4.2377	0.2808	1997.53	1997.255	1	478.5	50 F.KKPVFPGIDDAEENLNPL.K
		Nuclear protein that may have a role in nuclear protein import and maintenance of								
gi 6323738 ref NP_013809.1	YMR091C	proper telomere length; Npl6p	2	3.8699	0.3875	2083.97	2083.281	2	320.3	43.75 S.E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4.A
gil6323738/refINP_013809.1	YMR091C	proper telomere length: Npl6p	2	4.3978	0.4221	2148.71	2149.359	1	1384.3	70.588234 L.SEIPKEIYEDVVDEDVLR.A
34		Nuclear protein that may have a role in nuclear protein import and maintenance of	_							
gi 6323738 ref NP_013809.1	VMP001C	proper telemore length: Noles								61 11111 S1E111D1K2E111V1E1D1V1V1D1E1D1V11 1D4A1
-: 102222201 (IND_042800.4)	TWIRU91C	proper teromere rengin, rupiop	2	3.7479	0.2719	2245.75	2243.438	1	1013.3	01.11111 L.STETTFTKZETTTTETDTVTVTDTETDTVTLTK4AT.I
UI03237301101111 U13009.11	VMR001C	Nuclear protein that may have a role in nuclear protein import and maintenance of	2	3.7479	0.2719	2245.75	2243.438	1	1013.3	
3100001	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of	2 2	3.7479 5.3664	0.2719 0.4861	2245.75 2264.29	2243.438 2262.519	1 1	1013.3 1516.4	63.88889 G.LSEIPKEIYEDVVDEDVLR.A
gi 6323738 ref NP_013809.1	YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2 2 2	3.7479 5.3664 3.4018	0.2719 0.4861 0.2578	2245.75 2264.29 2271.01	2243.438 2262.519 2269.519	1 1 1	1013.3 1516.4 504.8	63.88889 G.LSEIPKEIYEDVVDEDVLR.A 47.22222 S.E11P1K2E111Y1E1D1V1V1D1E1D1V1L1R4A111.T
gi 6323738 ref NP_013809.1	YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of	2 2 2	3.7479 5.3664 3.4018	0.2719 0.4861 0.2578	2245.75 2264.29 2271.01	2243.438 2262.519 2269.519	1 1 1	1013.3 1516.4 504.8	63.88889 G.LSEIPKEIYEDVVDEDVLR.A 47.22222 S.E111P1K2E111Y1E1D1V1V1D1E1D1V1L1R4A111.T
gi 6323738 ref NP_013809.1 gi 6323738 ref NP_013809.1	YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2 2 2 2	3.7479 5.3664 3.4018 3.3013	0.2719 0.4861 0.2578 0.2658	2245.75 2264.29 2271.01 2332.45	2243.438 2262.519 2269.519 2333.598	1 1 1 1	1013.3 1516.4 504.8 753	 61.TTTT L.STETTT FIZZETT FEDDIVIDLE DIVIDLE DIVIDLE AT A CONTRACT AND A
gi 6323738 ref NP_013809.1 gi 6323738 ref NP_013809.1 gi 6323738 ref NP_013809.1	YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2 2 2 2	3.7479 5.3664 3.4018 3.3013	0.2719 0.4861 0.2578 0.2658	2245.75 2264.29 2271.01 2332.45	2243.438 2262.519 2269.519 2333.598	1 1 1 1	1013.3 1516.4 504.8 753	61.31111 E.STETHT FILZETT FED TVIDTE DI VIDTE DI VIDTE ATT 63.88889 G.LSEIPKEIYEDVVDEDVLR.A 47.22222 S.E111P1K2E111Y1E1D1V1V1D1E1D1V1L1R4A111.T 47.368423 L.SEIPKEIYEDVVDEDVLRAI.T 45.C LSEIPKEIYEDVVDEDVLRAI.T
gi[6323738 ref NP_013809.1 gi[6323738 ref NP_013809.1 gi[6323738 ref NP_013809.1	YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2 2 2 2 2 2	3.7479 5.3664 3.4018 3.3013 3.5125	0.2719 0.4861 0.2578 0.2658 0.2163	2245.75 2264.29 2271.01 2332.45 2444.91	2243.438 2262.519 2269.519 2333.598 2446.757	1 1 1 1 1	1013.3 1516.4 504.8 753 730.5	 63.88889 G.LSEIPKEIYEDVVDEDVLR.A 47.22222 S.E111P1K2E111Y1E1D1V1V1D1E1D1V1L1R4A111.T 47.368423 L.SEIPKEIYEDVVDEDVLRAI.T 45 G.LSEIPKEIYEDVVDEDVLRAI.T
gi[6323738 ref NP_013809.1 gi[6323738 ref NP_013809.1 gi[6323738 ref NP_013809.1 gi[6323738 ref NP_013809.1	YMR091C YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2 2 2 2 2 2 2	 3.7479 5.3664 3.4018 3.3013 3.5125 4.1986 	0.2719 0.4861 0.2578 0.2658 0.2163 0.3083	2245.75 2264.29 2271.01 2332.45 2444.91 2165.29	2243.438 2262.519 2269.519 2333.598 2446.757 2167.432	1 1 1 1 1 1	1013.3 1516.4 504.8 753 730.5 1005.1	 61.11111 E.STETHT FIGETITTE IDTVIDUE ID
gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1]	YMR091C YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2 2 2 2 2 2 2	 3.7479 5.3664 3.4018 3.3013 3.5125 4.1986 	0.2719 0.4861 0.2578 0.2658 0.2163 0.3083	2245.75 2264.29 2271.01 2332.45 2444.91 2165.29	2243.438 2262.519 2269.519 2333.598 2446.757 2167.432	1 1 1 1 1	1013.3 1516.4 504.8 753 730.5 1005.1	 61.1111 L.STETHT RZETITTE IDTVIDTE IDTVIDTETOTVIDTEAT.1 63.88889 G.LSEIPKEIYEDVVDEDVLR.A 47.22222 S.E1I1P1K2E111Y1E1D1V1V1D1E1D1V1L1R4A111.T 47.368423 L.SEIPKEIYEDVVDEDVLRAI.T 45 G.LSEIPKEIYEDVVDEDVLRAI.T 61.11111 K.F1K2K2P1V1F1P1G11ID1D1A1E1E1N2L1N2P1L1.K
gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1]	YMR091C YMR091C YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2 2 2 2 2 2 2 2 2 2	 3.7479 5.3664 3.4018 3.3013 3.5125 4.1986 4.9911 	0.2719 0.4861 0.2578 0.2658 0.2163 0.3083 0.4066	2245.75 2264.29 2271.01 2332.45 2444.91 2165.29 2145.63	2243.438 2262.519 2269.519 2333.598 2446.757 2167.432 2144.432	1 1 1 1 1 1 1	1013.3 1516.4 504.8 753 730.5 1005.1 1132	 61.11111 E.STETHTE INCENTIFIED VIDIE DIVIDIE DIVIDIE IN VIDIE IN VIDIE IN VIDIE IN VIDIE VIDI
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gi[6323738 ref NP_013809.1] gi[6323738 ref NP_013809.1] gi[6323738 ref NP_013809.1] gi[6323738 ref NP_013809.1] gi[6323738 ref NP_013809.1]	YMR091C YMR091C YMR091C YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2 2 2 2 2 2 2 2	3.7479 5.3664 3.4018 3.3013 3.5125 4.1986 4.9911	0.2719 0.4861 0.2578 0.2658 0.2163 0.3083 0.4066	2245.75 2264.29 2271.01 2332.45 2444.91 2165.29 2145.63	2243.438 2262.519 2269.519 2333.598 2446.757 2167.432 2144.432	1 1 1 1 1 1	1013.3 1516.4 504.8 753 730.5 1005.1 1132	 61.11111 E.STETHTE REETITTE IDTVIDUE ID
gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323751]ref[NP_013822.1]	YMR091C YMR091C YMR091C YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Protein kinase with similarityto serine/threonine protein kinase Ypk1p; functionally redundant with YPk1 at the genetic level; participates in a signaling pathway required for optimal cell wall integrity; homolog of mammalian kinase SGK; Ypk2p	2 2 2 2 2 2 2 2 2	3.7479 5.3664 3.4018 3.3013 3.5125 4.1986 4.9911 4.1084	0.2719 0.4861 0.2578 0.2658 0.2163 0.3083 0.4066	2245.75 2264.29 2271.01 2332.45 2444.91 2165.29 2145.63 2573.53	2243.438 2262.519 2269.519 2333.598 2446.757 2167.432 2144.432 2575.788	1 1 1 1 1 1 1	1013.3 1516.4 504.8 753 730.5 1005.1 1132 497.6	 61.1111 L.STETHTP IX2E IITTE IDTVIDUE I
gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323738]ref[NP_013809.1] gi[6323751]ref[NP_013822.1]	YMR091C YMR091C YMR091C YMR091C YMR091C YMR091C YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Protein kinase with similarityto serine/threonine protein kinase Ypk1p; functionally redundant with YPK1 at the genetic level; participates in a signaling pathway required for optimal cell wall integrity; homolog of mammalian kinase SGK; Ypk2p Protein kinase with similarityto serine/threonine protein kinase Yuk1p; functionally	2 2 2 2 2 2 2 2 2 2	3.7479 5.3664 3.4018 3.3013 3.5125 4.1986 4.9911 4.1084	0.2719 0.4861 0.2578 0.2658 0.2163 0.3083 0.4066 0.425	2245.75 2264.29 2271.01 2332.45 2444.91 2165.29 2145.63 2573.53	2243.438 2262.519 2269.519 2333.598 2446.757 2167.432 2144.432 2575.788	1 1 1 1 1 1 1	1013.3 1516.4 504.8 753 730.5 1005.1 1132 497.6	 61.1111 E.STETHTE RZETITTE IDTVIDTE IDTVIDTE IDTVIDTEATIONELIKAALT 63.88889 G.LSEIPKEIYEDVVDEDVLR.A 47.22222 S.E111P1K2E111Y1E1D1V1V1D1E1D1V1L1R4A111.T 47.368423 L.SEIPKEIYEDVVDEDVLRAI.T 45 G.LSEIPKEIYEDVVDEDVLRAI.T 61.11111 K.F1K2K2P1V1F1P1G11D1D1A1E1E1N2L1N2P1L1.K 69.44444 K.FKKPVFPGIDDAEENLNPL.K 40.476192 A.NFDQEFTKEKPIDSVVDEYLSA.S
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gi[6323738]ref[NP_013809.1] gi[6323738[ref[NP_013809.1] gi[6323738[ref[NP_013809.1] gi[6323738[ref[NP_013809.1] gi[6323738[ref[NP_013809.1] gi[6323751[ref[NP_013822.1] gi]6323751[ref[NP_013822.1]	YMR091C YMR091C YMR091C YMR091C YMR091C YMR091C YMR104C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p Protein kinase with similarityto serine/threonine protein kinase Ypk1p; functionally redundant with YPK1 at the genetic level; participates in a signaling pathway required for optimal cell wall integrity; homolog of mammalian kinase SGK; Ypk2p	2 2 2 2 2 2 2 2 2 2 2 2	3.7479 5.3664 3.4018 3.3013 3.5125 4.1986 4.9911 4.1084	0.2719 0.4861 0.2578 0.2658 0.2163 0.3083 0.4066 0.425 0.3963	2245.75 2264.29 2271.01 2332.45 2444.91 2165.29 2145.63 2573.53	2243.438 2262.519 2269.519 2333.598 2446.757 2167.432 2144.432 2575.788 2327.472	1 1 1 1 1 1 1 1	1013.3 1516.4 504.8 753 730.5 1005.1 1132 497.6 438.1	 61.11111 E.STETHTE INCENTIFIED VIDE EDIVIDIE IN VIDE EDIVIDIE IN VIDE EDIVIDIE IN VIDE EDIVIDE VIDE VIDE VIDE VIDE VIDE V

gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.6635	0.3779	2357.77	2359.605	1	454.7	45.238094 Q.N2V1D1T1V1F1G1Y1P1G1G1A111L1P1V1Y1D1A111H3N2.S
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	5.0018	0.3511	2033.05	2033.124	1	1324.5	58.823532 A.G1G1S1G1L1D1E1F111N2F1D1P1E1V1E1R4Q2.Q
gi 6323755 ref NP 013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	1	2.5068	0.2364	1380.28	1380.467	1	342.7	54.166668 E.S1L1V1I1D1I1D1G1D1A1S1F1N2.M
gil6323755lrefINP_013826.11	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria: expression of the gene is under general amino acid control. IIv2o	2	3.1879	0.1728	1843.69	1845.1	2	558	47.058823 A.T1S1G1R4P1G1P1V1L1V1D1L1P1K2D1V1T1A1 A
gil6323755lrefINP_013826.11	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria: expression of the gene is under general amino acid control. IIv2o	2	4.0048	0.3264	1917.19	1917.178	1	572.2	50 A.T1S1G1R4P1G1P1V1L1V1D1L1P1K2D1V1T1A1A1.I
ail6323755/refINP_013826.11	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria: expression of the opene is under general amino acid control. IV/20	2	3 264	0 2193	1895 73	1894 178	1	748 5	52 77778 A TSGRPGPVI VDI PKDVTAA I
oil6222755[ct]ND_012826_1	VMP109W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochoodic expression of the conce index several classes of inhibitors.	2	4.654	0.4007	2726.61	2728.002	1	677.7	
		Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the	2	4.034	0.4007	2730.01	2730.002	1	077.7	
gi 6323755 ref NP_013826.1	YMR108W	mitochondria; expression of the gene is under general amino acid control; Ilv2p Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the	2	3.4225	0.2111	1239.83	1240.433	1	671.3	77.77778 T.H3Q2L1N2P1D1F111K2L1.A
gi 6323755 ref NP_013826.1	YMR108W	mitochondria; expression of the gene is under general amino acid control; Ilv2p Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the	1	2.6559	0.2127	1224.51	1225.433	3	255.5	66.66667 T.HQLNPDFIKL.A
gi 6323755 ref NP_013826.1	YMR108W	mitochondria; expression of the gene is under general amino acid control; IIv2p Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inbititions, localizes to the	2	3.0289	0.2761	1654.45	1654.863	1	281.5	60.714287 A.SKRPEPAPSFNVDPLE
gi 6323755 ref NP_013826.1	YMR108W	mitochondria; expression of the gene is under general amino cid control; Ilv2p Acetolactate synthase, catalyses the first common step in isoleucine and valine	3	4.7044	0.3428	2737.7	2738.028	1	1074.8	34.375 A.S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1A1.k
gi 6323755 ref NP_013826.1	YMR108W	biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p Acetolactate synthase, catalyses the first common step in isoleucine and valine	2	3.5896	0.2817	2736.59	2738.028	1	306.1	39.583336 A.S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1A1.k
gi 6323755 ref NP_013826.1	YMR108W	biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p Acetolactate synthase, catalyses the first common step in isoleucine and valine	1	2.4953	0.205	1221.83	1222.385	1	537.1	70 D.P1L1E1Q2P1A1E1P1\$1K2L1.A
gi 6323755 ref NP_013826.1	YMR108W	biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	4.5437	0.336	2635.04	2634.949	1	1585.9	44.56522 A.SKRPEPAPSFNVDPLEQPAEPSKLA
gi 6323755 ref NP_013826.1	YMR108W	biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	3.7851	0.2912	2637.13	2634.949	1	437.9	45.652176 A.SKRPEPAPSFNVDPLEQPAEPSKLA
gi 6323755 ref NP_013826.1	YMR108W	Accordactate synthase, catalyses the inst common step in isoleccine and value biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.3174	0.3439	2223.53	2225.642	1	563.8	45 Q.S111N2K2A1A1D1L111N2L1A1K2K2P1V1L1Y1V1G1A1.G
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.6791	0.2375	2394.53	2393.615	1	569.5	50 A.SKRPEPAPSFNVDPLEQPAEPS.K
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	4.1112	0.3791	1655.43	1656.878	1	703	75 K.I1F1P1V1K2E1R4S1E1W2F1A1Q2.I
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.8955	0.2944	2705.87	2706.028	1	280	37.5 A.SKRPEPAPSFNVDPLEQPAEPSKLA.K
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.4652	0.2499	2735.57	2738.028	1	327	39.583336 A.S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1A1.K
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.6579	0.2126	2665.87	2665.949	2	269.6	36.95652 A.S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1.A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.7209	0.2772	2634.61	2634.949	2	341.5	41.304348 A.SKRPEPAPSFNVDPLEQPAEPSKLA
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	3	4.8443	0.3662	2668.37	2665.949	1	1690.6	41.304348 A.S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1.A

gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	4.7894	0.2949	2738.18	2738.028	1	868.5	32.291664 A.S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1A1.K
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	4.1542	0.3034	2705.3	2706.028	1	741.2	31.25 A.SKRPEPAPSFNVDPLEQPAEPSKLA.K
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	5.2573	0.3721	3365.9	3368.734	1	538.2	Y.S1A1S1P1L1P1A1S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L 28.225807 1A1.K
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	5.0937	0.3517	3295.55	3296.656	1	589.7	Y.S1A1S1P1L1P1A1S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L 26.666668 1.A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	4.5277	0.3323	3257.81	3258.656	1	669.3	27.5 Y.SASPLPASKRPEPAPSFNVDPLEQPAEPSKLA
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	4.2614	0.3387	3134.9	3136.499	2	655.8	27.67857 A.S1P1L1P1A1S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1.A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	3	4.9677	0.3453	3208.94	3208.577	1	601.1	S.A1S1P1L1P1A1S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1. 27.586206 A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	3.8657	0.3569	1874.85	1875.131	1	544.8	57.14286 M.S1K2I1F1P1V1K2E1R4S1E1W2F1A1Q2.I
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.2207	0.2018	1984.35	1984.323	1	571	50 M.MSKIFPVKERSEWFAQ.I
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	3	4.2905	0.3112	3102.11	3100.499	1	634	25.892857 A.SPLPASKRPEPAPSFNVDPLEQPAEPSKLA
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	4.7876	0.3658	1811.25	1808.942	1	1884.6	75 S.GLDEFINFDPEVERQ.Q
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	4.0529	0.2808	2419.53	2421.615	1	399.6	42.857143 A.S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1.K
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	2.9664	0.1939	1822.57	1823.1	1	701	52.941177 A.TSGRPGPVLVDLPKDVTA.A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	3	4.0437	0.2051	1822.22	1823.1	1	998.6	42.647057 A.TSGRPGPVLVDLPKDVTA.A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	3.2497	0.2619	1637.25	1637.878	2	556.6	66.66667 K.IFPVKERSEWFAQ.I
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	4.6868	0.3635	2664.77	2665.949	1	1353.3	39.130436 A.S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1.A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	3.7671	0.3032	2636.17	2634.949	1	454.2	45.652176 A.SKRPEPAPSFNVDPLEQPAEPSKL.A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	3	3.8841	0.2731	2637.5	2634.949	1	1468.5	41.304348 A.SKRPEPAPSFNVDPLEQPAEPSKL.A
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	5.1302	0.3723	1829.31	1828.942	1	1547.5	71.42857 S.G1L1D1E1F111N2F1D1P1E1V1E1R4Q2.Q
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	1	2.2737	0.2825	1152.6	1153.41	2	327.8	61.11111 A.ILRNPIPTKT.T
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; IIv2p	2	4.5478	0.3151	1655.09	1656.731	1	1459.8	75 L.D1E1F111N2F1D1P1E1V1E1R4Q2.Q
gi 6323755 ref NP_013826.1	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	2	3.984	0.2868	2007.51	2007.323	1	783.6	63.333332 M.M1S1K2I1F1P1V1K2E1R4S1E1W2F1A1Q2.I
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	2	2.9446	0.1558	1680.21	1680.769	3	266.5	57.692307 N.ETKSPNDYDDRQVL.H

gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	1	3.4674	0.427	1207.54	1208.406	1	299.5	72.22222 K.NRLEVPPHVF.A
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	1	3.688	0.2438	1223.61	1224.406	1	346.4	77.77778 K.N2R4L1E1V1P1P1H3V1F1.A
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	1	2.718	0.1886	1317.56	1318.521	1	289.9	66.66667 Q.IKNERNFHIF.Y
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	1	2.8677	0.2384	1335.62	1336.521	3	170	55.555557 Q.11K2N2E1R4N2F1H311F1.Y
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	2	3.7582	0.3763	1780.21	1779.987	1	676	68.75 A.YDFPGSGSPSELPLKKG.D
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	2	3.0595	0.2385	2228.59	2229.536	4	220.5	39.473686 D.GITDKNKDQLQKDLVELIGT.T
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	2	3.4565	0.3127	2330.53	2330.641	4	226.5	35 D.GITDKNKDQLQKDLVELIGTT.T
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	2	3.3809	0.3068	1234.79	1235.487	1	651.1	72.72727 H.SKKPAPPPPGMQ.N
gi 6323756 ref NP_013827.1	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	2	3.4278	0.2207	1924.63	1925.188	4	480.4	53.125 N.N2I1P1T1P1P1Q2N2R4D1V1P1K2P1V1L1N2.S
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	3	3.8638	0.2314	3905.15	3907.298	4	153.4	K.Q2E1N2F1A1P1V1L1P1I11E1Y1E1D1L1D1E1T111N2K2I1I1E1E1H3D1T1P1L1V1 18.75 Q2.Y
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	3	4.059	0.2356	3309.47	3310.693	1	371	25.925926 A.P1V1L1P1I1I1E1Y1E1D1L1D1E1T1I1N2K2I1I1E1E1H3D1T1P1L1V1Q2.Y
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	2	3.6969	0.3751	2967.19	2968.284	1	284.9	35.416664 L.PIIEYEDLDETINKIIEEHDTPLVQ.Y
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	3	4.4139	0.3908	3347.57	3348.772	1	358.4	25 F.APVLPIIEYEDLDETINKIIEEHDTPLVQ.Y
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	3	3.8625	0.2782	3866.66	3867.298	1	276.1	21.875 K.QENFAPVLPIIEYEDLDETINKIIEEHDTPLVQ.Y
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	3	3.8492	0.3247	3610.67	3610.052	1	248.7	25.833332 E.NFAPVLPIIEYEDLDETINKIIEEHDTPLVQ.Y
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	2	3.8038	0.3606	2337.01	2334.628	1	633.5	52.63158 E.NFAPVLPIIEYEDLDETINK.I
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	2	4.0297	0.3655	2714.59	2716.062	1	349.5	40.909092 E.N2F1A1P1V1L1P1111E1Y1E1D1L1D1E1T111N2K2I111E1.E
gi 6323757 ref NP_013828.1	YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	2	4.7015	0.3169	2689.79	2690.062	1	727.6	54.545456 E.NFAPVLPIIEYEDLDETINKIIE.E
gi 6323763 ref NP_013834.1	YMR116C	WD repeat protein (G-beta like protein) involved in translation regulation; required for repression of Gcn4p activity in the absence of amino-acid starvation; core component of the ribosome; ortholog of mammalian RACK1; Asc1p	2	3.6655	0.2486	1571.95	1572.715	1	853.8	65.38461 L.T1G1D1D1Q2K2F1G1V1P1V1R4S1F1.K
gi 6323763 ref NP_013834.1	YMR116C	WD repeat protein (G-beta like protein) involved in translation regulation; required for repression of Gcn4p activity in the absence of amino-acid starvation; core component of the ribosome; ortholog of mammalian RACK1; Asc1p	2	5.0182	0.3786	1815.77	1817.048	1	1362.1	66.66667 W.K2L1T1G1D1D1Q2K2F1G1V1P1V1R4S1F1.K
gi 6323763 ref NP_013834.1	YMR116C	WD repeat protein (G-beta like protein) involved in translation regulation; required for repression of Gcn4p activity in the absence of amino-acid starvation; core component of the ribosome; ortholog of mammalian RACK1; Asc1p	3	4.7719	0.2917	1815.14	1817.048	1	1480.6	46.666668 W.K2L1T1G1D1D1Q2K2F1G1V1P1V1R4S1F1.K
ail6323768/refINP 013839 11	YMR120C	Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4- carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine: Ade17o	2	3.7778	0,2684	2477.71	2478,807	1	443.4	44,736843 Q.SKFEEIPKPFTPEERKEWLS.K
	VMD(200	Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4- carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine	-	2.0040	0.000	2004.04	2.0007			
gijo323768[ret]NP_013839.1]	TMR120C	and hisudine; Ade17p	2	3.9942	0.289	2504.81	2505.807	9	359.6	39.47 3000 Q.STKZFTETETTTPTKZPTFTTTPTE1E1R4KZE1WZL1S1.K

		Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4- carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities; isozyme of Ade16p; ade16 ade17 mutants require adenine								
gi 6323768 ref NP_013839.1	YMR120C	and histidine; Adel7p Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4- carboxamide riborucleotide transformylase and inosine monophosphate	2	3.2658	0.2534	1928.17	1927.202	1	704.4	50 A.KVGVTIPEAVEEIDIGGVT.L
gi 6323768 ref NP_013839.1	YMR120C	cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine; Ade17p Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4- extremention is perspectively transformulase and inspire meanshappets.	2	3.1508	0.2141	2264.21	2263.555	1	604.7	52.941177 K.FEEIPKPFTPEERKEWLS.K
gi 6323768 ref NP_013839.1	YMR120C	carboxamice incurceoude transioninyiase and mosime monoprospitate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine; Ade17p Enzyme of 'de novo' ourine biosynthesis containing both 5-aminoimidazole-4-	2	3.8154	0.2937	2286.85	2287.555	1	1107.3	64.70589 K.F1E1E111P1K2P1F1T1P1E1E1R4K2E1W2L1S1.K
gi 6323768 ref NP_013839.1	YMR120C	carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine; Ade17p	3	5.0506	0.2613	2503.7	2505.807	1	834.4	39.473686 Q.S1K2F1E1E111P1K2P1F1T1P1E1E1R4K2E1W2L1S1.K
gi 6323768 ref NP_013839.1	YMR120C	carboxamic de roord punite disponies source annue de la construction d	2	2.9775	0.1827	1747.17	1745.932	1	528.8	57.14286 S.SDAFFPFPDNVYRAV.K
gi 6323768 ref NP_013839.1	YMR120C	carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine; Ade17p	3	4.26	0.3614	2288.27	2287.555	1	1262.9	47.058823 K.F1E1E111P1K2P1F1T1P1E1E1R4K2E1W2L1S1.K
gi 6323776 ref NP_013847.1	YMR128W	Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 18S rRNA synthesis; Ecm16p	2	2.9806	0.2061	1339.43	1338.649	1	968.1	72.72727 N.K2T1L1F1P1I1A1P1P1V1L1Q2.V
gi 6323776 ref NP_013847.1	YMR128W	Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 18S rRNA synthesis; Ecm16p	2	2.9431	0.2411	1704.65	1705.02	1	671.7	60.714287 T.N2R4T1S1111N2I1P1Y111P1V1L1A1.T
gi 6323776 ref NP_013847.1	YMR128W	Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 18S rRNA synthesis; Ecm16p	3	4.0776	0.2401	1718.9	1719.036	1	919.6	44.230766 A.R4I1Q2L1P1V1F1G1E1E1H3K2I1M1.E
gi 6323776 ref NP_013847.1	YMR128W	Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 18S rRNA synthesis; Ecm16p	2	3.8293	0.2714	2219.47	2220.579	1	399.5	47.368423 M.AIHNIINFPFPTPPDRVALS.K
gi 6323776 ref NP_013847.1	YMR128W	Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 18S rRNA synthesis; Ecm16p	2	4.5593	0.3165	2246.27	2247.579	1	640.8	47.368423 M.A111H3N21111N2F1P1F1P1T1P1P1D1R4V1A1L1S1.K
gi 6323776 ref NP_013847.1	YMR128W	Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 185 rRNA synthesis; Ecm16p	2	4.2034	0.2749	1831.71	1833.122	1	1016.7	63.333332 H.N2I1I1N2F1P1F1P1T1P1D1R4V1A1L1.S
gi 6323776 ref NP_013847.1	YMR128W	Essential DEAH-box AI IP-dependent KNA helicase specific to the US snoKNP, predominantly nucleolar in distribution, required for 185 rRNA synthesis; Ecm16p Essential DEAL-box ATE dependent RNA helicase specific to the U2 sopRIP	2	3.8232	0.3281	1717.33	1717.018	1	658.3	60.714287 N.1111N2F1P1F1P1T1P1P1D1R4V1A1L1.S
gi 6323776 ref NP_013847.1	YMR128W	predominantly nucleolar in distribution, required for 18S rRNA synthesis; Ecm16p Nuclear pore membrane dycoprotein; may be involved in duplication of nuclear	2	3.6553	0.2991	1811.31	1812.122	1	802.3	60.000004 H.NIINFPFPTPPDRVAL.S
gi 6323777 ref NP_013848.1	YMR129W	pores and nuclear pore complexes during S-phase; Pom152p Nuclear pore membrane divcoprotein; may be involved in duplication of nuclear	1	2.3604	0.4196	1281.56	1282.439	1	508.2	63.636364 Q.TVHPIPDVAFAD.G
gi 6323777 ref NP_013848.1	YMR129W	pores and nuclear pore complexes during S-phase; Pom152p	1	3.3083	0.2415	1489.63	1490.697	1	550.9	54.166668 L.K2L1P1N2Q2I1P1G1E1Y1I1T1T1.I
gi 6323777 ref NP_013848.1	YMR129W	pores and nuclear pore complexes during S-phase; Pom152p	1	3.0126	0.4128	1473.73	1474.697	1	620	58.333332 L.KLPNQIPGEYITT.I
gi 6323777 ref NP_013848.1	YMR129W	Nuclear pore membrane giycoprotein; may be involved in duplication of nuclear pores and nuclear pore complexes during S-phase; Pom152p	2	3.5986	0.292	2242.49	2243.428	1	423.1	52.941177 S.E1R4D1S1K2D1R4Y111N2G1D1K2K2V1D111Y1.S
gi 6323777 ref NP_013848.1	YMR129W	pores and nuclear pore complexes during S-phase; Pom152p	2	4.3242	0.3387	1834.97	1835.194	1	726.5	57.14286 N.KLFTEPIKLEPVKEY.T
gi 6323777 ref NP_013848.1	YMR129W	Nuclear pore membrane glycoprotein; may be involved in duplication of nuclear pores and nuclear pore complexes during S-phase; Pom152p	2	3.4777	0.4343	1742.69	1741.857	1	844.2	67.85714 K.AIFDGNYGESDIHFR.E
gi 6323777 ref NP_013848.1	YMR129W	Nuclear pore membrane glycoprotein; may be involved in duplication of nuclear pores and nuclear pore complexes during S-phase; Pom152p	2	3.7037	0.184	1684.61	1686.946	1	1109.9	69.230774 L.S1K2K2D1F1K2I1I1D1N2P1K2S1F1.L
ail6323777/refINP 013848.11	YMR129W	Nuclear pore membrane glycoprotein; may be involved in duplication of nuclear pores and nuclear pore complexes during S-phase; Pom152p	2	2.9645	0.2076	1243.37	1242.417	1	889.9	77.77778 A.FNFFEPIKEA.K
gil6323777/refINP_013848.1	YMR129W	Nuclear pore membrane glycoprotein; may be involved in duplication of nuclear	з	4 6914	0 3524	1667.9	1667 946	1	1829	
gil6323770[ref[ND_013950.1]	VMP1210	Essential nuclear protein involved in early steps of ribosome biogenesis; physically interact with the ribosome location Relax Relax	2	2 6057	0.0024	1007.5	1000.005		674	
gilosco779/rei/NP_013850.1	VADAGEO	Essential nuclear protein involved in early steps of ribosome biogenesis; physically	2	3.0957	0.3395	1966.57	1990.235	, ,	074	LLIK2D1D1N2E1G1E1D1D1E1E1D1D1E1D1D1V1D1P1V111E1N2E1N2I1P1L1R4E
gi 6323779 ret NP_013850.1	YMR131C	Interacts with the ribosomal protein RpI3p; Rb1p Essential nuclear protein involved in early steps of ribosome biogenesis; physically	3	3.8727	0.1647	3739.94	3742.684	5	358.1	20.161291 111.1
gi 6323779 ref NP_013850.1	YMR131C	interacts with the ribosomal protein Rpl3p; Rrb1p Essential nuclear protein involved in early steps of ribosome biogenesis; physically	2	4.0265	0.3507	1729.41	1727.927	1	644.7	60.000004 H.MSRPLGPDEVLEADPT.V
gi 6323779 ref NP_013850.1	YMR131C	interacts with the ribosomal protein Rpl3p; Rrb1p Essential nuclear protein involved in early steps of ribosome biogenesis; physically	2	3.6969	0.265	1746.61	1746.927	1	920.6	66.66667 H.M1S1R4P1L1G1P1D1E1V1L1E1A1D1P1T1.V L.L1K2D1D1N2E1G1E1D1D1E1E1D1D1E1D1D1V1D1P1V1I1E1N2E1N2I1P1L1R4[
gi 6323779 ref NP_013850.1	YMR131C	interacts with the ribosomal protein RpI3p; Rrb1p Essential nuclear protein involved in early steps of ribosome biogenesis; physically	3	5.5417	0.3096	4233.77	4235.24	1	501.8	24.285715 1T1T1N2R4L1.K
gi 6323779 ref NP_013850.1	YMR131C	interacts with the ribosomal protein Rpl3p; Rrb1p	3	6.3503	0.4249	4188.17	4188.24	1	693.4	27.142859 L.LKDDNEGEDDEEDDEDDVDPVIENENIPLRDTTNRL.K
gi 6323788 ref NP_013859.1	YMR139W	Protein kinase required for signal transduction during entry into meiosis; promotes the formation of the Ime1p-Ume6p complex by phosphorylating Ime1p and Ume6p; shares similarity with mammalian glycogen synthase kinase 3-beta; Rim11p	2	3.405	0.2656	2245.89	2245.405	2	206.3	36.842106 L.EFDENVELGHLSPDELSSVK.K
gi 6323788 ref NP_013859.1	YMR139W	Protein kinase required for signal transduction during entry into meiosis; promotes the formation of the Ime1p-Ume6p complex by phosphorylating Ime1p and Ume6p; shares similarity with mammalian glycogen synthase kinase 3-beta; Rim11p	2	3.1913	0.1988	2232.13	2231.447	1	396.2	42.105263 Y.Y1A1H3P1P1P1T111D1P1N2D1P1V1Q2I1S1F1P1T1.T
gi 6323798 ref NP_013869.1	YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p	2	3.1235	0.2903	1442.41	1442.758	5	371.6	54.166668 T.L1L1I1G1L1P1N2K2N2L1E1M1A1.F
gi 6323798 ref NP_013869.1	YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p	1	2.3245	0.217	1426.66	1426.758	1	489.5	58.333332 T.LLIGLPNKNLEMA.F

gi 6323798 ref NP_013869.1	YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p	2	3.7055	0.3456	1612.37	1611.705	1	701.2	61.538464 N.FDVDHSDSSLVDKF.G
gi 6323798 ref NP_013869.1	YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p	2	4.005	0.3819	1857.73	1858.968	1	1265.6	66.66667 N.L1N2F1D1V1D1H3S1D1S1S1L1V1D1K2F1.G
gi 6323798 ref NP_013869.1	YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p	2	5.3288	0.4825	1973.43	1975.072	1	1638.3	75 L.N2L1N2F1D1V1D1H3S1D1S1S1L1V1D1K2F1.G
gi 6323798 ref NP_013869.1	YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p	2	5.8741	0.4119	1954.65	1953.072	1	2520.3	81.25 L.NLNFDVDHSDSSLVDKF.G
gi 6323798 ref NP_013869.1	YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p	2	3.0195	0.3779	1724.59	1725.809	2	225.6	57.14286 L.NFDVDHSDSSLVDKF.G
gi 6323798 ref NP_013869.1	YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p Protein of uknown function; pronosed to be involved in responding to DNA	2	2.9523	0.2068	1753.67	1755.005	3	304.4	53.571426 A.S1S1T1A1K2P1K2E1N2L1F1R4E1I1L1.Q
gi 6323801 ref NP_013872.1	YMR152W	damaging agents; Yim1p	1	3.5901	0.3398	1452.48	1452.566	1	578.1	63.636364 V.G1N2H3D1F1F1P1V1I1D1Q2F1.L
gi 6323801 ref NP_013872.1	YMR152W	damaging agents; Yim1p	3	3.9329	0.2124	3097.82	3097.476	9	229.3	19.23077 I.IKAGKDVDNRWKVGDKVNGM@YSHIYGE.R
ail6323801/refINP 013872.1/	YMR152W	Protein of unknown function; proposed to be involved in responding to DNA damaging agents; Yim1p	2	3.5225	0.2491	1962.07	1963.046	1	378.3	50 M.V1E1V1P1K2D1E1N2D1P1Y1D1D1F1V1Y1.A
gil6323801/rofINIP_013872.1	VMP152W/	Protein of unknown function; proposed to be involved in responding to DNA	2	3 2755	0.2686	10// 13	1045.046	1	437	
gilo3230011rei14r_013072.11	11011113210	Protein of unknown function; proposed to be involved in responding to DNA	2	5.2755	0.2000	1344.13	1345.040		437	
gi 6323801 ref NP_013872.1	YMR152W	damaging agents; Yim1p	2	3.1817	0.2714	1574.25	1574.727	1	678.3	70.83333 G.TYKPPIDSVYEFD.Q
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	3	4.1405	0.2678	3047.84	3048.114	9	207.9	25 E.Q2Q2E1N2V1D1V1I1D1K2N2V1E1D1A1Q2Q2D1V1E1Q2G1V1G1H3T1N2.K
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	3	6.1161	0.3139	2537.93	2538.644	1	1437.3	39.772728 Q.ENVDVIDKNVEDAQQDVEQGVGH.T
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	2	5.5444	0.4556	2569.43	2569.644	1	1380.6	54.545456 Q.E1N2V1D1V111D1K2N2V1E1D1A1Q2Q2D1V1E1Q2G1V1G1H3.T
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	2	4.8099	0.4852	2536.53	2538.644	1	873.9	52.272724 Q.ENVDVIDKNVEDAQQDVEQGVGH.T
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	3	7.0969	0.3505	2697.11	2699.775	1	2165.9	42.391304 Q.Q2E1N2V1D1V1I1D1K2N2V1E1D1A1Q2Q2D1V1E1Q2G1V1G1H3.T
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	2	3.6262	0.245	2698.17	2699.775	1	386	41.304348 Q.Q2E1N2V1D1V1I1D1K2N2V1E1D1A1Q2Q2D1V1E1Q2G1V1G1H3.T
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	2	3.1302	0.181	2665.83	2666.775	1	385.8	43.47826 Q.QENVDVIDKNVEDAQQDVEQGVGH.T
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	3	5.0902	0.3032	2793.95	2794.905	1	1361.8	34.375 E.QQENVDVIDKNVEDAQQDVEQGVGH.T
gi 6323837 ref NP_013908.1	YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	3	5.0415	0.3952	2665.55	2666.775	1	1882.3	36.95652 Q.QENVDVIDKNVEDAQQDVEQGVGH.T
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	1	2.5303	0.2147	1293.74	1292.506	1	718.7	75 H.S1E1F1V1A1Y1P111Q2L1L1.V
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	1	2.3428	0.1766	1577.28	1578.689	1	339	50 T.D1E1A1E1D1L1I1P1E1W2L1S1F1.V
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	4.9004	0.2463	2495.81	2496.687	1	1276.1	40.789474 T.KDFELEETDEEKAEREKEIK.E
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	5.7498	0.4248	2496.41	2496.687	1	1022.2	57.894737 T.KDFELEETDEEKAEREKEIK.E
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.8422	0.2586	2366.43	2366.541	4	220.7	41.666664 E.ETDEEKAEREKEIKEYEPL.T
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.0216	0.274	1787.85	1788.995	1	326	60.714287 L.SDPKQLETEPDLFIR.I
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	4.0357	0.4066	1972.55	1973.233	1	524.5	59.375 Q.ALSDPKQLETEPDLFIR.I
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.2376	0.2769	1732.55	1733.012	1	309.3	56.666668 K.A1L1K2D1I1L1G1D1Q2V1E1K2V1V1V1S1.Y
		Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly								
gi 6323840 ref NP_013911.1	YMR186W	identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	4.2186	0.3947	1896.97	1897.188	1	526.7	59.375 K.A1L1K2D111L1G1D1Q2V1E1K2V1V1V1S1Y1.K

gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.5657	0.3609	1879.85	1877.188	1	487.7	56.25 K.ALKDILGDQVEKVVVSY.K
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	6.6511	0.4912	3356.48	3357.65	1	1317.7	34.615387 T.KDFELEETDEEKAEREKEIKEYEPLTK.A
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	4.0656	0.3694	1586.57	1586.828	1	967.8	75 D.PKQLETEPDLFIR.I
gi 6323840 ref NP 013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	5.0382	0.3967	3826.79	3825.135	1	1401.9	LV1D1I1T1K2D1F1E1L1E1E1T1D1E1E1K2A1E1R4E1K2E1I1K2E1Y1E1P1L1T1K2. 32.5 A
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	1	2.637	0.1994	1331.52	1332.556	1	784.6	68.181816 L.K2A1V1E1K2S1P1F1L1D1A1L1.K
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	2.9384	0.2794	2431.63	2433.756	1	446.8	42.105263 R.R4V1F111T1D1E1A1E1D1L111P1E1W2L1S1F1V1K2.G
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.237	0.2284	2089.81	2091.367	1	617.9	50 S.Y1K2L1L1D1A1P1A1A1I1R4T1G1Q2F1G1W2S1A1.N
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	4.3949	0.3146	3545.3	3547.065	1	299	23.275862 Q.A1L1S1D1P1K2Q2L1E1T1E1P1D1L1F111R4I1T1P1K2P1E1E1K2V1L1E111R4.D
ail6323840lrefINP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock: Hsc82p	2	2.9259	0.1925	2181.93	2180.471	1	344.6	39.473686 S.YKLLDAPAAIRTGOFGWSAN.M
qi 6323840 ref NP 013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	1	2.9382	0.1748	1459.56	1460.676	8	199.7	54.545456 K.RHSEFVAYPIQL.V
oil6323840/ref/NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by beat shock: Hsc82p	1	3,7399	0.3029	1477.59	1478.676	1	303.4	63 636364 K.R4H3S1E1E1V1A1Y1P11102L1.L
ail6323840lrefINP 013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock: Hsc82p	2	3.1518	0.1718	1926.47	1927.191	2	583.9	47.058823 Y.K2L1L1D1A1P1A1A1I1R4T1G1Q2F1G1W2S1A1.N
oil6323840/ref/NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by beat shock: Hsc82p	1	4.428	0.3153	1592.67	1592,835	1	330.4	62.5 K.R4H3S1E1E1V1A1Y1P111Q2L1L1 V
gil6323840/ref/NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSp82 and induced 2-3 fold by heat shock: Hsc82p	1	3.7613	0.269	1573.82	1573.835	1	275.8	58 333332 K.RHSEFVAYPIOLL V
oil6323840/refINP_013911_1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold binber basal levels that HSP82 and induced 2-3 fold by beat shock: Hss82p	2	3 1543	0 2791	1574 45	1572 625	1	1008.4	
oil6323840/refINP_013911_1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold binder brazal levels that HSP82 and induced 2-3 fold by beat shock: Hss82p	2	3 3976	0.2138	1809.09	1808 995	1	398.6	64 28571 SID1P1K202 1E1T1E1P1D1 1E111R4
oil6323840/refINP_013911_1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold binber basal levels that HSP82 and induced 2-3 fold by beat shock: Hss82p	3	4 5415	0.3302	1808 63	1808 995	1	835.7	48 2142871 S1D1P1K2021 151T151P1D11 15111841
oil6323840/refINP_013911_1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold hindre trasal levels that HSP82 and induced 2-3 fold by heat schock; Hsc82p	2	5 5222	0.4257	2495 77	2496 687	1	1052.8	57 894737 T KDFEI FETDEEKAEREKEIK E
oil6323840/refINP_013911_1	YMR186W	Cytoplasmic chapter beau event in the SP2 and induced 2.5 road by heat should have provide the second structure of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10-fold binder beau levels that HSp82 and induced 2.3 fold by beat should be the SP2 of the second structure of the second structure is the	3	4 7356	0.2453	3125 51	3128 37	1	1096.4	37.5 T KDFELEETDEEKAEREKEIKEVEPLIT
oil6323840/refINP_013911_1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher hspaal levels that HSp82 and induced 2-3 fold by heat shock: Hsp82p	1	2 6944	0 1564	1419.28	1417 648	2	571 5	
ail6323840]ref[NP_013911_1]	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold hv heat shock: Hsc82p	1	2.6881	0.3177	1317.74	1318.556	-	760.4	63 636364 L.KAVEKSPFLDAL.K
oil6323840[ref[NP_013011.1]	YMR186W/	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher hspaal levels that HSp82 and induced 2.3 fold by heat short-vir Hsp62p.	2	2 9535	0.2261	1593.83	1592 835	2	477 1	62.5 K R4H3S1E1E1V1A1Y1P110211111V
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.5989	0.2981	1479.25	1479.629	-	1006.5	68.181816 S.ISNDWEDPLYVK.H

gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.8713	0.2178	1493.17	1494.629	1	1050.9	68.181816 S.I1S1N2D1W2E1D1P1L1Y1V1K2.H
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.1839	0.1713	1203.17	1202.382	2	1000.3	80 K.A1V1E1K2S1P1F1L1D1A1L1.K
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	4.0386	0.2248	1727.67	1728.761	1	980.6	73.07692 T.K2D1F1E1L1E1E1T1D1E1E1K2A1E1.R
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	5.1068	0.3095	1998.03	1998.064	1	2144.1	80 T.KDFELEETDEEKAERE.K
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.8498	0.1896	2391.31	2391.541	6	261.3	44.44447 E.E1T1D1E1E1K2A1E1R4E1K2E111K2E1Y1E1P1L1.T
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	3.826	0.3246	1876.85	1877.058	1	1228.8	75 F.Y1K2S1I1S1N2D1W2E1D1P1L1Y1V1K2.H
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	5.8944	0.3554	3548.33	3548.859	1	962.1	31.25 K.E1V1E1K2E1V1P111P1E1E1E1K2K2D1E1E1K2K2D1E1D1D1K2K2P1K2L1E1.E
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	5.5688	0.4379	3509.18	3511.859	1	1344.6	33.035713 K.EVEKEVPIPEEEKKDEEKKDEDDKKPKLE.E
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	6.3453	0.3882	3839.03	3840.271	1	1180.6	28.225807 L.VTKEVEKEVPIPEEEKKDEEKKDEDKKPKLE.E
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	5.3535	0.1762	2495.39	2496.687	1	1810.4	47.368423 T.KDFELEETDEEKAEREKEIK.E
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	2	5.4438	0.3092	2522.69	2523.687	1	1211.5	60.526318 T.K2D1F1E1L1E1E1T1D1E1E1K2A1E1R4E1K2E1I1K2.E
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	6.3924	0.4285	3390.83	3392.65	1	1298.6	32.692307 T.K2D1F1E1L1E1E1T1D1E1E1K2A1E1R4E1K2E1I1K2E1Y1E1P1L1T1K2.A
gi 6323840 ref NP_013911.1	YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10- fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	3	5.2995	0.2172	3160.43	3160.37	1	871.3	34.375 T.K2D1F1E1L1E1E1T1D1E1E1K2A1E1R4E1K2E1I1K2E1Y1E1P1L1.T
gi 6323843 ref NP_013914.1	YMR189W	P subunit or the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gov2p P subunit of the mitochondrial glycine decarboxylase complex, required for the	2	3.0982	0.2412	1545.55	1544.748	1	880.4	66.66667 N.PDLKNIDRPLDTF.A
gi 6323843 ref NP_013914.1	YMR189W	catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gcv2p P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine 110-methylene-THF; expression is regulated by levels of	3	4.9167	0.2704	2481.5	2483.76	2	942.1	35.526314 T.Q2Y1S1R4I1F1N2P1D1L1K2N2I1D1R4P1L1D1T1F1.A
gi 6323843 ref NP_013914.1	YMR189W	levels of 5,10-methylene-THF in the cytoplasm; Gcv2p P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of	2	3.0084	0.2254	2161.47	2162.453	1	359.8	50 Y.SRIFNPDLKNIDRPLDTF.A
gi 6323843 ref NP_013914.1	YMR189W	levels of 5,10-methylene-THF in the cytoplasm; Gcv2p P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5 10-methylene. THE in the cytoplasm; Gcv2p	2	3.3464	0.2365	2099.95	2101.375	2	366	46.875 S.R411F1N2P1D1L1K2N211D1R4P1L1D1T1F1.A
gi 6323843 ref NP_013914.1	YMR189W	P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gcv2p	3	5.4512	0.3547	2454.41	2453.76	1	1353.9	38.157894 T.QYSRIFNPDLKNIDRPLDTF.A
gi 6323843 ref NP_013914.1	YMR189W	P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gcv2p P subunit of the mitochondrial glycine decarboxylase complex, required for the	2	2.9917	0.338	1574.71	1575.774	1	708.8	62.5 F.SIPHGGGGPAGAPICVK.S
gi 6323843 ref NP_013914.1	YMR189W	catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gcv2p Protein that recognizes and binds damaged DNA during nucleotide excision repair;	3	3.8218	0.2139	2325.23	2325.629	3	910	34.72222 Q.YSRIFNPDLKNIDRPLDTF.A
gi 6323857 ref NP_013928.1	YMR201C	Subunit of Nucleotide Excision Repair Factor 1 (NEF 1); contains zinc inger mour, homolog of human XPA protein; Rad14p Protein that recognizes and binds damaged DNA during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); contains zinc finger motif;	3	6.2802	0.4854	2699.78	2698.858	1	1217.4	43.75 E.C1K2E1D1Y1F1L1T1D1P1E1L1N2D1E1D1L1F1H3R4L1.E
gi 6323857 ref NP_013928.1	YMR201C	homolog of human XPA protein; Rad14p Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins;	3	4.2853	0.3154	2668.13	2670.858	2	773	33.75 E.CKEDYFLTDPELNDEDLFHRL.E
gi 6323859 ref NP_013930.1	YMR203W	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; constitutes the core element of the protein conducting pore; Tom40p	2	3.5338	0.1951	1669.39	1669.875	1	924.8	64.28571 H.RQSLELVNPGTVENLN
gi 6323859 ref NP_013930.1	YMR203W	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; constitutes the core element of the protein conducting pore; Tom40p	2	4.1901	0.3424	1902.43	1901.284	1	682.3	50 G.M1V1P1I1T1D1P1L1M1G1T1P1I1G1I1Q2P1T1.V

		Component of the TOM (translocase of outer membrane) complex responsible for								
gi 6323859 ref NP_013930.1	YMR203W	recognition and initial import steps for all mitochondrially directed proteins; constitutes the core element of the protein conducting pore; Tom40p Beta subunit of heterooctameric phosphofructokinase involved in qlycolysis,	2	4.4675	0.4627	1883.15	1882.284	1	1230.7	61.764706 G.MVPITDPLMGTPIGIQPT.V
gi 6323861 ref NP_013932.1	YMR205C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis,	1	2.4142	0.2722	1281.58	1280.42	1	372.1	54.166668 V.STKPTPPPAPEAS.A
gi 6323861 ref NP_013932.1	YMR205C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis,	1	3.1714	0.3858	1564.62	1565.782	1	386.1	53.846157 N.RVTPEEADLGMIAY.Y
gi 6323861 ref NP_013932.1	YMR205C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.4305	0.3355	1986.29	1987.139	1	494.2	52.941177 A.EADGRFDAKPAYPGHVQQ.G
gi 6323861 ref NP_013932.1	YMR205C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis,	3	3.8762	0.2164	2192.15	2191.489	2	642	33.82353 A.DLFRSEWPSLIEELLKTN.R
gi 6323861 ref NP_013932.1	YMR205C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.7858	0.1843	1598.65	1600.855	1	2163.3	87.5 F.RSEWPSLIEELLK.T
gi 6323861 ref NP_013932.1	YMR205C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; PR2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.6925	0.2352	1834.55	1837.064	1	953.7	71.42857 F.R4S1E1W2P1S1L1I1E1E1L1L1K2T1N2.R
gi 6323861 ref NP_013932.1	YMR205C	indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; PR2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.8912	0.3219	1570.35	1570.891	1	449.1	58.333332 A.VNENKIVRKPLME.S
gi 6323861 ref NP_013932.1	YMR205C	Indispensable for anaerobic growth, activated by tructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; PR2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis,	2	3.3213	0.2399	1858.53	1859.008	1	675.5	53.125 A.EADGRFDAKPAYPGHVQ.Q
gi 6323861 ref NP_013932.1	YMR205C	Indispensable for anaerobic growm, activated by tructose-z,b-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; PRzp Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, and the analysis of the second secon	2	3.8417	0.2863	1817.15	1816.064	1	1172.6	78.57143 F.RSEWPSLIEELLKTN.R
gi 6323861 ref NP_013932.1	YMR205C	Mappensable for anaerobic grown, activated by Incluse-2,o-hispinosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; PRzp Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indiaenocehic for concession arruth, orginized bu forchare 2 & bindparebits and	2	2.9849	0.2357	1749.47	1748.98	2	525.6	53.571426 N.SADHNEPKLPKDKRL.K
gi 6323861 ref NP_013932.1	YMR205C	Muspersaule for anaerobic grown, activated by incluse-conspirations and AMP, mutation inhibits glucose induction of cell cycle-related genes; PRzp Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indiaeocoshi for concession carryth, ordinated by forusted 2.6 kindparebota and	2	3.0285	0.3379	1590.51	1590.823	2	550.7	66.66667 A.DHNEPKLPKDKRL.K
gi 6323861 ref NP_013932.1	YMR205C	Indispensable for alteriobic growin, activated by indicase-2,onspinospirate and AMP, mutation inhibits glucose induction of cell cycle related genes; PR2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indicasonable for concession carryth, ordinated by forces 2 & binaparabeta and	2	3.0397	0.3779	2026.75	2028.316	1	590.9	52.941177 K.TTDTYPSLPKPLNRPQKA.I
gi 6323861 ref NP_013932.1	YMR205C	Indispensable for alteriotic growth, activated by indicase-2,onspinospirate and AMP, mutation inhibits glucose induction of cell cycle-related genes; PR2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indicasensehie for aparagehic growth, activated by furcherse, 2 & birspensphat and	2	3.0195	0.2442	1882.63	1883.255	4	274.1	46.666668 A.R4E1S1Y1P1A1F1R4I1P1M1V1L1I1P1A1.T
gi 6323861 ref NP_013932.1	YMR205C	Indispensable for alteriotic growth, activated by indicase-2,onspinospirate and AMP, mutation inhibits glucose induction of cell cycle-related genes; PR2p Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indicasensehie for aparagehic growth, activated by furcherse, 2 & birspensphat and	1	2.4812	0.2184	1084.49	1085.167	1	546	78.57143 F.HWEDVRGW.S
gi 6323861 ref NP_013932.1	YMR205C	AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	1	2.5226	0.1902	1276.69	1276.525	1	156.2	72.22222 M.EFKKREGRLL.G
gi 37362683 ref NP_013941.2	YMR214W	where it cooperates with Kar2p to mediate maturation of proteins; Scj1p	2	3.229	0.3408	2511.73	2512.75	1	778.4	50 Y.MDTRVGEAEKGPDFDAGDLVIEF.K
gi 37362683 ref NP_013941.2	YMR214W	One of several homologs of bacterial chaperone DnaJ, located in the ER lumen where it cooperates with Kar2p to mediate maturation of proteins; Scj1p	2	3.122	0.1839	1668.45	1668.857	1	460.5	64.28571 E.K2G1P1D1F1D1A1G1D1L1V1I1E1F1K2.E
gi 37362683 ref NP_013941.2	YMR214W	One of several homologs of bacterial chaperone DnaJ, located in the ER lumen where it cooperates with Kar2p to mediate maturation of proteins; Scj1p	3	4.3295	0.2198	1853.45	1853.122	2	1175.2	44.642857 W.Q2R4T1I1E1F1L1D1E1N2K2P1V1K2L1.S
gil37362683/refINP_013941.2	YMR214W	One of several homologs of bacterial chaperone DnaJ, located in the ER lumen where it cooperates with Kar2p to mediate maturation of proteins: Sci1p	3	4.6706	0.1558	1831.37	1831.122	1	1437.7	51,785713 W. ORTIEFL DENKPVKL S
gil272626821rofIND_012041.21	VMP214W	One of several homologs of bacterial chaperone DnaJ, located in the ER lumen	2	2 6724	0.2602	1920.91	1921 122		E12 E	
gij37362663 101 14F_013941.2		One of several homologs of bacterial chaperone DnaJ, located in the ER lumen	2	3.0724	0.2003	1029.01	1031.122		515.5	
gi 37362683 ref NP_013941.2	YMR214W	where it cooperates with Kar2p to mediate maturation of proteins; Sq1p GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5-phosphate (IMP); transcription is not subject to regulation by	2	4.1136	0.3311	1851.89	1853.122	1	431.7	67.85714 W.Q2R4T111E1F1L1D1E1N2K2P1V1K2L1.S
gi[6323873]ref[NP_013944.1]	YMR217W	guanine but is negatively regulated by nutrient starvation; Guarp GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5-phosphate (IMP); transcription is not subject to regulation by	2	3.3023	0.1959	1922.25	1923.155	3	262.2	53.333336 F.E.1K4E1A1E1K2I1K2P1K2D1G1K2E1I1Q2.F
gi[6323873 ref NP_013944.1]	YMR217W	guanine but is negatively regulated by nutrient starvation; Guanp GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5-phosphate (IMP); transcription is not subject to regulation by	2	3.1001	0.2582	1898.27	1899.155	1	334.9	60.000004 F.EREAEKIKPKDGKEIQ.F
gi[6323873 ref NP_013944.1]	YMR217W	guanine but is negatively regulated by nutrient starvation; Guanp GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5-phosphate (IMP); transcription is not subject to regulation by	3	5.131	0.3047	2186.21	2185.491	3	818.7	39./05883 F.E1R4E1A1E1K2I1K2P1K2D1G1K2E1I1Q2F1L1.L
gi 6323873 ref NP_013944.1	YMR217W	guanine but is negatively regulated by nutrient starvation; Gua1p Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is	2	4.4679	0.3845	2158.17	2159.491	1	424.7	55.88235 F.EREAEKIKPKDGKEIQFLL
gi 6323885 ref NP_013956.1	YMR229C	rRNA; component of small ribos romal subunit (SSU) processosome; Rrp5p	2	3.4447	0.2484	1803.49	1803.917	1	954.7	71.42857 Q.FEESEGDEKTIEYVK.A
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis or both 185 and 5.85 (RNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	3.8327	0.1991	1560.25	1560.758	1	558	69.230774 H.E1D1L1K2Q2G1E1I1V1D1G1I1V1K2.N
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; RpSp	2	3.6658	0.3081	1543.51	1543.758	1	593.3	73.07692 H.EDLKQGEIVDGIVK.N
		Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is								
gi 6323885 ref NP_013956.1	YMR229C	crucial for the formation of 185 rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	2.9497	0.2	2047.31	2047.24	5	507.3	46.875 L.T1Y1D1D1V1K2D1L1N2K2D1V1P1M1H3A1Y1.I
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	3.0677	0.3082	1658.27	1657.861	1	453.1	57.14286 H.EDLKQGEIVDGIVKN.V

gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	3.8919	0.3819	1767.55	1767.977	1	1011	63.333332 K.SHEDLKQGEIVDGIVK.N
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	4.1713	0.1532	2512.23	2513.654	8	229.9	37.5 K.R4K2R4D1E1D1F1P1L1S1R4E1D1S1T1K2Q2P1S1T1S1.S
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	4.3591	0.2495	1557.83	1558.8	1	1243.8	69.230774 T.K2D1S1V111V1E111P1D1V1G1L1R4.G
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	3.957	0.3098	1541.69	1540.8	1	1634.4	76.92308 T.KDSVIVEIPDVGLR.G
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	3.8562	0.1857	2481.73	2480.654	1	305.9	42.5 K.RKRDEDFPLSREDSTKQPSTS.S
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	2	4.3779	0.2827	1862.67	1863.208	1	1099.1	67.85714 K.DKKKVEDLFERIITK.K
gi 6323885 ref NP_013956.1	YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p Protein that colocalizes with clathrin-coated vesicles; involved in transport at the	2	4.4752	0.2541	1886.55	1885.208	1	786.7	64.28571 K.D1K2K2K2V1E1D1L1F1E1R4I1I1T1K2.K
gi 6323893 ref NP_013964.1	YMR237W	trans-Golgi; Bch1p	1	2.4537	0.2553	1231.47	1232.422	2	189.2	55 D.ENLHLPLPLDA.S
gi 6323893 ref NP 013964.1	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the trans-Golgi; Bch1p	2	3.9397	0.3333	1607.67	1606.86	1	1195.1	79.16667 K.K2I1T1D1L1F1L1D1T1P1Q2I1W2.F
ail62228021rofIND_012064_1	VMD007W/	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the	2	2 9205	0 2944	1705 62	1705 099	1	1645 1	
gilo323693[rei]ivP_013904.1]	TIVIR237 W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the	2	3.6295	0.3644	1795.05	1795.066	1	1045.1	75 K.KIIDEFEDIFQIWFG.K
gi 6323893 ref NP_013964.1	YMR237W	trans-Golgi; Bch1p Protein that colocalizes with clathrin-coated vesicles: involved in transport at the	2	3.5297	0.3158	2085.69	2086.396	1	604	52.77778 R.RIAPITSDENLHLPLPLDA.S
gi 6323893 ref NP_013964.1	YMR237W	trans-Golgi; Bch1p	2	3.4194	0.3132	1792.35	1790.112	1	1006.8	60.714287 F.AKKITDLFLDTPQIW.F
gi 6323893 ref NP_013964.1	YMR237W	trans-Golgi; Bch1p	2	4.4188	0.4063	2014.63	2015.341	1	1081.9	59.375 F.A1K2K2I1T1D1L1F1L1D1T1P1Q2I1W2F1G1.K
gi 6323893 ref NP 013964.1	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the trans-Golgi; Bch1p	3	3.8429	0.2559	3021.44	3022.533	1	523.6	25 F.A1K2K2I1T1D1L1F1L1D1T1P1Q2I1W2F1G1K2K2K2H3F1H3V1S1.K
gil6323803lrofIND_013064_11	VMP237W/	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the	2	4 4 4 1	0 387	1003 60	100/ 3/1	1	812.1	
giloszobsoliellitir _013304.1	1101123710	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the	2	4.441	0.507	1333.03	1334.341		012.1	
gi 6323893 ref NP_013964.1	YMR237W	trans-Golgi; Bch1p Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored	2	3.8293	0.3717	1812.43	1813.088	1	1247.6	67.85714 K.K2I1T1D1L1F1L1D1T1P1Q2I1W2F1G1.K
gi 6323894 ref NP_013965.1	YMR238W	membrane protein required for cell wall biogenesis in bud formation, involved in filamentous growth, homologous to Dcw1p; Dfg5p Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored	2	4.7984	0.4022	1998.15	1999.191	1	730	61.764706 L.LIHDRPAPYKEDNGGTSK.G
gi 6323894 ref NP_013965.1	YMR238W	membrane protein required for cell wall biogenesis in bud formation, involved in filamentous growth, homologous to Dcw1p; Dfg5p Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored membrane protein required for cell wall biogenesis in bud formation, involved in	2	5.2177	0.4433	2024.77	2025.191	1	668.9	58.823532 L.L111H3D1R4P1A1P1Y1K2E1D1N2G1G1T1S1K2.G
gi 6323894 ref NP_013965.1	YMR238W	filamentous growth, homologous to Dcw1p; Dfg5p	3	4.3498	0.3539	2022.68	2025.191	5	727.6	36.764706 L.L111H3D1R4P1A1P1Y1K2E1D1N2G1G1T1S1K2.G
gi 37362684 ref NP_013969.2	YMR242C	and has similarity to rat L18a ribosomal protein; Rpl20ap	1	3.2474	0.3234	1512.68	1513.777	1	286.2	54.166668 R.RLPTESVPEPKLF.R
gi 37362684 ref NP_013969.2	YMR242C	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp and has similarity to rat L18a ribosomal protein; Rpl20ap	2	3.0981	0.3364	2357.61	2359.731	4	218.6	36.842106 K.EYQVIGRRLPTESVPEPKLF.R
ail37362684/rofIND_013060.21	VMP242C	Protein component of the large (60S) ribosomal subunit, nearly identical to RpI20Bp	1	2 8028	0 1953	1367 71	1368 607	5	278 5	60 000004 K D1I 1K2E1D1I 1D1H3D4\/102 K
gij5/502004[rei]titr_015505.2]	1101172420	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp		2.0020	0.1000	1307.71	1300.007	5	270.5	
gi 37362684 ref NP_013969.2	YMR242C	and has similarity to rat L18a ribosomal protein; Rpl20ap Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp	1	2.978	0.2011	1350.7	1350.607	2	304.4	60.000004 K.DLKFPLPHRVQ.K
gi 37362684 ref NP_013969.2	YMR242C	and has similarity to rat L18a ribosomal protein; Rpl20ap	2	3.0778	0.2115	1366.85	1368.607	9	622.2	75 K.D1L1K2F1P1L1P1H3R4V1Q2.K
gi 37362684 ref NP_013969.2	YMR242C	and has similarity to rat L18a ribosomal protein; Rejust and rate international representation of the second state of the seco	1	3.7127	0.3184	1531.75	1530.777	6	291	54.166668 R.R4L1P1T1E1S1V1P1E1P1K2L1F1.R
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p	2	3.8937	0.3253	2177.55	2178.424	1	399.9	44.11765 A.K2D1E1V1E1L1H3F1P1K2P1E1D1P1A1C1I1M1.Y
gi 6323903 ref NP_013974.1	YMR246W	the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids; Faa4p Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in	2	4.2879	0.4202	2025.03	2025.349	1	937.8	52.77778 Y.A1D1E1N2K2V1K2P1V1G1I1V1V1P1N2L1G1H3L1.S
gi 6323903 ref NP_013974.1	YMR246W	the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids; Faa4p	2	4.3604	0.4157	2002.79	2000.349	1	1649.6	69.44444 Y.ADENKVKPVGIVVPNLGHL.S
gi 6323903 ref NP_013974.1	YMR246W	Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids; Faa4p	3	4.283	0.2658	2001.32	2000.349	1	921.9	41.666664 Y.ADENKVKPVGIVVPNLGHL.S
gi 6323903 ref NP_013974.1	YMR246W	Long chain tatty acyl-CoA synthetase, regulates protein modification during growth in the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids; Faa4p	2	4.4878	0.3967	2262.75	2262.657	1	829.7	50 C.VYADENKVKPVGIVVPNLGHL.S
gi 6323903 ref NP_013974.1	YMR246W	the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids; Faa4p Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in	2	4.3788	0.3349	2288.71	2289.657	1	927.3	50 C.V1Y1A1D1E1N2K2V1K2P1V1G1I1V1V1P1N2L1G1H3L1.S
gi 6323903 ref NP_013974.1	YMR246W	the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids; Faa4p Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in the presence of othered functions to incorporate activities and fails a	2	4.8105	0.4377	2031.13	2031.403	1	968.2	56.25 A.KDAVDKIKEVRPDIKIY.S
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p	3	4.7478	0.484	2261.18	2262.657	1	1537	41.25 C.VYADENKVKPVGIVVPNLGHL.S

		Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in								
gi 6323903 ref NP 013974.1	YMR246W	the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids; Faa4p	2	3.6289	0.3298	2227.61	2227.503	1	519.1	50 K.AKDEVELHFPKPEDPACIM.Y
		Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p	2	4.5266	0.3629	2249.45	2250.503	1	580.7	52.77778 K.A1K2D1E1V1E1L1H3F1P1K2P1E1D1P1A1C1I1M1.Y
		Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p	2	3.4907	0.3933	1572.35	1572.805	1	715.2	75 K.RVDGKDKPIEKTW.L
		Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in the presence of ethapol, functions to incorporate palmitic acid into phospholipids and								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p	2	4.3264	0.2845	1825.73	1826.147	1	1027.3	66.66667 A.AKDAVDKIKEVRPDIK.I
		Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in the presence of ethanol, functions to incorporate palmitic acid into phospholipids and								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p	2	3.9099	0.4113	2348.01	2349.735	1	1123.2	52.380955 C.VYADENKVKPVGIVVPNLGHLS.K
		Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in the presence of ethanol, functions to incorporate palmitic acid into phospholipids and								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p	2	4.0679	0.4152	2001.01	2000.349	1	1084.4	58.333332 Y.ADENKVKPVGIVVPNLGHL.S
		the presence of ethanol, functions to incorporate palmitic acid into phospholipids and								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p	2	4.2383	0.3903	2261.89	2262.657	1	1224.5	60.000004 C.VYADENKVKPVGIVVPNLGHL.S
		the presence of ethanol, functions to incorporate palmitic acid into phospholipids and								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in	2	5.3345	0.4583	2102.35	2102.482	1	1301.6	55.88235 A.AKDAVDKIKEVRPDIKIY.S
		the presence of ethanol, functions to incorporate palmitic acid into phospholipids and								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p Long chain fatty acvI-CoA synthetase, regulates protein modification during growth in	2	3.5236	0.4268	2155.19	2156.424	1	401.2	44.11765 A.KDEVELHFPKPEDPACIM.Y
	10.000	the presence of ethanol, functions to incorporate palmitic acid into phospholipids and								
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in	2	4.5254	0.4314	2087.55	2087.427	1	1130	57.894737 Y.ADENKVKPVGIVVPNLGHLS.K
		the presence of ethanol, functions to incorporate palmitic acid into phospholipids and		0 7004	0.004	0110.10	0110 107			
gi 6323903 ref NP_013974.1	YMR246W	neutral lipids; Faa4p Membrane protein of unknown function; overexpression suppresses NaCI sensitivity	2	3.7801	0.334	2112.49	2113.427	1	664.2	47.368423 Y.A1D1E1N2K2V1K2P1V1G111V1V1P1N2L1G1H3L1S1.K
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	2	3.1696	0.1921	1849.45	1850.05	3	429	46.42857 A.QCPELWIPRDPFGFS.K
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	2	3.4337	0.2743	1833.21	1834.05	1	611.7	60.714287 S.AQCPELWIPRDPFGF.S
ail63239221refINP_013993_11	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	3 8453	0 3719	2475 59	2476 847	1	311.6	
gilo323322[rei]re _013333.1]	11011120000	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	3.0455	0.5715	2473.33	2470.047		511.0	30.030304 E.SKVIF VDTWIKE EDGVSDTF SFKW.F
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p Membrane protein of unknown function: overexpression suppresses NaCl sensitivity	2	3.6874	0.2893	1745.45	1746.072	1	876.2	60.714287 N.IDMDGIKELPEFPIK.K
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	2	3.1475	0.237	1761.55	1763.072	1	935.8	60.714287 N.I1D1M1D1G1I1K2E1L1P1E1F1P1I1K2.K
ail6323922/refINP 013993.11	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCI sensitivity of sro7 mutant: Rsn1p	2	2.9383	0.1691	1815.95	1817.031	2	269.6	53.571426 Q.T1V1P1K2Q2Y1L1S1E1E1E1F1S1K2L1.F
3.1		Membrane protein of unknown function; overexpression suppresses NaCI sensitivity	_					-		
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p Membrane protein of unknown function; overexpression suppresses NaCI sensitivity	3	4.6716	0.2832	1874.06	1874.246	3	1045.1	45 N.IDMDGIKELPEFPIKK.Y
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	3	4.9362	0.1972	1896.14	1893.246	2	967.1	43.333332 N.I1D1M1D1G1I1K2E1L1P1E1F1P1I1K2K2.Y
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	2	3.8016	0.2715	1875.33	1874.246	1	724.4	56.666668 N.IDMDGIKELPEFPIKK.Y
ail63239221refINP_013993_11	YMR266W/	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	3 3721	0 2282	2057.07	2057 422	2	385.1	46 875 N 11D1M1D1G111K2E11 1P1E1E1P111K2K2V1 H
giloszoszzi cili i _010555.1]	11111220011	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	0.0721	0.2202	2001.01	2001.422	2	000.1	
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p Membrane protein of unknown function: overexpression suppresses NaCl sensitivity	2	3.5775	0.3437	1643.39	1645.998	1	601.5	61.538464 D.MDGIKELPEFPIKK.Y
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	2	3.5802	0.2964	2576.79	2575.947	1	584.5	40.476192 Y.H3A1P1L1F1M\$T1P1V1Y1I1G1I1E1P1S1D1V1V1W2F1N2.L
gi 6323922 ref NP 013993.1	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCI sensitivity of sro7 mutant; Rsn1p	2	3.5786	0.2389	2549.53	2549.947	1	364.5	35.714287 Y.HAPLFM@TPVYIGIEPSDVVWFN.L
	VMDaccW/	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	4 7000	0 4074	2550 52	0550.047		402.0	
gilo323922[rei]NP_013993.1]	TIVIR200VV	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	4.7606	0.4974	2008.03	2009.947		493.2	36.095236 T.H3ATPIETFIMITIPIVITIIGITEIPISIDIVIVIW2FINZ.L
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p Membrane protein of unknown function: overexpression suppresses NaCl sensitivity	2	3.8824	0.3321	2533.43	2533.947	1	645.4	42.857143 Y.HAPLFMTPVYIGIEPSDVVWFN.L
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	2	3.0955	0.1501	1415.11	1414.717	4	514.9	63.636364 D.G1I1K2E1L1P1E1F1P1I1K2K2.Y
ail63239221refINP_013993.11	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant: Rsn1p	1	2.9444	0.1975	1398.92	1399.717	4	517.7	63.636364 D.GIKELPEFPIKK Y
		Membrane protein of unknown function; overexpression suppresses NaCl sensitivity		2.0111	0.1070	1000.02				
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	3	3.8741	0.1984	3215.24	3214.684	1	726	28.57143 L.S1K2V1I1P1V1D1T1M1K2P1L1D1G1V1S1D1T1P1S1F1K2N2I1Y1K2G1I1E1.S
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	3	3.9214	0.235	1414.7	1414.717	8	1001.8	50 D.G1I1K2E1L1P1E1F1P1I1K2K2.Y
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	3	4.7017	0.3083	1578.35	1578.893	1	571.4	45.833336 D.G1I1K2E1L1P1E1F1P1I1K2K2Y1.H
ail63239221refINP_013993_11	YMR266W/	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	3 6496	0 2288	1922 27	1921 128	1	721.9	
giloszoszzitelini _010556.1	11111220011	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	0.0400	0.2200	1522.21	1021.120		721.5	
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p Membrane protein of unknown function; overexpression suppresses NaCl sensitivity	2	3.6185	0.382	1764.17	1762.971	1	745.9	69.230774 A.QCPELWIPRDPFGF.S
gi 6323922 ref NP_013993.1	YMR266W	of sro7 mutant; Rsn1p	2	3.2542	0.2079	1790.37	1791.1	1	855.3	63.333332 Y.H3A1P1L1F1M1T1P1V1Y1I1G1I1E1P1S1.D
gi 6323922 ref NP 013993.1	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCI sensitivity of sro7 mutant; Rsn1p	2	2.9738	0.2214	1780.17	1781.971	1	360.2	46.153847 A.Q2C1P1E1L1W2I1P1R4D1P1F1G1F1.S
	MADOOON	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity		0.4000	0 4070	1501.01	1500.000			
gilb323922[ref]NP_013993.1]	YNR266W	or sro/ mutant; Rsn1p	1	3.1923	0.4278	1561.81	1562.893	1	446.4	54.100008 D.GIKELPEFPIKKY.H
ail6323023[raf]ND_013004_41	YMR267\//	Mitochondrial inorganic pyrophosphatase, required for mitochondrial function and	2	3 011/	0 3557	102/63	1023 212	1	835 G	
8-10020020110114r _010004.11	. 1911 2207 11	posses, interved in energy generation norminorganic pyrophosphate, r pdzp	2	0.0114	0.0007	1024.00	1020.210		000.0	
gi 6323923 ref NP 013994.11	YMR267W	Mitochondrial inorganic pyrophosphatase, required for mitochondrial function and possibly involved in energy generation from inorganic pyrophosphate: Ppa2p	2	3.9613	0.3725	1938.37	1941.213	1	486	53.333336 S.K2I1D1D1L1E1K2I1E1E1Y1F1P1G1I1L1.D
0. · · · · · · · · · · · · · · · · · · ·		Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-	-					·		
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	2	3.1041	0.1831	1376.61	1376.701	2	902	75 H.KFLDLNRPLLM@.Q
=		.								

		Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-								
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain tatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-	2	3.6918	0.1744	1393.61	1392.701	2	1200.7	85 H.K2F1L1D1L1N2R4P1L1L1M\$.Q
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-	1	3.555	0.188	1488.87	1488.832	1	530.6	68.181816 H.KFLDLNRPLLMQ.I
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sphinoolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphinoolipid-	1	2.908	0.2712	1359.59	1360.701	2	541.1	70 H.KFLDLNRPLLM.Q
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sphinoglipia alpha-hydroxylase, functions in the alpha-hydroxylation of sphinoglipid-	1	3.1034	0.1588	1505.65	1506.832	2	482	63.636364 H.K2F1L1D1L1N2R4P1L1L1M1Q2.I
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sphinoglipia alpha-hydroxylase, functions in the alpha-hydroxylation of sphinoglipid-	1	2.5903	0.1662	1231.49	1232.527	1	700.7	77.77778 K.FLDLNRPLLM.Q
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sohinoolibid albha-hydroxylase, functions in the albha-hydroxylation of sohinoolibid-	2	4.0876	0.2004	1488.21	1488.832	1	1370.7	81.818184 H.KFLDLNRPLLMQ.I
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sphinoglipia alpha-hydroxylase, functions in the alpha-hydroxylation of sphinoglipid-	2	4.1763	0.1537	1507.53	1506.832	1	1631.3	86.36364 H.K2F1L1D1L1N2R4P1L1L1M1Q2.I
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sohinoolibid alpha-hydroxylase, functions in the alpha-hydroxylation of sohinoolibid-	2	3.6082	0.1707	1360.13	1360.701	6	1442	85 H.KFLDLNRPLLM.Q
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sphinoplinid alpha-hydroxylase, functions in the alpha-hydroxylation of sphinoplinid-	2	2.9966	0.2541	1481.27	1480.808	8	432.8	59.090908 M.DKYRLVMPPTLF.V
gi 6323928 ref NP_013999.1	YMR272C	associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p Sphinoplinia alpha-hydroxylase, functions in the alpha-hydroxylation of sphinoplinid-	2	3.4788	0.2459	1358.85	1360.701	8	1270.7	80 H.KFLDLNRPLLM.Q
gi 6323928 ref NP_013999.1	YMR272C	epinningunptic taptic on yo sing tasty acids, has both explort hyrothyrothere and associated even long chain faity acids, has both explort hyrothyrothere by hyrothyrothere and the second second acids and the second acids and hydroxylase/desaturase domains, not essential for growth; Scs7p ATP-dependent RNA belicase; localizes to both the nuclear periphery and nucleolus;	1	2.8386	0.3255	1359.83	1360.701	1	567.5	70 H.KFLDLNRPLLM.Q
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 65° pre-ribosomal particles; Hastp ATP-dependent RNA belicase; localizes to both the nuclear periohery and nucleolus;	2	3.6736	0.2727	1792.07	1792.042	1	821.3	64.28571 S.KVPLNEYEFPENKIA.N
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p ATP-dependent RNA belicase: localizes to both the nuclear periphery and nucleolus;	2	3.5395	0.1908	1810.29	1811.042	1	642.9	53.571426 S.K2V1P1L1N2E1Y1E1F1P1E1N2K2I1A1.N
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p ATP-dependent RNA helicase: localizes to both the nuclear periohery and nucleolus:	3	5.2575	0.2761	2449.22	2449.728	1	835.5	38.157894 I.D1E1A1D1R4I1L1E1I1G1F1E1D1E1M1R4Q2I1I1K2.I
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p ATP-dependent RNA helicase: localizes to both the nuclear periohery and nucleolus:	3	5.1246	0.2838	2421.26	2421.728	1	760.1	35.526314 I.DEADRILEIGFEDEMRQIIK.I
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p ATP-dependent RNA helicase: localizes to both the nuclear periohery and nucleolus;	3	6.3762	0.3554	2676.29	2678.047	1	1443.9	41.6666664 L.I1I1D1E1A1D1R4I1L1E1I1G1F1E1D1E1M1R4Q2I1I1K2.I
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p ATP-dependent RNA helicase: localizes to both the nuclear periohery and nucleolus:	3	6.4289	0.3167	2648.33	2648.047	1	1856.2	45.238094 LIIDEADRILEIGFEDEMRQIIK.I
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p ATP-dependent RNA helicase: localizes to both the nuclear periohery and nucleolus:	3	6.6049	0.3564	2679.2	2678.047	1	1322.8	41.6666664 L.1111D1E1A1D1R4I1L1E111G1F1E1D1E1M1R4Q21111K2.I
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p ATP-dependent RNA helicase: localizes to both the nuclear periohery and nucleolus:	2	3.346	0.2194	2678.55	2678.047	1	491.9	40.476192 L1111D1E1A1D1R4I1L1E111G1F1E1D1E1M1R4Q21111K2.I
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p ATP-dependent RNA helicase: localizes to both the nuclear periohery and nucleolus:	3	4.5175	0.2267	2330.9	2333.639	3	661.3	36.11111 D.E1A1D1R4I1L1E1I1G1F1E1D1E1M1R4Q2I1I1K2.I
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear por committed fractions; crusitiuent of 66S pre-ribosomal particles; Hastp ATP-dependent RNA helicase: localizes to both the nuclear periohery and nucleolus:	3	4.2793	0.2389	2824.19	2826.182	4	583.4	29.545454 LE111G1F1E1D1E1M1R4Q2I111K2I1L1P1N2E1D1R4Q2S1M1.L
gi 6323947 ref NP_014017.1	YMR290C	highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p Component of serine palmitovitransferase, responsible along with Lcb2p for the first	1	2.3449	0.1595	1348.46	1348.616	2	177.4	50 LK2F1K2P1R4N2G1T1G11111V1.I
gi 6323954 ref NP_014025.1	YMR296C	committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p Component of serine palmitoyltransferase, responsible along with Lcb2p for the first	2	4.0573	0.3452	2170.65	2170.557	1	891.8	52.941177 N.ELTEQEKLEKLPAIPRKF.I
gi 6323954 ref NP_014025.1	YMR296C	committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p Component of serine palmitoyltransferase, responsible along with Lcb2p for the first	2	4.3793	0.4166	2193.69	2195.557	1	1064.1	58.823532 N.E1L1T1E1Q2E1K2L1E1K2L1P1A1I1P1R4K2F1.I
gi 6323954 ref NP_014025.1	YMR296C	committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p Component of serine palmitoyltransferase, responsible along with Lcb2p for the first	3	5.03	0.1568	2312.9	2311.661	7	657.3	38.88889 L.N2E1L1T1E1Q2E1K2L1E1K2L1P1A111P1R4K2F1.I
gi 6323954 ref NP_014025.1	YMR296C	committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p Component of serine palmitoyltransferase, responsible along with Lcb2p for the first	2	5.0839	0.3383	2310.37	2311.661	1	1053.8	55.555557 L.N2E1L1T1E1Q2E1K2L1E1K2L1P1A1I1P1R4K2F1.I
gi 6323954 ref NP_014025.1	YMR296C	committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p Component of serine palmitoyltransferase, responsible along with Lcb2p for the first	2	4.1429	0.2552	2286.15	2284.661	1	985.7	52.77778 L.NELTEQEKLEKLPAIPRKF.I
gi 6323954 ref NP_014025.1	YMR296C	committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lob1p Component of serine palmitoyltransferase, responsible along with Lcb2p for the first	2	3.363	0.2722	1927.99	1928.282	1	1128	66.66667 L.TEQEKLEKLPAIPRKF.I
gi 6323954 ref NP_014025.1	YMR296C	committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p Component of serine palmitoyltransferase, responsible along with Lcb2p for the first	3	4.3917	0.2141	2171.06	2170.557	2	681.2	39.705883 N.ELTEQEKLEKLPAIPRKF.I
gi 6323954 ref NP_014025.1	YMR296C	committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	3	3.8664	0.1664	1950.92	1951.282	1	1198.2	45 L.T1E1Q2E1K2L1E1K2L1P1A1I1P1R4K2F1.I

		Ceramide synthase subunit; single-span ER membrane protein associated with								
-:::::::::::::::::::::::::::::::::::::	VMD200W	Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows	0	2 0007	0 4005	4047.07	4047.074	4	4470.0	
gilb323956[ref]NP_014027.1]	YMR298W	extremely slowly and is defective in ceramide synthesis; LIP1p Ceramide synthase subunit: single-span FR membrane protein associated with	2	3.9927	0.4035	1917.37	1917.974	1	1170.8	71.42857 R.1111R4D1Y1E1P1N2D1E1H3L151F1C1.I
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.4107	0.3344	2965.71	2967.264	1	494.6	32 C.IIENDNVPPVHYPIHEDKGEPGYVAY.V
		Lag1p and Lag1p and required for ceramide synthase activity, pull mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.7761	0.3234	2803.69	2804.088	1	377.7	35.416664 C.IIENDNVPPVHYPIHEDKGEPGYVA.Y
		Ceramide synthase subunit; single-span ER membrane protein associated with								
gil6323956[rof[NIP_014027_1]	VMP208W/	Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows	3	4 462	0 4336	2005 7	2007 227	1	502 5	27 000002 E C1111E1N/2D1N/2V1D1D1V/1H3V1D111H3E1D1K2C1E1D1C1V1/1A1 V
gil0323330[tel[14F_014027.1]	11011123000	Ceramide synthese subunit: single-span ER membrane protein associated with	5	4.402	0.4330	2333.1	2551.221	1	302.3	
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.0414	0.3766	2078.39	2078.161	7	570.9	50 K.R4I1T1R4D1Y1E1P1N2D1E1H3L1S1F1C1.I
		Lag1p and Lag1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.7355	0.3368	1892.31	1893.023	1	649	57.14286 K.RITRDYEPNDEHLSF.C
		Ceramide synthase subunit; single-span ER membrane protein associated with								
gil6323956/refINP_014027_11	YMR298W	extremely slowly and is defective in ceramide synthesis: Lin1p	2	3 607	0 2695	1915 59	1917 023	1	567.2	53 571426 K R4I1T1R4D1Y1E1P1N2D1E1H3I 1S1E1 C
910020000101111 _011021111	1111120011	Ceramide synthase subunit; single-span ER membrane protein associated with	-	0.001	0.2000	1010.00	10111020		007.2	
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p Ceramide synthese subunit: single-span ER membrane protein associated with	2	4.7058	0.4201	2245.31	2245.461	1	736.2	52.63158 D.N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1Y1V1A1.Y
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.1643	0.2734	2168.53	2169.401	1	761.1	52.77778 V.PPVHYPIHEDKGEPGYVAY.V
		Ceramide synthase subunit; single-span ER membrane protein associated with								
gil6323956/refINP_014027_11	YMR298W	extremely slowly and is defective in ceramide synthesis: Lin1p	2	3 026	0 2926	2331 51	2332 577	1	309.4	38 88889 N Y1E1W2E1H3C1T1P111K2E1P1Q2S1G1S1V111K2 I
giloozoooolioiliti _01102111		Ceramide synthase subunit; single-span ER membrane protein associated with	-	0.020	0.2020	2001.01	2002.077		000.1	
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p Ceramide synthese subunit: single-span EP membrane protein associated with	3	4.5126	0.2661	2535.65	2534.84	1	990.6	35 R.INYEWFHCTPIKEPQSGSVIK.L
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	3	3.8828	0.1654	2420.96	2420.736	1	1002.2	34.210526 N.YEWFHCTPIKEPQSGSVIKL.W
		Ceramide synthase subunit; single-span ER membrane protein associated with								
gil6323956/refINP_014027.1	YMR298W	Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis: Lip1p	2	4.2598	0.4348	2217.77	2219.461	1	696.1	52.63158 D.NVPPVHYPIHEDKGEPGYVA.Y
3.1		Ceramide synthase subunit; single-span ER membrane protein associated with								
- 1000000001 - (INID: 044007 4)		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows	0	0 7044	0.0705	0000 11	0000 007			
gi 6323956 ret NP_014027.1	YMR298W	extremely slowly and is detective in ceramide synthesis; Lip1p Ceramide synthese subunit: single-span ER membrane protein associated with	2	3.7211	0.3735	2383.41	2382.637	1	341.4	42.5 D.NVPPVHYPIHEDKGEPGYVAY.V
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.7408	0.2671	1906.59	1908.111	1	670	56.666668 E.W2F1H3C1T1P1I1K2E1P1Q2S1G1S1V1I1.K
		Ceramide synthase subunit; single-span ER membrane protein associated with								
ail6323956/refINP 014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis: Lip1p	3	4.3073	0.2493	2561.48	2562.84	1	1172	40 R.I1N2Y1E1W2F1H3C1T1P1I1K2E1P1Q2S1G1S1V111K2.L
31		Ceramide synthase subunit; single-span ER membrane protein associated with								
- 1000000001 - (INID: 044007 4)		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows	0	4 0000	0 1007	0500 70	0504.04		4405.4	
gilb323956[ref]NP_014027.1]	YMR298W	extremely slowly and is defective in ceramide synthesis; LIP1p Ceramide synthase subunit: single-span FR membrane protein associated with	2	4.6828	0.4627	2532.79	2534.84	1	1105.1	52.499996 R.INYEWFHCTPIKEPQSGSVIK.L
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.6576	0.4562	2419.45	2420.736	1	768.9	44.736843 N.YEWFHCTPIKEPQSGSVIKL.W
		Ceramide synthase subunit; single-span ER membrane protein associated with								
gi 6323956 ref NP 014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.7092	0.3866	2446.49	2446.736	1	762	44.736843 N.Y1E1W2F1H3C1T1P1I1K2E1P1Q2S1G1S1V1I1K2L1.W
		Ceramide synthase subunit; single-span ER membrane protein associated with								
ail6323056/rofIND_014027_11	VMP208///	Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows	3	4 7604	0.2654	2650.25	2648	1	780.6	
gilo323930[rei]inF_014027.1]	TIVINZ90W	Ceramide synthese subunit: single-span ER membrane protein associated with	3	4.7004	0.2004	2000.20	2048	1	780.0	32.142037 K.INTEWFROTFIKEPQ303 VIKE.W
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.8023	0.3876	2675.45	2677	1	680.6	40.476192 R.I1N2Y1E1W2F1H3C1T1P1I1K2E1P1Q2S1G1S1V111K2L1.W
		Lag1p and Lag1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.6071	0.402	2649.73	2648	1	461.4	40.476192 R.INYEWFHCTPIKEPQSGSVIKL.W
		Ceramide synthase subunit; single-span ER membrane protein associated with								
gil6323956[rof[NIP_014027_1]	VMP208W/	Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows	2	4 0270	0 2441	2151 /3	2152 445	1	623.8	52 041177 E W2E1H3C1T1P111K2E1P1O2S1C1S1\/111K2L1 W
gil0323330[rei]i4r_014027.1]	11011723000	Ceramide synthese subunit; single-span ER membrane protein associated with	2	4.0275	0.2441	2131.43	2152.445	1	023.0	
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	3	4.6447	0.2785	3001.88	3000.264	1	480.7	26 C.III1E1N2D1N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1Y1V1A1Y1.V
		Lag1p and Lag1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.3457	0.3996	2998.57	3000.264	1	286.1	28 C.III1E1N2D1N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1Y1V1A1Y1.V
		Ceramide synthase subunit; single-span ER membrane protein associated with								
ail63239561refINP_014027.11	YMR298W	extremely slowly and is defective in ceramide synthesis: Lip1p	2	3.7115	0.1701	2534.17	2534.84	1	930.1	50 R.INYEWEHCTPIKEPQSGSVIK.L
3.1		Ceramide synthase subunit; single-span ER membrane protein associated with								
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ret NP_014027.1	YMR298W	extremely slowly and is detective in ceramide synthesis; Lip1p Ceramide synthese subunit: single-span ER membrane protein associated with	3	3.9748	0.2248	2420.03	2420.736	1	1020.1	36.842106 N.YEWFHCTPIKEPQSGSVIKL.W
		Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.2607	0.4143	2420.57	2420.736	1	857.2	47.368423 N.YEWFHCTPIKEPQSGSVIKL.W
		Ceramide synthase subunit; single-span ER membrane protein associated with								
gi 6323956 ref NP_014027.1	YMR298W	extremely slowly and is defective in ceramide synthesis; Lip1p	2	2.9449	0.2537	1887.89	1887.111	1	303	43.333332 E.WFHCTPIKEPQSGSVI.K
= .		Ceramide synthase subunit; single-span ER membrane protein associated with								
ail6323956[ref]ND 014027 41	YMR209///	Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows	2	3 8695	0.4000	1907 73	1000 074	1	327 5	59 375 D N2\/1D1P1\/1H3V1P1 1H3E1D1K2C1E1D1C1 V
gij05255500[iCi]INF_014027.1]	11111723011	overeniery slowly and is delective in deranilde synthesis, Lip ip	2	0.0000	0.4099	1301.13	1303.074	1	521.5	55.575 D.WZVIEIERVINDER HINDEIDINZOTEIEIGI.T

	VMD200W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows	2	4 4000	0.4007	2407 77	0400 007	4	200.2	
gil6323956[rei]NP_014027.1]	TWR296W	Externelly slowly and is delective in certainde synthesis; Lip ip Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acatalyzed; involved in the production of contain cathowidate estars; regulated by	2	4.1002	0.4697	2407.77	2409.637	I	320.3	42.5 D.N2VIPIPIVIN3TIPIIINSEIDIN2GIEIPIGITIVIAITI.V
gi 6323961 ref NP_014032.1	YMR303C	ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	1	2.586	0.2784	1051.64	1052.335	1	367.8	61.11111 R.G1L1V1K2S1P1I1K2V1V1.G
gi 6323961 ref NP_014032.1	YMR303C	acetaidenyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	1	3.6608	0.2856	1531.91	1530.81	1	615.6	61.538464 W.HGDWPLPTKLPLVG.G
gi 6323961 ref NP_014032.1	YMR303C	acetal/dehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.3583	0.3535	1532.97	1530.81	1	1662.3	73.07692 W.HGDWPLPTKLPLVG.G
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	1	2.2786	0.2622	1209.63	1210.546	2	391.8	54.545456 R.GLVKSPIKVVGL.S
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.3045	0.4226	1984.69	1982.249	1	1089	58.333332 W.HGDWPLPTKLPLVGGHEGA.G
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	3	5.7004	0.3212	1856.42	1854.119	1	2096.9	56.25 W.HGDWPLPTKLPLVGGHE.G
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; Adr2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	1	2.2794	0.2457	1039.63	1040.335	2	371.2	61.11111 R.GLVKSPIKVV.G
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	1	2.6647	0.1672	1223.68	1224.546	2	398.2	54.545456 R.G1L1V1K2S1P1I1K2V1V1G1L1.S
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.4865	0.4029	2141.15	2138.434	1	1097.7	57.5 W.HGDWPLPTKLPLVGGHEGAGV.V
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adr2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	5.2313	0.339	1879.79	1877.119	1	905.1	65.625 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1.G
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	3	4.7776	0.3358	2167.46	2165.434	1	1391.9	40 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1G1A1G1V1.V
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	3.0002	0.2542	1855.65	1854.119	1	437.1	46.875 W.HGDWPLPTKLPLVGGHE.G
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	3	3.8835	0.2409	2009.9	2007.249	1	978.2	40.27778 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1G1A1.G
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	2.903	0.3122	1041.33	1040.335	6	576.7	77.77778 R.GLVKSPIKVV.G
gi 6323961 ref NP_014032.1	YMR303C	acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	3.725	0.3362	1377.55	1374.626	1	844.7	72.72727 W.HGDWPLPTKLPL.V
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; Adr2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.1469	0.326	1609.83	1606.862	1	1196.3	64.28571 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1.H
gi 6323961 ref NP_014032.1	YMR303C	abetaidenyde, involved in the production of certain carboxytate esters, regulated by ADR1; AdR2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.2282	0.3768	1551.37	1548.81	1	1458.3	69.230774 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1.G
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; Adr2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.6076	0.4271	1533.63	1530.81	1	1582.2	73.07692 W.HGDWPLPTKLPLVG.G
gi 6323961 ref NP_014032.1	YMR303C	actioneryoe, involved in the production of certain carboxylate esters, regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.1629	0.3169	1590.45	1587.862	1	1010.1	60.714287 W.HGDWPLPTKLPLVGG.H
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; Adr2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.1781	0.2032	1748.59	1747.003	1	1464.4	66.66667 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3.E
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; Adr2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	3	4.2899	0.2516	1983.86	1982.249	1	981.5	43.055553 W.HGDWPLPTKLPLVGGHEGA.G
gi 6323961 ref NP_014032.1	YMR303C	acteriatery de, involved in the production of certain carboxyrate esters, regulated by ADR1; AdR2 Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	3.9423	0.3421	1984.47	1982.249	1	475.4	52.77778 W.HGDWPLPTKLPLVGGHEGA.G
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; Adr2p Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	3	5.348	0.3145	1879.07	1877.119	1	1847.7	54.6875 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1.G
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.1147	0.3858	2009.61	2007.249	1	1287.2	61.11111 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1G1A1.G
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	4.262	0.3376	1727.63	1725.003	1	1265.4	66.66667 W.HGDWPLPTKLPLVGGH.E
gi 6323961 ref NP_014032.1	YMR303C	acetaioenyoe, involved in the production of certain carboxylate esters; regulated by ADR1; AdAp Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to	2	3.6984	0.2222	1879.47	1877.119	1	752.8	59.375 W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1.G
gi 6323961 ref NP_014032.1	YMR303C	ADR1; Adh2p Rota 1.2 alugaged/transferage, required for cell well accomply/ legelines to the cell	2	3.2825	0.3375	1855.15	1854.119	1	715.1	53.125 W.HGDWPLPTKLPLVGGHE.G
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p Bata 1.3-glycosylphosphatidylinositol (GPI) anchor; Gas1p Bata 1.3-glycosylphosphatidylinositol (GPI) anchor; Gas1p	2	2.9165	0.3253	1592.41	1592.748	1	962.5	70.83333 S.INRDDPTWTVDLF.N
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosyltanostrato, required to cell wall assembly, localizes to the cell Beta-1.3-diucanosyltanosterase, required for cell wall assembly localizes to the cell	2	3.2901	0.3135	1680.27	1679.827	1	989.5	69.230774 T.SINRDDPTWTVDLF.N
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosyltanostrato, required to cell wall assembly, localizes to the cell Beta-1.3-diucanosyltanosterase, required for cell wall assembly localizes to the cell	2	2.9695	0.331	2090.25	2091.285	1	272.6	41.666664 L.AAPATSINRDDPTWTVDLF.N
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p	2	2.9692	0.2277	1700.67	1698.827	1	542.9	53.846157 T.S1I1N2R4D1D1P1T1W2T1V1D1L1F1.N

		Beta-1.3-glucanosyltransferase, required for cell wall assembly; localizes to the cell								
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p Beta-1.3-olucanosyltransferase, required for cell wall assembly: localizes to the cell	1	2.825	0.2482	1123.56	1124.301	1	199.8	68.75 K.N2Y1R4K2I1P1V1G1Y1.S
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p	1	2.9565	0.2058	1552.8	1553.801	1	279.5	54.166668 Y.ISDKNYRKIPVGY.S
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p	1	3.2082	0.2832	1571.62	1572.801	1	290.6	58.333332 Y.I1S1D1K2N2Y1R4K2I1P1V1G1Y1.S
gi 6323967 ref NP_014038.1	YMR307W	Beta-1.3-glucanosyltransferase, required for cell wall assembly; localizes to the cell surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p	2	3.5641	0.2977	1610.27	1610.748	1	1490.8	79.16667 S.I1N2R4D1D1P1T1W2T1V1D1L1F1.N
gil6323967/refINP_014038.1	YMR307W	Beta-1.3-glucanosyltransferase, required for cell wall assembly; localizes to the cell surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p	2	2.9467	0.3536	1553.11	1553.801	1	698.3	70.83333 Y.ISDKNYRKIPVGY.S
gil0020007 : ci 11 _ c1 1000.1	VMD207W	Beta-1.3-glucanosyltransferase, required for cell wall assembly; localizes to the cell	-	2.0101	0.0000	4550.00	4552.004		204.0	
gilo323967 [rei]NP_014038.1]	TWR307W	Beta-1.3-glucanosyltransferase, required for cell wall assembly; localizes to the cell		3.7181	0.3673	1002.08	1003.601	1	321.2	58.333332 1.15DKN1KKIPVG1.5
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p Beta-1.3-glucanosyltransferase, required for cell wall assembly; localizes to the cell	1	3.3756	0.2795	1571.74	1572.801	1	286.2	58.333332 Y.I1S1D1K2N2Y1R4K2I1P1V1G1Y1.S
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p Beta-1 3-nucanosyltransferase, required for cell wall assembly: localizes to the cell	2	3.2133	0.257	1575.47	1572.801	2	601.7	66.66667 Y.I1S1D1K2N2Y1R4K2I1P1V1G1Y1.S
gi 6323967 ref NP_014038.1	YMR307W	surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p	1	2.5598	0.2631	1109.56	1110.301	1	229.9	68.75 K.NYRKIPVGY.S
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p	2	4.1416	0.3648	1772.67	1769.995	1	400.3	60.714287 L.SFQGPPETLRDYVLF.A
gi 6323969 ref NP_014040.1	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection; Nip1p	2	3.6868	0.372	2219.65	2221.32	2	377.1	38.88889 K.F1R4N2D1P1E1S1F1D1K2E1P1T1A1D1L1D1I1S1.A
ail63239691refINP 014040.11	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection; Nip1p	3	4.3194	0.3745	2529.74	2529.737	1	295	30.952381 F.A1D1P1I1D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.G
gil6222060/rofIND_014040_1	VMP200C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	-	4 4961	0 1055	0017 EE	2216 57	1	1291.0	
gilosz5909iteiline_014040.1	TWIK509C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	3	4.4001	0.1955	2317.55	2310.57		1201.9	42.103203 D.FIDFIEDEFREDBUGVRRIE.G
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	2	4.0273	0.3266	2531.49	2529.737	1	409.7	42.857143 F.A1D1P111D1F111E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.G
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Subunit of the eukarvotic translation initiation factor 3 (eIE3), involved in the	3	3.8397	0.2766	2838.29	2836.081	1	438.6	28.125 N.EFADPIDFIEDEPKEDSDGVKRILG.S
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p	3	4.8449	0.3239	2341.55	2341.57	1	1826	44.736843 D.P1I1D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.G
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p	2	3.7153	0.2084	2807.55	2808.03	1	304.6	41.304348 N.E1F1A1D1P1I1D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.G
gi 6323969 ref NP_014040.1	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection; Nip1p	2	3.6263	0.3425	2780.95	2779.029	1	444	45.652176 N.EFADPIDFIEDEPKEDSDGVKRIL.G
ail63239691refINP_014040.11	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection. Nip1p	2	4.5624	0.3786	1754.47	1754.008	1	1472.7	76.92308 A.KEKLLDEMODVYNK I
gil6222060/rofIND_014040_1	VMP200C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	-	2 9100	0.2062	1054.10	1054.246	1	E10.6	
gilosz5505itelini _014040.1	110113030	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	2	3.0103	0.2005	1954.19	1334.240		510.0	
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	3	4.0037	0.2087	1956.2	1954.246	1	731.6	45 A.KEKLLDEMQDVYNKIS.Q
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	2	3.757	0.4018	2025.61	2025.325	1	583.3	56.25 S.AKEKLLDEMQDVYNKIS.Q
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Suburit of the subaryotic translation initiation factor 3 (aIE3), involved in the	3	4.0111	0.3034	2027.6	2025.325	1	562.7	43.75 S.AKEKLLDEMQDVYNKIS.Q
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p	2	3.2903	0.3295	1862.83	1865.077	1	470.3	57.14286 T.L1K2D1E1H3D1L1E1R4A1L1T1R4P1F1.V
gi 6323969 ref NP_014040.1	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection; Nip1p	2	3.1802	0.4043	1838.83	1841.077	1	567.2	60.714287 T.LKDEHDLERALTRPF.V
gi 6323969 ref NP 014040.1	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection; Nip1p	2	3.0079	0.254	1787.69	1788.995	4	305.2	46.42857 L.S1F1Q2G1P1P1E1T1L1R4D1Y1V1L1F1.A
gil6323969/refINP_014040.1	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection. Nin1p	2	3 8833	0 3255	2530 17	2529 737	1	375	47 61905 F A1D1P1I1D1F1I1F1D1F1P1K2F1D1S1D1G1V1K2R4I1I 1 G
	VMD2000C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	-	2.0505	0.0200	4775.00	4770.000		024	
gilb323969[rei]NP_014040.1]	TMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	2	3.8595	0.241	1775.63	1773.008	1	931	73.07692 A.RZETRZETETDTETMTQ2DTVTTTNZRZ.I
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	2	3.687	0.2013	1175.21	1173.456	1	1191.2	83.33333 C.SLLIEIPRMT.A
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Subunit of the eukarvotic translation initiation factor 3 (eIE3), involved in the	2	4.0165	0.2089	1185.63	1186.456	1	1133.8	83.33333 C.S1L1L1I1E1I1P1R4M1T1.A
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p	2	3.3871	0.2187	1527.67	1526.73	1	646	72.72727 A.K2E1K2L1L1D1E1M1Q2D1V1Y1.N
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p	2	3.947	0.3372	2501.69	2502.737	1	569.9	52.380955 F.ADPIDFIEDEPKEDSDGVKRIL.G
gi 6323969 ref NP_014040.1	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection; Nip1p	2	3.6569	0.2237	2807.55	2808.03	2	239	36.95652 N.E1F1A1D1P1I1D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.G
ail63239691refINP 014040.11	YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection; Nip1p	3	3.8921	0.1857	2129.18	2129.294	2	918.4	41.17647 I.D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.G
gil6323969/rofINP_014040.1	VMP300C	Suburit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of projuitiation complex and start orden selection. Subon	3	4 3297	0.3050	2807 12	2808 03	-	574.1	31 52174 N E1E1A1D1E1I1D1E1I1E1D1E1D1K2E1D1S1D1G1V1K2P4I1I 1 G
gilosz5505itelini _014040.1	110113030	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the		4.3207	0.3033	2007.12	2000.03		574.1	
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the	2	3.5866	0.2621	1599.51	1598.809	2	401.2	58.333332 S.A1K2E1K2L1L1D1E1M1Q2D1V1Y1.N
gi 6323969 ref NP_014040.1	YMR309C	assembly of preinitiation complex and start codon selection; Nip1p Probable RNA-binding protein, functions in protein translation to promote G1	1	2.6412	0.1543	1195.45	1196.337	3	149.9	62.5 G.N2W2R4D1S1V1K2Y1L1.R
gi 6324327 ref NP_014397.1	YNL001W	progression and differentiation, required for meiotic cell division; Dom34p Brobable BNA-binding protein, functions in protein translation to promote G1	1	2.9772	0.3784	1482.56	1483.618	2	227.7	42.307693 L.HSLGEELDQLTGIA.C
gi 6324327 ref NP_014397.1	YNL001W	progression and differentiation, required for meiotic cell division; Dom34p	2	4.6389	0.4231	2024.39	2024.293	1	1452.1	66.66667 K.VISEDFDMKDEYLKYK.G
gi 6324327 ref NP_014397.1	YNL001W	Probable RNA-binding protein, functions in protein franslation to promote G1 progression and differentiation, required for meiotic cell division; Dom34p	2	4.9044	0.4556	2044.55	2043.293	1	1623	70 K.V1I1S1E1D1F1D1M1K2D1E1Y1L1K2Y1K2.G
gi 6324327 ref NP_014397.1	YNL001W	Probable RNA-binding protein, functions in protein translation to promote G1 progression and differentiation, required for meiotic cell division; Dom34p	2	3.8601	0.2749	1651.25	1650.678	1	855.4	69.230774 L.K2Y1P1L1P1D1L1D1E1D1D1G1E1E1
gil6324327/refINP_014397_1	YNL001W	Probable RNA-binding protein, functions in protein translation to promote G1 progression and differentiation, required for mejotic cell division. Dom34n	2	3,7065	0.3353	1635.65	1635.678	1	742 4	65.38461 L.KYPI PDI DEDDGEE -
	VNI 004W	Probable RNA-binding protein, functions in protein translation to promote G1	-	4 9 4 9 0	0.4000	1077.04	1070 007	4	1057.0	
gijo324327 (ret[NP_014397.1]	rnL001W	Probable RNA-binding protein, functions in protein translation to promote G1	2	4.2439	0.4089	1877.21	1878.997	1	1057.2	70 C.HLIKZYIPILIPIDILIDIEIDIDIGIEIEI
gi 6324327 ref NP_014397.1	YNL001W	progression and differentiation, required for meiotic cell division; Dom34p Type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1p; not	2	3.8488	0.4567	1861.15	1861.997	1	1193.7	70 C.ILKYPLPDLDEDDGEE
gil6324321/refINP_014391_1	YNL007C	functionally redundant with Ydj1p due to due to substrate specificity; shares similarity with bacterial Dna.Loroteins; Sis1p	2	4,1453	0.3726	1847 33	1848.065	1	1086	63.333332 A ALKYHPDKPTGDTEKE.K
5-1-5- 10-11-01-01-001-11			-		0.0120		.0.000			

gi 6324321 ref NP_014391.1	YNL007C	Type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1p; not functionally redundant with Ydj1p due to due to substrate specificity; shares similarity with bacterial DnaJ proteins; Sis1p Type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1p; not	2	3.6375	0.2896	1681.31	1682.827	1	850	61.538464 L.K2Y1H3P1D1K2P1T1G1D1T1E1K2F1.K
gi 6324321 ref NP_014391.1	YNL007C	functionally redundant with Ydj1p due to due to substrate specificity; shares similarity with bacterial DnaJ proteins; Sis1p Type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1p; not	2	3.2703	0.3467	1956.85	1959.103	1	292.7	53.333336 Q.E1K2S1H3P1N2F1K2R4D1G1D1D1L111Y1.T
gi 6324321 ref NP_014391.1	YNL007C	functionally redundant with Ydj1p due to due to substrate specificity; shares similarity with bacterial DnaJ proteins; Sis1p	2	3.165	0.3044	1662.17	1663.827	1	444.6	57.692307 L.KYHPDKPTGDTEKF.K
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	1	2.7271	0.2085	1471.65	1472.682	1	379.9	59.090908 E.N2I1P1I1D1W2E1T1I1N2I1K2.Q
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	3	3.9199	0.2308	1793.39	1791.999	1	1451.9	43.75 I.PGDGVGKEITDSVRTIF.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	3	4.2374	0.3245	1813.19	1812.999	1	2144.9	51.5625 I.P1G1D1G1V1G1K2E1I1T1D1S1V1R4T1I1F1.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	4.1784	0.3165	1812.31	1812.999	1	893.2	59.375 I.P1G1D1G1V1G1K2E1I1T1D1S1V1R4T1I1F1.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	4.1271	0.4491	1794.59	1791.999	1	1086.2	65.625 I.PGDGVGKEITDSVRTIF.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.9768	0.1564	1323.51	1323.622	1	1285.1	85 T.RIPDIDLIVIR.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	4.0613	0.2821	1440.69	1442.727	1	1447.1	81.818184 K.T1R4I1P1D111D1L111V11R4.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.6037	0.2305	1472.21	1470.737	8	518.3	63.636364 T.R4I1P1D1I1D1L1I1V11R4E1.N
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.2912	0.2593	1365.79	1364.6	2	585.3	72.72727 M.K2L1G1D1G1L1F1R4N2I1I1T1.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	4.0436	0.3455	1422.73	1424.727	1	1490.7	81.818184 K.TRIPDIDLIVIR.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	1	2.5948	0.2227	1322.79	1323.622	1	237.7	65 T.RIPDIDLIVIR.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	1	2.7709	0.2436	1339.55	1340.622	3	250.5	65 T.R4I1P1D1I1D1L111V111R4.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	4.2101	0.3375	1338.57	1340.622	1	1469.2	90 T.R4I1P1D1I1D1L111V11R4.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	2.9274	0.2999	2018.67	2018.318	1	549.6	63.88889 T.LIPGDGVGKEITDSVRTIF.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.4842	0.2633	1452.65	1452.737	1	1200.5	81.818184 T.RIPDIDLIVIRE.N
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	1	2.6398	0.246	1322.84	1323.622	1	235	65 T.RIPDIDLIVIR.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	1	2.2619	0.176	1342.34	1340.622	1	197	60.000004 T.R4I1P1D1I1D1L1I1V11R4.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	4.2304	0.3114	1338.79	1340.622	1	1540.2	90 T.R4I1P1D1I1D1L111V11R4.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.7056	0.2035	1323.69	1323.622	2	1129.8	80 T.RIPDIDLIVIR.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.3046	0.275	1900.91	1903.232	3	424.8	46.875 M.KLGDGLFRNIITEIGOK.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.7726	0.2871	1785.83	1785.992	2	345.3	57.14286 F.EAENIPIDWETINIK.Q
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	1	3.2703	0.1745	1471.46	1472.682	1	478.8	63.636364 E.N2I1P111D1W2E1T11N2I1K2.Q
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	1	3.0883	0.3	1456.61	1456.682	1	446.4	63.636364 E.NIPIDWETINIK.Q
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.4877	0.2513	1474.57	1472.682	1	576.5	81.818184 E.N2I1P1I1D1W2E1T1I1N2I1K2.Q
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	2.9134	0.1693	2322.09	2319.66	2	378.6	40.476192 F.TVTLIPGDGVGKEITDSVRTIF.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	1	2.5899	0.1818	1323.42	1323.622	2	183.8	60.000004 T.RIPDIDLIVIR.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	4.2329	0.2569	1341.15	1340.622	1	1310.8	85 T.R4I1P1D1I1D1L1I1V111R4.E

gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	2	3.8584	0.1983	1323.71	1323.622	1	1467.2	90 T.RIPDIDLIVIR.E
gi 6324291 ref NP_014361.1	YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	1	2.7028	0.1945	1339.71	1340.622	4	217.2	60.000004 T.R4I1P1D1I1D1L1I1V1I1R4.E
gi 6324280 ref NP_014350.1	YNL048W	the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	2	3.1629	0.1699	1578.65	1578.808	1	767.2	75 T.KDPLRYPNLSDLF.L
gi 6324280 ref NP_014350.1	YNL048W	the ManSGIcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	1	3.0503	0.2437	1572.64	1572.916	1	249.9	57.692307 L.K2N2L1P1D1S1V1S1P111K2L111M1.A
gi 6324280 ref NP_014350.1	YNL048W	the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	2	3.8795	0.3316	1668.59	1669.076	1	534.2	64.28571 F.LKNLPDSVSPIKLIM.A
gi 6324280 ref NP_014350.1	YNL048W	the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	2	5.427	0.3445	2166.43	2167.479	1	1921.7	71.875 L.KFDKDWENFVLNPICKL.L
gi 6324280 ref NP_014350.1	YNL048W	the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	2	6.2968	0.4694	2190.27	2190.479	1	2213.2	75 L.K2F1D1K2D1W2E1N2F1V1L1N2P1I1C1K2L1.L
gi 6324280 ref NP_014350.1	YNL048W	the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	2	3.5699	0.1519	1839.91	1841.098	5	526.7	53.571426 T.K2D1P1L1R4Y1P1N2L1S1D1L1F1L1Q2.I
gi 6324280 ref NP_014350.1	YNL048W	the Ran5GlCNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	2	3.9819	0.2838	1819.33	1820.098	1	629	60.714287 T.KDPLRYPNLSDLFLQ.I
gi 6324280 ref NP_014350.1	YNL048W	the Rinh GiCNAC2-YP-dolichol intermediate during asparagine-linked giycosylation in the ER; Alg11p Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to	2	3.5795	0.1886	1691.43	1691.968	2	690.2	69.230774 T.KDPLRYPNLSDLFL.Q
gi 6324280 ref NP_014350.1	YNL048W	the Rinh GiCNAC2-YP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p Probable component of COPII coated vesicles that binds to Sec23p; similar to and	2	3.4872	0.173	1708.31	1710.968	1	834	73.07692 T.K2D1P1L1R4Y1P1N2L1S1D1L1F1L1.Q
gi 6324279 ref NP_014349.1	YNL049C	Tunctionally redundant with sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy; Stb2p Probable component of COPII coated vesicles that binds to Sec23p; similar to and	2	3.7779	0.3552	1826.25	1826.021	2	539.9	53.571426 C.RFKNDVPFGFDQNLQ.G
gi 6324279 ref NP_014349.1	YNL049C	Tunctionally redundant with sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy; Stb2p Probable component of COPII coated vesicles that binds to Sec23p; similar to and	2	3.8148	0.3461	1670.83	1671.894	1	841.1	64.28571 L.YIIRGPSINEPANLN.S
gi 6324279 ref NP_014349.1	YNL049C	Tunctionally redundant with sec249, but expressed at low levels; involved in ER to Golgi transport and in autophagy; Stb2p Probable component of COPII coated vesicles that binds to Sec23p; similar to and	2	3.8465	0.323	1703.09	1704.833	1	1114.5	71.42857 L.H3D1M1P1D1E1V1G1L1P1D1F1E1G1K2.T
		functionally redundant with Sec24p, but expressed at low levels; involved in ER to								
gi 6324279 ref NP_014349.1	YNL049C	Golgi transport and in autophagy; Sto2p	2	4.6932	0.3633	1906.27	1907.071	1	845.9	53.125 Y.SILIH3DIMIPIDIEIVIGILIPIDIFIEIGIK2.1
gi 0324278 rel NP_014348.1	YNLUSUC	hypothetical protein; mitosocp	2	2.9225	0.2159	1700.69	1700.885	2	494	
gi 6324278 ref NP_014348.1	VNL 050C	hypothetical protein; Ynl050cp	2	3.0275	0.1019	1935.13	1935.14	1	029	53.57 1420 Q.NEENQEEFEFFLF5F.G
gi 0324278 rel NP_014348.1	YNLUSUC	hypothetical protein; mitosocp	2	3.7044	0.2003	1/1/.49	17 10.000		133	
gij6324278 ret NP_014348.1	YNLU50C	nypometical protein; Ynuouop Mitochondrial portin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	4.6555	0.3754	1954.03	1953.14	1	1105.3	/1.4285/ Q.KZE1E1KZQZE1E1F1E1F1P1L1F1S1F1.G
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	3.3845	0.2132	1550.11	1551.706	1	812.8	75 T.M1N2C1K2L1P1N2S1N2V1N2I1E1.F
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Portp Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	4.3971	0.4433	1709.81	1710.85	1	1154.4	67.85714 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1.L
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Portp Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	4.8369	0.2596	1690.53	1690.85	1	1612.1	75 M.SPPVYSDISRNINDL.L
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	3.3104	0.2398	1916.57	1918.114	1	388	50 M.SPPVYSDISRNINDLLN.K
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability: Portp Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial gemetic stability and mitochondrial	2	4.1564	0.2945	1805.55	1804.01	1	877.9	70 M.SPPVYSDISRNINDLL.N
gi 6324273 ref NP_014343.1	YNL055C	regenterate remeability. Portp Mitochondrial porin (voltage-dependent anion channel), outer mebrane protein enuired for the maintenance of mitochondrial commit catalitity and mitochondrial	2	3.7701	0.4317	1750.79	1751.961	1	1111	64.28571 T.MNCKLPNSNVNIEFA.T
gi 6324273 ref NP_014343.1	YNL055C	required for the metaliteticable of initiation and stratus statuting and micochondria membrane permeability; Por1p Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenange of mitochondrial gemetic tability and mitochondrial	2	4.3445	0.3817	1698.63	1699.882	1	1079.4	69.230774 T.M1N2C1K2L1P1N2S1N2V1N2I1E1F1.A
gi 6324273 ref NP_014343.1	YNL055C	required for the maintenance of minochonania conoce stability and minochonania membrane permeability; Portp Mitochondrial porin (voltage-dependent anion channel), outer membrane protein manufard for the maintenange-of entenbergdial permetion protein dial	1	2.3567	0.2524	1310.44	1309.563	1	457.6	54.545456 C.LKSPTFVGDLTM.A
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability: Portp Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	2	3.5733	0.2193	1977.79	1977.181	4	719.8	56.25 P.PVYSDISRNINDLLNKD.F
gi 6324273 ref NP_014343.1	YNL055C	required for the maintenance or microtronatal ostrouc stability and microtronatal membrane permeability. Port p Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	2	5.056	0.3476	2071.07	2071.288	1	1643.2	70.588234 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2.D
gi 6324273 ref NP_014343.1	YNL055C	required on the maintenance or minocrionolial osmotic stability and mitochondrial membrane permeability. Port p Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	2	4.3633	0.3623	2160.33	2161.376	1	829	55.555557 M.SPPVYSDISRNINDLLNKD.F
gi 6324273 ref NP_014343.1	YNL055C	required ou the maintenance or mitochondrial osmotic stability and mitochondrial membrane permeability. Port p Mitochondrial porin (voltage-dependent anion channe), outer membrane protein	2	4.4348	0.2236	2187.19	2187.376	1	1080.1	58.333332 M.S1P1P1V1Y1S1D111S1R4N2I1N2D1L1L1N2K2D1.F
gi 6324273 ref NP_014343.1	YNL055C	required on the maintenance or mitochondrial osmotic stability and mitochondrial membrane permeability; Portp Mitochondrial porti (voltage-dependent anion channel), outer membrane protein	2	3.3993	0.1503	1375.23	1372.534	2	399.6	70.83333 K.A1K2Q2P1V1K2D1G1P1L1S1T1N2.V
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	1	2.5018	0.211	1354.57	1355.534	1	159.1	58.333332 K.AKQPVKDGPLSTN.V

		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
ail6324273/refINP_014343.1	YNL055C	required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability: Por1p	1	2.7477	0.2366	1371.45	1372,534
9.1442 1 1		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
-:::::::::::::::::::::::::::::::::::::		required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	5 5005	0 4007	2004 45	2004 240
gilo324273[rei]inP_014343.1]	TINLUSSU	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	3	5.5065	0.4267	2981.45	2984.249
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	3.9307	0.2712	2981.77	2984.249
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	5.281	0.4326	2709.41	2711.949
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
gil6324273/refINP_014343.11	YNI 055C	required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability. Por1p	3	5 0752	0.373	3753.02	3755 067
gilooz4270/cilita _014040.11	INCOSSO	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	5	0.07.02	0.070	0100.02	0/00.00/
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p Mitrahandrial paris (voltage dependent opion channel), outer membrane protein	3	4.7774	0.2821	3552.65	3550.857
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	2.9952	0.2438	1356.39	1355.534
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
gil6324273/refINP_014343.1	YNL055C	membrane permeability: Por1p	2	3.5292	0.2675	2445.37	2445.819
34444		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	-				
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p Mitochondrial porin (voltage-dependent anion chappel), outer membrane protein	2	4.6201	0.3803	2384.73	2385.74
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	4.1492	0.316	2947.81	2949.249
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
gil6324273/refINP_014343.1	YNL055C	membrane permeability: Por1p	2	4,7603	0.2669	2679.81	2679.949
34444		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	-				
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p Mitochondrial porin (voltage-dependent anion chappel), outer membrane protein	3	4.3529	0.33	2766.17	2765.054
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	3	5.6272	0.4078	3204.05	3204.505
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
gi 6324273 ref NP 014343.1	YNL055C	membrane permeability; Por1p	2	3.5841	0.3922	1782.67	1783.035
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
cil62242721cofIND_014242.11	VNI OFFC	required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	2 7990	0 272	2250 62	2250 74
gilo324273[rei]I4F_014343.1]	INL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	2	3.7009	0.272	2330.03	2330.74
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	4.6176	0.3459	1758.41	1756.924
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	3	3.8539	0.1825	3412.55	3414.924
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
gil6324273/refINP_014343.11	YNI 055C	required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability. Por1p	3	4 2664	0 204	3528.38	3529 028
gilooz izrolioitii _orioioiti		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	0	1.2001	0.201	0020.00	0020.020
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p Mitochondrial porin (voltage-dependent apion chappel), outer membrane protein	3	6.1724	0.4371	3731.15	3731.185
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	3	4.7526	0.3087	3485.33	3486.003
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
gil6324273/refINP_014343.1	YNL055C	membrane permeability: Por1p	3	4.5379	0.3633	3146.6	3148.637
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
-:::::::::::::::::::::::::::::::::::::		required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	4 00 4 0	0.0040	2074 50	2070 704
gij6324273 ret NP_014343.1	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	3	4.2618	0.2948	3271.58	3270.794
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	3.609	0.351	1620.35	1620.769
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	3.4685	0.2903	1638.63	1639.769
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
gil6324273/rofINP_014343_1	VNI 055C	required for the maintenance of mitochondrial osmotic stability and mitochondrial	2	3 5608	0 2044	1540.63	1540.60
gilooz4270/cilita _014040.11	III E0000	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	2	0.0000	0.2044	1040.00	1040.00
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	3.739	0.3575	1772.27	1771.961
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	3.5959	0.2431	1681.35	1680.882
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein					
gil6324273/refINP_014343_1	YNL055C	required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability: Por1p	2	3,199	0.2985	1524.37	1523.665
9-1-2-12-10-10-10-10-10-10-10-10-10-10-10-10-10-		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	2	0.100	0.2000		.020.000
		required for the maintenance of mitochondrial osmotic stability and mitochondrial	-		a 100-		
gijb324273 ret NP_014343.1	YNL055C	memorane permeability; Por1p Mitochondrial porin (voltage-dependent apion channel), outer membrane protein	3	4.8243	0.4363	2679.83	2679.949
		required for the maintenance of mitochondrial osmotic stability and mitochondrial					
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	2	2.9967	0.2284	1237.97	1237.405

1	2.7477	0.2366	1371.45	1372.534	2	203.8	62.5 K.A1K2Q2P1V1K2D1G1P1L1S1T1N2.V
3	5.5085	0.4267	2981.45	2984.249	1	639.1	31 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1.A
2	3.9307	0.2712	2981.77	2984.249	1	479.8	36 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1.A
2	5.281	0.4326	2709.41	2711.949	1	693.7	45.454548 M.S1P1P1V1Y1S1D111S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1.T
3	5.0752	0.373	3753.02	3755.067	1	1024.3	M.S1P1P1V1Y1S1D111S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1A1F1D1V1Q 23.4375 2T1T1.T
3	4.7774	0.2821	3552.65	3550.857	2	580.9	M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1A1F1D1V1Q 23.333334 2.T
2	2.9952	0.2438	1356.39	1355.534	2	339.6	62.5 K.AKQPVKDGPLSTN.V
2	3.5292	0.2675	2445.37	2445.819	1	535	45.238094 N.NLQTKLEFANLTPGLKNELITS.L
2	4.6201	0.3803	2384.73	2385.74	1	901.5	50 N.N2L1Q2T1K2L1E1F1A1N2L1T1P1G1L1K2N2E1L111T1.S
2	4.1492	0.316	2947.81	2949.249	1	581.3	40 M.SPPVYSDISRNINDLLNKDFYHATPA.A
2	4.7603	0.2669	2679.81	2679.949	2	691.5	45.454548 M.SPPVYSDISRNINDLLNKDFYHA.T
3	4.3529	0.33	2766.17	2765.054	2	412.9	30.434782 P.PVYSDISRNINDLLNKDFYHATPA.A
3	5.6272	0.4078	3204.05	3204.505	1	764.1	26.85185 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1A1F1.D
2	3.5841	0.3922	1782.67	1783.035	1	487.9	59.375 K.AKQPVKDGPLSTNVEAK.L
2	3.7889	0.272	2358.63	2358.74	1	565	42.5 N.NLQTKLEFANLTPGLKNELIT.S
2	4.6176	0.3459	1758.41	1756.924	1	1117.2	76.92308 S.R4N2I1N2D1L1L1N2K2D1F1Y1H3A1.T
3	3.8539	0.1825	3412.55	3414.924	1	740.3	24.193548 N.TNNLQTKLEFANLTPGLKNELITSLTPGVAKS.A
3	4.2664	0.204	3528.38	3529.028	1	659.8	24.21875 W.SNTNNLQTKLEFANLTPGLKNELITSLTPGVAK.S
3	6.1724	0.4371	3731.15	3731.185	1	1468.6	W.S1N2T1N2N2L1Q2T1K2L1E1F1A1N2L1T1P1G1L1K2N2E1L1I1T1S1L1T1P1G1V 27.941175 1A1K2S1A1.V
3	4.7526	0.3087	3485.33	3486.003	1	957	25.78125 N.TNNLQTKLEFANLTPGLKNELITSLTPGVAKSA.V
3	4.5379	0.3633	3146.6	3148.637	2	517.3	25 N.N2L1Q2T1K2L1E1F1A1N2L1T1P1G1L1K2N2E1L1I1T1S1L1T1P1G1V1A1K2.S
3	4.2618	0.2948	3271.58	3270.794	1	726	26.666668 N.NLQTKLEFANLTPGLKNELITSLTPGVAKSA.V
2	3.609	0.351	1620.35	1620.769	1	779.1	69.230774 M.NCKLPNSNVNIEFA.T
2	3.4685	0.2903	1638.63	1639.769	1	604.6	57.692307 M.N2C1K2L1P1N2S1N2V1N2I1E1F1A1.T
2	3.5608	0.2944	1549.63	1549.69	1	1195.5	70.83333 M.NCKLPNSNVNIEF.A
2	3.739	0.3575	1772.27	1771.961	1	758.7	60.714287 T.M1N2C1K2L1P1N2S1N2V1N2I1E1F1A1.T
2	3.5959	0.2431	1681.35	1680.882	1	931	65.38461 T.MNCKLPNSNVNIEF.A
2	3.199	0.2985	1524.37	1523.665	2	490.5	58.333332 N.C1K2L1P1N2S1N2V1N2I1E1F1A1.T
3	4.8243	0.4363	2679.83	2679.949	1	513.4	30.681818 M.SPPVYSDISRNINDLLNKDFYHA.T
2	2.9967	0.2284	1237.97	1237.405	2	716.8	70 L.CLKSPTFVGDL.T

		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial								
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	1	2.2271	0.1815	1007.49	1008.122	1	377.4	64.28571 L.LNKDFYHA.T
ail63242731rofIND_014343_1	YNI 055C	required for the maintenance of mitochondrial osmotic stability and mitochondrial	3	4 8902	0 4446	2710 55	2711 949	1	655.4	30 681818 M S1P1P1V1V1S1D111S1R4N21N2D11 11 1N2K2D1E1V1H3A1 T
gilosz4275itelini _014545.1	INLOSSE	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	5	4.0302	0.4440	2710.55	2711.343		055.4	
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p	3	4.4431	0.2913	2948.57	2949.249	6	316.9	23 M.SPPVYSDISRNINDLLNKDFYHATPA.A
		Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial								
gi 6324273 ref NP_014343.1	YNL055C	membrane permeability; Por1p Mitochondrial porin (voltage-dependent anion chappel), outer membrane protein	3	4.249	0.2956	2982.62	2984.249	1	545.5	27.000002 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1.A
gi 6324273 ref NP_014343.1	10110550	required for the maintenance of mitochondrial osmotic stability and mitochondrial		4 004 4	0 0005	4000.04	1050 100		704.0	
	TINLUSSC	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein	2	4.3314	0.2665	1960.01	1959.162	I	724.9	60.000004 D.ITSTR4NZTINZDTETETNZRZDTFTYTH3AT.T
gi 6324273 ref NP_014343.1	YNL055C	required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability: Por1p	2	3.9393	0.3896	1935.17	1934.162	1	1188.3	66.66667 D.ISRNINDLLNKDFYHA.T
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pro-rPNA and large ribosomal subunit biogenesis. localized to the nucleolus:								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p	2	4.3486	0.4207	2096.37	2097.166	1	1313.6	67.64706 L.SKKLDEEEAEEAEEAEME.L
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p Probable RNA m(5)C methyltransferase, essential for processing and maturation of	2	3.2005	0.2176	1352.45	1352.533	1	631	72.72727 Y.D1A1R4E1F1P1K2V1I1G1G1F1.D
		27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;	2	4 0070	0 2000	0070 57	2072 057		044.0	
gi 6324268 ref NP_014338.1	YNL061W	Constituent of 665 pre-ribosomal particles; Nop2p Probable RNA m(5)C methyltransferase, essential for processing and maturation of	2	4.8079	0.3868	2672.57	2672.857	1	811.2	45.238094 S.RKEEEEVVEEDKDLPEVDLEEL.S
gi 6324268 ref NP_014338.1	YNL061W	27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles: Nop2p	2	5.0286	0.328	2447.83	2445.515	1	1716.9	55 K.K2L1D1E1E1E1A1E1E1A1E1E1A1E1M1E1L1V1E1A1E1.N
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of	_							
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p	2	4.6218	0.2659	2424.35	2423.515	1	1648.5	52.499996 K.KLDEEEAEEAEEAEMELVEAE.N
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p Probable RNA m(5)C methyltransferase, essential for processing and maturation of	2	3.1896	0.2928	1442.55	1440.645	2	700.3	66.66667 L.VNRGVNLQPIGSW.T
gi 6324268 ref NP_014338.1		27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;								
	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p Probable RNA m(5)C methyltransferase, essential for processing and maturation of	2	4.972	0.3529	2117.27	2117.166	1	1203.1	58.823532 L.S1K2K2L1D1E1E1E1A1E1E1A1E1E1A1E1M1E1.L
gi 6324268 ref NP_014338.1	YNL061W	27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Noo2p	2	5.1575	0.3706	2699.83	2699.857	1	805.7	45.238094 S.R4K2E1E1E1E1V1V1E1E1D1K2D1L1P1E1V1D1L1E1E1L1.S
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of								
gi 6324268 ref NP_014338.1	YNL061W	27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	3.8669	0.2569	1644.87	1646.868	1	1255.6	87.5 S.R4T1E1K2D1F1I1Q2I1P1H3L1Q2.K
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p Brobable RNA m(5)C methyltrapsforace, essential for processing and maturation of	2	3.0877	0.2644	1811.41	1812.079	1	461.7	53.571426 K. VSRTEKDFIQIPHLQ.K
gi 6324268 ref NP_014338.1		27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;								
	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p Probable RNA m(5)C methyltransferase, essential for processing and maturation of	2	4.0825	0.3438	1882.27	1881.914	1	1514.4	73.333336 K.KLDEEEAEEAEEAEME.L
gi 6324268 ref NP_014338.1	YNL061W	27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles: Nop2p	2	4.6662	0.3545	1899.19	1898.914	1	1513.2	73.333336 K.K2L1D1E1E1E1A1E1E1A1E1E1A1E1M1E1.L
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p	2	3.5922	0.3419	1458.61	1460.645	1	982.5	83.33333 L.V1N2R4G1V1N2L1Q2P1I1G1S1W2.T
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p Brobable RNA m(5)C methyltrapsforace, assertial for processing and maturation of	3	4.0193	0.2778	2700.65	2699.857	1	531.1	33.333336 S.R4K2E1E1E1E1V1V1E1E1D1K2D1L1P1E1V1D1L1E1E1L1.S
		27S pre-rRNA and large ribosonal subunit biogenesis; localized to the nucleolus;								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p Probable RNA m(5)C methyltransferase, essential for processing and maturation of	3	3.8964	0.208	2672.78	2672.857	1	692.7	34.523808 S.RKEEEEVVEEDKDLPEVDLEEL.S
gi 6324268 ref NP_014338.1	YNL061W	27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles: Nop2p	2	5.2153	0.3575	2700.45	2699.857	1	1006.2	47.61905 S.R4K2E1E1E1E1V1V1E1E1D1K2D1L1P1E1V1D1L1E1E1L1.S
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p	3	4.3294	0.2791	1625.3	1625.868	1	1391.3	54.166668 S.RTEKDFIQIPHLQ.K
		Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;								
gi 6324268 ref NP_014338.1	YNL061W	constituent of 66S pre-ribosomal particles; Nop2p Probable RNA m(5)C methyltransferase, essential for processing and maturation of	2	4.8274	0.4121	2944.25	2945.969	1	581.9	39.583336 S.LFDDEEDDDEAGLVDEELKDEFDLE.Q
		27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus;	2	4 7004	0.2422	2074 42	2074 000		640.4	
gilo324208[rei]NP_014338.1]	TINLUGIVV	Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.7304	0.3133	2971.13	2971.909	I	649.1	39.563336 S.LIFIDIDIEIEIDIDIDIEIAIGILIVIDIEIEILIKZDIEIFIDILIEI.Q
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p	1	2.3196	0.2314	1295.74	1296.571	1	351.1	62.5 V.GIVPGEVIAPGMR.K
		Protein chaperone involved in regulation of the HSP90 and HSP70 functions;								
gi 6324265 ref NP_014335.1	YNL064C	Ydj1p	1	2.5323	0.1714	1311.56	1312.571	1	383.1	58.333332 V.G111V1P1G1E1V111A1P1G1M1R4.K
		Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family;								
gi 6324265 ref NP_014335.1	YNL064C	Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions:	1	2.2639	0.2198	1123.65	1124.409	1	442.5	60.000004 W.LKVGIVPGEVI.A
gi 6324265 ref NP_014335.1	YNL 064C	involved in protein translocation across membranes; member of the DnaJ family;	2	3 079	0.214	1583 3F	1582 669	1	567 7	
	INLU04C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	3.078	0.314	1303.33	1302.000	1	507.7	
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p	1	2.7609	0.2919	1426.57	1426.48	1	310.6	54.545456 F.K2R4D1G1D1D1L1V1Y1E1A1E1.I
		Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family;								
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gi 6324265 ref NP_014335.1	YNL064C	Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	3.8868	0.3479	1890.2	1891.047	1	1172.8	46.666668 L.KYHPDKNPSEEAAEKF.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.9676	0.5253	2074.07	2075.285	1	1413.3	64.70589 C.ALKYHPDKNPSEEAAEKF.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	5.2105	0.3701	2100.14	2099.285	1	1367	48.52941 C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	1	3.334	0.2869	1596.86	1597.767	1	446.7	66.66667 K.FTIKFPENHFTSE.E
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.728	0.3983	1913.97	1913.047	1	1191.3	70 L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.2543	0.4223	1892.03	1891.047	1	1470.3	73.333336 L.KYHPDKNPSEEAAEKF.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.2825	0.4156	2026.53	2027.349	1	555.6	52.941177 L.EVHVEPGMKDGQRIVFKG.E
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	3.8696	0.2602	1994.45	1995.297	1	578.6	59.375 L.E1V1H3V1E1P1G1M1K2D1G1Q2R4I1V1F1K2.G
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	3.3155	0.3356	1523.59	1523.877	1	668.5	67.85714 LKVGIVPGEVIAPGMR.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	3.926	0.2219	1912.4	1913.047	1	1009	43.333332 LK2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	5.6759	0.4487	2098.35	2099.285	1	1410.5	64.70589 C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	1	4.0835	0.5011	1522.67	1523.877	1	548.8	64.28571 L.KVGIVPGEVIAPGMR.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	5.3696	0.4536	2347.51	2347.742	1	1217.2	54.761906 E.H3V1S1G1D1W2L1K2V1G1I1V1P1G1E1V1I1A1P1G1M1R4.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	4.0079	0.3794	1893.8	1891.047	1	930.7	46.666668 L.KYHPDKNPSEEAAEKF.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	1	3.2142	0.2379	1465.72	1466.591	2	219.7	50 F.T111K2F1P1E1N2H3F1T1S1E1.E
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	1	3.1091	0.349	1449.61	1450.591	3	207.8	50 F.TIKFPENHFTSE.E
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	3.0663	0.1886	1861.57	1859.966	7	346.6	50 C.HGTGDIIDPKDRCKSC.N
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	3.9877	0.3765	1613.77	1614.767	1	1014.6	75 K.F1T111K2F1P1E1N2H3F1T1S1E1.E
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.3046	0.3912	1892.25	1891.047	1	1243.7	70 L.KYHPDKNPSEEAAEKF.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.7249	0.3576	1911.65	1913.047	1	1059.9	66.66667 L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	5.8082	0.4399	2100.55	2099.285	1	1133.9	61.764706 C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	4.8848	0.3416	2101.64	2099.285	1	1731.8	48.52941 C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	1	3.011	0.4524	1522.71	1523.877	1	493.3	57.14286 L.KVGIVPGEVIAPGMR.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	4.0344	0.3178	1912.91	1913.047	7	428.3	35 L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.3601	0.3913	1822.89	1823.25	1	1131.8	68.75 D.WLKVGIVPGEVIAPGMR.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	4.999	0.338	1847.93	1845.25	1	1553.9	48.4375 D.W2L1K2V1G1I1V1P1G1E1V1I1A1P1G1M1R4.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	4.1585	0.308	1823.15	1823.25	1	1275.1	45.3125 D.WLKVGIVPGEVIAPGMR.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	3.466	0.2017	1410.45	1412.703	1	512.3	61.538464 K.V1G1I1V1P1G1E1V1I1A1P1G1M1R4.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.0954	0.3683	1890.89	1891.047	1	1359	70 L.KYHPDKNPSEEAAEKF.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein transiocation across membranes; member of the DnaJ family; Ydj1p	3	4.5157	0.3532	1890.71	1891.047	1	895.3	46.666668 L.KYHPDKNPSEEAAEKF.K

		Protein chaperone involved in regulation of the HSP90 and HSP70 functions;								
gi 6324265 ref NP_014335.1	YNL064C	Involved in protein translocation across memoranes; member of the Dinaj family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	3	5.0373	0.3615	1915.82	1913.047	1	1267.2	50 L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions:	2	5.57	0.4352	2099.85	2099.285	1	1497.8	67.64706 C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein chaperone involved in regulation of the HSP90 and HSP70 functions;	2	4.3204	0.3337	2155.31	2156.464	1	698.6	58.333332 L.EVHVEPGMKDGQRIVFKGE.A
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; member of the DnaJ family; Ydj1p Protein changrone involved in regulation of the HSP00 and HSP70 functions:	2	4.5759	0.328	1911.19	1913.047	1	1324.9	70 L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; membra of the DnaJ family; Ydj1p Protein concerns involved in regulation of the VEDD0 and VEDD0 functions;	2	3.1526	0.2844	2025.11	2027.207	1	499.7	50 A.L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	involved in protein translocation across membranes; membranes of the DnaJ family; Ydj1p	3	6.1385	0.5049	2096.33	2099.285	1	2263.1	51.47059 C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.K
gi 6324265 ref NP_014335.1	YNL064C	Protein chaperone involved in regulation of the HSP30 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family; Ydj1p	2	3.6008	0.2624	1970.51	1970.297	1	469.1	53.125 L.EVHVEPGMKDGQRIVFK.G
gi 6324265 ref NP_014335.1	YNL064C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family; Ydj1p	2	4.6241	0.3187	2053.47	2053.349	1	587	52.941177 LE1V1H3V1E1P1G1M1K2D1G1Q2R4I1V1F1K2G1.E
gi 6324265 ref NP_014335.1	YNL064C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family; Ydj1p	2	4.2578	0.4395	1525.47	1523.877	1	902.5	78.57143 L.KVGIVPGEVIAPGMR.K
gi 6324265 ref NP 014335.1	YNL064C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family; Yd(1p	1	3.9202	0.4939	1522.82	1523.877	1	600.1	67.85714 L.KVGIVPGEVIAPGMR.K
gil6324265lrefINP_014335.1	YNI 064C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family; Yri1n	1	4 1776	0 4479	1541 63	1542 877	1	647.3	67 86714 K2V1G111V1P1G1E1V111A1P1G1M1R4 K
ail6324265irefINP_014335_1	YNL064C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family; Vitin	2	3 2776	0.1951	1791 81	1793 184	1	445.8	50 000004 E1E111 1P1P1P411/1P14111P1K2K241 T
gilo324205[ref NP_014335.1]	VNI 064C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family;	2	4 2028	0.1551	1820.01	1923.25	1	1157 /	
gilos24205/rel/NF_014335.1	1NL004C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family;	2	4.2030	0.3007	1020.91	1023.25		1000.4	
gi 6324265 ret NP_014335.1	YNL064C	Yojip Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family;	2	5.0701	0.5001	1843.73	1845.25	1	1220.4	71.8/5 D.WZL1KZVIGIIIVIPIGIEIVIIIAIPIGIMIK4.K
gi 6324265 ref NP_014335.1	YNL064C	Ydj1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA;	3	4.3966	0.3542	1821.17	1823.25	1	1509.9	48.4375 D.WLKVGIVPGEVIAPGMR.K
gi 6324258 ref NP_014328.1	YNL071W	Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA;	2	5.2201	0.4046	1952.25	1951.061	1	1521.6	64.70589 K.K2E1G1D1Q2L1S1P1G1E1V1I1A1E1I1E1T1D1.K
gi 6324258 ref NP_014328.1	YNL071W	Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarbox/dation of ovruvate to acetyl-CoA-	2	4.577	0.3962	1914.09	1913.051	1	1883.5	67.64706 A.TVERVAVEDAAAENGFSF.D
gi 6324258 ref NP_014328.1	YNL071W	Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the ryidative decadovylation of pyruvate to acetyl_CA	2	3.1885	0.2609	1700.59	1701.871	1	619.2	56.666668 W.TKKEGDQLSPGEVIAE.I
gi 6324258 ref NP_014328.1	YNL071W	Dihydrolipoamide acetytetansferase component (E2) of pyruate to acetyt Con- complex which acetytetansferase component (E2) of pyruate dehydrogenase	2	4.3314	0.1867	1807.39	1805.168	1	688.9	59.375 K.ILVPEGTKDIPVNKPIA.V
gi 6324258 ref NP_014328.1	YNL071W	Dihydrolipoanie acetytransferase component (E2) of pyruvate dehydrogenase	2	4.3795	0.2095	1769.97	1771.166	1	825.8	67.85714 M.KELKTVIENPLEMLL-
gi 6324258 ref NP_014328.1	YNL071W	Complex, which catalyzes the oxidative decarboxylation of pyrovate to acetyr-Cox, Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyrovate dehydrogenase	2	4.5204	0.1674	1788.49	1789.166	1	784.1	67.85714 M.K2E1L1K2T1V111E1N2P1L1E1M1L1L1
gi 6324258 ref NP_014328.1	YNL071W	Complex, which catalyzes the oxidative decarboxylation of pyrovate to acetyr-Cox, Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyrovate dehydrogenase	1	2.4208	0.2395	1415.65	1416.666	2	240.6	55 Y.WLPNENVIRKF.K
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	3	5.0962	0.254	1936.28	1933.342	1	1684.6	52.941177 A.KILVPEGTKDIPVNKPIA.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	4.9681	0.4853	2218.47	2219.651	1	903	52.63158 A.K2I1L1V1P1E1G1T1K2D1I1P1V1N2K2P1I1A1V1Y1.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	3.1131	0.297	2052.83	2055.475	1	496.9	55.555557 A.K2I1L1V1P1E1G1T1K2D1I1P1V1N2K2P1I1A1V1.Y
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	2.93	0.2318	1760.49	1761.025	3	397.4	46.666668 V.P1E1G1T1K2D1I1P1V1N2K2P1I1A1V1Y1.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	3.1684	0.1855	1429.63	1430.717	1	983.7	77.27273 LK2T1V11E1N2P1L1E1M\$L1L1
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrooenase	1	3.7983	0.4036	1480.77	1481.645	1	1284.8	70.83333 Y.VEDKADVPAFKDF.K
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; LatTp Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrooenase	1	3.9785	0.2711	1495.55	1496.645	1	1001	62.5 Y.V1E1D1K2A1D1V1P1A1F1K2D1F1.K
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	3.5445	0.1812	1415.31	1414.717	6	390.5	72.72727 LK2T1V111E1N2P1L1E1M1L1L1

		Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase								
gi 6324258 ref NP_014328.1	YNL071W	Latip Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	4.39	0.2287	1512.79	1513.876	1	1773.1	83.33333 E.LKTVIENPLEMLL
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	5.0075	0.3789	2183.01	2183.34	1	1273	52.63158 W.T1K2K2E1G1D1Q2L1S1P1G1E1V111A1E111E1T1D1.K
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	3.3562	0.2877	2067.65	2067.477	5	385.1	38.88889 K.ILVPEGTKDIPVNKPIAVY.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	4.4414	0.3727	2091.65	2089.477	1	694.3	50 K.I1L1V1P1E1G1T1K2D1I1P1V1N2K2P1I1A1V1Y1.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	4.0323	0.3816	1931.95	1933.342	1	774.3	55.88235 A.KILVPEGTKDIPVNKPIA.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	3.9564	0.4711	2194.91	2195.651	1	654.8	47.368423 A.KILVPEGTKDIPVNKPIAVY.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	3.5824	0.3033	1400.45	1400.717	1	703.2	86.36364 L.KTVIENPLEMLL
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lattp Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	1	2.5788	0.1965	1433.64	1434.666	3	186.2	50 Y.W2L1P1N2E1N2V111R4K2F1.K
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	4.7236	0.3887	1954.95	1955.342	1	1101.5	64.70589 A.K2I1L1V1P1E1G1T1K2D1I1P1V1N2K2P1I1A1.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	2	4.2533	0.296	1933.71	1933.342	1	706.3	50 A.KILVPEGTKDIPVNKPIA.V
gi 6324258 ref NP_014328.1	YNL071W	complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p Protein that forms a complex with Pbp1p that may mediate posttranscriptional	2	4.5034	0.387	2033.19	2032.475	1	1085.5	58.333332 A.KILVPEGTKDIPVNKPIAV.Y
gi 6324244 ref NP_014314.1	YNL085W	regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p Protein that forms a complex with Pbp1p that may mediate posttranscriptional	1	2.3108	0.2767	1341.4	1341.593	1	445	60.000004 F.KDFNITPIFVF.N
gi 6324244 ref NP_014314.1	YNL085W	regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mk1p Protein that forms a complex with Pbp1p that may mediate posttranscriptional	1	2.5907	0.1822	1354.68	1354.593	1	408.3	60.000004 F.K2D1F1N2I1T1P1I1F1V1F1.N
gi 6324244 ref NP_014314.1	YNL085W	regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mk1p Protein that forms a complex with Pbp1p that may mediate posttranscriptional	2	3.8078	0.1547	1368.55	1366.643	1	1086.4	85 A.KLIDENVFKLF.T
gi 6324244 ref NP_014314.1	YNL085W	regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mk1p Protein that forms a complex with Pbp1p that may mediate posttranscriptional	1	2.816	0.1576	1365.57	1366.643	1	517.1	65 A.KLIDENVFKLF.T
gi 6324244 ref NP_014314.1	YNL085W	regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mk1p Protein that forms a complex with Pbp1p that may mediate posttranscriptional	2	3.7311	0.3754	2163.59	2165.375	1	452.5	52.941177 K.E1V1R4K2P1R4D111P1N2D1V1H3D1F1I1G1Q2.M
gi 6324244 ref NP_014314.1	YNL085W	regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mk11p Protein that forms a complex with Pbp1p that may mediate posttranscriptional	2	2.9455	0.2207	1355.23	1354.593	5	506.5	65 F.K2D1F1N2I1T1P1I1F1V1F1.N
gi 6324244 ref NP_014314.1	YNL085W	regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mk1p	2	3.3543	0.368	2136.21	2136.375	1	294	47.058823 K.EVRKPRDIPNDVHDFIGQ.M
gi 6324241 ref NP_014311.1	YNL088W	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re- sealing the phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; Top2p	3	4.4323	0.3064	2212.79	2211.529	1	1209.8	38.157894 S.LADNIRSIPNVLDGFKPGQR.K
gi 6324241 ref NP_014311.1	YNL088W	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re- sealing the phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; Top2p	3	4.624	0.4085	2298.44	2298.607	1	526.5	36.25 F.SLADNIRSIPNVLDGFKPGQR.K
gi 6324241 ref NP_014311.1	YNL088W	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re- sealing the phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; Top2p	3	5.3947	0.3738	2331.35	2329.607	4	1081.8	35 F.S1L1A1D1N2I1R4S1I1P1N2V1L1D1G1F1K2P1G1Q2R4.P
gi 6324241 ref NP_014311.1	YNL088W	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re- sealing the phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; Top2p	2	4.5327	0.3484	1559.51	1559.708	1	2098.3	86.36364 L.MNDEELEQMHPW.F
gi 6324241 ref NP_014311.1	YNL088W	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re- sealing the phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; Top2p	2	3.0882	0.2348	1574.21	1576.708	1	720.9	68.181816 L.M1N2D1E1E1L1E1Q2M1H3P1W2.F
gi 6324241 ref NP_014311.1	YNL088W	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re- sealing the phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; Top2p	2	3.5668	0.3294	2289.83	2289.483	1	337.7	53.125 F.YNMPDYEKWREEESHKF.T
ail6324241/refINP_014311_1	YNI 088W/	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re- sealing the phosphodiester backbone of both positively and negatively supercoiled DNA: cleaves complementary strandis' localizes to avail cores in mainsis: Too?a	3	4 3503	0 3154	2098 55	2008 37	1	1256 3	
gil6324230/rofINE_014300.11		Putative protein tyrosine phosphatase, required for cell cycle arrest in response to ovidetive damage of DNA: Oca1p	2	3 5036	0.2337	1855 /0	1857 144	1	960.3	
aile2242200101141_014300.1	VNILOOOC	Putative protein tyrosine phosphatase, required for cell cycle arrest in response to	2	4 2022	0.2307	000.40	2010 405	1	610 5	
gijb324230 ret NP_014300.1	YNLU99C	oxidative damage of DNA; Uca1p Putative protein tyrosine phosphatase, required for cell cycle arrest in response to	2	4.2032	0.3795	2211.19	2212.485	1	619.5	52.941177 H.A1P1Q2E1R4I1V1P1P1L1N2F1C1P1V1E1R4Y1.L
gi 6324230 ref NP_014300.1	YNL099C	oxidative damage of DNA; Oca1p Putative protein tyrosine phosphatase, required for cell cycle arrest in response to	2	3.657	0.2666	2188.53	2186.485	1	567.7	52.941177 H.APQERIVPPLNFCPVERY.L
gi 6324230 ref NP_014300.1	YNL099C	oxidative damage of DNA; Oca1p Putative protein tyrosine phosphatase, required for cell cycle arrest in response to	2	3.3653	0.2109	1628.89	1628.825	1	721.6	57.692307 Y.L1Y1R4S1G1Q2P1S1P1V1N2F1P1F1.L
gi 6324230 ref NP_014300.1	YNL099C	oxidative damage of DNA; Oca1p	2	2.9556	0.2677	1837.41	1836.144	1	617.3	53.333336 Y.LYRSGQPSPVNFPFLL.N

		Catalytic subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes								
ail6324211/refINP 014281.11	YNL118C	the 5' cap structure from mRNAs prior to their degradation; member of the Nudix hvdrolase family: Dcp2p	3	4.0828	0.2401	2131.64	2132.223	1	785.5	39.0625 N.C1P1N2E1D1L1S1S1V1E1R4E1L1F1H3F1E1.E
51		Catalytic subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes								
gi 6324211 ref NP 014281.1	YNL118C	the 5' cap structure from mRNAs prior to their degradation; member of the Nudix hydrolase family; Dcp2p	2	3.6694	0.3863	2623.63	2624.822	1	577.3	47.5 R.F1I1I1N2C1P1N2E1D1L1S1S1V1E1R4E1L1F1H3F1E1.E
		Catalytic subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes								
gi 6324211 ref NP_014281.1	YNL118C	hydrolase family; Dcp2p	2	3.9963	0.2841	1841.23	1840.089	1	1262.5	73.07692 Q.VRNEIDKIEWFDFK.K
		Component of the TOM (translocase of outer membrane) complex responsible for								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	2	3.5466	0.1919	1605.89	1606.816	1	1057	75 A.KELDPENIFPYIQ.L
		Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	2	3.2439	0.176	1719.97	1719.975	2	709.9	65.38461 A.KELDPENIFPYIQL.A
		Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	2	4.5352	0.3064	2103.41	2103.291	1	663.2	68.75 F.EEQLDKNNEDEKLKEKL.A
		Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	2	3.1004	0.2118	1376.01	1376.636	4	795.9	63.636364 K.ALELKPDYSKVL.L
		recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	1	2.8634	0.2024	1375.64	1376.636	4	632.2	63.636364 K.ALELKPDYSKVL.L
		recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p Component of the TOM (translocase of outer membrane) complex responsible for	2	4.2668	0.2903	2158.49	2157.389	1	723.2	52.77778 L.STQPAKERKDKQENLPSVT.S
		recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p Component of the TOM (translocase of outer membrane) complex responsible for	2	4.9035	0.3971	2398.47	2399.663	1	377.6	42.5 T.ELSTQPAKERKDKQENLPSVT.S
		recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p Component of the TOM (translocase of outer membrane) complex responsible for	2	4.4711	0.301	2428.49	2429.663	2	456.5	45 T.E1L1S1T1Q2P1A1K2E1R4K2D1K2Q2E1N2L1P1S1V1T1.S
100040001- (INID: 044070-4	1011 4040	recognition and initial import steps for all mitochondrially directed proteins; acts as a		0.0040	0.4504	4500.00	1500 700			
gij6324208 ret NP_014278.1	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for	2	3.6042	0.1521	1538.39	1536.728	1	690	69.230774 L.KNDPLGAHEDIKKA.I
ail6324208/rofIND_014278_1	VNI 121C	recognition and initial import steps for all mitochondrially directed proteins; acts as a	2	4 5 2 3	0.3627	1706 / 1	1700.005	1	507.2	57 14286 K P4K2E1D1E1A1D1E1\/1D1N2E1E1A1E1
gil0524200[rei]14r_014270.1]	INCIZIO	Component of the TOM (translocase of outer membrane) complex responsible for	2	4.525	0.3027	1730.41	1733.003	'	551.2	
ail6324208/refINP_014278_1	YNI 121C	recognition and initial import steps for all mitochondrially directed proteins; acts as a recentor for incoming precursor proteins; Tom70p	2	3 0509	0 2674	1669 11	1670 888	1	581.2	60 714287 E L 1K2N2D1P1L1G1A1H3E1D1L1K2K2A1 L
giloo24200/10/141_014210.11	INCIZIO	Component of the TOM (translocase of outer membrane) complex responsible for	2	0.0000	0.2014	1003.11	1070.000		501.2	
ail6324208/refINP 014278.11	YNL121C	recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.6014	0.4924	1776.03	1779.005	1	604.1	57.14286 K.RKFPEAPEVPNFFAE.I
2/1102		Component of the TOM (translocase of outer membrane) complex responsible for								
ail6324208/refINP 014278.11	YNL121C	recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins: Tom70p	2	3.2524	0.2516	1376.53	1376.636	1	829.8	63.636364 K.ALELKPDYSKVL.L
51		Component of the TOM (translocase of outer membrane) complex responsible for								
gi 6324208 ref NP_014278.1	YNL121C	recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.3481	0.2267	2184.39	2185.389	3	224.8	38.88889 L.S1T1Q2P1A1K2E1R4K2D1K2Q2E1N2L1P1S1V1T1.S
		Component of the TOM (translocase of outer membrane) complex responsible for								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	2	3.6424	0.3169	2130.45	2131.373	1	445.7	47.058823 S.E1A1K2R4K2F1P1E1A1P1E1V1P1N2F1F1A1E1.I
		Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	2	3.9457	0.4148	1581.57	1578.811	1	771.2	75 K.RKFPEAPEVPNFF.A
		Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	2	3.3573	0.2953	1594.65	1596.811	1	451.3	62.5 K.R4K2F1P1E1A1P1E1V1P1N2F1F1.A
		Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a								
gi 6324208 ref NP_014278.1	YNL121C	receptor for incoming precursor proteins; Tom70p	2	3.772	0.3679	2000.41	2001.258	1	481.1	50 E.A1K2R4K2F1P1E1A1P1E1V1P1N2F1F1A1E1.I
gi 42742307 ref NP_014269.2	YNL130C	inositol-dependent regulation of EPT1 transcription; Cpt1p	1	3.0487	0.2475	1303.62	1303.461	5	140.4	54.545456 R.RTGQQGPLGELF.D
ail42742307/refINP_014269.21	YNI 130C	Cholinephosphotransferase, required for phosphatidylcholine biosynthesis and for institutedependent regulation of EPT1 transcription; Cotto	1	2 6802	0 2092	1320 73	1320.461	8	132.3	54 545456 R R4T1G10202G1P1I 1G1E1I 1E1 D
31 121 12001 [101] 11 _01 120012]	11121000	Cholinephosphotransferase, required for phosphatidylcholine biosynthesis and for	·	2.0002	0.2002	1020.10	10201101	0	102.0	
gi 42742307 ref NP_014269.2	YNL130C	inositol-dependent regulation of EPT1 transcription; Cpt1p Essential protein of unknown function: heterozvoous mutant shows haploinsufficiency	2	3.8239	0.2507	2199.57	2199.321	1	554	56.666668 L.Y1Y1D1P1Y1F1D1Q2E1S1P1R4W2T1Y1F1.S
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p	2	3.4177	0.2564	2587.51	2589.006	2	207.9	34.090908 L.F1V1L1L1P1P1I1D1P1K2D1G1G1R4I1P1D1P1L1C1V1I1Q2.I
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p	2	3.4504	0.2934	2414.67	2413.682	1	524.3	47.368423 L.R4E1I1S1L1D1E1P1I1R4Y1A1P1G1D1P1I1E1K2W2.L
ail6224107/rofIND_014267.1	VNI 122W/	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency	2	2 0490	0.2152	2560.17	2561.006	4	202.2	
gil0524197 [rei]142 014207.1]	TINETSZW	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency	2	2.3403	0.2155	2300.17	2301.000	4	202.2	34.030300 E.I. VEELI HEI KEGGKIE DI EGVIQ.I
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p Essential protein of unknown function: beterozygous mutant shows banloinsufficiency	2	3.4866	0.2239	2224.79	2226.537	3	289.1	36.842106 L.L1P1P1I1D1P1K2D1G1G1R4I1P1D1P1L1C1V1I1Q2.I
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p	2	3.7	0.3146	2237.61	2239.5	1	464	47.058823 N.R4D1T1L1F1S1Y1H3P1V1S1E1N2F1L1E1K2M1.M
gi 6324197 ref NP 014267.1	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.0267	0.365	1938.79	1940.996	1	501.6	53.333336 Q.D1L1S1D1D1E1K2H3D1N2K2E1L1T1R4T1.H
	XAU 400144	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency		0.4077	0 4777	4000.04	1005 000		101.0	
gijo324197 ret NP_014267.1	TNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency	2	3.4077	0.1777	1936.81	1935.268	1	491.9	อบ ค.ขานานาคาคาเกมาคาหรุมาได้าดาหล่าคามาคาและ
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p Essential protein of unknown function: beterozygous mutant shows bankingufficiency	2	3.4152	0.2952	2384.93	2385.682	1	634.5	50 L.REISLDEPIRYAPGDPIEKW.L
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p	3	3.9612	0.2637	2868.44	2870.238	2	395.3	30.434782 Q.SRQLREISLDEPIRYAPGDPIEKW.L
gi 6324197 ref NP 014267.1	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	1	2.2264	0.1635	1090.7	1091.208	7	365.3	68.75 T.HLDDIFSPF.D
		Essential protein of unknown function; heterozygous mutant shows haploinsufficiency	~	0.7440	0.0400	0050 51	0050 404		440.0	
gij0324197[rei]NP_014267.1]	TINE 13200	in Ki kiler toxin resistance; Krebbp	2	3.7449	0.3466	2202.51	2203.494	1	419.8	49.999997 R.ETHSTLIDTETPTTR4T1A1P1G1D1P111E1K2W2.L

-:::::::::::::::::::::::::::::::::::::		Essential protein of unknown function; heterozygous mutant shows haploinsufficiency	0	0.4074	0.0400	4044.20	1012 200		502 5	
gi 6324197 ref NP_014267.1	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency	2	3.4674	0.2462	1914.39	1913.268	1	503.5	50 F.VLLPPIDPKDGGRIPDPL.C
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p Essential protein of unknown function: beterozygous mutant shows hanloinsufficiency	2	4.6656	0.3009	2441.63	2440.829	1	558.8	47.61905 F.V1L1L1P1P1I1D1P1K2D1G1G1R4I1P1D1P1L1C1V1I1Q2.I
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p	2	3.0299	0.3045	2242.53	2244.583	1	325.2	42.105263 L.F1V1L1L1P1P1I1D1P1K2D1G1G1R4I1P1D1P1L1C1.V
gi 6324197 ref NP_014267.1	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.1467	0.3013	2058.81	2060.444	1	471.4	52.77778 L.FVLLPPIDPKDGGRIPDPL.C
ail6324197/refINP_014267_1	YNI 132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance: Kre33p	2	2 9398	0 1664	2085 83	2083 444	6	361.7	47 222221 E1V11 1I 1P1P1I1D1P1K2D1G1G1R4I1P1D1P1I 1 C
		Essential protein of unknown function; heterozygous mutant shows haploinsufficiency	-	2.0000		2000.00	2000.111			
gi 6324197 ret NP_014267.1	YNL132W	IN K1 killer toxin resistance; Kre33p Essential protein of unknown function; heterozygous mutant shows haploinsufficiency	2	4.1649	0.3138	2414.73	2413.829	1	854.2	57.14286 F.VLLPPIDPKDGGRIPDPLCVIQ.I
gi 6324197 ref NP_014267.1	YNL132W	in K1 killer toxin resistance; Kre33p Pentidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs EK506 and	2	3.6611	0.278	2079.93	2081.382	2	517.3	47.058823 K.N2V1K2P1L1P1P1K2E1D1D1E1L1P1P1K2Q2L1.E
		rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and	2	3.584	0.1822	1960.23	1960.194	4	507.7	47.22222 K.IDRISPGDGATFPKTGDLV.T
ail6224104/rofIND_014264_1	VNI 1250	rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may	2	4 5240	0.2522	0007 40	2220 6	1	1040	
gilo324194 101 14F_014204.1	TNLISSC	Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and	2	4.3249	0.3523	2337.43	2339.0	1	1040	52.360935 K.HUIK4HSTETGIDTGIATTIETEKZTIGIDTETVITTIII63.1
ail6324194/refINP 014264.1	YNL135C	rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; For1p	2	3.7941	0.2527	1753.65	1752.946	2	1013.8	59.375 D.R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1.T
51		Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p	1	3.2963	0.3096	1522.55	1523.775	1	487.7	60.714287 Y.GPRGFPGLIPPNSTL.V
		Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and ranamycin: also binds to the pophistope chromatin binding protein Hmo1n and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p	1	3.2919	0.3097	1541.57	1542.775	1	397.6	57.14286 Y.G1P1R4G1F1P1G1L1I1P1P1N2S1T1L1.V
		Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p Particular regulate its assembly or function; Fpr1p	3	5.2247	0.334	2084.03	2083.352	1	1454.4	43.421055 D.RISPGDGATFPKTGDLVTIH.Y
		rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p Peotidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and	2	5.708	0.4697	2109.43	2109.352	1	1461.9	68.42105 D.R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T111H3.Y
-:::::::::::::::::::::::::::::::::::::	VAII 4250	rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may	2	5 0700	0 2005	2400.00	0400.050		4074.0	
gilo324194[rei]INP_014264.1]	TINE 1350	Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and	3	5.6728	0.3665	2109.68	2109.352	I	1271.0	42.105263 D.R41151P1G1D1G1A111F1P1R211G1D1E1V1111183.1
gil6324194/refINP_014264_1	YNI 135C	rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function: Epr1p	2	5 3038	0.3608	2084 79	2083 352	1	1682.3	71 05263 D RISPGDGATEPKTGDI VTIH Y
3.1		Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and	-					-		
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p	2	4.5467	0.3322	2541.53	2538.907	1	756.2	50 N.VKIDRISPGDGATFPKTGDLVTIH.Y
		Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p	1	2.2258	0.151	916.44	917.096	2	172.3	78.57143 A.RLTIPGPY.A
		Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p	2	4.9373	0.3641	2214.27	2213.501	1	947.6	57.5 N.V1K2I1D1R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1.T
		rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and	2	4.0433	0.2921	2190.13	2187.501	1	665.5	50 N.VKIDRISPGDGATFPKTGDLV.T
ail6224104/rofIND_014264_1	VNI 1250	rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may	2	E 222	0 2005	2100.21	2100 252	1	1075.0	
gilo324194 101 14F_014204.1	TNLISSC	Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and	2	5.525	0.3995	2109.21	2109.332	I	1375.5	00.42103 D.R4H31F101D101A111F1F1R21101D1E1V1111173.1
ail6324194/refINP 014264.1	YNL135C	rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function: For1p	2	4,7743	0.3816	2084.27	2083.352	1	1545.3	68.42105 D.RISPGDGATEPKTGDLVTIH Y
9.1442 · · · · · · · · · · · · · · · · · ·		Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and	_					-		
gi 6324194 ref NP_014264.1	YNL135C	rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	3	5.0897	0.3569	2109.29	2109.352	1	1240.3	42.105263 D.R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T1I1H3.Y
		Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and ranamycin: also binds to the poppistone chromatin binding protein Hmo1p and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p	3	4.3064	0.2908	2539.88	2538.907	1	775.1	35.869564 N.VKIDRISPGDGATFPKTGDLVTIH.Y
		Peptidyl-prolyl cis-trans isomerase (PPlase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p Particular regulate its assembly or function; Fpr1p	3	5.229	0.2958	2572.82	2569.907	1	885.2	38.04348 N.V1K2I1D1R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T1I1H3.Y
		rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may								
gi 6324194 ref NP_014264.1	YNL135C	regulate its assembly or function; Fpr1p Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and	2	4.4168	0.3426	2568.71	2569.907	1	514.5	41.304348 N.V1K2I1D1R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T11H3.Y
ail6224104/rofIND_014264_1	VNI 1250	rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may	2	2 1 2 2	0.2204	1724.00	1721 046	1	057	
gilo324194 101 14F_014204.1	TNLISSC	Subunit of the NuA4 histone acetyltransferase complex, which acetylates the N-	2	3.123	0.2304	1734.09	1731.940	I	937	59.575 D.RIS-GDGATFERTGDLV.T
gi 6324193 ref NP_014263.1	YNL136W	terminal tails of histones H4 and H2A; Eaf7p Subunit of the NuA4 histone acetyltransferase complex, which acetylates the N-	2	3.4082	0.2756	1772.49	1772.921	1	604.6	53.846157 R.K2Q2D1F1T1L1P1W2E1E1Y1G1E1L1.I
gi 6324193 ref NP_014263.1	YNL136W	terminal tails of histones H4 and H2A; Eaf7p	2	3.2119	0.2679	1983.65	1982.24	1	603	53.333336 R.KQDFTLPWEEYGELIL.E
gi 6324193 ref NP_014263.1	YNL136W	terminal tails of histories H4 and H2A; Eaf7p	2	3.1687	0.1546	1082.35	1084.29	6	827.8	87.5 W.T1I1V1D1E1I1R4L1L1.R
		Essential protein required for maturation of Gas1p and Pho8p: GEP-fusion protein								
	100	localizes to the endoplasmic reticulum (ER) and YFP-fusion protein to the nuclear	0	5 4 4 9 9		0404.00	0101 101		0.40.4	
gijo324180[ret]NP_014250.1]	rnl149C	envelope-ER network; null mutants have a cell separation defect; Pga2p	3	5.1183	0.3282	3131.66	3131.424	1	846.4	
		Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum (ER) and YEP-fusion protein to the pucker								
gi 6324180 ref NP_014250.1	YNL149C	envelope-ER network; null mutants have a cell separation defect; Pga2p	3	4.4769	0.2015	3003.8	3002.309	1	626.1	28 Q.VEKDKRDKEEKRSKDLIDKPDDAATA.E
gi 6324177 ref NP_014247.1 gi 6324177 ref NP_014247.1	YNL152W YNL152W	Protein required for cell viability; Yni152wp Protein required for cell viability; YnI152wp	2	4.1736 4.3391	0.3903	2392.47 2393.93	2391.719 2391.719	1 1	705.3 962.7	36.25 S.MAMKPIPPLPTESEYDYVHGS.T
gi 6324177 ref NP_014247.1	YNL152W	Protein required for cell viability; YnI152wp	2	3.4747	0.1802	2304.97	2304.641	1	409.1	44.736843 S.MAMRPIPPLPTESEYDYVHG.S
gij0324177[rei]NP_014247.1]	TINL 15200	Frotein required for cell viability; thirtszwp	2	3.7459	0.3968	2007.03	2007.317	1	020.5	50.25 A.MIR4PHIPIPILIPITIEIS1E1Y1D1Y1V1H3.G

gil6324177/refINP_014247.1	YNL152W	Protein required for cell viability: YnI152wp	3	4.5288	0.2703	2416.97	2417.719	1	910.8	33.75 S.M1A1M1R4P1I1P1P1L1P1T1E1S1E1Y1D1Y1V1H3G1S1.T
gil6324177/refINP_014247_1	YNI 152W	Protein required for cell viability: Vol152wp	2	4 0166	0 3574	2418.09	2417 719	1	770 7	50 S M1A1M1R4P111P1P11 1P1T1E1S1E1Y1D1Y1//1H3G1S1 T
gil6324177 rofIND 014247.1	VNI 152W	Protein required for cell viability; Vnl152wp	2	3 0478	0.2036	2212.03	2213 447	1	308.4	
silcoo44c4lastNID_044004_4	VNL4COC	The extrement of the viability, THI 52 wp	2	3.3470	0.2330	4507.55	4500.000	1	530.4	
gilb324161[rei]NP_014231.1]	TINLIBOC	The authentic, non-tagged protein was localized to milochondria, Emp41p	1	3.0127	0.2271	1597.55	1598.809		5/6	53.846157 1.K2M1K2PTETETVTT1D1511151G1V1.A
gi 6324161 ref NP_014231.1	YNL168C	The authentic, non-tagged protein was localized to mitochondria; Fmp41p	2	3.6343	0.3471	1801.47	1802	2	456.6	53.333336 A.G1V1G1E1L1K2P1G1D1R4V1H3C1E1L1L1.C
gi 6324161 ref NP_014231.1	YNL168C	The authentic, non-tagged protein was localized to mitochondria; Fmp41p	2	4.5268	0.4243	2133.55	2132.353	1	662.2	50 T.G1T1P1A1G1V1G1E1L1K2P1G1D1R4V1H3C1E1L1L1.Q
gi 6324161 ref NP_014231.1	YNL168C	The authentic, non-tagged protein was localized to mitochondria; Fmp41p	2	3.9359	0.3287	1581.73	1582.809	1	1173	65.38461 T.KMKPEEVYDSISGV.A
gil6324161/refINP_014231.11	YNL168C	The authentic, non-tagged protein was localized to mitochondria: Emp41p	2	4.1345	0.2818	1597.45	1598.809	1	1524.3	73.07692 T.K2M1K2P1E1E1V1Y1D1S1I1S1G1V1.A
gil6324161/refINP_014231_1	YNI 168C	The authentic, non-tagged protein was localized to mitochondria: Emp41p	2	4 2907	0 4228	2233.83	2234 483	1	566.5	45 T. GTPAGVGELKEGDRVHCELLON
gil6224161[rof[NID_014221.1]	VNI 169C	The authentic, non-tagged protein was localized to mitochondria; Emp41p	2	2 66 19	0.4542	2105.00	2106 252	1	500.5 522 5	
gil032410111e11NF_014231.11	TINE TOOC	The authentic, non-tagged protein was localized to milochondina, Filip4 ip	2	3.0010	0.4042	2105.25	2100.333		000.0	47.300423 T.GTFAGVGELKFGDKVHCELLQ
		Protein component of the small (405) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	3	4.0541	0.2917	2276.33	2276.632	1	1094.9	38.75 L.PDAVTIIEPKEEEPILAPSVK.D
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity: essential for viability: has similarity to E, coli S3 and rat								
gil6324151/refINP_014221_1	YNI 178W	S3 ribosomal proteins: Rps3p	2	5 7336	0 3819	2297.63	2200 632	1	1442	65 P1D141V1T1111F1P1K2F1F1F1P1111141P1S1V1K2 D
gilosz4101/101/101/101/14221.11	INC. INC.	Brotein appropriate of the small (40S) ribesamel subunit, hes apprinis/appr/imidinis	2	0.7000	0.0010	2201.00	2200.002		1442	
		Protein component of the small (403) hoosonial subunit, has apulline/apyliniumic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coll S3 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	3	5.3631	0.3381	2297.06	2299.632	1	1432.6	42.5 L.P1D1A1V1T1111E1P1K2E1E1E1P111L1A1P1S1V1K2.D
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
gil6324151/refINP_014221.1	YNL178W	S3 ribosomal proteins: Rps3p	2	3.0064	0.215	1795.81	1793.111	1	409.1	50 T.IJEPKEEEPILAPSVK.D
3.1		Protein component of the small (40S) ribosomal subunit has anurinic/anvrimidinic								
		(AB) and any alage and with a second of the single for visibility has similarity to E and S2 and rat								
	1011 47014	(AF) endonuclease activity, essential for viability, has similarity to E. coil 55 and fat	0	0.5700	0.0054	4 407 45	4 407 070		1017 5	
gilo324151[rei]NP_014221.1]	TINLITOW	S3 hbosomai proteins; Rps3p	2	3.5738	0.3251	1437.45	1437.070		1047.5	75 E.PREEEPILAPSVK.D
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	2	6.2757	0.4445	2278.55	2276.632	1	2030	70 L.PDAVTIIEPKEEEPILAPSVK.D
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity: essential for viability: has similarity to E_coli S3 and rat								
ail62244541rofIND_014224_41	VNII 179\//	22 riboomal proteins: Days	2	4 60 4 1	0.2601	2045 04	2011 210	1	024.0	
gil032415111eiline_014221.11	TINLITOW	So housoniai proteins, rupsop	3	4.0041	0.3091	2040.91	2044.310	1	024.9	30.109232 R. IGFRALFDAV HIEFREEFILAFSVR.D
		Protein component of the small (405) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	2	4.1683	0.3909	2773.29	2773.199	1	464.2	36 S.RTGPKALPDAVTIIEPKEEEPILAPS.V
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity: essential for viability: has similarity to E, coli S3 and rat								
gil6324151/refINP_014221.1	YNL178W	S3 ribosomal proteins: Rps3p	2	4.2648	0.3344	2803.77	2804,199	1	711.9	44 S.R4T1G1P1K2A1L1P1D1A1V1T1111E1P1K2E1E1E1P111L1A1P1S1.V
91002 110 110 110 110 <u>_</u> 01 122 111		Protein component of the small (40S) ribosomal subunit, has any rinic/any rimidinic	-	1.2010	0.0011	2000.11	2001.100			
		(AD) and any alagase activity appartial for viability has similarity to E call S2 and rat								
	1011 47014	(AF) endonuclease activity, essential for viability, has similarity to E. coll 35 and fat		5 0700	0 4450	0450.05	0400 074		1005 0	
gil6324151 [ref]NP_014221.1]	YNL178W	S3 ribosomai proteins; Rps3p	2	5.3709	0.4152	2459.95	2460.871	1	1065.2	54.545456 K.ALPDAV HIEPKEEEPILAPSVK.D
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	2	5.7495	0.3283	2488.09	2485.871	1	1281	56.81818 K.A1L1P1D1A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1V1K2.D
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity: essential for viability: has similarity to E_coli S3 and rat								
gil6324151/refINP_014221_1	YNI 178W	S3 ribosomal proteins: Ros30	3	4 0693	0 4334	2460.95	2460 871	1	649.2	38 636364 K ALPDAVTIERKEEERILAPSVK D
gil05241511ieiliui _014221.11	INLI70W	Detain component of the empli (40C) sitesemple whereit her equivisio(equivisidinie	5	4.0033	0.4334	2400.33	2400.071		043.2	30.00004 K.AELDAV HIELKEELEN SVK.D
		Protein component of the small (405) hoosomal subunit, has apunnic/apynnidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coll 53 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	2	2.985	0.2532	1136.61	1136.353	1	978.4	77.77778 F.K2Y1A1P1G1T1I1V1L1Y1.A
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
ail6324151/refINP 014221.1	YNL178W	S3 ribosomal proteins: Rps3p	2	3.0219	0.2461	1895.01	1894.216	1	467.7	46.875 V.TIIEPKEEEPILAPSVK.D
3.1		Protein component of the small (40S) ribosomal subunit has anurinic/anvrimidinic								
		(AP) and on uclease activity, assential for viability, has similarity to E, coli S3 and rat								
	1011 47014	(AF) endonuclease activity, essential for viability, has similarity to E. coll 35 and fat		5 4500	0 4400	0000 07	0004 407		740 5	
gil6324151 [ref]NP_014221.1]	YNL178W	S3 ribosomai proteins; Kps3p	2	5.4592	0.4198	2063.37	2064.427	1	746.5	55.555557 D.AV HIEPKEEEPILAPSVK.D
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	3	4.0161	0.3728	2772.95	2773.199	1	551.8	36 S.RTGPKALPDAVTIIEPKEEEPILAPS.V
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity: essential for viability: has similarity to E_coli S3 and rat								
gil6324151/rofIND_014221_1	VNI 178W/	S3 ribosomal proteins: Pps3p	2	4 2778	0 321	1954 21	1955 12	1	710.3	62.5 D A1/(1711)1151D1K251515111111A1D151 \/
gil032415111eiline_014221.11	TINLITOW	So housonal ploteins, rupsop	2	4.2770	0.321	1004.21	1000.12	1	/19.5	02.5 D.ATVTTTTTTEFFTRZETETETFTTTETATFTST.V
		riberin component of the small (403) hobsonial subunit, has apulnicapy initialine								
		(AP) endonuclease activity; essential for viability; has similarity to E. coll 53 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	2	3.7553	0.2595	1837.39	1837.12	1	618.4	59.375 D.AVTIIEPKEEEPILAPS.V
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
ail6324151/refINP 014221.1	YNL178W	S3 ribosomal proteins: Rps3p	2	3.2361	0.1928	2232.41	2233.564	1	465.8	45 K.ALPDAVTIJEPKEEEPILAPS.V
3100 0 1 0 1 <u>-</u>		Protein component of the small (40S) ribosomal subunit has any ripic/apyrimidinic								
		(AB) and any alage and with a second of the single for visibility has similarity to E and S2 and rat								
	1011 47014	(AF) endonuclease activity, essential for viability, has similarity to E. coil 55 and fat	0	5 40 40	0 1077	0004.00	0005 407		704.0	
gilb324151[rei]NP_014221.1]	TINL 178VV	So housomai proteins; Rpsop	2	5.4849	0.4277	2084.03	2085.427	1	761.9	55.555557 D.ATVTTTTTTTETPTKZETETETPTTTLTATPTSTVTKZ.D
		Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic								
		(AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat								
gi 6324151 ref NP_014221.1	YNL178W	S3 ribosomal proteins; Rps3p	2	3.7575	0.1569	2256.79	2255.564	8	260.6	37.5 K.A1L1P1D1A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1.V
		Protein kinase that stabilizes several plasma membrane amino acid transporters by								
ail6324146/refINP 014216.1	YNL183C	antagonizing their ubiguitin-mediated degradation: Npr1p	2	5.1904	0.4651	2324.15	2323.585	1	1143.9	58.333332 L.N2H3P1N2I1I1E1T1I1E1I1V1Y1E1N2D1R4I1L1.Q
		Protein kinase that stabilizes several plasma membrane amino acid transporters by								
gil6324146lrofIND_014216_1	VNI 1830	antagonizing their ubiguitin-mediated degradation: Nor1n	2	5 5614	0 4 4 1 7	2208 61	2206 585	1	1358 5	
gil0524140[rei]14F_014210.1]	INLIGGO	Brotein kinges that stabilizes several plasma membrane amine said transporters by	2	5.5014	0.4417	2230.01	2230.303		1556.5	30.333352 E.NHI MIE HEN TENDRE.Q
	1000	Frotein kinase that stabilizes several plasma memorane amino acid transporters by		4 9 4 4 9	0 40 40	0.400.00	0407 745			
gil6324146[ref]NP_014216.1]	YNL183C	antagonizing their ubiquitin-mediated degradation; Npr1p	2	4.8446	0.4242	2436.69	2437.745	1	811.4	50 I.LINZH3PINZHITETTTTETTVTYTETNZDTR4HLT.Q
		Protein kinase that stabilizes several plasma membrane amino acid transporters by								
gi 6324146 ref NP_014216.1	YNL183C	antagonizing their ubiquitin-mediated degradation; Npr1p	2	3.3015	0.2579	1934.17	1935.079	1	565.4	50 L.N2H3P1N2I1I1E1T1I1E1I1V1Y1E1N2D1.R
		Ubiquitin-specific protease that deubiquitinates ubiquitin-protein moieties: may								
		regulate silencing by acting on Sir4p; involved in posttranscriptionally regulating								
gil6324143/refINP_014213_1	VNI 186W/	Gan1n and nossibly other transporters: primarily located in the nucleus: Ubn10n	3	5 487	0.4187	2588 84	2587 777	1	1411 1	41 25 T Y1D1D1E1Y111N2I111S1E1R4D1V1L1K2E1P1N2A1Y1 Y
910024140110110F_014213.1	111210000	Sup in and possibly other transporters, printally located in the nucleus, Obp10p	3	5.407	0.410/	2000.04	2301.111	'	1411.1	
		I libiquitin appointion protococo that doubliquiting the unbiquiting protocols and intervention								
		obiquiun-specific protease that deubiquitinates ubiquitin-protein moleties; may								
		regulate silencing by acting on Sir4p; involved in posttranscriptionally regulating	-		o	0005 55	0000		705 5	K.E1R4D1N2A1D1K2G1D1G1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1E1D1IIG1EID1IIGIEIDIIGIEIDIIGIEIDIIGIEIDIIIGIEIDIIIGIEIDIIIGIEIDIIIGIEIDIIIGIEIDIIIGIEID
gijo324143 ret NP_014213.1	1NL186W	Gap (p and possibly other transporters; primarily located in the nucleus; Ubp10p	3	5.7623	0.4098	3960.86	3962.924	1	182.3	ZI.5ZITTI DIITGTETNZET.G

gi 6324143 ref NP_014213.1	YNL186W	Ubiquitin-specific protease that deubiquitinates ubiquitin-protein moieties; may regulate silencing by acting on Sir4p; involved in posttranscriptionally regulating Gap1p and possibly other transporters; primarily located in the nucleus; Ubp10p	3	6.7452	0.4399	4293.5	4295.336	1	1312.8	A.S1L1K2E1R4D1N2A1D1K2G1D1G1E1D111G1E1D111G1E1D111G1E1D111G1E1D111G1E1D111G1E1D111G1E1N2L1.G
gi 6324143 ref NP_014213.1 gi 6324123 ref NP_014193.1 gi 6324123 ref NP_014193.1 gi 6324123 ref NP_014193.1	YNL186W YNL206C YNL206C YNL206C	Ubiquitin-specific protease that deubiquitinates ubiquitin-protein moieties; may regulate silencing by acting on Sir4p; involved in posttranscriptionally regulating Gap1p and possibly other transporters; primarily located in the nucleus; Ubp10p Protein with a role in regulation of Ty1 transposition; Rtt106p Protein with a role in regulation of Ty1 transposition; Rtt106p Protein with a role in regulation of Ty1 transposition; Rtt106p	3 1 1 2	5.9968 2.3206 2.3117 3.0255	0.448 0.2855 0.2541 0.2199	4248.17 1517.49 1531.74 2156.77	4248.336 1517.808 1532.808 2157.508	1 1 1	1280.6 376.8 592.9 180.9	 23.717949 A.SLKERDNADKGDGEDIGEDIGEDIGEDIGEDIGEDIGEDIGEDIGEDIGE
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	1	2.427	0.1689	1191.68	1191.431	7	222.2	50 M.LERVIDFMPA.G
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	2	3.8727	0.2638	1925.93	1925.158	1	745.8	59.375 L.L111D1F1K2D1Y1P1D1V1P1K2V1P1G1N2S1.K
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	2	3.2522	0.3813	1423.19	1422.494	1	760.3	75 S.HLGEEHGDKITAD.L
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	3	3.8558	0.2721	1310.9	1310.554	1	986	63.88889 Q.KMYDEVLKHF.S
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	2	3.9791	0.2338	2609.11	2610.069	1	593.5	34.782608 L.LIDFKDYPDVPKVPGNSKIPPIGV.G
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	3	4.996	0.3634	2609.96	2610.069	1	1593.6	40.217392 L.LIDFKDYPDVPKVPGNSKIPPIGV.G
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	1	2.4861	0.2645	1309.52	1310.554	1	511.4	72.22222 Q.KMYDEVLKHF.S
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	3	3.8325	0.2144	2667.44	2667.12	2	923.1	32.291664 L.LIDFKDYPDVPKVPGNSKIPPIGVG.K
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	3	5.1311	0.3566	2638.85	2638.069	1	951.7	32.608696 L.L111D1F1K2D1Y1P1D1V1P1K2V1P1G1N2S1K2I1P1P1I1G1V1.G
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	2	4.3953	0.4036	2608.85	2610.069	1	641.9	39.130436 L.LIDFKDYPDVPKVPGNSKIPPIGV.G
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	3	4.4324	0.2281	2796.08	2795.294	1	926.5	30.000002 L.LIDFKDYPDVPKVPGNSKIPPIGVGK.E
gi 6324098 ref NP_014168.1	YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	3	4.3082	0.3028	2611.04	2610.069	1	723.3	30.434782 L.LIDFKDYPDVPKVPGNSKIPPIGV.G
gi 27808714 ref NP_014160.2	YNL239W	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p; Lap3p	2	4.4701	0.2777	2074.31	2075.409	1	787.6	55.555557 F.T1S1G1K2E1E1P111V1L1P111W2D1P1M1G1A1L1.A
gi 27808714 ref NP_014160.2	YNL239W	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p; Lap3p	2	3.9402	0.3149	2054.45	2054.409	1	820.9	55.555557 F.TSGKEEPIVLPIWDPMGALA
gi 27808714 ref NP_014160.2	YNL239W	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p; Lap3p	2	3.5343	0.2501	1642.23	1640.935	1	755	61.538464 S.G1K2E1E1P111V1L1P111W2D1P1M1.G
gi 27808714 ref NP_014160.2	YNL239W	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p; Lap3p	2	3.26	0.2762	1865.21	1866.226	1	541.1	53.125 S.GKEEPIVLPIWDPMGAL.A
gi 27808714 ref NP_014160.2	YNL239W	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p; Lap3p	2	4.1753	0.3157	1961.63	1961.249	1	1094.9	61.764706 F.T1S1G1K2E1E1P111V1L1P111W2D1P1M1G1A1.L
gi 27808714 ref NP_014160.2	YNL239W	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p; Lap3p	2	3.361	0.2375	1812.45	1813.119	1	715.5	56.666668 F.TSGKEEPIVLPIWDPM.G
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	1	2.6306	0.1847	1471.63	1472.74	8	478.1	58.333332 M.TQDKMNPILDAILE
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	2.9355	0.2068	1474.31	1472.74	1	712.4	75 M.TQDKMNPILDAILE
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	3.4882	0.1953	1475.69	1474.698	2	614.4	66.66667 Q.D1K2M1N2P111L1D1A111L1E1S1.G

gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	3.262	0.3506	1964.69	1965.384	1	691.8	50 T.LVTIPKLPVDAPDVFLIN.D
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	4.1332	0.4711	1985.89	1985.384	1	554.5	50 T.L1V1T111P1K2L1P1V1D1A1P1D1V1F1L111N2.D
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	4.0968	0.3661	1873.33	1871.224	1	701.9	53.125 L.V1T111P1K2L1P1V1D1A1P1D1V1F1L111N2.D
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	2.9807	0.2022	1490.71	1488.724	1	677.5	66.66667 L.KTLPLANDEVQLF.K
ail63240861refINP 014156.11	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip: dimer in vivo: Sla2p	2	5.2838	0.4067	1992.79	1995.249	1	2036.9	73.52941 M.T1Q2D1K2M1N2P111L1D1A111L1E1S1G111N2.T
ail6324086/rofIND_014156.11	VNI 243W/	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin certical patch of the emprained build in; direct avec 1920.	2	5 1105	0 3935	1072 40	1073 240	1	1021.0	
gilos24060 161 14F_014150.1	11124300	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis;	2	5.1195	0.3635	1972.49	1973.249		1921.9	
gi 6324086 ref NP_014156.1	YNL243W	present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis;	2	4.1573	0.3099	2315.45	2315.644	1	674	47.5 M.TQDKMNPILDAILESGINTIQ.E
gi 6324086 ref NP_014156.1	YNL243W	present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	3.5656	0.193	1704.49	1706.934	1	1204	67.85714 M.T1Q2D1K2M1N2P1I1L1D1A1I1L1E1S1.G
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	3.7044	0.2583	1690.79	1688.934	1	1007.4	67.85714 M.TQDKMNPILDAILES.G
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	3.9619	0.3012	1992.05	1989.249	3	675.8	52.941177 M.TQDKM@NPILDAILESGIN.T
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	2.9691	0.2689	1826.39	1827.171	1	442	46.875 L.TTLVTIPKLPVDAPDVF.L
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	3.9001	0.2889	1474.47	1472.74	1	810	83.33333 M.TQDKMNPILDAIL.E
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	3.8787	0.2204	1487.75	1488.74	1	638.7	79.16667 M.T1Q2D1K2M1N2P1I1L1D1A1I1L1.E
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	1	2.8241	0.371	1510.62	1511.802	1	869.5	57.692307 L.VTIPKLPVDAPDVF.L
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	1	3.0373	0.3339	1525.59	1526.802	1	864.5	61.538464 L.V1T111P1K2L1P1V1D1A1P1D1V1F1.L
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	1	2.9208	0.1848	1472.55	1472.74	6	465.2	58.333332 M.TQDKMNPILDAIL.E
ail63240861refINP_014156_11	YNI 243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin contrical patch of the emerging bud tin; dimer in vivo; Sla2n	2	3 8071	0.3571	1641.37	1640 961	1	733.4	60 714287 T I 1V1T111P1K2I 1P1V1D141P1D1V1F1 I
9,002,000,0,0,0, _0, 7,00, 1		Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis;	-	0.0071	0.0071					
gi 6324086 ref NP_014156.1	YNL243W	present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p Transmembrane actin-binding protein involved in membrane cytoskeleton assembly	2	3.9118	0.4168	1627.61	1624.961	1	866.6	64.28571 T.LVTIPKLPVDAPDVF.L
gi 6324086 ref NP_014156.1	YNL243W	and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	3.4501	0.294	2303.67	2304.605	1	489.1	44.736843 N.DVDESKEIKFKKREPSVTPA.R
gi 6324086 ref NP_014156.1	YNL243W	rransmemorane actin-oinding protein involved in memorane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	2	4.0565	0.2074	2330.63	2331.605	1	474	39.473686 N.D1V1D1E1S1K2E1I1K2F1K2K2R4E1P1S1V1T1P1A1.R
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	1	2.3993	0.1916	1319.69	1320.547	1	184.2	65 S.E1H3L1R4V1D1V1P1K2P1L1.L
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	1	2.3248	0.2676	1302.72	1303.547	1	174.6	60.000004 S.EHLRVDVPKPL.L
gi 6324086 ref NP_014156.1	YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	1	2.7442	0.3849	1415.81	1416.707	1	207.3	59.090908 S.EHLRVDVPKPLL.S

		Transmembrane actin-binding protein involved in membrane cytoskeleton assembly								
aile224096 rofIND 014156 1	VNI 242W	and cell polarization; adaptor protein that links actin to clathrin and endocytosis;	2	2 002	0.150	1422 50	1424 707	1	700 7	72 72727 8 64421 4 64/4 64/4 64/2 64/ 41 4 8
gij6324086/rei/NP_014156.1	YNL243W	RNA polymerase I subunit A49: Rpa49p	2	3 9449	0.159	2051.01	2052 419	1	829.7	56 25 S SILKEADKEKKI ELEPY O
gi 6324081 ref NP_014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	4.3968	0.2185	2071.57	2073.419	1	362.8	50 S.S1I1L1K2E1A1D1K2E1K2K2L1E1L1F1P1Y1.Q
gi 6324081 ref NP_014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	4.5925	0.3771	2142.61	2143.485	1	850.5	55.88235 T.DVEQIYPIESIIPKKELQ.F
gi 6324081 ref NP_014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	3.1236	0.1554	2034.47	2036.165	1	429.5	53.333336 K.D1R4S1Y1F1I1D1P1Q2N2E1D1K2I1L1C1.Y
gi 6324081 ref NP_014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	2.9602	0.2262	2167.77	2166.339	1	363.1	50 S.K2D1R4S1Y1F1I1D1P1Q2N2E1D1K2I1L1C1.Y
gi 6324081 ref NP_014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	4.7793	0.2769	2338.53	2339.669	1	1147.5	57.894737 D.A1T1D1V1E1Q2I1Y1P1I1E1S1I1I1P1K2K2E1L1Q2.F
gi 6324081 ref NP_014151.1 gi 6324081 ref NP_014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	3.9316	0.3477	2315.43	2315.669	1	904.3 716.0	52.63158 D.ATDVEQITPLESIIPKKELQ.F 50 T.D1//1E10211V10111E1S1111101K2K2E11 102 E
gi[6324081]refINP_014151.1]	VNI 248C	RNA polymerase I subunit A49, Rpa49p	2	4.7509	0.3310	2035.19	2035 354	1	800 4	56 25 T D1//1E102/1Y1P1/1E151/1/1P1K2K2E1L102.F
gil6324081/refINP_014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	3.2199	0.2564	2014.81	2015.354	1	727.1	50 T.DVEOIYPIESIIPKKELQ
gil6324081/refINP 014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	3.9372	0.4332	2587.59	2588.009	1	908.2	55 T.D1V1E1Q2I1Y1P1I1E1S1I1I1P1K2K2E1L1Q2F1I1R4.V
gi 6324081 ref NP_014151.1	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	3.7087	0.4566	2560.11	2560.009	1	687.4	47.5 T.DVEQIYPIESIIPKKELQFIR.V
		Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate								
		synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin								
gi 37362687 ref NP_014143.2	YNL256W	aldolase activities; Fol1p	2	3.3164	0.1857	2198.45	2199.492	1	740.5	50 A.G1E1D1I111V1N2E1P1D1L1N2I1P1H3P1R4M1L1.E
		Multifunctional enzyme of the folic acid biosynthesis pathway, has dinydropteroate								
gil37362687/rofIND_014143.21	VNI 256W/	synthetase, any aro-o-ny aroxymethylptenn pyrophosphokinase, and any aroneoptenn aldelase activities: Fol1p	2	/ 1959	0 3270	2404 37	2404 712	1	111 0	47.5 C1E1 1 1\$1P1\/1H3 1H3P1\/1T1A1E1P1 1\/1D1H3 1 K
gij5/50200/[rei]i4/_014145.2]	111223000	Multifunctional enzyme of the folic acid biosynthesis pathway, has dibydropteroate	2	4.1000	0.5275	2404.57	2404.712	'	441.5	47.5 E.GTETETHOR TVHISEHISETVH IATER HIVE HIGH.K
		synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin								
gi 37362687 ref NP_014143.2	YNL256W	aldolase activities; Fol1p	3	4.1287	0.2745	2403.29	2404.712	1	825.8	33.75 L.C1E1L1I1S1P1V1H3L1H3P1V1T1A1E1P1I1V1D1H3L1.K
		Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate								
		synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin								
gi 37362687 ref NP_014143.2	YNL256W	aldolase activities; Fol1p	3	4.5003	0.4191	2375.99	2377.712	1	1150	37.5 L.CELISPVHLHPVTAEPIVDHL.K
		Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate								
-1072020214ND 044442 01	VAL OF CW	synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin	2	4 0045	0.0004	0000.04	0004 040		040.0	
gij37362687 [rei]NP_014143.2]	TINL200VV	Audolase activities; Folip Multifunctional annume of the falia acid biographical notheray, has dihudranteraate	3	4.9015	0.2601	2332.34	2331.049	1	842.0	30.25 N.SAGEDIIVNEPDLNIPHPRMLE
		synthetase, dibydro-6-bydroxymethyloterin pyrophosphokinase, and dibydroneonterin								
gil37362687/refINP_014143.2	YNL256W	aldolase activities: Fol1p	2	3.5831	0.2659	2016.57	2017.37	2	372.9	41.17647 K.K2A1E1L1P1P1P1V1Q2S1I1I1D1N2V1V1K2E1.V
3.10.00_00.1.0.1.00.0.01		Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate	-					-		
		synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin								
gi 37362687 ref NP_014143.2	YNL256W	aldolase activities; Fol1p	2	3.4666	0.2981	1993.19	1995.37	1	377.5	41.17647 K.KAELPPPVQSIIDNVVKF.V
		Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate								
		synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin								
gi 37362687 ref NP_014143.2	YNL256W	aldolase activities; Fol1p	2	3.2884	0.2858	2377.03	2377.712	1	242.4	37.5 L.CELISPVHLHPVTAEPIVDHL.K
		Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate								
ail27262697/rofIND 014142.21	VNII DECW	synthetase, and anydro-o-hydroxymethylptenn pyrophosphokinase, and anydroneoptenn	2	2 50 42	0.0521	1707 62	1726.07	1	705	
gij5/30206/[lei]NF_014143.2]	TINE230W	Multifunctional enzyme of the folic acid biosynthesis nathway, has dihydronteroate	2	3.3042	0.2551	1727.03	1720.97		795	73.07092 Q.HDEDTEWREVELET.R
		synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin								
gi 37362687 ref NP 014143.2	YNL256W	aldolase activities; Fol1p	2	4.8573	0.4282	1948.41	1949.216	1	1409.9	70 A.HNEYFQKFPDSPLVVK.V
31		Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate								
		synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin								
gi 37362687 ref NP_014143.2	YNL256W	aldolase activities; Fol1p	3	3.9043	0.2539	1950.02	1949.216	1	1114	46.666668 A.HNEYFQKFPDSPLVVK.V
		Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate								
	100000	synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin		0.0404	0.004	4070.04	1071 010		000.0	
gi 37362687 ret NP_014143.2	YNL256W	aldolase activities; Fol1p Phosphatidulinosital 4-kinase: cataluzes first step in the biosynthesis of	3	3.9494	0.294	1970.84	1971.216	1	906.3	43.333332 A.H3N2E111F1Q2K2F1P1D151P1L1V1V1K2.V
		phosphatidylinositol-4-kinase, calalyzes inst step in the biosynthesis of								
gil6324062[refINP_014132_1]	YNI 267W	cytoskeleton: Pik1n	3	4 7747	0.3395	2196 71	2197 456	1	722.3	35 526314 S S1N2R4S1S1T1P1T1S1P1I1D1I 1I1D1P1I1K2T1K2 F
gilooz iooziloitti _ottilozitti		Phosphatidylinositol 4-kinase: catalyzes first step in the biosynthesis of	Ũ		0.0000	2100.71	21011100		122.0	
		phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin								
gi 6324062 ref NP_014132.1	YNL267W	cytoskeleton; Pik1p	2	4.1001	0.3182	1990.83	1993.274	1	470.4	55.88235 N.R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
		Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of								
		phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin								
gi 6324062 ref NP_014132.1	YNL267W	cytoskeleton; Pik1p	2	3.3752	0.1837	2170.85	2171.456	1	369.7	44.736843 S.SNRSSTPTSPIDLIDPIKTK.E
		Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of								
gil6324062/refINP_014132_1	YNI 267W	prosphalidylinositol-4,5-biphosphale; may control cytokineses through the actin	з	4 5819	0 1567	2173 1	2171 456	2	1129.5	
giloo24002[ici]i4i _014102.1]	THEZOT	Phosphatidylinositol 4-kinase: catalyzes first step in the biosynthesis of	0	4.0010	0.1007	2170.1	2111.400	2	1125.5	
		phosphatidylinositol-4.5-biphosphate: may control cytokineses through the actin								
gi 6324062 ref NP_014132.1	YNL267W	cytoskeleton; Pik1p	3	5.2048	0.1701	1993.49	1993.274	3	1799.9	50 N.R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
		Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of								
		phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin								
gi 6324062 ref NP_014132.1	YNL267W	cytoskeleton; Pik1p	2	3.1058	0.2319	1970.71	1970.274	1	564.1	58.823532 N.RSSTPTSPIDLIDPIKTK.E
		Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of								
-::C2240C2I#ND_0444224		phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin	2	4.047	0.4070	4070 57	4070 074	4	2200 5	
gil0324002[rei]INF_014132.1]	TINL207W	Desphatidulinesitel 4-kinase: cataluzes first step in the biosynthesis of	3	4.017	0.1079	1970.57	1970.274		2309.5	50 N.KSSTFTSFIDLIDFIKTK.E
		phosphatidylinositol-4.5-biphosphate: may control cytokineses through the actin								
ail63240621refINP 014132.11	YNL267W	cvtoskeleton: Pik1p	3	5.9931	0.2181	1994.18	1993.274	1	3418.5	52.941177 N.R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
31		Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of								
		phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin								
gi 6324062 ref NP_014132.1	YNL267W	cytoskeleton; Pik1p	2	4.3178	0.3251	1992.05	1993.274	1	523.3	58.823532 N.R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
		Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of								
-: 102240021 END 04442241		phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin	0	0 5005	0.2075	4070.05	4070 074	2	540.0	
gil0324062[rei]NP_014132.1]	TINL267W	суюткенской, МКТр	2	3.3625	0.3075	1970.35	19/0.2/4	2	518.8	00.00200 N.KOOTHTOHULIUMIKTK.E
		C-14 sterol reductase, acts in ergosterol biosynthesis: mutants accumulate the								
		abnormal sterol ignosterol (ergosta-8,14 dienol), and are viable under anaerobic								
gi 6324049 ref NP_014119.1	YNL280C	growth conditions but inviable on rich medium under aerobic conditions; Erg24p	2	3.709	0.3127	1669.81	1669.837	1	1170.8	64.28571 L.GGNSGNIIYDWFIGR.E
		с.,								
		C-14 sterol reductase, acts in ergosterol biosynthesis; mutants accumulate the								
gil6324040/rofIND_044440_4	VNI 2000	aphormal sterol Ignosterol (ergosta-8,14 dienol), and are viable under anaerobic	•	4 1 4 0 9	0 2472	2606.00	2604 007	4	520.0	28 2608681 6161N28161N21111V1D4W2541464D45414N2D4D4L4C4D4L4 D
91002404010110F_014119.1	TINEZOUC	growar contaitons put invitable on non medium under derobic contaitions, Erg24p	3	4.1400	0.3473	2030.33	2034.007	I	520.9	20.200000 E.010114201011421111101192F11101R4E1E1192F1R4E101P1E1.D

gij6324049 ref NP_014119.1	YNL280C	C-14 sterol reductase, acts in ergosterol biosynthesis; mutants accumulate the abnormal sterol ignosterol (ergosta-8,14 dienol), and are viable under anaerobic growth conditions but inviable on rich medium under aerobic conditions; Erg24p	3	4.6168	0.3213	2659.79	2660.007	2	439.2	25 L.GGNSGNIIYDWFIGRELNPRLGPL.D
gi 6324049 ref NP_014119.1	YNL280C	C-14 sterol reductase, acts in ergosterol biosynthesis; mutants accumulate the abnormal sterol ignosterol (ergosta-8,14 dienol), and are viable under anaerobic growth conditions but inviable on rich medium under aerobic conditions; Erg24p	2	3.3167	0.2927	2316.95	2314.602	4	198.6	41.17647 Y.GENWEEYERKVPYKIJPY.V
gi 6324049 ref NP_014119.1	YNL280C	C-14 sterol reductase, acts in ergosterol biosynthesis; mutants accumulate the abnormal sterol ignosterol (ergosta-8,14 dienol), and are viable under anaerobic growth conditions but inviable on rich medium under aerobic conditions; Erg24p	2	3.2652	0.2709	2127.59	2128.435	2	365.7	50 E.NWEEYERKVPYKIIPY.V
gi 6324042 ref NP_014112.1	YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	2	3.2666	0.2554	1606.59	1606.857	1	742.8	61.538464 T.KNDPTLYESIISLL.K
gi 6324042 ref NP_014112.1	YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	2	2.9212	0.187	1292.87	1294.538	7	397.4	65 Y.H3L1L1P1I1S1E1V1T1I1R4.R
gi 6324042 ref NP_014112.1	YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	2	3.2836	0.3081	1444.39	1441.714	7	689.2	68.181816 S.YHLLPISEVTIR.R
gi 6324042 ref NP_014112.1	YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	2	3.2765	0.3068	1683.45	1680.901	1	565.5	60.000004 L.HLLGKEGPSAPNPSLY.V
gi 6324042 ref NP_014112.1	YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	2	3.5859	0.3316	1963.15	1964.245	1	774.2	50 S.M1V1S1P1E1K2I1V1V1C1N2P1E1L1E1S1L1.I
gi 6324042 ref NP_014112.1	YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	2	4.044	0.4267	1958.71	1960.08	1	2156.3	78.57143 LCDFIEDCEFNEILVR.I
gi 6324042 ref NP_014112.1	YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	1	2.3065	0.2228	1332.98	1332.441	9	232.7	41.666664 L.G1K2E1G1P1S1A1P1N2P1S1L1Y1.V
gi 6324042 ref NP_014112.1	YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	2	3.9732	0.2086	1700.17	1700.901	1	1060.2	63.333332 L.H3L1L1G1K2E1G1P1S1A1P1N2P1S1L1Y1.V
gi 6324036 ref NP_014106.1	YNL293W	GTPase-activating protein for Sec4p and several other Rab GTPases, regulates exocytosis via its action on Sec4p, also required for proper actin organization; similar to Msb4p; both Msb3p and Msb4p localize to sites of polarized growth; Msb3p	2	4.1151	0.3822	1783.21	1784.072	1	1443.5	73.07692 Q.K2N2E1F1L1Y1R4L1P1P1I1T1L1C1.T
gi 6324036 ref NP_014106.1	YNL293W	GTPase-activating protein for Sec4p and several other Rab GTPases, regulates exocytosis via its action on Sec4p, also required for proper actin organization; similar to Msb4p; both Msb3p and Msb4p localize to sites of polarized growth; Msb3p	2	3.9209	0.2988	1766.09	1765.072	1	1273.6	73.07692 Q.KNEFLYRLPPITLC.T
gi 6324036 ref NP_014106.1	YNL293W	GTPase-activating protein for Sec4p and several other Rab GTPases, regulates exocytosis via its action on Sec4p, also required for proper actin organization; similar to Msb4p; both Msb3p and Msb4p localize to sites of polarized growth; Msb3p Peripheral membrane protein with a role in endocytosis and vacuole integrity,	3	3.8631	0.3303	2504.51	2503.72	1	702.7	35.526314 Q.D1L1D11111E1R4D1L1N2R4T1F1P1D1N2I1H3F1Q2.S
gi 6324033 ref NP_014102.1	YNL297C	Interacts with Arth p and localizes to the endosome; member of the Sec/p family of proteins; Mon2p Peripheral membrane protein with a role in endocytosis and vacuole integrity,	2	5.072	0.3292	2202.61	2201.329	1	1530.3	70.588234 Q.R4I1N2P1E1L1D1N2L1T1E1I1D1D1L1N2E1Y1.S
gi 6324033 ref NP_014102.1	YNL297C	interacts with Art Ip and localizes to the endosome; member of the Sec7p family of proteins; Mon2p Peripheral membrane protein with a role in endocytosis and vacuole integrity,	2	4.2034	0.3828	2176.49	2177.329	1	1256.8	61.764706 Q.RINPELDNLTEIDDLNEY.S
gi 6324033 ref NP_014102.1	YNL297C	interacts with Art Ip and localizes to the endosome; member of the Sec7p family of proteins; Mon2p Peripheral membrane protein with a role in endocytosis and vacuole integrity,	2	4.0297	0.3281	2304.13	2305.46	1	1041.8	58.333332 LQRINPELDNLTEIDDLNEY.S
gi 6324033 ref NP_014102.1	YNL297C	Interacts with Art p and localizes to the endosome; member of the Sec/p family of proteins; Mon2p Peripheral membrane protein with a role in endocytosis and vacuole integrity,	2	4.5154	0.3542	2331.21	2331.46	1	770.7	50 LQ2R4I1N2P1E1L1D1N2L1T1E1I1D1D1L1N2E1Y1.S
gi 6324033 ref NP_014102.1	YNL297C	Interacts with Antip and localizes to the endosome; member of the Sec/p family of proteins; Mon2p Peripheral membrane protein with a role in endocytosis and vacuole integrity,	2	4.3504	0.3879	2444.41	2445.62	1	749.1	50 T.L1Q2R4I1N2P1E1L1D1N2L1T1E1I1D1D1L1N2E1Y1.S
gi 6324033 ref NP_014102.1	YNL297C	Interacts with Anti-pain localizes to the endoscome, memory or the Sec/p family of proteins; $Mos2p$ Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacting the Anti-pain endormal to the compares of the Sec/p family of	2	3.867	0.3255	2417.79	2418.62	1	720.6	50 T.LQRINPELDNLTEIDDLNEY.S
gi 6324033 ref NP_014102.1	YNL297C	neerads with Arth participation to the endosphere, member of the Sec/ pranning of proteins; Mon2p	2	3.6127	0.3162	2095.85	2097.456	1	579.9	50 S.A1I1K2Y1P1L1L1P1E1F1V1Q2D1K2T1K2P1S1.S
gi 6324031 ref NP_014101.1	YNL298W	Cocc2p activated signal transoucting kinase of the PAR (b21-activated kinase) family, involved in septin ring assembly and cytokinesis; directly phosphorylates septins Cdc3p and Cdc10p; other yeast PAK family members are Ste20p and Skm1p; Cla4p	2	4.0026	0.5024	1971.59	1972.167	1	649	55.555557 Q.GPSPSPSPSPSPLNPYRPH.H
gi 6324031 ref NP_014101.1	YNL298W	Cdc42p activated signal transducing kinase of the PAK (p21-activated kinase) family, involved in septin ring assembly and cytokinesis; directly phosphorylates septins Cdc3p and Cdc10p; other yeast PAK family members are Ste20p and Skm1p; Cla4p	2	3.6181	0.4613	1998.01	1997.167	1	613.6	52.77778.Q.G1P151P151P151P151P151P1L1N2P1Y1R4P1H3.H
gi 6324016 ref NP_014086.1 gi 6324016 ref NP_014086.1	YNL313C YNL313C	Protein required for cell viability; Ynl313cp Protein required for cell viability; Ynl313cp	2	3.4591 3.817	0.2593	1843.25 2034.43	1842.053 2033.339	1	321 854.1	50 K.NTTPAKDPLVEEELTALL 58.823532 Q.K2S1L1F1D1V1T1P1D1Q2E1I1P1L1P1I1IS1.A
gi 6324016 ref NP_014086.1	YNL313C	Protein required for cell viability; Ynl313cp	2	3.5356	0.333	2858.13	2860.09	2	363.9	30.434782 L.E1S1D1L1L1L1E1K2P1H3F1E1S1I1A1D1E1P1L1D1E1Q2I1Y1.S
gi 6324016 ref NP_014086.1	YNL313C	Protein required for cell viability; Ynl313cp Protein required for cell viability; Ynl313cp	2	3.3457	0.3672	3046.53	3046.328	1	322.5	30.000002 F.A1L1E1S1D1L1L1L1E1K2P1H3F1E1S1I1A1D1E1P1L1D1E1Q2I1Y1.S
gij6324016/ref/NP_014086.1	YNL313C	Protein required for cell viability; Ynl313cp	∠ 3	3.8491	0.3553	1871.42	1871.141	1	492 1031.1	42.1875 R.RDKSGEGSIDLPIIEKL.V
gi 6324016 ref NP_014086.1	YNL313C	Protein required for cell viability; Ynl313cp	2	3.6102	0.2622	1872.39	1871.1	1	755.6	60.714287 T.KELPESIHEDFKREL.C
gi 6324016 ref NP_014086.1	YNL313C	Protein required for cell viability; Ynl313cp	2	4.0764	0.3245	1891.59	1893.1	1	1032.5	67.85714 T.K2E1L1P1E1S111H3E1D1F1K2R4E1L1.C
gijb324016 ret NP_014086.1 gij6324016 ret NP_014086.1	YNL313C YNL313C	Protein required for cell viability; Ynl313cp Protein required for cell viability; Ynl313cp	2	3.3862	0.3482	2159.65 2861.36	2160.432	1	443.1 576 4	61.764706 K.RQKVDLNEGYEEDKLLPL.A 32.608696 L.E1S1D1L1L1L1E1K2P1H3E1E1S1I1A1D1E1P1I 1D1E1O2I1V1 S
gi 6324016 ref NP_014086.1	YNL313C	Protein required for cell viability; Ynl313cp	3	4.1631	0.3459	3048.83	3046.328	1	713.8	30.000002 F.A1L1E1S1D1L1L1L1E1K2P1H3F1E1S1I1A1D1E1P1L1D1E1Q2I1Y1.S
gi 6324016 ref NP_014086.1	YNL313C	Protein required for cell viability; Ynl313cp	2	3.5043	0.3641	2106.11	2105.417	1	484.6	41.666664 Q.K2S1L1F1D1V1T1P1D1Q2E1I1P1L1P1I1I1S1A1.E
gi 6324016 ref NP_014086.1 gi 6324016 ref NP_014086.1	YNL313C	Protein required for cell viability; Ynl313cp Protein required for cell viability; Ynl313cp	2	3.0886	0.2004	2276.85	2274.489	2	448.5 573 8	41.666664 L.LEKPHFESIADEPLDEQIY.S 67.64706 K R4O2K2V/1D11 1N2E1G1Y1E1E1D1K2L11 1D1L1 A
gi 6324009 ref NP_014079.1	YNL320W	hypothetical protein; Ynl320wp	2	3.807	0.2658	2752.23	2753	1	295.6	34.090908 F.EFPLGSHNDTIIQDGYWDIIRDF.L

gi 6324009 ref NP_014079.1	YNL320W	hypothetical protein; Ynl320wp	2	3.0659	0.3483	2123.45	2122.301	8	159	40.625 S.HNDTIIQDGYWDIIRDF.L
gi 6324009 ref NP_014079.1	YNL320W	hypothetical protein; Ynl320wp	2	3.5565	0.29	2268.13	2266.431	1	395.6	47.22222 L.GSHNDTIIQDGYWDIIRDF.L
gil6324009/refINP_014079.11	YNL320W	hypothetical protein: YnI320wp	2	4,1536	0.3637	1539.13	1539.836	1	871.2	70.83333 S.GLKDEIVPPFHMR.K
gil6224000/rofIND_014070.1	VNI 220W	hypothetical protein, This20wp	2	4.1000	0.0007	1560.20	1550.000	1	707.9	70.00000 0.0EKBEINTTTTIMIKIK
gil6324009[rei]NP_014079.1]	TINL320VV	hypothetical protein; miszowp	2	4.0793	0.3232	1560.39	1008.830		797.8	70.63333 S.GTLTK2DTETTIVTPTPTFTH3WTR4.K
		Membrane protein of the plasma membrane and ER, involved in translocation of								
	VAL 20214/	wend and protein of the plasma memorale and Lik, movied in translocation of	0	4 4 4 9 0	0.04	4000.07	4000 004		4400.0	C2 222222 O LADAIA CALALIOW2D4)/4LAE4E4N2C4//2//2 O
gil6324006[rei]NP_014076.1]	TINL323VV	phospholipids and alkylphosphocholine drugs across the plasma memorane; Lemop	2	4.1420	0.24	1000.07	1869.201		1169.6	03.333332 Q.LTDTTGTLTH3W2PTVTLTETFTN2GTK2K2.G
		Membrane protein of the plasma membrane and ER, involved in translocation of								
gi 6324006 ref NP_014076.1	YNL323W	phospholipids and alkylphosphocholine drugs across the plasma membrane; Lem3p	3	3.9798	0.2917	1889.84	1889.201	1	2271.9	56.666668 Q.L1D1I1G1L1H3W2P1V1L1E1F1N2G1K2K2.G
		Membrane protein of the plasma membrane and EP, involved in translocation of								
		wentbraite protein of the plasma membrane and Erk, involved in translocation of	~	0.0074	0.04.47	4 400 00	4 400 740		4 400 4	
gi 6324006 ret NP_014076.1	YNL323W	phospholipids and alkylphosphocholine drugs across the plasma membrane; Lem3p	3	3.9671	0.2147	1486.28	1486.742	1	1436.1	63.636364 G.L1H3W2P1V1L1E1F1N2G1K2K2.G
		Membrane protein of the plasma membrane and ER, involved in translocation of								
gil6324006/refINP_014076_11	VNI 323W/	phospholipids and alkylphosphocholine drugs across the plasma membrane: Lem3p	2	3 1414	0 2098	1568 17	1570 801	3	737 1	66 66667 O L1D111G1L1H3W2P1V1L1E1E1N2 G
gil0024000[ici]i4i _014010.1]	114202011	prosprolipids and any prosprocholine drugs across the plasma memorane, certop	2	0.1414	0.2000	1000.17	1070.001	0	707.1	
		Membrane protein of the plasma membrane and ER, involved in translocation of								
gi 6324006 ref NP_014076.1	YNL323W	phospholipids and alkylphosphocholine drugs across the plasma membrane; Lem3p	1	2.3781	0.1944	1168.62	1168.341	7	368.5	56.25 G.L1H3W2P1V1L1E1F1N2.G
		Membrane protein of the plasma membrane and ER, involved in translocation of								
aile224006trofIND_014076_11	VNII 2021/1/	phonobaliside and allaulabaanbaahalina da aa aaraa tha alaama mambrana: Lam2n	2	4 077	0 2074	1000 51	1000 201	1	1502 5	
gil0324000[tet]INF_014076.1]	TINESZOVV	phospholipids and akylphosphocholine drugs across the plasma memorane, Lemop	3	4.077	0.2974	1009.01	1009.201	1	1505.5	51.000004 Q.EIDHIGIEIH3W2FTVIEIEIFTN2GTK2K2.G
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
ail63243431refINP 014413.11	YNR016C	fatty acids: Acc1p	1	2.5449	0.1569	1195.51	1196.418	1	271.7	55 Q.K2I1I1E1E1A1P1V1T1I1A1.K
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		Access of a form relation of the service of the service the service of the servic								
		acety-CoA to form malonyi-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP_014413.1	YNR016C	fatty acids; Acc1p	1	3.7457	0.1794	1337.56	1338.491	1	364.3	75 S.N2F1N2I1K2P1I1F1T1D1N2.R
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA: required for de novo biosynthesis of long-chain								
gil6324343lrefINP_014413_1	VNR016C	fatty acids: Acc1n	1	3 4745	0 2722	1322.49	1323 401	2	328.8	75 S NENIKPIETON R
gil0324343[rei]14F_014413.1]	TNIKUTUC	actus, Accup		5.4745	0.2722	1322.43	1323.431	2	520.0	
		Acetyl-CoA carboxylase, blotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP 014413.1	YNR016C	fatty acids; Acc1p	1	2.7342	0.3668	1316.49	1317.467	1	503.5	59.090908 Q.S1A1K2V1P1C1I1P1W2S1G1T1.G
3100 0 01 01 =0 0 01		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		Access of a form relation of the service of the service the service of the servic								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP_014413.1	YNR016C	fatty acids; Acc1p	1	3.9072	0.3892	1573.53	1574.713	1	598.6	57.14286 T.G1V1D1T1V1H3V1D1E1K2T1G1L1V1S1.V
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA: required for de novo biosynthesis of long-chain								
gil6324343lrefINP_014413_1	VNR016C	fatty acids: Acc1n	1	2 4 4 5	0 3534	1365.6	1365 572	1	628.4	68 181816 R VHEGVTVPIVEW K
gil0324343[rei]14F_014413.1]	TNIKUTUC	actus, Accup		2.445	0.3334	1303.0	1303.372		020.4	00.101010 K.VILEGVTVFTVEW.K
		Acetyl-CoA carboxylase, blotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP_014413.1	YNR016C	fatty acids; Acc1p	1	2.3838	0.1885	1392.77	1392.51	2	405.8	55 L.YSHDDGKFYFL.E
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		active CoA to form malony CoA: required for do novo biosynthesis of long-chain								
	VAIDALOO	active to form mainty-cox, required for de novo biosynthesis of long-chain	~	0 7044	0 0000	0744 50	0740 400		504.4	
gi 6324343 ret NP_014413.1	YNR016C	fatty acids; Acc1p	2	3.7214	0.2292	2711.53	2713.163	1	581.4	43.75 H.ALPFEGMLPDFGSPVIEGTKPAYKF.K
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA: required for de novo biosynthesis of long-chain								
gil6324343/rofIND_014413_1	VNP016C	fatty acide: Acc1n	2	3 25/3	0 3257	2202 17	2200 747	1	632.8	
gil0324343[rei]14F_014413.1]	TNIKUTUC	latty actus, Accup	2	3.2343	0.5257	2302.17	2300.747		032.0	44.730043 D.AEVD INCENTIFY FOLLOW
		Acetyl-COA carboxylase, blotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP 014413.1	YNR016C	fatty acids; Acc1p	2	4.3396	0.3403	2140.03	2139.508	1	729.7	55.88235 L.V1D1Y1K2Q2P1I1I11Y1I1P1P1T1G1E1L1R4.G
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA: required for do novo biosynthesis of long-chain								
	VAIDALOO	active to form mainty-cox, required for de novo biosynthesis of long-chain	~	4 0700	0.0500	0000 70	0005 747		744.0	
gi 6324343 ret NP_014413.1	YNR016C	fatty acids; Acc1p	2	4.2768	0.3502	2326.79	2325.747	1	/11.2	50 D.A1L1V1D1Y1K2Q2P111111Y11P1P111G1E1L1R4.G
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gil6324343lrefINP_014413_1	VNR016C	fatty acids: Acc1n	2	3 2204	0 1744	2232.63	2233 565	2	296.5	34 210526 R V1H3E1G1V1T1V1P1I1V1E1W2K2E1O2I 1P1S1A1A1 F
gil0324343[rei]14F_014413.1]	TNIKUTUC	latty actus, Accup	2	3.22.54	0.1744	2202.00	2200.000	2	230.5	
		Acetyl-COA carboxylase, blotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP_014413.1	YNR016C	fatty acids; Acc1p	2	3.434	0.2637	1734.43	1732.971	1	854	73.07692 S.V1K2E1R4T1E1Q2I1E1H3I1L1K2S1.S
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA: required for do novo biosynthesis of long-chain								
-:::C2242421#IND_04444241	VND0400	active order to form matching con, required for de novo biosynthesis of long-chain	0	4 0000	0 2204	1005 50	4000 400		000 4	
gilb324343[rei]NP_014413.1]	TINKUIGO	faity acids, Accip	2	4.0933	0.3301	1805.59	1803.199		666.1	65.625 K.IIIKDPQTGAPVPLKALI
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
ail6324343lrefINP 014413.1	YNR016C	fatty acids: Acc1p	2	3,9493	0.3993	2869.71	2870.337	1	437.2	36 H.A1L1P1F1E1G1M1L1P1D1F1G1S1P1V1I1E1G1T1K2P1A1Y1K2F1K2.S
3.1		Acatul-CoA carboxulase, biotic containing enzyme that catalyzes the carboxulation of	-					-		
		Acetyl-CoA carboxylase, bloth containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP_014413.1	YNR016C	fatty acids; Acc1p	2	4.2259	0.3853	2840.13	2841.337	1	713	42 H.ALPFEGMLPDFGSPVIEGTKPAYKFK.S
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA: required for de novo biosynthesis of long-chain								
ail62242421rofIND_014412_11	VND016C	fotty colde: A colta	2	4 0777	0.2500	2002 51	2002 207	1	401.0	50 L D1D1E1C1S1D1\/11E1C1T1V3D1A1V1V3E1V3 S
gil0324343[iei]INF_014413.1]	TINKUTOC	latty actos, Accip	2	4.0777	0.3369	2003.51	2003.207		401.2	50 L.F IDIFIGISTETVITETGTTR2FTATTR2FTA2.5
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
ail63243431refINP 014413.11	YNR016C	fatty acids: Acc1p	2	3.1749	0.1755	1710.67	1710.971	1	855.5	69.230774 S.VKERTEQIEHILKS.S
3100 0 01 01 =0 0 01		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		sector Control boxylation, block to containing of an and the analyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP_014413.1	YNR016C	fatty acids; Acc1p	2	3.9065	0.4098	1639.19	1639.912	1	573.1	70.83333 T.MFPVDFIHEGKRY.K
		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA: required for de novo biosynthesis of long-chain								
gil6324343/rofIND_014413_1	VNP016C	fatty acide: Acc1n	2	4 4108	0.401	1650 37	1658 012	1	615.2	75 T M1E1D1/1D1E1/1H3E1G1K2D4V1 K
gil0324343[iei]INF_014413.1]	TINKUTOC	latty actos, Accip	2	4.4190	0.401	1039.37	1000.912		015.2	73 1.WIFTETVIDTETITISETGTK2K411.K
		Aceiyi-CoA carboxylase, blotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP_014413.1	YNR016C	fatty acids; Acc1p	2	3.0967	0.2457	1289.83	1290.464	8	449.7	66.66667 L.RNPKLPYSEW.K
=		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetuleCoA to form malonyleCoA: required for de novo biosynthesis of long-chain								
	VNDC100	accor controllorin malony-con, required for de novo biosynthesis of long-chain	~	4 0500	0.4000	4047.04	4040 000		000 5	
gijo324343 ret NP_014413.1	TNKU16C	ratty actors, ACC1p	2	4.3529	0.4336	1817.61	1819.036	1	983.5	07.00714 L.H351K4L1P1A1K2L1D1E1Q2M1E1E1L1.V
		AcetyI-COA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
		acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain								
gi 6324343 ref NP_014413.11	YNR016C	fatty acids; Acc1p	2	3.0183	0.1778	1707.45	1707.886	3	252.9	53.571426 Y.SERHTELPGHFIGLN.T

		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of								
gi 6324343 ref NP_014413.1	YNR016C	acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of	2	3.0958	0.2876	1526.67	1526.72	1	417.9	68.181816 M.F1P1V1D1F1I1H3E1G1K2R4Y1.K
gi 6324343 ref NP_014413.1	YNR016C	acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p Acetyl-CoA carboxylase biotin containing enzyme that catalyzes the carboxylation of	1	2.8577	0.3163	1592.69	1593.783	2	351.6	50 Y.SERHTELPGHFIGL.N
gi 6324343 ref NP_014413.1	YNR016C	actly/LocA to form malony/LoA; required for de nev biosynthesis of long-chain fatty acids; Acc1p Acety/LoA to compute activity acids; activity activity acids; acids; acids; activity acids; a	2	2.9851	0.2938	1871.53	1871.062	1	430.3	53.333336 T.NYSERHTELPGHFIGL.N
gi 6324343 ref NP_014413.1	YNR016C	actly/LocA to form malony/LoA; required for de nev biosynthesis of long-chain fatty acids; Acc1p Acety/LoA to compute activity acids; activity activity acids; acids; acids; activity acids; a	2	3.3624	0.3751	1896.77	1895.062	1	566.2	56.666668 T.N2Y1S1E1R4H3T1E1L1P1G1H3F1I1G1L1.N
gi 6324343 ref NP_014413.1	YNR016C	Activity CoA to form malonyth-CoA; requiring the yine visit damy you the consolvation of activity-CoA to form malonyth-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p Acetui-CoA carbovidase, biotic containing anzyme that catalyzes the carbovidation of	3	4.3063	0.2941	1872.92	1871.062	2	948.1	41.666664 T.NYSERHTELPGHFIGL.N
gi 6324343 ref NP_014413.1	YNR016C	Activity CoA to form malonyth-CoA; requiring the yine visit damy you the consolvation of activity-CoA to form malonyth-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p Acetui-CoA carbovidase, biotic containing anzyme that catalyzes the carbovidation of	2	3.7387	0.3179	1740.07	1739.111	1	882.7	67.85714 Y.KQPIIIYIPPTGELR.G
gi 6324343 ref NP_014413.1	YNR016C	Activity CoA to form malonyth-CoA; requiring the yine visit damy you the consolvation of activity-CoA to form malonyth-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p Acetui-CoA carbovidase, biotic containing anzyme that catalyzes the carbovidation of	2	3.8082	0.3927	1980.41	1981.274	1	929.4	62.5 S.ALHSRLPAKLDEQMEEL.V
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA to form malonyh-CoA; requiring on 2 more that catalyzes the completion of fatty acids; Acc1p Acetyl-CoA to form malonyh-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p Acetyl-CoA cathoxylase. biotic containing enzyme that catalyzes the cathoxylation of	2	2.9134	0.1945	1382.31	1380.572	2	569.5	63.636364 R.V1H3E1G1V1T1V1P1I1V1E1W2.K
gi 6324343 ref NP_014413.1	YNR016C	acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p Acetyl-CoA carboxvlase, biotin containing enzyme that catalyzes the carboxvlation of	2	4.0473	0.2737	1557.75	1558.775	1	724.6	65.38461 A.VKNPEYNPDKLLGA.V
gi 6324343 ref NP_014413.1	YNR016C	acety/-CA to form malenylCA; requiring the J-ne matching but the dispersion of the set	2	2.9122	0.2133	1694.61	1694.91	2	275.7	50 Q.L1A1D1R4E1R4E1L1L1P1I1Y1G1Q2.I
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA calosynade, joint containing enzyme that calaryzes the calosynation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	3	4.0497	0.1535	2116.4	2116.508	2	711.6	41.17647 L.VDYKQPIIIYIPPTGELR.G
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA calosynade, joint containing enzyme that calaryzes the calosynation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	3.8768	0.2669	1641.19	1640.922	1	1216.9	65.38461 R.VHEGVTVPIVEWKF.Q
gi 6324343 ref NP_014413.1	YNR016C	Activity CoA to form malonyin-CoA; required for de noval objective that catalyzes the comparison of activity-CoA to form malonyin-CoA; required for de noval objective to de long-chain fatty acids; Acc1p Acetui-CoA cathowlass, biotic containing enzyme that catalyzes the cathowlation of	2	3.4846	0.3876	1658.33	1658.922	1	1169.7	76.92308 R.V1H3E1G1V1T1V1P1I1V1E1W2K2F1.Q
gi 6324343 ref NP_014413.1	YNR016C	Activity CoA to form malonyin-CoA; required for de noval objective that catalyzes the comparison of activity-CoA to form malonyin-CoA; required for de noval objective to de long-chain fatty acids; Acc1p Acetui-CoA cathowlass, biotic containing enzyme that catalyzes the cathowlation of	2	3.7244	0.1548	1777.53	1777.024	2	719.2	60.714287 L.K2L1R4D1E1N2P1K2D1L1D1K2V1A1L1.T
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA calboxytase, joint containing enzyme that calabyzes the calboxytation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	3.0503	0.3043	1292.35	1290.464	5	592.4	72.22222 L.RNPKLPYSEW.K
gi 6324343 ref NP_014413.1	YNR016C	Acety-CoA caloxyrabe, joint comaining enzyme that calaryzes the caloxyrabit of acety-CoA to form malonyi-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p code (CoA) sortex-loss biotic contribute carging carging that calobrate the achevidation of	2	3.2847	0.4224	1612.49	1614.783	1	509.9	53.846157 Y.S1E1R4H3T1E1L1P1G1H3F1I1G1L1.N
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA calboxylaste, joldin colmaining enzyme unat calaryzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	3.3653	0.199	1305.25	1306.464	1	929.1	83.33333 L.R4N2P1K2L1P1Y1S1E1W2.K
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA calboxylaste, joldin colmaining enzyme unat calaryzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	1	2.6032	0.1929	1289.58	1290.464	1	230.4	61.11111 L.RNPKLPYSEW.K
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA carboxylase, block containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	3	3.9103	0.1656	2140.58	2139.508	1	806.5	42.647057 L.V1D1Y1K2Q2P1I1I11Y1I1P1P1T1G1E1L1R4.G
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-LoA carooxylase, blouin containing enzyme that catalyzes the carooxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	3.2102	0.1913	1569.75	1570.786	1	888.6	75 L.KLRDENPKDLDKV.A
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	1	2.962	0.2315	1327.61	1328.412	1	259.9	60.000004 Y.S1E1R4H3T1E1L1P1G1H3F1.I
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-LoA carboxylase, blobin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	3	4.8589	0.2408	1774.79	1777.024	1	1516.1	53.571426 L.K2L1R4D1E1N2P1K2D1L1D1K2V1A1L1.T
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-LoA carboxylase, blobin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	4.5535	0.3578	1882.93	1883.235	1	847.3	59.375 A.E111R411111K2D1P1Q2T1G1A1P1V1P1L1.R
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	4.7869	0.426	1861.65	1861.235	1	946.1	62.5 A.EIRIIIKDPQTGAPVPL.R
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	4.8011	0.3737	2139.77	2139.508	1	956.9	58.823532 L.V1D1Y1K2Q2P1I1I1I1Y1I1P1P1T1G1E1L1R4.G
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	4.105	0.4178	2116.23	2116.508	2	903.3	58.823532 L.VDYKQPIIIYIPPTGELR.G
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	2	4.2321	0.2063	1777.21	1779.043	2	465.4	64.28571 E.K2L1F1N2G1P1N2V1R4E1E1N2I1I1L1.K
gi 6324343 ref NP_014413.1	YNR016C	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	1	2.2066	0.1729	1583.67	1585.948	1	338.6	53.846157 M.SYVPAKRNMPVPIL.E
	VND0400	Acetyr-uoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fortu-cride: log1e.	2	2 0547	0 224 4	1505 57	1595 040	4	091.9	
gijuuz4040jreijiNP_014413.1	ALD C LOU	Essential protein of the mitochondrial inner membrane, component of the	2	3.0317	0.3214	1000.07	1000.948		301.0	
gi 6324344 ref NP_014414.1	YNR017W	mitochondrial import system; Mas6p Essential protein of the mitochondrial inner membrane, component of the	2	3.3041	0.3087	1812.81	1811.955	1	649.8	63.333332 Q.GLIPSRGWTDDLCYGT.G
gi 6324344 ref NP_014414.1	YNR017W	mitochondrial import system; Mas6p	2	3.7303	0.2401	1940.05	1938.095	2	358.6	46.875 A.GLDKGVEYLDLEEEQLS.S

		Essential protein of the mitochondrial inner membrane, component of the								
gi 6324344 ref NP_014414.1	YNR017W	mitochondrial import system; Mas6p	2	4.7912	0.4463	2008.45	2009.174	1	1398.3	64.70589 L.AGLDKGVEYLDLEEEQLS.S
	VND047W	Essential protein of the mitochondrial inner membrane, component of the	2	4 5504	0.0405	2020 75	2020 474		4400.0	
gilo324344[rei]NP_014414.1]	TINKUT7W	Essential protein of the mitochondrial inner membrane, component of the	2	4.5561	0.3425	2026.75	2029.174	1	1136.3	61.764706 LAIGILIDINZGIVIEITILIDILIEIEIEIQZLISI.S
gi 6324344 ref NP_014414.1	YNR017W	mitochondrial import system; Mas6p	2	4.8483	0.1933	1986.93	1987.122	1	2136	71.875 L.D1K2G1V1E1Y1L1D1L1E1E1E1Q2L1S1S1L1.E
ail6324344/refINP_014414_1	VNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system: Mas6n	2	4 3778	0.406	1967 53	1968 122	1	1268.4	
gilooz io i filoifiai _o i i i i i i		Essential protein of the mitochondrial inner membrane, component of the	-		0.100	1007.00	1000.122		1200.1	
gi 6324344 ref NP_014414.1	YNR017W	mitochondrial import system; Mas6p	2	4.6048	0.3653	2231.45	2231.412	1	1634.7	63.15789 L.A1G1L1D1K2G1V1E1Y1L1D1L1E1E1E1Q2L1S1S1L1.E
gi 6324344 ref NP 014414.1	YNR017W	mitochondrial import system; Mas6p	2	5.0021	0.4248	2140.37	2138.333	1	1755.8	58.333332 A.GLDKGVEYLDLEEEQLSSL.E
		Essential protein of the mitochondrial inner membrane, component of the								
gi 6324344 ref NP_014414.1	YNR017W	mitochondrial import system; Mas6p Essential protein of the mitochondrial inner membrane, component of the	2	3.4658	0.1939	2206.73	2209.412	1	842.9	50 L.AGLDKGVEYLDLEEEQLSSL.E
gi 6324344 ref NP_014414.1	YNR017W	mitochondrial import system; Mas6p	2	4.1446	0.2975	2159.73	2159.333	2	1036.8	55.555557 A.G1L1D1K2G1V1E1Y1L1D1L1E1E1E1Q2L1S1S1L1.E
		Essential protein of the mitochondrial inner membrane, component of the								
gi 6324344 ret NP_014414.1	YNR017W	mitochondrial import system; Mas6p	2	4.0613	0.2119	1956.35	1957.095	3	519.9	50 A.G1L1D1K2G1V1E1Y1L1D1L1E1E1Q2L1S1.S
gi 6324348 ref NP_014418.1 gi 6324348 ref NP_014418.1	YNR021W	hypothetical protein; Yhr021wp	2	4.2153	0.2716	1854.73	1855.141	1	1/93./	75 K.S1K2Q2L1E1E1F1M1E111V111K4P1N2.G 77 27273 A HTSENDKI DNNE V
gil6324348/refINP_014418.1	YNR021W	hypothetical protein; Ynr021wp	2	3 2992	0.4371	2453.63	2453 668	5	178.3	35 F TDI PVNPPRDDKEWESSIEPK A
gi 6324348 ref NP_014418.1	YNR021W	hypothetical protein; Ynr021wp	2	4.1103	0.2139	2481.63	2481.668	1	234.4	37.5 F.T1D1L1P1V1N2P1P1R4D1D1K2E1W2E1S1S1I1E1P1K2.A
		73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved								
		in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin		=						
gi 6324350 ref NP_014420.1	YNR023W	remodeling complex; deletion mutants are temperature-sensitive; Snf12p	2	4.1786	0.3037	1828.25	1828.945	1	967.7	60.714287 V.K2W2Q2Y1D1P1N2N2P1V1D1F1D1G1L1.D
		73 kDa aubunit of the 11 aubunit SWI/SNE obromatin remodeling complex involved								
		in transcriptional regulation; homolog of Pecen subunit of the PSC chromatin								
ail6324350/refINP_014420_1	YNR023W	remodeling complex: deletion mutants are temperature-sensitive: Sof12p	2	4 064	0 4378	1807 87	1808 944	1	882.6	57 14286 V KWOYDPNNPVDEDGL D
giloo24000[ici]i4i _014420.1]	111102011	remodeling complex, deletion matanta are temperature sensitive, om rzp	-	4.004	0.4070	1007.07	1000.044		002.0	51.14200 V.KWQTDI NIN VDI DOLD
		73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved								
		in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin								
gi 6324350 ref NP_014420.1	YNR023W	remodeling complex; deletion mutants are temperature-sensitive; Snf12p	2	3.0069	0.2122	1741.19	1740.994	1	637.1	53.571426 N.STHLLPLQPIEIDYT.V
		73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved								
	MIDOCOM	in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin		0.005	0.0070	4750.07	1750.001		040.0	
gi 6324350 ref NP_014420.1	YNR023W	remodeling complex; deletion mutants are temperature-sensitive; Shf12p	2	2.985	0.2372	1758.87	1758.994	1	610.9	50 N.S111H3L1L1P1L1Q2P111E111D1Y111.V
		73 kDa subunit of the 11-subunit SWI/SNE chromatin remodeling complex involved								
		in transcriptional regulation: homolog of Rsc6p subunit of the RSC chromatin								
gi 6324350 ref NP 014420.1	YNR023W	remodeling complex; deletion mutants are temperature-sensitive; Snf12p	2	3.3984	0.2884	1554.05	1552.811	1	575.1	62.5 T.HLLPLQPIEIDYT.V
51		<u>9</u>								
		Guanine nucleotide exchange factor (GEF); glycosylated integral membrane protein								
		of the endoplasmic reticulum, important for the initiation of transport vesicle budding								
gi 6324353 ref NP_014423.1	YNR026C	from the endoplasmic reticulum through activation of the GTPase Sar1p; Sec12p	2	3.2475	0.191	1512.17	1512.703	3	736.4	68.181816 F.KYDKVNDQLEFL.T
		Guanine nucleotide exchange factor (GEF); glycosylated integral membrane protein								
-:::::::::::::::::::::::::::::::::::::	VND0000	of the endoplasmic reticulum, important for the initiation of transport vesicle budding	2	4 4004	0.000	4070.00	4004 404		4407.0	
gil0324353[rei]iNF_014423.1]	TNR020C	from the endoplasmic reaction inforger activation of the GTP ase Sality, Sec12p	2	4.4031	0.309	1979.33	1901.194		1107.0	00.00007 L.R4VIDIFITIR2DITIETR2ETQ2FTH3HET.3
		Guapine nucleotide exchange factor (GEE): divcosvlated integral membrane protein								
		of the endoplasmic reticulum, important for the initiation of transport vesicle budding								
gi 6324353 ref NP_014423.1	YNR026C	from the endoplasmic reticulum through activation of the GTPase Sar1p; Sec12p	2	4.4397	0.4427	1955.69	1957.194	1	990.5	63.333332 L.RVDPTKDTEKEQFHIL.S
		Alpha-1,6-mannosyltransferase localized to the ER; responsible for the addition of								
		the alpha-1,6 mannose to dolichol-linked Man7GlcNAc2, acts in the dolichol pathway								
gi 6324357 ref NP_014427.1	YNR030W	for N-glycosylation; Alg12p	2	4.3455	0.3638	2027.07	2025.277	1	566.7	62.5 F.H3L1I1Q2A1P1F1T1K2V1E1E1S1F1N2I1Q2.A
		Alpha-1,6-mannosyltransferase localized to the ER; responsible for the addition of								
	MIDOCOM	the alpha-1,6 mannose to dolichol-linked Man/GicNAc2, acts in the dolichol pathway		4 0000	0.0054	0000 07	0000 077		100.0	
gi 6324357 ret NP_014427.1	YNRU30W	for N-glycosylation; Alg12p	2	4.3906	0.3851	2003.87	2002.277	1	426.9	56.25 F.HLIQAPFTKVEESFNIQ.A
		Alpha-1,6-mannosyltransierase localized to the ER; responsible for the addition of the alpha-1,6-mannosyltransierase to delichel-linked Man7ClcNAc2, acts in the delichel nathway								
ail6324357/refINP_014427_1	YNR030W	for N-alvcosvlation: Ala12p	2	3 0518	0 2416	1531 67	1532 783	1	511.6	62.5 Y D1H3I 1K2E1P1G1V1V1P1R4T1E1 V
giloo24007 [rei]14 _014427.11	111100001	Essential protein involved in ribosome biogenesis: putative ATP-dependent RNA	-	0.0010	0.2410	1001.07	1002.100		011.0	
gi 6324366 ref NP_014436.1	YNR038W	helicase of the DEAD-box protein family; Dbp6p	2	3.1932	0.2908	2479.47	2480.74	4	244.6	32.5 E.RTFFDDLNKDLDRDGKSVQPL.E
		Essential protein involved in ribosome biogenesis; putative ATP-dependent RNA								
gi 6324366 ref NP_014436.1	YNR038W	helicase of the DEAD-box protein family; Dbp6p	2	4.3791	0.395	2248.41	2249.447	1	621.1	50 T.F1F1D1D1L1N2K2D1L1D1R4D1G1K2S1V1Q2P1L1.E
		DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in								
		transcriptional repression of meiosis-specific genes during vegetative growth and								
gi 6324570 ref NP_014639.1	YOL004W	silencing; involved in telomere maintenance; Sin3p	2	3.5934	0.2602	2462.39	2463.8	2	294.2	36.842106 H.W2L1T1P1K2P1K2S1Q2L1D1F1D1F1P1D1K2N2I1F1.Y
		DNA binding subunit of Sin3p-Rpd3p historie deacetylase complex, involved in								
gil6324570/rofINP_014639_1		transcriptional repression of melosis-specific genes during vegetative growth and silencing; involved in telemere maintenance; Sin3n	2	2 0707	0 2006	2436 67	2437.8	1	116.8	
gil0524570[rei]141_014059.1]	10100411	DNA hinding subunit of Sin3n-Rod3n histone deacetylase complex, involved in	2	2.5757	0.2000	2430.07	2437.0	'	440.0	33.47 3000 H.WETHARAGEDI DI PDANIL I
		transcriptional repression of meiosis-specific genes during vegetative growth and								
gi 6324570 ref NP_014639.1	YOL004W	silencing; involved in telomere maintenance; Sin3p	2	3.3102	0.316	2027.73	2028.337	1	401.3	52.941177 S.GLPSIQQPEMPAHRQIPQ.S
		DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in								
		transcriptional repression of meiosis-specific genes during vegetative growth and								
gi 6324570 ref NP_014639.1	YOL004W	silencing; involved in telomere maintenance; Sin3p	3	4.2361	0.2528	4263.32	4265.495	1	497.8	21.527777 S.NDEDGKVPQLSEPPEEEPNTIEEEELIDEEAKNPWLT.G
		DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in								
	VOI 00 /04/	transcriptional repression of meiosis-specific genes during vegetative growth and		0 4004	0 4074	1000 55	1000 105		4000.0	S.N2D1E1D1G1K2V1P1Q2L1S1E1P1P1E1E1E1P1N211I1E1E1E1E1L1I1D1E1E1A1
gijo324570[rei]NP_014639.1]	TOL004W	Silenoing, involved in telomere maintenance; SIR3p DNA binding subunit of Sin3p-Pod3p bistops descetulase complex, involved in	3	0.1884	0.4674	4309.55	4309.495	1	1006.2	20.094440 NZ(NZM1WZL111.0
		transcriptional repression of mejosic-specific genes during vegetative growth and								
ail6324570/refINP 014639 11	YOL004W	silencing: involved in telomere maintenance: Sin3n	2	3,1414	0,1581	1388.41	1387.57	1	1037.4	77.27273 Q.DILDLDDLVEKV.D
51		DNA binding subunit of Sin3p-Rpd3p histone deacetvlase complex. involved in	-		2.1001			•		
		transcriptional repression of meiosis-specific genes during vegetative growth and								
gi 6324570 ref NP_014639.1	YOL004W	silencing; involved in telomere maintenance; Sin3p	2	3.4414	0.2036	1401.81	1400.57	1	1078.7	77.27273 Q.D111L1D1L1D1L1V1E1K2V1.D
		I opoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving								
aileoodEcolinating oddoor d		and re-sealing the phosphodiester backbone; relaxes both positively and negatively	~	2 2070	0.2045	1617.04	1616 047	4	600.4	
gil0324500[rei]NP_014637.1]	TULUU6C	superconed DIVA; functions in replication, transcription, and recombination; Top1p	2	3.3973	0.3045	1017.21	118.0101	1	092.4	04.2007 I LONDARVPPAPEGIINW.G

gi 6324568 ref NP_014637.1	YOL006C	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination; Top1p	2	3.4708	0.3149	1635.67	1636.817	1	586.1	60.714287 L.S1K2D1A1P1V1P1P1A1P1E1G1H3K2W2.G
gi 6324568 ref NP_014637.1	YOL006C	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination; Top1p	3	5.8978	0.498	2710.58	2711.081	1	1809.9	41.666664 Q.LDKDLLKKEPKYFEEIDDLTKE.D
gi 6324568 ref NP_014637.1	YOL006C	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination; Top1p	2	4.4198	0.3065	2712.09	2711.081	1	572.5	45.238094 Q.LDKDLLKKEPKYFEEIDDLTKE.D
gi 6324568 ref NP_014637.1	YOL006C	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination; Top1p	2	3.7201	0.2789	1812.33	1813.09	1	407.5	46.666668 L.K2H3N2G1V111F1P1P1P1Y1Q2P1L1P1S1.H
gi 6324568 ref NP_014637.1	YOL006C	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination; Top1p	3	4.0783	0.3951	2239.97	2239.571	2	666.4	36.764706 D.LLKKEPKYFEEIDDLTKE.D
gi 6324568 ref NP_014637.1	YOL006C	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination; Top1p Protein involved in determination of longevity; LAG2 gene is preferentially expressed	2	3.1217	0.2751	2237.89	2239.571	2	432.2	44.11765 D.LLKKEPKYFEEIDDLTKE.D
gi 6324548 ref NP_014617.1	YOL025W	in young cells; overexpression extends the mean and maximum life span of cells; Lag2p Protein involved in determination of longevity; LAG2 gene is preferentially expressed	3	4.0343	0.3337	3081.02	3083.478	1	848.5	27.000002 N.R4L1L1P1V1L1F1P1P1Q2M1G1E1E1C1N2V1E1D1V1L1E1I1V1H3N2.F
gi 6324548 ref NP_014617.1	YOL025W	in young cells; overexpression extends the mean and maximum life span of cells; Lag2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to	2	3.8918	0.3946	1804.83	1806.093	1	627	64.28571 N.R4L1L1P1V1L1F1P1P1Q2M1G1E1E1C1.N
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to	2	4.0362	0.4433	1866.51	1868.989	1	1312.5	66.66667 F.D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to	2	4.3959	0.3394	2607.57	2609.798	1	993.7	52.499996 V.Y1N2N2V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to	2	5.6653	0.3028	2114.77	2117.298	1	2714.9	76.47059 W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxyoen-independent signaling pathway required to	2	4.5471	0.2624	2447.25	2445.622	1	961.7	57.894737 Y.N2N2V1R4M1E1D1L1P1E1M111E1E1L1D111D1D1E1
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, everyasion is controlled by an ovygen-independent cirpation pathway required to	2	3.7455	0.2662	2581.97	2583.798	1	359.2	42.5 V.YNNVRMEDLPEMIEELDIDDE
gi 6324513 ref NP_014582.1	YOL059W	expression to controlled by an oxygen-independent signaling patienty required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, averageing in socialide bu op ownee independent septimer to patients of the	3	6.5468	0.3166	2115.14	2117.298	1	2338.6	50 W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi 6324513 ref NP_014582.1	YOL059W	expression is controlled by an oxygen-independent signaling patiway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is occulled to be a owner independent signaling of topd1p.	3	3.8675	0.1862	2331.32	2329.518	1	1257.6	37.5 N.N2V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1
gi 6324513 ref NP_014582.1	YOL059W	expression is controlled by an oxygen-independent signaling patrway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling patrway required to	2	6.5187	0.3799	2329.31	2329.518	1	2103.6	69.44444 N.N2V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anxic conditions; located in cytamity patring for thicknown Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling patring required to	2	4.5953	0.4573	2259.39	2259.486	1	493	50 A.Y1Q2L1P1K2D1Y1Q2G1D1G1K2D1V1D1H3K2I1L1.K
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to	2	3.2551	0.2191	1940.73	1941.19	1	1079	63.333332 R.H3Q2N2V1K2Y1L1P1N2I1D1L1P1H3N2L1.V
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to	2	3.5095	0.2648	2358.77	2361.518	1	322.5	38.88889 N.N2V1R4M\$E1D1L1P1E1M\$I1E1E1L1D1I1D1D1E1
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to	2	5.9164	0.4473	2093.05	2093.298	1	2398.4	76.47059 W.VFDEKIGDENLTDIINTR.H
gi 6324513 ref NP_014582.1	YOL059W	equitate metabolism under anoxic conditions; located in cytosol and mitopatient of Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, averagesion is controlled by an overgoe ideopendent sizesling patients are control to	2	5.8611	0.3256	2114.81	2117.298	1	2343.8	73.52941 W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi 6324513 ref NP_014582.1	YOL059W	expression is controlled by an oxygen intogentionen signaling patriway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p,	3	6.6297	0.2753	2117.3	2117.298	1	3115.4	54.411762 W.V1F1D1E1K2I1G1D1E1N2L1T1D11111N2T1R4.H
gi 6324513 ref NP_014582.1	YOL059W	expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	6.196	0.3845	2329.15	2329.518	1	2174.6	69.44444 N.N2V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1

		NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p,								
		regulate metabolism under anoxic conditions; located in cytosol and mitochondria;								
gi 6324513 ref NP_014582.1	YOL059W	Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p,	2	5.4883	0.4171	2305.43	2306.518	1	1874.2	66.66667 N.NVRMEDLPEMIEELDIDDE
		expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions: located in cytosol and mitochondria:								
gi 6324513 ref NP_014582.1	YOL059W	Gpd2p	2	4.5299	0.2287	2193.67	2192.415	1	1646.3	64.70589 N.VRMEDLPEMIEELDIDDE
		expression is controlled by an oxygen-independent signaling pathway required to								
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	5.4075	0.3458	2214.77	2213.415	1	1901.3	64.70589 N.V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1
		NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to								
	20105010	regulate metabolism under anoxic conditions; located in cytosol and mitochondria;		0.0074	0.0005	4070 47	1070 010			
gi 6324513 ret NP_014582.1	YOL059W	Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p,	2	3.6871	0.2605	1673.17	1670.918	1	684.6	57.692307 Q.N2V1K2Y1L1P1N2I1D1L1P1H3N2L1.V
		expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria;								
gi 6324513 ref NP_014582.1	YOL059W	Gpd2p NAD-dependent division 3-phosphate depydrogenase, homolog of Gpd1p	1	2.7435	0.2528	1160.74	1160.418	1	288.1	66.66667 Q.R4L1G1L1G1E11111K2F1.G
		expression is controlled by an oxygen-independent signaling pathway required to								
gi 6324513 ref NP_014582.1	YOL059W	Gpd2p	2	4.2488	0.3088	1956.21	1957.111	1	1551	65.625 W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1.R
		NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to								
gil6324513/refINP_014582_1	YOI 059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria;	1	3 1245	0.3016	1323 48	1324 508	2	549.8	70 K Y1I 1P1N2I1D1I 1P1H3N2I 1 V
giloo2 io iolioinii _o i ioo2.iij	10200011	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p,		0.1210	0.0010	1020.10	102 1.000	-	0.0.0	
		regulate metabolism under anoxic conditions; located in cytosol and mitochondria;								
gi 6324513 ref NP_014582.1	YOL059W	Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p,	1	2.6112	0.2229	1308.44	1309.508	5	324.9	60.000004 K.YLPNIDLPHNL.V
		expression is controlled by an oxygen-independent signaling pathway required to								
gi 6324513 ref NP_014582.1	YOL059W	Gpd2p	2	3.0616	0.2309	1323.43	1324.508	1	460.3	75 K.Y1L1P1N2I1D1L1P1H3N2L1.V
		expression is controlled by an oxygen-independent signaling pathway required to								
qi 6324513 ref NP 014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	3	5.0371	0.275	1868.45	1868.989	1	1485.5	48.333332 F.D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
		NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p,								
		regulate metabolism under anoxic conditions; located in cytosol and mitochondria;								
gi 6324513 ref NP_014582.1	YOL059W	Gpd2p NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p,	2	4.9288	0.2893	2114.29	2113.282	1	1388.7	62.5 V.R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1
		expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions: located in cvtosol and mitochondria:								
gi 6324513 ref NP_014582.1	YOL059W	Gpd2p	2	3.0369	0.1943	1854.55	1855.006	1	893	56.666668 W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2.T
		expression is controlled by an oxygen-independent signaling pathway required to								
gi 6324513 ref NP_014582.1	YOL059W	regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	3.7343	0.2755	1938.43	1937.111	1	982.5	68.75 W.VFDEKIGDENLTDIINT.R
ail6324512lrefINP 014581.11	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	2.92	0.1516	1625.45	1624.829	1	754.7	61.538464 S.A1D1T1I1L1D1D1K2T1V1E1K2I1F1.N
gil6324512kofIND_014581_1		Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	3 0010	0 3204	2369 37	2365 712	1	610.2	
gilosz4512liellitir_014501.1	1020000	Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	3.3013	0.3234	2300.37	2303.712		010.2	
gi 6324512 ref NP_014581.1	YOL060C	Mam3p Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	3.7185	0.2777	1851.79	1851.109	1	818.8	63.333332 F.S1R4I1P11F1L1P1N2E1P1N2N2F1I1G1.M
gi 6324512 ref NP_014581.1	YOL060C	Mam3p Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	3.4015	0.1739	1960.47	1960.301	3	453	46.875 F.SRIPIFLPNEPNNFIGM.L
gi 6324512 ref NP_014581.1	YOL060C	Mam3p Protein required for normal mitochondrial morphology, has similarity to homolysins:	2	3.5977	0.1997	1980.53	1983.301	3	424.3	50 F.S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1M1.L
gi 6324512 ref NP_014581.1	YOL060C	Mam3p	2	4.1845	0.268	2164.43	2164.53	1	1006.1	55.555557 S.GFSRIPIFLPNEPNNFIGM.L
gi 6324512 ref NP_014581.1	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	4.8377	0.3075	2305.43	2303.689	1	766.5	47.368423 S.G1F1S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1M1L1.L
gi 6324512 ref NP 014581.1	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	4.0781	0.2503	2279.81	2277.689	1	1067	55.263157 S.GFSRIPIFLPNEPNNFIGML.L
gil6324512lrefINP_014581_1	YOI 060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	3 8233	0.3216	2244 47	2245 637	1	541 1	44 444447 G E1S1R4I1P1I1E1I 1P1N2E1P1N2N2E1I1G1M1I 1 I
sil0224542 still _ 044584.4	VOLOCOC	Protein required for normal mitochondrial morphology, has similarity to hemolysins;	-	2.0422	0.4054	2404.54	2105 502		220.0	
gi 6324512 ret NP_014581.1	YOLUGUC	Mam3p Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	3.0433	0.1954	2104.51	2105.583	3	330.8	38.235294 L.VILIMIYILIMIYIPIVIAIYIPIIIAIIILILIDI.Y
gi 6324512 ref NP_014581.1	YOL060C	Mam3p Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	4.8996	0.4276	1830.99	1829.134	1	1058.1	67.85714 K.R4V1E1E111M1T1P111E1N2V1F1T1M1.S
gi 6324512 ref NP_014581.1	YOL060C	Mam3p Protein required for normal mitochondrial morphology, has similarity to bemolysins:	2	3.0737	0.3552	1808.33	1810.134	1	730.2	60.714287 K.RVEEIMTPIENVFTM.S
gi 6324512 ref NP_014581.1	YOL060C	Mam3p Destein required for normal mitochondrial morphology, has similarly to homolysins;	2	3.4219	0.2045	2293.31	2293.689	1	612.8	42.105263 S.GFSRIPIFLPNEPNNFIGM@L.L
gi 6324512 ref NP_014581.1	YOL060C	Mam3p	2	3.1078	0.2268	2318.31	2319.689	2	464.9	42.105263 S.G1F1S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1M\$L1.L
gi 6324512 ref NP_014581.1	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.6283	0.1703	2072.71	2073.461	2	457	44.11765 F.SRIPIFLPNEPNNFIGML.L
gil6324512lrefINP_014581.11	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.4232	0.2734	2095.89	2097.461	3	382	38.235294 F.S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1M1L1.L
ail6324512lrofIND_014591.41	VOI 060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins;	-	3 0600	0.2274	2222 47	2220 627	-	914	
9103243121101NP_014361.1		Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	3.3003	0.23/4	2222.17	2220.037	1	011	
gijo324512 ret NP_014581.1	YOL060C	Mam3p Protein required for normal mitochondrial morphology, has similarity to hemolysins;	2	3.3208	0.2622	2030.75	2031.386	1	599.3	46.875 K.A1K2K4V1E1E111M111P111E1N2V1F1T1M1.S
gi 6324512 ref NP_014581.1	YOL060C	Mam3p Protein required for normal mitochondrial morpholoay, has similarity to hemolysins:	2	3.545	0.2403	1998.17	1999.285	1	357.9	43.75 G.F1S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1.M
gi 6324512 ref NP_014581.1	YOL060C	Mam3p	2	4.6877	0.252	2190.39	2189.53	1	1161.5	58.333332 S.G1F1S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1M1.L

		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide,								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p	3	3.9506	0.1887	2981.33	2979.27	1	1632.7	38.541664 M.D1L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1Y1C1K2P1I1A1Q2.N
		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p	2	4.5036	0.4281	2977.61	2979.27	1	681.2	43.75 M.D1L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1Y1C1K2P1I1A1Q2.N
		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in hucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p 5-phospho-ribosyl-1/alpha)-pyrophosphate synthetase, involved in nucleotide	2	4.5994	0.3894	2948.73	2948.27	1	534.1	39.583336 M.DLHDPQFPGFFDIPVDNLYCKPIAQ.N
		histidine, and tryptophan biosynthesis; one of a five related enzymes, which are								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p 5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide.	3	4.7069	0.2711	3111.77	3111.463	1	2271.7	39 T.M1D1L1H3D1P1Q2F1P1G1F1F1D111P1V1D1N2L1Y1C1K2P111A1Q2.N
		histidine, and tryptophan biosynthesis; one of a five related enzymes, which are								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p 5-phospho-ribosvl-1(alpha)-pvrophosphate svnthetase, involved in nucleotide.	2	3.1066	0.3388	2862.35	2863.182	1	188.4	36.95652 D.L1H3D1P1Q2F1P1G1F1F1D11P1V1D1N2L1Y1C1K2P1I1A1Q2.N
-102045441	VOLOCAW	histidine, and tryptophan biosynthesis; one of a five related enzymes, which are	2	2 0 4 0 7	0.0405	2022.04	0000 400		C 42 0	
gil6324511[rei]NP_014560.1]	TOLUGIW	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide,	2	3.8407	0.3425	2632.01	2033.102	1	643.8	43.47826 D.LEDPQFPGFFDIPVDNLTCKPIAQ.N
ail63245111refINP_014580_1	YOI 061W	histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as beteromultimeric complexes; Prs5p.	2	3 4386	0 2283	2138 25	2137 334	1	369.8	42 105263 Q H3R4I1P1D1Y1Q2D1A1V1I1V1S1P1D1A1G1G1A1K2 R
gilooz io i filoifi i _o i looo.if	10200111	5-phospho-ribosyl-1 (alpha)-pyrophosphate synthetase, involved in nucleotide,	-	0.1000	0.2200	2100.20	2101.001	•	000.0	
gi 6324511 ref NP 014580.1	YOL061W	histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	3	4.8645	0.3309	2862.05	2863.182	1	788	28.260868 D.L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1Y1C1K2P1I1A1Q2.N
		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide,								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p	3	4.8069	0.2658	2832.38	2833.182	1	811.7	28.260868 D.LHDPQFPGFFDIPVDNLYCKPIAQ.N
		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptonban biosynthesis; one of a five related enzymes, which are								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p	2	3.5342	0.2423	1584.51	1582.809	1	1007.7	69.230774 K.G1A1P1I1I1S1K2P1K2E1N2Y1T1F1.E
		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p	2	4.2977	0.3872	2380.55	2381.624	1	438.6	42.857143 Y.I1Q2H3R4I1P1D1Y1Q2D1A1V1I1V1S1P1D1A1G1G1A1K2.R
		histidine, and tryptophan biosynthesis; one of a five related enzymes, which are								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p	2	3.9372	0.3744	2353.67	2351.624	1	565.1	45.238094 Y.IQHRIPDYQDAVIVSPDAGGAK.R
		histidine, and tryptophan biosynthesis; one of a five related enzymes, which are								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p 5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide.	2	3.3338	0.1957	2108.25	2109.296	3	447	47.058823 M.D1L1H3D1P1Q2F1P1G1F1F1D111P1V1D1N2L1.Y
	VOI 004144	histidine, and tryptophan biosynthesis; one of a five related enzymes, which are		0.0075	0.0400	400457	4000 007		700.0	
gi 6324511 ret NP_014580.1	YOL061W	S-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide,	2	3.6375	0.3198	1994.57	1993.207	1	783.9	65.625 D.L1H3D1P1Q2F1P1G1F1F1D111P1V1D1N2L1.Y
ail63245111rofIND_014580_1	VOI 061W	histidine, and tryptophan biosynthesis; one of a five related enzymes, which are	2	3 0501	0 171	1550.23	1550 857	1	535 5	61 539464 L S1E1S1P411P1M11P1C1C1C1K2L1O2 N
gil03243111ieijini _014300.1j	IOLOOIW	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide,	2	3.0301	0.171	1330.23	1550.657		333.5	
ail63245111refINP_014580.11	YOL061W	histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	4.3569	0.475	2273.53	2273.472	1	874	61.11111 M.D1L1H3D1P1Q2E1P1G1E1E1D11P1V1D1N2L1Y1.C
24		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide,								
gi 6324511 ref NP_014580.1	YOL061W	active as heteromultimeric complexes; Prs5p	2	3.7636	0.4117	2250.63	2250.472	1	587.5	52.77778 M.DLHDPQFPGFFDIPVDNLY.C
ail6324510/refINP_014579_1	YOL 062C	Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in vesicle transport: Apm4p	2	3 2234	0 2721	1715 73	1716.02	1	436.7	57 14286 N HILFEVPPDGSMELM K
gilooz iorolioitii _orioro.ii	1020020	Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in	-	0.2201	0.2721		11 10:02	•	100.1	
gi 6324510 ref NP_014579.1	YOL062C	vesicle transport; Apm4p Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in	2	3.163	0.3143	1738.45	1737.934	7	238.2	50 N.G1H3C1K2F1V1P1E1E1N2A1M111W2.R
gi 6324510 ref NP_014579.1	YOL062C	vesicle transport; Apm4p	2	3.4399	0.2415	2101.43	2100.415	1	456.7	52.941177 F.NRNHIIEFVPPDGSMELM.K
gi 6324510 ref NP_014579.1	YOL062C	vesicle transport; Apm4p	2	4.2439	0.3553	2124.07	2125.415	1	489.5	55.88235 F.N2R4N2H3I1I1E1F1V1P1P1D1G1S1M1E1L1M1.K
		Nucleolar protein, constituent of 66S pre-ribosomal particles; depletion leads to								
gi 6324496 ref NP_014565.1	YOL077C	possesses a sigma(70)-like RNA-binding motif; Brx1p	3	4.4214	0.2622	2580.89	2579.723	1	902.7	35.714287 S.T1K2N2K2E1E1Y1E1D1G1E1E1D111S1L1V1E1I1G1P1R4.F
		Nucleolar protein, constituent of 66S pre-ribosomal particles; depletion leads to defects in rRNA processing and a block in the assembly of large ribosomal subunits:								
gi 6324496 ref NP_014565.1	YOL077C	possesses a sigma(70)-like RNA-binding motif; Brx1p	2	4.2096	0.3728	2320.91	2322.444	1	428.6	44.736843 K.NKEEYEDGEEDISLVEIGPR.F
		defects in rRNA processing and a block in the assembly of large ribosomal subunits;								
gi 6324496 ref NP_014565.1	YOL077C	possesses a sigma(70)-like RNA-binding motif; Brx1p	2	5.2044	0.3812	2579.69	2579.723	1	1076.5	54.761906 S.T1K2N2K2E1E1Y1E1D1G1E1E1D1I1S1L1V1E1I1G1P1R4.F
		defects in rRNA processing and a block in the assembly of large ribosomal subunits;								
gi 6324496 ref NP_014565.1	YOL077C	possesses a sigma(70)-like RNA-binding motif; Brx1p Nucleolar protein, constituent of 66S pre-ribosomal particles: depletion leads to	2	3.3288	0.3076	1999.65	1999.092	8	315.6	43.75 S.TKNKEEYEDGEEDISLV.E
		defects in rRNA processing and a block in the assembly of large ribosomal subunits;								
gi 6324496 ret NP_014565.1	YOLUTTC	possesses a sigma(70)-like RNA-binding motif; Brx1p	2	6.1441	0.4423	25/8./3	2579.723	1	1756.9	64.285/1 S.11K2N2K2E1E1Y1E1D1G1E1E1D111S1L1V1E111G1P1K4.F
		GTPase-activating protein that negatively regulates RAS by converting it from the								
gi 6324491 ref NP_014560.1	YOL081W	nutrient limiting conditions, has similarity to Ira1p and human neurofibromin; Ira2p	2	3.2377	0.3463	1598.65	1597.762	1	619.2	68.181816 Q.C1Q2W2L1N2Y1P1D1L1L1T1R4.E
		GTPase-activating protein that negatively regulates RAS by converting it from the								
ail62244041rofIND_044560.41		GTP- to the GDP-bound inactive form, required for reducing cAMP levels under	2	2 0008	0.2602	2050.01	2061 252	2	227.0	
9il002449111811NP_014000.1	1 OLUG I W	noment immung conditions, has similarity to traitp and numari neurolibromini, irazp	2	2.9900	0.2003	2009.91	2001.252	2	331.8	40.070 H.F ID0R40 IF IETVITIVIE IETUITITITETUITITETUITITETUI
		GTPase-activating protein that negatively regulates RAS by converting it from the GTP- to the GDP-bound inactive form, required for reducing cAMP levels under								
gi 6324491 ref NP_014560.1	YOL081W	nutrient limiting conditions, has similarity to Ira1p and human neurofibromin; Ira2p	2	3.1399	0.1708	1580.47	1579.762	1	703	68.181816 Q.CQWLNYPDLLTR.E
gij6324489[ref]NP_014558.1] gij6324489[ref]NP_014558.1]	YOL083W YOL083W	nypotneucai protein; Yol083wp hypothetical protein; Yol083wp	2	2.969	0.2708	1990.43 2009.61	1991.388 2010.388	1 7	569.9 337.4	OU N.KUILPEDKPELIKFF.S 40 K.K2C1111L1P1E1D1K2P1E1L111K2F1F1.S
gi 6324489 ref NP_014558.1	YOL083W	hypothetical protein; Yol083wp	2	3.471	0.3212	1778.19	1779.073	1	724.7	57.14286 K.G1Q2K2E1L1W2F1F1P1S1L1P1T1P1L1.S
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	3.3605	0.3635	1423.97	1424.523	1	563.7	58.333332 L.G1I1D1G1G1E1G1K2E1E1L1F1R4.S

		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
ail6324486/rofIND_014555_11		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	3	4 0204	0 3432	1626 17	1626 761	1	1088.4	51 795713 L C1I1D1C1C1C1E1C1K2E1E11 1E1D4S111 C
gilo244001e114F_014555.1	TOLUGOC	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	3	4.0204	0.3432	1020.17	1020.701		1000.4	51.765713 L.GIIIDIGIGIEIGIKZETETETETETETK45111.G
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol debydrogenase, fermentative isozyme active as homo, or beterotetramers;	2	4.4459	0.4291	2097.51	2097.289	1	666	52.63158 L.GIDGGEGKEELFRSIGGEVF.I
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	1	3.259	0.2044	1515.77	1516.75	1	228.8	62.5 L.E1Y1K2D1I1P1V1P1K2P1K2A1N2.E
		Alconol denydrogenase, termentative isozyme active as nomo- or neterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	2.9051	0.1964	2101.75	2103.419	1	453.7	44.11765 L.S1T1L1P1E1I1Y1E1K2M1E1K2G1Q2I1V1G1R4.Y
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
gil6324486/refINP 014555.1	YOL086C	pathway: Adh1p	1	2,7292	0.3167	1387.61	1388.653	2	365.1	54.545456 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
31		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
ail6224496IrofIND_044666_41	VOLOREC	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	1	2 5024	0 2201	1371.66	1070 650	1	400 E	
gilo224400[rei]inF_014555.1]	TOLUGOC	Alcohol dehvdrogenase, fermentative isozvme active as homo- or heterotetramers;	1	2.3024	0.3201	1371.00	1372.033		420.0	39.090906 W.HODWFLFVRLFL.V
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol debudrogenase, fermentative isozume active as homo- or beterotetramers;	1	2.586	0.2784	1051.64	1052.335	1	367.8	61.11111 R.G1L1V1K2S1P1I1K2V1V1.G
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	4.0213	0.1743	1373.51	1372.653	2	903.2	77.27273 W.HGDWPLPVKLPL.V
		Alconol denydrogenase, termentative isozyme active as nomo- or neterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the divcolvtic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	3.9028	0.3171	1389.17	1388.653	1	913.2	77.27273 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
gil6324486/refINP_014555.1	YOL086C	required for the reduction of acetaidenyde to ethanol, the last step in the glycolytic pathway: Adh1p	2	3.3747	0.5021	1526.81	1528.838	1	977.8	61.538464 W.HGDWPLPVKLPLVG.G
3.1		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	-					-		
	VOLABOO	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic		2 0 7 5	0 5040	4504.04	4505 000		744 5	
gilo324466[rei]NP_014555.1]	TOLUBBC	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	1	3.0275	0.5242	1064.01	1282.889	1	/11.5	60.714287 W.HGDWPLPVKLPLVGG.H
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol debudrogenase, fermentative isozume active as homo- or beterotetramers;	1	3.9187	0.3257	1548.73	1546.838	1	763.7	65.38461 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	1	4.2403	0.196	1530.76	1528.838	1	669.9	61.538464 W.HGDWPLPVKLPLVG.G
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the divcolutio								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	4.0285	0.3654	1544.83	1546.838	1	1584	73.07692 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
gil6324486/refINP 014555.1	YOL086C	required for the reduction of acetaidenyde to ethanol, the last step in the glycolytic pathway: Adh1p	1	2.2786	0.2622	1209.63	1210.546	2	391.8	54.545456 R.GLVKSPIKVVGLS
31002 1 1001 01 11 _01 10001 1	1020000	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	•	2.2700	0.LOLL	1200.00	12101010	-	00110	
	201 0000	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic		4 4000	0.0070	1007 50	4007.004		757.0	
gi 6324486 ret NP_014555.1	YOL086C	patnway; Adn1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers:	2	4.1809	0.3378	1807.53	1807.084	1	/5/.9	59.375 G.D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.G
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alashal dahudragangga, formantativa isastuma activa sa hama, ar hataratatramara:	2	4.213	0.3331	2061.67	2063.329	1	950.3	52.63158 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1.V
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	3.393	0.1672	2035.93	2037.329	1	929.2	52.63158 W.HGDWPLPVKLPLVGGHEGAG.V
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the divcolutio								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	1	3.1869	0.2966	1502.89	1502.782	2	347.7	50 W.P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.G
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
gil6324486/refINP_014555.1	YOL086C	required for the reduction of acetaidenyde to ethanol, the last step in the glycolytic pathway: Adh1p	2	4.0856	0.2109	1911.37	1909,198	2	635.3	50 W.HGDWPLPVKLPLVGGHEG.A
3.1		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	-					_		
	VOLABOO	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	0	5 2000	0 5400	4070 75	4075 440		0700.0	
gilo324466[rei]NP_014555.1]	TOLUBBC	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	5.3908	0.5128	18/2./5	1875.146	1	2720.6	78.125 W.H3G1D1W2P1E1P1V1K2E1P1E1V1G1G1H3E1.G
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol debydrogenase, fermentative isozyme active as homo, or beterotetramers;	2	3.9274	0.3104	1933.63	1933.198	1	968.1	55.88235 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1.A
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	5.3715	0.1849	2164.61	2163.461	1	1184.9	57.5 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.V
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the divcolutio								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	3	6.2355	0.4098	1872.29	1875.146	1	2287.5	59.375 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
gi 6324486 ref NP 014555.1	YOL086C	pathway; Adh1p	2	4.9812	0.2428	2135.53	2136.461	1	1256.1	57.5 W.HGDWPLPVKLPLVGGHEGAGV.V
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
gil6324486lrofINP_014555_1	YOI 086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	3	4 4151	0 2057	2163 32	2163.461	1	925.3	36 25 W H3G1D1W2P1I 1P1V1K2I 1P1I 1V1G1G1H3E1G1A1G1V1 V
gilosz4400/10/14/ _014000.1/	1020000	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	0	4.4101	0.2007	2100.02	2100.401		525.5	
	201 0000	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic		4 5000	0.0000	0400.44	0100 101		4474.0	
gi 6324486 ret NP_014555.1	YOL086C	patnway; Adn1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers:	3	4.5296	0.2323	2136.11	2136.461	1	1171.9	40 W.HGDWPLPVKLPLVGGHEGAGV.V
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol debudrogenase, fermentative isozume active as home- or beteretetromore:	2	3.2336	0.3097	2260.61	2263.594	1	339.1	35.714287 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1V1.V
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	4.3629	0.2311	2334.91	2334.726	1	606.5	45.454548 W.HGDWPLPVKLPLVGGHEGAGVVV.G
		Accorol denydrogenase, termentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the alveolvtic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	3.5639	0.3331	1406.73	1407.523	1	701.2	62.5 L.GIDGGEGKEELFR.S

		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers:	2	3.3694	0.3433	1607.43	1607.761	1	552.1	57.14286 L.GIDGGEGKEELFRSI.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	2	4.1663	0.3509	1628.47	1626.761	1	629.9	57.14286 L.G1I1D1G1G1E1G1K2E1E1L1F1R4S1I1.G
gi 6324486 ref NP_014555.1	YOL086C	Alcohol dehydrogenase, termentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	2	4.1478	0.3979	1875.85	1872.98	1	540.4	52.941177 L.G1I1D1G1G1E1G1K2E1E1L1F1R4S1I1G1G1E1.V
gi 6324486 ref NP_014555.1	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	2	3.0165	0.2792	2118.43	2121.289	1	352.6	36.842106 L.G1I1D1G1G1E1G1K2E1E1L1F1R4S1I1G1G1E1V1F1.I
ail6324486lrefINP_014555.1	YOI 086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathwarv. And the	1	2 2794	0 2457	1039.63	1040 335	2	371.2	
	1020000	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic		0.5004	0.2107	1000.00	4070.050	-	404.7	
gilb324486 ret NP_014555.1	YOLU86C	partway; Adh tp Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	1	2.5284	0.2438	1371.68	1372.653	1	491.7	63.636364 W.HGDWPLPVKLPL.V
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the dycolvtic	1	2.8215	0.2997	1387.71	1388.653	1	473.3	63.636364 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of actal dehydra to othanol, the last stop in the alcoholic	2	4.1543	0.2945	1389.27	1388.653	1	794.6	72.72727 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	3.2467	0.4238	1584.61	1585.889	1	754.8	53.571426 W.HGDWPLPVKLPLVGG.H
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	4.5673	0.3791	1602.57	1604.889	1	1399.2	67.85714 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1.H
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	1	3.8202	0.4412	1527.82	1528.838	1	830.4	65.38461 W.HGDWPLPVKLPLVG.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	1	4.0913	0.34	1547.81	1546.838	1	934.5	69.230774 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh 1p Alcohol dehydropenase fermentative isozyme active as homo- or heterotetramers:	2	3.7892	0.311	1546.45	1546.838	2	1584	73.07692 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway: Adh1p Acebel dehydrogenese, formentative issume active as home, or beterstetramers:	2	3.6967	0.1943	1528.03	1528.838	2	1105.1	65.38461 W.HGDWPLPVKLPLVG.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	1	2.6647	0.1672	1223.68	1224.546	2	398.2	54.545456 R.G1L1V1K2S1P111K2V1V1G1L1.S
gi 6324486 ref NP_014555.1	YOL086C	Alcohol dehydrogenase, termentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	2	3.69	0.2842	1371.73	1372.653	4	575.6	63.636364 W.HGDWPLPVKLPL.V
gi 6324486 ref NP_014555.1	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	2	3.0099	0.2501	1788.35	1786.084	1	417.7	50 G.DWPLPVKLPLVGGHEGA.G
ail6324486 refINP 014555.1	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway: Adh to	2	3.5887	0.2915	1820.81	1819.136	1	635.3	60.000004 H.G1K2L1E1Y1K2D1I1P1V1P1K2P1K2A1N2.E
gil6324486/refINP_014555_1	YOI 086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic nathway. 4dd 10	2	4 7241	0.4506	1979.05	1980 277	1	1216.4	
	1010000	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	4.7241	0.4000	0005.00	0005.077		1210.4	
gi 6324486 ret NP_014555.1	YOL086C	pathway; Adh 1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	3	6.2768	0.1857	2005.28	2005.277	1	1495.5	47.22222 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.G
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	3	4.4812	0.1615	1722.65	1723.031	3	1188.6	43.333332 W.HGDWPLPVKLPLVGGH.E
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	5.0083	0.4635	1872.73	1875.146	1	2044.3	71.875 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the divolutio	2	4.8911	0.4199	1743.59	1745.031	1	1408.3	66.66667 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E
gi 6324486 ref NP_014555.1	YOL086C	Pathway: Adh 1p Alcohol de hydrogenase, fermentative isozyme active as homo- or heterotetramers; reveloted repto adhadation of a cetabetrian and a set of the transmission of the transmission of the set of the transmission of t	2	5.0732	0.4569	1850.97	1852.146	1	2194.1	75 W.HGDWPLPVKLPLVGGHE.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldenyde to errariol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	4.851	0.2868	1722.53	1723.031	1	2158.6	76.666664 W.HGDWPLPVKLPLVGGH.E
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	3	6.3864	0.463	1872.47	1875.146	1	1846.9	53.125 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	4.8889	0.4433	2160.73	2163.461	1	1124.1	57.5 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.V
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh J, Adh All and Al	2	5.0006	0.1972	2136.17	2136.461	1	1036.8	55 W.HGDWPLPVKLPLVGGHEGAGV.V
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh tp Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers:	3	5.9524	0.4437	1849.85	1852.146	1	2719.1	62.5 W.HGDWPLPVKLPLVGGHE.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	3	5.2536	0.3403	1742.9	1745.031	1	1579.1	51.666664 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E

gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway: Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	3.1536	0.2337	1560.89	1560.864	1	834.4	65.38461 D.W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	3	4.8128	0.1633	1982	1980.277	1	962.6	41.666664 W.HGDWPLPVKLPLVGGHEGA.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	4.8422	0.3295	2004.39	2005.277	1	1530.1	63.88889 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	3	4.9838	0.2384	2262.86	2263.594	1	939.3	38.095238 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1V1.V
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	3	4.124	0.1777	2237.69	2235.594	2	669.2	33.333336 W.HGDWPLPVKLPLVGGHEGAGVV.V
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	2.9069	0.2938	1715.17	1715.005	5	354.1	50 H.GDWPLPVKLPLVGGHE.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	2	2.903	0.3122	1041.33	1040.335	6	576.7	77.77778 R.GLVKSPIKVV.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway: Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	1	2.7936	0.2432	1387.78	1388.653	1	406.1	59.090908 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of acetaloenyde to emanol, the last step in the glycolytic pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;	1	2.5366	0.3597	1371.62	1372.653	2	457.9	59.090908 W.HGDWPLPVKLPL.V
gi 6324486 ref NP_014555.1	YOL086C	required ior me reduction of actelationaryde to entantia, me last step in me glycorydc pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; rewind for the advision of actelatived to sthead, the left step is the advised this	2	4.3253	0.3016	1389.25	1388.653	1	964.5	77.27273 W.H3G1D1W2P1L1P1V1K2L1P1L1.V
gi 6324486 ref NP_014555.1	YOL086C	required to me doubtion of acceleration you to entando, the last step in the glycolytic pathway; Adh 1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; routined for the production of accelerative to pathway to abased the last torie in the alvecteding	1	4.0372	0.2692	1529.96	1528.838	1	702.8	61.538464 W.HGDWPLPVKLPLVG.G
gi 6324486 ref NP_014555.1	YOL086C	required for the reduction of a catalobergue to entand, the last step in the gypodyte pathway; Adh 1p Alcohol dehydrogenase, fermentative isozene active as homo- or heterotetramers; required for the reduction of a catalobergue to athaool, the last term in the divocibilit	1	3.2679	0.2435	1586.92	1585.889	1	406.5	46.42857 W.HGDWPLPVKLPLVGG.H
gi 6324486 ref NP_014555.1	YOL086C	Pathway; Adh tp Alcohol dehydrogenase, fermentative isozma active as homo- or heterotetramers; required for the reduction of a cataldehyde to ethanol. the last step in the dycolvic	2	3.4332	0.2331	1487.81	1488.786	1	1007.8	66.66667 W.H3G1D1W2P1L1P1V1K2L1P1L1V1.G
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehvde to ethanol. the last step in the divcolvtic	1	4.0023	0.3302	1547.6	1546.838	1	985.2	69.230774 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the divcolvtic	2	4.1249	0.3893	1584.69	1585.889	1	1560.6	71.42857 W.HGDWPLPVKLPLVGG.H
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	3.931	0.2191	1547.31	1546.838	2	1279.6	69.230774 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.G
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	3.9058	0.1778	1375.33	1372.653	4	664.6	68.181816 W.HGDWPLPVKLPL.V
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	3	4.426	0.2886	1797.2	1798.136	1	1553.2	46.666668 H.GKLEYKDIPVPKPKAN.E
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	3.5255	0.3463	1613.25	1612.953	1	1244.1	76.92308 H.GKLEYKDIPVPKPK.A
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	4.0178	0.1737	1528.61	1528.838	2	1290.1	69.230774 W.HGDWPLPVKLPLVG.G
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	5.166	0.5049	1873.97	1875.146	1	1755.5	65.625 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	5.2552	0.4408	2002.81	2005.277	1	1189.3	
gil6324486/rel/NP_014555.1	VOLOBEC	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic optimum, det no.	2	4.0330	0.4932	1/21.59	1952 146	1	2161.5	
gil6324486/refINP_014555.1	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic natiware. 4dh n	3	5 1465	0.4155	1981.67	1980 277	1	1548.3	
gil6324486/refINP_014555.1	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic nattway: Adh1n	2	5.0269	0.5071	1849.89	1852.146	1	3140.9	84.375 W HGDWPI PVKI PI VGGHE G
gil6324486lrefINP 014555.11	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway: Adh1p	3	6.0883	0.3685	1743.38	1745.031	1	1820.2	56.666668 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E
gi 6324486 ref NP_014555.1	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	2	4.5257	0.435	1978.47	1980.277	1	1250.1	61.11111 W.HGDWPLPVKLPLVGGHEGA.G
gi 6324486 ref NP_014555.1	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	3	5.9576	0.2427	2006.42	2005.277	1	1006.6	41.6666664 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.G
gi 6324486 ref NP_014555.1	YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	3	5.3805	0.2526	1723.46	1723.031	1	2156.4	60.000004 W.HGDWPLPVKLPLVGGH.E

Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;

		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
ail6224496IrofIND_014EEE_1		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	2	E 1661	0.2695	1746 20	1745 021	1	1501 1	
gil0324480[10]10F_014555.1]	TOLUGUC	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers:	2	5.1551	0.2005	1740.29	1745.031		1301.1	00.00007 W.H301D1W2F1E1F1V1K2E1F1E1V10101H3.E
		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	3	5.867	0.3839	1872.68	1875.146	1	1782.6	53.125 W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.G
		Alconol denydrogenase, termentative isozyme active as nomo- or neterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the alycolytic								
gi 6324486 ref NP_014555.1	YOL086C	pathway; Adh1p	2	4.015	0.3807	2135.43	2136.461	1	640.2	45 W.HGDWPLPVKLPLVGGHEGAGV.V
		Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers;								
ail6324486/rofINP_014555_1		required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic	3	1 3812	0 1753	2127 7	2136 461	1	016.0	
gil6324485/refINP_014554.1	YOL087C	hypothetical protein: Yol087cp	2	4.0447	0.4218	2352.45	2353.692	1	414.4	47.22222 N.EKKKPEEMPDLI EOIQESY.K
gi 6324485 ref NP_014554.1	YOL087C	hypothetical protein; Yol087cp	2	3.8639	0.3403	2376.29	2377.692	1	326.8	44.444447 N.E1K2K2K2P1E1F1M1P1D1L1L1E1Q2I1Q2E1S1Y1.K
gi 6324485 ref NP_014554.1	YOL087C	hypothetical protein; Yol087cp	3	4.9057	0.3589	2980.64	2982.346	1	659.8	31 A.S1D1K2A1I1D1D1S1L1E1L1V1Q2P1L1P1A1S1K2K2P1Y1F1R4T1Q2.S
gi 6324485 ref NP_014554.1	YOL087C	hypothetical protein; Yol087cp	2	4.008	0.3611	1831.51	1831.027	1	1053.2	68.75 A.S1D1K2A1I1D1D1S1L1E1L1V1Q2P1L1P1A1.S
ail6324485/refINP_014554.1	YOL087C	hypothetical protein; Yol087cp	2	3.9025	0.2631	2119.81	2119.512	1	481.4	41.666664 Q.DAHILPITKILYPDIPGKN.Y
gi 6324485 ref NP_014554.1	YOL087C	hypothetical protein; Yol087cp	2	3.3181	0.2256	1979.51	1979.379	1	694.5	46.875 H.I1L1P1I1T1K2I1L1Y1P1D1I1P1G1K2N2Y1.F
gi 6324485 ref NP_014554.1	YOL087C	hypothetical protein; Yol087cp	2	3.6541	0.3259	2280.93	2282.688	2	353.4	34.210526 Q.DAHILPITKILYPDIPGKNY.F
gilo324465[rei]NP_014554.1]	TULU8/C	Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity:	2	5.2599	0.2973	2308.13	2307.688	1	1211.2	57.694737 Q.DTATH3HETPTHTTR2HETPTDHTPTGTR2N211.F
		overexpression suppresses the lethality of a pdi1 deletion but does not complement								
gi 6324484 ref NP_014553.1	YOL088C	all Pdi1p functions; undergoes oxidation by Ero1p; Mpd2p	2	4.6703	0.3626	1874.47	1876.866	1	762.7	73.333336 L.S1H3I1E1D1Q2L1E1D1T1S1S1H3D1E1L1
		Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity;								
ail6324484/refINP 014553.1/	YOL088C	all Pdi1p functions: undergoes oxidation by Ero1p: Mpd2p	2	3.6437	0.3595	1625.27	1625.859	1	836	61.538464 C.KTLAPVYEELGELY.A
5100 111 _0 001		Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity;								
		overexpression suppresses the lethality of a pdi1 deletion but does not complement								
gi 6324484 ref NP_014553.1	YOL088C	all Pdi1p functions; undergoes oxidation by Ero1p; Mpd2p Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity;	2	3.4656	0.287	1967.19	1969.341	1	656.6	59.375 T.LCTDLPGFPIIELVKPR.T
		overexpression suppresses the lethality of a pdi1 deletion but does not complement								
gi 6324484 ref NP_014553.1	YOL088C	all Pdi1p functions; undergoes oxidation by Ero1p; Mpd2p	2	2.918	0.229	1312.25	1310.622	3	400.2	70 R.TKPLVLPKLDW.S
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	3	5.1749	0.37	3503.75	3501.8	1	828.8	27.586206 Q.CLWYDNEEKPAVDPIHLSPANPINENVLHD.V
gi 6324480 ret NP_014549.1 gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	2	3.566	0.2837	2929.51 3476 51	2930.229	1	244.6 1240.4	32 N.E1E1K2P1A1V1D1P111H3L1S1P1A1N2P111N2E1N2V1L1H3D1V1F1.N 33 62069 L WYDNEEKPAVDPIHLSPANPINENVLHDVE N
gil0324400[rei]i4r_014343.1]	10103210	nypotnetical protein, roloszwp	5	5.6700	0.0000	3470.31	3474.011		1240.4	C.L1W2Y1D1N2E1E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1V1F
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	3	6.3344	0.3975	3628.91	3628.97	1	1248.3	30.833334 1.N
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	3	4.0121	0.1723	4684.91	4685.129	7	195.3	15.384616 Q.CLWYDNEEKPAVDPIHLSPANPINENVLHDVFNEQQPLLN.S
gij6324480[ref]NP_014549.1] gij6324480[ref]NP_014549.1]	YOL092W	hypothetical protein; Yol092wp	2	4.4316	0.3091	2798 53	2800 114	1	536.6 478.7	24. 100000 C.LWYDNEERPAVDPIRLSPANPINENVLRDVF.N 39 583336 E E1K2P1A1V1D1P1I1H3I 1S1P1A1N2P1I1N2E1N2V1I 1H3D1V1E1 N
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	2	3.5214	0.3682	2765.89	2767.114	1	505.5	43.75 E.EKPAVDPIHLSPANPINENVLHDVF.N
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	3	4.3451	0.3486	2764.94	2767.114	1	396.6	28.125 E.EKPAVDPIHLSPANPINENVLHDVF.N
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	2	3.53	0.3284	2153.29	2153.407	1	608.2	50 D.P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1V1F1.N
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	3	6.8011	0.5094	3512.72	3514.811	1	1421.8	33.62069 L.W2Y1D1N2E1E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1V1F1.N
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	3	4.8149	0.424	3747.86	3748.109	1	1080.1	29.032257 Q.CLWYDNEEKPAVDPIHLSPANPINENVLHDVF.N
ail6324480/rofIND_014549_11		hypothetical protein: Vol092wp	3	5 9517	0 4743	3780 38	3700 100	1	1072.0	Q.C1L1W2Y1D1N2E1E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1\ 20.032257.1E1 N
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	3	4.6882	0.3799	4412.03	4411.831	1	588.5	20.945946 L.WYDNEEKPAVDPIHLSPANPINENVLHDVFNEQQPLLN.S
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	2	3.6553	0.3306	1845.45	1847.003	1	468.3	57.14286 L.W2Y1D1N2E1E1K2P1A1V1D1P1I1H3L1.S
gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	2	4.7289	0.39	2793.93	2795.98	1	607.4	45.652176 L.W2Y1D1N2E1E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2.V
gi 6324480 ref NP_014549.1 gi 6324480 ref NP_014549.1	YOL092W	hypothetical protein; Yol092wp	3	7.1836	0.4867	3265.73	3266.502 2800 114	1	1522.7	33.333336 L.W2Y1D1N2E1E1K2P1A1V1D1P111H3L1S1P1A1N2P111N2E1N2V1L1H3D1.V 30.208334 E E1K2P1A1V1D1P111H3L1S1P1A1N2P111N2E1N2V1L1H3D1V1E1 N
gilooz i loolioiliti _or lo loiil	10200211	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone	0	0.0202	0.001	2100.00	2000.111		0LL	
		(Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing								
gi 37362692 ref NP_014545.2	YOL096C	complex; Coq3p	2	4.7225	0.2682	1914.23	1915.224	1	992.1	66.66667 Q.V1K2I1Q2N2P1E1I1F1V1P1G1F1N2Y1K2.E
		(Coenzyme Q) biosynthesis: component of a mitochondrial ubiquinone-synthesizing								
gi 37362692 ref NP_014545.2	YOL096C	complex; Coq3p	2	4.8664	0.18	1894.83	1894.224	1	1307.4	76.666664 Q.VKIQNPEIFVPGFNYK.E
		O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone								
ail272626021rofIND 014545 21		(Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing	1	2 0 2 2	0 2220	1450 71	1460 710	2	226	
gij3/302092[lei]litF_014545.2]	TOL090C	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone	'	2.933	0.3329	1439.71	1400.719	2	320	59.090906 C.WSREINFERGIEF.L
		(Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing								
gi 37362692 ref NP_014545.2	YOL096C	complex; Coq3p	2	3.4731	0.2702	1512.61	1511.78	1	558.6	66.66667 A.KEHAKKDPMLEGK.I
		O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme O) biosynthesis: component of a mitochondrial ubiquinone-synthesizing								
gi 37362692 ref NP 014545.2	YOL096C	complex; Coq3p	2	3.2788	0.3448	1458.45	1460.719	1	835.8	68.181816 C.WSRLNPEKGILF.L
31		O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone								
	201 0000	(Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing		0 40 40	0.0500	4574 57	1570.070		740.0	
gi 37362692 ref NP_014545.2	YOL096C	complex; Coq3p	2	3.1343	0.2589	15/1.5/	1573.878	1	713.2	62.5 C.WSKLNPEKGILFL.S
		Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway								
		that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling								
gi 6324472 ref NP_014541.1	YOL100W	cascade required for maintenance of cell wall integrity; redundant with Pkh1p; Pkh2p	2	3.2766	0.324	2032.55	2032.481	1	792.5	50 S.KVPMPPYTPPMSPPMTPY.D
		Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway								
		that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling								
gi 6324472 ref NP_014541.1	YOL100W	cascade required for maintenance of cell wall integrity; redundant with Pkh1p; Pkh2p	2	4.4642	0.4502	1639.83	1640.935	1	672.8	69.230774 Q.Y1A1F1T1P1G1F1P1L1I1I1R4D1L1.V
		Serine/threonine protein kinase involved in sphingolinid-mediated signaling pathway								
		that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling								
gi 6324472 ref NP_014541.1	YOL100W	cascade required for maintenance of cell wall integrity; redundant with Pkh1p; Pkh2p	2	3.1467	0.2377	2225.97	2227.638	2	343	39.473686 L.S1S1K2V1P1M1P1P1Y1T1P1P1M1S1P1P1M1T1P1Y1.D
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating can-dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP 014502.1	YOL139C	initiation factor elF4G (Tif4631p or Tif4632p); Cdc33p	1	3.1313	0.371	1573.52	1574.718	1	497.9	66.66667 L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for								
ail62044221rofIND_044500_1	VOI 1000	mediating cap-dependent mRNA translation via interactions with the translation	4	2 000	0.444	1665 54	1666 740		E04 C	
gij0324433[rei]NP_014502.1]	1011390	initiation raciol ell'4G (1114031) or 1114032p); CCC33p	1	2.926	0.411	1000.51	1000./18	1	0.1≤C	00.00007 L.KLIDDGHLEFFFH.3

		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for								
gi 6324433 ref NP_014502.1	YOL139C	mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	3	4.5575	0.3186	1574.99	1574.718	1	1222.9	54.166668 L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.8263	0.5098	1554.25	1556.718	1	1214	83.33333 L.KLTDDGHLEFFPH.S
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.4462	0.2587	2034.59	2036.294	1	599.4	56.25 Q.NIPEPHELPLKSDYHVF.R
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediation cap dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.6626	0.3066	2712.83	2714.05	1	566.4	40.909092 L.WYTKPAVDKSESWSDLLRPVTSF.Q
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.638	0.3027	1425.89	1426.615	1	668.5	72.72727 S.A1H3F1D1V1K2H3P1L1N2T1K2.W
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	4.6892	0.3071	1782.79	1781.914	1	1320.2	76.666664 K.KFEENVSVDDTTATPK.T
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediation cap dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	3	3.8163	0.3017	1574.72	1574.718	1	862.1	50 L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediation cap dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.4852	0.3121	1391.45	1390.552	1	1209.3	77.27273 R.G1K2G1A1D111D1E1L1W2L1R4.T
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediation cap dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	4.4975	0.4601	1576.21	1574.718	1	1249.6	83.33333 L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.7892	0.3643	1573.61	1574.718	1	442.2	62.5 L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.6958	0.4083	1555.77	1556.718	1	506.6	62.5 L.KLTDDGHLEFFPH.S
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediation cap dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	4.0793	0.3062	2059.05	2059.295	1	665.8	56.25 Q.N2I1P1E1P1H3E1L1P1L1K2S1D1Y1H3V1F1.R
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	2.9857	0.1678	1078.59	1078.232	4	734.2	81.25 S.A1H3F1D1V1K2H3P1L1.N
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor elF4G (Tif4631p or Tif4632p); Cdc33p	1	2.3949	0.2696	1257.45	1257.429	6	285.5	55 K.SEDKEPLLRIG.G
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.6665	0.1577	1005.35	1006.153	9	258.7	78.57143 A.H3F1D1V1K2H3P1L1.N
		Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation								
gi 6324433 ref NP_014502.1	YOL139C	initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.7564	0.2369	992.39	993.153	9	263.4	78.57143 A.HFDVKHPL.N
		Endosomal terric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by								
gi 6324415 ref NP_014484.1	YOL158C	Rcs1p and affected by chloroquine treatment; Enb1p	2	3.3757	0.17	1107.57	1108.366	9	688.4	81.25 A.G1G1M1I1R4F1P1M1W2.T
		deprivation; member of the major facilitator superfamily; expression is regulated by								
gi 6324415 ref NP_014484.1	YOL158C	Rcs1p and affected by chloroquine treatment; Enb1p	2	3.9292	0.1811	1824.75	1826.898	8	771.9	67.85714M1L1E1T1D1H3S1R4N2D1N2L1D1D1K2.S
		deprivation; member of the major facilitator superfamily; expression is regulated by								
gi 6324415 ref NP_014484.1	YOL158C	Rcs1p and affected by chloroquine treatment; Enb1p	2	4.1986	0.3064	2144.53	2146.16	1	596.8	52.941177 M.L1E1T1D1H3S1R4N2D1N2L1D1D1K2S1T1V1C1.Y
		deprivation; member of the major facilitator superfamily; expression is regulated by								
gi 6324415 ref NP_014484.1	YOL158C	Rcs1p and affected by chloroquine treatment; Enb1p Endocomal farric enterchartin transporter, expressed upder conditions of iron	2	4.2443	0.3224	2278.11	2278.353	1	835.2	52.77778M1L1E1T1D1H3S1R4N2D1N2L1D1D1K2S1T1V1C1.Y
		deprivation; member of the major facilitator superfamily; expression is regulated by								
gi 6324415 ref NP_014484.1	YOL158C	Rcs1p and affected by chloroquine treatment; Enb1p Endosomal ferric enterobactin transporter, expressed under conditions of iron	2	3.4924	0.2315	2252.17	2251.353	1	689	50MLETDHSRNDNLDDKSTVC.Y
		deprivation; member of the major facilitator superfamily; expression is regulated by								
gi 6324415 ref NP_014484.1	YOL158C	Rcs1p and affected by chloroquine treatment; Enb1p Endosomal ferric enterobactin transporter, expressed under conditions of iron	3	3.8086	0.2974	2441.51	2442.529	1	1091.6	38.157894M1L1E1T1D1H3S1R4N2D1N2L1D1D1K2S1T1V1C1Y1.S
		deprivation; member of the major facilitator superfamily; expression is regulated by								
gi 6324415 ref NP_014484.1	YOL158C	Rcs1p and affected by chloroquine treatment; Enb1p Endosomal ferric enterobactin transporter, expressed under conditions of iron	2	4.5	0.454	2696.23	2698.009	1	1005.7	42 S.T1T1H3N2E1M1A1T1V1T1G1L1L1M1S1V1Y1Q2I1G1D1A1V1G1A1S1.I
		deprivation; member of the major facilitator superfamily; expression is regulated by								
gi 6324415 ref NP_014484.1	YOL158C	Rcs1p and affected by chloroquine treatment; Enb1p Endosomal ferric enterobactin transporter, expressed under conditions of iron	2	5.1993	0.4917	2608.47	2609.931	1	1360.2	47.916664 S.T1T1H3N2E1M1A1T1V1T1G1L1L1M1S1V1Y1Q2I1G1D1A1V1G1A1.S
-10224445161010-04440441	VOI 4590	deprivation; member of the major facilitator superfamily; expression is regulated by	2	0.4000	0 4040	4000.05	4000 000	4	c22.2	
gilo324415/rei/iNP_014464.1/	TULISBU	Endosomal ferric enterobactin transporter, expressed under conditions of iron	2	3.4229	0.4019	1062.00	1083.092	1	033.3	65.36461 D.H351K4N2D1N2L1D1D1K25111V1C1.1
ail622441ElrofIND_014494_1	VOI 1590	deprivation; member of the major facilitator superfamily; expression is regulated by	2	2 2016	0 2277	1500.95	1510 969	1	075	66 66667 C 14 41C1 C 1M11/10 4E4 D 1M1W/2T41 4 V
giloszarioliciliai _orada.ii	TOETODO	Endosomal ferric enterobactin transporter, expressed under conditions of iron	2	0.2010	0.2011	1000.00	1010.000		515	
gil6324415/refINP_014484_1	YOI 158C	deprivation; member of the major facilitator superfamily; expression is regulated by Restp and affected by chloroguine treatment: Ephtp.	1	2 4263	0 1592	1051 43	1052 225	1	418.5	71 42857 M I 1H3F1Y1P1H3P1K2 V
gilooz i riolioilui _orrio ilii	1021000	Endosomal ferric enterobactin transporter, expressed under conditions of iron	·	2.1200	0.1002	1001110	1002.220	•	110.0	
gi 6324415 ref NP 014484.1	YOL158C	deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment: Enb1p	2	3.4609	0.2672	1428.21	1430.688	4	304.3	70 A.EEREKEKLKIK.Q
or			-							
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component or the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	4.1723	0.2697	3018.65	3020.081	3	418.6	27.173912 L.R4L1V1D1D1D1E1N2N2P1S1H3Y1P1H3P1Y1E1Y1E1I1D1H3Q2.E
		Exonuclease component of the nuclear exosome: contributes to the quality-control								
gi 6324574 ref NP_014643.1	YOR001W	system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.903	0.2801	2433.57	2433.869	1	527	37.5 L.A1N2L1E1D11111F1E111E1K2P1L1V1V1P1V1K2L1E1.E

gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.6708	0.2715	2208.33	2209.675	1	632.6	44.444447 A.NLEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	4.3302	0.2125	2231.72	2231.675	3	725	41.6666664 A.N2L1E1D11111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	4.2347	0.2228	2209.52	2209.675	1	941.9	43.055553 A.NLEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	4.2582	0.3717	2546.35	2548.028	1	570.9	40.476192 A.L1A1N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1E1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	4.464	0.345	2523.79	2523.028	1	1183.6	52.380955 A.LANLEDIIFEIEKPLVVPVKLE.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.3939	0.1997	1853.29	1853.296	1	579	50 E.DIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.3145	0.2535	1870.79	1871.296	1	562.2	50 E.D1111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.2955	0.2672	1983.93	1982.411	3	447.1	46.875 L.EDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	4.3185	0.3658	2097.59	2095.571	1	1072.8	55.88235 N.LEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	4.7939	0.3578	2924.66	2922.477	1	963.9	29.166666 A.L1A1N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1E1E111K2.T
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.9493	0.1931	2230.53	2231.675	1	541.6	41.6666664 A.N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	3.9793	0.2288	2393.03	2393.913	1	872.3	37.5 A.LANLEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	5.172	0.3563	2420.42	2417.913	1	1151.3	42.5 A.L1A1N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	4.7263	0.2663	2395.65	2393.913	1	815.1	47.5 A.LANLEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	4.2705	0.2439	2894.69	2893.477	3	753.9	26.041666 A.LANLEDIIFEIEKPLVVPVKLEEIK.T
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	4.1628	0.2094	3410.12	3410.999	1	548.8	23.275862 A.L1A1N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1E1E111K2T1V1D1P1A1.S
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	4.7469	0.3116	2416.03	2417.913	1	964.6	45 A.L1A1N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.0471	0.1947	2077.81	2077.299	1	210.4	44.444447 A.SAPNHSPEIDNLDDLVVLK.K
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.6432	0.2495	2114.31	2115.571	1	971.8	50 N.L1E1D11111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	4.3325	0.2214	3295.94	3296.839	1	482.1	25 L.A1N2L1E1D11111F1E111E1K2P1L1V1V1P1V1K2L1E1E111K2T1V1D1P1A1.S
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	4.2699	0.284	2230.39	2231.675	1	867.1	52.77778 A.N2L1E1D11111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	5.2624	0.3266	2211.17	2209.675	1	1016.2	44.444447 A.NLEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	4.889	0.3808	2210.83	2209.675	1	1064.7	55.555557 A.NLEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	5.0894	0.4421	2521.85	2523.028	1	865.4	34.523808 A.LANLEDIIFEIEKPLVVPVKLE.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	6.1746	0.448	2545.52	2548.028	1	1316.3	39.285713 A.L1A1N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1E1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	5.0874	0.3758	2393.75	2393.913	1	999.5	41.25 A.LANLEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	5.0273	0.2605	2394.49	2393.913	1	1058.9	50 A.LANLEDIIFEIEKPLVVPVKL.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	5.5898	0.3519	2417.65	2417.913	1	1703.3	60.000004 A.L1A1N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	4.3921	0.23	2418.47	2417.913	1	776.9	37.5 A.L1A1N2L1E1D1111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	2	3.438	0.2348	2117.69	2115.571	1	557	47.058823 N.L1E1D11111F1E111E1K2P1L1V1V1P1V1K2L1.E

gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	3	5.2449	0.3574	2117.36	2115.571	1	1313.9	44.11765 N.L1E1D11111F1E111E1K2P1L1V1V1P1V1K2L1.E
gi 6324574 ref NP_014643.1	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl	1	2.6738	0.1855	1265.51	1266.555	1	423.9	65 L.L1K2E1K2P1N2A1L1K2P1L1.S
gi 6324575 ref NP_014644.1	YOR002W	pyrophosphate to asparagine residues of proteins during N-linked protein glycosylation; mutations in human ortholog are associated with disease; Alg6p Glucosyltransferase, involved in transfer of oligosaccharides from dolicityl	2	3.5816	0.3771	1814.13	1815.076	1	620.6	63.333332 R.L1L1V1N2K2P1A1E1E1S1F1Y1A1S1P1M1.Y
gi 6324575 ref NP_014644.1	YOR002W	pyrophosphate to asparagine residues of proteins during N-linked protein glycosylation; mutations in human ortholog are associated with disease; Alg6p Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl	2	3.1898	0.1878	1590.27	1593.032	6	360.9	53.846157 H.E1K2T1I1L1I1P1L1L1P1I1T1L1L1.Y
gi 6324575 ref NP_014644.1	YOR002W	pyrophosphate to asparagine residues or proteins during v-inited protein glycosylation; mutations in human ortholog are associated with disease; Alg6p Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl evrophosphate to asparagine residues of proteins during Nulriked northin	2	3.9602	0.2874	1579.59	1578.032	1	577.8	65.38461 H.EKTILIPLLPITLL.Y
gi 6324575 ref NP_014644.1	YOR002W	py oprinciplinate routparticipante reasonable of hip operations outling in which proteins a glycosylation; mutations in human orthogo are associated with disease; Alg6p Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparatione residues of proteins during N-linked rortein	2	3.9967	0.2892	1479.37	1478.872	1	539.4	70.83333 H.E1K2T111L111P1L1L1P111T1L1.L
gi 6324575 ref NP_014644.1	YOR002W	glycosylation; mutations in human ortholog are associated with disease; Alg6p	2	3.6399	0.3622	1466.57	1464.872	1	678	75 H.EKTILIPLLPITL.L
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p	2	3.3673	0.4059	2933.75	2935.216	1	661.5	44 L.FRPIPPPVNPVGDIYDPDEDEPVNEL.A
gi 6324588 ref NP_014657.1	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A; Rts1p	3	4.6372	0.3442	3049.52	3048.376	1	961.7	30.769232 N.LFRPIPPPVNPVGDIYDPDEDEPVNEL.A
ail63245881rofIND_014657_11		B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	3 0/15	0 4010	3046 73	3049 376	1	371.0	
gil0324366[10110F_014037.1]	10K014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	3.9415	0.4019	3040.73	3040.370	1	371.9	34.01336/ N.LENFIFFF VIEVGDITDEDEEVINEL.A
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	5.4018	0.3439	2340.65	2341.674	1	844.3	47.368423 L.T1K2L1P1N2F1N2E1V1S1P1E1E1R4I1P1L1F1I1A1.K
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p	3	5.7006	0.2783	2551.13	2549.886	1	1166	39.285713 F.E1R4L1P1T1P1T1K2L1N2P1D1T1D1L1E1L111K2T1P1Q2.R
gi 6324588 ref NP_014657.1	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A; Rts1p	2	3.531	0.2665	2547.09	2549.886	1	411.9	42.857143 F.E1R4L1P1T1P1T1K2L1N2P1D1T1D1L1E1L1I1K2T1P1Q2.R
ail63245881rofIND_014657.11		B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	4 4286	0.2448	2443 55	2443 840	1	709	
gilo324300[tel[14F_014037.1]	101(01410	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	4.4200	0.2440	2443.33	2445.045		700	
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	4.6644	0.3555	2469.05	2471.849	1	1017.7	50 L.T1K2L1P1N2F1N2E1V1S1P1E1E1R4I1P1L1F1I1A1K2.V
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p	3	4.7494	0.3683	2893.4	2892.282	1	795.7	35.416664 S.HSFERLPTPTKLNPDTDLELIKTPQ.R
gi 6324588 ref NP_014657.1	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A; Rtstp B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	3.5644	0.216	1561.95	1560.741	1	918.7	66.66667 L.NEIEDIFEVIEPL.E
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	3	4.5465	0.4058	3079.76	3080.376	1	499.9	24.038462 N.L1F1R4P1I1P1P1P1V1N2P1V1G1D1I1Y1D1P1D1E1D1E1P1V1N2E1L1.A
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p	3	5.6465	0.424	3050.9	3048.376	1	828.8	29.807693 N.LFRPIPPPVNPVGDIYDPDEDEPVNEL.A
gi 6324588 ref NP_014657.1	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A; Rts1p	2	3.6755	0.2629	3048.71	3048.376	1	526.5	38.46154 N.LFRPIPPPVNPVGDIYDPDEDEPVNEL.A
ail6324588/refINP_014657_1	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A: Rts1p	3	5 1078	0 2848	3540 71	3539 926	1	1094.6	
		B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the			0.2010					
gi 6324588 ret NP_014657.1	YOR014W	B-type regulatory subunit of PP2A; Rts1p	3	5.2807	0.335	2549.09	2549.886	1	814.2	34.523808 F.ETR4L1P111P111K2L1N2P1D111D1L1E1L111K211P1Q2.R
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	3.9021	0.2388	2549.17	2549.886	1	285.4	38.095238 F.E1R4L1P1T1P1T1K2L1N2P1D1T1D1L1E1L111K2T1P1Q2.R
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p	2	4.4813	0.4017	2965.79	2966.216	1	514.9	42 L.F1R4P1I1P1P1P1V1N2P1V1G1D1I1Y1D1P1D1E1D1E1P1V1N2E1L1.A
gi 6324588 ref NP_014657.1	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A; Rts1p	2	4.618	0.4282	3078.47	3080.376	1	527.2	38.46154 N.L1F1R4P1I1P1P1P1V1N2P1V1G1D1I1Y1D1P1D1E1D1E1P1V1N2E1L1.A
ail6324588/refINP_014657_1	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A. Bts1p	2	3 2376	0 4283	2031.95	2031 094	1	503.1	
giloo24000[rel[tit _014001.1]	1010141	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	2	0.2010	0.4200	2001.00	2001.004		000.1	
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the	3	4.6969	0.4072	3047.42	3048.376	1	1213.8	31.730768 N.LFRPIPPPVNPVGDIYDPDEDEPVNEL.A
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p	2	4.1465	0.3383	3048.67	3048.376	1	485.3	38.46154 N.LFRPIPPPVNPVGDIYDPDEDEPVNEL.A
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p	2	4.6109	0.3382	2313.71	2315.674	1	1055.8	52.63158 L.TKLPNFNEVSPEERIPLFIA.K
ail6324588/refINP 014657.1	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A; Rts1p	3	6.1089	0.4399	3576.38	3578.926	1	858.1	N.L1F1R4P1I1P1P1P1V1N2P1V1G1D1I1Y1D1P1D1E1D1E1P1V1N2E1L1A1W2P1H 24.166666 3.M
	VODALIN	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the		0.0507	0.0000	1015 50	1015 101	•	007.0	
gi 6324588 ret NP_014657.1	YOR014W	B-type regulatory subunit of PP2A; Rts1p	2	3.0587	0.3202	1815.59	1815.134	2	397.3	46.666668 N.L1F1R4P11P1P1P1P1V1N2P1V1G1D111Y1.D
gi 6324588 ref NP_014657.1	YOR014W	mammalian B' subunit of PP2A; Rts1p	2	4.6506	0.4222	2018.35	2019.308	1	1500.1	68.75 T.KLNPDTDLELIKTPQRH.S
gi 6324595 ret NP_014664.1 gi 6324595 ref NP_014664.1	YOR021C	hypothetical protein; Yor021cp	2	3.2264 5.4351	0.1936	2320.49	2321.64	1	424.1	44.11765 D.RIAFEDIKFIDYPEFRFN.K 42.647057 D.R4I141E1E1D11K2E1I1D1Y1D1E1E1R4E1N2 K
gil6324595/refINP_014664.1	YOR021C	hypothetical protein; Yor021cp	2	3.2389	0.1838	2346.51	2347.64	3	503.3	44.11765 D.R4I1A1F1E1D111K2F1I1D1Y1P1E1F1R4F1N2.K
gi 6324595 ref NP_014664.1	YOR021C	hypothetical protein; Yor021cp	2	3.5901	0.2671	1833.57	1834.038	1	624.9	61.538464 F.EDIKFIDYPEFRFN.K
gi 6324595 ref NP_014664.1	YOR021C	hypothetical protein; Yor021cp	2	3.785	0.3231	1980.03	1981.215	1	557.7	57.14286 A.FEDIKFIDYPEFRFN.K
gi 6324595 ref NP_014664.1 gi 6324595 ref NP_014664.1	YOR021C	hypothetical protein; Yor021cp	2	3.5141	0.2518	2000.13	2001.215	1	583	60./1428/ A.F1E1D111K2F111D1Y1P1E1F1R4F1N2.K
gil6324595/refINP_014664.1	YOR021C	hypothetical protein; Yor021cp	2	3.2106	0.2020	1589.23	1589.834	1	1052.8	77.27273 D.IKFIDYPEFRFN.K
gil6324617/refINP_014686.1	YOR043W	Protein required, with binding partner Psr1p, for full activation of the general stress response, possibly through Msn2p dephosphory/ation; regulates growth during the diauxic shift: negative requilator of G1 cyclin expression: Whi2p	2	4.0743	0.3217	1754.39	1753.033	2	460.6	53 571426 N N2E102D1111 1H302K2P1A11111V11 1 R
3-1-1-1 (0.1 point) _01-000.1		Protein required, with binding partner Psr1p, for full activation of the general stress response, possibly through Msn2p dephosphorylation; regulates growth during the	2		0.0217			~		
gi 6324617 ref NP_014686.1	YOR043W	diauxic shift; negative regulator of G1 cyclin expression; Whi2p Protein required, with binding partner Psr1p, for full activation of the general stress response. Dossibly through Msr2p dephosphorulation; regulates growth during the	2	3.6618	0.241	1731.85	1732.033	1	452.4	53.571426 N.NEQDILHQKPAIIVL.R
gi 6324617 ref NP_014686.1	YOR043W	diauxic shift; negative regulator of G1 cyclin expression; Whi2p	2	3.391	0.331	1838.37	1836.995	1	611.5	64.28571 Y.T1K2A1H3D1D1L1Y1N2H3P1V1E1K2F1.F
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	2	4.3323	0.1756	1850.35	1851.048	3	891.1	64.28571 T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2.K
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p	3	6.0212	0.2868	1979.96	1981.222	1	1362.8	51.666664 T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.V

		Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in								
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	2	4.7609	0.3397	1978.65	1981.222	1	866.2	56.666668 T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.V
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p	2	3.9563	0.277	2189.71	2190.519	1	370.8	50 E.MTRVPTDDWDEVEKIVKK.V
gi 6324620 ref NP_014689.1	YOR046C	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus; Dbp5p	2	4.6015	0.1672	2214.55	2215.519	2	604.5	52.941177 E.M1T1R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.V
ail6224620/rofIND_014690.11	VORMAC	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	2	2 4404	0.244	1696 21	1695 017	1	220.2	
gil0324020[10][NF_014009.1]	10K040C	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	2	3.4494	0.244	1000.31	1005.017	1	320.2	05.56401 A.ERLVFRVEERRING.E
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	3	5.4181	0.3434	1832.06	1830.048	1	1895.9	53.571426 T.RVPTDDWDEVEKIVK.K
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p	3	5.2758	0.3061	1957.37	1958.222	1	2091.2	53.333336 T.RVPTDDWDEVEKIVKK.V
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p	2	4.2325	0.2751	1958.13	1958.222	1	667.4	56.666668 T.RVPTDDWDEVEKIVKK.V
gil6324620/refINP_014689.1	YOR046C	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus: Dbp5p	2	4 2038	0 2625	1979 95	1981 222	1	588.4	50 T R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2 V
		Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	-		0.2020					
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	3	5.4028	0.2944	1978.34	1981.222	1	1441.3	51.6666664 I.R4V1P111D1D1W2D1E1V1E1K2I1V1K2K2.V
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p Cytoplasmic ATP-dependent RNA belicase of the DEAD-box family involved in	2	3.3929	0.3432	1555.91	1556.886	1	433.3	62.5 A.EKLVPKVEEKKTK.Q
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p	2	3.663	0.2553	1575.59	1574.886	1	447.2	62.5 A.E1K2L1V1P1K2V1E1E1K2K2T1K2.Q
gi 6324620 ref NP_014689.1	YOR046C	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus; Dbp5p	2	3.487	0.1587	1829.47	1830.048	4	497.9	46.42857 T.RVPTDDWDEVEKIVK.K
ail6324620/rofINP_014680_1	VORMEC	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA expect from the nucleur: Dbp5p	3	6.0300	0 3113	1079 92	1081 222	1	2001	55 T P4//1P1T1D1D1///2D1E1//1E1K2I1//1K2K2 \/
gilo324020[rei]14r_014003.1]	101(0400	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	5	0.0303	0.5115	1370.02	1301.222	1	2001	33 1.K4VII 1110101W201E1VIE1K2IIVIK2K2.V
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p Cvtoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in	2	4.4144	0.3288	1979.91	1981.222	2	520.2	50 T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.V
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p	3	5.6612	0.312	1959.44	1958.222	1	1617.2	55 T.RVPTDDWDEVEKIVKK.V
gi 6324620 ref NP_014689.1	YOR046C	mRNA export from the nucleus; Dbp5p	3	4.7741	0.1606	2191.46	2190.519	1	1511.2	44.11765 E.MTRVPTDDWDEVEKIVKK.V
gil6324620/refINP_014689.1	YOR046C	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus: Dbp5p	2	2 9429	0 2908	1493 85	1494 79	1	459 1	59 090908 K R4E1I 1P1K2D1T102I 1V1I 1E1 S
giloo2 io20 io1111 _01100011	10110100	Probable cochaperone, regulates activity of Cyr1p (adenylyl cyclase); involved in	-	2.0.20	0.2000	1100.00		·	10011	
gi 6324631 ref NP_014700.1	YOR057W	assembly of the kinetochore complex, associates with the SCF (Skp1p/Cdc53p/F box protein) ubiquitin ligase complex; Sgt1p	2	4.5987	0.2957	2073.45	2073.26	1	1033.9	62.5 L.G1Y1V1D1D1T1L1P1L1W2E1D1R4L1E1T1K2.L
		Probable cochaperone, regulates activity of Cyr1p (adenylyl cyclase); involved in assambly of the kinetechore complex associates with the SCE (Skp1p)Cdc53p/E box								
gi 6324631 ref NP_014700.1	YOR057W	protein) ubiquitin ligase complex; Sgt1p	2	4.1915	0.3429	2050.67	2051.26	1	756.9	56.25 L.GYVDDTLPLWEDRLETK.L
		Protein component of the large (60S) ribosomal subunit, has similarity to E. coli L3 and rat L3 ribosomal proteins; involved in the replication and maintenance of killer								
gi 6324637 ref NP_014706.1	YOR063W	double stranded RNA virus; Rpl3p	2	3.4691	0.2725	1694.17	1696.841	2	469.2	58.333332 S.E1K2V1D1W2A1R4E1H3F1E1K2T1.V
		and rat L3 ribosomal proteins; involved in the replication and maintenance of killer								
gi 6324637 ref NP_014706.1	YOR063W	double stranded RNA virus; Rpl3p Protein component of the large (60S) ribosomal subunit, has similarity to E, coli I 3	1	2.6232	0.3053	1355.57	1356.527	1	321.1	63.636364 F.GKGRFQTPAEKH.A
		and rat L3 ribosomal proteins; involved in the replication and maintenance of killer								
gi 6324637 ref NP_014706.1	YOR063W	double stranded RNA virus; Rpl3p Protein component of the large (60S) ribosomal subunit, has similarity to E. coli L3	2	3.962	0.4298	1674.67	1675.841	1	580.2	70.83333 S.EKVDWAREHFEKT.V
ail6224627/rofIND_014706.11	VOROCOW	and rat L3 ribosomal proteins; involved in the replication and maintenance of killer	2	2 40 4 1	0.2574	1671 61	1671.09	1	659.2	
gil0324037 iei i4F_014700.1	TORUGSW	Protein component of the large (60S) ribosomal subunit, has similarity to E. coli L3	2	3.4041	0.3374	10/1.01	1071.90	I	030.3	00.714207 R.VRAFFRDDRSRFVAL.I
ail6324637/refINP 014706.1	YOR063W	and rat L3 ribosomal proteins; involved in the replication and maintenance of killer double stranded RNA virus: Rpl3p	2	3.0719	0.1875	1693.89	1692.98	1	472.2	60.714287 R.V1K2A1F1P1K2D1D1R4S1K2P1V1A1L1.T
51		Protein component of the large (60S) ribosomal subunit, has similarity to E. coli L3								
gi 6324637 ref NP_014706.1	YOR063W	double stranded RNA virus; Rpl3p	1	2.2592	0.1894	1208.49	1208.365	1	353.2	61.11111 R.KYEAPRHGHL.G
		Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated glucose-repressed Hap2p/3p/4p/5p CCAAT-binding								
gi 6324639 ref NP_014708.1	YOR065W	complex; Cyt1p	2	3.6112	0.2351	2692.09	2692.855	1	674.9	43.18182 M.AEEFEYDDEPDEQGNPKKRPGKL.S
		Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding								
gi 6324639 ref NP_014708.1	YOR065W	complex; Cyt1p	3	5.6883	0.4105	2724.95	2723.855	1	1481.8	42.045452 M.A1E1E1F1E1Y1D1D1E1P1D1E1Q2G1N2P1K2K2R4P1G1K2L1.S
		regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding								
gi 6324639 ref NP_014708.1	YOR065W	complex; Cyt1p Cytochrome c1, component of the mitochondrial respiratory chain; expression is	2	3.6758	0.281	2722.31	2723.855	3	298	34.090908 M.A1E1E1F1E1Y1D1D1E1P1D1E1Q2G1N2P1K2K2R4P1G1K2L1.S
ail6224620/rofIND_014709.11	VOROGEW	regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding	2	6 2669	0.4206	0704 47	2722 955	1	1504.2	
gilo324039[rel[NP_014708.1]	TURU65W	Cytochrome c1, component of the mitochondrial respiratory chain; expression is	3	0.2008	0.4296	2724.17	2123.800		1594.3	42.043432 M.ATETETETETETETETETETETETETETETETETETETE
gil6324639/refINP_014708.1	YOR065W	regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex: Cvt1p	2	4.0343	0.2515	2722.63	2723.855	1	695.9	45.454548 M.A1E1E1E1E1Y1D1D1E1P1D1E1Q2G1N2P1K2K2R4P1G1K2L1.S
giloo2 iooojioinii _011100111	10100011	Cytochrome c1, component of the mitochondrial respiratory chain; expression is	-	1.0010	0.2010	2122.00	2120.000	·	000.0	
gi 6324639 ref NP_014708.1	YOR065W	regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAA1-binding complex; Cyt1p	3	4.7342	0.4688	2690.72	2692.855	1	1005.4	35.227272 M.AEEFEYDDEPDEQGNPKKRPGKL.S
		Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which								
gi 6324659 ref NP_014728.1	YOR085W	important for N-glycosylation of a subset of proteins; Ost3p	2	3.3505	0.2923	1275.97	1274.549	1	637.1	85 K.SPAYPFPLLRL.S
		Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is								
gi 6324659 ref NP_014728.1	YOR085W	important for N-glycosylation of a subset of proteins; Ost3p	2	4.0248	0.4049	2144.09	2145.376	1	575.1	50 L.KDSSFENILAPPHENAYIV.A
		catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is								
gi 6324659 ref NP_014728.1	YOR085W	important for N-glycosylation of a subset of proteins; Ost3p Gamma subunit of the oligosaccharyltransferase complex of the ER lumen which	2	3.8707	0.3196	2170.73	2169.376	1	515.1	50 L.K2D1S1S1F1E1N2I1L1A1P1P1H3E1N2A1Y1I1V1.A
	VODOCINI	catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is	•	0.0004	0.047	4400.05	4400.07	-	100.0	
gilp324659[ret]NP_014728.1	TURU85W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which	2	2.9294	0.247	1460.35	1460.67	5	400.9	24. 100000 V.NLEUPSK IIPKAF.Q
ail6324659/refINP_014729_1	YOR085\M	catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is important for N-plycosylation of a subset of proteins; Ost3p	2	3 0708	0 2747	1288 45	1288 549	1	4Q1 R	70 K S1P1A1Y1P1F1P1 1 1R4 1 S
9.1-32 (000) 0.1 m _0 (4/20.1)			~	0.07 00	0.2171	.200.40	.200.040			

		Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which								
gi 6324659 ref NP_014728.1	YOR085W	catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is important for N-glycosylation of a subset of proteins; Ost3p	2	3.3463	0.182	1708.39	1706.977	1	664.6	60.714287 T.K2V1N2L1E1D1P1S1K2T1I1P1K2A1F1.Q
		Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which								
gi 6324659 ref NP_014728.1	YOR085W	important for N-glycosylation of a subset of proteins; Ost3p is	2	3.5857	0.352	1634.31	1634.987	1	389	61.538464 F.T1I1K2S1P1A1Y1P1F1P1L1L1R4L1.S
		Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which								
gi 6324659 ref NP_014728.1	YOR085W	important for N-glycosylation of a subset of proteins; Ost3p	2	3.4646	0.3647	1618.69	1616.987	1	1085.7	76.92308 F.TIKSPAYPFPLLRL.S
		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-								
ail6324660/refINP_014729_1	YOR086C	fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and Tcb3p interact: Tcb1p	2	4 5754	0.3163	1871.31	1869 079	1	1081.3	67 64706 K KI PDGSVEELPDI NTGIA K
gilooz iooolioinii _01112011	10110000	Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-	-		0.0100	101 1.01	1000.010	•	1001.0	
	VODORCO	fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and	0	0 40 47	0.0000	4040 47	40.40.040		744.0	
gilo324000/rei/iNP_014729.1	TURU86C	Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-	2	3.4247	0.3206	1642.17	1843.012		/ 14.6	60.714287 R.11V IR4DITIEIN2PIV IVV2DIEITIEITI.V
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p Contains three calcium and linid hinding domains; green fluorescent protein (GEP)-	2	3.3937	0.3359	1822.79	1823.012	2	663.5	57.14286 R.TVRDTLNPVWDETLY.V
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	2.9982	0.2238	1377.71	1378.612	1	996	72.72727 Q.L1L1K2V1P1D1F1D1F1V1A1T1.L
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	4.3733	0.3409	1984.19	1984.081	1	743.3	56.25 K.DENDKYEETIDEKAKVG.R
		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)- fusion protein localizes to the cell periphery: C-terminal portion of Tcb1p. Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	3.6923	0.2844	2006.47	2005.081	1	617.8	59.375 K.D1E1N2D1K2Y1E1E1T1I1D1E1K2A1K2V1G1.R
		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-								
gi 6324660 ref NP 014729.1	YOR086C	Tcb3p interact; Tcb1p	2	4.0632	0.4098	2069.81	2070.248	1	829.6	59.375 W.EDKDELTLDDELMDMTR.E
		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-								
gil6324660/refINP_014729.1	YOR086C	tusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and Tcb3p interact: Tcb1p	2	4.3817	0.3587	2495.43	2496.817	1	793.2	45.454548 T.LEEKKLPDGSVEELPDLNTGIAK.V
2.1		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-								
ail6324660/rofIND_014720.11	VOPORC	fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and	2	5 4207	0 4324	1006 47	1007 253	1	1563 1	
gilo324000 101 14729.1	TORUGUC	Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-	2	5.4207	0.4324	1990.47	1997.200		1505.1	00.00007 N.KEPUGSVEELPULINTGIAN.V
	VODAAAA	fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and	•	4 0040	0 1010	0050.00	0057 004		550.0	
gilo324000/rei/iNP_014729.1	TURU86C	Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-	2	4.0210	0.4019	2056.33	2057.304		559.6	59.375 R.11V IR4DITIEIN2PIV IW2DIEITIEITIVIEI.E
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p Contains three calcium and linid hinding domains; green fluorescent protein (GEP)-	2	4.3735	0.2858	2056.55	2055.251	1	791.9	68.75 T.RETFLDNIIPDSLYGDW.Y
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	3.5163	0.1855	1645.93	1643.835	1	902.9	63.333332 M.AKEDTGVTAPKKPETA.Q
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	3	4.6396	0.4144	3017.6	3020.392	1	656.3	29.807693 R.F1F1P1T1L1E1E1K2K2L1P1D1G1S1V1E1E1L1P1D1L1N2T1G111A1K2.V
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	3.8369	0.328	2542.51	2541.779	1	1069.2	55 T.RETFLDNIIPDSLYGDWYHSV.A
		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)- fusion protein localizes to the cell periphery: C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	3.1454	0.217	2776.03	2776.006	3	232.2	35.714287 E.DKAKFDQEWNEVKELEDMYSNR.Q
		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)- fusion protein localizes to the cell peripheny. Caterminal portion of Tch1n, Tch2n and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	2.9227	0.2368	2173.27	2171.464	1	388.8	44.11765 R.T1V1R4D1T1L1N2P1V1W2D1E1T1L1Y1V1L1L1.N
		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	3.5144	0.2989	2370.25	2368.643	8	176.3	35.714287 T.LEEKKLPDGSVEELPDLNTGIA.K
		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-								
gil6324660/refINP_014729.1	YOR086C	tusion protein localizes to the cell periphery; C-terminal portion of 1cb1p, 1cb2p and Tcb3p interact: Tcb1p	2	3.1967	0.2477	2076.17	2077.251	1	291.7	43.75 T.R4E1T1E1L1D1N2I1I1P1D1S1L1Y1G1D1W2.Y
51		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-								
gil6324660/refINP_014729_1	YOR086C	tusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and Tcb3p interact: Tcb1p	2	3 8546	0 3784	2150.31	2148 464	1	585.5	52 941177 R TVRDTI NPVWDETI YVLL N
3.i		Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-								
ail6324660/refINP_014729_11	YOR086C	fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and Tcb3p interact; Tcb1p	2	3 3057	0 252	1366.41	1365 612	1	1115.9	
gilo324000[rei]NF_014723.1]	10100000	Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-	2	5.5057	0.232	1300.41	1303.012		1113.5	TT.27273 Q.LERVEDI DI VAT.E
	VODAAAA	fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and		0.5400	0.0707	1070 70	4070.040		400	
gilo324000/rei/INP_014729.1	TURU86C	Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-	1	2.5438	0.2707	13/6./6	13/8.012		432	50 Q.LILIKZVIPIDIFIDIFIVIATIT.L
	VODAAAA	fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and		0.4450	0.0400	000450	0005 004		100.1	
gi 6324660 ref NP_014729.1	YOR086C	Contains three calcium and lipid binding domains; green fluorescent protein (GEP)-	2	3.4456	0.3406	2034.59	2035.304	1	489.4	50 R.TVRDTLNPVWDETLYVL.L
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p Contains three calcium and linid binding domains; green fluorescent protein (CEP)-	2	3.8098	0.3752	1620.29	1620.991	2	512	57.692307 K.K2Y1M1G1P1I1L1L1P1P1F1S1L1Q2.L
		fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and								
gi 6324660 ref NP_014729.1	YOR086C	Tcb3p interact; Tcb1p	2	3.1717	0.1608	1606.91	1604.991	1	520.5	57.692307 K.KYMGPILLPPFSLQ.L
gi 6324673 ref NP_014742.1	YOR099W	member of the KRE2/MNT1 mannosyltransferase family; Ktr1p	2	3.6628	0.4203	2004.39	2003.135	1	493.3	53.333336 K.EHWSFPEWIDEEKAAQ.V
	VORCOOM	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation;	2	2 0242	0.000	1667.0	1666 040	4	1007	
gijo324673[rei]NP_014742.1]	10K099W	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation;	3	3.9213	0.289	1007.3	1000.843	1	1337	33.70923 1. TVYTTSCHUTSIK.L
gi 6324673 ref NP_014742.1	YOR099W	member of the KRE2/MNT1 mannosyltransferase family; Ktr1p	3	4.444	0.2689	2307.62	2307.535	1	1074.4	39.0625 L.M1D1D1Y1D1W2Y1W2R4V1E1P1D111K2L1H3.C
gi 6324673 ref NP_014742.1	YOR099W	member of the KRE2/MNT1 mannosyltransferase family; Ktr1p	2	3.6528	0.2632	1707.55	1708.824	1	1022.5	70.83333 A.Y1F1D1Y1L1D1R4E1G1G1F1F1Y1.E
	VODG	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation;	-	10	0.0.00				005 5	
gijo324673[ret]NP_014742.1]	10K099W	member of the KKE2/MNT1 mannosyltransferase family; Ktr1p	3	4.2671	0.2483	2034.17	2032.234	1	939.3	

		Phosphatidylinositol 4,5-bisphosphate 5-phosphatase, synaptojanin-like protein with an N-terminal Sact domain, plays a role in a TGN (trans Golgi network)-to-early endosome pathwar, byperspective trans cause transforation to actin pathware byperspective and the second seco								
gi 6324683 ref NP_014752.1	YOR109W	Inp53p Phosphatidylinositol 4 5-bisphosphate 5-phosphatase synantojanin-like protein with	3	4.1004	0.3161	2583.02	2583.908	1	498.5	32.5 N.N2F1M1D1K2E1K2Q2Q2N2l1D1T1L1L1G1R4L1P1Y1Q2.K
		an N-terminal Sac1 domain, plays a role in a TGN (trans Golgi network)-to-early endosme nathway: hyperosmotic stress causes translocation to actin patches:								
gi 6324683 ref NP_014752.1	YOR109W	Inp53p Bhosphatidylinasital 4 5 bischoophata 5 phosphatasa, synaptaiania-lika pratain with	2	3.4156	0.3035	1718.61	1716.117	1	772.9	71.42857 W.LFPIGEKFKPDIVVL.G
		an N-terminal Sac1 domain, plays a role in a TGN (trans Golgi network)-to-early								
gi 6324683 ref NP_014752.1	YOR109W	endosome patnway; nyperosmotic stress causes translocation to actin patches; Inp53p	3	4.069	0.2784	2786.6	2786.161	1	826.2	32.954548 N.N2F1M1D1K2E1K2Q2Q2N2I1D1T1L1L1G1R4L1P1Y1Q2K2A1.V
		Phosphatidylinositol 4,5-bisphosphate 5-phosphatase, synaptojanin-like protein with an N-terminal Sac1 domain, plays a role in a TGN (trans Golgi network)-to-early								
ail63246831refINP_014752.11	YOR109W	endosome pathway; hyperosmotic stress causes translocation to actin patches;	2	3 0389	0 2203	1732 01	1733 117	1	532.4	64 28571 W I 1E1P11/G1E1K2E1K2P1D111//1/11 1 G
gi 6324686 ref NP_014755.1	YOR112W	hypothetical protein; Yor112wp	2	3.5202	0.2258	1372.57	1372.566	2	674.3	70 T.ERVVPFPWDNL.G
gi 6324686 ref NP_014755.1	YOR112W	hypothetical protein; Yor112wp	2	3.9952	0.3287	1630.05	1629.856	1	926.7	69.230774 T.ERVVPFPWDNLGSL.S
gi 6324686 ref NP_014755.1	YOR112W	hypothetical protein; Yor112wp	2	4.5406	0.3017	1646.83	1648.856	1	1061.9	73.07692 T.E1R4V1V1P1F1P1W2D1N2L1G1S1L1.S
gil6324686[ref]NP_014755.1]	YOR112W	hypothetical protein; Yor112wp	2	3 5660	0.2103	1720.47	1720.792	1	714.5	70.92306 N.KSWINDELINDUGWIQ.D 61 538464 N.K2S1W2N2D1E1I 1N/2D1D1C1W/2I1O2 D
gil6324686lrefINP 014755.1	YOR112W	hypothetical protein; Yor112wp	2	3.7334	0.3698	1500.35	1500.74	1	929.3	75 E.RVVPFPWDNLGSL.S
gi 6324705 ref NP_014774.1	YOR131C	hypothetical protein; Yor131cp	2	3.5663	0.3265	1688.35	1689.056	1	963.1	60.714287 K.AMKEMQPQPGLVDIM.R
gi 6324705 ref NP_014774.1	YOR131C	hypothetical protein; Yor131cp	3	4.3062	0.2433	2680.1	2682.007	5	400.7	26.190477 L.H3F1I1D1T1L1P1T1E1K2E1K2K2E1A1H3D1R4I1E1L1V1.E
gi 6324705 ref NP_014774.1	YOR131C	hypothetical protein; Yor131cp	2	3.1343	0.2208	1923.15	1924.164	1	183.2	53.333336 L.HFIDTLPTEKEKKEAH.D
gil6324705[ref]NP_014774.1]	VOR131C	hypothetical protein; Yor131cp	2	3.0205	0.2307	2650.82	2650.007	1	491	
gilo324705[tel[147_014774.1]	101(1310	hypothetical protein, for rarep	5	4.5577	0.2710	2000.02	2030.007	'	000	30.033230 E.HI DTEFTERERREAHDRIEEV.E
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	1	3.5107	0.4008	1322.58	1323.486	1	523.1	63.636364 S.G111E1H311V1C1P1G1V1V1Q2.S
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	1	2.5791	0.3179	1307.52	1308.486	1	528.5	63.636364 S.GIEHIVCPGVVQ.S
		Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which								
gi 6324709 ref NP_014779.1	YOR136W	catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; ldh2p	2	3.2391	0.3143	1351.45	1350.543	1	976.7	75 T.T1Y1E1N2V1D1L1V1L11R4.E
		Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which								
gi 6324709 ref NP_014779.1	YOR136W	catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	2	4.1332	0.4395	1583.31	1582.822	1	1550.7	79.16667 F.K2T1T1Y1E1N2V1D1L1V1L1I1R4.E
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	1	2.8684	0.2005	1573.53	1574.817	1	405.5	46.42857 L.G1L1T1P1S1A1N2I1G1H3K2I1S111F1.E
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	1	2.4805	0.3611	981.69	982.211	1	325.3	66.66667 L.KGPLATPIGK.G
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	2	3.5879	0.3206	1556.59	1555.817	1	453.2	57.14286 L.GLTPSANIGHKISIF.E
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	2	4.7469	0.3785	1797.49	1795.981	1	1234.4	71.42857 A.KELSKEYPDLTLETE.L
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	2	4.2213	0.4073	1565.49	1564.822	1	1506.4	79.16667 F.KTTYENVDLVLIR.E
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	2	3.1055	0.3344	993.49	994.211	1	937	88.88889 L.K2G1P1L1A1T1P1I1G1K2.G
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; IdA2p	2	3.1629	0.3191	1176.43	1176.404	1	704.6	77.27273 L.KGPLATPIGKGH.R
gi 6324709 ref NP_014779.1	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; (ld2p	2	3.2691	0.3831	1194.37	1192.404	1	586.9	72.72727 L.K2G1P1L1A1T1P1I1G1K2G1H3.R
gi 6324709 ref NP_014779.1	YOR136W	Subunit or mitochonorial VAU(+)-dependent isocitrate denyarogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; (ldh2p	2	3.8733	0.4255	1469.15	1469.64	1	410.4	66.66667 G.RYTGKPNPSTGKY.T
gi 6324709 ref NP_014779.1	YOR136W	Subunit or mitochondrial VAU(+)-dependent isocitrate denyarogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; (Id2p	2	3.0941	0.2807	1235.17	1234.438	1	1288.2	83.33333 T.YENVDLVLIR.E
gi 6324709 ref NP_014779.1	YOR136W	Subulit of milliocholdrain VAD(+)-appendent sociate denyorgenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; (ldpp	1	2.4606	0.3271	1233.69	1234.438	1	499.3	72.22222 T.YENVDLVLIR.E
gi 6324709 ref NP_014779.1	YOR136W	catalyzes the oxidation of isocitrate dalpha-ketoglutarate in the TCA cycle; Idh2p	1	3.157	0.3182	1436.7	1436.645	1	995.3	68.181816 A.KELSKEYPDLTL.E
gi 6324709 ref NP_014779.1	YOR136W	Subunit or mitochonorrai NAU(+)-dependent isocitrate denyarogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; (Idpp	1	2.4154	0.2519	993.91	994.211	1	345.1	66.66667 LK2G1P1L1A1T1P111G1K2.G
gi 6324709 ref NP_014779.1	YOR136W	Subunit of minocholdran MAD(+) response to appha-ketoglutarate in the TCA cycle; (ldh2p	1	3.3565	0.3326	1191.59	1192.404	1	517.7	72.72727 L.K2G1P1L1A1T1P111G1K2G1H3.R
gi 6324709 ref NP_014779.1	YOR136W	catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; ldh2p Nuclear actin-related protein involved in chromatin remodeling, component of	1	3.5449	0.3891	1176.63	1176.404	1	756	72.72727 L.KGPLATPIGKGH.R
gi 6324715 ref NP_014784.1	YOR141C	chromatin-remodeling enzyme complexes; Arp8p	2	4.4044	0.2797	2253.31	2253.466	1	952.3	55.88235 E.K2N2D1P1S1P1I1E1W2I1F1D1D1S1K2L1Y1Y1.G
gi 6324715 ref NP_014784.1	YOR141C	chromatin-remodeling enzyme complexes; Arp8p	2	4.282	0.2978	1886.49	1885.167	1	412.8	59.375 N.S1I1K2I1G1F1P1K2D1D1H3P1V1V1V1P1N2.C
gi 6324715 ref NP 014784.1	YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes; Arp8p	2	3.3033	0.2748	1682.39	1680.781	1	1096.3	65.38461 E.K2N2D1P1S1P111E1W2I1F1D1D1S1.K
ail6324715/refIND_014784_1	YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of	2	4 2047	0 3376	186/ 51	1863 167	1	574 1	
8-1002-11 TOPOINT_014/04.1	10111410	enternation for the complexes, rupop	2	4.2047	0.0210	100-1.01	1000.107		0.4.1	

		Nuclear actin-related protein involved in chromatin remodeling, component of								
gi 6324715 ref NP_014784.1	YOR141C	chromatin-remodeling enzyme complexes; Arp8p Nuclear actin-related protein involved in chromatin remodeling, component of	2	2.9109	0.1541	1577.13	1576.703	1	828.8	66.66667 E.KNDPSPIEWIFDD.S
gi 6324715 ref NP_014784.1	YOR141C	chromatin-remodeling enzyme complexes; Arp8p	2	4.5829	0.3109	2069.37	2068.29	1	821.3	62.5 E.KNDPSPIEWIFDDSKLY.Y
gi 6324715 ref NP_014784.1	YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes; Arp8p	2	4.0644	0.3892	2089.53	2089.29	1	593	53.125 E.K2N2D1P1S1P1I1E1W2I1F1D1D1S1K2L1Y1.Y
gi 6324715 ref NP 014784.1	YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes; Arp8p	2	4.8025	0.2912	2233.97	2231.466	1	939.9	64.70589 E.KNDPSPIEWIFDDSKLYY.G
5100 0101 _0 01		Diadenosine polyphosphate hydrolase, member of the MutT family of nucleotide								
gil6324737/refINP 014806.1	YOR163W	hydrolases with high specificity for diadenosine hexa- and pentaphosphates, required for efficient hydrolysis of diohosphorylated inositol polyphosphates; Ddo1p	2	4.2429	0.2516	1941.69	1943.208	1	757	67.85714 E.D1M1R4P1P1K2D1W2N2K2D1I1K2Q2F1.E
34444		Diadenosine polynhosphate bydrolase, member of the Mutt family of nucleotide								
		hydrolases with high specificity for diadenosine hexa- and pentaphosphates, required								
gi 6324737 ret NP_014806.1	YUR163W	Protein of unknown function, contains two predicted GTP-binding motifs GXXXXGKS	2	4.1038	0.2664	1920.51	1919.208	2	509.9	60.714287 E.DMRPPKDWNKDIKQF.E
gi 6324739 ref NP_014808.1	YOR165W	and DXXG near the N-terminus, homolog of the Arabidopsis gene RHD3 (Root Hair Defective); Sey1p	2	3.906	0.3767	1562.61	1562.822	1	747.5	75 K.K2N2L1V1P1E1L1K2D1H3V1I1H3.L
		Protein of unknown function, contains two predicted GTP-binding motifs GXXXXGKS and DXXG near the N-terminus, homolog of the Arabidopsis gene RHD3 (Root Hair								
gi 6324739 ref NP_014808.1	YOR165W	Defective); Sey1p Protein of unknown function, contains two predicted GTP-binding motifs GXXXXGKS	2	3.6543	0.1623	2146.17	2146.287	1	848.6	53.125 E.NCWDQIERNKDLDLPTQ.Q
ail62247201rofIND_014909_11	VOR165W	and DXXG near the N-terminus, homolog of the Arabidopsis gene RHD3 (Root Hair Defective): Sevice	1	0 0750	0.2450	1401 50	1400 54	1	154.6	
gilo324739/rei/NP_014808.1/	TUK 165W	Protein of unknown function, contains two predicted GTP-binding motifs GXXXXGKS	1	2.3753	0.2459	1421.52	1422.54	I	154.6	00.00007 L.R4DIR4FTETDTVTFTR4TT.D
gi 6324739 ref NP_014808.1	YOR165W	and DXXG near the N-terminus, homolog of the Arabidopsis gene RHD3 (Root Hair Defective); Sey1p	2	3.1662	0.2219	1543.47	1542.822	1	524.6	66.66667 K.KNLVPELKDHVIH.L
		Glutamine tRNA synthetase, monomeric class I tRNA synthetase that catalyzes the specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in								
gi 6324742 ref NP_014811.1	YOR168W	enzyme-tRNA interactions; GIn4p Glutamine tRNA synthetase monomeric class I tRNA synthetase that catalyzes the	3	4.1501	0.3181	3051.56	3053.401	1	511.3	25 E.RSDFSENVDDKEFFRLTPNQPVGLIK.V
ail62247421rofIND_014811_1	VOP169W	specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in	2	2 1520	0.2105	1621 52	1620.966	1	227.2	
gilb324742[rei]NP_014811.1]	TUK IBBW	Glutamine tRNA synthetase, monomeric class I tRNA synthetase that catalyzes the	2	3.1529	0.3105	1631.53	1630.866	1	337.3	61.536464 K.STETETK2DTETATGTK2TTTK4TTH3.V
gi 6324742 ref NP_014811.1	YOR168W	specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in enzyme-tRNA interactions; GIn4p	1	2.8055	0.2221	1105.89	1106.357	6	269.9	68.75 E.R4Y1K2L1V1P1G1I1F1.A
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of								
ail6324750/rofIND_014810_1	VOP176W	ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic	1	2 /397	0 2171	1169 54	1160 277	2	552.2	
gilosz4756/101/14 _014015.1	TORTION			2.4007	0.2171	1100.04	1103.277	2	002.2	66 EITEIDEGVIGEO.E
		ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic								
gi 6324750 ref NP_014819.1	YOR176W	pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	1	2.5993	0.1599	1435.57	1435.573	5	328.8	60.000004 S.KVEETYDFLYQ.L
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic								
gi 6324750 ref NP_014819.1	YOR176W	pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	2	3.6652	0.3316	1518.85	1519.746	1	325.6	70.83333 Q.YREIGGGSPIRKW.S
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of								
gi 6324750 ref NP_014819.1	YOR176W	pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	2	3.4328	0.2117	1667.67	1668.977	9	384.1	53.846157 K.LQEFPQPVRDKVVL.L
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of								
gi 6324750 ref NP 014819.1	YOR176W	ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	2	4.1778	0.3133	1630.51	1628.869	1	1237.1	73.07692 W.SVIDRWPTNEGLIK.A
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of								
	VOD470W	ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic	2	2.000	0.0444	454440	4544.07	4	450.0	
gilb324750[rei]NP_014819.1]	TOR 176W	pathway; thin ip mediates the use of iron by Hem isp; Hem isp	2	3.008	0.2144	1544.13	1544.67	I	459.9	62.5 L.DKTCPETAPRKPT.V
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic								
gi 6324750 ref NP_014819.1	YOR176W	pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	1	2.7209	0.2477	1518.7	1519.746	1	320.8	66.66667 Q.YREIGGGSPIRKW.S
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic								
gi 6324750 ref NP_014819.1	YOR176W	pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	2	2.9396	0.2434	1562.67	1561.67	1	418.1	66.66667 L.D1K2T1C1P1E1T1A1P1H3K2P1Y1.V
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of								
gi 6324750 ref NP_014819.1	YOR176W	pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	2	4.318	0.1912	1647.31	1648.869	1	931.1	61.538464 W.S1V1I1D1R4W2P1T1N2E1G1L1I1K2.A
		Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of								
gil6324750/refINP_014819.1	YOR176W	ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic pathway: Yfh1p mediates the use of iron by Hem15p; Hem15p;	1	3.0317	0.3501	1518.72	1519.746	1	225.7	62.5 Q.YREIGGGSPIRKW.S
3-1		Ferrochelatase a mitochondrial inner membrane protein, catalyzes the insertion of								
-1020475014ND 04404041	VOD470W	ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic	2	2 60 42	0.0000	4520.47	4540 740	4	202.0	
gi 6324750 ret NP_014819.1	YUR176W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine	2	3.6043	0.2893	1538.47	1540.746	1	303.6	66.66667 Q.Y1R4E111G1G1G1S1P111R4K2W2.S
gi 6324761 ref NP_014830.1	YOR187W	nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.1137	0.253	1732.03	1731.956	1	957.6	64.28571 F.VNKVDTIDDPEMLEL.V
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p Mitochondrial translation elongation factor Tu: comprises both GTPase and guarance	2	3.8906	0.3456	2239.49	2241.512	1	844.5	55.555557 F.V1N2K2V1D1T1I1D1D1P1E1M1L1E1L1V1E1M1E1.M
ail6324761 rofIND 044820 4	VOD10714/	nucleotide exchange factor activities, while these activities are found in separate	2	3 705	0 3469	2000 97	2007 275	4	710.1	
gij0324701[tet]NP_014630.1]		proteins in 5. pombe and numans, rump	2	3.705	0.3408	2009.87	2001.215		119.1	33.123 N.N.YD HDDFEMLELVEME.M

		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6224761 IrofIND 014920 1		nucleotide exchange factor activities, while these activities are found in separate	2	4 247	0.2269	21/2 25	21 42 222	1	666 G	
gil0324701110110F_014030.11	IOK IO/W	Mitochondrial translation elongation factor Tu: comprises both GTPase and quanine	2	4.347	0.2300	2142.33	2143.323	1	000.0	52.9411/7 L.DTATVIDTETTITIFTETR4DTETR2RZFTFT.L
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	5.2202	0.3762	3386.33	3386.78	1	567.8	25 L.D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1S1I1S1.G
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6324761/refINP 014830.11	YOR187W	proteins in S, pombe and humans: Tuf1p	3	4.1386	0.3128	3352.37	3352.78	1	466.8	23.214285 L.DAVDEYIPTPERDLNKPFLMPVEDIFSIS.G
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
	VODACTIN	nucleotide exchange factor activities, while these activities are found in separate		0 5 400	0.4047	0045.07	00.40.040		000	
gi 6324761 ret NP_014830.1	YOR187W	proteins in S. pompe and numans; Turip Mitochondrial translation elongation factor Tur comprises both GTPase and guanine	2	3.5428	0.1917	2345.67	2346.642	1	323	39.473686 K.LLDAVDEYIPTPERDLNKPF.L
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	2	3.146	0.1604	2282.01	2283.625	1	472.8	41.666664 I.P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
gi 6324761 ref NP 014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	2	2.9262	0.1774	3065.73	3065.465	1	401.6	32 L.DAVDEYIPTPERDLNKPFLMPVEDIF.S
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6224761 rofIND 014820 1		nucleotide exchange factor activities, while these activities are found in separate	2	2 0624	0.2150	2062.08	2065 465	1	600.7	
gil0324701110110F_014030.11	IOK IO/W	Mitochondrial translation elongation factor Tu: comprises both GTPase and quanine	3	3.9034	0.3159	3003.00	3003.403	1	090.7	30.000002 L.DAVDETIFTFENDLINNFFLMFVEDIF.3
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	2	3.2632	0.2696	2545.79	2546.941	1	381.7	35.714287 I.PTPERDLNKPFLMPVEDIFSIS.G
		Nitochondrial translation elongation factor 1 u; comprises both G I Pase and guanine nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	4.1604	0.2774	3324.8	3324.783	1	702.8	26.85185 K.L1L1D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6224761 rofIND 014820 1		nucleotide exchange factor activities, while these activities are found in separate	2	4 6925	0.2016	2612 77	2615.000	1	661 E	K.L1L1D1A1V1D1E1Y111P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D111F1S111S1.
gil03247011eiliNF_014830.11	TOK 167 W	Mitochondrial translation elongation factor Tu: comprises both GTPase and quanine	3	4.0033	0.3010	3012.77	3015.099	1	001.5	23.333334 0
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	4.7156	0.3635	3576.14	3579.099	1	716.1	25.833332 K.LLDAVDEYIPTPERDLNKPFLMPVEDIFSIS.G
		Nitochondrial translation elongation factor 1 u; comprises both G I Pase and guanine nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	4.4145	0.3402	3453.14	3454.958	1	1136.2	28.57143 M.K2L1L1D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6224761 rofIND 014820 1		nucleotide exchange factor activities, while these activities are found in separate	2	4 2296	0.274	2466.46	2465.04	2	766.0	
gil03247011eilini _014030.11	101(1071)	Mitochondrial translation elongation factor Tu: comprises both GTPase and quanine	5	4.2200	0.274	3400.40	3403.34	2	700.5	
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	3.8152	0.2617	3289.01	3291.783	1	881.5	27.777779 K.LLDAVDEYIPTPERDLNKPFLMPVEDIF.S
		Nitochondrial translation elongation factor 1 u; comprises both G I Pase and guanine nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	2	4.4382	0.4528	2474.09	2474.816	1	772.9	47.5 M.KLLDAVDEYIPTPERDLNKPF.L
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6324761/refINP_014830.11	YOR187W	nucleotide exchange factor activities, while these activities are found in separate	2	4 2946	0.4369	2501.85	2501 816	1	691.4	47.5 M K2I 1I 1D141V1D1E1Y1I1P1T1P1E1R4D1I 1N2K2P1E1 I
gil03247011eilini _014030.11	101(10710	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine	2	4.2340	0.4303	2001.00	2301.010	1	031.4	
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p Mitageographical translation elegation factor Tur comprises both CTBase and guarance	3	4.3136	0.3877	3436.64	3435.958	1	537.3	24.107143 M.KLLDAVDEYIPTPERDLNKPFLM@PVEDIF.S
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	5.9035	0.4244	3419.36	3419.958	1	1916.9	33.035713 M.KLLDAVDEYIPTPERDLNKPFLMPVEDIF.S
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6324761 refINP 014830.1	YOR187W	proteins in S, pombe and humans: Tuf1p	2	3.8481	0.2027	2119.43	2120.323	1	598.1	52.941177 L.DAVDEYIPTPERDLNKPF.L
5111		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
- 1000 4704 L- (IND. 04 4000 4)	VOD407W	nucleotide exchange factor activities, while these activities are found in separate		0.0004	0.0447	0007.05	0000 405		500.4	
gi 6324761 ret NP_014830.1	YOR187W	proteins in S. pombe and humans; 1ut1p Mitochondrial translation elongation factor Tu: comprises both GTPase and quanine	2	3.8084	0.3417	2807.65	2808.165	1	588.1	38.636364 V.D1E1Y111P111P1E1R4D1L1N2K2P1F1L1M1P1V1E1D111F1.S
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	2	3.5084	0.322	2778.49	2780.165	1	564.3	36.363636 V.DEYIPTPERDLNKPFLMPVEDIF.S
		Mitochondrial translation elongation factor 1 u; comprises both G I Pase and guanine nucleotide exchange factor activities, while these activities are found in separate.								
gi 6324761 ref NP 014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	2	3.3103	0.1666	2979.85	2980.376	1	401.9	33.333336 D.A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6224761 IrofIND 014920 1		nucleotide exchange factor activities, while these activities are found in separate	2	2 5609	0.4266	2049 11	2050 276	1	470.6	
gilo324761[rei[NP_014630.1]	TOR 187W	Mitochondrial translation elongation factor Tu: comprises both GTPase and quanine	2	3.3698	0.4366	2946.11	2950.376	1	479.0	33.410004 D.AVDETIPTPERDLINKPFLMPVEDIF.S
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	4.1874	0.3371	2978.57	2980.376	1	499.5	29.166666 D.A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	3.9599	0.2835	2949.41	2950.376	1	726.2	32.291664 D.AVDEYIPTPERDLNKPFLMPVEDIF.S
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6324761 refINP 014830.1	YOR187W	nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans: Tuf1p	2	3.4637	0.259	3095.65	3096.465	1	331.7	30.000002 L.D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
3.1		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
- 1000 4704 L- (IND. 04 4000 4)	VOD407W	nucleotide exchange factor activities, while these activities are found in separate		0.0004	0.0040	0000 45	0005 405		454	
gi 6324761 ret NP_014830.1	YOR187W	proteins in S. pombe and humans; 1ut1p Mitochondrial translation elongation factor Tu: comprises both GTPase and quanine	2	2.9991	0.3242	3063.15	3065.465	1	451	32 L.DAVDEYIPTPERDLNKPFLMPVEDIF.S
		nucleotide exchange factor activities, while these activities are found in separate								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	4.1095	0.3106	3065.78	3065.465	1	652	32 L.DAVDEYIPTPERDLNKPFLMPVEDIF.S
		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
gi 6324761 ref NP_014830.1	YOR187W	proteins in S. pombe and humans; Tuf1p	3	4.006	0.3215	3209.15	3210.624	1	684.4	28.846153 L.L1D1A1V1D1E1Y11P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D111F1.S
=		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
ail6324761 refIND 014830 41	YOR1971/	nucleotide exchange factor activities, while these activities are found in separate	2	3 4766	0.2597	2561 31	2561 961	1	280.0	35 E V111P1T1P1E1R4D11 1N2K2P1E11 1M1P1\/1E1D111E1 S
9-1002-10 (perfor _014000.1]		protonio in ol pomoc and namano, rump	4	0.4700	0.2007	2001.01	2001.001		200.0	

		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine								
gil6324761/refINP_014830_1	YOR187W	nucleotide exchange factor activities, while these activities are found in separate	2	3 0227	0 185	1926 65	1927 211	3	296	46 875 T GRVERGNI KKGEELEIV G
gil0324701[tel[14]_014030.1]	101(10/10	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine	2	5.0227	0.105	1320.05	1327.211	5	230	40.073 T.GRVERGNERRGEELEN.G
-1000470414ND 044000 41	VOD407W	nucleotide exchange factor activities, while these activities are found in separate	2	2 0022	0 4000	4050.00	4052 244		247.0	
gil6324761[ref]NP_014830.1]	YOR187W	Proteins in S. pombe and humans; 1011p Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in	2	3.0932	0.1993	1952.39	1953.211	1	347.2	53.125 1.G1R4V1E1R4G1N2L1K2K2G1E1E1L1E111V1.G
gi 6324775 ref NP_014844.1	YOR201C	mitochondrial 21S rRNA; Mrm1p	2	3.8509	0.4002	2660.59	2662.019	1	679	47.826088 D.F1F1V1E1I1P1F1G1G1I1E1K2G1N2R4A1P1E1P1I1V1D1S1L1.N
ail6324775/rofIND_014844_1	VOP201C	Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in mitochondrial 21S rPNA: Mrm1n	2	4 0310	0 4003	2632.65	2633.010	1	684.6	
gilo324775/10/14644.1	TORZUIC	Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in	2	4.0319	0.4093	2032.05	2033.019		004.0	43.032176 D.FF VEIFFOOIEKONKAFEFIVD3L.N
gi 6324775 ref NP_014844.1	YOR201C	mitochondrial 21S rRNA; Mrm1p	3	4.2546	0.3343	2662.55	2662.019	1	734.8	32.608696 D.F1F1V1E1I1P1F1G1G1I1E1K2G1N2R4A1P1E1P1I1V1D1S1L1.N
		ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase, required for translation								
gi 6324778 ref NP 014847.1	YOR204W	cause of male infertility; Ded1p	2	5.5094	0.4482	2055.47	2056.267	1	1052.8	65.625 Q.IRHIVEDCDMTPVGERQ.T
		ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase, required for translation								
ail6224770irofIND_014947_1	VOR204W	initiation of all yeast mRNAs; mutations in human DEAD-box DBY are a frequent	2	6 0152	0 519	2082 50	2022 267	1	007 E	50 375 O 1104H314/14E1D1C1D1M1T1D1/14C1E1D4O3 T
gil0324770110110F_014047.11	10K204W	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase, required for translation	2	0.0152	0.516	2062.39	2002.207		027.5	59.575 Q.TR4H5HVTETDTCTDTMTTTFTVTGTETR4Q2.T
		initiation of all yeast mRNAs; mutations in human DEAD-box DBY are a frequent								
gi 6324778 ref NP_014847.1	YOR204W	cause of male infertility; Ded1p Protein that forms a nucleolar complex with Mak21p that binds to 00S and 66S pro-	1	2.6601	0.2187	1364.68	1365.618	5	158.4	50 A.RFTKPTPVQKY.S
		ribosomes, as well as a nuclear complex with Noc3p that binds to 66S pre-								
		ribosomes; both complexes mediate intranuclear transport of ribosomal precursors;								
gi 6324780 ref NP_014849.1	YOR206W	Noc2p Brotein that forms a nucleolar complex with Mak21p that hinds to 00S and 66S pro-	2	3.6164	0.3505	1933.35	1934.29	2	581.3	46.875 Y.C1K2N2I1A1F1P1E1L1V1T1P1V1I1I1S1L1.R
		ribosomes, as well as a nuclear complex with Noc3p that binds to 66S pre-								
		ribosomes; both complexes mediate intranuclear transport of ribosomal precursors;								
gi 6324780 ref NP_014849.1	YOR206W	Noc2p Brotein that forms a publicator complex with Mak21n that hinds to 005 and 665 pro	2	3.5983	0.323	1801.67	1802.167	1	205.7	57.14286 F.FEKGIEIPKENKKLK.K
		ribosomes, as well as a nucleor complex with Noc3p that binds to 66S pre-								
		ribosomes; both complexes mediate intranuclear transport of ribosomal precursors;								
gi 6324780 ref NP_014849.1	YOR206W	Noc2p Brotein that forms a publicator complex with Mak21p that binds to 005 and 665 pro	2	5.1937	0.3192	2378.59	2379.548	4	481.4	47.22222 M.R4E1S1M1E1E1Q2D1K2E1R4E1T1E1E1A1K2L1L1.N
		ribosomes, as well as a nucleor complex with Noc3p that binds to 66S pre-								
		ribosomes; both complexes mediate intranuclear transport of ribosomal precursors;								
gi 6324780 ref NP_014849.1	YOR206W	Noc2p	2	3.4072	0.2676	1774.89	1773.151	4	680.3	50 C.K2N2I1A1F1P1E1L1V1T1P1V1I1I1S1L1.R
		Protein that forms a nucleolar complex with Mak21p that binds to 90S and 66S pre- ribosomes, as well as a nuclear complex with Noc3p that binds to 66S pre-								
		ribosomes; both complexes mediate intranuclear transport of ribosomal precursors;								
gi 6324780 ref NP_014849.1	YOR206W	Noc2p	2	3.3033	0.1943	1389.23	1389.656	2	516	70 Q.REVKEEKARLM.R
		Protein that forms a nucleolar complex with Mak21p that binds to 905 and 665 pre-								
		ribosomes; both complexes mediate intranuclear transport of ribosomal precursors;								
gi 6324780 ref NP_014849.1	YOR206W	Noc2p	2	3.7138	0.1692	1692.15	1692.993	1	797	65.38461 F.F1E1K2G1I1E1I1P1K2E1N2K2K2L1.K
		Mitochondrial GTPase related to dynamin, present in a complex containing Lloo1p								
		and Fzo1p; required for normal morphology of cristae and for stability of Tim11p;								
gi 6324785 ref NP_014854.1	YOR211C	homolog of human OPA1 involved in autosomal dominant optic atrophy; Mgm1p	2	4.4138	0.3324	1858.39	1860.117	1	1230.8	71.875 K.SSRVPDLSLVDLPGYIQ.V
		Mitochondrial GTPase related to dynamin, present in a complex containing Lloo1p								
		and Fzo1p; required for normal morphology of cristae and for stability of Tim11p;								
gi 6324785 ref NP_014854.1	YOR211C	homolog of human OPA1 involved in autosomal dominant optic atrophy; Mgm1p	2	4.2242	0.2792	1705.19	1704.961	1	1053.7	71.42857 S.R4V1P1D1L1S1L1V1D1L1P1G1Y1I1Q2.V
		Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p								
		and Fzo1p; required for normal morphology of cristae and for stability of Tim11p;								
gi 6324785 ref NP_014854.1	YOR211C	homolog of human OPA1 involved in autosomal dominant optic atrophy; Mgm1p	2	3.3531	0.252	1880.21	1881.117	1	650.9	50 K.S1S1R4V1P1D1L1S1L1V1D1L1P1G1Y1I1Q2.V
		Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p								
		and Fzo1p; required for normal morphology of cristae and for stability of Tim11p;								
gi 6324785 ref NP_014854.1	YOR211C	homolog of human OPA1 involved in autosomal dominant optic atrophy; Mgm1p	2	3.8081	0.3023	1685.29	1685.961	1	1105.7	71.42857 S.RVPDLSLVDLPGYIQ.V
		Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p								
		and Fzo1p; required for normal morphology of cristae and for stability of Tim11p;								
gi 6324785 ref NP_014854.1	YOR211C	homolog of human OPA1 involved in autosomal dominant optic atrophy; Mgm1p	2	2.9067	0.1876	1485.35	1484.698	2	313.1	63.636364 F.KVEFNDRHLTPK.S
		and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT								
gi 6324787 ref NP_014856.1	YOR213C	activity; Sas5p	2	4.7748	0.3459	2354.65	2354.726	1	1360	63.88889 S.KYFDLPWKVVSPEEEMSLR.I
		Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones								
ail6324787/refINP_014856.1	YOR213C	and nucleosomes and regulates transcriptional silencing; stimulates Saszp HAT	2	4.6018	0.3456	2379.61	2379.726	1	1338.7	63.88889 S.K2Y1F1D1L1P1W2K2V1V1S1P1E1E1E1M1S1L1R4.
3.1		Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones								
-: 100047071 (IND 044050 4)	VODAAOO	and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT	2	4 4 4 7 7	0.407	0054.54	0054 700		4040.4	
gilo324787 [rei]INP_014856.1]	TURZISC	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetvlates free histones	3	4.1177	0.197	2304.01	2354.726		1019.1	41.000004 S.RTFDLPWRVVSPEEEMSLR.I
		and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT								
gi 6324787 ref NP_014856.1	YOR213C	activity; Sas5p	3	4.8682	0.3334	2381.39	2379.726	1	1289.7	43.055553 S.K2Y1F1D1L1P1W2K2V1V1S1P1E1E1E1M1S1L1R4.I
		mitochondrial fatty acid synthase that produces intermediates for phospholipid								
gi 6324795 ref NP_014864.1	YOR221C	remodeling; Mct1p	2	4.7353	0.3671	2236.59	2234.6	1	406.2	52.941177 S.TVLRPVQEPLYDYIWDIL.K
		Predicted malonyl-CoA:ACP transferase, putative component of a type-II								
ail6324795/refINP_014864_1	YOR221C	mitochondrial fatty acid synthase that produces intermediates for phospholipid remodeling: Mct1p	2	3 9172	0 1682	2257 27	2257.6	1	268.7	47 058823 S T1//1 1R4P1//102E1P1 1Y1D1Y1I1W2D1 1 1 K
gilo24/30[cill4]_014004.1]	10102210	Predicted malonyl-CoA:ACP transferase, putative component of a type-II	-	0.0172	0.1002	2201.21	2201.0		200.7	
		mitochondrial fatty acid synthase that produces intermediates for phospholipid								
gijb324795 ret NP_014864.1	YUR221C	remodeling; Mct1p Protein of the mitochondrial matrix involved in protein import into mitochondria: acts	2	3.021	0.2196	1892.45	1893.192	1	312.7	53.571426 S. IVLRPVQEPLYDYIW.D
		as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli								
gi 6324806 ref NP_014875.1	YOR232W	GrpE; Mge1p	2	4.7172	0.3406	2022.49	2023.072	1	770.9	65.625 E.ESKENNEDLTEEQSEIK.K
		erotein or the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of F_coli								
gi 6324806 ref NP_014875.1	YOR232W	GrpE; Mge1p	2	3.8212	0.2423	2043.21	2045.072	1	350	53.125 E.E1S1K2E1N2N2E1D1L1T1E1E1Q2S1E1I1K2.K

		Protein of the mitochondrial matrix involved in protein import into mitochondria; acts								
gi 6324806 ref NP_014875.1	YOR232W	as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p Protein of the mitochondrial matrix involved in protein import into mitochondria; acts	2	4.412	0.3902	2209.41	2208.433	1	547.2	50 H.GIEKLDPLGEPFDPNKHEAT.F
gi 6324806 ref NP_014875.1	YOR232W	as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p Protein of the mitochondrial matrix involved in protein import into mitochondria: acts	2	4.0648	0.3935	2232.37	2233.433	1	662.9	52.63158 H.G111E1K2L1D1P1L1G1E1P1F1D1P1N2K2H3E1A1T1.F
gi 6324806 ref NP_014875.1	YOR232W	as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p Protein of the mitochondrial matrix involved in protein import into mitochondria: acts	3	4.3377	0.42	3793.07	3794.209	1	562.7	24.242424 H.GIEKLDPLGEPFDPNKHEATFELPQPDKEPGTVF.H
gi 6324806 ref NP_014875.1	YOR232W	as a cochaperone and a nucleotide release factor for Soc1p; here homolog of E. coli GrpE; Mge1p Protein of the mitochondrial matrix involved in protein import into mitochondria; acts	3	5.1792	0.3007	3835.97	3835.209	1	1054.2	H.G111E1K2L1D1P1L1G1E1P1F1D1P1N2K2H3E1A1T1F1E1L1P1Q2P1D1K2E1P1G 30.303032 1T1V1F1.H
gi 6324806 ref NP_014875.1	YOR232W	Frozen drine immessive management and matching the product for Society have interrupted in the interrupt of the society interrupt of the society interrupt of the society interrupt of the society interrupt of the interchandrial matrix involved in protein into mitochondria: acts	3	3.8462	0.2927	3494.69	3494.882	1	536.2	22.5 E.KLDPLGEPFDPNKHEATFELPQPDKEPGTVF.H
gi 6324806 ref NP_014875.1	YOR232W	as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p Ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to	2	3.035	0.4085	1906.51	1907.133	1	635.8	59.375 H.GIEKLDPLGEPFDPNKH.E
gi 6324808 ref NP_014877.1	YOR234C	RpI33Ap and has similarity to rat L35a; rpI33b null mutant exhibits normal growth while rpI33a rpI33b double null mutant is inviable; RpI33bp Ribosomal protein L37 of the large (6005) ribosomal subunit, nearly identical to	1	2.7508	0.1985	1207.57	1208.406	1	223.3	66.66667 T.FRNNLPAKTF.G
gi 6324808 ref NP_014877.1	YOR234C	Rpl33Ap and has similarity to rat L35a; rpl33b null mutant exhibits normal growth while rpl33a rpl33b double null mutant is inviable; Rpl33bp	1	2.8126	0.2359	1223.65	1224.406	2	168.6	61.11111 T.F1R4N2N2L1P1A1K2T1F1.G
gi 6324825 ref NP_014894.1	YOR251C	catalyzes transfer of the sulfane atom of thiosulfate to cyanide to form sulfite and thiocyanate; Yor251cp	2	4.188	0.3926	3192.81	3193.5	1	530.6	34.482758 L.GRFEGTEPEPRSDIPSGHIPGTQPLPYGSLL
gi 6324825 ref NP 014894.1	YOR251C	catalyzes transfer of the sulfane atom of thiosulfate to cyanide to form sulfite and thiocyanate; Yor251cp	3	5.2469	0.4358	3233.09	3232.5	1	729.1	30.172413 L.G1R4F1E1G1T1E1P1E1P1R4S1D1I1P1S1G1H3I1P1G1T1Q2P1L1P1Y1G1S1L1.L
gil6324825lrefINP_014894_1	YOR251C	catalyzes transfer of the sulfane atom of thiosulfate to cyanide to form sulfite and thiocyanate. Yor251cp	3	3 976	0.333	3191 99	3193.5	1	569.8	
gil6324825[rofIND_014804.1]	VOR2510	catalyzes transfer of the sulfane atom of thiosulfate to cyanide to form sulfite and	2	4 2104	0.000	2074.25	2072.21	1	620.0	
gilo32482511e11NF_014894.11	TOR251C	catalyzes transfer of the sulfane atom of thiosulfate to cyanide to form sulfite and	3	4.2194	0.204	2974.25	2972.21		029.9	
gi 6324825 ref NP_014894.1	YOR251C	thiocyanate; Yor251cp catalyzes transfer of the sulfane atom of thiosulfate to cyanide to form sulfite and	2	3.9887	0.4017	2969.99	2972.21	1	421.9	36.53846 L.G1R4F1E1G111E1P1E1P1R4S1D111P1S1G1H31P1G111Q2P1L1P1Y1.G
gi 6324825 ref NP_014894.1	YOR251C	thiocyanate; Yor251cp Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP- dependent and post-translational SPP-independent protein tarretion and import into	2	3.3058	0.2096	2936.13	2936.21	1	270.8	30.769232 L.GRFEGTEPEPRSDIPSGHIPGTQPLPY.G
gi 6324828 ref NP_014897.1	YOR254C	the ER; Sec63p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	3.4933	0.1718	2150.55	2151.405	1	668.5	53.125 H.E1F1K2Q2F1F1P1D1L1Q2P1T1D1F1E1K2L1.L
gi 6324828 ref NP_014897.1	YOR254C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	4.0881	0.3368	2129.23	2130.405	1	1120.7	62.5 H.EFKQFFPDLQPTDFEKL.L
gi 6324828 ref NP_014897.1	YOR254C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	3.4411	0.2783	2865.89	2866.232	1	370.1	37.5 N.D1W2E1I1G1T111K2I1P1L1G1Q2P1A1P1E1T1V1G1D1F1F1F1F1R4.V
gi 6324828 ref NP_014897.1	YOR254C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	3.3851	0.3392	2834.37	2835.232	1	261.7	35.416664 N.DWEIGTIKIPLGQPAPETVGDFFFR.V
gi 6324828 ref NP_014897.1	YOR254C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	5.226	0.4459	2361.67	2363.624	1	1670.8	63.88889 F.A1H3E1F1K2Q2F1F1P1D1L1Q2P1T1D1F1E1K2L1.L
gi 6324828 ref NP_014897.1	YOR254C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	3.7356	0.424	2235.61	2234.603	1	756.2	60.526318 G.TIKIPLGQPAPETVGDFFFR.V
gi 6324828 ref NP_014897.1	YOR254C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	4.2974	0.397	1784.51	1784.062	1	2197.9	75 G.TIKIPLGQPAPETVGDF.F
gi 6324828 ref NP_014897.1	YOR254C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	4.6784	0.388	1805.27	1803.062	1	2242.6	78.125 G.T111K211P1L1G1Q2P1A1P1E1T1V1G1D1F1.F
gi 6324828 ref NP_014897.1	YOR254C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p	2	3.2548	0.24	2098.89	2099.415	1	498.2	44.444447 G.T111K211P1L1G1Q2P1A1P1E1T1V1G1D1F1F1F1.R
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	3	5.0752	0.2513	3604.91	3604.612	1	825	31.034481 Q.SHEQQPEQPQETEEHHEEEPSRVDPEQEAH.N
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	2	4.3379	0.2967	1950.43	1951.127	1	592.9	60.000004 F.A1I1R4D1D1R4D1H3I1N2P1D1D1L1M1K2.A
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	2	4.0934	0.3225	1925.53	1925.127	1	428.2	53.333336 F.AIRDDRDHINPDDLMK.A
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	2	3.8251	0.3517	1995.11	1996.205	1	316.4	46.875 F.AIRDDRDHINPDDLMKA.V
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	2	3.5132	0.2685	1708.43	1707.971	1	587.9	67.85714 L.DRKVEIPLPNEAGRL.E

gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	1	2.3607	0.3226	1491.88	1490.728	8	189.7	45.454548 M.R4I1L1P1R4E1T1D1P1L1V1Y1.N
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	3	3.9098	0.2026	3779.51	3780.742	3	292.4	Q.Q2S1H3E1Q2Q2P1E1Q2P1Q2E1T1E1E1H3H3E1E1E1P1S1R4V1D1P1E1Q2E1A 25.833332 1H3.N
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	3	6.1566	0.3446	3648.38	3650.612	1	1611.4	Q.S1H3E1Q2Q2P1E1Q2P1Q2E1T1E1E1H3H3E1E1E1P1S1R4V1D1P1E1Q2E1A1H 38.793106 3.N
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	2	3.8969	0.3922	1696.93	1698.015	1	1266.7	73.07692 L.REVIELPLKNPEIF.Q
gi 6324833 ref NP_014902.1	YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p Subunit of vacular-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p);	2	4.1075	0.257	1715.91	1717.015	1	1090.2	65.38461 L.R4E1V111E1L1P1L1K2N2P1E111F1.Q
gi 6324844 ref NP_014913.1	YOR270C	Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V- ATPase complexes of the Golgi and endosomes; Vph1p 1 Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p);	1	2.6526	0.256	1583.72	1584.813	1	437	53.846157 L.IAEGWIPRDELATL.Q
gi 6324844 ref NP_014913.1	YOR270C	Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V- ATPase complexes of the Golgi and endosomes; Vph1p Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V/ATPase complexes of the vacuola while Stv1p is located in V-	2	3.7008	0.2939	1402.37	1399.59	1	1316.1	86.36364 E.GWIPRDELATLQ.A
gi 6324844 ref NP_014913.1	YOR270C	ATPase complexes of the Golgi and endosomes; Vph1p Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Volation is corrected in V/ATBase expendingene of the unrevelop while Stv1p is located in V/	2	3.3208	0.292	1731.73	1732.943	1	643.9	60.714287 L.I1A1E1G1W2I1P1R4D1E1L1A1T1L1Q2.A
gi 6324844 ref NP_014913.1	YOR270C	ATPase complexes of the Golgi and endosomes; Vph1p Subunit of vacualar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Subunit of vacualar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p);	1	2.4231	0.175	1416.55	1416.59	9	156.2	45.454548 E.G1W2I1P1R4D1E1L1A1T1L1Q2.A
gi 6324844 ref NP_014913.1	YOR270C	ATPase complexes of the Golgi and endosomes; Vph1p Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p);	2	3.8318	0.2213	1418.49	1416.59	1	1012	77.27273 E.G1W2I1P1R4D1E1L1A1T1L1Q2.A
gi 6324844 ref NP_014913.1	YOR270C	Vph1p is located in V-AIPase complexes of the vacuole while Stv1p is located in V- ATPase complexes of the Golgi and endosomes; Vph1p Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p);	2	3.7379	0.2454	1988.45	1989.275	1	690	53.125 A.Q2Y1R4E1I1N2A1G1L1P1T1I1V1T1F1P1F1.M
gi 6324844 ref NP_014913.1	YOR270C	Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V- ATPase complexes of the Golgi and endosomes; Vph1p Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p);	2	3.7574	0.274	2342.73	2341.723	1	501.9	39.473686 A.Q2Y1R4E111N2A1G1L1P1T111V1T1F1P1F1M1F1A1.I
gi 6324844 ref NP_014913.1	YOR270C	Vph1 p is located in V-ATPase complexes of the vacuole while Stv1p is located in V- ATPase complexes of the Golgi and endosomes; Vph1p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	1	2.4634	0.1861	1415.62	1416.574	5	136.5	45.454548 A.E1G1W2I1P1R4D1E1L1A1T1L1.Q
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	3	4.456	0.4466	3076.1	3077.181	1	994.2	32.692307 N.NMTGGEPIDPRDLDWDGPDDPDNPHNW.S
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	2	4.1711	0.5174	3074.53	3077.181	1	1031.3	46.153847 N.NMTGGEPIDPRDLDWDGPDDPDNPHNW.S
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	2	3.0937	0.4342	2095.89	2098.447	1	437.6	50 A.RDAETGELLPVVPEKFLIA.C
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	2	3.6553	0.2549	2121.61	2121.447	1	377.8	47.22222 A.R4D1A1E1T1G1E1L1L1P1V1V1P1E1K2F1L1I1A1.C
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	1	3.2643	0.2964	1436.63	1436.796	2	583.6	58.333332 F.IALMPETHKGIIL.R
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	1	2.9853	0.1582	1451.64	1452.796	1	551.3	58.333332 F.I1A1L1M1P1E1T1H3K2G1I1IL1.R
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	2	2.9413	0.2714	2350.83	2351.794	1	475.9	33.333336 L.GLSTVIGAPLSEVFGRKPVYLF.S
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	1	3.215	0.3547	1343.24	1342.64	1	674.2	54.166668 L.S1P1F1L1G1P1V1L1S1P1I1M1A1.G
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	3	5.5368	0.4399	3113.75	3114.181	1	800.3	31.730768 N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	2	3.0769	0.2646	3113.87	3114.181	1	365.3	28.846153 N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	3	4.3542	0.1965	1820.69	1821.05	3	1150.9	46.666668 A.R4D1A1E1T1G1E1L1L1P1V1V1P1E1K2F1.L
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	2	3.5363	0.3665	1799.81	1801.05	1	521.3	60.000004 A.RDAETGELLPVVPEKF.L
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	2	3.8949	0.2375	1822.55	1821.05	1	457.9	60.000004 A.R4D1A1E1T1G1E1L1L1P1V1V1P1E1K2F1.L
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine:	3	4.4479	0.3013	3533.33	3534.671	5	432.6	N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2S1S1L 23.333334 1K2.K
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p Polyamine transport protein, recognizes spermine, putrescine, and spermidine:	2	3.1211	0.1754	1453.53	1452.796	8	549.7	66.66667 F.I1A1L1M1P1E1T1H3K2G1I1IL1.R
gi 6324847 ref NP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	3.5762	0.2839	2029.85	2031.226	1	457.6	53.125 L.R4T1M1E1T1D1P1S1T1R4E1K2P1G1E1R4L1.S

		Polyamine transport protein, recognizes spermine, putrescine, and spermidine;								
ail6324847/refINP_014916.1	YOR273C	localizes to the plasma membrane; member of the major facilitator superfamily;	3	5.4956	0.4147	3130.64	3130.181	1	579.7	29.807693 N.N2M\$T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gilooz to tritolitit _of to total	10112100	Polyamine transport protein, recognizes spermine, putrescine, and spermidine;	0	0.1000	0.1111	0100.01	0100.101	•	0.0.1	
	VODOZOC	localizes to the plasma membrane; member of the major facilitator superfamily;	2	2 50 44	0.004	0704.00	0700 70	2	200.7	
gilo324647 [rei]NP_014916.1]	TUR2/3C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine:	2	3.5241	0.221	2764.23	2/03.78	3	309.7	30.95652 T.GTGTETPTTDTPTR4DTLTDTW2DTGTPTDTDTPTDTN2PTH3N2W2.5
		localizes to the plasma membrane; member of the major facilitator superfamily;								
gi 6324847 ref NP_014916.1	YOR273C	Tpo4p Balvamina transport protein, recognized apermina, putrassing, and apermiding:	3	6.0002	0.3794	2762.9	2763.78	1	1438.2	40.217392 T.G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
		localizes to the plasma membrane; member of the major facilitator superfamily;								
gi 6324847 ref NP_014916.1	YOR273C	Тро4р	3	5.9982	0.4331	3113.42	3114.181	1	831.7	30.769232 N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
		Polyamine transport protein, recognizes spermine, putrescine, and spermidine;								
gi 6324847 ref NP_014916.1	YOR273C	Tpo4p	2	4.8266	0.4188	3111.67	3114.181	1	967.7	44.230766 N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
		Phosphoprotein of the mRNA cap-binding complex involved in translational control,								
ail6224950[rofIND_014010_1]	VOROZEW	repressor of cap-dependent translation initiation, competes with eIF4G for binding to	2	1 0051	0.2551	2112.05	2112 255	1	E 4 E 4	50 S S4N/2D4D141D4T1D4D114//141D4K/2D11411C1E1 N
gilo324030/rei/iNF_014919.1/	10K2/6W	Phosphoprotein of the mRNA cap-binding complex involved in translational control.	2	4.0004	0.2551	2113.05	2113.335		040.4	50 5.5 IN2R4F IAIDTT R4DITTY IAIDTR2F ITTE IGTF 1.N
		repressor of cap-dependent translation initiation, competes with eIF4G for binding to								
gi 6324850 ref NP_014919.1	YOR276W	elF4E; Caf20p	2	3.8685	0.2262	2084.55	2086.355	1	515.8	47.22222 S.SNRPADTRDIVADKPILGF.N
gi 6324857 ref NP_014926.1 gi 6324857 ref NP_014926.1	YOR283W	hypothetical protein; Yor283wp	3	4.2824	0.3713	2416.25	2416.577	1	980.8	37.5 M. I1K2E1V1P1Y1Y1C1D1N2D1D1N2N2I1I1R4L1F1.
gil6324857 refINP_014926.1	YOR283W	hypothetical protein; Yor283wp	3	4.8591	0.4368	2414.72	2416.577	1	1203.3	44.444447 M.TIK2ETV1P1Y1Y1C1D1N2D1D1N2N2I1I1R4L1F1
gi 6324857 ref NP_014926.1	YOR283W	hypothetical protein; Yor283wp	2	5.6112	0.494	2416.41	2416.577	1	1189	66.66667 M.T1K2E1V1P1Y1Y1C1D1N2D1D1N2N2I1I1R4L1F1.
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VOD240C	synthesis; component of the small subunit processome complex, which is required	2	0.0440	0.0455	4000.05	4005 044		4042.0	
gi 6324886 ret NP_014955.1	YOR310C	for processing of pre-185 rRNA; Nop58p Protein involved in pre-rRNA processing 18S rRNA synthesis, and spoRNA	2	2.9418	0.2155	1636.25	1635.641	1	1043.8	67.85714 L.AEDRDDSGDIGLESR.A
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.5248	0.2913	1656.15	1656.641	1	819.8	64.28571 L.A1E1D1R4D1D1S1G1D1I1G1L1E1S1R4.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VOD240C	synthesis; component of the small subunit processome complex, which is required	2	4 9745	0.0000	0400.05	0400 045		700 5	
gil6324886[rei]NP_014955.1]	TORSTOC	Protein involved in pre-r8X RNA; N0p38p	2	4.3745	0.3000	2138.25	2139.315	1	700.5	56.623532 A.STETTIDILISTETTLIPTETETTETETR4VTK2.1
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	5.5005	0.3507	2190.51	2188.394	1	913.3	63.88889 K.ASETDLSEILPEEIEERVK.T
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VOD240C	synthesis; component of the small subunit processome complex, which is required	2	2 025	0.0400	4000.00	4004 404		750.0	
gil6324886[fei]NP_014955.1]	TORSTOC	Protein involved in pre-rRNA processing 18S rRNA synthesis and snoRNA	2	3.035	0.2186	1699.99	1901.121	1	/52.0	60.000004 E.IDLSEILPEEIEERVK.I
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.1769	0.2534	1919.53	1921.121	1	566.3	56.666668 E.T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/rofIND 014955 1	VOP310C	synthesis; component of the small subunit processome complex, which is required for processing of pro-18S rBNA: Nop58p	2	3 2170	0 1930	2120 43	2121 3/2	3	352.2	
gil0324000[rei]NF_014333.1]	101(3100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	2	5.2175	0.1000	2130.43	2131.342	5	332.2	44.11703 S.ETDESELF ELIELININ.A
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.6212	0.2301	2312.29	2313.499	1	630.7	50 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/refINP_014955_11	YOR310C	for processing of pre-18S rRNA: Non580	2	3 6299	0 1895	2217 71	2218 42	1	719.4	52 77778 A SETDI SEILPEEIEERVKT A
giloo2 iccolicit ii _c i iccoli i	10110100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	-	0.0200	0.1000		2210.12		110.1	
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.2595	0.3275	2288.71	2289.499	1	769.8	57.894737 K.ASETDLSEILPEEIEERVKT.A
		Protein involved in pre-rkina processing, 185 rkina synthesis, and snokina synthesis: component of the small subunit processome complex, which is required								
ail6324886/refINP 014955.11	YOR310C	for processing of pre-18S rRNA: Nop58p	1	2.8348	0.1704	1416.47	1416.72	6	274.6	59.090908 A.I1K2E1Y1L1P1E1L1L1P1G1M1.S
3.1		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	5.2788	0.3415	2386.91	2385.577	1	996	57.5 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.1714	0.1517	1316.75	1316.439	1	493.2	65 L.P1E1E1I1E1E1R4V1K2T1A1.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VODOLOO	synthesis; component of the small subunit processome complex, which is required		5 40 47	0.0000	0044.00	0040 400		700.0	
gi 6324886 ret NP_014955.1	YOR310C	for processing of pre-185 rRNA; Nop58p Protein involved in pre-rRNA processing 18S rRNA synthesis, and spoRNA	2	5.1247	0.2696	2314.63	2313.499	1	798.3	60.526318 A.S1E111D1L1S1E111L1P1E1E111E1E1R4V1K211A1.A
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	1	2.3054	0.1536	1315.31	1316.439	5	306.7	55 L.P1E1E1I1E1E1R4V1K2T1A1.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VOD240C	synthesis; component of the small subunit processome complex, which is required	2	2 4002	0.0040	4050 54	4050 074	2	240	
gil6324886[fei]NP_014955.1]	TORSTOC	Protein involved in pre-rRNA processing 18S rRNA synthesis and snoRNA	2	3.1603	0.2243	1000.01	1000.874	2	346	57.092307 S.EILPEEIEERVKTA.A
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.8859	0.2725	2071.67	2073.305	1	569.8	55.88235 E.TDLSEILPEEIEERVKTA.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/refINP_014955_11	YOR310C	synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA: Non580	2	4 6046	0 3888	2200 30	2289 499	1	549.6	52 63158 & SETDI SEILPEELEERVIKTA A
gilosz4000[rei]til _014303.1]	1010100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	-	4.0040	0.0000	2200.00	2203.433		040.0	
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.4005	0.337	1676.29	1674.874	1	788.8	73.07692 S.E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
gi 6324886 ref NP 014955.11	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.4364	0.2358	1301.35	1301.439	1	636.4	70 L.PEEIEERVKTA.A
an and an arrest of		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	-							
		synthesis; component of the small subunit processome complex, which is required	-							
gi 6324886 ref NP_014955.1	YOR310C	tor processing of pre-18S rRNA; Nop58p Protein involved in pre-rRNA processing 18S rPNA synthesis, and spoPNA	2	4.8636	0.4402	2358.53	2360.577	1	1257.3	60.000004 K.ASETDLSEILPEEIEERVKTA.A
		synthesis; component of the small subunit processione complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.0784	0.3283	1745.61	1743.952	1	796.6	67.85714 L.SEILPEEIEERVKTA.A

		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.0498	0.1699	1416.93	1414.599	3	394.9	59.090908 I.LPEEIEERVKTA.A
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	3	5.151	0.3566	2358.77	2360.577	1	2148.5	47.5 K.ASETDLSEILPEEIEERVKTA.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VOD240C	synthesis; component of the small subunit processome complex, which is required	0	0.0740	0.0570	4074 54	1070.0	-	205.2	
gil6324886[rei]NP_014955.1]	TORSTOC	Protein involved in pre-rRNA processing 18S rRNA synthesis and snoRNA	2	3.3748	0.2573	1974.51	1972.2	5	365.2	40.875 T.DLSEILPEEIEERVKTA.A
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.5512	0.3873	2225.03	2225.42	1	617.4	55.555557 S.E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VODALAO	synthesis; component of the small subunit processome complex, which is required		5 0504	0.0757	0.400.00	0.400.040		074.0	
gi 6324886 ret NP_014955.1	YOR310C	for processing of pre-185 rRNA; Nop58p Protein involved in pre-rRNA processing 18S rRNA synthesis and spoRNA	3	5.3501	0.3757	2402.39	2403.646	1	971.6	42.5 R.SKASET DLSEILPEEIEERVK.T
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.896	0.3219	2602.33	2603.83	1	1203.4	50 R.S1K2A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VODALAO	synthesis; component of the small subunit processome complex, which is required		0.0004	0 4500	0000.00	0000.00		1007	
gi 6324886 ret NP_014955.1	YOR310C	for processing of pre-185 rRNA; Nop58p Protein involved in pre-rRNA processing 18S rRNA synthesis and spoRNA	3	6.8684	0.4589	2606.09	2603.83	1	1267	40.909092 R.S1K2A1S1E111D1L1S1E111L1P1E1E111E1E1R4V1K211A1.A
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	3	4.0472	0.2243	2211.29	2211.394	2	804.7	34.72222 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VODALAO	synthesis; component of the small subunit processome complex, which is required		5 00 4	0.0705	0004.47	0000 504		4400	
gi 6324886 ret NP_014955.1	YOR310C	for processing of pre-185 rkNA; Nop58p Protein involved in pre-rPNA processing 18S rPNA synthesis, and snoPNA	2	5.394	0.3795	2204.47	2203.524	1	1180	66.666671.K2E1Y1L1P1E1L1L1P1G1M1S1D1N2D1L1S1K2M1.S
		synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	5.4545	0.415	2296.43	2294.683	1	1585.1	65.789474 A.IKEYLPELLPGMSDNDLSKM.S
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p Brotein involved in pre-rBNA processing, 18S rBNA synthesis, and appBNA	3	4.1028	0.3196	2295.35	2294.683	1	2251.9	47.368423 A.IKEYLPELLPGMSDNDLSKM.S
		synthesis: component of the small subunit processome complex, which is required								
ail6324886/refINP 014955.11	YOR310C	for processing of pre-18S rRNA: Nop58p	1	2.7789	0.2514	1194.42	1195.348	2	463.9	65 L.PGMSDNDLSKM.S
5111		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	3	4.7146	0.3033	2944.55	2944.374	1	648.2	30.208334 L.D1I1Y1R4A1I1K2E1Y1L1P1E1L1L1P1G1M1S1D1N2D1L1S1K2M1.S
		synthesis: component of the small subunit processome complex, which is required								
ail6324886/refINP 014955.11	YOR310C	for processing of pre-18S rRNA: Nop58p	1	3.0279	0.3172	1287.64	1288.489	1	396.6	70 L.KTKHDTPKYGL.L
5111		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.8565	0.3582	2007.13	2007.392	1	881.7	58.333332 R.M1K2A1I1A1P1N2L1T1Q2L1V1G1E1L1V1G1A1R4.L
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/refINP_014955_11	YOR310C	for processing of pre-18S rRNA: Nop58p	2	4 6711	0.312	2362 79	2360 577	1	941.3	55 K ASETDI SEIL PEELERVKTA A
gilooz isocitolitit _ot isociti	10110100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	-		0.012	2002.10	2000.011	·	011.0	
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.2113	0.3746	2202.25	2202.42	1	510	50 S.ETDLSEILPEEIEERVKTA.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/refINP 014955.1	YOR310C	for processing of pre-18S rRNA: Nop58p	2	4,2625	0.3388	2208.73	2211.394	1	531	52,77778 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
gilooz isocitolitit _ot isociti	10110100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	-	1.2020	0.0000	2200.10	2211.001	·	001	
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.6712	0.393	2119.69	2117.315	1	753.5	61.764706 A.SETDLSEILPEEIEERVK.T
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/refINP_014955_11	YOR310C	for processing of pre-18S rRNA: Nop58p	3	4 2753	0 2519	2209 7	2211 394	2	699.2	34 72222 K A1S1E1T1D1I 1S1E1I1I 1P1E1E1I1E1E1R4V1K2 T
gil0024000[rei]14 _014000.1]	1010100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	0	4.2700	0.2010	2200.1	2211.004	-	000.2	
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	3	4.7239	0.3253	2387.54	2385.577	1	914.7	33.75 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/refINP_014955_1	YOR310C	for processing of pre-18S rRNA: Nop580	з	4 4601	0 3213	2360.09	2360 577	1	1281 7	40 K ASETDI SEIL PEELEERVIKTA A
gil0324000[rei]147_014333.1]	1013100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	5	4.4001	0.3213	2300.03	2300.377	1	1201.7	
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	5.0396	0.3407	2403.47	2403.646	1	1250.9	60.000004 R.SKASETDLSEILPEEIEERVK.T
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
aile224996 rofIND 014055 1	VOP210C	synthesis; component of the small subunit processome complex, which is required	2	4 756	0 4000	2574 57	2575 02	1	1252.0	
gilo324860[rei]i4F_014955.1]	TORSTOC	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	2	4.750	0.4099	2014.01	2575.65	1	1333.9	52.272724 R.SRASET DESELFECTER VRTA.A
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.8621	0.3689	2601.91	2603.83	1	1245.8	52.272724 R.S1K2A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/refINP_014955_1	YOR310C	synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA: Nop580	2	6.031	0.4018	2316 53	2317 683	1	1752 4	68 42105 & HK2E1V1I 1P1E1I 1I 1P1G1M1S1D1N2D1I 1S1K2M1 S
gil0024000[rei]14 _014000.1]	1010100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	-	0.001	0.4010	2010.00	2017.000		1102.4	
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	5.2646	0.4343	2293.57	2294.683	1	1232.8	60.526318 A.IKEYLPELLPGMSDNDLSKM.S
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
gil6324886/refINP_014955_1	YOR310C	syntnesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA: Nop58p	3	4 6075	0.370/	2519 57	2521 95	1	917 2	38 095238 Y RAIKEYI PELI PGMSDNDI SKM S
9-1002-0001-0114F_014000.1	. 010100	Protein involved in pre-rRNA processing, 18S rRNA synthesis. and snoRNA	5	4.0070	0.07.04	2013.01	2021.30	'	511.2	
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.8505	0.4729	2521.39	2521.95	1	940.1	54.761906 Y.RAIKEYLPELLPGMSDNDLSKM.S
		Protein involved in pre-rKNA processing, 18S rRNA synthesis, and snoRNA								
gi 6324886 ref NP 014955.11	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.7727	0.4005	1915.93	1916.309	1	1626.9	70 Q.LEKLLEEIKKDKKSTL.I
2 <u>-</u>			-							

		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
	VODOLOO	synthesis; component of the small subunit processome complex, which is required				4 400 74				
gij6324886 ret NP_014955.1	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	1	3.44	0.3388	1400.74	1401.649	1	682.8	72.72727 L.KIKHDIPKYGLL.Y
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ret NP_014955.1	YOR310C	tor processing of pre-185 rRNA; Nop58p Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	2	3.1468	0.2183	1564.19	1564.825	1	530.4	70.83333 L.KTKHDTPKYGLLY.H
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p Protein involved in pre-rRNA processing 18S rRNA synthesis and spoRNA	2	3.9847	0.2957	2074.37	2073.35	1	485.2	50 K.E1Y1L1P1E1L1L1P1G1M1S1D1N2D1L1S1K2M1.S
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	1	3.297	0.208	1504.51	1504.798	1	410.7	62.5 A.I1K2E1Y1L1P1E1L1L1P1G1M1S1.D
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	1	3.3032	0.1853	1490.6	1490.798	1	509.2	66.66667 A.IKEYLPELLPGMS.D
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	5.0593	0.3457	2048.85	2051.237	1	951.2	71.875 S.E1T1D1L1S1E111L1P1E1E1I1E1E1R4V1K2.T
		Protein involved in pre-rRNA processing, 185 rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.1764	0.3504	2027.73	2030.237	1	799.1	59.375 S.ETDLSEILPEEIEERVK.T
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	4.9844	0.427	2209.79	2211.394	1	832.1	63.88889 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis: component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	1	2.8408	0.2019	1415.56	1416.72	2	280.9	59.090908 A.I1K2E1Y1L1P1E1L1L1P1G1M1.S
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	1	2.6325	0.2364	1402.48	1403.72	6	272.7	54.545456 A.IKEYLPELLPGM.S
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
gi 6324886 ref NP 014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.6729	0.2765	1414.69	1416.72	4	764.7	77.27273 A.I1K2E1Y1L1P1E1L1L1P1G1M1.S
		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA								
ail6324886/refINP_014955.11	YOR310C	synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.4365	0.3878	2294.61	2294.683	1	1803.9	68.42105 A.IKEYLPELLPGMSDNDLSKM.S
3-1		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	-							
gil6324886lrefINP_014955.11	YOR310C	synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA: Nop58p	3	4.473	0.2905	2295.86	2294.683	1	2339.7	48.684208 A.IKEYLPELLPGMSDNDLSKM.S
3-1		Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	-							
ail6324886/refINP_014955_11	YOR310C	synthesis; component of the small subunit processome complex, which is required	3	4 5179	0 2535	2386 52	2385 577	1	1091 5	37.5 K & 1S1E1T1D1 1S1E1 1 1P1E1E1 1E1E1B4\/1K2T1&1 &
gilooz isocholitik _orrisocrif	1010100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	0		0.2000	2000.02	2000.011		100110	
ail6324886/refINP_014955_11	YOR310C	synthesis; component of the small subunit processome complex, which is required	2	3 912	0 3262	2384 43	2385 577	1	508	47.5 K &1S1E1T1D1 1S1E1 1 1P1E1E1 1E1E1B4\/1K2T1&1 &
gil0524000[rei]i4r_014955.1]	1013100	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	2	5.512	0.3202	2304.43	2303.311	,	500	
ail6224996IrofIND_014055_1	VOP210C	synthesis; component of the small subunit processome complex, which is required	2	4 5207	0.2251	2522.11	2521.05	1	1106.2	
gilo324866/rei/INP_014955.1/	TURSIUC	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	3	4.5207	0.2251	2023.11	2021.90	1	1106.2	40.476192 T.KAIKETLPELLPGMSDINDLSKM.S
	VODOLOO	synthesis; component of the small subunit processome complex, which is required		4 00 4 0	0.0500	1005 17	4007 000		1050.0	
gi 6324886 ret NP_014955.1	YOR310C	Protein involved in pre-185 rRNA; Nop58p Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	2	4.9212	0.3506	1935.47	1937.309	1	1359.6	66.66667 Q.L1E1K2L1L1E1E111K2K2D1K2K2S111L1.I
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ret NP_014955.1	YOR310C	tor processing of pre-185 rRNA; Nop58p Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA	2	3.2349	0.2354	1304.23	1304.489	1	286.3	70 L.K211K2H3D111P1K2Y1G1L1.L
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p Protein involved in pre-rRNA processing 18S rRNA synthesis and spoRNA	1	2.5434	0.2873	1305.43	1304.489	1	350.7	60.000004 L.K2T1K2H3D1T1P1K2Y1G1L1.L
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p Protein involved in pre-rRNA processing, 18S rRNA synthesis, and spoRNA	1	3.738	0.3718	1581.46	1582.825	1	607.7	62.5 L.K2T1K2H3D1T1P1K2Y1G1L1L1Y1.H
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p Protein involved in pre-rRNA processing 18S rRNA synthesis and spoRNA	2	4.0859	0.2365	1583.53	1582.825	1	592.7	70.83333 L.K2T1K2H3D1T1P1K2Y1G1L1L1Y1.H
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p Protein involved in pre-rRNA processing, 18S rRNA synthesis, and spoRNA	2	2.9782	0.2818	1504.47	1504.798	3	452.2	58.333332 A.I1K2E1Y1L1P1E1L1L1P1G1M1S1.D
		synthesis; component of the small subunit processome complex, which is required								
gi 6324886 ref NP_014955.1	YOR310C	for processing of pre-18S rRNA; Nop58p	2	3.5721	0.3084	2053.65	2053.35	1	836.4	61.764706 K.EYLPELLPGMSDNDLSKM.S
		involved in the activation of imported fatty acids; not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	2	4.1733	0.4467	1954.47	1955.174	1	960.3	66.66667 M.G1W2R4D1V1K2E1I1H3E1E1S1K2S1V1M1.K
		involved in the activation of imported fatty acids; not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	2	3.3893	0.3125	1930.29	1931.174	1	968.9	66.66667 M.GWRDVKEIHEESKSVM.K
		involved in the activation of imported fatty acids; not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	2	3.9948	0.4212	2058.57	2059.348	1	781.6	68.75 M.GWRDVKEIHEESKSVMK.K
		Long chain fatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids; involved in the activation of imported fatty acids: not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	2	4.4883	0.4303	2262.39	2261.407	1	830.9	52.77778 E.SCNEIDVHPPGKDDLCCIM.Y
		Long chain tatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids; involved in the activation of imported fatty acids; not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	2	3.7318	0.2594	2576.43	2575.748	1	379.9	38.095238 L.GKESCNEIDVHPPGKDDLCCIM.Y
		Long chain fatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids; involved in the activation of imported fatty acids; not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	2	2.9244	0.1674	2712.75	2714.97	3	219.6	27.272728 P.D1I1K2T1F1S1F1D1D1I1L1K2L1G1K2E1S1C1N2E1I1D1V1.H
		Long chain fatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids; involved in the activation of imported fatty acids; not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	3	4.5828	0.3589	1954.58	1955.174	1	1060.3	41.666664 M.G1W2R4D1V1K2E1I1H3E1E1S1K2S1V1M1.K

		Long chain fatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids;								
gil63248931refINP_014962_11	VOR317W	involved in the activation of imported fatty acids; not required for growth on	2	4 4386	0 2889	1870 79	1869 171	1	824.4	
gilo324693[ter]INF_014902.1]	TORSITW	Long chain fatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids;	2	4.4300	0.2009	10/0./9	1809.171	1	024.4	00.000004 L.VRIGERFINDDDREITET.A
		involved in the activation of imported fatty acids; not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	2	4.4898	0.3944	2282.71	2284.407	1	859.3	55.555557 E.S1C1N2E1I1D1V1H3P1P1G1K2D1D1L1C1C1I1M1.Y
		involved in the activation of imported fatty acids; not required for growth on								
gi 6324893 ref NP_014962.1	YOR317W	nonfermentable carbon sources; essential for stationary phase; Faa1p	1	2.2932	0.1654	991.63	991.181	1	230.5	66.66667 Q.RLHIPGGGAL.G
		One of two type V myosins, involved in polarized distribution of mitochondria;								
gil6324902/refINP_014971.1	YOR326W	moves multiple cargo: reversibly phosphorylated in vivo: Mvo2p	2	3.4468	0.2714	2122.67	2121.222	1	244.8	41.666664 L.SLLDEESRLPAGSDESWTO K
giloon isochoiltin To Lion in Li	101102011	One of two type V myosins, involved in polarized distribution of mitochondria;	-	0.1100	0.2711	2122.01			211.0	
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	4.54	0.4141	2249.59	2249.396	1	1223.4	57.894737 L.SLLDEESRLPAGSDESWTQK.L
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation:								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.6056	0.3571	2821.91	2822.145	1	461.3	37.5 V.DTKDLNNDKDQSLPLLRNPPILEAT.E
		One of two type V myosins, involved in polarized distribution of mitochondria;								
gil6324902/refINP_014971.1	YOR326W	moves multiple cargo: reversibly phosphorylated in vivo: Mvo2p	2	3.5402	0.3103	2854.37	2856.145	1	561.5	43.75 V.D1T1K2D1L1N2N2D1K2D1Q2S1L1P1L1L1R4N2P1P1I1L1E1A1T1.E
9.1		One of two type V myosins, involved in polarized distribution of mitochondria;								
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.8013	0.3162	2175.99	2176.478	1	513	41.666664 K.DLNNDKDQSLPLLRNPPIL.E
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.8312	0.2344	2202.31	2203.478	1	535	44.444447 K.D1L1N2N2D1K2D1Q2S1L1P1L1L1R4N2P1P1I1L1.E
		One of two type V myosins, involved in polarized distribution of mitochondria;								
gil6324902lrefINP_014971.11	YOR326W	moves multiple cargo: reversibly phosphorylated in vivo: Myo2p	2	4.6922	0.372	2707.65	2707.056	1	689.6	43 47826 D. TKDI NNDKDOSL PLI RNPPILEAT E
3.1		One of two type V myosins, involved in polarized distribution of mitochondria;	-							
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	4.1701	0.3772	2740.49	2740.056	1	690.4	43.47826 D.T1K2D1L1N2N2D1K2D1Q2S1L1P1L1L1R4N2P1P1I1L1E1A1T1.E
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.4025	0.2493	1314.63	1313.499	1	908.9	88.88889 I.PHEQWDLIFK.K
		One of two type V myosins, involved in polarized distribution of mitochondria;								
gil6324902/refINP_014971.1	YOR326W	moves multiple cargo: reversibly phosphorylated in vivo: Mvo2p	2	4.2487	0.2693	1747.59	1748.048	1	498.9	65.38461 K.VKENKEMTERIKEL Q
5100 00101 =0 001		One of two type V myosins, involved in polarized distribution of mitochondria;								
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria:	2	4.5569	0.353	2405.55	2405.757	1	835.1	47.5 D. IKDLINNDKDQSLPLLKNPPIL.E
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	1	3.0557	0.3195	1545.39	1546.734	1	318.6	63.636364 R.CWYPHKELGWIG.A
		One of two type V myosins, involved in polarized distribution of mitochondria;								
ail6324902lrefINP 014971.11	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Mvo2p	1	3.2119	0.4002	1562.42	1563.734	1	312.2	59.090908 R.C1W2Y1P1H3K2E1L1G1W2I1G1.A
5100 00101 =0 001		One of two type V myosins, involved in polarized distribution of mitochondria;								
-100040001(IND-044074-4)	VODAGOW	required for mitochondrion and vacuole inheritance and nuclear spindle orientation;		4 0000	0.0704	4077.00	4070.000		000	
gi 6324902 ref NP_014971.1	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria:	3	4.0608	0.2734	1877.99	1876.222	2	632	42.857143 S.KVKENKEMTERIKEL.Q
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	4.6409	0.2201	2314.19	2313.631	2	457.8	52.77778 M.KKEHLIDIDNQKSKDMELQ.K
		One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuale inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.8115	0.2829	2477.17	2477.777	1	592.8	42.857143 K.DLNNDKDQSLPLLRNPPILEAT.E
		One of two type V myosins, involved in polarized distribution of mitochondria;								
ail62240021rofIND_014071_1	VORSSEW	required for mitochondrion and vacuole inheritance and nuclear spindle orientation;	2	4 1765	0.2024	1505 65	1506 670	2	456 7	62 5 K K2E1T1T1E1E1D1111861\/1\/1/2 M
gilo324902 tet 14F_014971.1	10K320W	One of two type V myosins, involved in polarized distribution of mitochondria:	2	4.1705	0.2021	1505.65	1506.679	3	400.7	62.5 K.K2E11111E1E1D1111310101K2.W
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	3	3.9332	0.3864	2251.22	2249.396	1	1318.8	38.157894 L.SLLDEESRLPAGSDESWTQK.L
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation:								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.1492	0.2508	1978.31	1979.329	1	282.7	50 R.YYILIPHEQWDLIFK.K
		One of two type V myosins, involved in polarized distribution of mitochondria;								
ail6324002lrofIND_014071_1	VOP326W	required for mitochondrion and vacuole inheritance and nuclear spindle orientation;	3	4 0625	0.2848	2425 22	2435 757	2	1073 5	38 75 D T1K2D1I 1N2N2D1K2D1O2S1I 1D1I 1I 1D4N2D1D1I1I 1 E
gilo324902 tet 14F_014971.1	10K320W	One of two type V myosins, involved in polarized distribution of mitochondria;	3	4.0025	0.2040	2430.33	2433.737	2	1073.5	36.75 D.11K2D1E1N2N2D1K2D1Q231E1F1E1E1K4N2F1F111E1.E
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation;								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	4.3091	0.3529	2404.51	2405.757	1	803.3	47.5 D.TKDLNNDKDQSLPLLRNPPIL.E
		required for mitochondrion and vacuole inheritance and nuclear spindle orientation:								
gi 6324902 ref NP_014971.1	YOR326W	moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	3	3.9439	0.2867	2405.09	2405.757	1	1199.6	41.25 D.TKDLNNDKDQSLPLLRNPPIL.E
		Protein required for normal cortical actin organization and endocytosis; multicopy								
ail6324905/refINP_014974_1	YOR329C	suppressor of clathrin deficiency; acts as a targeting subunit for protein phosphatase type 1: Scd5p	2	3 1204	0 2081	1893 99	1895 04	1	332.1	53 333336 S S1I 1P1S1E10202E1T1E1E1E1K2K2V1I 1 E
gilooz iocolioitai _oriior iiif	10110200	Protein required for normal cortical actin organization and endocytosis; multicopy	-	0.1201	0.2001	1000.00	1000.01		002.1	
		suppressor of clathrin deficiency; acts as a targeting subunit for protein phosphatase								
gi 6324905 ref NP_014974.1	YOR329C	type 1; Scd5p Protein required for normal cortical actin organization and endocutoris; multiconv	2	3.8139	0.2448	1874.65	1875.04	1	381	56.666668 S.SLPSEQQETEEEKKVL.E
		suppressor of clathrin deficiency: acts as a targeting subunit for protein phosphatase								
gi 6324905 ref NP_014974.1	YOR329C	type 1; Scd5p	3	4.3359	0.2622	4041.08	4040.099	1	823.4	23.571428 E.SSNNSEARKQDPDAEDEDQDSNNDSPLDFTLPMDQL.L
		Protein required for normal cortical actin organization and endocytosis; multicopy								
gi 6324905 ref NP 014974.1	YOR329C	type 1; Scd5p	3	5.46	0.4043	4086.17	4087.099	1	639.1	26.428572 L1P1M1D1Q2L1.L
		Protein required for normal cortical actin organization and endocytosis; multicopy								
gil6324005lrofIND_044074_4	VOP320C	suppressor of clathrin deficiency; acts as a targeting subunit for protein phosphatase	2	3 00 40	0.2400	2124 15	2125 077	4	505.0	
9100240001011NF_014974.1	10113280	(ypo 1, 0000p	2	J.JZ4Z	0.3409	2124.10	2123.011	1	000.9	

		Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		A Pase (V-A Pase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6324907 ref NP_014977.1	YOR332W	membrane; Vma4p	1	2.7989	0.1643	1407.51	1406.579	8	460.5	54.545456 K.A1L1E1R4D1V1D1L1I1E1S1M1.K
		Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6324907 ref NP_014977.1	YOR332W	membrane; Vma4p	1	2.5528	0.2323	1392.55	1391.579	9	277.8	45.454548 K.ALERDVDLIESM.K
		Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6324907 ref NP_014977.1	YOR332W	membrane; Vma4p	2	4.3771	0.2759	1814.17	1814.136	1	522.6	64.28571 F.IRKEAEEKAKEIQLK.A
		Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6324907 ref NP_014977.1	YOR332W	membrane; Vma4p	2	3.2325	0.229	1573.93	1572.802	1	537.3	70.83333 F.IRKEAEEKAKEIQ.L
		Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		endomembrane system; required for the V1 domain to assemble onto the vacuolar								
gi 6324907 ref NP_014977.1	YOR332W	membrane; Vma4p	2	5.2722	0.2335	1835.77	1837.136	1	699.6	64.28571 F.I1R4K2E1A1E1E1K2A1K2E1I1Q2L1K2.A
		Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64.1 allele) causes cell cycle arrest at C1; lethality of null mutation is functionally								
gi 6324911 ref NP_014980.1	YOR335C	complemented by human homolog; Ala1p	2	3.976	0.4529	1968.69	1970.1	1	1114.7	62.5 T.YFEGDEKLGLEPDTEAR.E
		Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation								
ail63249111refINP_014980_11	VOR335C	(cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog: Ala1p	3	4 0371	0 2556	2212 01	2212 375	1	979 3	
gilo324311[tel[t4:_014300.1]	101(3550	Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation	5	4.0371	0.2000	2212.31	2212.375	1	515.5	40.27770 T.TEGDEREGELF DIEAREE.W
		(cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally								
gi 6324911 ref NP_014980.1	YOR335C	complemented by human homolog; Ala1p	2	4.6984	0.3647	2097.79	2097.196	1	898.9	52.77778 Y.S1G1N2F1G1E1N2D1K2D1G1I1D1T1A1Y1R4V1L1.A
		(cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally								
gi 6324911 ref NP_014980.1	YOR335C	complemented by human homolog; Ala1p	3	3.8033	0.1973	2096.57	2097.196	1	1366.5	40.27778 Y.S1G1N2F1G1E1N2D1K2D1G1I1D1T1A1Y1R4V1L1.A
		Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation								
gi 6324911 ref NP 014980.1	YOR335C	complemented by human homolog; Ala1p	2	3.3046	0.2746	1990.51	1991.1	2	401.6	46.875 T.Y1F1E1G1D1E1K2L1G1L1E1P1D1T1E1A1R4.E
gi 6324916 ref NP_014985.1	YOR340C	RNA polymerase I subunit A43; Rpa43p	2	3.3549	0.3508	1237.63	1236.453	1	1062.2	90 L.IKITPDTPFGF.T
gi 6324916 ref NP_014985.1	YOR340C	RNA polymerase I subunit A43; Rpa43p	1	2.7351	0.3763	1235.68	1236.453	1	513.8	
gi 6324916 ref NP_014985.1	YOR340C	RNA polymerase I subunit A43; Rpa43p	1	2.7557	0.3188	1235.61	1236.453	2	394.6	65 L.IKITPDTPFGF.T
gi 6324916 ref NP_014985.1	YOR340C	RNA polymerase I subunit A43; Rpa43p	1	2.4402	0.2225	1041.76	1041.288	6	386.7	75 N.CIVRVPIAL.Y
gi 6324932 ref NP_015001.1 gi 6324932 ref NP_015001.1	YOR356W	hypothetical protein; Yor356wp	2	3.0044	0.2903	1910.71	1912.233	1	884.3 670.8	59.375 E.LFPDEKSDIGIPLPKEL.A 47 727272 E S111515151142G11 1P1//1115151//151D151D161D161K2M1A1 M
gi 6324932 ref NP_015001.1	YOR356W	hypothetical protein; Yor356wp	2	3.6854	0.2908	2189.75	2191.523	1	594.8	50 W.K2E1L1F1P1D1E1K2S1D1I1G11P1L1P1K2E1L1.A
gi 6324932 ref NP_015001.1	YOR356W	hypothetical protein; Yor356wp	2	3.8937	0.3027	2262.31	2263.602	1	470.5	42.105263 W.K2E1L1F1P1D1E1K2S1D1I1G1I1P1L1P1K2E1L1A1.T
gi 6324932 ref NP_015001.1	YOR356W	hypothetical protein; Yor356wp	2	4.7102	0.3284	1991.61	1989.288	1	874.4	59.375 A.S1K2Y1K2P1I1E1Y1P1K2P1D1G1V1I1S1F1.D
gil6324932 ref NP_015001.1	YOR356W	hypothetical protein; Yor356wp	2	4.2246	0.2417	2454.87	2454.866	1	771.8	45.238094 W.KELFPDEKSDIGIPLPKELATL.V
gi 6324932 ref NP_015001.1	YOR356W	hypothetical protein; Yor356wp	2	2.9483	0.2089	1745.67	1745.939	4	283.3	46.666668 K.GLPVLEEVEDEDAKMA.M
gi 6324932 ref NP_015001.1 gi 6324932 ref NP_015001.1	YOR356W	hypothetical protein; Yor356wp	3	4.1588	0.2691	1927.97	1927.248	1	1229.3	43.75 W.KELFPDEKSDIGIPLPK.E
gi 6324932 ref NP_015001.1	YOR356W	hypothetical protein; Yor356wp	2	4.5042	0.3898	1968.17	1969.288	1	849.2	59.375 A.SKYKPIEYPKPDGVISF.D
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for								
gil6324037lrofIND_015006_1	VOP361C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mPNA and tPNA(i)Met to ribocomes: Prt1p.	2	3 004	0.2452	2072.00	2070 21	1	365.6	
gilooz4007 [rei]r4 _010000.1]	1010010	Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	0.004	0.2402	2012.00	2010.21		000.0	
		translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p Subupit of the core complex of translation initiation factor 3(eIE3), essential for	2	3.827	0.1825	1608.19	1607.865	1	1331.3	83.33333 W.LMDDKVRDQFVLQ.D
		translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	3.2213	0.1992	2305.85	2305.568	1	391.3	47.22222 L.T1E1R4D111P1V1E1K2V1E1L1K2D1S1V1F1E1F1.G
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation: part of a subcomplex (Prt1p-Rog1p-Nin1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	3.1711	0.2809	1864.57	1865.139	1	625.6	60.714287 F.YAPETKEKTDVIKRW.S
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for								
gil6324037lrofIND_015006_1	VOP361C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mPNA and tPNA(i)Met to ribocomes: Prt1p.	2	2 0006	0 2301	2577 77	2570 015	2	177.0	35 C P4I 1T1E1P4D1I1P1\/1E1K2\/1E1I 1K2D1S1\/1E1E1E1 G
gil0324337 [rei]14r_013000.1]	1010010	Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	2.3030	0.2301	2311.11	2373.313	2	111.5	55 G.N.4ETTEIN.4DTHFTVTEIN.2VTETEIN.2DT5TVTFTEITT.6
		translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p Subunit of the core complex of translation initiation factor 3(eIE3) essential for	2	4.0417	0.3098	1846.71	1849.147	1	416.3	57.14286 C.R4L1T1E1R4D111P1V1E1K2V1E1L1K2.D
		translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	3.4583	0.3466	2010.83	2012.316	1	1007.6	66.66667 R.FYAPETKEKTDVIKRW.S
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	5.0215	0.2759	1818.65	1821.001	1	1159.2	71.42857 E.E1I1V1E1E1V1L1E1E1T1K2E1K2V1E1
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for								
ail6324937/refINP_015006.11	YOR361C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes: Prt1p	2	4 1423	0 1703	1806.91	1804 001	1	1106.2	
gilooz4007 [rei]r4 _010000.1]	1010010	Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	4.1420	0.1700	1000.01	1004.001		1100.2	IS E.EIVEEVILLE INERVE.
		translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p Subunit of the core complex of translation initiation factor 3(eIE3) essential for	3	3.9868	0.1895	2996.27	2998.21	2	440.3	27.083334 F.E1D111K2L1E1D111P1V1D1D1111D1F1S1D1L1E1E1Q2Y1K2V1T1.E
		translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	2.926	0.3609	2027.27	2028.313	1	200.6	50 C.RLTERDIPVEKVELKDS.V
		Suburnit or the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpo1p-Nin1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	3.9736	0.3658	2360.49	2361.543	1	707.9	52.63158 E.T1F1E1D1I1K2L1E1D1I1P1V1D1D1I1D1F1S1D1L1.E
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for								
ail6324937/refINP 015006 1	YOR361C	mansiation, part of a subcomplex (Prtrp-rkpg/tp-htp/tp) that stimulates binding of mRNA and tRNA(i)Met to ribosomes: Prt1p	2	4,6949	0,4287	2339.51	2340,543	1	700.1	52.63158 E.TFEDIKLEDIPVDDIDFSDL.F
31			-							
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for								
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gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	3.1988	0.2552	2018.23	2019.154	1	596.4	50 T.F1S1T1E1P1I1I1V1E1E1D1N2E1F1S1P1F1.T
		translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	3.356	0.3279	1724.13	1722.963	1	434	57.692307 Y.A1P1E1T1K2E1K2T1D1V111K2R4W2.S
gil6324937/refINP_015006.1	YOR361C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes: Prt1p	2	3.6864	0.3036	2262.91	2263.398	1	715.9	52.77778 E.D1I1P1V1D1D1I1D1F1S1D1L1E1E1Q2Y1K2V1T1.E
24		Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation, and a cube market (Bt4). Pag1a Nin1a) that stimulate binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p-kpg rp-kip rp) that stimulates binding of	2	3.4646	0.2574	1475.27	1474.698	1	938.4	77.27273 C.R4L1T1E1R4D1I1P1V1E1K2V1.E
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	5.4446	0.3823	2033.89	2035.316	1	1731.6	76.666664 R.F1Y1A1P1E1T1K2E1K2T1D1V111K2R4W2.S
ail6224027trofIND_045006_1	VOP261C	translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(iWat to ribecome). Bt1p	2	4 6265	0.2699	2244 74	2242 209	1	066.9	
gilo324337 [relinit _013000.1]	1010010	Subunit of the core complex of translation initiation factor 3(eIF3), essential for	2	4.0205	0.5000	2241.71	2242.330		300.0	
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	4.2607	0.4369	2370.57	2371.471	1	712.3	52.63158 Y.N2S1D1D1F1D1T1E1F1R4E1P1D1M1P1T1F1V1P1S1.S
		Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of								
gi 6324937 ref NP_015006.1	YOR361C	mRNA and tRNA(i)Met to ribosomes; Prt1p	2	3.9184	0.3879	2346.83	2347.471	1	830.9	55.263157 Y.NSDDFDTEFREPDMPTFVPS.S
gi 6324949 ref NP_015018.1	YOR373W	Nud1p	2	3.2914	0.2999	1999.43	2000.302	1	835.4	56.25 R.DFTHLPVDLSKELPFLQ.E
gi 6324949 ref NP_015018.1	YOR373W	Component of the spinale pole body outer plaque, required for exit from mitosis; Nud1p	2	2.9234	0.17	2618.29	2617.893	1	379.7	34.090908 L.Q2E1V1N2L1S1Y1N2S1I1Q2S1L1E1G1I1G1S1S1R4M\$K2K2.L
gi 6324949 ref NP_015018.1	YOR373W	Component of the spindle pole body outer plaque, required for exit from mitosis; Nud1p	2	3.5694	0.3751	1754.35	1757.037	1	511.6	53.571426 F.T1H3L1P1V1D1L1S1K2E1L1P1F1L1Q2.E
gil6324949/refINP_015018_1	YOR373W	Component of the spindle pole body outer plaque, required for exit from mitosis;	2	3 2984	0 3122	1739 95	1738 037	1	562.8	
gilosz4345irelini _015010.11	1010701	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from	2	0.2004	0.0122	1100.00	1100.001		002.0	
gi 6324951 ref NP_015020.1	YOR375C	Gdh3p; expression regulated by nitrogen and carbon sources; Gdh1p	3	4.9434	0.3476	3409.4	3410.861	1	833.6	28.703705 L.E1D1S1T1L1F1E1Q2H3P1E1Y1R4K2V1L1P1I1V1S1V1P1E1R4I1I1Q2F1.R
		NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from								
gi 6324951 ref NP_015020.1	YOR375C	Gdh3p; expression regulated by nitrogen and carbon sources; Gdh1p NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from	2	3.8761	0.3264	1759.89	1759.155	1	648.6	57.14286 R.K2V1L1P1I1V1S1V1P1E1R4I1I1Q2F1.R
	VODATEO	ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from	2	2 5002	0.0700	4000.00	4004 047	2	400.0	
gil6324951 [rei]NP_015020.1]	TUR3/5C	Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	3.5963	0.2736	1009.09	1091.217	2	420.3	50 I.LIFTETQ2H5PTETTTR4K2VTETPTTV1.5
gi 6325253 ref NP_015321.1	YPL004C	with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	3.2559	0.2976	1619.33	1620.598	1	455.3	69.230774 T.E1V1P1V1D1D1E1A1H3E1A1D1H3H3.V
		Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and								
gi 6325253 ref NP_015321.1	YPL004C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	1	3.1759	0.2647	1523.52	1524.801	1	510.2	62.5 T.KIPVLEQELVRAE.A
		with Pillp to down-regulate heat by Pill 4 and Pillp and		0 5050	0.404	1515 55	1510.001		500 7	
gi 6325253 ref NP_015321.1	YPL004C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	3.5253	0.191	1545.55	1542.801	2	592.7	66.66667 T.K2IIPTVILIEIQ2EILIVIR4AIEI.A
gi 6325253 ref NP_015321.1	YPL004C	with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	3.7852	0.3137	1725.91	1724.958	1	308.4	61.538464 S.RDRKEKITDEIAHL.K
		Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Pil1p to down-regulate beat stress resistance via regulation of the Pkc1p and								
gi 6325253 ref NP_015321.1	YPL004C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	3.7512	0.2357	2138.77	2136.416	1	667.1	55.88235 S.VQPSRDRKEKITDEIAHL.K
		with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and								
gi 6325253 ref NP_015321.1	YPL004C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	4.3755	0.2647	2162.87	2165.416	1	703.2	55.88235 S.V1Q2P1S1R4D1R4K2E1K2I1T1D1E1I1A1H3L1.K
ail63252531refINP 015321.11	YPL004C	with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and Yok1p pathways: phosphorylated by Phk1p and Phk2p: Lsp1p	2	2.9979	0.2383	1802.51	1800.973	2	521.3	43.75 L.L1E1L1L1D1D1S1P1V1T1P1G1E1A1R4P1A1.Y
51		Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Pil1p to down regulate bast stores resistance via regulation of the Pkg1p and								
gi 6325253 ref NP_015321.1	YPL004C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	3.2387	0.3011	1701.11	1701.703	1	593.8	64.28571 T.TEVPVDDEAHEADHH.V
		with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and								
gi 6325253 ref NP_015321.1	YPL004C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	2	3.6764	0.2386	1810.37	1808.809	1	320.2	60.000004 T.E1V1P1V1D1D1E1A1H3E1A1D1H3H3V1S1.Q
gil6325253lrefINP_015321.1	YPL004C	with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and Yok1p pathways: phosphorylated by Phk1p and Phk2p; Lsp1p	2	3,1537	0.3284	1789.67	1786.809	2	186.1	53.333336 T. EVPVDDEAHEADHHVS Q
24.000000000000000000000000000000000000		Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Dilate down exclusion participation of the Pketh and	_					-		
gi 6325253 ref NP_015321.1	YPL004C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	3	4.1671	0.2852	3653.96	3654.7	1	389	27.419355 H3H3.V
		with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and								E.E1E1E1P1E1I1Q2N2G1D1I1P1G1Q2V1V1E1E1E1E1V1E1W2T1T1E1V1P1V1D1
gi 6325253 ref NP_015321.1	YPL004C	Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along	3	4.0906	0.2436	4517.51	4517.568	1	506.5	19.078947 D1E1A1H3E1A1D1H3H3.V
gil6325253/refINP_015321_1	YPI 004C	with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ynk1p pathways: phosphorylated by Phk1p and Phk2p; I sn1p	2	3 5713	0.236	1525 69	1524 801	1	891.3	79 16667 T KIPVI FOFI VRAF A
sil0325245irefiND_045343.4	VDL 04 0W/	Protein required for export of the ribosomal subunits; associates with the RNA	2	0.0710	0.200	4054.00	4055.050		500.0	
gilo325245[rei]NP_015313.1]	TPLUIZW	Protein required for export of the ribosomal subunits; associates with the RNA	2	3.2082	0.2705	1654.39	1600.200	I	500.2	53.333336 L.GTEIPTETETETIMTR4PTR2VTPTETETETETET.K
gi 6325245 ref NP_015313.1	YPL012W	components of the pre-ribosomes; contains HEAT-repeats; Rrp12p Protein required for export of the ribosomal subunits; associates with the RNA	2	4.0252	0.2068	1983.97	1985.43	1	618.2	50 L.G1L1P1E1E1L1M1R4P1K2V1P1E1L1L1L1K2.L
gi 6325245 ref NP_015313.1	YPL012W	components of the pre-ribosomes; contains HEAT-repeats; Rrp12p Protein required for export of the ribosomal subunits: associates with the RNA	2	3.3542	0.3869	1916.69	1915.265	1	479	50 K.T1I1V1E1L1L1P1L1D1H3L1D1F1I1V1R4.T
gi 6325245 ref NP_015313.1	YPL012W	components of the pre-ribosomes; contains HEAT-repeats; Rrp12p	2	3.7745	0.2404	1893.77	1894.265	1	575.4	60.000004 K.TIVELLPLDHLDFIVR.T
gi 6325245 ref NP_015313.1	YPL012W	components of the pre-ribosomes; contains HEAT-repeats; Rrp12p	2	3.1646	0.2357	1961.95	1963.43	1	691.7	53.125 L.GLPEELMRPKVPELLLK.L
gi 6325245 ref NP_015313.1	YPL012W	components of the pre-ribosomes; contains HEAT-repeats; Rrp12p	2	2.9818	0.2073	1953.95	1955.388	1	372.7	37.5 C.V1L1G1L1P1E1E1L1M1R4P1K2V1P1E1L1L1.L

gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.5068	0.1592	2785.67	2786.929	1	970.9	32.608696 V.PNENDDFVDNLESDVRVQPEARLN.I
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.0742	0.1671	3081.49	3082.218	2	252.8	26.923079 Y.A1S1V1P1N2E1N2D1D1F1V1D1N2L1E1S1D1V1R4V1Q2P1E1A1R4L1N2.I
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.7932	0.361	2083.43	2081.27	1	386.2	53.333336 N.D1V1Y1P1P1W2K2D1S1Y111D1Y1E1R4L1.K
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	4.2677	0.249	1341.49	1340.607	1	1245.8	80 F.I1V1E1E1K2L1Q2P1V1L1R4.A
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.7173	0.3651	2977.89	2980.271	1	437.8	36.95652 F.W2L1P1D1L1E1T1D111R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1.Q
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.8793	0.4631	2979.98	2980.271	1	616.3	35.869564 F.W2L1P1D1L1E1T1D111R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1.Q
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.3943	0.3481	2947.25	2947.271	1	892.6	41.304348 F.WLPDLETDIRKNPQEAYEEEKKTL.Q
gi]6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.8073	0.428	2806.76	2808.029	1	425.4	30.681818 L.P1D1L1E1T1D11R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1Q2.K
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.9702	0.383	2383.61	2383.612	1	554.5	50 K.L1A1N2D1V1Y1P1P1W2K2D1S1Y1I1D1Y1E1R4L1.K
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.7762	0.345	2384.99	2383.612	1	1577	43.055553 K.L1A1N2D1V1Y1P1P1W2K2D1S1Y111D1Y1E1R4L1.K
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	4.0323	0.3821	2360.51	2358.612	1	794.6	58.333332 K.LANDVYPPWKDSYIDYERL.K
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.1065	0.3335	2545.25	2543.882	2	489.9	34.210526 A.NDVYPPWKDSYIDYERLKKL.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.168	0.2807	2726.87	2728.12	6	375.2	28.57143 K.LANDVYPPWKDSYIDYERLKKL.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.4641	0.2922	2313.77	2312.627	2	238	36.11111 Q.VRLKELPFNNSEEYSPLLY.R
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.8343	0.2718	1754.13	1752.974	4	331.6	53.846157 Q.L1R4E1R4G1T1Q2K2E1E1L1E1K2L1.S
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.2882	0.237	1949.19	1949.139	5	548.1	53.333336 W.H3R4D1D1I1D1S1N2I1P1N2P1L1R4F1L1.R
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	1	2.9437	0.2556	1434.6	1435.625	1	555.8	68.181816 K.HDKLHPNYPSVK.S
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.7314	0.2676	1797.65	1798.972	1	742.9	64.28571 R.L1K2E1L1P1F1N2N2S1E1E1Y1S1P1L1.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.4725	0.3701	1779.91	1780.972	1	744	67.85714 R.LKELPFNNSEEYSPL.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	2.9221	0.1845	2816.27	2816.955	7	193.3	29.166666 Y.ASVPNENDDFVDNLESDVRVQPEAR.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.3767	0.3045	1284.19	1284.441	4	725.4	77.77778 L.D1K2E1L1E1K2V1Y1T1F1.Q
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.7203	0.2958	2382.61	2383.612	1	444.5	44.444447 K.L1A1N2D1V1Y1P1P1W2K2D1S1Y1I1D1Y1E1R4L1.K
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.6616	0.3452	2060.47	2060.27	1	308.1	50 N.DVYPPWKDSYIDYERL.K

gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	5.6117	0.4526	3108.53	3110.402	1	1192.5	38.541664 F.W2L1P1D1L1E1T1D111R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1Q2.K
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	2.9386	0.1592	2727.99	2728.12	7	243.1	28.57143 K.LANDVYPPWKDSYIDYERLKKL.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.2455	0.1865	1922.49	1923.139	4	453	50 W.HRDDIDSNIPNPLRFL.R
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	5.0303	0.349	2729.51	2728.12	1	561	32.142857 K.LANDVYPPWKDSYIDYERLKKL.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	5.4029	0.3951	2758.4	2758.12	1	626.7	34.523808 K.L1A1N2D1V1Y1P1P1W2K2D1S1Y1I1D1Y1E1R4L1K2K2L1.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	4.0152	0.4071	1434.77	1435.625	1	800.3	77.27273 K.HDKLHPNYPSVK.S
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.3503	0.2259	1640.13	1638.835	5	701.3	58.333332 D.NSQMPNYEWIKDL.T
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.4081	0.1908	1688.09	1688.745	1	496.6	57.692307 D.S1W2S1E1R4N2E1S1D1F1V1E1A1L1.D
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.0301	0.1581	1527.21	1526.615	4	469.9	66.66667 W.H3R4D1D111D1S1N2I1P1N2P1L1.R
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.1354	0.2821	2000.39	2001.225	1	853.5	45 D.11R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1.Q
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.353	0.3007	2452.94	2455.778	1	875	40.27778 N.D1V1Y1P1P1W2K2D1S1Y111D1Y1E1R4L1K2K2L1.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.3732	0.2905	2429.99	2429.778	4	298	38.88889 N.DVYPPWKDSYIDYERLKKL.L
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	4.0007	0.3802	1977.74	1977.225	1	1032.9	48.333332 D.IRKNPQEAYEEEKKTL.Q
gi 6325238 ref NP_015306.1	YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	2	3.8503	0.2976	1772.47	1772.924	1	1147.1	69.230774 Q.D1N2S1Q2M1P1N2Y1E1W2I1K2D1L1.T
gi 6325220 ref NP_015288.1	YPL037C	Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in protein targeting, associated with cytoplasmic ribosomes; enhances DNA binding of the Gal4p activator; homolog of human BTF3b; Egd1p Subunit beta1 of the assequent polypeptide-associated complex (NAC) involved in	2	3.6295	0.2067	1620.45	1620.828	1	1496.2	73.07692 Q.E1K2N2L1Q2D1L1F1P1G11111S1Q2.L
gi 6325220 ref NP_015288.1	YPL037C	protein targeting, associated with cytoplasmic ribosomes; enhances DNA binding of the Gal4p activator; homolog of human BTF3b; Egd1p Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in	2	3.5658	0.215	1603.11	1602.828	1	1041	69.230774 Q.EKNLQDLFPGIISQ.L
gi 6325220 ref NP_015288.1	YPL037C	protein targeting, associated with cytoplasmic ribosomes; enhances DNA binding of the Gal4p activator; homolog of human BTF3b; Egd1p Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in	1	2.4749	0.248	1473.46	1474.697	1	306.2	54.166668 Q.EKNLQDLFPGIIS.Q
gi 6325220 ref NP_015288.1	YPL037C	protein targeting, associated with cytoplasmic nbosomes; enhances UNA binding of the Gal4p activator; homolog of human BTF3b; Egd1p Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in DNA bine of	2	3.1295	0.2545	1475.27	1474.697	1	850.4	66.66667 Q.EKNLQDLFPGIIS.Q
gi 6325220 ref NP_015288.1	YPL037C	protein targeting, associated with cytoplasmic hoosomes; enhances DNA binding or the Gal4p activator; homolog of human BTF3b; Egd1p Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in DNA bine of	2	2.9366	0.3579	1868.85	1870.156	2	325.2	46.875 Y.GLPQEKNLQDLFPGIIS.Q
gi 6325220 ref NP_015288.1	YPL037C	protein rangening, associated with cryopastime indosonies, eminances DNA biologina of the Gal4p activator; homolog of human BTF3b; Egd1p Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in protein torgeting, associated with cryopastic largenic indepension, and process. DNA bioling of	2	4.5407	0.3497	2032.55	2033.193	4	409.2	52.77778 K.A1P1A1D1A1E1K2K2D1E1A111P1E1L1V1E1G1Q2.T
gi 6325220 ref NP_015288.1	YPL037C	protein rangeming associated in opportation inducedness primatices private intermediate the Galap activitator; homologi of human BTF2b; Egd complex (NAC) involved in protein targeting, associated with cycholasmic (thoseness: enhances DNA binding of the start of the start of	2	3.9143	0.3407	2364.07	2365.561	2	370.1	40.476192 H.E1A1K2A1P1A1D1A1E1K2K2D1E1A1I1P1E1L1V1E1G1Q2.T
gi 6325220 ref NP_015288.1	YPL037C	the Gal4p activator; homolog of human BTF3b; Egd1p Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in protein targeting, associated with cytoplasmic ribosomes; enhances DNA binding of	2	4.0435	0.4642	2338.69	2339.562	1	446.1	42.857143 H.EAKAPADAEKKDEAIPELVEGQ.T
gi 6325220 ref NP_015288.1	YPL037C	the Gal4p activator; homolog of human BTF3b; Egd1p Translational cofactor elongation factor-1 gamma, participates in the regulation of GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of	2	3.3371	0.2315	1997.05	1998.287	1	463.2	52.941177 Y.GLPQEKNLQDLFPGIISQ.L
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p Translational cofactor elongation factor: 1 gamma, participates in the regulation of GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of	1	2.2603	0.1662	1240.35	1240.288	1	617.7	72.22222 A.F1D1V1A1P1D1W2E1S1Y1.E
gil6325209 ref NP_015277.1	YPL048W	protein synapsis or another GT-dependent process; Cam to Translational cofactor elongation factor-1 gamma, participates in the regulation of GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of protein synthesis or another GTP-dependent process: Cam to	2	2.5259	0.1784	1386.52	1386.594	1	570.6	66 66667 T F1V11 1D101W2K2R4K2Y1 S
9.1-9-9-901, 9.1.10.10211.11		present cynansolo o'r anothor o'r acoponaent procese, oannip		2.0200	0+	.000.02			0.0.0	

		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
ail6325200/rofIND_015277_1		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of	2	3 0470	0 1706	1373 57	1370 594	1	706.6	
gilo32320910110F_013277.1	IFL040W	Translational cofactor elongation factor-1 gamma, participates in the regulation of	2	3.0479	0.1700	13/3.37	1370.394	1	790.0	TT.TTTTO T.F VEDDWKKKT.S
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	3.3893	0.1854	1389.43	1386.594	1	1074.3	88.88889 T.F1V1L1D1D1W2K2R4K2Y1.S
		I ranslational cofactor elongation factor-1 gamma, participates in the regulation of								
gil6325209 ref NP 015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	2.9058	0.2643	1065.79	1066.236	1	451.4	81.25 W.R4A1Q2H3P1A1I1V1R4.W
51		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	3	4.6564	0.2105	2770.16	2770.09	1	523.6	36.904762 T.F1V1L1D1D1W2K2R4K2Y1S1N2E1D1T1R4P1V1A1L1P1W2.F
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP 015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	4.0486	0.154	1930.35	1931.063	1	769	60.000004 A.K2L1D1P1T1N2D1D1D1K2E1F1I1N2N2M1.W
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	3	4.7974	0.2861	2281.31	2281.535	1	2209	44.736843 M.W2A1W2D1K2P1V1S1V1N2G1E1P1K2E1I1V1D1G1K2.V
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	3.3375	0.2242	1696.79	1696.869	2	467.9	53.846157 R.K2Y1S1N2E1D1T1R4P1V1A1L1P1W2.F
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p Translational cofactor elongation factor-1 gamma, participates in the regulation of	2	3.4619	0.195	1385.95	1386.594	1	954.7	//.////8 I.F1V1L1D1D1W2K2R4K2Y1.S
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	3.6219	0.267	1489.31	1488.699	1	846.4	80 S.T1F1V1L1D1D1W2K2R4K2Y1.S
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	3.4127	0.1716	1472.35	1471.699	3	574	70 S.TFVLDDWKRKY.S
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP 015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	1	2.4315	0.1741	1385.59	1386.594	1	486.2	66.666667 T.F1V1L1D1D1W2K2R4K2Y1.S
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	3.7398	0.2308	2035.89	2035.11	1	698.6	53.125 Y.D1Y1A1K2L1D1P1T1N2D1D1D1K2E1F1I1N2.N
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	3.6956	0.2485	2013.59	2014.11	1	670.4	53.125 Y.DYAKLDPTNDDDKEFIN.N
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of	0	0.0000	0.0070	4040.00	4040.055		4400.4	00 00000 M WOAAWODAKODAYACAYAANO C
gi 6325209 ret NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p Translational cofactor elongation factor-1 gamma, participates in the regulation of	2	2.9896	0.2272	1216.39	1216.355	1	1108.1	88.88889 M.W2A1W2D1K2P1V1S1V1N2.G
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	1	2.2461	0.1894	1265.61	1266.495	3	295.1	50 A.MDAVDKIVDIF.E
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of		0.0050	0 4705	4070 50	4070 405	6	004.0	
gi 6325209 ret NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p Translational cofactor elongation factor-1 gamma, participates in the regulation of	1	2.2252	0.1735	1279.58	1278.495	6	281.6	55 A.M1D1A1V1D1K2I1V1D111F1.E
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	3.9671	0.2987	1277.57	1278.495	1	1536.1	90 A.M1D1A1V1D1K2I1V1D1I1F1.E
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
ail6225200 rofIND 015277 1		G I P-binding protein EF-1 alpha, may play a redundant role in the regulation of	1	2 7201	0 1012	1407.0	1400 470	1	404 E	
gilo323209/10/INF_013277.1	1FL046W	Translational cofactor elongation factor-1 gamma, participates in the regulation of	1	2.7201	0.1013	1427.3	1420.473		404.0	01.11111 W.FTW2ETH311N2FTETETT1.5
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	1	2.6707	0.2866	1414.53	1414.473	1	572.5	72.22222 W.FWEHYNPEEY.S
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
gil6325209/rofINP_015277_1		G I P-binding protein EF-1 alpha, may play a redundant role in the regulation of protein synthesis or another GTP-dependent process: Cam1p	2	4 9437	0 3330	2118.00	2110 276	1	867.5	56 25 A K2I 1D1P1T1N2D1D1D1K2E1E1I1N2N2M1W2 A
gil0323203[rel[NF_013277.1]	11 204000	Translational cofactor elongation factor-1 gamma, participates in the regulation of	2	4.0437	0.3333	2110.33	2113.270	'	007.5	
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	1	2.2021	0.1755	1387.79	1386.594	2	455.2	61.11111 T.F1V1L1D1D1W2K2R4K2Y1.S
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
gil6325209/refINP_015277_1	YPI 048W	G I P-binding protein EF-1 alpha, may play a redundant role in the regulation of protein synthesis or another GTP-dependent process: Cam1p	2	3 3668	0 2264	1387 39	1386 594	1	770.8	77 77778 T E1V1I 1D1D1W2K2R4K2Y1 S
giloszszssileiliti _013277.11	11 204000	Translational cofactor elongation factor-1 gamma, participates in the regulation of	2	3.3000	0.2204	1307.33	1500.534	'	110.0	
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	2	4.0728	0.2351	1560.09	1560.892	1	628.2	73.07692 R.D1F1P1L1K2K2V1P1A1F1V1G1P1K2.G
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
gil6325209/rofINP_015277_1		G I P-binding protein EF-1 alpha, may play a redundant role in the regulation of protein synthesis or another GTP-dependent process: Cam1p	2	3 9056	0 340	1544.27	15/3 802	9	531	
gil0323203[rel[NF_013277.1]	11 204000	Translational cofactor elongation factor-1 gamma, participates in the regulation of	2	3.0000	0.343	1344.27	1040.092	0	331	03.230774 N.DITERRATAI VOLN.G
		GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of								
gi 6325209 ref NP_015277.1	YPL048W	protein synthesis or another GTP-dependent process; Cam1p	1	4.4135	0.2466	1560.83	1560.892	1	700.7	65.38461 R.D1F1P1L1K2K2V1P1A1F1V1G1P1K2.G
		Translational cofactor elongation factor-1 gamma, participates in the regulation of								
ail6325209/refINP_015277.11	YPL048W	protein synthesis or another GTP-dependent process: Cam1p	2	3.6434	0.3361	1267.85	1266.495	1	1094.1	85 A.MDAVDKIVDIE.E
3.1		Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p,	_							
		Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan								
		backbone; forms a separate complex with Van1p that is also involved in backbone								
gi 6325207 ref NP_015275.1	YPL050C	elongation; Mnn9p Subusit of Colgi manageultransferage complex also containing App1p, Map10p	2	4.1457	0.3581	1981.41	1981.196	1	823.4	67.85/14 Q.R4F1Y1D1E1E1K2K2Q2P1S1I1R4P1Y1.D
		Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan								
		backbone; forms a separate complex with Van1p that is also involved in backbone								
gi 6325207 ref NP_015275.1	YPL050C	elongation; Mnn9p	2	3.871	0.328	1955.91	1957.196	1	786.2	60.714287 Q.RFYDEEKKQPSIRPY.D
		Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p,								
		backbone; forms a separate complex with Van1p that is also involved in backbone								
gi 6325207 ref NP_015275.1	YPL050C	elongation; Mnn9p	2	3.3726	0.2816	1559.21	1559.676	1	797.2	65.38461 F.NDHVEDIIPEGHIA.H
=										

		Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone: forms a separate complex with Van1o that is also involved in backbone								
gi 6325207 ref NP_015275.1	YPL050C	elongation; Mnn9p Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan	2	3.2533	0.2301	1578.13	1578.676	2	649.9	61.538464 F.N2D1H3V1E1D1I11P1E1G1H31A1.H
gi 6325207 ref NP_015275.1	YPL050C	backbone; forms a separate complex with Van1p that is also involved in backbone elongation; Mnn9p Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p,	2	3.1578	0.1867	1665.23	1664.879	1	1028.5	65.38461 A.EVHRDGAMFPNFPF.Y
gi 6325207 ref NP_015275.1	YPL050C	Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone; forms a separate complex with Van1p that is also involved in backbone elongation; Mnn9p Subpit of Color managesultransforms complex also containing Aprila Mon10	2	3.779	0.2217	1537.69	1535.763	1	898.6	70.83333 E.VHRDGAMFPNFPF.Y
gi 6325207 ref NP_015275.1	YPL050C	Supplier of Congrinal integritariates are conjusted also containing with promotop, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone; forms a separate complex with Van1p that is also involved in backbone elongation; Mnn9p	1	2.7448	0.1633	1534.54	1535.763	4	299.5	54.166668 E.VHRDGAMFPNFPF.Y
		Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone; forms a separate complex with Van1p that is also involved in backbone								
gi 6325207 ref NP_015275.1	YPL050C	elongation; Mnn8p Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backhope: forms a searcrate complex with Van1 that is also involved in backhope	1	2.6389	0.2283	1553.52	1554.763	1	306.4	54.166668 E.V1H3R4D1G1A1M1F1P1N2F1P1F1.Y
gi 6325207 ref NP_015275.1	YPL050C	elongation; Minn\$p elongation; Minn\$p Subunit of Golgi mannosyltransferase complex also containing Anp1p, Min10p, Min11p, and Hoc1p that mediates elongation of the polysaccharide mannan	2	3.2912	0.1943	1537.21	1535.763	2	880.6	70.83333 E.VHRDGAMFPNFPF.Y
gi 6325207 ref NP_015275.1	YPL050C	backbone; forms a separate complex with Van1p that is also involved in backbone elongation; Mnn9p	2	3.9563	0.3258	1553.57	1554.763	1	817.3	70.83333 E.V1H3R4D1G1A1M1F1P1N2F1P1F1.Y
gi 6325199 ref NP_015267.1	YPL058C	Plasma membrane weak-acid-inducible AI P-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by sorbate and benzoate, regulated by War1p, mutants exhibit sorbate hypersensitivity; Pdr12p	2	3.6597	0.3215	1898.91	1898.16	1	923.5	60.714287 Y.V111Y1C1P1E1L1D1F1H3F1P1K211T1.V
gi 6325199 ref NP_015267.1	YPL058C	Plasma membrane weak-acid-inducible ATP-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by sorbate and benzoate, regulated by War1p, mutants exhibit sorbate hypersensitivity; Pdr12p	2	3.7539	0.4066	1878.77	1880.16	1	877	64.28571 Y.VIYCPELDFHFPKIT.V
gi 6325199 ref NP_015267.1	YPL058C	Plasma membrane weak-acid-inducible ATP-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by sorbate and benzoate, regulated by War1p, mutants exhibit sorbate hypersensitivity; Pdr12p	2	3.7851	0.2727	2254.95	2254.626	6	368.8	38.88889 Q.SSVPLEEKYEYVEKIITLL.G
gi 6325199 ref NP_015267.1	YPL058C	Plasma membrane weak-acid-inducible ATP-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by sorbate and benzoate, regulated by War1p, mutants exhibit sorbate hypersensitivity; Pdr12p	2	3.1852	0.3297	2346.61	2347.58	1	403.9	55.263157 K.KVVCNPHEYNIMDPPSGKTC.G
gi 6325199 ref NP_015267.1	YPL058C	Plasma membrane weak-acid-inducible ATP-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by sorbate and benzoate, regulated by War1p, mutants exhibit sorbate hypersensitivity; Pdr12p	2	2.9231	0.3095	1591.95	1592.896	1	487	62.5 C.G1I1L1Q2P1R4E1K2M1P1A1F1W2.R
gi 6325199 ref NP_015267.1	YPL058C	Plasma membrane weak-acid-inducible ATP-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by sorbate and benzoate, regulated by War1p, mutants exhibit sorbate hypersensitivity; Pdr12p Constituent of the mitochondrial inner membrane presequence translocase (TIM23	2	3.0914	0.3295	1575.79	1573.896	1	589.1	62.5 C.GILQPREKMPAFW.R
gi 6325194 ref NP_015262.1	YPL063W	complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23	2	3.3668	0.345	2056.25	2056.301	1	396.7	58.823532 E.NAIPMEPWNGEADDKLVR.L
gi 6325194 ref NP_015262.1	YPL063W	complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complexity and u carmate binding of incoming occur precare stratistics to the intercomplexity.	2	5.5391	0.3954	2321.49	2320.62	1	1911.3	71.05263 F.TLKDYVEGNLPSPEEQMKIQ.L
gi 6325194 ref NP_015262.1	YPL063W	compex), may promote bintang or incoming precorso proteins to the memerine notate space domain of Tom229 during translocation; Tim50 Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane	2	5.6064	0.369	2344.57	2345.62	1	2106.7	73.68421 F.T1L1K2D1Y1V1E1G1N2L1P1S1P1E1E1Q2M1K2l1Q2.L
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane	3	4.1947	0.1788	2321.45	2320.62	1	1334.7	44.736843 F.TLKDYVEGNLPSPEEQMKIQ.L
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane	1	2.7403	0.1919	1545.72	1546.822	1	363.2	59.090908 K.MIEEEKEKIRIQ.Q
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane	2	4.4134	0.2271	1546.61	1546.822	1	1052.1	
gij6325194/ref/NP_015262.1	YPL063W	space domain or non-zp outing transucation, import Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom270 during translocation: Tim50n	2	4.3983	0.2402	2525.03	2526.913	1	345.9	40.476192 F. NAIPMEPWNGFADDKI.VRUPF I.
gi 6325194 ref NP_015262.1	YPL063W	constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p	2	3.2684	0.3106	2341.75	2341.73	1	528.2	47.368423 I.PMEPWNGEADDKLVRLIPFL.E
gi 6325194 ref NP_015262.1	YPL063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p	2	4.1329	0.3708	2650.73	2651.997	1	496.1	47.727272 Y.KLQPENAIPMEPWNGEADDKLVR.L
gi 6325194 ref NP_015262.1	YPL063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23	2	4.3606	0.3608	1987.65	1987.183	1	1130.6	65.625 L.N2R4D1L1S1K2V11111D1T1D1P1N2S1Y1.K
gi 6325194 ref NP_015262.1	YPL063W	complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23	2	4.1063	0.3443	2417.67	2419.791	1	664.6	55 F.Q2E1P1P1F1P1D1L1L1P1P1P1P1P1P1P1Y1Q2R4P1L1.T
gi 6325194 ref NP_015262.1	YPL063W	complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p	3	3.8701	0.349	2606.18	2608.055	2	321.2	30.681818 F.QEPPFPDLLPPPPPPYQRPLTL.V

		Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane								
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23	3	4.1777	0.2916	2633.3	2636.055	1	354.1	32.954548 F.Q2E1P1P1F1P1D1L1L1P1P1P1P1P1P1P1Y1Q2R4P1L1T1L1.V
gi 6325194 ref NP_015262.1	YPL063W	complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p Constituent of the mitcohondrial inner membrane presequence translocase (TIM23	2	4.6624	0.2409	1674.67	1674.996	1	1422.6	87.5 M.KMIEEEKEKIRIQ.Q
gi 6325194 ref NP_015262.1	YPL063W	complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23)	2	4.47	0.3115	1668.27	1668.89	1	852.4	73.07692 T.KFPLDLIHEEGQKN.Y
gi 6325194 ref NP_015262.1	YPL063W	complex), may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p Constituent of the mitochooding inone monthrane precontingence translocate. (TIM22)	2	5.3061	0.372	2566.49	2567.967	1	725	52.380955 Y.F1Q2E1P1P1F1P1D1L1L1P1P1P1P1P1P1P1P1Y1Q2R4P1L1.T
gi 6325194 ref NP_015262.1	YPL063W	complex), may promote binding of incoming precursor proteins to the intermediate complex), may promote binding of incoming precursor proteins to the intermediate space domain of Tom22p during translocation; Tim50p Constituent of the mitherpodicip longer membrane programme translocator (TIM22)	2	4.4342	0.4268	1946.57	1945.225	1	644.6	56.666668 T.KFPLDLIHEEGQKNYL.M
gi 6325194 ref NP_015262.1	YPL063W	consistent of the interview interview in the interview provide the transaction of the interview of the inter	2	3.1408	0.2012	2394.89	2393.791	1	500.1	50 F.QEPPFPDLLPPPPPPYQRPL.T
gi 6325194 ref NP_015262.1	YPL063W	considerity in any promote binding of incoming precision protections to the intermembrane space domain of Tom22p during translocation; Tim50p	3	4.4029	0.266	3627.56	3627.163	1	374.3	A.R4F1N2S1M1F1T1Y1F1Q2E1P1P1F1P1D1L1L1P1P1P1P1P1P1P1P1Q2R4P1L1. 25 T
gi 6325194 ref NP_015262.1	YPL063W	Constituent or the mitochondnai inner memorane presequence transiocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p	3	4.9478	0.3306	3158.18	3158.609	1	606.1	26.923079 Y.K2L1Q2P1E1N2A111P1M1E1P1W2N2G1E1A1D1D1K2L1V1R4L111P1F1.L
gi 6325194 ref NP_015262.1	YPL063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p	2	4.0679	0.3506	1965.65	1967.225	1	697.6	56.666668 T.K2F1P1L1D1L111H3E1E1G1Q2K2N2Y1L1.M
gi 6325194 ref NP_015262.1	YPL063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p	2	4.9345	0.3654	2318.69	2320.62	1	1423.6	65.789474 F.TLKDYVEGNLPSPEEQMKIQ.L
gi 6325194 ref NP_015262.1	YPL063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p	2	4.3943	0.1734	1564.25	1564.822	1	889	77.27273 K.M11E1E1E1K2E1K2I1R4I1Q2.Q
ail6325194/refINP 015262.1/	YPL063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom220 during translocation: Tim50o	3	4.6708	0.3953	2651.87	2651.997	4	625.1	30.681818 Y.KLOPENAIPMEPWNGEADDKLVR.L
gil6325194/ref/NP_015262.1	YPL063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22 o during translocation: Tim50o	2	3.1085	0.2063	2247.85	2247.513	2	255.9	36.842106 L.GGSTKEPLDLIHEEGQKNYLM
gil6325194/refINP_015262_1	YPI 063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom270 during translocation: Tim50n	3	4 3781	0 3228	3138 17	3138 609	3	396.4	
ail6225104/rofIND_015262.1	VDL 062W/	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane ensers dympine of Emo20 during threadenation: Time For the intermembrane	2	4.0000	0.0220	2121.99	2122.600	1	550.4 556 1	
gilo323194[lei]linF_013262.1[TFLOOSVV	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane	3	4.3908	0.3125	5121.00	3122.009		550.1	
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane	3	4.0328	0.3337	1947.38	1945.225	1	1296.6	53.333336 T.KFPLDLIHEEGQKNYL.M
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane	3	4.0554	0.3493	3287.27	3288.769	1	497	24.074074 Y.K2L1Q2P1E1N2A111P1M\$E1P1W2N2G1E1A1D1D1K2L1V1R4L111P1F1L1.E
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane	3	4.466	0.3734	3249.8	3251.769	1	654.4	27.777779 Y.KLQPENAIPM@EPWNGEADDKLVRLIPFL.E
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex): may promote binding of incoming precursor proteins to the intermembrane	3	4.0578	0.1729	3271.37	3272.769	7	446.7	21.296297 Y.K2L1Q2P1E1N2A1I1P1M1E1P1W2N2G1E1A1D1D1K2L1V1R4L11P1F1L1.E
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex): may reprodue binding of incoming presures represents to the intermembrane	2	2.9574	0.2775	1547.79	1548.762	1	353.1	62.5 L.Q2K2E1T1K2D1D1K2P1K2S11L1.T
gi 6325194 ref NP_015262.1	YPL063W	space domain of Tom22p during translocation; Tim50p	2	4.2177	0.3732	2540.05	2540.967	1	501.4	45.238094 Y.FQEPPFPDLLPPPPPPPQRPL.T
gi 6325175 ref NP_015243.1	YPL082C	(TBP) from DNA via its C-terminal ATPase activity, forms a complex with TBP that binds TATA DNA with high affinity but with altered specificity; Mottp	3	4.0729	0.1804	2197.22	2199.563	9	673.1	38.235294 Q.L1L1N2R4D1E1F1P1V1F1R4E1L1V1P1S1L1K2.A
gi 6325175 ref NP_015243.1	YPL082C	Essential abundant protein involved in regulation of transcription, removes Sp115p (TBP) from DNA via its C-terminal ATPase activity, forms a complex with TBP that binds TATA DNA with high affinity but with altered specificity; Mot1p	3	4.3481	0.3145	2171.3	2173.563	1	910.8	45.588234 Q.LLNRDEFPVFRELVPSLK.A
gi 6325175 ref NP_015243.1	YPL082C	Essential abundant protein involved in regulation of transcription, removes Spt15p (TBP) from DNA via its C-terminal ATPase activity, forms a complex with TBP that binds TATA DNA with high affinity but with altered specificity; Mot1p	2	3.0771	0.2535	1223.35	1221.485	1	779.6	83.33333 S.EVFTRFPVLL.T
gi 6325175 ref NP_015243.1	YPL082C	Essential abundant protein involved in regulation of transcription, removes Spt15p (TBP) from DNA via its C-terminal ATPase activity, forms a complex with TBP that binds TATA DNA with high affinity but with altered specificity; Mot1p	3	3.9195	0.1842	1853.36	1855.141	1	836	42.857143 N.R4D1E1F1P1V1F1R4E1L1V1P1S1L1K2.A
gi 6325175 ref NP_015243.1	YPL082C	Essential abundant protein involved in regulation of transcription, removes Spt15p (TBP) from DNA via its C-terminal ATPase activity, forms a complex with TBP that binds TATA DNA with high affinity but with altered specificity. Mot1p COPII vesicle coat protein required for ER transport vesicle budding and	2	3.0516	0.3948	1520.93	1521.803	1	776.8	70.83333 LAKKPLEDSKHRVL.M
gi 6325172 ref NP_015240.1	YPL085W	aurupriagusome formation; sectop is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and	2	3.3667	0.2568	1593.49	1592.854	4	393.4	58.333332 S.RYKPIIEEEAGMR.Q
gi 6325172 ref NP_015240.1	YPL085W	autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p	2	3.7581	0.3142	2317.87	2319.612	1	338.3	42.105263 S.V1A1P1P1R4Q2E1N2N2P111K2I1D1N2E1A1L1L1R4.R

		COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize nitral COPII complexes: interacts with Sec230, Sec240, and								
gi 6325172 ref NP_015240.1	YPL085W	Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and	2	3.1392	0.2162	2286.59	2288.612	3	188.8	39.473686 S.VAPPRQENNPIKIDNEALLR.R
gi 6325172 ref NP_015240.1	YPL085W	may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and cutophageage formation; Sec16p is bound to the periphere of ER membranes and	2	3.0517	0.2461	1614.73	1612.854	3	460.9	62.5 S.R4Y1K2P1I1I1E1E1E1A1G1M1R4.Q
gi 6325172 ref NP_015240.1	YPL085W	may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and	3	5.8715	0.5142	4097.51	4099.515	1	811.4	T.S1V11P1N2N2P11T1G1E1P1L1P111K2T1S1P1S1P1T1G1P1N2P1N2N2S1P1S1 28.846153 P1S1S1P111S1R411S1.G
gi 6325172 ref NP_015240.1	YPL085W	autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p	2	3.1032	0.2649	1663.33	1660.867	1	570.3	50 V.HATSVIPNNPITGEPL.P
gi 6325172 ref NP_015240.1	YPL085W	autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p	2	3.623	0.3933	2362.31	2363.795	1	256	33.333336 H.A1N2I1Q2P1P1T1G1I1L1P1L1A1P1L1R4P1L1D1P1L1Q2.A
		COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Content of the second secon	2	4 4 2 4 2	0.0750	2226.40	2222 005		0447	
gij6325172 ret NP_015240.1	YPL085W	Sec3rp; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23o, Sec24p and	2	4.1312	0.2753	2236.19	2233.665	1	814.7	52.499996 H.AINZIIQZPIPIIIGIILIPILIAIPILIK4PILIDIPILI.Q
gi 6325172 ref NP_015240.1	YPL085W	Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and	2	4.1687	0.4461	2206.55	2207.665	1	863.3	57.5 H.ANIQPPTGILPLAPLRPLDPL.Q
gi 6325172 ref NP_015240.1	YPL085W	may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and	3	3.8801	0.2899	2209.94	2207.665	1	569.8	33.75 H.ANIQPPTGILPLAPLRPLDPL.Q
gi 6325172 ref NP_015240.1	YPL085W	may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation: Sec16p is bound to the periphery of ER membranes and	2	4.0868	0.3662	2046.55	2045.482	1	265.7	52.77778 N.I1Q2P1P1T1G111L1P1L1A1P1L1R4P1L1D1P1L1.Q
gi 6325172 ref NP_015240.1	YPL085W	may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and	2	3.227	0.3107	2024.45	2022.482	2	261.2	50 N.IQPPTGILPLAPLRPLDPL.Q
gi 6325172 ref NP_015240.1	YPL085W	may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and exterbacement formation. Sec16p is bound to be periphered for ER membranes and	2	4.145	0.2772	2161.41	2161.586	1	783.8	57.894737 A.N2I1Q2P1P1T1G1I1L1P1L1A1P1L1R4P1L1D1P1L1.Q
gi 6325172 ref NP_015240.1	YPL085W	autophagosome formation, sec top is bound to the periprety of EX memoranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and	3	3.8205	0.2279	3816.62	3818.102	1	659.7	24.21875 Q.PTIRKASTNQYRAFKPLESDADKYNDVIEDESD.D
gi 6325172 ref NP_015240.1	YPL085W	autophagosome formation; Sec16p is bound to the perphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p COPII vesicle coat protein required for ER transport vesicle budding and	3	4.4429	0.4845	3896.63	3897.277	1	858.1	T.S1V111P1N2N2P111T1G1E1P1L1P111K2T1S1P1S1P1T1G1P1N2P1N2N2S1P1S1 29.054054 P1S1S1P111S1R4.I
gi 6325172 ref NP_015240.1	YPL085W	autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p	3	4.2696	0.4388	3849.5	3850.277	1	370.1	22.972973 T.SVIPNNPITGEPLPIKTSPSPTGPNPNNSPSPSSPISR.I
gi 6325172 ref NP_015240.1	YPL085W	autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p	3	5.5177	0.5671	4050.35	4050.515	1	490.3	23.717949 T.SVIPNNPITGEPLPIKTSPSPTGPNPNNSPSPSSPISRIS.G
gi 6325164 ref NP_015232.1	YPL093W	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre- ribosomal particles; member of the ODN family of nucleolar G-proteins; Nog1p	2	4.3784	0.3326	2047.61	2048.229	1	1196.3	68.75 L.EDDEWKNDIMPEILDGK.N
gi 6325164 ref NP_015232.1	YPL093W	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre- ribosomal particles; member of the ODN family of nucleolar G-proteins; Nog1p	2	3.84	0.2628	2221.81	2219.521	1	830.5	50 L.S1W2K2D111P1T1V1A1P1A1N2D1L1L1D111V1L1N2.R
gi 6325164 ref NP_015232.1	YPL093W	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre- ribosomal particles; member of the ODN family of nucleolar G-proteins; Nog1p	2	3.5657	0.1871	2155.77	2155.413	6	651.7	47.058823 N.KTDIIRPEDLDEERAQLL.E
gi 6325164 ref NP_015232.1	YPL093W	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre- ribosomal particles; member of the ODN family of nucleolar G-proteins; Nog1p	2	3.6122	0.3216	2130.53	2131.442	1	474	44.44447 S.W2K2D1I1P1T1V1A1P1A1N2D1L1L1D111V1L1N2.R
ail6325164 refINP 015232.11	YPL093W	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre- ribosomal particles; member of the ODN family of nucleolar G-proteins; Noo1o	3	3.9688	0.2531	2952.29	2952.32	1	559.8	30.434782 N.L1K2D1K2Y1L1L1E1D1D1E1W2K2N2D1I1M1P1E1I1L1D1G1K2.N
aile225164/refIND_015222.41	VDI 002W	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre-	2	3 0026	0.2101	2240.92	2240.66	1	759.0	
gilo325164[rei]NP_015232.1]	1PL093W	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus	3	3.9920	0.3191	3249.83	3249.00	I	/58.2	25.30 1538 F.INVNERDKTELEDDEWKNDIMPEILDGK.IN
gi 6325164 ref NP_015232.1	YPL093W	and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre- ribosomal particles; member of the ODN family of nucleolar G-proteins; Nog1p Essential subunit of Sec63 complex (Sec63p, Sec66p, Sec66p and Sec72p); with Sec61 complex, Kar20BiP and Lhs1p forms a channel competent for SRP-	2	4.1136	0.3966	2133.11	2131.439	1	811.9	58.823532 E.KFEDILKGFPNINDVHPF.H
gi 41629689 ref NP_015231.2	YPL094C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p	2	3.6384	0.2343	2368.65	2369.67	1	354.7	44.736843 S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2.S

		Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP- dependent and post-translational SRP-independent protein targeting and import into								
gi 41629689 ref NP_015231.2	YPL094C	the ER; Sec62p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	3	4.3265	0.323	2671.07	2672.013	1	994.4	37.5 K.SARQPEIYPTIPSNKIEDQLKSR.E
gi 41629689 ref NP_015231.2	YPL094C	the ER; Sec62p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	3	6.089	0.2747	2703.71	2706.013	1	1888.9	44.31818 K.S1A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi 41629689 ref NP_015231.2	YPL094C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	2	4.0719	0.258	2616.43	2617.935	1	426.9	42.857143 S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi 41629689 ref NP_015231.2	YPL094C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex Kar2n/BiP and the 1n forms a channel completent for SRP.	2	4.9272	0.4207	2670.89	2672.013	1	800	50 K.SARQPEIYPTIPSNKIEDQLKSR.E
gi 41629689 ref NP_015231.2	YPL094C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex (Sec63p, March 1, forme a changed complete for SPP.	3	6.4794	0.4431	2703.14	2706.013	1	1185.1	35.227272 K.S1A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi 41629689 ref NP_015231.2	YPL094C	dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with	2	4.9013	0.4025	2704.81	2706.013	1	562.9	45.454548 K.S1A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi 41629689 ref NP_015231.2	YPL094C	Secci complex, Kar2pisiP and Lns1p forms a channel competent for SKP- dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with	3	4.6882	0.2848	2616.92	2617.935	1	807.5	32.142857 S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi 41629689 ref NP_015231.2	YPL094C	Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP- dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p Essential subunit of Sec63 complex (Sec63p. Sec62p. Sec66p and Sec72p); with	3	5.0336	0.2839	2368.67	2369.67	1	994.5	42.105263 S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2.S
gi 41629689 ref NP_015231.2	YPL094C	Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP- dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p Example a suburit of Cos62 complex (Sec62p, Cos62p, Cos62p, and Sec72p); with	3	5.2353	0.4366	2584.91	2584.935	1	1175.8	39.285713 S.ARQPEIYPTIPSNKIEDQLKSR.E
gi 41629689 ref NP_015231.2	YPL094C	Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP- dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p	3	6.2987	0.3591	2617.49	2617.935	1	1883	47.61905 S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi 41629689 ref NP_015231.2	YPL094C	Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec65p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP- dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p	2	4.4697	0.2449	2616.45	2617.935	1	530.5	45.238094 S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi 6325151 ref NP_015219.1	YPL106C	ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p	2	3.275	0.3347	1600.23	1600.712	1	869.1	72.72727 A.V1P1P1W2Y1T1E1E1Q2R4Y1N2.I
gi 6325151 ref NP_015219.1	YPL106C	A Pase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex;	2	3.1399	0.3494	1581.77	1582.712	1	769.8	68.181816 A.VPPWYTEEQRYN.I
gi 6325151 ref NP_015219.1	YPL106C	binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex;	2	4.3547	0.3473	1847.83	1848.989	1	1314.1	78.57143 A.E1E1W2L1Y1D1E1G1F1D1S1I1K2A1K2.Y
gi 6325151 ref NP_015219.1	YPL106C	binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; See1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;	2	3.312	0.3022	1830.19	1830.989	1	655.5	57.14286 A.EEWLYDEGFDSIKAK.Y
gi 6325151 ref NP_015219.1	YPL106C	Danus undozed proteins, methode on the near shock protein 70 (HSF70) raining, localized to the cytoplasm; Seetp ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSF70) family;	2	3.8248	0.3062	1591.81	1592.787	1	1412.9	84.61539 K.L1V1E1L1D1D1K2K2T1G1A1E1V1R4.F
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;	2	3.9686	0.4494	1572.51	1573.787	1	1135.2	73.07692 K.LVELDDKKTGAEVR.F
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the ordenlarem; Sce1e.	2	3.8078	0.2209	1714.49	1714.969	1	926	66.66667 T.G1V1Q2L1P1E1G1Q2D1S1V1P1V1K2L1K2L
gi 6325151 ref NP_015219.1	YPL106C	ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p	2	3.5086	0.2716	1585.25	1584.795	6	351.5	57.14286 T.GIV1Q2L1P1E1G1Q2D1S1V1P1V1K2L1.K
gi 6325151 ref NP_015219.1	YPL106C	ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p	3	3.982	0.1704	2998.79	2998.226	1	501.2	28 E.D111E1V1E1E1P111P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1T1.K
gi 6325151 ref NP_015219.1	YPL106C	A Page that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex;	2	3.0411	0.2414	2176.05	2175.394	3	265.9	33.333336 E.P111P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1.T
gi 6325151 ref NP_015219.1	YPL106C	binds unfolded proteins: member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex;	2	4.2447	0.4417	2894.59	2896.121	1	680.2	43.75 E.D111E1V1E1E1P111P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1.T
gi 6325151 ref NP_015219.1	YPL106C	uncs unrouged proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;	2	4.296	0.3685	2867.67	2868.121	1	428.8	37.5 E.DIEVEEPIPLPEDAPEDAEQEFKKV.T
gi 6325151 ref NP_015219.1	YPL106C	Incalized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;	2	3.1253	0.262	2998.69	2998.226	3	220.6	28 E.D111E1V1E1E1P111P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1T1.K
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;	2	3.4903	0.3634	2967.23	2969.226	1	420.4	32 E.DIEVEEPIPLPEDAPEDAEQEFKKVT.K
gij6325151 ret NP_015219.1	1PL106C	iocalized to the cytoplasm; Sse1p	2	4.0525	0.3729	1610.77	1611.836	1	1652.6	80.769226 F.KTDLPEGEEKPRIV.A

		ATPase that is a component of the heat shock protein Hsp90 chaperone complex;								
gil63251511refINP_015219_1	YPI 106C	binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm: Sse1p	2	4 5172	0.3686	1997 01	1997 124	1	586.4	63 333332 S W2D1K2Q2V1E1D1E1D1H3M1E1V1E1P1A1 G
giloozo io inolini _010210111	11 21000	ATPase that is a component of the heat shock protein Hsp90 chaperone complex;	-		0.0000	1001.01	10011121	•	000.1	
ail6325151/rofIND_015210_1	VPI 106C	binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;	2	4 4912	0 4320	1076 25	1076 124	1	81/1 1	
gil0525151[lei]i4F_015215.1]	TETOOC	ATPase that is a component of the heat shock protein Hsp90 chaperone complex;	2	4.4012	0.4323	1370.23	1370.124	'	014.1	00.00007 S.WERQVEBEDHINE VITA.G
-:::02054541{IND_045040_4		binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;	2	4 0000	0.0000	2044.04	2244 504	0	504.4	
gilo325151[rei]NP_015219.1]	TPLIUGG	ATPase that is a component of the heat shock protein Hsp90 chaperone complex;	3	4.2693	0.2006	3211.01	3211.501	2	504.1	25.925920 T. HEDIEVEEPIPLPEDAPEDAEQEFKKV.I
		binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;								
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex:	3	4.3646	0.2395	3245.15	3242.501	1	494.7	25 Y.1111E1D111E1V1E1E1P111P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1.1
		binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;								
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex:	2	5.0691	0.393	2664.33	2665.814	1	1003.9	59.090908 E.D111E1V1E1E1P111P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2.K
		binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;								
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex:	1	2.5417	0.1853	1174.6	1174.33	1	146.7	66.66667 A.R4N2R4G111D111V1V1N2.E
		binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;								
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex:	3	4.3251	0.2155	2896.79	2896.121	1	601.2	33.333336 E.D111E1V1E1E1P111P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1.T
		binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;								
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex:	2	4.7713	0.4459	2639.59	2640.814	1	695.3	52.272724 E.DIEVEEPIPLPEDAPEDAEQEFK.K
		binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;								
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p ATPase that is a component of the heat shock protein Hsp90 chaperone complex:	2	3.7438	0.2393	1583.53	1584.769	1	360.9	57.692307 F.G1P1K2N2R4Y1L1G1E1T1G1K2N2K2.Q
		binds unfolded proteins; member of the heat shock protein 70 (HSP70) family;								
gi 6325151 ref NP_015219.1	YPL106C	localized to the cytoplasm; Sse1p	2	3.2358	0.2187	1565.37	1562.769	1	404.5	65.38461 F.GPKNRYLGETGKNK.Q
		Glycerophosphocholine (GroPCho) phosphodiesterase; hydrolyzes GroPCho to								
ail6325147/rofIND_015215_1	VPI 110C	choline and glycerolphosphate after its uptake by Git1p permease, for use as a	1	2 8154	0.201	1170.64	1190 509	1	026.3	72 22222 K20201//1101111161111
giloszs147 [rei]14F_015215.1]	TREITIO	prospirate source and as a precursor for prospiracionine synthesis, due ip		2.0134	0.201	1173.04	1100.000	'	320.3	
		Glycerophosphocholine (GroPCho) phosphodiesterase; hydrolyzes GroPCho to								
gi 6325147 ref NP_015215.1	YPL110C	phosphate source and as a precursor for phosphocholine synthesis; Gde1p	2	3.6639	0.2769	1381.79	1382.746	1	542.7	63.636364 L.S1L1K2Q2P1V11P111L1F1L1.T
		Pho GTPase activating protein (PhoGAP) involved in control of the cytoskeleton								
		organization; targets the essential Rho-GTPase Cdc42p, which controls								
gi 6325142 ref NP_015210.1	YPL115C	establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	4.4157	0.3536	1935.49	1935.184	1	1161.6	59.375 L.KSDIPLFVQPEDFGTIQ.I
		Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton								
ail62251421rofIND_015210_1	VDI 1150	organization; targets the essential Rho-GTPase Cdc42p, which controls	2	E 0926	0 3731	1056 57	1055 194	1	11/2 /	
giloszs14zireiltar_015z10.1	TELISO	establishment and maintenance of cell polanty, including bud-site assembly, behisp	2	5.0050	0.5751	1330.37	1999.104	'	1145.4	
		Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton								
gi 6325142 ref NP_015210.1	YPL115C	establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	3.5131	0.3154	2158.45	2157.422	1	677.8	52.77778 Q.S1L1K2S1D1I1P1L1F1V1Q2P1E1D1F1G1T1I1Q2.I
		Pho GTPase activating protein (PhoGAP) involved in control of the cytoskeleton								
		organization; targets the essential Rho-GTPase Cdc42p, which controls								
gi 6325142 ref NP_015210.1	YPL115C	establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	3.995	0.3495	2073.55	2074.387	1	865.8	58.823532 K.SHVPDLPLPTLPDRQLFQ.T
		Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton								
ail6325142/rofIND_015210_1	VDI 1150	organization; targets the essential Rho-GTPase Cdc42p, which controls	2	4 0779	0 3137	1068 47	1060 257	1	630.2	53 125 K S1H3V1P1D11 1P11 1P171 1P1D1P4O2I 1E1 O
giloszs14zireiltar_015z10.1	TELISO	establishment and maintenance of cell polanty, including bud-site assembly, behisp	2	4.0773	0.5157	1300.47	1303.237	'	030.2	33.123 K.SHISVIFIDTEIFIEIFIEIFIEIFIDTK4Q2EIFI.Q
		Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton								
gi 6325142 ref NP_015210.1	YPL115C	establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	3.6957	0.3207	1987.31	1987.309	2	465.2	50 S.HVPDLPLPTLPDRQLFQ.T
		Rho GTPase activating protain (RhoGAP) involved in control of the cytoskeleton								
		organization; targets the essential Rho-GTPase Cdc42p, which controls								
gi 6325142 ref NP_015210.1	YPL115C	establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	3.7681	0.4278	1880.81	1881.104	1	569	53.333336 S.S1I1E1L111P1N2L1P1E1D1R4F1G1T1R4.N
		Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton								
ail63251/2/rofIND_015210_1	VDI 1150	organization; targets the essential Rho-GTPase Cdc42p, which controls	2	3 3203	0 371	1857.60	1959 104	1	770 5	
giloszs14zirelini _015z10.1	TETISO	establishment and maintenance of cell polarity, including buc-site assembly, beinsp	2	3.3203	0.571	1057.05	1030.104	'	110.5	00.000004 S.SIEEFNEFEDRI GTRIN
		Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton								
gi 6325142 ref NP_015210.1	YPL115C	establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	4.2968	0.2688	2098.81	2099.387	1	1177.2	61.764706 K.S1H3V1P1D1L1P1L1P1T1L1P1D1R4Q2L1F1Q2.T
		Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA								
gi 6325128 ref NP_015196.1	YPL129W	YEATS domain; Taf14p	2	4.764	0.2361	2443.79	2445.757	1	883.8	57.894737 K.T1Q2Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
		Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA								
gi 6325128 ref NP_015196.1	YPL129W	YEATS domain; Taf14p	3	3.9427	0.3642	2418.14	2415.757	1	1854.2	51.315792 K.TQQHILPEVPPVENFPVRQW.S
		Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA								
gi 6325128 ref NP_015196.1	YPL129W	YEATS domain; Taf14p	2	3.8255	0.3158	1744.39	1745.072	1	673.4	60.714287 E.HVIQIPLNKPLLTEE.L
		Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a								
gi 6325128 ref NP_015196.1	YPL129W	YEATS domain; Taf14p	2	3.7669	0.3077	1763.69	1765.072	1	748.4	64.28571 E.H3V111Q2I1P1L1N2K2P1L1L1T1E1E1.L
		Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a								
gi 6325128 ref NP_015196.1	YPL129W	YEATS domain; Taf14p	2	2.941	0.2536	1385.79	1386.566	2	837.1	65 V.P1P1V1E1N2F1P1V1R4Q2W2.S
		Subunit (30 KDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification. contains a								
gi 6325128 ref NP_015196.1	YPL129W	YEATS domain; Taf14p	2	4.436	0.2254	2415.99	2415.757	1	899.1	57.894737 K.TQQHILPEVPPVENFPVRQW.S

		Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA								
gi 6325128 ref NP_015196.1	YPL129W	VEATS domain; Tafl4p Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	2	3.3879	0.2374	1635.61	1634.957	7	442.8	53.846157 E.H3V111Q211P1L1N2K2P1L1L1T1E1.E
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 kDa) of TFIID. TFIIF, and SWI/SNF complexes, involved in RNA	2	3.29	0.2599	2215.83	2213.521	1	493	55.88235 Q.Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Tat14p Subunit (30 Kba) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	2	3.3651	0.1819	2059.65	2058.39	1	785.5	59.375 Q.HILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 Kba) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	2	3.3039	0.2249	1877.61	1879.232	1	544.6	50 E.H3V1I1Q2I1P1L1N2K2P1L1L1T1E1E1L1.A
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 KDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	3	3.8441	0.2972	2415.71	2415.757	1	1219	40.789474 K.TQQHILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 kDa) of TFIID. TFIIF, and SWI/SNF complexes, involved in RNA	2	4.6094	0.2084	2414.95	2415.757	1	961.3	60.526318 K.TQQHILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Ta114p Subunit (30 Kba) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	2	3.3682	0.3908	1856.39	1858.232	1	897.3	63.333332 E.HVIQIPLNKPLLTEEL.A
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 Kba) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	3	5.9989	0.3712	2213.99	2213.521	1	1077.7	47.058823 Q.Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subuni (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	1	2.7708	0.164	1457.72	1458.657	1	289.6	54.545456 A.G1E1R4K2I1P1H3D1L1N2F1L1.Q
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 KDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	2	3.1553	0.2981	1430.37	1430.598	1	1248.3	83.33333 L.TKLNEDDLVGVVQ.M
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 KDa) of TFID, TFIIF, and SWI/SNF complexes, involved in RNA	2	3.2033	0.1637	2103.55	2101.413	6	413.5	47.058823 K.TQQHILPEVPPVENFPVR.Q
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	3	5.0954	0.3121	2416.73	2415.757	1	1825.2	50 K.TQQHILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	2	4.4074	0.1961	2415.87	2415.757	1	957.6	57.894737 K.TQQHILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	2	4.5151	0.238	2442.79	2445.757	1	1108.1	63.15789 K.T1Q2Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf149 Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	3	4.8919	0.29	2445.14	2445.757	1	1188.1	47.368423 K.T1Q2Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	3	4.889	0.2904	2060.03	2058.39	1	1922.4	51.5625 Q.HILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf149 Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	2	4.4147	0.4193	2082.31	2083.39	1	1650	81.25 Q.H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf149 Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA	3	6.3139	0.4265	2184.56	2186.521	1	1698	57.352943 Q.QHILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf149 Subunit (30 kDa) of TFIID, TFIIF, and SW/SNF complexes, involved in RNA	2	4.255	0.44	2057.45	2058.39	1	1227.7	71.875 Q.HILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	polymerase in danscription initiation and in chromatin modulication, contains a YEATS domain; Taf149 Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA soluminges (Interpreting initiation and in chromoting readimentary contains a	3	6.6271	0.4173	2213.42	2213.521	1	1574.7	54.411762 Q.Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi 6325128 ref NP_015196.1	YPL129W	Polymerase in danschippon initiation and in criminal incollication, contains a YEATS domain; Taf14p Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA solvmorase a largeoretime initiation and in chromotilin prodification contains a	2	3.3887	0.2312	2185.47	2186.521	1	879.5	64.70589 Q.QHILPEVPPVENFPVRQW.S
gi 6325128 ref NP_015196.1	YPL129W	Polymerade in data bippon initiation and in crimonian incompany polymerade in data bippony and the polymerade in the pol	1	2.9926	0.3306	1438.6	1439.657	3	317.4	54.545456 A.GERKIPHDLNFL.Q
gi 6325128 ref NP_015196.1	YPL129W	VEATS domain; Tat14p Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a	1	2.6008	0.2367	1485.73	1486.841	1	595.2	58.333332 E.HVIQIPLNKPLLT.E
gi 6325128 ref NP_015196.1	YPL129W	VEATS domain; Tat14p Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a	1	2.2904	0.2525	1503.38	1504.841	5	398.6	50 E.H3V111Q211P1L1N2K2P1L1L1T1.E
gi 6325128 ref NP_015196.1	YPL129W	VEATS domain; Tai14p YEATS domain; Tai14p Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat I.5 ribosomal norticine; binds 55 rRNA and is required for 60S subunit	2	3.4091	0.3102	1486.55	1486.841	1	719.3	66.66667 E.HVIQIPLNKPLLT.E
gi 6325126 ref NP_015194.1	YPL131W	and rate be indecember process, which controls the required on exclusions assembly: Rpl5p Protein component of the large (60S) ribosomal subunit with similarity to E: coli L18 and rat L5 ribosomal proteins; binds 55; RPA and is required for RoS subunit	2	4.259	0.4017	1614.29	1614.668	1	1621.4	79.16667 H.SENRFPGWDFETE.E
gi 6325126 ref NP_015194.1	YPL131W	and rate be indecember process, which consider interview in required on occusation assembly; Rpl5p Protein component of the large (60S) ribosomal subunit with similarity to E: coli L18 and rat L5 ribosomal proteins; binds 55; RPA and is required for RoS subunit	2	4.7879	0.4074	2449.81	2449.582	1	1133.3	63.15789 H.S1E1N2R4F1P1G1W2D1F1E1T1E1E1I1D1P1E1L1L1.R
gi 6325126 ref NP_015194.1	YPL131W	assembly: Rpl5p Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rel L5 ribosomal proteins; binds 55 (RNA and is required for RoS subunit	2	4.1739	0.3906	2106.57	2104.25	1	1487.8	65.625 Y.MEELADDDEERFSELFK.G
gi 6325126 ref NP_015194.1	YPL131W	assembly: Rpl5p Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat L5 ribosomal proteins: binds 55 rRNA and is required for 605 subunit	2	3.012	0.2606	1312.57	1310.455	2	300.6	65 Y.SHELPRYGITH.G
gi 6325126 ref NP_015194.1	YPL131W	assembly; Rpl5p	3	4.2276	0.3743	4011.56	4013.325	1	580.4	26.470589 L.KGASDGGLYVPHSENRFPGWDFETEEIDPELLRSY.I

gi 6325126 ref NP_015194.1	YPL131W	Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat L5 ribosomal proteins; binds 5S rRNA and is required for 60S subunit assembly; Rpl5p	3	5.0282	0.4431	4058.75	4059.325	1	391.2	L.K2G1A1S1D1G1G1L1Y1V1P1H3S1E1N2R4F1P1G1W2D1F1E1T1E1E1I1D1P1E1 26.470589 L1L1R451Y1.I
		Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat L5 ribosomal proteins; binds 5S rRNA and is required for 60S subunit								
gi 6325126 ref NP_015194.1	YPL131W	assembly; RpI5p Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat IS fibosomal proteins: binds 55 rRNA and is required for 60S subunit	2	3.6904	0.3591	2181.25	2181.281	1	754.3	50 L.G1L1D1E1T1Y1K2G1V1E1E1V1E1G1E1Y1E1L1T1.E
gi 6325126 ref NP_015194.1	YPL131W	assembly; Rpl5p Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rol L5 incomponent of the large (60S) ribosomal subunit with similarity to E. coli L18	3	4.7695	0.2533	2831.96	2831.024	1	1875.9	39.772728 H.SENRFPGWDFETEEIDPELLRSY.I
gi 6325126 ref NP_015194.1	YPL131W	and fait to housening proteins, binks so rick want is required to doo subunit assembly: Rpl5p Protein component of the large (60S) ribosomal subunit with similarity to E, coli L18	2	3.2876	0.1734	2861.13	2862.024	2	304.5	40.909092 H.S1E1N2R4F1P1G1W2D1F1E1T1E1E111D1P1E1L1L1R4S1Y1.I
gi 6325126 ref NP_015194.1	YPL131W	and ratio indestinal proteins, once so inversion and is required on eos subunit assembly: Rpl5p Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and ratio. Fibosomal proteins; binds 55; RPNA and is required for R65 subunit	2	3.3673	0.2122	1493.39	1492.631	1	824.8	72.72727 A.Y1S1H3E1L1P1R4Y1G1I1T1H3.G
gi 6325126 ref NP_015194.1	YPL131W	and at 2 in busine proteins, binds 50 ritks and is required to 000 subunit assembly; Rpl5p Protein component of the large (60S) ribosomal subunit with similarity to E, coli L18 end at LE friesmand proteins, binds FC, 42NU, and is required for 60S publicit.	2	3.5841	0.3938	2162.41	2161.281	1	874.1	52.77778 L.GLDETYKGVEEVEGEYELT.E
gi 6325126 ref NP_015194.1	YPL131W	and not be however in a proteins, which and is required to not subunit assembly; RplSp Member of the oxysterol binding protein family, which includes seven yeast bomolons: involved in practice regulation of Sect 40-depandent Colici complex	2	4.4928	0.3159	1630.57	1632.668	1	1407.9	79.16667 H.S1E1N2R4F1P1G1W2D1F1E1T1E1.E
gi 6325112 ref NP_015180.1	YPL145C	services involves in regards regulation or detail reproduction object on place secretory functions, peripheral membrane protein that localizes to the Golgi complex; Kestp Momber of the overtered binding particle family, which includes eaven used	2	3.854	0.3052	1789.73	1788.992	1	673.5	63.333332 T.PEEGALVPEKDDTFLK.L
ail62264421cofIND_046480.41		homologs; involved in negative regulation of Sec14p-dependent Golgi complex secretory functions, peripheral membrane protein that localizes to the Golgi complex;	2	4 6961	0 2424	1099 51	1080.32	1	692.6	
gij6325112[rei]NP_015180.1]	TPL1450	Nets ip Member of the oxysterol binding protein family, which includes seven yeast homologs; involved in negative regulation of Sect4p-dependent Golgi complex	2	4.0001	0.3431	1966.51	1969.23	I	083.0	30.823932 S. VIPEEGALVPENDUIFLK.L
gi 6325112 ref NP_015180.1	YPL145C	secretory functions, peripheral memorane protein that localizes to the Golg complex; Kes1p Member of the oxysterol binding protein family, which includes seven yeast borndown: investing and ensuing of Section 4 decondent Colici complex;	2	3.7968	0.3036	1841.41	1842.016	1	840	63.333332 T.LVGDKEDRKEDLSSIH.W
gi 6325112 ref NP_015180.1	YPL145C	secretory functions, peripheral membrane protein that localizes to the Golgi complex; Kes1p	2	4.6467	0.3883	2125.65	2123.389	1	625.3	52.77778 S.V1T1P1E1E1G1A1L1V1P1E1K2D1D1T1F1L1K2L1.A
ail62264121cofIND_016180_11		Memory with a second se	2	2 170	0 2202	2211 65	2211 579	1	442.2	
gilo323112[rei]NF_013160.1]	TFE1450	Member of the oxysterol binding protein family, which includes seven yeast homologs, involved in negative regulation of Sect 4p-dependent Golgi complex correcting functions, precisional membrane protein that localizes to the Golgi complex.	2	3.179	0.2302	2211.05	2211.576	I	443.2	36.00009 I.WEDIKDESTEV IPPPENIE/G
gi 6325112 ref NP_015180.1	YPL145C	Kestp Member of the oxysterol binding protein family, which includes seven yeast homoloas: involved in nearbive regulation of Sect4-ocleanednet Golia complex	2	4.21	0.2714	2027.79	2028.229	1	1169.1	65.625 T.LVGDKEDRKEDLSSIHW.R
gi 6325112 ref NP_015180.1	YPL145C	secretory functions, peripheral membrane protein that localizes to the Golgi complex; Kes1p Member of the oxysterol binding protein family, which includes seven yeast	2	2.9806	0.2607	1403.35	1403.707	1	730.2	72.72727 E.KKPLNPFLGELF.V
gi 6325112 ref NP_015180.1	YPL145C	homologs; involved in negative regulation of Sec14p-dependent Golgi complex secretory functions, peripheral membrane protein that localizes to the Golgi complex; Kes1p	2	3.606	0.2968	1629.87	1628.786	1	678.9	65.38461 H.CLIDPEVESPELAR.M
		Member of the oxysterol binding protein family, which includes seven yeast homologs; involved in negative regulation of Sec14p-dependent Golgi complex secretory functions, peripheral membrane protein that localizes to the Golgi complex;								
gi 6325112 ref NP_015180.1	YPL145C	Kes1p Member of the oxysterol binding protein family, which includes seven yeast homologs; involved in negative regulation of Sec14p-dependent Golgi complex	2	4.4885	0.3656	1644.95	1645.786	1	955.3	73.07692 H.C1L111D1P1E1V1E1S1P1E1L1A1R4.M
gi 6325112 ref NP_015180.1	YPL145C	secretory functions, peripheral membrane protein that localizes to the Golgi complex; Kes1p Member of the oxysterol binding protein family, which includes seven yeast	2	4.3926	0.3454	2491.81	2491.732	1	429.6	42.857143 F.D1Y1S1V1T1P1E1E1G1A1L1V1P1E1K2D1D1T1F1L1K2L1.A
gi 6325112 ref NP_015180.1	YPL145C	homologs; involved in negative regulation of Sec14p-dependent Golgi complex secretory functions, peripheral membrane protein that localizes to the Golgi complex; Kes1p	2	4.0394	0.4233	2465.93	2467.732	1	718.5	52.380955 F.DYSVTPEEGALVPEKDDTFLKL.A
		Member of the oxysterol binding protein family, which includes seven yeast homologs; involved in negative regulation of Sect4p-dependent Golgi complex secretory functions, peripheral membrane protein that localizes to the Golgi complex;								
gi 6325112 ref NP_015180.1	YPL145C	Kes1p Activator of the phosphotyrosyl phosphatase activity of PP2A; regulates G1 phase	2	4.1505	0.3176	2104.77	2102.389	1	565	50 S.VTPEEGALVPEKDDTFLKL.A
gi 6325105 ref NP_015173.1	YPL152W	progression, the osmoresponse and microtubule dynamics; implicated in the spindle assembly check; subunit of the Tap42p-Pph21p-Rrd2p complex; Rrd2p	2	3.9069	0.3067	1813.37	1812.94	1	1198.4	71.42857 L.R4S1E1F1P1S1L1T1D1E1Q2L1E1Q2L1.S
gi 6325105 ref NP_015173.1	YPL152W	Activator of the phosphotyrosyl phosphatase activity of PP2A; regulates G1 phase progression, the osmoresponse and microtubule dynamics; implicated in the spindle assembly check; subunit of the Tap42p-Pph21p-Rrd2p complex; Rrd2p	2	3.8352	0.3189	2006.61	2009.426	1	1004.8	66.666667M1L1P1E1K2R4L1L1T1P1D1D1M1K2L1W2.E
gi 6325105 ref NP_015173.1	YPL152W	Activator of the phosphotyrosyl phosphatase activity of PP2A; regulates G1 phase progression, the osmoresponse and microtubule dynamics; implicated in the spindle assembly check; subunit of the Tap42p-Pph21p-Rrd2p complex; Rrd2p	2	4.6059	0.357	1794.59	1792.94	1	1535.3	78.57143 L.RSEFPSLTDEQLEQL.S
gi 6325105 ref NP_015173.1	YPL152W	Activator of the phosphotyrosyl phosphatase activity of PP2A; regulates G1 phase progression, the osmoresponse and microtubule dynamics; implicated in the spindle assembly check; subunit of the Tap42p-Pph21p-Rrd2p complex; Rrd2p	2	3.5973	0.3508	1985.71	1987.426	2	483.3	50MLPEKRLLTPDDMKLW.E
gi 6325103 ref NP_015171.1	YPL154C	Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self-activates; Pep4p	2	3.2891	0.2624	1723.55	1725.859	1	730.7	61.538464 T.L1D1C1N2T1R4D1N2L1P1D1L111F1.N
gi 6325103 ref NP_015171.1	YPL154C	Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self-activates; Pep4p	1	2.3262	0.2683	1045.49	1046.231	1	278.4	68.75 D.K2V1V1P1P1F1Y1N2A1.I

gi 6325103 ref NP_015171.1	YPL154C	Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self-activates; Pep4p	3	3.8774	0.2526	3490.34	3490.937	2	386.5	22.413794 L.GYDTISVDKVVPPFYNAIQODLLDEKRFAF.Y
gi 6325103 ref NP_015171.1	YPL154C	Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self-activates; Pep4p	2	3.2986	0.314	1780.51	1780.076	1	1070.9	64.28571 L.AIVGDAFLRKYYSIY.D
gi 6325103 ref NP_015171.1	YPL154C	Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self-activates; Pep4p	1	2.2488	0.1705	1254.86	1254.428	5	340.8	61.11111 Q.DLLDEKRFAF.Y
gi 6325103 ref NP_015171.1	YPL154C	Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self-activates; Pep4p	2	3.0875	0.251	1806.75	1807.964	1	528.3	57.14286 Y.TLDCNTRDNLPDLIF.N
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	3	4.1452	0.1738	3476.36	3476.689	1	692.6	26.724138 F.GKNFDNVPAEEEEIKEETPAEKDHEDVTKF.K
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	2	4.1915	0.275	2207.33	2208.436	1	713.8	50 Q.RLANEKPEDVFERELQFS.E
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	2	4.6941	0.2903	2234.43	2235.436	3	626.5	47.058823 Q.R4L1A1N2E1K2P1E1D1V1F1E1R4E1L1Q2F1S1.E
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	2	2.9322	0.2687	1775.81	1777.03	1	482.2	50 Y.GLGTRLPWDEKYLVE.S
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	1	2.4124	0.1504	1333.8	1334.618	1	622.6	63.636364 F.Y1K2P1I1V1T1V1P1G1K2A1F1.I
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	2	3.1961	0.1552	1851.45	1851.122	2	367.1	53.571426 T.K2D1L1L1H3K2P1E1Y1Y1G1I1K2P1E1.W
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	2	4.224	0.4138	2216.59	2217.366	1	791.3	52.77778 E.EHQFEIDAPSIEDEPITMD.S
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	2	2.9685	0.1933	2101.35	2102.277	2	456.9	38.235294 E.EHQFEIDAPSIEDEPITM.D
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	2	3.8852	0.366	2123.95	2123.277	1	785.8	50 E.E1H3Q2F1E1I1D1A1P1S1I1E1D1E1P1I1T1M1.D
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	3	4.3641	0.3803	3062.9	3062.182	1	502.1	31 F.D1N2V1P1A1E1E1E1E1I1K2E1E1T1P1A1E1K2D1H3E1D1V1T1K2F1.K
gi 6325097 ref NP_015165.1	YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	3	5.7814	0.4424	3513.02	3514.689	1	836.6	F.G1K2N2F1D1N2V1P1A1E1E1E1E111K2E1E1T1P1A1E1K2D1H3E1D1V1T1K2F1 26.724138 K
gi 6325041 ref NP_015109.1	YPL215W	Mitochondrial protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex); interacts with Cbp4p and function is partially redundant with that of Cbp4p; Cbp3p	1	3.3927	0.2749	1419.6	1420.68	1	702	65 S.K2Y1E1L1P1K2W2K2E1A1L1.G
gi 6325041 ref NP_015109.1	YPL215W	minochondria protein required of assembly oubliquinor cytochrome-c reouctase complex (cytochrome bc1 complex); interacts with Cbp4 and function is partially redundant with that of Cbp4p; Cbp3p Mitochondrial protein required for assembly of ubiauinol cytochrome-c reductase	1	3.0649	0.2736	1404.78	1405.68	1	743.6	65 S.KYELPKWKEAL.G
gi 6325041 ref NP_015109.1	YPL215W	complex (cytochrome bc1 complex); interacts with Cbp4p and function is partially redundant with that of Cbp4p; Cbp3p Mitochondrial protein required for assembly of ubiauinol cytochrome-c reductase	2	3.8826	0.1919	1738.27	1739.009	1	1043.5	62.5 A.K2Y1F1Y1E1D1L1K2L1P1R4T1F1.S
gi 6325041 ref NP_015109.1	YPL215W	complex (cytochrome bc1 complex); interacts with Cbp4p and function is partially redundant with that of Cbp4p; Cbp3p Mitochondrial protein required for assembly of ubiquinol cytochrome-c reductase	2	3.2667	0.195	1404.85	1405.68	4	677.1	75 S.KYELPKWKEAL.G
gi 6325041 ref NP_015109.1	YPL215W	complex (cytochrome bc1 complex); interacts with Cbp4p and function is partially redundant with that of Cbp4p; Cbp3p Mitochondrial protein required for assembly of ubiquinol cytochrome-c reductase	1	3.0517	0.2835	1405.65	1405.68	1	714.3	65 S.KYELPKWKEAL.G
gi 6325041 ref NP_015109.1	YPL215W	complex (cytochrome bc1 complex); interacts with Cbp4p and function is partially redundant with that of Cbp4p; Cbp3p GTPase, GTP-binding protein of the ARF family, component of COPII coat of weides: rowing for greened useled formation during EB to Colling rotation transport.	2	2.9474	0.2307	1720.13	1721.009	1	646.5	54.166668 A.KYFYEDLKLPRTF.S
gi 6325038 ref NP_015106.1	YPL218W	resules, required to transport vesicle romation during Eric Goog protein datsport, Sartp GTPase, GTP-binding protein of the ARF family, component of COPII cost of vesicles: required for transport vesicle formation during EP to Gold increase transport.	2	4.2375	0.1703	1630.45	1630.841	1	1329.4	83.33333 L.W2K2D1Y1F1P1E1V1N2G111V1F1.L
gi 6325038 ref NP_015106.1	YPL218W	Sartp GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles: required for transport vesicle formation during ER to Gold protein transport	2	4.7275	0.2747	1707.31	1706.847	1	1798.2	80 L.G1N2K2I1D1A1P1N2A1V1S1E1A1E1L1R4.S
gi 6325038 ref NP_015106.1	YPL218W	Sar1p GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport;	2	3.6814	0.3244	2266.43	2267.534	1	681.8	45.238094 L.G1N2K2I1D1A1P1N2A1V1S1E1A1E1L1R4S1A1L1G1L1L1.N
gi 6325038 ref NP_015106.1	YPL218W	Sartp GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport;	2	4.9939	0.4088	2237.77	2239.534	1	1688.4	64.28571 L.GNKIDAPNAVSEAELRSALGLLN
gi 6325038 ref NP_015106.1	YPL218W	Sar1p GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport;	2	3.3693	0.2063	1743.47	1745	1	1142.6	73.07692 L.W2K2D1Y1F1P1E1V1N2G111V1F1L1.V
gi 6325038 ref NP_015106.1	YPL218W	Sar1p GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport;	1	2.5467	0.1808	1348.59	1348.53	6	103.8	55 Q.R4I1E1G1Q2R4P1V1E1V1F1.M
gi 6325038 ref NP_015106.1	YPL218W	Sartp GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport;	2	3.1724	0.1603	1485.27	1484.667	1	723.3	85 R.R4L1W2K2D1Y1F1P1E1V1N2.G
gij6325038 ref NP_015106.1	YPL218W	Sarip GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport;	1	3.0334	0.2634	1484.56	1484.667	2	135.7	
gil6325038/ref/NP_015106.1	YPI 218W	GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport;	2	2.410	0.2397	1460.69	1467.667	1	881 3	
gij6325038/ref/NP_015106.1	YPI 218W	GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport;	2	3,8752	0.2200	1904 29	1905 188	1	1334 7	71 42857 R R4I 1W2K2D1Y1F1P1F1V1N2G1I1V1F1 L
gil6325038lrefINP_015106.1	YPL218W	GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport; Sarto	-	2,231	0.159	1466.66	1467,667	1	97.6	50 R.RLWKDYFPEVN.G
Strategicalia Totorograf		GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport.	•		2			•		
gi 6325038 ref NP_015106.1	YPL218W	Sar1p	1	2.5176	0.1803	1483.65	1484.667	1	194.3	70 R.R4L1W2K2D1Y1F1P1E1V1N2.G

		GTPase, GTP-binding protein of the ARF family, component of COPII coat of								
gi 6325038 ref NP_015106.1	YPL218W	vesicles; required for transport vesicle formation during ER to Goigi protein transport; Sar1p ATP binding cassette family member; Asn/GIn-rich rich region supports [NU+] prion	2	3.1418	0.2093	1486.01	1484.667	1	866.9	85 R.R4L1W2K2D1Y1F1P1E1V1N2.G
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member: Asn/GIn-rich rich region supports (NU+) prion	1	2.9734	0.2417	1346.55	1346.409	2	457.7	59.090908 K.H3F1E1D1V1G1L1D1S1E1I1A1.N
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member: San/Ghr-rich rich region supports [NU+] prion	2	3.0031	0.1873	1420.45	1422.541	2	525.9	68.181816 A.LDCISDKENTVK.R
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member: Sav(Gh-rich rich region supports [NU+] prion	2	3.0666	0.2998	1881.79	1881.994	1	564.1	63.333332 L.KEDDEADKENKFSGRL.T
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member: Sav(Gh-rich rich region supports [NU+] prion	1	2.4811	0.1728	1039.54	1040.301	2	548.1	68.75 Q.M1R4F1P1P1P1G111L1.T
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member: Sav(Gh-rich rich region supports [NU+] prion	2	3.4611	0.2628	1678.55	1679.781	1	429.9	53.571426 L.DEPTNYLDRDSLGALA
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member: Sav(Gh-rich rich region supports [NU+] prion	2	3.7145	0.2942	1436.45	1437.541	1	825.3	77.27273 A.L1D1C111S1D1K2E1N2T1V1K2.R
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member: Sav(Gh-rich rich region supports [NU+] prion	2	4.0373	0.3718	1820.99	1820.932	1	775.9	68.75 S.N2L1A1K2P1S1V1D1D1D1D1S1P1A1N2I1K2.V
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member; Sav(Sh-rich rich region supports [NI]+] prion	2	3.6697	0.2602	1904.43	1904.994	1	769.9	56.666668 L.K2E1D1D1E1A1D1K2E1N2K2F1S1G1R4L1.T
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibilities (PSH) prior induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding reassett 6 amily member: Sav(Ghu-rich rich region supports [N] H1 prior	2	2.9127	0.3016	1640.65	1639.852	5	245.1	54.166668 W.RYQFGDDREVLLK.E
gi 6325030 ref NP_015098.1	YPL226W	formation, susceptibility, [PBH-] prior induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p 4TP biolific reasestit family member; Se/(Shu-tik rich renion supports [N]] Al prior	2	3.3976	0.1688	2071.09	2071.205	1	469.8	46.875 L.FYQEKERADEDEGIEIV.N
gi 6325030 ref NP_015098.1	YPL226W	Arr binang sessetti anny method, for induction and aggregation opports (Nev) prior formation, susceptibility (FSH) prior induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p ATP binding cassette family member; Se/(Shu-tich rich region supports [NI] Al prior	2	3.9317	0.2824	2092.15	2093.205	1	924.3	59.375 L.F1Y1Q2E1K2E1R4A1D1E1D1E1G111E1I1V1.N
gi 6325030 ref NP_015098.1	YPL226W	Arris of an angle case the same processing of the second s	2	3.7428	0.3282	1661.23	1660.852	1	385.3	62.5 W.R4Y1Q2F1G1D1D1R4E1V1L1L1K2.E
gi 6325025 ref NP_015093.1	YPL231W	submatching and the second sec	2	3.7031	0.3266	2133.37	2134.301	3	383.4	47.058823 L.KLEAEEIPSEDONEFLLE.R
gi 6325025 ref NP_015093.1	YPL231W	Applied build for high your synthesis, which catalyzes and beta ketaoxy synthesis of one of the saturated faity acids; contains beta-ketaoxy reductase and beta-ketaoxy isynthese activities; Fas2p. Albha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	3	5.1229	0.4372	2647.97	2650.039	1	1092.4	35.714287 S.G111R4L111E1P1E1L1F1N2G1Y1N2P1E1K2K2E1M111Q2.E
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids, contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Albha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.3224	0.3549	1681.47	1679.868	1	262.6	57.14286 A.AIPEQGIELEHIDSK.S
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Aloha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.918	0.4554	1770.37	1770.946	1	537.8	70 F.A1A1I1P1E1Q2G111E1L1E1H3I1D1S1K2.S
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.0215	0.3878	1750.29	1750.946	1	467.4	60.000004 F.AAIPEQGIELEHIDSK.S
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.9505	0.3132	2603.53	2605.805	1	521.4	38.636364 L.G1K2E1F1G1T1T1P1E1K2P1E1E1T1P1L1E1E1L1A1E1T1F1.Q
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Albha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.2156	0.2753	2120.29	2119.287	1	800.4	52.77778 F.GTTPEKPEETPLEELAETF.Q
gi 6325025 ref NP_015093.1	YPL231W	submode in the state years of the state of t	1	3.1844	0.2795	1421.8	1422.535	1	441.3	63.636364 R.N2A1D1N2V1D1K2I1L1E1Q2F1.E
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	1	3.071	0.3066	1405.55	1406.535	1	540.4	63.636364 R.NADNVDKILEQF.E
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.2932	0.1983	1760.53	1760.926	1	542.4	53.571426 LI1E1F1I1Y1D1T1E1K2N2G1G1L1G1W2.D
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.5273	0.3757	2242.27	2241.351	1	1029.4	61.11111 K.E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1A1.R
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	1	2.3394	0.1703	1066.63	1068.219	3	195.7	61.11111 E.R4V1V1E1I1G1P1S1P1T1.L
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Aloha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.9286	0.296	2092.67	2091.235	1	1127.3	61.764706 E.HAPYTDELEEDVYLDPLA.R
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.4827	0.2516	1724.97	1726.878	1	790.8	62.5 L.A1A1K2E1E1P1A1K2E1E1A1P1A1P1T1P1A1.A
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	2.9202	0.1926	1709.87	1707.878	1	342.2	53.125 L.AAKEEPAKEEAPAPTPA.A
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	1	2.2209	0.1527	1432.54	1433.535	6	157.2	50 LEEFEHGRTPAEM.S
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p	1	2.4095	0.1882	1054.75	1055.219	7	155.6	61.11111 E.RVVEIGPSPT.L

		Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids: contains beta-ketoacyl reductase and beta-ketoacyl synthase								
gi 6325025 ref NP_015093.1	YPL231W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.0456	0.2975	1666.49	1666.8	1	535.4	57.692307 N.T1L1E1E1F1E1H3G1R4T1P1A1E1M1.S
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.4938	0.3433	1697.87	1698.868	1	325.7	64.28571 A.A111P1E1Q2G111E1L1E1H3I1D1S1K2.S
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Aloha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.6277	0.2564	1876.23	1875.024	1	1193.1	66.66667 Y.S1K2D1A1K2E1I1Y1Y1T1P1D1P1S1E1L1.A
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha suburit of fatty acid synthetase which catalyzes the synthesis of long-chain	3	3.8716	0.1783	2376.65	2377.603	1	691.5	38.157894 M.D1L1D1N2G1E1R4K2F1L1K2E1K2D1T1V1A1E1L1Q2.A
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Albha subwini of fatty acid synthetase which catalyzas the synthesis of long-chain	2	4.9174	0.4239	2152.33	2153.329	1	1022.4	58.333332 L.G1K2E1F1G1T1T1P1E1K2P1E1E1T1P1L1E1E1L1.A
gi 6325025 ref NP_015093.1	YPL231W	reprint bubblish that a constraint beta-ketoacyl reductable and Synthesis of high straint saturated fatty acids; constraints beta-ketoacyl reductable and beta-ketoacyl synthase activities; Fas2p	2	4.4568	0.3994	2298.27	2299.446	2	403.5	50 S.K2E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1.A
gi 6325025 ref NP_015093.1	YPL231W	Appressibility acids, contains beta-ketoacyl reductase and beta-ketoacyl synthesis saturated faity acids, contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p	2	3.584	0.3391	2560.63	2559.736	2	139.6	35.714287 F.V1S1K2E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1A1.R
gi 6325025 ref NP_015093.1	YPL231W	Alpha subunit of ratify acid synthetase, which catalyzes the synthesis of long-chain saturated faity acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p	2	3.7541	0.312	2370.31	2371.525	1	422.4	47.368423 S.K2E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1A1.R
gi 6325025 ref NP_015093.1	YPL231W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p	2	4.2786	0.324	2347.01	2348.525	1	658.1	50 S.KEHAPYTDELEEDVYLDPLA.R
gi 6325025 ref NP_015093.1	YPL231W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p	2	3.6458	0.3177	2580.17	2580.805	1	290.9	36.363636 L.GKEFGTTPEKPEETPLEELAETF.Q
ail6325025lrefINP_015093.1	YPL231W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2n	2	3.73	0.2588	1902.45	1903.14	2	518.4	53.125 W VDSKTKEPVDDKDVKAK Y
ail63250251refINP_015093_1	VPI 231W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Ess20.	2	4 8753	0 3077	2377.61	2377 603	-	524.3	50 M D11 1D1N2G1E1R4k2E11 1K2E1K2D1T1V1A1E11 1O2 A
ail6225025[ref NP_015033.1]	VDI 221W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activition; Ear2	2	4.0733	0.0007	23/7.01	2311.003	0	524.5	
	TPL231W	Activities, rascp Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase	2	4.5978	0.2367	2346.43	2345.546	°	501.7	37.5 LIN25 IG TITTE IG IN274IN24 ID IN27 ID IN21 LIE IQ2F I.E
gi 6325025 ref NP_015093.1	YPL231W	activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase	2	4.4219	0.2704	2315.09	2315.548	1	761.2	47.5 L.NSGIIPGNRNADNVDKILEQF.E
gi 6325025 ref NP_015093.1	YPL231W	activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase	2	4.3235	0.3413	2139.69	2141.366	1	721.5	50 S.G1111P1G1N2R4N2A1D1N2V1D1K211L1E1Q2F1.E
gi 6325025 ref NP_015093.1	YPL231W	activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase	2	3.6724	0.3027	2113.55	2114.366	1	839.7	50 S.GIIPGNRNADNVDKILEQF.E
gi 6325025 ref NP_015093.1	YPL231W	activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids: contains beta-ketoacyl reductase and beta-ketoacyl synthase	2	3.6942	0.2297	1543.13	1542.688	1	551.1	77.27273 M.F1K2D1R4F1K2D1E1P1V1Q2N2.D
gi 6325025 ref NP_015093.1	YPL231W	activities (FpS2pa) Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain equivated fatty acids (synthetase), which catalyzes and beta ketacad synthesis	2	4.4174	0.334	2146.39	2147.342	1	834.8	59.375 M.F1K2D1R4F1K2D1E1P1V1Q2N2D111L1Q2E1.S
gi 6325025 ref NP_015093.1	YPL231W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.2579	0.3447	2120.77	2122.342	1	1146.6	65.625 M.FKDRFKDEPVQNDILQE.S
gi 6325025 ref NP_015093.1	YPL231W	saturated ratif actus, contains beia-keloacy reductase and beia-keloacy synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	3	4.9423	0.3457	2142.83	2143.44	1	1230.3	41.17647 S.G111R4L11E1P1E1L1F1N2G1Y1N2P1E1K2K2.E
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.5462	0.3625	2648.45	2650.039	1	500.5	47.61905 S.G111R4L111E1P1E1L1F1N2G1Y1N2P1E1K2K2E1M111Q2.E
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	2.9546	0.1791	1526.37	1523.688	1	462	72.72727 M.FKDRFKDEPVQN.D
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.2187	0.3022	1992.55	1993.227	1	941.7	63.333332 M.FKDRFKDEPVQNDILQ.E
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	4.5418	0.3141	2017.47	2017.227	1	862.8	60.000004 M.F1K2D1R4F1K2D1E1P1V1Q2N2D111L1Q2.E
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Aloha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.7733	0.2143	1889.69	1887.096	1	880.7	67.85714 M.F1K2D1R4F1K2D1E1P1V1Q2N2D111L1.Q
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha suburit of fatty acid synthetase which catalyzes the synthesis of long-chain	2	3.345	0.298	1863.97	1865.096	1	510.5	57.14286 M.FKDRFKDEPVQNDIL.Q
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids, contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Albha subwini of fatty acid synthatase which catalyzas the synthesis of long-chain	3	4.5037	0.2209	2638.91	2639.97	1	647.2	36.904762 L.K2M1D1L1D1N2G1E1R4K2F1L1K2E1K2D1T1V1A1E1L1Q2.A
gi 6325025 ref NP_015093.1	YPL231W	saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alpha subwini of fatty acid synthetase, which catalyras the synthesis of long abain	2	3.9102	0.1899	2637.61	2639.97	1	452.7	45.238094 L.K2M1D1L1D1N2G1E1R4K2F1L1K2E1K2D1T1V1A1E1L1Q2.A
gi 6325025 ref NP_015093.1	YPL231W	subtracted data years years synthesized, mind tradayced ine synthesize on blightfaill saturated data years and beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p Alnha sithunit of data acid synthesized, which catalycers the synthesized fuers abain	3	4.8169	0.2911	2621.18	2620.039	1	1197	40.476192 S.GIRLIEPELFNGYNPEKKEMIQ.E
gi 6325025 ref NP_015093.1	YPL231W	saturated faitly acids; contains beta-ketoacyl reductase and beta-ketoacyl synthese activities; Fas2p	2	3.4553	0.3468	1804.27	1805.093	1	799.8	52.941177 T.A1T1D1K2I1G1R4S1V1P1A1P1G1K2G1I1L1T1.T

ail62250251rofIND_015002_11		saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase	2	2 4006	0.2600	1007.25	1007 100	1	CCE O	47 00000 A T4 A4T4 D4/2010 (D4 A4D4 A4D4 C4/2010) 4T4 T
gil6325025 ret NP_015093.1	YPL231W	activities; Fas2p Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain	2	3.4906	0.3699	1907.35	1907.199	1	665.9	47.22222 A.TTATTTD1K2I1G1R4S1V1P1A1P1G1K2G111L1T1.T
		saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase								
gi 6325025 ref NP_015093.1	YPL231W	activities; Fas2p	2	3.226	0.3547	1705.93	1702.988	1	885.2	56.25 T.A1T1D1K2I1G1R4S1V1P1A1P1G1K2G1I1L1.T
		Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
ail6325025/refINP 015093.1	YPL231W	activities: Fas2p	2	3.8819	0.183	2150.07	2149.272	1	655.5	50 K.EHAPYTDELEEDVYLDPL.A
31		Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
		saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase								
gi 6325025 ref NP_015093.1	YPL231W	activities; Fas2p	2	3.8548	0.3782	2219.19	2220.351	1	682.5	52.77778 K.EHAPY I DELEED VYLDPLA.R
		saturated fatty acids: contains beta-ketoacyl reductase and beta-ketoacyl synthesis								
gi 6325025 ref NP_015093.1	YPL231W	activities; Fas2p	3	4.1435	0.2362	1733.6	1733.015	4	1006.8	39.0625 A.T1D1K2I1G1R4S1V1P1A1P1G1K2G1I1L1T1.T
		Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain								
ail62250251rofINB_015002.1		saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase	1	4 0259	0 4422	1507.67	1509 904	4	204.2	
gil0323025[lei]litP_015095.1]	TFL23TW	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain		4.0200	0.4423	1507.07	1308.804		304.3	00.714207 1.DRIGR3VFAFGRGIE.1
		saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase								
gi 6325025 ref NP_015093.1	YPL231W	activities; Fas2p	2	4.6187	0.2392	2170.49	2169.272	1	918.1	58.823532 K.E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1.A
		Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids: contains beta-ketoacyl reductase and beta-ketoacyl synthese								
ail6325025/refINP 015093.1	YPL231W	activities: Fas2p	2	4.556	0.3455	2139.97	2139.287	1	633.9	47.22222 F.G1T1T1P1E1K2P1E1E1T1P1L1E1E1L1A1E1T1F1.Q
31		Beta subunit of the translation initiation factor eIF2, involved in the identification of								
gi 6325018 ref NP_015087.1	YPL237W	the start codon; proposed to be involved in mRNA binding; Sui3p	1	2.7162	0.2714	1133.42	1134.253	3	231.2	68.75 L.H3R4S1P1E1H3L1I1Q2.Y
gil6325018/rofINP_015087_1	VDI 237W/	Beta subunit of the translation initiation factor eIF2, involved in the identification of	1	2 0103	0.2833	1247 41	1248 412	1	241.2	66 66667 K I 1H3P4S1P1E1H3I 1102 V
gil0323010[tel[14F_013007.1]	11 2237 11	Beta subunit of the translation initiation factor eIF2, involved in the identification of		2.3133	0.2000	1247.41	1240.412		241.2	00.00007 N.Emor43 TFTE moemoz.T
gi 6325018 ref NP_015087.1	YPL237W	the start codon; proposed to be involved in mRNA binding; Sui3p	1	2.5476	0.249	1101.54	1102.206	2	427.4	55.555557 K.K2V111P1D1D1F1D1A1A1.V
		Beta subunit of the translation initiation factor eIF2, involved in the identification of								
gi 6325018 ref NP_015087.1	YPL237W	the start codon; proposed to be involved in mRNA binding; Sui3p	1	2.3058	0.2018	1116.47	1117.253	4	210.1	62.5 L.HRSPEHLIQ.Y
		proteins: involved in heme A biosynthesis: homologous to human adrenodoxin:								
gi 6325004 ref NP_015071.1	YPL252C	Yah1p	2	3.5755	0.253	2933.63	2934.111	1	458.1	39.583336 C.HVIVDPDYYDALPEPEDDENDMLDL.A
		Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur								
ail6325004/rofINB_015071_1		proteins; involved in heme A biosynthesis; homologous to human adrenodoxin;	2	4 9754	0 4651	2002.61	2004.25	4	502.2	
gil6323004[tel[INP_013071.1]	TFL2520	Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur	2	4.2704	0.4031	3092.01	3094.25		093.Z	40 T.CHVIVDFDTTDALFEFEDDENDIVIEDE.A
		proteins; involved in heme A biosynthesis; homologous to human adrenodoxin;								
gi 6325004 ref NP_015071.1	YPL252C	Yah1p	2	4.4394	0.4116	2932.35	2934.111	1	435.8	41.666664 C.HVIVDPDYYDALPEPEDDENDMLDL.A
		Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur								
ail6325004/refINP_015071.1	YPL252C	Yah1p	3	4.6654	0.3008	2933.21	2934.111	1	922.5	33.333336 C.HVIVDPDYYDALPEPEDDENDMLDL A
3.1		Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and	-							
		mitochondrial localization determined by the N-terminal mitochondrial targeting								
gi 6324993 ref NP_015061.1	YPL262W	sequence and protein conformation; Fum1p	3	3.939	0.2334	2172.2	2172.46	1	1129.6	47.058823 L.TEKEFDEWVVPEHMLGPK
		mitochondrial localization determined by the N-terminal mitochondrial targeting								
gi 6324993 ref NP_015061.1	YPL262W	sequence and protein conformation; Fum1p	2	4.7486	0.28	2172.95	2172.46	1	1056.3	61.764706 L.TEKEFDEWVVPEHMLGPK
		Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and								
ail62240021rofINB_015061_1		mitochondrial localization determined by the N-terminal mitochondrial targeting	2	4 7046	0.252	2102 65	2105.46	4	1261.2	48 52044 T1E1K2E1E1D1E1W2\/1\/1D1E1H2M111C1D1K2
gil0324993[iei]inF_015061.1]	TFL202W	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle: cytosolic and	3	4.7040	0.202	2193.00	2195.40	'	1301.2	40.52541 L.TTETKZETFTDTETW2VTVTFTETH5MTETGTFTK2
		mitochondrial localization determined by the N-terminal mitochondrial targeting								
gi 6324993 ref NP_015061.1	YPL262W	sequence and protein conformation; Fum1p	2	5.2577	0.3673	2172.69	2172.46	1	1272.4	67.64706 L.TEKEFDEWVVPEHMLGPK
		Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and								
ail6324993/refINP_015061.1	YPL262W	sequence and protein conformation: Fum1p	1	2.3361	0.3744	1256.43	1257.434	1	556.8	70 E.IHVPADKYWGA.Q
3.1		Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and	-							
		mitochondrial localization determined by the N-terminal mitochondrial targeting								
gi 6324993 ref NP_015061.1	YPL262W	sequence and protein conformation; Fum1p	2	3.1337	0.2619	1777.99	1776.958	4	368.7	50 L.TEKEFDEWVVPEHM.L
gi 6324992 ref NP_015060.1	YPL263C	Cytoplasmic protein of unknown function; Kel3p	2	3.8811	0.373	2347.65	2349.672	1	760.9	50 Q.MTE111P1D1E1R4S1W2L1P1H3P1K2P1F1E1T1L1.K 43 055553 O.M1E111P1D1E1P4S1W2L1P1H3P1K2P1E1E1T1L1.R
gil6324992[ref]NP_015060.1]	VPL 263C	Cytoplasmic protein of unknown function, Kelsp	2	3 8608	0.3201	2349.44	2349.072	1	1228.6	43.033333 Q.MIETTETDTETRASTWZETETIGETRZETETETTET.K
gil6324992[ref[NP_015060.1]	VPI 263C	Cytoplasmic protein of unknown function; Kel3p	2	1 7802	0.2341	2351.06	23/0 672	1	1468.3	45 833336 O M1E11101D1E104S1W2I 101H301K201E1E1T1L1 P
gil6324992/refINP_015060.1	YPI 263C	Cytoplasmic protein of unknown function; Kel3p	2	3 622	0.2713	2347 75	2349.672	1	505.3	41.666664 O M1E111P1D1E1R4S1W2L1P1H3P1K2P1E1E1T1L1 R
gil6324992[rofIND_015060.1]	VPI 263C	Cytoplasmic protein of unknown function; Kel3p	2	3 6575	0.0001	1081 21	1080 202	3	3/3 1	
gil6324992[rofIND_015060.1]	VPI 263C	Cytoplasmic protein of unknown function; Kel3p	2	3 7237	0.2253	2004.03	2003 202	7	410.1	56 666668 O M1E1I1D1D1E1D4S1W2I 1D1H3D1K2D1E1 E
gil6324992/refINP_015060.1	YPI 263C	Cytoplasmic protein of unknown function; Kel3p	2	2 9777	0.2249	2216 41	2217 479	1	394.4	47 058823 M E111P1D1E1R4S1W2I 1P1H3P1K2P1E1E1T1I 1 R
gi[6324992]refINP_015060.1]	YPI 263C	Cytoplasmic protein of unknown function; Kel3p	2	3 1767	0.312	1848 61	1849 099	1	632.1	60 714287 M EIPDERSWI PHPKPE E
gi[6324992]refINP_015060.1]	YPI 263C	Cytoplasmic protein of unknown function; Kel3p	2	3 7458	0.2501	2001 77	2003 292	4	531.9	60 000004 O M1E111P1D1E1R4S1W2L1P1H3P1K2P1E1 E
gil6324992/refINP_015060.1	YPL263C	Cytoplasmic protein of unknown function; Kel3p	3	4.2155	0.2275	2002.88	2003.292	9	609.6	41.6666664 Q.M1E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1.E
ail6324992/refINP 015060.1	YPL263C	Cytoplasmic protein of unknown function: Kel3p	2	3.3344	0.2329	2113.87	2115.341	1	321.8	56.25 S.K2R4K2S1N2K2D1Q2E1K2E1L1Q2D1L1L1N2.S
		High-affinity S-adenosylmethionine permease, required for utilization of S-								
		adenosylmethionine as a sulfur source; has similarity to S-methylmethionine								
gi 6324981 ref NP_015049.1	YPL274W	permease Mmp1p; Sam3p High-affinity S-adenosylmethioning permease, required for utilization of S-	2	4.9663	0.4299	2523.37	2523.674	1	1016	62.5 S.N2L1H3V11P1E1D1L1E1N2S1E1Q211E1Q2E1K2I1Q2.W
		adenosylmethionine as a sulfur source: has similarity to S-methylmethionine								
gi 6324981 ref NP_015049.1	YPL274W	permease Mmp1p; Sam3p	2	3.6794	0.321	2711.71	2711.888	1	757.4	47.61905 S.N2L1H3V1I1P1E1D1L1E1N2S1E1Q2T1E1Q2E1K2I1Q2W2.K
		High-affinity S-adenosylmethionine permease, required for utilization of S-								
		adenosylmethionine as a sulfur source; has similarity to S-methylmethionine								
gi 6324981 ref NP_015049.1	YPL274W	permease Mmp1p; Sam3p	3	4.1424	0.3543	2841.56	2842.062	1	470.6	26.136362 S.N2L1H3V11P1E1D1L1E1N2S1E1Q2T1E1Q2E1K2I1Q2W2K2.L
gijo325267 [ret]NP_015335.1	TPRU10C	KINA polymerase i subunit A135; Kpa135p	1	2.7478	0.2939	1451.54	1452.665	1	/36.2	00.101010 K.KWPTIDMPESET.G
gijo325267 [ret]NP_015335.1	TPRU10C	KIVA polymerase i subunit A135; Kpa135p	2	2.9156	0.1582	2137.79	2137.329	4	312	
gijo325267 [ret]NP_015335.1	TPRU10C	KIVA polymerase i subunit A135; Kpa135p BNA polymerase i subunit A135; Bps125p	2	3.4057	0.2672	1682.37	1682.896	1	661.3	
gilo325267 [ref]NP_015335.1	VPP010C	NNA polymerase Leubunit A135: Pra135n	2	J.0344	0.2012	166/ 71	1662 026	1	332.0	
gi[6325267]refINP_015335.1	YPR010C	RNA polymerase Lsubunit A135: Rpa135p	2	3 5638	0.2041	2880 33	2890 300	1	267.6	30 769232 E GKTPGI PIDI FIGY/PPSTRGOVPGI V I
gil6325267/ref/NP_015335_1	YPR010C	RNA polymerase I subunit A135: Rpa135p	2	5.1145	0.362	2131 71	2133 37	1	1292.4	62.5 Q.HEGEGNDEWPKEWLEKI D
gil6325267/ref/NP_015335_1	YPR010C	RNA polymerase I subunit A135: Rpa135p	2	4,9501	0.3792	2159.97	2157.37	1	1328.5	68.75 Q.H3F1G1F1G1N2D1E1W2P1K2E1W2L1E1K2L1.D
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	1	2.5035	0.3136	1228.68	1229.465	1	367.4	66.66667 T.TVRKLLPESW.G

Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain

ail6325267/refINP 015335.11	YPR010C	RNA polymerase Lsubunit A135: Rpa135p	2	3.6973	0.3402	1694.73	1695.931	1	790.8	65.38461 C.SRKWPTIDMPESET.G
gil6325267/refINP_015335_1	YPR010C	RNA polymerase Lsubunit A135: Rpa135n	2	4 9167	0 4682	2466 73	2467 868	1	1198.9	56 81818 W KVEGKTPGI PIDI EIGYVPPSTR G
gil6325267/refINP_015335_1	VPR010C	RNA polymerase I subunit A135: Rpa135p	2	3 3035	0.3504	1664 75	1664 896	1	1169.7	
gil6225267 [ref[ND_015225_1]	VPR010C	BNA polymoroso Loubunit A135: Bpo135p	2	2 2012	0.0004	2409.20	2405 542	1	206.6	
gil0323207 [rei]NF_015355.1]	VPPotoC	RNA polymerase i suburili A105, Rpa105p	2	3.3012	0.3243	2406.29	2403.342		590.0	
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	4.4036	0.3711	2889.11	2890.309	2	519.4	28.846153 E.GKTPGLPIDLEIGYVPPSTRGQYPGLY.L
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	3.9606	0.2627	2157.32	2157.37	4	451.2	32.8125 Q.H3F1G1F1G1N2D1E1W2P1K2E1W2L1E1K2L1.D
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.722	0.2149	1715.03	1714.931	1	680.3	61.538464 C.S1R4K2W2P1T1I1D1M1P1F1S1E1T1.G
gi 6325267 ref NP 015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	4.7658	0.3091	2497.76	2495.868	1	1164.1	39.772728 W.K2V1E1G1K2T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4.G
gil6325267/refINP_015335.11	YPR010C	RNA polymerase Lsubunit A135; Rpa135p	2	5.3502	0.4855	2494.97	2495,868	1	1161.6	54.545456 W.K2V1E1G1K2T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4 G
gil6325267/refINP_015335_1	VPR010C	RNA polymerase I subunit A135; Rpa135p	3	5.0735	0 4411	2465 33	2467 868	1	1170.5	42 045452 W KVEGKTPGI PIDI EIGYVPPSTR G
sil0225267 [ref[ND_045225_4]	VDD040C			2,000	0.4411	2400.00	2407.000		704.5	
gi[6325267]ref[NP_015335.1]	YPR010C	RNA polymerase i subunit A135; Rpa135p RNA polymerase i subunit A135; Rpa135p	3	3.829 4.0233	0.306	2134.91	3246 731	1	724.5 913.6	30.9375 Q.FFGFGNDEWPREWLERLD 32 75862 W KVEGKTPGI PIDI FIGYVPPSTRGQYPGI Y I
giloozozor (rol) ti _o roboo. rj		na repolymolado rododine rrido, repartoop	0		0.2201	0210.0	02101101		010.0	W K2//16161K2T1P161L1P11/D111161/16171/12P1P181T1P16102Y1P161L1Y1
	VERALAO	DNA - I - I - I - I A 405 D - 405	0	4 7404	0.0700	0000 50	0000 704		707 7	
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	4.7124	0.3796	3282.59	3282.731	1	121.1	30.172413 L
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.8843	0.3349	2112.65	2113.329	(430	41.6666664 A.SPDQSDLEVGQEVLDRIVL.V
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	4.7714	0.369	2184.57	2184.408	1	816.6	57.894737 Q.ASPDQSDLEVGQEVLDRIVL.V
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.4611	0.2752	1925.69	1926.22	2	489.4	44.11765 K.TPGLPIDLEIGYVPPSTR.G
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	4.9323	0.4082	1946.23	1947.22	1	1023.8	61.764706 K.T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4.G
ail6325267/refINP 015335.11	YPR010C	RNA polymerase I subunit A135: Rpa135p	2	4.3578	0.3124	1684.45	1684.955	1	945.2	63.333332 W.K2V1E1G1K2T1P1G1L1P1I1D1L1E1I1G1.Y
gil6325267/refINP_015335_1	YPR010C	RNA polymerase subunit A135: Rpa135n	2	4 8136	0 4948	2134 39	2135 446	1	1199.3	57 894737 E G1K2T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4 G
gil6325267/refINP_015335_1	VPR010C	RNA polymerase I subunit A135; Rpa135p	3	4 2008	0 2171	2112.86	2111 446	1	1374 5	43 421055 E GKTPGI PIDI EIGY//PPSTR G
silcooport at ND_045005.1	VDD040C	DNA polymerase Louburit A105, Rea105p	5	4.2330	0.2171	2112.00	2111.440		040.0	
gilb325267 [rel]NP_015335.1]	VPR010C	RNA polymerase i subunit A135; Rpa135p	3	4.5809	0.2996	2495.72	2495.868	2	949.9	
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	5.8828	0.5286	2495.69	2495.868	1	1432.4	59.090908 W.K2V1E1G1K211P1G1L1P111D1L1E111G1Y1V1P1P1S111R4.G
gi 6325267 ref NP_015335.1	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.356	0.2559	1732.75	1732.01	1	862.7	64.28571 L.VHLGKDGSQDKFRML.L
		Essential helicase component of heterohexameric MCM2-7 complexes which bind								
		pre-replication complexes on DNA and melt the DNA prior to replication;								
ail6325276/refINP 015344.11	YPR019W	accumulates in the nucleus in G1; homolog of S, pombe Cdc21p; Cdc54p	2	3.8736	0.275	2716.47	2716.017	1	957.5	43.18182 L.TNLYLEDKPEHISQDDVLPVEFL.T
3111 1 1 1		Essential helicase component of heterohexameric MCM2-7 complexes which bind								
		pre-replication complexes on DNA and melt the DNA prior to replication:								
-: 102252701 FIND 045244 41	VDD040W	pre-replication complexes on Drive and mentine Drive prior to replication,	0	2 05 22	0.0047	4044.00	4044.005		007.0	
gilo325276[rei]inP_015344.1]	TPRUI9W	accumulates in the nucleus in GT; nomolog of S. pombe Cdc2Tp; Cdc54p	2	3.9533	0.3647	1611.33	1811.005	1	697.6	11.42637 L.DKVDEKNDRELAKHL.I
		Essential helicase component of heterohexameric MCM2-7 complexes which bind								
		pre-replication complexes on DNA and melt the DNA prior to replication;								
gi 6325276 ref NP_015344.1	YPR019W	accumulates in the nucleus in G1; homolog of S. pombe Cdc21p; Cdc54p	2	4.1338	0.4113	1909.91	1910.042	1	1150.5	66.66667 L.IVDNNLDYDLDEIETK.F
		Essential helicase component of heterohexameric MCM2-7 complexes which bind								
		pre-replication complexes on DNA and melt the DNA prior to replication:								
ail6325276/refINP_015344_1	VPR010W	accumulates in the nucleus in G1: homolog of S, nombe Cdc21n; Cdc54n	2	4 1873	0.4115	2263.97	2263 599	1	531.3	52 63158 S RYNPNI PVTENIDI PPPI I S R
gil0525270[rei]rii _015544.1]	111101344	Essential belicase component of beterobevameric MCM2-7 complexes which bind	2	4.1075	0.4115	2203.37	2203.333		551.5	32.05136 S.KTHEREFTELBLEFTELS.K
		Essential hericase component of heteronexamenc wow2-7 complexes which bind								
		pre-replication complexes on DINA and melt the DINA prior to replication;								
gi 6325276 ref NP_015344.1	YPR019W	accumulates in the nucleus in G1; homolog of S. pombe Cdc21p; Cdc54p	2	3.639	0.283	2289.63	2289.599	2	321.4	42.105263 S.R4Y1N2P1N2L1P1V1T1E1N2I1D1L1P1P1P1L1L1S1.R
		Actin-related protein involved in transcriptional regulation; subunit of the chromatin								
gi 6325291 ref NP_015359.1	YPR034W	remodeling Snf/Swi complex; Arp7p	2	3.6502	0.266	1452.41	1452.748	1	889.6	75 Q.L1K2V1S1P1E1E1L1P1L1V1I1T1.M
		Actin-related protein involved in transcriptional regulation; subunit of the chromatin								
ail6325291/refINP_015359.11	YPR034W	remodeling Snf/Swi complex: Arp7p	2	3.4641	0.16	1440.63	1438.748	1	1061.5	75 Q.LKVSPEELPLVIT.M
3.1		Actin-related protein involved in transcriptional regulation: subunit of the chromatin	-							
ail62252011rofIND_015250_11	VDD024W	remodeling Spf/Sui complex: Arn7n	2	2 1267	0 2477	1969 97	1966 367	1	251.0	
gil03232911eiline_015559.11	16803400	Astin related eastein involved in transmistional annulation, subwit of the abarrantia	2	3.1207	0.3477	1000.07	1000.207	1	331.9	40.025 T.QLKVSFEELFLVIIIWFA.1
		Actin-related protein involved in transcriptional regulation; subunit of the chromatin								
gi 6325291 ref NP_015359.1	YPR034W	remodeling Snf/Swi complex; Arp7p	2	3.1166	0.2223	1952.49	1953.345	1	676.8	50 Q.LKVSPEELPLVITMPATN.G
		Actin-related protein involved in transcriptional regulation; subunit of the chromatin								
gi 6325291 ref NP_015359.1	YPR034W	remodeling Snf/Swi complex; Arp7p	2	3.0062	0.4158	1382.13	1382.643	1	859.6	75 C.NVTPIIDGIVVKN.A
		Actin-related protein involved in transcriptional regulation; subunit of the chromatin								
ail6325291/refINP 015359.11	YPR034W	remodeling Snf/Swi complex: Arp7p	2	4.0475	0.3176	1485.33	1485.73	1	783.7	69.230774 S.GCNVTPIIDGIVVK.N
31		Actin-related protein involved in transcriptional regulation: subunit of the chromatin								
ail6325291 refINP 015359 1	VPR034W	remodeling Snf/Swi complex: Arn7p	2	3 6857	0 2802	1277 55	1275 401	1	1875 5	86 36364 S DKESPEDGI GPL M
gil03232311feiliar_013333.11	11103400	Cubusit I of the sight subusit V/4 assistent membrane demois of the vesseles I i	2	3.0037	0.2002	1211.55	12/ 3.401		10/0.0	0.30304 S.DKI SI EDGESI E.W
		Subunit H of the eight-subunit vil peripheral membrane domain of the vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system; serves as an activator or a structural stabilizer of the V-								
gi 6325293 ref NP_015361.1	YPR036W	ATPase; Vma13p	2	3.8014	0.4101	1721.51	1723.761	1	842.8	69.230774 L.C1W2S1P1P1H3V1D1N2G1F1W2S1D1.N
		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system: serves as an activator or a structural stabilizer of the V-								
-: 102252021 END 045204 41	VDDOOCM	ATDess Vised 2s	0	2 0700	0 4704	2070 70	2004 404	0	400 5	
gilo325293[rei]inP_015361.1]	TPRUSOW	Al Pase, vina isp	2	3.0798	0.1794	2079.79	2081.194	2	422.5	43.75 Q.STETSTETR4K211STDTETETETR4Q2DTT51.N
		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system; serves as an activator or a structural stabilizer of the V-								
gi 6325293 ref NP 015361.1	YPR036W	ATPase; Vma13p	2	3.0988	0.1952	2109.55	2109.219	1	396.8	46.875 L.S1E1R4K2Y1S1D1E1E1L1R4Q2D111S1N2L1.K
		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		ATPase (V-ATPase) an electrogenic proton nump found throughout the								
		and amembrane system: service as an activator or a structural stabilizer of the V								
	VDD000W	ATBase Marchine System; serves as an activator of a structural stabilizer of the v-	0	0 00 40	0.0070	101115	1011 001		704 7	
gi 6325293 ref NP_015361.1	YPR036W	ATPase; Vma13p	2	3.0246	0.2272	1614.45	1611.884	1	/31./	66.66667 L.AVIPEYRDVIWLH.E
		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system; serves as an activator or a structural stabilizer of the V-								
ail6325293/refINP 015361.11	YPR036W	ATPase: Vma13p	2	3.4745	0.3401	1630.79	1630.884	1	937.8	70.83333 L.A1V1I1P1E1Y1R4D1V1I1W2L1H3.E
3.1		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacualar H+-								
		ATPase (V-ATPase) an electrogenic proton nump found throughout the								
		A rase (V-A rase), an electrogenic proton pump round throughout the								
		endomembrane system; serves as an activator or a structural stabilizer of the v-								
gi 6325293 ref NP_015361.1	YPR036W	ATPase; Vma13p	2	3.3554	0.2787	1980.77	1982.29	1	410.7	46.666668 L.QELAVIPEYRDVIWLH.E
		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		endomembrane system: serves as an activator or a structural stabilizer of the V-								
gil6325293/refINP_015361_1	YPR036W	ATPase: Vma130	2	3 0656	0 2423	1853.01	1854 159	1	460.3	
		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacualar H+-	-	2.2000						
		ATPase (V/ATPase) an electrogenic protoc sume found throughout the								
		and emembrane evidence and an endotre state that the state of the Market state of the								
		encomemorane system; serves as an activator or a structural stabilizer of the V-			o					
gi 6325293 ref NP_015361.1	YPR036W	ATPase; Vma13p	2	3.0003	0.1598	1558.57	1558.805	1	494.8	63.636364 A.V1I1P1E1Y1R4D1V1I1W2L1H3.E
		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-								
		ATPase (V-ATPase), an electrogenic proton pump found throughout the								
		· · · ·								
		endomembrane system; serves as an activator or a structural stabilizer of the V-								
gi 6325293 ref NP 015361.1	YPR036W	endomembrane system; serves as an activator or a structural stabilizer of the V- ATPase; Vma13p	2	3.2394	0.2475	2004.59	2005.29	1	373	46.666668 L.Q2E1L1A1V111P1E1Y1R4D1V111W2L1H3.E

		Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H+- ATPase (V-ATPase), an electrogenic proton pump found throughout the								
gi 6325293 ref NP_015361.1	YPR036W	endomembrane system; serves as an activator or a structural stabilizer of the V- ATPase; Vma13p Translation initiation factor eIF-5: N-terminal domain functions as a GTPase-	2	4.1346	0.4329	1872.47	1875.159	1	917.1	67.85714 Q.E1L1A1V111P1E1Y1R4D1V111W2L1H3.E
gi 6325298 ref NP_015366.1	YPR041W	activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p Translation initiation factor eIF-6; N-terminal domain functions as a GTPase-	1	2.2043	0.1745	1046.41	1046.185	8	412.4	68.75 A.K2L1Q2D1V1L1D1G1F1.I
gi 6325298 ref NP_015366.1	YPR041W	radiation indication indicate by A commencement of the second of the second and the second of the se	2	3.7675	0.1968	1774.37	1774.807	6	443.1	61.538464 Q.H3H3D1E1D1E1D1E1L1S1R4Q2I1K2.A
gi 6325298 ref NP_015366.1	YPR041W	Translation introduction factor en-os, re-reinination domain inductions as a Grasse- activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; TiSp Trackative with the UE for the series of CTD as	2	5.35	0.2979	2193.33	2193.238	1	1133.8	58.823532 S.S1T1P1Q2H3H3D1E1D1E1D1E1L1S1R4Q2I1K2.A
gi 6325298 ref NP_015366.1	YPR041W	rearisation initiation factor eir-3, N-termina domain functions as a G rease- activating protein to mediate hydrolysis of ribosome-bound GPr; C-terminal domain is the core of ribosomal preinitiation complex formation; TifSp	1	3.7524	0.1711	1546.72	1546.907	1	317.3	62.5 L.E1H3K2D1L11P1L1L1P1K2I1L1.V
gi 6325298 ref NP_015366.1	YPR041W	Translation initiation factor eIF-5; N-terminal domain functions as a GTPase- activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p	2	3.1902	0.3516	1546.01	1546.907	1	609.7	79.16667 L.E1H3K2D1L111P1L1L1P1K2I1L1.V
qi 6325298 ref NP 015366.1	YPR041W	Translation initiation factor eIF-5; N-terminal domain functions as a GTPase- activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p	1	3.4644	0.2538	1531.78	1529.907	3	253.3	58.333332 L.EHKDLIPLLPKIL.V
gil6325298/refINP_015366.1	YPR041W	Translation initiation factor eIF-5; N-terminal domain functions as a GTPase- activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation: Tifso	2	3,1073	0.3943	1528.01	1529.907	1	749.3	79 16667 I. EHKDI IPI I PKIL V
gil6225209/rofIND_015266_1	VPP041W	Translation initiation factor eIF-5; N-terminal domain functions as a GTPase- activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain to the area of theorem domain densitieting exempler formation: Tiffs	2	2.9554	0.0010	1996 22	1997 114		056.4	
gilo325296[rei]NP_015366.1]	TPR041W	Translation initiation factor eIF-5; N+terminal domain functions as a GTPase- activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain	2	3.8554	0.2842	1000.33	1007.114		956.4	04.2007 I Q.LTNIDIJƏEELIMIKF.G
gi 6325298 ref NP_015366.1	YPR041W	is the core of ribosomal preinitiation complex formation; Tif5p Translation initiation factor eIF-5; N-terminal domain functions as a GTPase- activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain	2	3.8456	0.2655	1761.81	1763.015	1	402.7	50 D.K2D1R4Y1L1V1N2G1V1H3E1P1A1K2L1.Q
gi 6325298 ref NP_015366.1	YPR041W	is the core of ribosomal preinitiation complex formation; Tif5p Translation initiation factor eIF-5; N-terminal domain functions as a GTPase- activation protein to mediate burdness of ribosome-bound GTP. C-terminal domain	1	2.7161	0.2036	1529.96	1529.907	2	223.5	54.166668 L.EHKDLIPLLPKIL.V
gi 6325298 ref NP_015366.1	YPR041W	is the core of ribosomal preinitiation complex formation; Tifsp Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-	1	3.1087	0.174	1548.21	1546.907	1	222	54.166668 L.E1H3K2D1L111P1L1L1P1K2I1L1.V
gi 6325298 ref NP_015366.1	YPR041W	to the core of ribosomal preinitiation complex formation, Tif5p Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-	2	3.027	0.3508	1529.61	1529.907	1	651.1	79.16667 L.EHKDLIPLLPKIL.V
gi 6325298 ref NP_015366.1	YPR041W	activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinititation complex formation; Tif5p Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-	2	3.1073	0.1728	1534.53	1532.64	2	425.3	65 C.R4D1N2H3D1P1F1Y1R4Y1K2.M
gi 6325298 ref NP_015366.1	YPR041W	activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-	2	3.1097	0.2796	1546.29	1546.907	1	403.3	70.83333 L.E1H3K2D1L11P1L1L1P1K2I1L1.V
gi 6325298 ref NP_015366.1	YPR041W	activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p Translation initiation factor eIF-5; N+terminal domain functions as a GTPase-	2	3.7189	0.2166	1630.11	1630.81	1	449.6	65.38461 L.V1T1P1E1Y1E1K2N2F1M1G1G1I1E1.R
gi 6325298 ref NP_015366.1	YPR041W	activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p Translation initiation factor eIE-5: N-terminal domain functions as a GTPase-	2	3.8821	0.1872	1908.01	1907.114	7	309.1	53.571426 Q.L1Y1N2N2D1I1I1S1E1E1E1I1M1R4F1.G
gi 6325298 ref NP_015366.1	YPR041W	activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p Translation initiation factor eIE-5: N-terminal domain functions as a GTPase-	3	4.5232	0.2695	2310.5	2311.605	1	1662.2	46.05263 S.I1S1V1D1K2D1R4Y1L1V1N2G1V1H3E1P1A1K2L1Q2.D
gi 6325298 ref NP_015366.1	YPR041W	activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p Transleting: initiation factor LTE; it: I complex formation; Tif5p	1	2.8667	0.1572	1317.61	1318.588	9	263.7	65 L.E1H3K2D1L111P1L1L1P1K2.I
gi 6325298 ref NP_015366.1	YPR041W	ransiadul midulu radul er-s, refermina dontan rutudus as a Grase activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p	2	2.9911	0.3343	1531.55	1529.907	1	368.5	75 L.EHKDLIPLLPKIL.V
gi 6325298 ref NP_015366.1	YPR041W	Translation initiation factor eit-s; N-terminal domain functions as a G Pase- activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p	1	2.3812	0.1524	1528.85	1529.907	3	266	58.333332 L.EHKDLIPLLPKIL.V
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	3.6389	0.2914	1714.27	1714.918	1	747.7	62.5 A.FQNPLFNDELKYW.L
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	4.3579	0.3306	1994.45	1995.19	1	1316.3	66.66667 K.K2V1K2E1G1I1E1D1F1D1D111Y1E1K2F1.Q
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	3	3.8895	0.2357	1974.95	1976.19	1	814.1	38.333332 K.KVKEGIEDFDDIYEKF.Q
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	3.0087	0.2894	2239.91	2239.524	1	414.1	47.058823 L.L1K2K2V1K2E1G111E1D1F1D1D111Y1E1K2F1.Q
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	2.9087	0.3334	1746.69	1748.883	1	309.9	50 V.KEGIEDFDDIYEKF.Q
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	3	4.8856	0.3129	1865.27	1865.016	1	1378	53.571426 K.V1K2E1G111E1D1F1D1D111Y1E1K2F1.Q
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	4.6786	0.2983	1863.63	1865.016	1	1351.2	71.42857 K.V1K2E1G111E1D1F1D1D111Y1E1K2F1.Q
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	3.3454	0.3872	1978.89	1980.359	1	533.6	50 E.ALTNPDIIKDPKELKKR.D
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	3.2215	0.1858	1856.63	1857.075	1	1044.5	64.28571 N.AAFQNPLFNDELKYW.L

gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	4.2877	0.2283	1731.65	1732.918	1	1067.3	70.83333 A.F1Q2N2P1L1F1N2D1E1L1K2Y1W2.L
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	2	4.7566	0.3676	1976.15	1976.19	1	1479.4	70 K.KVKEGIEDFDDIYEKF.Q
gi 6325329 ref NP_015397.1	YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	3.7654	0.3019	2218.45	2217.524	1	632.8	47.058823 L.LKKVKEGIEDFDDIYEKF.Q
gi 6325331 ref NP_015399.1	YPR074C	in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tki1p Transketolase, similar to Tki2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	4.5608	0.2463	2330.49	2329.587	1	921.4	52.499996 R.K2L1S1E1T1V1L1E1D1V1Y1N2Q2L1P1E1L1I1G1G1S1.A
gi 6325331 ref NP_015399.1	YPR074C	in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	3.9938	0.2913	1933.31	1933.093	2	556.1	52.941177 L.G1S1R4T1P1G1H3P1E1F1E1L1P1G1V1E1V1T1.T
gi 6325331 ref NP_015399.1	YPR074C	in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tk1p Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	3.8971	0.3589	1788.43	1786.963	5	479.4	50 S.R4T1P1G1H3P1E1F1E1L1P1G1V1E1V1T1.T
gi 6325331 ref NP_015399.1	YPR074C	in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	3.6095	0.3389	1765.69	1765.963	1	588.9	56.666668 S.RTPGHPEFELPGVEVT.T
gi 6325331 ref NP_015399.1	YPR074C	in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	4.1971	0.3694	2104.03	2104.238	1	1602.8	57.894737 A.THDSIGVGEDGPTHQPIETL.A
gi 6325331 ref NP_015399.1	YPR074C	in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	3.8764	0.3786	2465.87	2463.709	1	623.7	43.47826 L.GSRTPGHPEFELPGVEVTTGPLGQ.G
gi 6325331 ref NP_015399.1	YPR074C	in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	3.1888	0.3034	2494.39	2493.709	4	197.5	30.434782 L.G1S1R4T1P1G1H3P1E1F1E1L1P1G1V1E1V1T1T1G1P1L1G1Q2.G
gi 6325331 ref NP_015399.1	YPR074C	in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate	2	3.1348	0.2241	2306.35	2307.639	1	188.8	50 Q.M1R4M1N2P1T1N2P1D1W2l1N2R4D1R4F1V1L1.S
gi 6325331 ref NP_015399.1	YPR074C	In the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tki1p	2	3.4968	0.2803	2277.93	2276.639	1	215.4	47.058823 Q.MRMNPTNPDWINRDRFVL.S
gi 6325343 ref NP_015411.1	YPR086W	Iranscription factor TFIB, a general transcription factor required for transcription initiation and start site selection by RNA polymerase II; Sua7p	2	4.7538	0.4546	2044.43	2045.3	1	1106.9	73.333336 L.T1C1P1E1C1K2V1Y1P1P1K2I1V1E1R4F1.S
gi 6325343 ref NP_015411.1 gi 6325349 ref NP_015416.1 gi 6325349 ref NP_015416.1 gi 6325349 ref NP_015416.1	YPR086W YPR091C YPR091C YPR091C	Infrastorption factor Finb, a general transcription factor required for transcription initiation and start site selection by RNA polymerase II; Sua7p hypothetical protein; Ypr091cp hypothetical protein; Ypr091cp	2 2 2 2	4.3835 3.9971 3.3367 3.0139	0.3775 0.2929 0.3425 0.1736	2026.63 1884.91 2013.43 1795.83	2024.3 1883.121 2014.153 1795.042	1 1 1	832 903.9 509 662.3	63.333332 L.TCPECKVYPPKIVERF.S 70 F.RAT1E1P1I1M1D1F1E111E1P1I1V1S1S1.S 56.25 K ELDHDTABEIDEKTRLLA 64.28571 F.R4T1E1P1I1M1D1F1E111E1P1I1V1S1.S
gi 6325349 ref NP_015416.1 gi 6325349 ref NP_015416.1	YPR091C YPR091C	hypothetical protein; Ypr091cp hypothetical protein; Ypr091cp	2	2.9395 3.5665	0.1598 0.3351	2012.37 2262.63	2011.297 2263.555	1 1	805.6 800.2	56.25 A.FRTEPIMDFEIEPIVSS.S 52.77778 T.IWPRFDELGKEELPDASLF.T
gi 6325349 ref NP_015416.1 gi 6325349 ref NP_015416.1	YPR091C YPR091C	hypothetical protein; Ypr091cp	2	3.8449 4.853	0.2277	2286.47 2384.63	2287.555 2385.58	1	704.3 930.2	50 T.I1W2P1R4F1D1E1L1G1K2E1E1L1P1D1A1S1L1F1.T 57 894737 A S1K2K2E1L1D1H3D1T1A1D1E1IJD1E1K2T1R4L1L1 A
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	3	6.8696	0.3553	2386.31	2385.58	1	1849.6	44.736843 A.S1K2K2E1L1D1H3D1T1A1D1E1I1D1E1K2T1R4L1L1.A
gi 6325349 ref NP_015416.1 gi 6325349 ref NP_015416.1	YPR091C YPR091C	hypothetical protein; Ypr091cp hypothetical protein; Ypr091cp	2	5.1014 3.5617	0.4044	2359.61 1575 15	2357.58 1574.858	1	983.8 862.6	57.894737 A.SKKELDHDTADEIDEKTRLL.A 65.38461 N KIKTPGELDDI VVE K
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	2	4.3318	0.2239	1591.33	1590.858	1	994.1	73.07692 N.K2I1K2T1P1G1F1L1D1D1L1V1V1E1.K
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	2	3.4153	0.1973	1490.05	1490.74	2	801.6	66.666667 K.L1N2K2I1K2T1P1G1F1L1D1D1L1.V
gi 6325349 ref NP_015416.1 gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	2	3.7664	0.2612	1917.59	1916.268	1	692.2 1244.2	53.125 L.NKIKTPGFLDDLVVEKV.D 65.625 KT1N2K211K2T1P1G1E1L1D1D1L1V1V1E1K2 V
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	3	5.0256	0.2663	2052.77	2051.428	1	1677.9	45.588234 K.L1N2K2I1K2T1P1G1F1L1D1D1L1V1V1E1K2V1.D
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	2	4.5952	0.3391	2050.11	2051.428	1	708.5	50 K.L1N2K2I1K2T1P1G1F1L1D1D1L1V1V1E1K2V1.D
gi 6325349 ret NP_015416.1 gi 6325349 ref NP_015416.1	YPR091C YPR091C	hypothetical protein; Ypr091cp hypothetical protein; Ypr091cp	2	3.1111	0.216	1866.39	1864.121	1	593.7 1073.5	60.000004 F.RTEPIMDFEIEPIVSS.S 64.28571 L N2K2I1K2T1P1G1E1L1D1D1L1V1V1E1 K
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	2	4.4169	0.2791	1688.97	1688.962	2	670.8	53.571426 L.NKIKTPGFLDDLVVE.K
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	2	3.8523	0.3945	1799.73	1802.121	1	394.3	53.333336 K.LNKIKTPGFLDDLVVE.K
gi 6325349 ref NP_015416.1 gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	2	4.0194	0.2741	1821.57	1821.121	4	552.4 1347 3	53.333336 K.L1N2K2I1K211P1G1F1L1D1D1L1V1V1E1.K 42.647057 K LNKIKTPGELDDL VVEKV D
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	2	3.6774	0.3042	2029.31	2029.428	1	697.3	50 K.LNKIKTPGFLDDLVVEKV.D
gi 6325349 ref NP_015416.1	YPR091C	hypothetical protein; Ypr091cp	3	5.4877	0.3799	2357.09	2357.58	1	1919.3	46.05263 A.SKKELDHDTADEIDEKTRLL.A
gi 6325382 ref NP_015450.1	YPR125W	Mitochondrial inner membrane protein exposed to the mitochondrial matrix, associates with mitochondrial ribosomes, NOT required for respiratory growth; homolog of human Letm1, a protein implicated in Wolf-Hirschhorn syndrome; Ylh47p	2	5.0054	0.3929	1889.27	1890.011	2	738.9	56.25 S. VKDELSLDDQDKNIDAA.A
gi 6325382 ref NP_015450.1	YPR125W	Mitochondrial inner membrane protein exposed to the mitochondrial matrix, associates with mitochondrial ribosomes, NOT required for respiratory growth; homolog of human Letm1, a protein implicated in Wolf-Hirschhorn syndrome; Ylh47p	2	4.7582	0.3262	2477.35	2477.606	1	1010.1	47.368423 L.R4E1Q2E1E111M1K2E1E1E1Q2Q2E1E1N2A1I1V1S1.V
gi 6325382 ref NP_015450.1	YPR125W	Mitochondrial inner membrane protein exposed to the mitochondrial matrix, associates with mitochondrial ribosomes, NOT required for respiratory growth; homolog of human Letm1, a protein implicated in Wolf-Hirschhorn syndrome; Ylh47p	2	4.3061	0.2245	1903.37	1901.133	1	1099.1	76.666664 L.CDVLIGIPDELYHEVK.V
gi 6325382 ref NP_015450.1	YPR125W	Mitochondrial inner membrane protein exposed to the mitochondrial matrix, associates with mitochondrial ribosomes, NOT required for respiratory growth; homolog of human Letm1, a protein implicated in Wolf-Hirschhorn syndrome; Ylh47p	2	3.8132	0.3287	2448.59	2449.606	1	611.2	44.736843 L.REQEEIMKEEEQQEENAIVS.V

		Mitochondrial inner membrane protein exposed to the mitochondrial matrix,								
gi 6325382 ref NP_015450.1	YPR125W	associates with mitochondrial ribosomes, NOT required for respiratory growth; homolog of human Letm1, a protein implicated in Wolf-Hirschhorn syndrome; YIh47p GTP-binding protein of the rho subfamily of Ras-like proteins, involved in	2	3.1491	0.1946	1603.61	1602.914	1	454.6	61.538464 A.SKVSPVKEKEKVPF.K
gi 6325423 ref NP_015491.1	YPR165W	establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1.3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p GTP-binding protein of the rho subfamily of Ras-like proteins, involved in ent-bibliobarget of cell orientive conditionar certains binser C (Digta) over the cell well.	1	2.3708	0.166	1351.63	1352.53	1	234.9	45.454548 F.SKGQFPEVYVPT.V
gi 6325423 ref NP_015491.1	YPR165W	establishment of cell polarity, regulates protein knase C (PKC) plant the cell wail synthesizing enzyme 1,3-beta-glucan synthase (FKst pland Gsc29); Rho1p GTP-binding protein of the rho subfamily of Ras-like proteins, involved in the binding content of the rho subfamily of Ras-like proteins, involved in	2	3.2236	0.3196	1352.47	1352.53	1	568.8	72.72727 F.SKGQFPEVYVPT.V
gi 6325423 ref NP_015491.1	YPR165W	establishment of cell polarity, regulates protein narase (Rest p and Sc2p); Rhotp synthesizing enzyme 1,3-beta-glucan synthase (Fkst p and Gsc2p); Rhotp GTP-binding protein of the rho subfamily of Ras-like proteins, involved in setablishment of cell polarity; canultee protein kines (2, (Rest p), and the cell wall	2	3.9749	0.1576	1688.87	1690.875	1	1123.6	69.230774 C.K2V1D1L1R4N2D1P1Q2T1I1E1Q2L1.R
gi 6325423 ref NP_015491.1	YPR165W	establishment of cell polarity, regulates protein narase C (Pacto I) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fkstp and Gsc2p); Rhotp GTP-binding protein of the rho subfamily of Ras-like proteins, involved in setablishment of cell polarity; regulates protein kinase C (Pacto) and the cell wall	1	2.4295	0.2084	1365.5	1366.53	1	338.9	59.090908 F.S1K2G1Q2F1P1E1V1Y1V1P1T1.V
gi 6325423 ref NP_015491.1	YPR165W	establishment of earl polarity, regulates protein names e (Rest p and Sc2p); Rhotp synthesizing or care polarity, resultance synthase (Fkst p and Gsc2p); Rhotp GTP-binding protein of the rho subfamily of Ras-like proteins, involved in setablishment of cell polarity, regulates protein place (C (Rest p)) and the cell wall	2	3.0304	0.2546	1354.51	1352.53	1	432.2	63.636364 F.SKGQFPEVYVPT.V
gi 6325423 ref NP_015491.1	YPR165W	establishment of cell polarity, regulates protein market or (Rs1p and the Cen wai synthesizing on centre and the synthese (Fks1p and Gs2p); Rho1p GTP-binding protein of the rho subfamily of Ras-like proteins, involved in setablishment of cell polarity, regulates protein kinese C (Psrc1) and the cell wall	2	3.8823	0.2722	1920.51	1921.114	1	870.5	63.333332 C.FSIDLPDSLENVQEKW.I
gi 6325423 ref NP_015491.1	YPR165W	contabilities on portuging galaxies procession influebo of (No try) and Scz(2), Rho tp synthesizing enzyme 1,3beta-gilucan synthase (Fks tp and Gsc2)), Rho tp GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPU vesicle const involved in FR to Gold intersport and autombary:	2	3.5122	0.2404	2105.79	2105.352	3	336.2	47.058823 C.FSIDLPDSLENVQEKWIA.E
gi 6325439 ref NP_015507.1	YPR181C	of the Gorth sets the GDP-board for of Sartip: Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPU vesicle conti involved in ER to Gold intersport and automany:	2	3.2678	0.2141	2384.69	2385.642	1	381.3	39.473686 L.YTPLKEYDELNVAPYNPVVC.S
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sartp; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPU vesicle cont involved in ER to Gold intersport and automany:	2	3.1117	0.2913	1406.47	1406.71	2	525.2	68.181816 T.NKPVTVPPIFFF.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sartp; Sec29 GTPase-activating protein; component of the Sec29-Sec24p heterodimeric complex of the COPU vesicle coat: involved in ER to Gold intensport and autophary:	2	3.7009	0.2919	1421.71	1420.711	3	510	68.181816 T.N2K2P1V1T1V1P1P111F1F1F1.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sartp; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPI vesicle coat: involved in ER to Gold intensort and autophagy:	1	2.8298	0.3435	1405.66	1406.71	3	328.3	59.090908 T.NKPVTVPIFFF.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPI vesicle coat: involved in ER to Gold intensort and autophaov:	1	2.7475	0.2213	1419.61	1420.71	3	278.4	54.545456 T.N2K2P1V1T1V1P1P1I1F1F1F1.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPI vesicle coat, involved in ER to Golgi transport and autophagy;	2	3.2703	0.1978	1303.91	1304.607	1	888.3	80 N.K2P1V1T1V1P1P111F1F1F1.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPI vesicle coat, involved in ER to Golgi transport and autophagy;	2	3.1632	0.3046	1291.75	1292.607	1	801.5	75 N.KPVTVPPIFFF.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPI vesicle coat, involved in ER to Golgi transport and autophagy;	1	2.724	0.285	1303.55	1304.607	2	297.7	60.000004 N.K2P1V1T1V1P1P111F1F1F1.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	1	2.6047	0.2396	1293.61	1292.607	2	370.5	65 N.KPVTVPPIFFF.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	2	3.7505	0.3974	1518.93	1520.843	3	459.8	62.5 T.N2K2P1V1T1V1P1P1I1F1F1F1F1V1.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	2	3.0025	0.2844	1402.49	1404.739	2	984.7	77.27273 N.K2P1V1T1V1P1P1I1F1F1F1V1.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	2	3.1407	0.1802	2118.29	2119.449	1	467.6	37.5 F.S1L1N2R4F1F1L1P1L1E1Q2V1E1F1K2L1N2.Q
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	2	2.9997	0.2071	1389.77	1391.739	2	929.8	72.72727 N.KPVTVPPIFFFV.V
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	2	3.5302	0.3213	1436.23	1435.689	1	509.3	63.636364 Q.G1C1Y1K2N2I1P1A1R4I1I1L1.F
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	2	3.0038	0.1547	1783.89	1784.151	1	396.3	57.14286 E.YITNKPVTVPPIFFF.V
gi 6325439 ret NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	3	3.8359	0.4009	2359.85	2361.66	1	1008.5	42.5 A.ELLVDRFPLPRFIDI EAGGSQ.A
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of SarTp; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	3	4.3652	0.3715	2388.89	2389.66	1	870.8	41.25 A.E1L11V1D1R4F1P1L1P1R4F1I1D111E1A1G1G1S1Q2.A
gij6325439 ret NP_015507.1	YPR181C	Stimulates the GDP-polund form of SarTp; SeC24p GTPase-activating protein; component of the SeC23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	1	2.5551	0.3646	1405.64	1406.71	1	416.8	
gij6325439 ret NP_015507.1	VPD484C	stimulates the GDP-pound form of Sartp; Sec24p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;	1	2.661	0.2307	1292.88	1292.607	2	429.1	
gil6325439/refIND_015507_1	VPR1910	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; etimulates the GDP-hound form of Sarth: Sec23p.	1 2	2.0914	0.2170	1305.40	1304.007	4	304.7 801 1	80 N K221/4T1/4D1011F4E4E4 V
gil6325439/refINP_015507.1	VPR181C	of Trass-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; etimulates the GDP-hound form of Sarth: Sec23n	2	3 3702	0.3702	1363.85	1364 674	2	718.8	75 C V1K2N2I1P101R41111 1F1 0
9.1112 0 100 0 0 100 0 1 1			-	0.0700	0.2100			-		. S GIT INERENT IN THIS INTELLE IN THE

		GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex								
gi 6325439 ref NP_015507.1	YPR181C	of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.7589	0.2448	1347.63	1348.674	2	374.3	60.000004 C.YKNIPARIILF.A
		GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex								
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p	2	3.5126	0.3245	1421.67	1420.711	4	546.7	68.181816 T.N2K2P1V1T1V1P1P1I1F1F1F1.V
		GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex								
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p	2	3.0058	0.2271	2127.53	2127.531	1	296.7	47.058823 T.TIEYITNKPVTVPPIFFF.V
		GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy:								
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p	1	2.571	0.2774	1405.63	1406.71	3	344.9	59.090908 T.NKPVTVPPIFFF.V
		GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;								
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p	1	2.5598	0.2019	1422.38	1420.711	5	223.7	50 T.N2K2P1V1T1V1P1P1I1F1F1F1.V
		of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;								
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p	2	3.0665	0.2561	1406.51	1406.71	1	717.1	77.27273 T.NKPVTVPPIFFF.V
		of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;								
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein: component of the Sec23p-Sec24p beterodimeric complex	1	2.6364	0.327	1303.46	1304.607	9	261.2	55 N.K2P1V1T1V1P1P1I1F1F1F1.V
		of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;								
gi 6325439 ref NP_015507.1	YPR181C	stimulates the GDP-bound form of Sar1p; Sec23p GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex	2	3.3535	0.3599	1303.55	1304.607	1	1038.9	85 N.K2P1V1T1V1P1P1I1F1F1F1.V
	VERANO	of the COPII vesicle coat, involved in ER to Golgi transport and autophagy;		0.0000	0.0004	4504.04	1505 040	0	100.0	
gi 6325439 ret NP_015507.1	IPR181C	Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes	2	3.3226	0.3884	1504.91	1505.843	2	433.3	58.333332 1.NKPV1VPPIFFFV.V
		the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p	1	2.9464	0.2517	1446.47	1447.588	1	452.8	62.5 M.DADLQHPPETVPK.L
		Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl								
		phosphatidylinositol membrane anchoring, O mannosylation, and protein								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes	1	3.3175	0.2616	1463.53	1464.588	1	576.7	66.66667 M.D1A1D1L1Q2H3P1P1E1T1V1P1K2.L
		the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p	2	3.3079	0.2827	1861.63	1859.116	1	686.9	60.000004 C.M1D1A1D1L1Q2H3P1P1E1T1V1P1K2L1F1.E
		Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes								
		phosphatidylinositol membrane anchoring, O mannosylation, and protein								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p Dolichol phosphate manages (Dol.P.Map) synthese of the EP membrane, catalyzes	2	3.7178	0.4017	1762.71	1764.009	1	1335.9	66.66667 L.GTRYAPGVGIDKDWPM.Y
		the formation of DoI-P-Man from DoI-P and GDP-Man; required for glycosyl								
ail6325441/refINP_015509.1	YPR183W	phosphatidylinositol membrane anchoring, O mannosylation, and protein alvcosylation: Dpm1p	1	2.8247	0.2687	1421.53	1422.668	1	578.2	68.181816 D.I.102H3P1P1E1T1V1P1K2L1E1.E
3.1		Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes								
		the formation of DoI-P-Man from DoI-P and GDP-Man; required for glycosyl phosphatidylinositol membrane anchoring, O mannosylation, and protein								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p Deliabel absorbets menances (Del B Man) synthese of the EB membrane, estelyzes	2	4.8872	0.3317	1904.31	1904.034	1	891.9	75 Q.K2K2Y1L1E1N2C1N2P1R4D1I1N2S1Q2.G
		the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl								
gil6325441/refINP_015509_11	YPR183W	phosphatidylinositol membrane anchoring, O mannosylation, and protein alvcosylation: Dpm1p	2	3 2155	0 1897	1579.05	1578 78	3	576	57 692307 C MDADI OHPPETVPK I
giloo2044 (itelii 4 _010000.1)	111(1001)	Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes	2	0.2100	0.1007	101 0.00	10/0./0	5	5/0	
		the formation of DoI-P-Man from DoI-P and GDP-Man; required for glycosyl phosphatidylinositol membrane anchoring. O mannosylation, and protein								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p	3	4.1309	0.2317	1728.08	1726.924	2	914.3	48.214287 M.D1A1D1L1Q2H3P1P1E1T1V1P1K2L1F1.E
		Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl								
ail6325441/rofIND_015500_1	VDD193\//	phosphatidylinositol membrane anchoring, O mannosylation, and protein	2	2 01/0	0 3363	1939 35	1930 116	1	407.2	
gilo32344 (reijini _013303.1)	1110300	Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes	2	2.3143	0.5505	1030.33	1055.110		437.2	30 C.MDADEQITITET TITLE .E
		the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p	2	4.2199	0.2972	1783.51	1785.009	1	726.4	53.333336 L.G1T1R4Y1A1P1G1V1G1I1D1K2D1W2P1M1.Y
		Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes the formation of Dol-P-Man from Dol-P and GDP-Man: required for glycosyl								
		phosphatidylinositol membrane anchoring, O mannosylation, and protein		0.0000	0.0101	1070 10	1000.001			
gilo32544 [[rei]NP_015509.1]	TPRIBBW	Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes	2	3.8036	0.2101	1879.43	1660.034		415.1	57.14286 Q.KKTLENCNPRDINSQ.G
		the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p	1	2.6572	0.3355	1405.55	1406.668	1	545.6	63.636364 D.LQHPPETVPKLF.E
		Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes the formation of Dol-P-Man from Dol-P and GDP-Man: required for glycosyl								
		phosphatidylinositol membrane anchoring, O mannosylation, and protein								
gijo325441 ret NP_015509.1	1PK183W	giycosylation; Upm1p Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes	3	4.4448	0.238	2108.66	2109.372	1	/60./	38.239294 L.GTTTR4YTATPTGTV1G111D1K2D1W2P1M1Y1R4.R
		the formation of DoI-P-Man from DoI-P and GDP-Man; required for glycosyl								
gi 6325441 ref NP_015509.1	YPR183W	glycosylation; Dpm1p	2	4.4478	0.3821	2107.39	2109.372	2	467.9	52.941177 L.G1T1R4Y1A1P1G1V1G1I1D1K2D1W2P1M1Y1R4.R
		Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes the formation of Dol-P-Man from Dol-P and GDP-Man; required for alycosyl								
		phosphatidylinositol membrane anchoring, O mannosylation, and protein	_	1.05.11	0.4000	0000	0000		o	
gilb325441 ret NP_015509.1	YPR183W	giycosylation; Upm1p	2	4.6841	0.4881	2082.55	2083.372	1	619.5	58.823532 L.GTRYAPGVGIDKDWPMYR.R