Supplemental Table I: Zybailov et al.

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.

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LocusID	Y Name	Description	Z	XCorr	DeltCN	M+H+	CalcM+H+	SpR	SpScore	IonProportion	Sequence
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	3.9915	0.3211	1991.35	1991.102	4	445.9	50	L.V1T1D1Y1F1N2G1K2E1P1N2R4S1I1N2P1D1.E
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	3.3497	0.3254	2671.49	2671.882	1	338.3	33.333336	N.D1A1V1V1T1V1P1A1Y1F1N2D1S1Q2R4Q2A1T1K2D1A1G1T1I1A1.G
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	1	2.2812	0.1939	1159.47	1160.188	1	232.8	61.11111	T.HLGGEDFDNR.L
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	1	2.4155	0.1761	1175.36	1176.188	1	270.5	66.66667	T.H3L1G1G1E1D1F1D1N2R4.L
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	1	3.2904	0.2992	1533.7	1531.795	1	484.2	53.571426	T.GIPPAPRGVPQIEVT.F
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	4.5176	0.354	1937.45	1938.101	1	1077.3	66.66667	E.AEKFKEEDEKESQRIA.S
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	1	3.2817	0.3412	1353.69	1354.59	1	714.8	72.72727	F.KLIDVDGKPQIQ.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	2	4.413	0.3052	1354.01	1354.59	1	1864.4	86.36364	F.KLIDVDGKPQIQ.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	3.6138	0.2801	1370.51	1370.59	1	807.7	72.72727	F.K2L1I1D1V1D1G1K2P1Q2I1Q2.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	2	3.7753	0.3391	1403.79	1404.522	1	435.4	68.181816	A.H3F1A1N2D1R4V1D1I1I1A1N2.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	3.2621	0.152	1461.33	1460.686	8	321.8	68.181816	L.D1K2K2G1K2E1E1H3V1L1I1F1.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	1	2.9359	0.2362	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	3.3168	0.3578	1443.01	1443.686	8	230.9	63.636364	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	3.1942	0.3995	1631.77	1632.897	1	283.5	57.692307	Y.G1L1D1K2K2G1K2E1E1H3V1L1I1F1.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	3.2304	0.2693	1606.29	1605.618	1	521.8	57.14286	A.TAGDTHLGGEDFDNR.L
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	3.499	0.2675	2028.13	2029.092	1	523	47.22222	K.A1T1A1G1D1T1H3L1G1G1E1D1F1D1N2R4L1V1N2.H
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	3.2338	0.2465	2003.43	2003.092	1	407.8	44.444447	K.ATAGDTHLGGEDFDNRLVN.H
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	3.1664	0.2432	1352.11	1354.59	1	699.3	77.27273	F.KLIDVDGKPQIQ.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	2	3.6415	0.269	2532.11	2529.684	1	436	40.476192	L.V1T1D1Y1F1N2G1K2E1P1N2R4S1I1N2P1D1E1A1V1A1Y1.G
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	3.5399	0.163	2019.61	2020.305	3	606.9	46.875	E.EFDDKLKELQDIANPIM.S
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	3.5598	0.1511	2041.83	2041.305	5	683.5	50	E.E1F1D1D1K2L1K2E1L1Q2D1I1A1N2P1I1M1.S

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	4.4116	0.1919	1372.31	1370.59	1	1475	81.818184	F.K2L1I1D1V1D1G1K2P1Q2I1Q2.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	3.3319	0.341	1353.73	1354.59	1	805.8	72.72727	F.KLIDVDGKPQIQ.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	2	3.5609	0.2739	2500.89	2500.684	1	597.6	40.476192	L.VTDYFNGKEPNRSINPDEAVAY.G
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	3.1143	0.3749	2020.49	2022.181	1	374.7	41.17647	Y.FNGKEPNRSINPDEAVAY.G
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	3.8942	0.3645	2212.49	2211.357	4	290.7	38.88889	D.Y1F1N2G1K2E1P1N2R4S1I1N2P1D1E1A1V1A1Y1.G
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	3.9763	0.4749	1622.85	1623.725	1	456.5	65.38461	T.HLGGEDFDNRLVNH.F
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	1	3.1629	0.2045	1461.71	1460.686	1	451.3	63.636364	L.D1K2K2G1K2E1E1H3V1L1I1F1.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	1	2.9325	0.2937	1442.68	1443.686	1	507.8	63.636364	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	3.1015	0.2784	1882.57	1883.2	1	564.1	50	K.HFPFKLIDVDGKPQIQ.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	2.4512	0.1775	1247.54	1248.381	2	131.9	60.000004	H.FANDRVDIIAN.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	3.221	0.1753	1371.39	1370.59	1	702	72.72727	F.K2L1I1D1V1D1G1K2P1Q2I1Q2.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	1	3.6795	0.3253	1370.57	1370.59	1	842.4	72.72727	F.K2L1I1D1V1D1G1K2P1Q2I1Q2.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 chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	2	4.4942	0.3686	2326.43	2327.446	1	482.3	42.105263	T.D1Y1F1N2G1K2E1P1N2R4S1I1N2P1D1E1A1V1A1Y1.G
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	4.1382	0.3494	2298.75	2300.446	2	481.6	39.473686	T.DYFNGKEPNRSINPDEAVAY.G
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	3.1681	0.1549	1396.27	1397.481	3	351.7	70	E.KFKEEDEKESQ.R
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	5.026	0.2624	1756.47	1758.907	1	1455.9	76.92308	E.K2F1K2E1E1D1E1K2E1S1Q2R4I1A1.S
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	4.8959	0.3685	1737.35	1737.907	1	1472.4	76.92308	E.KFKEEDEKESQRIA.S
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	1	3.2424	0.3812	1549.7	1550.795	2	302.9	46.42857	T.G1I1P1P1A1P1R4G1V1P1Q2I1E1V1T1.F
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	1	2.4917	0.1594	1598.68	1599.828	1	489.4	57.692307	F.RSTLDPVEKVLRDA.K
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	2.9663	0.1828	1600.39	1599.828	1	589.2	61.538464	F.RSTLDPVEKVLRDA.K
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	3.0745	0.3087	1444.73	1443.686	1	297.1	68.181816	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	1	2.8026	0.3393	1442.64	1443.686	1	438	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	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	2	4.2975	0.3776	1873.37	1871.996	1	713.9	63.333332 T.LEKEKTLTDEHEADVN.N
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	2	3.0344	0.2332	1783.21	1780.985	3	198.9	50 N.N2A1V1E1E1I1D1R4N2L1N2K2I1T1K2.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.G1D1N2V1V1G1D1N2K2D1N2W2V1I1E1I1M1.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.Y1I1P1P1S1H3V1L1P1E1E1T1I1D1L1D1A1D1D1D1N2I1E1N2D1V1H3E1N2L1.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	28.225807	Y.Y1I1P1P1S1H3V1L1P1E1E1T1I1D1L1D1A1D1D1D1N2I1E1N2D1V1H3E1N2L1F1M1.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.Y1I1P1P1S1H3V1L1P1E1E1T1I1D1L1D1.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 18S rRNA; Drs2p	2	2.9958	0.1529	1259.39	1258.372	4	702	60.000004	A.E1K2L1D1E1A1A1N2L1I1E1.K
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	3.8897	0.3524	2606.59	2607.836	1	756.8	45.454548	N.SFENDDDHPTLPVLRNPPILEST.D
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	4.244	0.4104	2637.55	2637.836	1	820.7	45.454548	N.S1F1E1N2D1D1D1H3P1T1L1P1V1L1R4N2P1P1I1L1E1S1T1.D
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	3.0431	0.1574	1957.73	1955.215	1	483.9	53.333336	Y.LNDLENETLKVFDKIY.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	3.3544	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-tRNAiMet 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.HENEDQNQGEEEEEGEEEEEEEEERAHVH.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	4.818	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-tRNAiMet 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-tRNAiMet 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.V1I1E1E1K2K2D1G1K2P1I1L1K2.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.NEDQNQGEEEEEGEEEEEEEEERAHVH.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.N2E1D1Q2N2Q2G1E1E1E1E1E1G1E1E1E1E1E1E1E1E1E1R4A1H3V1H3.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.K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L1I1D1D1W2E1N2L1.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.H3E1N2E1D1Q2N2Q2G1E1E1E1E1E1G1E1E1E1E1E1E1E1E1E1R4A1H3V1H3.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.ASHENEDQNQGEEEEEGEEEEEEEEERAHVH.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.SKKDSEVVPDDELKESEDVLIDDWENL.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	5.8958	0.2754	3266.15	3263.447	1	1418.7	31.48148	S.DSKKDSEVVPDDELKESEDVLIDDWENL.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	6.4723	0.4089	3481.85	3482.685	1	2030.7	35.344826	S.D1S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L1I1D1D1W2E1N2L1A1L1.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.S1A1S1P1N2K2K2D1L1R4S1P1I1C1.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	32.5	T.A1S1H3E1N2E1D1Q2N2Q2G1E1E1E1E1E1G1E1E1E1E1E1E1E1E1E1R4A1H3V1H3.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	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.D1S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L1I1D1.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-tRNAiMet 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.D1S1K2K2D1S1E1V1V1P1D1D1E1L1K2E1S1E1D1V1L1I1D1D1W2E1N2L1.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	5.6161	0.2529	2347.65	2347.416	1	199.4	58.823532	L.E1R4E1E1E1E1R4L1E1K2E1E1E1E1R4L1A1N2.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	3.6759	0.2699	1762.37	1762.944	1	486.8	64.28571	A.V1R4L1E1D1P1S1G1Q2Q2P1I1W2G1R4.H
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	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-tRNAiMet 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-tRNAiMet 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-tRNAiMet 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.S1I1G1L1G1P1V1Y1K2R4.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	4.1127	0.3007	1905.61	1905.282	1	700.8	66.66667	Q.E1K2K2V1I1E1E1K2K2D1G1K2P1I1L1K2.S
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	2.9592	0.2231	1184.44	1184.335	1	358.7	65	T.IGPKTNNPETL.V
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	2.6177	0.2194	1508.61	1509.743	1	559.3	53.571426	H.KGVNLPGTDVDLPAL.S
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.8673	0.3985	1797.47	1796.854	1	862.3	67.85714	F.E1K2E1P1V1S1D1W2T1D1D1V1E1A1R4.I
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	4.0387	0.375	1495.64	1496.717	1	490.1	65.38461	A.R4G1D1L1G1I1E1I1P1A1P1E1V1L1.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	3.618	0.212	1481.79	1479.717	2	582.3	69.230774	A.RGDLGIEIPAPEVL.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.0839	0.2968	2007.37	2008.173	1	369.2	46.666668	A.Y1L1P1N2Y1D1D1M1R4N2C1T1P1K2P1T1.S
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.8629	0.3544	2251.73	2250.427	1	628	52.77778	F.VFEKEPVSDWTDDVEARIN.F
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.2248	0.1971	2273.65	2275.427	3	340.8	44.444447	F.V1F1E1K2E1P1V1S1D1W2T1D1D1V1E1A1R4I1N2.F
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.7569	0.4649	2659.15	2659.927	1	820.3	50	K.G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.2204	0.2792	1827.67	1829.103	1	890.6	63.333332	N.N2F1D1E1I1L1K2V1T1D1G1V1M1V1A1R4.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.3537	0.4645	1549.11	1548.736	1	924.1	79.16667	L.PALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	5.1414	0.5418	2755.91	2758.101	1	1167.3	54.166668	H.KGVNLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	5.2992	0.4832	2787.67	2790.101	1	1138.1	54.166668	H.K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.2782	0.3084	2816.09	2815.153	2	501.1	36	H.KGVNLPGTDVDLPALSEKDKEDLRFG.V
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	4.608	0.288	2815.91	2815.153	1	804.1	31	H.KGVNLPGTDVDLPALSEKDKEDLRFG.V

gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.7632	0.3623	1464.37	1464.662	2	689	77.27273 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.9192	0.3104	2709.31	2709.956	1	714.8	50 C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1.R
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.157	0.4292	2354.73	2355.701	1	340.8	42.5 S.V1I1D1N2A1R4K2S1E1E1L1Y1P1G1R4P1L1A1I1A1L1.D
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	2.9249	0.2972	2079.21	2078.33	6	251.9	34.210526 C.SHKGVNLPGTDVDLPALSEK.D
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	3.2777	0.1917	1463.65	1464.662	2	263	63.636364 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.5442	0.37	1447.25	1445.662	1	652.8	72.72727 A.RKSEELYPGRPL.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.7149	0.2868	3038.81	3039.372	1	758.7	38.88889 C.SHKGVNLPGTDVDLPALSEKDKEDLRFG.V
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.6499	0.3731	3017.73	3018.32	1	853.9	46.153847 C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.267	0.4026	2980.83	2982.32	1	1023.4	50 C.SHKGVNLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	2.9832	0.2955	1526.6	1526.743	2	487	53.571426 H.K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1.S
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	5.6553	0.4536	2044.37	2045.163	1	1564.5	81.25 F.V1F1E1K2E1P1V1S1D1W2T1D1D1V1E1A1R4.I
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.5315	0.2602	2003.71	2004.117	1	434.2	59.375 F.EKEPVSDWTDDVEARIN.F
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	5.2682	0.2622	2024.18	2023.163	1	2560	53.125 F.VFEKEPVSDWTDDVEAR.I
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	5.2134	0.3127	2044.67	2045.163	1	1647.1	45.3125 F.V1F1E1K2E1P1V1S1D1W2T1D1D1V1E1A1R4.I
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.2459	0.2799	1984.77	1986.173	1	426.2	53.333336 A.YLPNYDDMRNCTPKPT.S
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.957	0.3395	2473.11	2473.742	1	900.5	47.61905 V.NLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.4578	0.45	2628.75	2629.927	1	885.9	50 K.GVNLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.3585	0.3703	1413.57	1412.614	1	774.6	72.72727 G.R4I1I1Y1V1D1D1G1V1L1S1F1.Q
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	6.7234	0.45	2787.14	2790.101	1	1132.9	40.625 H.K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	3.9263	0.3402	2757.2	2758.101	1	632.4	30.208334 H.KGVNLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.1795	0.2855	1820.73	1821.04	1	387.7	47.058823 C.SHKGVNLPGTDVDLPALS.E
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	5.26	0.3201	2680.76	2678.956	1	1448.3	34.375 C.SHKGVNLPGTDVDLPALSEKDKEDL.R
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	2.9265	0.2214	1666.53	1666.884	1	408.1	46.666668 S.H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1.S
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.6133	0.3004	1463.71	1464.662	2	685.3	72.72727 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	3.0193	0.1526	1464.73	1464.662	1	220.1	59.090908 A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.6166	0.3832	1445.49	1445.662	1	953.5	77.27273 A.RKSEELYPGRPL.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	3.0563	0.311	1444.73	1445.662	1	272.2	63.636364 A.RKSEELYPGRPL.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	5.0551	0.3342	2981.24	2982.32	1	1166.8	35.576923 C.SHKGVNLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	5.3145	0.325	3018.11	3018.32	1	1104.9	33.653847 C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	2.918	0.192	1236.63	1238.42	3	570.5	72.22222 F.S1H3L1Y1R4G1V1F1P1F1.V

gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	2.9137	0.1839	1323.48	1323.529	1	702.6	62.5	R.GDLGIEIPAPEVL.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.4481	0.2392	1237.19	1236.367	1	1400	88.88889	F.VFEKEPVSDW.T
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.5071	0.3813	1682.47	1682.781	1	999.9	61.538464	F.V1F1E1K2E1P1V1S1D1W2T1D1D1V1.E
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.9518	0.2489	1668.35	1666.781	1	1162.2	69.230774	F.VFEKEPVSDWTDDV.E
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	2.8892	0.3036	1197.42	1198.335	1	347.3	60.000004	T.I1G1P1K2T1N2N2P1E1T1L1.V
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	2.4417	0.2253	1281.41	1282.381	2	376.9	61.11111	L.S1E1K2D1K2E1D1L1R4F1.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	2.3456	0.2861	1266.55	1267.381	1	403.3	61.11111	L.SEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.3426	0.2944	1776.33	1776.854	1	534.4	57.14286	F.EKEPVSDWTDDVEAR.I
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	5.0172	0.47	2022.01	2023.163	1	1672.9	84.375	F.VFEKEPVSDWTDDVEAR.I
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.8297	0.2773	2500.57	2501.742	1	1216.7	54.761906	V.N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.2227	0.3923	1970.63	1973.156	1	1012.7	52.77778	C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1.K
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.1884	0.4936	1948.49	1950.156	1	839.7	52.77778	C.SHKGVNLPGTDVDLPALSE.K
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	5.3844	0.4036	2759.84	2758.101	1	853	35.416664	H.KGVNLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert 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
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	6.0313	0.377	2710.19	2709.956	1	1419.1	35.416664	C.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1.R
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	2.9447	0.2839	1732.41	1733.962	2	646.2	53.125	S.HKGVNLPGTDVDLPALS.E
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.2081	0.3378	1733.41	1733.962	1	1077.6	65.625	C.SHKGVNLPGTDVDLPAL.S
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.0162	0.2311	1646.13	1646.884	1	621.7	56.666668	S.HKGVNLPGTDVDLPAL.S
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	3.7436	0.3511	1463.63	1464.662	1	1178.4	86.36364	A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	2.6179	0.2387	1273.48	1274.515	2	304.5	66.66667	S.KYRPNCPIIL.V
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	3.1672	0.169	1463.61	1464.662	1	297.8	68.181816	A.R4K2S1E1E1L1Y1P1G1R4P1L1.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	1	3.0602	0.2939	1445.7	1445.662	1	252.4	63.636364	A.RKSEELYPGRPL.A
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	3	5.1481	0.3258	2982.41	2982.32	1	1383.9	35.576923	C.SHKGVNLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	2.9605	0.3262	1225.75	1223.42	1	612.4	72.22222	F.SHLYRGVFPF.V
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	2	4.0306	0.3728	2983.07	2982.32	1	635.7	42.307693	C.SHKGVNLPGTDVDLPALSEKDKEDLRF.G
gi|6319279|ref|NP_009362.1|	YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert 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.S1H3K2G1V1N2L1P1G1T1D1V1D1L1P1A1L1S1E1K2D1K2E1D1L1R4F1.G
gi|6319278|ref|NP_009361.1|	YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role in microphthalmia with linear skin defects (MLS); Cyc3p	2	3.9557	0.304	2109.91	2109.256	1	344.4	50	S.SIPKSPDSNEFWEYPSPQ.Q
gi|6319278|ref|NP_009361.1|	YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role in microphthalmia with linear skin defects (MLS); Cyc3p	2	3.1512	0.1617	2368.47	2368.579	1	333.5	39.473686	S.SIPKSPDSNEFWEYPSPQQM.Y
gi|6319278|ref|NP_009361.1|	YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role in microphthalmia with linear skin defects (MLS); Cyc3p	1	2.6729	0.2581	1557.67	1558.762	1	189.6	54.545456	Q.E1L1P1F1D1R4H3D1W2I1V1L1.R
gi|6319278|ref|NP_009361.1|	YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role in microphthalmia with linear skin defects (MLS); Cyc3p	1	2.6512	0.2776	1540.69	1540.762	1	188.6	54.545456	Q.ELPFDRHDWIVL.R

gi|6319278|ref|NP_009361.1|	YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-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
gi|6319278|ref|NP_009361.1|	YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role 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
gi|6319278|ref|NP_009361.1|	YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role 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
gi|6319278|ref|NP_009361.1|	YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role 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
gi|6319258|ref|NP_009341.1|	YAL060W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during 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
gi|6319258|ref|NP_009341.1|	YAL060W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth; Bdh1p	2	4.7226	0.3627	1695.05	1692.94	1	1901.4	76.92308	S.D1L1H3E1Y1L1D1G1P1I1F1M1P1K2.D
gi|6319258|ref|NP_009341.1|	YAL060W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during 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
gi|6319258|ref|NP_009341.1|	YAL060W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth; Bdh1p	2	3.4174	0.2507	1945.43	1945.12	5	502.1	50	T.G1K2Q2R4I1E1D1G1W2E1K2G1F1Q2E1L1.M
gi|6319258|ref|NP_009341.1|	YAL060W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during 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
gi|6319258|ref|NP_009341.1|	YAL060W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth; Bdh1p	2	3.0049	0.2009	2691.07	2688.939	3	403.4	36.363636	C.G1S1D1L1H3E1Y1L1D1G1P1I1F1M1P1K2D1G1E1C1H3K2L1.S
gi|6319258|ref|NP_009341.1|	YAL060W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during 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
gi|6319319|ref|NP_009402.1|	YAR002C-A	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 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
gi|6319319|ref|NP_009402.1|	YAR002C-A	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 transport and localized to COPII-coated vesicles; Erp1p	2	4.9266	0.4012	1797.03	1796.931	1	1842	82.14286	L.IDIEETFDDNHLVVH.Q
gi|6319319|ref|NP_009402.1|	YAR002C-A	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 transport and localized to COPII-coated vesicles; Erp1p	2	3.2835	0.3879	2088.29	2089.275	1	917.6	55.88235	F.G1V1L1I1D1I1E1E1T1F1D1D1N2H3L1V1V1H3.Q
gi|6319319|ref|NP_009402.1|	YAR002C-A	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 transport and localized to COPII-coated vesicles; Erp1p	2	4.7111	0.3651	2065.55	2066.275	1	1055.8	64.70589	F.GVLIDIEETFDDNHLVVH.Q
gi|6319319|ref|NP_009402.1|	YAR002C-A	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 transport and localized to COPII-coated vesicles; Erp1p	2	3.2288	0.1884	1761.27	1761.01	8	272.7	50	D.E1K2L1D1S1K2G1K2A1T1I1D1I1L1H3A1.K
gi|37362612|ref|NP_009421.2|	YAR042W	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; 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	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; 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
gi|37362612|ref|NP_009421.2|	YAR042W	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; localizes to the Golgi and the nucleus-vacuole junction; Swh1p	2	3.7986	0.39	1822.15	1821.086	1	710.1	70	T.TNRVSKPFNPLLGETF.E
gi|37362612|ref|NP_009421.2|	YAR042W	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; localizes to the Golgi and the nucleus-vacuole junction; Swh1p	2	4.2299	0.4213	1966.17	1967.111	1	475.8	56.666668	T.I1R4P1D1H3N2I1S1V1P1E1E1T1Y1S1W2.K
gi|37362612|ref|NP_009421.2|	YAR042W	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; 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	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; 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
gi|37362612|ref|NP_009421.2|	YAR042W	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; localizes to the Golgi and the nucleus-vacuole junction; Swh1p	2	3.1041	0.2807	1921.73	1922.191	4	376.3	40.625	S.TTNRVSKPFNPLLGETF.E
gi|14270688|ref|NP_009551.2|	YBL004W	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of the 18S rRNA; Utp20p	2	3.3247	0.3107	1885.65	1886.028	1	513.5	53.333336	A.DSIIRNPVNDDHYVDL.V
gi|14270688|ref|NP_009551.2|	YBL004W	Component of the small-subunit (SSU) processome, which is involved in the 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	Component of the small-subunit (SSU) processome, which is involved in the 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	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of the 18S rRNA; Utp20p	2	3.2699	0.2556	1859.77	1858.148	2	525.9	53.333336	F.SESGRKIPDWNKITIL.I
gi|14270688|ref|NP_009551.2|	YBL004W	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of the 18S rRNA; Utp20p	2	4.0113	0.2175	1983.97	1985.182	3	491.5	53.333336	F.I1K2L1P1D1E1N2Q2N2L1D1Y1Y1Q2P1L1.L
gi|14270688|ref|NP_009551.2|	YBL004W	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of the 18S rRNA; Utp20p	2	2.9791	0.2704	1495.95	1496.724	1	750.1	85	S.R4M1H3E1Y1D1F1P1R4I1L1.S
gi|14270688|ref|NP_009551.2|	YBL004W	Component of the small-subunit (SSU) processome, which is involved in the 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	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of the 18S rRNA; Utp20p	2	4.2988	0.3324	2199.37	2198.437	1	914.1	61.764706	L.SFIKLPDENQNLDYYQPL.L
gi|14270688|ref|NP_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.S1E1S1G1R4K2I1P1D1W2N2K2I1T1I1L1.I
gi|6319464|ref|NP_009546.1|	YBL007C	Cytoskeletal protein binding protein required for assembly of the cortical actin 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

gi|6319464|ref|NP_009546.1|	YBL007C	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin dynamics and with proteins required for endocytosis; Sla1p	2	4.3095	0.3589	2054.85	2056.226	1	983.6	68.75	N.FDREQLTEDMMPDINNS.M
gi|6319464|ref|NP_009546.1|	YBL007C	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin dynamics and with proteins required for endocytosis; Sla1p	2	3.6493	0.2508	1874.15	1875.044	1	526.1	60.714287	N.F1D1R4E1Q2L1T1E1D1M1M1P1D1I1N2.N
gi|6319464|ref|NP_009546.1|	YBL007C	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin dynamics and with proteins required for endocytosis; Sla1p	2	3.4607	0.3042	1853.77	1855.044	1	618.2	67.85714	N.FDREQLTEDMMPDIN.N
gi|6319464|ref|NP_009546.1|	YBL007C	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin 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
gi|6319464|ref|NP_009546.1|	YBL007C	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin 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	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	2	3.7259	0.4223	2258.51	2257.546	1	575.3	54.545456	T.AIKEDGSIVPGPSVGGSPEFITV.S
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	2	3.5209	0.2179	2532.51	2533.907	1	464.5	40	S.FEGIHDIDMPVNPPFRKPYPY.L
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	3	5.4148	0.3435	2673.74	2676.066	4	614.9	29.761904	S.F1E1G1I1H3D1I1D1M1P1V1N2P1P1F1R4K2P1Y1P1Y1L1.K
gi|6319456|ref|NP_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
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	3	3.8414	0.1658	3138.26	3138.55	1	477.4	25.961538	N.T1A1T1P1S1F1E1G1I1H3D1I1D1M1P1V1N2P1P1F1R4K2P1Y1P1Y1L1.K
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	3	5.028	0.217	2647.34	2647.066	1	1391.4	41.666664	S.FEGIHDIDMPVNPPFRKPYPYL.K
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	2	4.7663	0.4268	2645.01	2647.066	1	978	54.761906	S.FEGIHDIDMPVNPPFRKPYPYL.K
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate 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	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	3	4.1999	0.2968	3106.19	3104.55	1	483.5	26.923079	N.TATPSFEGIHDIDMPVNPPFRKPYPYL.K
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	2	4.0538	0.2361	2064.29	2063.422	1	405.1	50	H.DIDMPVNPPFRKPYPYL.K
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	2	3.8648	0.2185	2532.65	2533.907	1	714.3	47.5	S.FEGIHDIDMPVNPPFRKPYPY.L
gi|6319456|ref|NP_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.FEGIHDIDMPVNPPFRKPYPY.L
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	2	4.3462	0.3111	2646.87	2647.066	1	973.2	52.380955	S.FEGIHDIDMPVNPPFRKPYPYL.K
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	3	4.0895	0.1841	2674.91	2676.066	1	552.3	29.761904	S.F1E1G1I1H3D1I1D1M1P1V1N2P1P1F1R4K2P1Y1P1Y1L1.K
gi|6319456|ref|NP_009538.1|	YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	3	4.9535	0.3219	2648.24	2647.066	1	663.3	36.904762	S.FEGIHDIDMPVNPPFRKPYPYL.K
gi|6319454|ref|NP_009536.1|	YBL017C	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles between the late-Golgi and prevacuolar endosome-like compartments; Pep1p	2	5.0196	0.2621	2340.09	2340.334	1	905.6	63.88889	F.N2D1K2T1C1E1E1N2D1F1E1D1W2N2L1A1E1G1K2.C
gi|6319454|ref|NP_009536.1|	YBL017C	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles 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
gi|6319454|ref|NP_009536.1|	YBL017C	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles 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
gi|6319454|ref|NP_009536.1|	YBL017C	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles 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
gi|6319454|ref|NP_009536.1|	YBL017C	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles 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
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	1	2.9277	0.3507	1362.59	1363.615	2	169.6	59.090908	D.RLYETTPPGVVM.G
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	3	5.109	0.2922	3890.63	3890.068	1	1114.6	27.142859	Q.AKDTDTETTVVEDANNPEDQESTSPATPKLEDIVVE.R
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	1	2.4778	0.1841	1421.59	1422.566	1	183.4	54.166668	L.I1D1E1I1D1K2I1G1H3G1G1I1H3.G
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	2	3.7682	0.4234	2132.57	2132.304	1	463.7	40	A.SIHLHCPEGATPKDGPSAGVT.M
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	1	3.0989	0.2631	1388.3	1386.593	1	549.8	65	S.HIIKSPTWQEF.Q
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	3	4.6674	0.1831	3075.38	3072.397	1	531.8	32	K.T1I1I1F1P1K2D1N2L1N2D1W2E1E1L1P1D1N2V1K2E1G1L1E1P1L1.A
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; 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
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; 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	36	K.TIIFPKDNLNDWEELPDNVKEGLEPL.A
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	2	4.5185	0.3459	2364.31	2365.505	1	507.9	44.736843	K.D1N2L1N2D1W2E1E1L1P1D1N2V1K2E1G1L1E1P1L1.A
gi|6319449|ref|NP_009531.1|	YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	2	4.4975	0.2889	2338.93	2340.505	1	1050	57.894737	K.DNLNDWEELPDNVKEGLEPL.A

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.K2I1P1V1D1D1T1G1M1E1P1D1V1C1I1I1E1L1.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	2	4.5357	0.3834	2115.89	2116.397	1	813.9	52.77778	V.AKIPVDDTGMEPDVCIIEL.G
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	2.9102	0.2704	1794.49	1795.984	1	340.8	43.333332	N.SILPVKDEFDDEFAGL.E
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	3.8869	0.296	2244.33	2245.357	1	414.6	47.058823	M.E1Q2F1E1T1I1D1H3K2D1L1D1D1E1L1Q2M1N2.A
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	3.8156	0.3102	2447.65	2446.587	1	666.7	47.5	Q.SVRDDVELPETLEERDTINNT.A
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	1	2.8232	0.1522	1511.62	1512.731	9	286.1	53.846157	Q.K2K2N2A1G1V1E1L1P1D1V1I1P1N2.E
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	3.0926	0.2336	2431.09	2429.819	1	381.3	38.636364	T.KVATPSIPQQPIPLKNDPIVDAS.L
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	3.6007	0.2415	2459.11	2457.819	2	355.9	36.363636	T.K2V1A1T1P1S1I1P1Q2Q2P1I1P1L1K2N2D1P1I1V1D1A1S1.L
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	3.483	0.3701	1616.41	1616.829	2	415.5	57.692307	S.R4A1S1K2P1S1L1Q2D1M1P1H3Q2V1.S
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	3.3506	0.256	1835.81	1836.934	3	206.5	53.571426	F.E1T1I1D1H3K2D1L1D1D1E1L1Q2M1N2.A
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	4.3314	0.2416	1945.33	1945.091	1	919.9	66.66667	Q.SIIKEEPEEQEQLRES.S
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	3.2408	0.3165	1490.83	1489.798	1	862.2	65.38461	T.KVATPSIPQQPIPL.K
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	3	4.3947	0.359	3680.03	3680.239	1	923.4	28.030304	Q.KKNAGVELPDVIPNELLQSPALGLYPPNPLPQQQ.S
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	3	4.0336	0.2742	3721.1	3723.239	1	487.5	22.727274	Q.K2K2N2A1G1V1E1L1P1D1V1I1P1N2E1L1L1Q2S1P1A1L1G1L1Y1P1P1N2P1L1P1Q2Q2Q2.S
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	4.3505	0.4321	1924.09	1925.099	1	629.4	56.25	N.SILPVKDEFDDEFAGLE.Q
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	2	3.7984	0.3392	1812.91	1812.984	2	634.1	53.333336	N.S1I1L1P1V1K2D1E1F1D1D1E1F1A1G1L1.E
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	3	4.2784	0.2292	3762.11	3760.97	1	460.8	24.13793	L.SNKDTDLTDREKQLEERNRQIEEQENLYHQ.H
gi|6319424|ref|NP_009506.1|	YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	3	3.9906	0.3783	2429.57	2429.819	1	492.3	32.954548	T.KVATPSIPQQPIPLKNDPIVDAS.L
gi|6319420|ref|NP_009502.1|	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; Pin4p	3	3.811	0.3039	2060.75	2060.41	1	791.5	40.625	K.KEQLLDIIEEMDLPLPY.A
gi|6319420|ref|NP_009502.1|	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; Pin4p	2	5.8258	0.4532	2076.59	2079.41	1	1201.1	68.75	K.K2E1Q2L1L1D1I1I1E1E1M1D1L1P1L1P1Y1.A
gi|6319420|ref|NP_009502.1|	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; Pin4p	2	5.1115	0.3485	2059.11	2060.41	1	1192	68.75	K.KEQLLDIIEEMDLPLPY.A
gi|6319420|ref|NP_009502.1|	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; Pin4p	3	4.1099	0.3488	2078.12	2079.41	2	801.1	37.5	K.K2E1Q2L1L1D1I1I1E1E1M1D1L1P1L1P1Y1.A

gi|6319420|ref|NP_009502.1|	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; Pin4p	2	4.0062	0.3092	2075.97	2076.41	1	805.4	56.25	K.KEQLLDIIEEM@DLPLPY.A
gi|6319420|ref|NP_009502.1|	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; Pin4p	2	3.8341	0.3316	2316.87	2315.666	1	619.9	47.22222	K.K2E1Q2L1L1D1I1I1E1E1M$D1L1P1L1P1Y1A1F1.N
gi|6319420|ref|NP_009502.1|	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; Pin4p	2	5.6005	0.4819	2058.79	2060.41	1	1237.6	68.75	K.KEQLLDIIEEMDLPLPY.A
gi|6319420|ref|NP_009502.1|	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; Pin4p	2	5.3703	0.3795	2078.41	2079.41	1	1179.3	65.625	K.K2E1Q2L1L1D1I1I1E1E1M1D1L1P1L1P1Y1.A
gi|6319420|ref|NP_009502.1|	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; Pin4p	2	3.8885	0.3151	2277.47	2278.666	1	889.6	52.77778	K.KEQLLDIIEEMDLPLPYAF.N
gi|6319420|ref|NP_009502.1|	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; Pin4p	2	3.6819	0.2904	2299.15	2299.666	1	423.6	38.88889	K.K2E1Q2L1L1D1I1I1E1E1M1D1L1P1L1P1Y1A1F1.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.S1I1K2F1P1P1S1S1V1T1P1E1V1I1Q2Q2.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.Y1R4T1P1D1E1I1F1E1D1L1I1D1N2P1L1P1F1.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.N2R4E1E1K2L1L1D1I1E1T1P1F1I1L1P1Y1.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.N2R4E1E1K2L1L1D1I1E1T1P1F1I1L1P1Y1L1.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.K2N2V1Q2D1S1E1F1I1F1P1I1F1E1L1F1P1I1V1C1.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.R4L1E1S1I1K2F1P1P1S1S1V1T1P1E1V1I1Q2Q2.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.Q2N2R4E1E1K2L1L1D1I1E1T1P1F1I1L1P1Y1.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
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	3.851	0.3848	2158.65	2156.487	1	632.8	52.77778	L.RLESIKFPPSSVTPEVIQQ.E
gi|6319391|ref|NP_009473.1|	YBL080C	Protein required for mitochondrial translation; mutation is functionally complemented by a Bacillus subtilis ortholog; Pet112p	2	3.2041	0.3811	1922.69	1925.358	1	625.8	50	S.GVRGLMPQLPDDIMRIL.M
gi|6319391|ref|NP_009473.1|	YBL080C	Protein required for mitochondrial translation; mutation is functionally complemented by a Bacillus subtilis ortholog; Pet112p	2	3.3182	0.2477	1991.87	1989.227	1	877.4	58.823532	N.LSKELDDIDESAKEIGIL.Q
gi|6319391|ref|NP_009473.1|	YBL080C	Protein required for mitochondrial translation; mutation is functionally complemented 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.GIKVTNPKGRL.A
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	2.2375	0.1723	1103.54	1104.354	1	378.8	66.66667	M.A1S1L1P1H3P1K2I1V1K2.K
gi|6319367|ref|NP_009449.1|	YBL101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements; Ecm21p	3	4.1199	0.2786	2930	2932.243	1	961.4	30.000002	K.N2E1E1S1G1E1E1D1I1F1A1E1Y1P1I1K2V1I1R4T1P1P1P1V1A1V1.S
gi|6319367|ref|NP_009449.1|	YBL101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements; Ecm21p	3	4.7679	0.1553	3149.54	3150.495	3	858.6	26.85185	L.K2N2E1E1S1G1E1E1D1I1F1A1E1Y1P1I1K2V1I1R4T1P1P1P1V1A1V1S1.T
gi|6319367|ref|NP_009449.1|	YBL101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements; Ecm21p	3	5.1647	0.3878	3305.87	3306.707	1	579.9	22.321428	H.Q2L1K2N2E1E1S1G1E1E1D1I1F1A1E1Y1P1I1K2V1I1R4T1P1P1P1V1A1V1.S
gi|6319367|ref|NP_009449.1|	YBL101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements; Ecm21p	2	4.3796	0.3905	1659.29	1659.887	1	501.6	69.230774	M.L1R4I1S1K2P1D1P1E1C1P1S1K2L1.R
gi|6319367|ref|NP_009449.1|	YBL101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements; Ecm21p	3	5.034	0.3999	3620.96	3623.004	5	361.1	20.967741	S.S1H3Q2L1K2N2E1E1S1G1E1E1D1I1F1A1E1Y1P1I1K2V1I1R4T1P1P1P1V1A1V1 S1.T
gi|6319367|ref|NP_009449.1|	YBL101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements; Ecm21p	2	4.1219	0.4134	2686.59	2686.023	1	519.8	36.95652	E.E1S1G1E1E1D1I1F1A1E1Y1P1I1K2V1I1R4T1P1P1P1V1A1V1.S
gi|6319367|ref|NP_009449.1|	YBL101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements; Ecm21p	3	5.6996	0.518	3059.99	3062.417	1	1259.3	33.653847	L.K2N2E1E1S1G1E1E1D1I1F1A1E1Y1P1I1K2V1I1R4T1P1P1P1V1A1V1.S
gi|6319481|ref|NP_009563.1|	YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf1p	1	2.5228	0.3078	1503.61	1504.726	1	211.1	58.333332	L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi|6319481|ref|NP_009563.1|	YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf1p	2	4.6301	0.3826	1502.59	1504.726	1	816.2	79.16667	L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi|6319481|ref|NP_009563.1|	YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf1p	3	4.1497	0.175	1503.29	1504.726	2	1435.8	58.333332	L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi|6319481|ref|NP_009563.1|	YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf1p	3	4.0401	0.1596	1502.6	1504.726	1	985.3	50	L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi|6319481|ref|NP_009563.1|	YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf1p	3	4.2628	0.1755	1483.31	1482.726	4	1006.3	50	L.RDNIQGITKPAIR.R
gi|6319481|ref|NP_009563.1|	YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf1p	2	4.1063	0.2973	1503.71	1504.726	1	482.6	70.83333	L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi|6319481|ref|NP_009563.1|	YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin 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

gi|6319481|ref|NP_009563.1|	YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf1p	2	3.7896	0.3267	1504.31	1504.726	1	339.4	66.66667	L.R4D1N2I1Q2G1I1T1K2P1A1I1R4.R
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	3.2598	0.1975	1712.15	1712.925	1	865.1	61.538464	N.D1I1E1D1V1E1K2Y1F1P1G1L1L1R4.A
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	3.4767	0.2994	1711.77	1708.865	1	814.6	65.38461	F.H3D1I1P1L1Y1A1D1K2E1N2N2I1F1.N
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	3.2843	0.2681	2639.99	2641.998	3	202.6	36.363636	D.I1N2D1P1L1A1P1K2L1N2D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	3.6715	0.2317	2871.39	2872.246	1	287.8	35.416664	A.I1D1I1N2D1P1L1A1P1K2L1N2D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	3	4.8575	0.2962	2871.8	2872.246	1	877.2	37.5	A.I1D1I1N2D1P1L1A1P1K2L1N2D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	4.1195	0.2566	2846.05	2843.246	1	360.9	37.5	A.IDINDPLAPKLNDIEDVEKYFPGLL.R
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	3.6715	0.3056	1558.21	1558.629	1	1080.5	79.16667	Q.T1W2E1D1P1N2V1S1H3P1E1T1K2.A
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	3.1169	0.1884	2613.79	2614.998	2	287.7	38.636364	D.INDPLAPKLNDIEDVEKYFPGLL.R
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	3.0011	0.1587	1508.37	1508.687	1	983.6	75	Y.K2I1P1D1G1K2P1E1N2Q2F1A1F1.S
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	3.2777	0.2139	1552.25	1552.737	1	477.4	66.66667	N.D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	2	4.0891	0.3462	1694.39	1694.925	1	1569.5	73.07692	N.DIEDVEKYFPGLLR.A
gi|6319483|ref|NP_009565.1|	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	3	4.1402	0.1879	2871.11	2872.246	6	540.1	27.083334	A.I1D1I1N2D1P1L1A1P1K2L1N2D1I1E1D1V1E1K2Y1F1P1G1L1L1.R
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	4.157	0.3778	2905.75	2905.215	1	459.7	44	L.RNMGTTLPVEVLIPPGDEGETEFCNK.I
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	4.8183	0.3847	2268.27	2268.541	1	1901	76.47059	F.KYLDDLLGQDKTEWKRVC.G
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	5.4895	0.3938	2293.15	2294.541	1	1524.3	67.64706	F.K2Y1L1D1D1L1L1G1Q2D1K2T1E1W2K2R4V1C1.G
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	4.9359	0.2522	1685.41	1684.871	1	1544.8	80.769226	N.K2N2P1F1K2Y1L1D1D1L1L1G1Q2D1.K
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	4.6546	0.2025	1570.23	1568.783	1	1542.3	79.16667	N.K2N2P1F1K2Y1L1D1D1L1L1G1Q2.D
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	5.2535	0.4439	2032.73	2034.279	1	978.3	65.625	L.KGDIGDRPDHYKDLYKL.S
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	2.9895	0.2049	2017.11	2018.101	1	531.5	52.941177	A.DDSTPLRDNDEAGNEKLK.S
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	4.9573	0.4237	1864.55	1863.975	1	2267.7	82.14286	E.KYTEEFFDNEDLNAK.N
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	3.6165	0.2928	1792.35	1792.946	1	910.1	60.714287	L.KGDIGDRPDHYKDLY.K
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	3.6617	0.1749	1551.47	1551.783	2	923.5	66.66667	N.KNPFKYLDDLLGQ.D
gi|6319489|ref|NP_009571.1|	YBR015C	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, localizes to an early Golgi compartment; Mnn2p	2	4.1516	0.352	2059.85	2059.279	1	563.1	56.25	L.K2G1D1I1G1D1R4P1D1H3Y1K2D1L1Y1K2L1.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	2	4.1169	0.2729	1900.11	1899.163	1	554.8	56.666668	L.Q2D1H3T1E1F1L1I1P1V1L1E1P1I1I1N2.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.E1A1S1N2D1D1D1A1F1L1E1D1K2D1E1D1I1K2P1I1A1P1R4I1V1.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.E1A1S1N2D1D1D1A1F1L1E1D1K2D1E1D1I1K2P1I1A1P1R4I1V1.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.S1Q2D1L1L1F1P1Q2G1T1K2D1L1T1I1L1.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.D1H3T1E1F1L1I1P1V1L1E1P1I1I1N2.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.N2D1D1D1A1F1L1E1D1K2D1E1D1I1K2P1I1A1P1R4.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.E1A1S1N2D1D1D1A1F1L1E1D1K2D1E1D1I1K2P1I1A1P1R4I1V1.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	3.7559	0.2459	1877.77	1879.163	1	522.3	53.333336	L.QDHTEFLIPVLEPIIN.T
gi|6319497|ref|NP_009579.1|	YBR023C	Chitin synthase III, catalyzes the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for synthesis of the majority of cell wall chitin, the chitin ring during bud emergence, and spore wall chitosan; Chs3p	2	3.7828	0.3468	2045.11	2045.385	1	766.4	59.375	T.I1I1H3P1D1I1V1Q2Q2P1P1L1D1F1M1P1Y1.G
gi|6319497|ref|NP_009579.1|	YBR023C	Chitin synthase III, catalyzes the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for synthesis of the majority of cell wall chitin, the chitin ring during bud emergence, and spore wall chitosan; Chs3p	2	4.1359	0.3993	2023.39	2024.385	1	843.6	62.5	T.IIHPDIVQQPPLDFMPY.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
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	1	4.3594	0.1833	1531.51	1532.645	3	817.2	66.66667	M.S1P1E1D1A1E1E1E1L1K2K2L1Q2.T
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	3.6686	0.1754	1388.41	1388.514	3	1478.8	81.818184	M.SPEDAEEELKKL.Q
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	3	4.0454	0.2706	1388.63	1388.514	1	1809.5	70.454544	M.SPEDAEEELKKL.Q
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	4.3441	0.2421	1646.91	1647.838	1	1015.3	73.07692	H.MSPEDAEEELKKLQ.T
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	2.9662	0.2041	1300.51	1301.436	1	702.8	75	S.PEDAEEELKKL.Q
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	3.9661	0.3755	1635.27	1633.795	1	815.2	69.230774	K.GKDYVVEDGDIIYF.R
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	3.584	0.2835	2179.37	2179.326	1	760	50	C.F1D1D1A1E1I1I1H3V1E1G1D1V1D1P1V1R4D1L1.E
gi|6319499|ref|NP_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|ref|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|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	3.7613	0.3683	2040.87	2041.292	1	810.2	56.25	L.M1Q2K2G1K2D1Y1V1V1E1D1G1D1I1I1Y1F1.R
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	3	4.7335	0.1708	2211.77	2209.513	1	698.6	38.88889	A.T1I1D1P1E1E1A1R4V1I1V1P1S1P1R4F1D1K2L1.C
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	3	3.9371	0.2232	2471.51	2471.742	1	850.7	35	V.SLEERLSHMSPEDAEEELKKL.Q
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	3.4393	0.2797	2816.29	2818.083	1	407.1	41.304348	F.S1V1S1L1E1E1R4L1S1H3M1S1P1E1D1A1E1E1E1L1K2K2L1Q2.T
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	3.5291	0.2267	2784.91	2786.083	1	376.7	39.130436	F.SVSLEERLSHMSPEDAEEELKKLQ.T
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	3.771	0.3762	2687.25	2687.953	1	867	50	F.S1V1S1L1E1E1R4L1S1H3M1S1P1E1D1A1E1E1E1L1K2K2L1.Q
gi|6319499|ref|NP_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|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	3	3.9273	0.2947	2252.96	2254.591	3	650.3	35.526314	F.ATIDPEEARVIVPSPRFDKL.C
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	3	4.6405	0.2828	2685.77	2687.953	1	1401	36.363636	F.S1V1S1L1E1E1R4L1S1H3M1S1P1E1D1A1E1E1E1L1K2K2L1.Q
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	1	2.339	0.3098	1112.5	1113.241	1	365	61.11111	A.I1T1R4C1P1L1G1N2P1A1.N
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	3.1086	0.3012	1504.27	1504.606	1	564.2	63.636364	V.RCFDDAEIIHVE.G
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	2	4.2475	0.1814	1663.59	1664.838	1	940.4	73.07692	H.M1S1P1E1D1A1E1E1E1L1K2K2L1Q2.T
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	3	4.3315	0.2154	2182.34	2183.513	1	655.2	40.27778	A.TIDPEEARVIVPSPRFDKL.C
gi|6319499|ref|NP_009581.1|	YBR025C	hypothetical protein; Ybr025cp	3	3.8711	0.212	2280.98	2281.591	1	728.4	34.210526	F.A1T1I1D1P1E1E1A1R4V1I1V1P1S1P1R4F1D1K2L1.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	4.2936	0.3273	1688.39	1688.961	1	1045.6	60.714287	Q.V1E1E1K2K2V1L1L1G1R4P1G1N2N2L1.K
gi|6319500|ref|NP_009582.1|	YBR026C	2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase family; localized to in mitochondria, where it has a probable role in fatty acid synthesis; Etr1p	1	2.3524	0.1869	1295.61	1296.553	3	242.1	54.545456	K.GDLKLGDRVIPL.Q
gi|6319500|ref|NP_009582.1|	YBR026C	2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase family; localized to in mitochondria, where it has a probable role in fatty acid synthesis; Etr1p	2	3.1417	0.151	1921.67	1921.117	2	408.6	46.666668	M.YNYGHIISPRDEIETL.T
gi|6319500|ref|NP_009582.1|	YBR026C	2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase family; localized to in mitochondria, where it has a probable role in fatty acid synthesis; Etr1p	2	3.8464	0.1994	1876.61	1877.108	1	489.4	53.333336	L.SVIRDRDNFDEVAKVL.E
gi|6319500|ref|NP_009582.1|	YBR026C	2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase 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-diaclglyerol, 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.Q2I1I1E1L1I1D1I1L1I1R4.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.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	2.9052	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 of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	1	2.3631	0.184	1197.63	1196.473	5	470.2	55 E.KIPEIPLVVST.D
gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	1	3.1445	0.2072	1478.68	1479.803	1	390.3	58.333332 H.RVEKIPEIPLVVS.T
gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	1	2.7687	0.18	1597.9	1598.908	2	352.3	57.692307 H.R4V1E1K2I1P1E1I1P1L1V1V1S1T1.D
gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	1	2.8167	0.1834	1391.78	1392.725	3	312.8	59.090908 H.RVEKIPEIPLVV.S
gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	2	2.9906	0.3225	2041.13	2039.406	1	296.6	38.88889 N.A1L1P1L1P1A1V1F1S1A1P1I1R4P1D1I1V1H3T1.V
gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	2	2.928	0.2551	2287.57	2287.715	1	285.8	35 N.A1L1P1L1P1A1V1F1S1A1P1I1R4P1D1I1V1H3T1V1F1.T
gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	1	2.4115	0.3017	1106.65	1106.368	3	369.5	55.555557 E.K2I1P1E1I1P1L1V1V1S1.T
gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	1	2.9851	0.2846	1208.75	1208.473	1	536	60.000004 E.K2I1P1E1I1P1L1V1V1S1T1.D
gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	2	2.9059	0.2134	1198.17	1196.473	1	495.3	75 E.KIPEIPLVVST.D

gi|6319505|ref|NP_009587.1|	YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	1	3.19	0.3688	1495.69	1496.803	1	452	58.333332 H.R4V1E1K2I1P1E1I1P1L1V1V1S1.T
gi|41629676|ref|NP_009597.2|	YBR041W	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a complex with Faa1p or Faa4p that imports and activates exogenous fatty acids; Fat1p	2	2.9645	0.2187	1606.05	1604.846	1	1276.1	80.769226 Q.KLPKGLDGNDTIFW.L
gi|41629676|ref|NP_009597.2|	YBR041W	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a complex with Faa1p or Faa4p that imports and activates exogenous fatty acids; Fat1p	2	3.1606	0.2906	1621.71	1622.846	1	857.2	69.230774 Q.K2L1P1K2G1L1D1G1N2D1T1I1F1W2.L
gi|41629676|ref|NP_009597.2|	YBR041W	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a complex with Faa1p or Faa4p that imports and activates exogenous fatty acids; Fat1p	1	2.4954	0.156	1468.6	1469.723	3	400.7	54.545456 R.IFFPKKPETSFQ.G
gi|41629676|ref|NP_009597.2|	YBR041W	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a complex with Faa1p or Faa4p that imports and activates exogenous fatty acids; Fat1p	3	4.9633	0.2555	3154.67	3154.501	1	726.1	27.777779 Q.VFIDPDASNPIRESEEEIKNALPDVKLN.Y
gi|41629676|ref|NP_009597.2|	YBR041W	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a complex with Faa1p or Faa4p that imports and activates exogenous fatty acids; Fat1p	2	2.9179	0.1595	1470.59	1469.723	3	445.8	63.636364 R.IFFPKKPETSFQ.G
gi|6319516|ref|NP_009598.1|	YBR042C	hypothetical protein; Ybr042cp	2	3.8343	0.3829	1761.19	1760.086	1	892.4	64.28571 K.SIFLEGKYPKLVDIH.I
gi|6319516|ref|NP_009598.1|	YBR042C	hypothetical protein; Ybr042cp	3	4.712	0.3469	3663.08	3663.043	1	513.1	25.833332 S.L1A1G1K2S1P1E1R4I1T1E1E1G1E1S1I1W2N2P1E1V1I1D1P1K2Q2I1H3W2P1Y1.N
gi|6319516|ref|NP_009598.1|	YBR042C	hypothetical protein; Ybr042cp	3	3.8377	0.2294	3508.34	3507.884	2	397.1	23.275862 L.AGKSPERITEEGESIWNPEVIDPKQIHWPY.N
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	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	3.1952	0.2925	1341.73	1342.544	4	722.8	70 S.YIDKKCPFTGL.V
gi|6319522|ref|NP_009604.1|	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	1	3.2515	0.3198	1341.66	1342.544	1	612.4	65 S.YIDKKCPFTGL.V
gi|6319522|ref|NP_009604.1|	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	1	2.6984	0.376	1201.57	1202.371	1	421.7	60.000004 R.H3K2N2V1P1V1H3V1S1P1A1.F
gi|6319522|ref|NP_009604.1|	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
gi|6319522|ref|NP_009604.1|	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	1	2.4666	0.3671	1184.6	1185.371	1	463.4	60.000004 R.HKNVPVHVSPA.F
gi|6319522|ref|NP_009604.1|	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	3.3618	0.3764	1202.97	1202.371	1	1279.2	80 R.H3K2N2V1P1V1H3V1S1P1A1.F
gi|6319522|ref|NP_009604.1|	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	3.5335	0.4235	1331.95	1332.548	1	806.2	68.181816 R.HKNVPVHVSPAF.R
gi|6319522|ref|NP_009604.1|	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	3.1764	0.3641	1469.77	1470.683	1	580.7	62.5 K.N2V1P1V1H3V1S1P1A1F1R4V1Q2.V
gi|6319522|ref|NP_009604.1|	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	3.105	0.3196	1202.57	1202.371	1	467.1	65 R.H3K2N2V1P1V1H3V1S1P1A1.F
gi|6319522|ref|NP_009604.1|	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	1	2.7734	0.3704	1201.52	1202.371	1	441.3	60.000004 R.H3K2N2V1P1V1H3V1S1P1A1.F
gi|6319522|ref|NP_009604.1|	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	1	2.3308	0.2944	1184.54	1185.371	1	380.3	55 R.HKNVPVHVSPA.F
gi|6319522|ref|NP_009604.1|	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	1	3.2481	0.2448	1354.34	1355.544	7	549.6	60.000004 S.Y1I1D1K2K2C1P1F1T1G1L1.V
gi|6319522|ref|NP_009604.1|	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	1	2.752	0.2327	1507.6	1508.689	7	227.8	50 Q.S1E1R4A1F1Q2K2Q2P1H3I1F1.N
gi|6319522|ref|NP_009604.1|	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	3.0962	0.3575	1185.79	1185.371	1	885.6	75 R.HKNVPVHVSPA.F
gi|6319522|ref|NP_009604.1|	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	1	2.4031	0.3867	1184.61	1185.371	1	503.5	65 R.HKNVPVHVSPA.F
gi|6319523|ref|NP_009605.1|	YBR049C	RNA polymerase I enhancer binding protein; DNA binding protein which binds to 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
gi|6319523|ref|NP_009605.1|	YBR049C	RNA polymerase I enhancer binding protein; DNA binding protein which binds to 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
gi|6319523|ref|NP_009605.1|	YBR049C	RNA polymerase I enhancer binding protein; DNA binding protein which binds to genes transcribed by both RNA polymerase I and RNA polymerase II; required for termination of RNA polymerase I transcription; Reb1p	2	3.0079	0.1759	2055.85	2055.26	5	299.2	41.17647 T.E1D1S1Q2V1D1W2D1E1L1A1A1L1K2P1G1M1K2.L
gi|6319523|ref|NP_009605.1|	YBR049C	RNA polymerase I enhancer binding protein; DNA binding protein which binds to genes transcribed by both RNA polymerase I and RNA polymerase II; required for termination of RNA polymerase I transcription; Reb1p	2	3.2504	0.2238	1252.25	1252.41	1	610.8	83.33333 N.LLEEEQHLLQ.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
gi|6319529|ref|NP_009611.1|	YBR055C	Splicing factor, component of the U4/U6-U5 snRNP complex; Prp6p	2	3.3442	0.2169	1664.55	1662.926	1	497.3	58.333332 N.S1F1R4K2I1L1P1Q2E1P1E1I1W2.I
gi|6319529|ref|NP_009611.1|	YBR055C	Splicing factor, component of the U4/U6-U5 snRNP complex; Prp6p	2	3.5972	0.2166	2000.43	2001.283	1	808.9	53.125 R.S1I1L1D1R4G1L1L1K2N2P1D1D1V1L1F1Y1.I
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.S1I1I1K2D1L1P1N2T1V1N2F1P1H3E1D1A1D1Y1T1V1G1.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
gi|6319530|ref|NP_009612.1|	YBR056W	hypothetical protein; Ybr056wp	2	3.0899	0.2372	1577.45	1576.749	2	655.9	59.090908 Y.IDRIDWEWLSKD.A
gi|6319530|ref|NP_009612.1|	YBR056W	hypothetical protein; Ybr056wp	2	3.9777	0.3975	1795.73	1797.002	1	579.4	60.000004 W.H3V1E1D1G1K2H3L1D1S1L1P1F1A1P1L1.R
gi|6319530|ref|NP_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
gi|6319546|ref|NP_009628.1|	YBR072W	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 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
gi|6319546|ref|NP_009628.1|	YBR072W	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 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

gi|6319546|ref|NP_009628.1|	YBR072W	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 by heat, upon entry into stationary phase, and during sporulation; Hsp26p	1	2.4617	0.1616	1530.73	1531.706	3	281.9	46.153847	K.RVITLPDYPGVDAD.N
gi|6319546|ref|NP_009628.1|	YBR072W	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 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
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	4.476	0.3404	3010.79	3011.901	1	599.7	30.000002	Q.E1E1K2E1E1T1D1E1A1L1G1P1Q2E1T1E1D1G1E1E1K2E1E1E1S1D1.P
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.8501	0.3245	3189.75	3191.251	2	286.7	29.62963	A.SKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	6.2343	0.3395	3295.64	3296.33	1	837.2	33.035713	T.A1S1K2E1V1S1E1E1E1N2T1E1P1E1V1Q2E1E1K2E1E1T1D1E1A1L1G1P1Q2.E
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	6.1462	0.406	3192.14	3191.251	1	1044	37.037037	A.SKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	6.2074	0.3814	3398.51	3398.435	1	1183.8	35.344826	S.T1A1S1K2E1V1S1E1E1E1N2T1E1P1E1V1Q2E1E1K2E1E1T1D1E1A1L1G1P1Q2.E
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	5.9175	0.4516	3363.35	3363.435	1	1319.8	34.482758	S.TASKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	5.3326	0.3787	3675.98	3675.76	1	685.9	26.612906	Q.EEKEETDEALGPQETEDGEEKEEESDPVIIRN.S
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	5.5203	0.3573	3562.19	3561.656	1	1169.5	31.666666	Q.EEKEETDEALGPQETEDGEEKEEESDPVIIR.N
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	5.9334	0.4118	3599.99	3598.656	1	1108.8	30.833334	Q.E1E1K2E1E1T1D1E1A1L1G1P1Q2E1T1E1D1G1E1E1K2E1E1E1S1D1P1V1I1I1R4.N
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.3197	0.3042	1169.79	1170.299	1	910.9	83.33333	I.P1S1I1G1Y1D1P1H3L1R4.M
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.6465	0.3368	1938.65	1941.19	1	774.5	60.000004	Q.L1D1E1I1P1S1I1G1Y1D1P1H3L1R4M1Y1.R
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	1	2.7048	0.1905	1130.56	1130.262	2	455.3	75	Y.R4S1I1E1D1V1F1H3L1.M
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	1	3.0702	0.2969	1261.51	1262.455	5	369.3	72.22222	Y.R4S1I1E1D1V1F1H3L1M1.K
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	1	2.8335	0.2762	1246.5	1247.455	1	445.1	77.77778	Y.RSIEDVFHLM.K
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.1941	0.4329	2525.21	2525.795	5	155.8	23.076923	A.G1G1S1S1P1A1T1P1A1T1P1A1T1P1A1T1P1T1P1S1S1G1P1K2K2M1T1.M
gi|6319553|ref|NP_009635.1|	YBR079C	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 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(eIF3), 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
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.7784	0.386	2422.45	2423.69	1	503	38	A.G1G1S1S1P1A1T1P1A1T1P1A1T1P1A1T1P1T1P1S1S1G1P1K2K2M1.T
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.7724	0.4548	2394.25	2395.69	1	477.7	36	A.GGSSPATPATPATPATPTPSSGPKKM.T
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	5.6608	0.4527	3190.58	3191.251	1	1021.2	37.962963	A.SKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.7137	0.3246	3189.91	3191.251	1	297.1	29.62963	A.SKEVSEEENTEPEVQEEKEETDEALGPQ.E
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	5.5049	0.3464	3715.04	3714.76	1	886.1	28.225807	Q.E1E1K2E1E1T1D1E1A1L1G1P1Q2E1T1E1D1G1E1E1K2E1E1E1S1D1P1V1I1I1R4N2.S
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	4.1894	0.2417	1837.47	1839.019	1	1167.6	67.85714	K.V1D1E1E1L1K2E1L1Y1D1I1I1E1V1N2.F
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.8722	0.2379	1821.37	1822.019	1	1474	75	K.VDEELKELYDIIEVN.F
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.3902	0.2887	1918.79	1920.19	1	1066.9	63.333332	Q.LDEIPSIGYDPHLRMY.R
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	1	3.2415	0.2579	1497.59	1498.709	1	387.7	59.090908	E.A1Y1R4S1I1E1D1V1F1H3L1M1.K
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	1	3.0619	0.2895	1481.82	1481.709	1	402.8	59.090908	E.AYRSIEDVFHLM.K
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.258	0.3445	1596.57	1596.781	1	355.2	53.571426	G.NREPPSTPSTLPKAT.V

gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	3.9347	0.1895	1498.58	1498.709	1	1512.8	59.090908	E.A1Y1R4S1I1E1D1V1F1H3L1M1.K
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.4001	0.2541	2242.15	2243.277	1	362.7	52.77778	Q.E1T1E1D1G1E1E1K2E1E1E1S1D1P1V1I1I1R4N2.S
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.2155	0.3678	2218.57	2219.277	1	277.5	50	Q.ETEDGEEKEEESDPVIIRN.S
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.6732	0.3573	2125.91	2127.174	3	350.7	47.058823	Q.E1T1E1D1G1E1E1K2E1E1E1S1D1P1V1I1I1R4.N
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.4362	0.1974	1111.25	1110.259	1	797.4	87.5	T.F1A1K2D1P1F1D1I1F1.A
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	3.7806	0.3431	1626.63	1625.822	1	732	69.230774	Q.LDEIPSIGYDPHLR.M
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	3.8137	0.2963	1777.55	1774.952	1	783	46.42857	T.Q2L1D1E1I1P1S1I1G1Y1D1P1H3L1R4.M
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	2	4.126	0.2157	1969.45	1969.193	1	726	60.000004	G.K2V1D1E1E1L1K2E1L1Y1D1I1I1E1V1N2.F
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	3	4.2033	0.2153	1366.28	1366.517	2	1626.5	65	E.A1Y1R4S1I1E1D1V1F1H3L1.M
gi|6319553|ref|NP_009635.1|	YBR079C	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 tRNA(i)Met to ribosomes; Rpg1p	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 core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-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
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	1	2.4465	0.224	1408.58	1409.536	2	324.3	50	L.HLESPVPSDIDIS.R
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	4.3965	0.431	2132.87	2132.332	1	776.2	61.764706	L.DIEKEDPDALTPEEVKRF.A
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	3	5.2167	0.3672	2154.44	2155.332	1	1668.1	47.058823	L.D1I1E1K2E1D1P1D1A1L1T1P1E1E1V1K2R4F1.A
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.9193	0.1958	1997.19	1999.296	1	630	59.375	L.L1I1Q2L1P1L1P1R4H3L1D1E1T1T1I1T1N2.A
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.4394	0.1581	1884.11	1883.192	1	506.4	63.333332	L.L1I1Q2L1P1L1P1R4H3L1D1E1T1T1I1T1.N
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.4487	0.1982	1860.51	1861.192	1	555.2	56.666668	L.LIQLPLPRHLDETTIT.N
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.6892	0.2558	2204.85	2203.411	1	542.3	52.77778	L.DIEKEDPDALTPEEVKRFA.R
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.5226	0.2738	2068.99	2068.294	1	426.1	44.11765	S.EKNPLNDKNIHEPGYVVT.E
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.2097	0.3174	1496.49	1497.738	1	693.4	66.66667	F.ARLNINPDTITIR.R
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.4137	0.306	2790.51	2790.102	5	164.2	34	H.GGAPNVKPGQSLPKEYTEENIDFVAK.G
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	1	3.4068	0.2737	1333.84	1334.685	4	642.5	59.090908	E.SEKLPVIKPLPL.H
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.0295	0.1544	1863.91	1862.136	1	281.8	53.333336	L.IQLPLPRHLDETTITN.A
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	4.2148	0.3296	2067.59	2068.294	2	567.2	50	E.KNPLNDKNIHEPGYVVTE.A
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	4.3139	0.3977	2552.55	2553.831	1	854.4	47.727272	K.LVGSEKNPLNDKNIHEPGYVVTE.A

gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	3	4.1722	0.2887	1812.65	1813.234	1	920	38.333332	F.VESEKLPVIKPLPLHL.E
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	1	2.4213	0.1526	1129.93	1130.492	1	964.8	77.77778	E.K2L1P1V1I1K2P1L1P1L1.H
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	1	3.4055	0.2884	1118.67	1118.492	1	989.3	77.77778	E.KLPVIKPLPL.H
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	3	4.088	0.2955	2132.54	2132.332	2	558.9	36.764706	L.DIEKEDPDALTPEEVKRF.A
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	3.3893	0.1841	2396.49	2393.699	1	657.3	52.499996	N.VKPGQSLPKEYTEENIDFVAK.G
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	4.2675	0.2836	1976.89	1975.296	1	545.4	56.25	L.LIQLPLPRHLDETTITN.A
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	4.0758	0.2881	1486.41	1486.724	1	839.4	73.07692	A.N2V1R4Q2P1S1L1G1P1T1L1G1V1K2.G
gi|6319558|ref|NP_009640.1|	YBR084W	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; Mis1p	2	4.4235	0.4125	1469.63	1466.724	1	969.8	76.92308	A.NVRQPSLGPTLGVK.G
gi|6319558|ref|NP_009640.1|	YBR084W	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; 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	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	1	2.2028	0.1838	1254.54	1255.518	1	491.2	72.22222	Y.LKYTNPLFMQ.S
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	2	3.3447	0.2801	1267.73	1268.518	1	979.7	77.77778	Y.L1K2Y1T1N2P1L1F1M1Q2.S
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	2	3.489	0.2987	1304.37	1304.505	3	375.1	68.181816	F.G1K2P1A1T1G1D1L1K2R4P1F1.K
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	2	3.4769	0.349	1288.43	1287.505	1	408	68.181816	F.GKPATGDLKRPF.K
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	1	2.3898	0.233	1118.46	1119.266	2	382.1	68.75	A.LEHNEVKIH.L
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	2	2.9396	0.1784	1135.37	1134.266	4	545.4	75	A.L1E1H3N2E1V1K2I1H3.L

gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double 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.GQTGPKTDKKSIEEAERAGNAGVKAE.-
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	3	5.8787	0.477	2505.77	2505.718	1	1040.5	41.304348	M.G1Q2T1G1P1K2T1D1K2K2S1I1E1E1A1E1R4A1G1N2A1G1V1K2.A
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	2	4.9333	0.3717	2505.51	2505.718	1	388.8	43.47826	M.G1Q2T1G1P1K2T1D1K2K2S1I1E1E1A1E1R4A1G1N2A1G1V1K2.A
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	2	4.1741	0.3492	2472.55	2472.718	1	448	43.47826	M.GQTGPKTDKKSIEEAERAGNAGVK.A
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	1	2.6789	0.2254	1286.6	1287.505	6	309.7	59.090908	F.GKPATGDLKRPF.K
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	2	3.1322	0.2824	1257.17	1255.518	1	947.4	77.77778	Y.LKYTNPLFMQ.S
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	1	2.9543	0.2665	1546.81	1547.841	2	382.2	57.692307	H.LFGKPATGDLKRPF.K
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced 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
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	1	2.4715	0.2739	1546.68	1547.841	1	464.6	61.538464	H.LFGKPATGDLKRPF.K
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	1	3.0949	0.3122	1565.72	1566.841	1	478.5	61.538464	H.L1F1G1K2P1A1T1G1D1L1K2R4P1F1.K
gi|6319582|ref|NP_009664.1|	YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	2	3.5047	0.2111	1547.55	1547.841	1	541.2	69.230774	H.LFGKPATGDLKRPF.K
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	3.6147	0.2884	1786.23	1786.889	1	586.5	66.66667	A.T1V1P1A1E1A1S1P1V1E1D1E1V1R4Q2H3.S
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	4.1602	0.3957	2585.31	2586.893	1	456.8	44.736843	L.E1C1F1R4Y1I1L1P1Q2P1P1A1P1L1Q2E1W2D1I1W2.F
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	3.096	0.2173	2834.55	2835.2	2	384.4	38.095238	L.ECFRYILPQPPAPLQEWDIWFQ.L
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	2.9243	0.1898	2862.71	2865.2	2	240.1	33.333336	L.E1C1F1R4Y1I1L1P1Q2P1P1A1P1L1Q2E1W2D1I1W2F1Q2.L
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	3.0262	0.1513	1381.75	1380.574	1	644.6	72.72727	L.S1N2P1N2V1P1K2L1W2H3G1I1.G
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	1	2.3374	0.1607	1361.59	1362.574	1	681.7	63.636364	L.SNPNVPKLWHGI.G
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	1	2.6963	0.2205	1379.59	1380.574	1	708.2	68.181816	L.S1N2P1N2V1P1K2L1W2H3G1I1.G
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	4.2716	0.445	2401.51	2398.769	1	805	55.555557	F.RYILPQPPAPLQEWDIWFQ.L
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	3.695	0.2427	2561.51	2559.893	1	543.6	47.368423	L.ECFRYILPQPPAPLQEWDIW.F
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	4.1852	0.2256	2148.55	2147.462	4	372	46.875	F.R4Y1I1L1P1Q2P1P1A1P1L1Q2E1W2D1I1W2.F
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	3.961	0.4333	2423.27	2425.769	1	574	50	F.R4Y1I1L1P1Q2P1P1A1P1L1Q2E1W2D1I1W2F1Q2.L
gi|6319589|ref|NP_009670.1|	YBR112C	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 to promoters; Cyc8p	2	3.6632	0.2183	2125.37	2123.462	2	543	53.125	F.RYILPQPPAPLQEWDIW.F
gi|6319591|ref|NP_009673.1|	YBR115C	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	2	2.966	0.2214	2190.01	2187.544	4	342.9	39.473686	V.GFLPPPTHNDKLPLPSIELT.Q
gi|6319591|ref|NP_009673.1|	YBR115C	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	2	3.4868	0.3072	1713.79	1714.974	1	475.6	57.692307	F.M1V1P1R4F1D1K2P1D1D1L1S1K2F1.Q
gi|6319591|ref|NP_009673.1|	YBR115C	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	3	4.2989	0.2612	1847.54	1845.105	1	1117.8	50	F.M1V1P1R4F1D1K2P1D1D1L1S1K2F1Q2.S
gi|6319591|ref|NP_009673.1|	YBR115C	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	2	3.6641	0.2059	1845.43	1845.105	1	631.9	57.14286	F.M1V1P1R4F1D1K2P1D1D1L1S1K2F1Q2.S
gi|6319591|ref|NP_009673.1|	YBR115C	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	2	2.9917	0.1896	2153.41	2153.492	1	215.2	44.444447	G.F1L1P1P1P1T1H3N2D1K2L1P1L1P1S1I1E1L1T1.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	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	41.666664 K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	3.7529	0.2738	1560.13	1560.643	1	1021.3	73.07692 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1.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	3.0031	0.3027	1559.51	1560.643	1	243.5	61.538464 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1.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	3.7237	0.2802	2578.39	2579.876	2	449.9	36.363636 G.Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	3.0936	0.3071	2705.89	2708.061	1	583.1	37.5 K.VGYNPKTVPFVPISGWNGDNMIEAT.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	3.6142	0.1697	2636.69	2635.956	1	583.9	36.95652 K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1.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	3.3216	0.3216	1484.33	1482.682	1	445.2	70.83333 T.VIDAPGHRDFIKN.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	1	2.9759	0.2141	1413.39	1414.487	1	456	75 M.D1S1V1K2W2D1E1S1R4F1Q2.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	3.2889	0.2899	1101.71	1102.397	2	719.5	72.22222 G.V1I1K2P1G1M1V1V1T1F1.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	3.4313	0.3435	2607.45	2608.928	1	561.6	41.304348 V.GYNPKTVPFVPISGWNGDNMIEAT.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	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
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	2.7549	0.2122	1397.61	1397.487	1	331.7	65 M.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	3.1255	0.2337	1881.63	1881.093	5	478.5	53.125 L.EAIDAIEQPSRPTDKPL.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	5.5963	0.503	1995.59	1993.133	1	1188.1	73.52941 H.H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.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	3.6477	0.3074	2227.49	2226.383	1	302.3	44.736843 K.SVEM@HHEQLEQGVPGDNVGF.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	3.4864	0.3132	2252.33	2253.383	1	327.2	44.736843 K.S1V1E1M$H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1.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	4.2164	0.1987	2019.33	2019.184	1	1278.1	66.66667 M.D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1.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	4.0168	0.3043	2119.61	2121.289	2	656.2	53.125 M.D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1.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	3.6517	0.1988	2231.71	2233.517	3	468.1	44.736843 K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1.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	3.5285	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
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	5.4426	0.4888	2364.67	2365.582	1	1418.9	65 V.EMHHEQLEQGVPGDNVGFNVK.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	3.3552	0.3915	1763.31	1763.864	1	620.7	70 M.HHEQLEQGVPGDNVGF.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	5.4909	0.4893	2584.43	2583.793	1	1132	59.090908 K.S1V1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.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	5.2897	0.3647	2635.94	2635.935	1	1460.1	36.363636 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1.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	1	2.4298	0.2617	1213.45	1214.45	9	249.5	61.11111 K.PLRLPLQDVY.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	2.7781	0.2141	1227.44	1228.45	3	271.7	66.66667 K.P1L1R4L1P1L1Q2D1V1Y1.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	3.885	0.4275	1342.07	1342.597	1	785.9	77.27273 N.P1K2T1V1P1F1V1P1I1S1G1W2.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	4.5	0.2669	2094.98	2095.295	1	1064.6	43.75 W.D1E1S1R4F1Q2E1I1V1K2E1T1S1N2F1I1K2.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	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
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	4.6606	0.3105	1326.95	1326.552	1	1057	60.416668 V.P1V1G1R4V1E1T1G1V1I1K2P1G1.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	1	2.6773	0.3376	1508.66	1509.789	3	168.3	39.285713 G.TVPVGRVETGVIKPG.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	1	2.858	0.2713	1529.6	1528.789	1	186.7	42.857143 G.T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1.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	6.4288	0.4253	2943.11	2944.215	1	707.6	36 T.E1V1K2S1V1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.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	4.3544	0.3232	2943.67	2944.215	1	427	40 T.E1V1K2S1V1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.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	3.6507	0.3988	1897.49	1895.056	1	778.3	71.875 E.MHHEQLEQGVPGDNVGF.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	3.5759	0.2201	1757.93	1759.053	4	466.7	50 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1.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	1	2.4618	0.2519	1308.68	1309.552	2	159.4	50 V.PVGRVETGVIKPG.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	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

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	3.2236	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.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	3.0469	0.152	2901.61	2900.244	6	222.8	31.25	L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	2.3355	0.3624	1327.59	1328.597	1	643.9	63.636364	N.PKTVPFVPISGW.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	4.4177	0.3407	2552.75	2552.89	6	544.4	29.761904	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	6.1175	0.3043	3014.54	3014.403	1	797.1	28	L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	4.9356	0.339	2963.6	2966.359	1	711.3	27.000002	K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1.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	4.5525	0.2553	2716.37	2717.981	1	403.5	42.857143	M.D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1N2F1I1K2.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	4.3377	0.3287	2687.37	2686.981	1	415.1	40.476192	M.DSVKWDESRFQEIVKETSNFIK.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	4.4473	0.3889	1309.7	1309.552	1	948.4	56.25	V.PVGRVETGVIKPG.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	6.1794	0.5098	3506.51	3505.884	1	1011.8	28.90625	F.APAGVTTEVKSVEMHHEQLEQGVPGDNVGFNVK.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	4.9031	0.2911	2470.73	2471.734	1	1095.8	55.263157	N.K2M1D1S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1.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	5.234	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	24.242424	T.F1A1P1A1G1V1T1T1E1V1K2S1V1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.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
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	3.5088	0.408	1328.87	1328.597	1	817.3	77.27273	N.PKTVPFVPISGW.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	3.147	0.2216	1140.56	1140.329	1	635.3	75	K.K2L1E1D1H3P1K2F1L1.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	4.1051	0.3934	1706.33	1704.92	1	546.8	64.28571	Q.V1T1V1I1D1A1P1G1H3R4D1F1I1K2N2.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	5.7197	0.4062	2500.94	2503.875	1	1113.7	39.285713	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	4.7276	0.4115	2339.42	2341.792	1	641.6	34.090908	G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.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	4.0786	0.3577	1907.73	1909.291	1	595.4	52.941177	V.P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.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	4.5956	0.4284	2361.32	2360.716	1	1035.7	37.5	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	2.6292	0.2906	1126.54	1127.329	1	565.3	75	K.KLEDHPKFL.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	5.6297	0.4635	2265.45	2265.467	1	1534.3	73.68421	E.M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.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	5.3763	0.4759	2235.35	2236.467	1	1641.7	76.31579	E.MHHEQLEQGVPGDNVGFNVK.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	3.3817	0.2613	1715.57	1714.98	1	523.2	60.714287	V.TVIDAPGHRDFIKNM.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	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
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	3.6418	0.2436	2342.45	2341.792	8	289	36.363636	G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.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	3.7033	0.4145	1885.87	1887.291	1	701.1	58.823532	V.PVGRVETGVIKPGMVVTF.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	5.2671	0.4165	2817.8	2816.227	1	1399.2	35.416664	L.LEAIDAIEQPSRPTDKPLRLPLQDV.Y
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	3.953	0.1726	2616.63	2618.035	1	616.4	45.454548	T.L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.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	5.727	0.3245	2615.45	2618.035	1	1762.3	43.18182	T.L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.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	2	3.9983	0.3944	2866.21	2868.235	1	443.7	34	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	5.0189	0.3216	2693.66	2694.051	1	1174.4	38.04348	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	3.4693	0.2936	2692.73	2694.051	1	711.9	43.47826	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	3	4.9595	0.4573	2865.71	2868.235	1	930.7	31	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	4.4333	0.2893	2384.73	2385.682	1	487	50	V.KWDESRFQEIVKETSNFIK.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	5.2729	0.4538	2688.65	2688.14	1	1337	34.782608	K.TLLEAIDAIEQPSRPTDKPLRLPL.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	2	5.043	0.4873	2068.37	2069.428	1	687.2	57.894737	Q.T1V1A1V1G1V1I1K2S1V1D1K2T1E1K2A1A1K2V1T1.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	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

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	6.5846	0.326	2746.19	2748.166	1	2634.7	43.47826	T.L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.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	3.7382	0.2834	2412.41	2413.682	2	519.8	47.22222	V.K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1N2F1I1K2.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	5.0598	0.4039	3030.71	3030.492	1	1599.5	36.53846	K.TLLEAIDAIEQPSRPTDKPLRLPLQDV.Y
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	6.1227	0.3867	2720	2720.14	1	1352.5	35.869564	K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.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	5.0223	0.298	2390.15	2389.731	1	1738.5	43.75	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	3	4.0586	0.3072	2465.06	2467.801	2	554.7	33.75	D.A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	3.5842	0.271	1758.45	1756.098	1	776.9	67.85714	T.DKPLRLPLQDVYKIG.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	3.969	0.2683	2394.11	2393.704	1	889.5	35	K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4.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	2	2.9219	0.2032	1258.11	1255.503	8	345.3	66.66667	K.KLEDHPKFLK.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	3.0493	0.2086	1312.76	1312.555	1	587.8	65	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	2	5.8545	0.2642	2407.73	2407.736	1	855.1	52.499996	T.T1N2A1P1W2Y1K2G1W2E1K2E1T1K2A1G1V1V1K2G1K2.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	4.8675	0.3638	2192.91	2193.51	1	1031.6	61.11111	T.TNAPWYKGWEKETKAGVVK.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	5.8692	0.3191	2219.57	2219.51	1	733.7	55.555557	T.T1N2A1P1W2Y1K2G1W2E1K2E1T1K2A1G1V1V1K2.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	3.919	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
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	3.6008	0.2752	1358.63	1358.624	2	334.1	70	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	3	4.2147	0.3821	2394.32	2395.723	1	858.1	36.842106	A.I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	3.6533	0.3339	1889.71	1890.235	1	968.1	65.625	K.KVGYNPKTVPFVPISGW.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	3.5403	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
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	4.941	0.437	3532.31	3533.053	1	924	26.666668	K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1G
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	4.5696	0.2878	3547.4	3549.105	1	611.1	24.193548	K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYKIGG.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	3	4.9533	0.331	3493.79	3492.053	1	1139.7	29.166666	K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYKIG.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	2.3049	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
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	4.14	0.4007	1741.59	1740.827	1	703.1	66.66667	H.HEQLEQGVPGDNVGFN.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	4.1633	0.4494	1761.71	1762.827	1	627.6	66.66667	H.H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2.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	1	2.5093	0.3283	1359.61	1360.466	1	213.9	50	E.QLEQGVPGDNVGF.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	3.476	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
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	3.4128	0.2147	1585.57	1586.681	1	416	58.333332	W.D1E1S1R4F1Q2E1I1V1K2E1T1S1.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	3.3577	0.3461	1567.7	1568.681	1	355.4	58.333332	W.DESRFQEIVKETS.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	4.2175	0.3561	1680.35	1680.929	1	853.3	67.85714	V.G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.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	3.5239	0.3588	1607.63	1605.877	1	569.2	65.38461	G.YNPKTVPFVPISGW.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	3.3413	0.2178	2320.01	2319.602	1	386.4	37.5	K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1.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	3	3.8342	0.1834	1780.46	1781.061	3	719.9	41.666664	K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.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	3.9075	0.4051	1779.71	1781.061	1	651.3	63.333332	K.V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.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	3.3691	0.2507	1622.29	1622.877	2	528.8	61.538464	G.Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.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	3.191	0.2814	1761.57	1762.061	4	371.1	50	K.VGYNPKTVPFVPISGW.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	3.6003	0.3508	1412.41	1414.487	1	708.1	75	M.D1S1V1K2W2D1E1S1R4F1Q2.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	1	3.1538	0.3402	1396.64	1397.487	1	468.4	75	M.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	4.0023	0.3863	2297.67	2299.596	1	769.4	47.5	N.P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	1	2.6076	0.2628	841.44	841.873	1	519.9	78.57143	G.H3V1D1S1G1K2S1T1.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	1	2.4437	0.325	830.38	830.873	1	418.4	71.42857	G.HVDSGKST.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	1	2.3959	0.2656	1095.53	1096.188	2	292.2	71.42857	V.KWDESRFQ.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	3.7783	0.3476	1993.89	1996.184	1	906.8	56.666668	M.DSVKWDESRFQEIVKE.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	3.8194	0.1795	2210.84	2209.367	4	711.7	35.294117	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	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
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	3.9591	0.236	1385.51	1386.578	1	665.6	68.181816	T.V1I1D1A1P1G1H3R4D1F1I1K2.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	4.0811	0.3922	1919.25	1919.056	1	616.7	65.625	E.M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1.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	3.4229	0.2312	2387.19	2389.716	3	467.4	47.5	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	1	3.1497	0.1787	1473.67	1474.713	1	305.8	63.636364	T.D1K2P1L1R4L1P1L1Q2D1V1Y1.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	4.4094	0.2163	2583.77	2583.89	1	606.5	32.142857	I.D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	5.5709	0.4761	2864.18	2866.244	1	1008.7	29.166666	L.EAIDAIEQPSRPTDKPLRLPLQDVY.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	3.002	0.2936	1341.92	1342.597	1	516.7	59.090908	N.P1K2T1V1P1F1V1P1I1S1G1W2.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	2.8586	0.3208	1327.77	1328.597	6	420.7	54.545456	N.PKTVPFVPISGW.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	3.196	0.2028	2020.39	2021.317	6	287.8	46.875	Q.P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	3.8956	0.2356	1807.57	1808.957	1	479.9	65.38461	V.N2K2M$D1S1V1K2W2D1E1S1R4F1Q2.E
gi|6319594|ref|NP_009676.1|	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.5311	0.2544	1786.13	1786.957	1	688.9	73.07692	V.NKM@DSVKWDESRFQ.E
gi|6319594|ref|NP_009676.1|	YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	2	3.4469	0.3138	1909.65	1909.09	1	474.8	64.28571	A.V1N2K2M$D1S1V1K2W2D1E1S1R4F1Q2.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	3.4435	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
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	4.208	0.3851	2068.47	2069.279	1	1235.6	62.5	D.SVKWDESRFQEIVKETS.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	4.6701	0.4051	2090.63	2093.279	1	1211.3	62.5	D.S1V1K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1.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	6.103	0.4227	2501.51	2503.875	1	1423.2	41.666664	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	2	2.947	0.1573	2503.73	2503.875	2	327.7	42.857143	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	2	3.6217	0.1892	2168.73	2169.348	5	437.1	43.75	V.K2W2D1E1S1R4F1Q2E1I1V1K2E1T1S1N2F1.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	3	6.5006	0.4503	3126.05	3128.563	1	1786.6	35.576923	T.L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	5.3722	0.2735	2931.17	2931.359	1	949.6	29	K.TLLEAIDAIEQPSRPTDKPLRLPLQD.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	5.4792	0.4285	3065.54	3066.492	1	1748.9	34.615387	K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1.Y
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	4.8969	0.2837	3474.17	3475.001	1	862.6	24.13793	K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1.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	3.1995	0.1871	1138.55	1140.329	1	828.5	87.5	K.K2L1E1D1H3P1K2F1L1.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	4.0495	0.3037	1401.23	1400.646	1	760.3	69.230774	Y.K2I1G1G1I1G1T1V1P1V1G1R4V1E1.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	3.9978	0.2253	1561.51	1560.803	2	625.9	56.666668	Y.K2I1G1G1I1G1T1V1P1V1G1R4V1E1T1G1.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	3.655	0.2843	1541.47	1540.803	1	785.6	63.333332	Y.KIGGIGTVPVGRVETG.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	3.7517	0.3451	1882.43	1883.068	1	938.9	60.714287	V.KWDESRFQEIVKETS.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	4.0858	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_009676.1|	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	3.0971	0.2494	1357.83	1358.624	1	306.3	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	3	6.7566	0.4114	2633.57	2634.006	1	2594	45.454548	L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.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	4.1576	0.3129	2330.9	2330.792	1	703.9	36.363636	G.GIGTVPVGRVETGVIKPGM@VVTF.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	4.4387	0.3749	2358.02	2357.792	1	644.2	36.363636 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M$V1V1T1F1.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	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
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	4.3698	0.2426	2868.68	2868.235	1	691.2	29 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	4.3146	0.3674	2865.67	2868.235	1	471.8	34 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	4.6739	0.3317	2606.93	2605.98	1	771.8	35.227272 K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1.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	5.7165	0.4191	3194.99	3193.668	1	1465.8	30.555555 K.TLLEAIDAIEQPSRPTDKPLRLPLQDVY.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	6.6026	0.4081	3230.45	3230.668	1	1581.7	32.407406 K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	2.9501	0.1687	1140.58	1140.329	3	522.1	68.75 K.K2L1E1D1H3P1K2F1L1.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	3.4753	0.2884	1682.13	1682.92	1	551.1	67.85714 Q.VTVIDAPGHRDFIKN.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	4.3513	0.3367	2285.81	2288.652	1	1023.3	39.473686 A.IDAIEQPSRPTDKPLRLPLQ.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	4.718	0.4116	2158.88	2160.522	1	1449.7	47.22222 A.IDAIEQPSRPTDKPLRLPL.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	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
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	3.9092	0.4567	2884.75	2884.235	7	185.9	30.000002 K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M$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	3.4308	0.2472	2339.93	2341.792	1	335.4	38.636364 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.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	4.0797	0.3443	2344.4	2341.792	1	669.2	34.090908 G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.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	4.0645	0.3721	2693.79	2694.051	1	653.6	41.304348 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	3	5.9365	0.3336	2694.8	2694.051	1	1467.8	40.217392 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	3	6.187	0.4504	2813.51	2816.271	1	1627.8	36.458336 K.TLLEAIDAIEQPSRPTDKPLRLPLQ.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	6.3694	0.3887	2852.09	2850.271	1	1252.3	32.291664 K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.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	3.7103	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
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	3.6803	0.2138	1356.47	1358.581	1	1279.2	85 K.K2L1E1D1H3P1K2F1L1K2S1.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	3.0904	0.3501	1356.91	1358.624	1	574.5	85 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	3.0299	0.3082	1774.11	1777.098	2	390.3	50 T.D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.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	4.114	0.3692	2367.11	2364.704	1	1589.7	42.5 K.TLLEAIDAIEQPSRPTDKPLR.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	2	3.1324	0.1769	2391.87	2393.704	7	204.7	37.5 K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4.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	5.2742	0.4204	3431.87	3432.892	1	509.7	22.5 L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1G1I1G1 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	4.9857	0.4696	3390.29	3391.892	1	793.3	26.666668 L.EAIDAIEQPSRPTDKPLRLPLQDVYKIGGIG.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	4.2764	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
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	4.1566	0.3461	2999.18	3000.435	1	489.2	27.000002 A.I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.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	4.7605	0.364	2964.02	2964.435	1	800.3	33 A.IDAIEQPSRPTDKPLRLPLQDVYKIG.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	3.2734	0.2309	2998.21	3000.435	6	211.8	32 A.I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.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	3.9501	0.1917	3073.85	3072.514	1	523.1	28.846153 E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.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	4.2366	0.3428	3162.2	3164.629	8	443.9	21.296297 L.EAIDAIEQPSRPTDKPLRLPLQDVYKIG.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	4.2346	0.3017	2853.47	2852.235	1	854.6	31 K.KVGYNPKTVPFVPISGWNGDNM@IEAT.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	5.1786	0.372	3357.95	3360.842	4	432.9	20.535715 K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2.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	1	3.2547	0.1906	1256.72	1255.503	5	337.4	66.66667 K.KLEDHPKFLK.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	3.2124	0.2324	2668.27	2669.013	1	239.7	38.095238 F.DELLEKNDRRSGKKLEDHPKFL.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	3.9935	0.2832	2062.01	2060.404	1	808.7	44.11765	D.AIEQPSRPTDKPLRLPLQ.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	4.2001	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
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	2.9613	0.2782	1116.21	1114.306	1	448.5	83.33333	K.T1V1P1F1V1P1I1S1G1W2.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	3.2973	0.179	1654.51	1652.847	2	472	53.571426	K.T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1.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	3.341	0.2141	1897.69	1897.122	1	679.3	53.125	K.T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.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	1	2.2989	0.2496	1241.64	1242.418	8	228.3	45.833336	G.GIGTVPVGRVETG.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	1	2.4328	0.2576	1418.54	1419.663	1	561.9	62.5	V.GYNPKTVPFVPIS.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	3.5468	0.213	1227.23	1226.378	1	515.6	77.77778	A.F1S1E1Y1P1P1L1G1R4F1.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	1	2.6715	0.2625	1115.5	1114.306	1	464.5	66.66667	K.T1V1P1F1V1P1I1S1G1W2.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	3.3383	0.3	2070.53	2071.306	1	461.5	41.666664	K.T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	4.0872	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
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	3.3536	0.1936	1585.91	1586.739	3	1136.9	69.230774	I.D1A1I1E1Q2P1S1R4P1T1D1K2P1L1.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	3.1748	0.1541	969.33	968.145	9	669.3	77.77778	G.G1I1G1T1V1P1V1G1R4V1.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	1	2.7715	0.2082	1434.52	1434.663	1	468.4	62.5	V.G1Y1N2P1K2T1V1P1F1V1P1I1S1.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	3.1022	0.1738	1421.07	1419.663	1	632.3	75	V.GYNPKTVPFVPIS.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	2.5898	0.2265	1369.49	1370.536	1	443.7	59.090908	E.A1F1S1E1Y1P1P1L1G1R4F1A1.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	1	2.4533	0.2659	1517.65	1518.796	1	506.9	57.692307	K.VGYNPKTVPFVPIS.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	3.9019	0.3199	1369.67	1370.536	1	679.1	77.27273	E.A1F1S1E1Y1P1P1L1G1R4F1A1.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	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
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	4.8478	0.3599	2463.21	2463.744	1	681	45.238094	V.G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1.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	3.9895	0.2917	2638.49	2637.928	1	437	36.95652	V.G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	1	2.4312	0.1739	1025.52	1026.169	4	238.3	64.28571	L.E1D1H3P1K2F1L1K2.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	3.2113	0.2449	1469.35	1470.651	1	796.2	66.66667	D.A1I1E1Q2P1S1R4P1T1D1K2P1L1.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	3.8427	0.2281	1771.93	1772.977	3	725	56.666668	E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1.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	3.8495	0.2105	1903.17	1903.093	6	505.2	53.125	L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1.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	4.5781	0.2718	2015.79	2017.252	1	1003.7	58.823532	L.L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1.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	3.2821	0.2095	1664.19	1662.929	1	760.4	60.714287	V.GYNPKTVPFVPISGW.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	3.7546	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
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	3.3115	0.2304	2538.31	2535.877	1	790.3	47.727272	K.VGYNPKTVPFVPISGWNGDNMIE.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	3.484	0.2216	1569.39	1568.816	2	458.5	57.692307	Q.VTVIDAPGHRDFIK.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	2.9101	0.1932	1475.37	1474.713	3	392.6	68.181816	T.D1K2P1L1R4L1P1L1Q2D1V1Y1.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	4.7091	0.2558	2899.67	2900.244	3	582.9	25	L.E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1.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	3.1377	0.2537	1458.49	1458.701	1	575.8	62.5	Y.N2P1K2T1V1P1F1V1P1I1S1G1W2.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	3.8575	0.4059	1330.53	1328.597	1	904.3	81.818184	N.PKTVPFVPISGW.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	3.6065	0.3432	1445.37	1442.701	1	895.1	79.16667	Y.NPKTVPFVPISGW.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	4.1459	0.395	1460.13	1458.701	1	1136.9	87.5	Y.N2P1K2T1V1P1F1V1P1I1S1G1W2.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	3.7279	0.3468	1367.87	1368.578	1	825.9	72.72727	T.VIDAPGHRDFIK.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	3.4493	0.3442	1853.65	1852.967	1	934	62.5	L.NHPGQISAGYSPVLDCH.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	3.5133	0.4181	1632.73	1634.875	1	467.6	57.692307	T.V1I1D1A1P1G1H3R4D1F1I1K2N2M1.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	3	4.6875	0.2234	2942.78	2944.215	1	459.5	30.000002	T.E1V1K2S1V1E1M1H3H3E1Q2L1E1Q2G1V1P1G1D1N2V1G1F1N2V1K2.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	3.9846	0.2794	2908.43	2908.215	3	321.6	25	T.EVKSVEMHHEQLEQGVPGDNVGFNVK.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	4.127	0.3618	2173.79	2175.493	1	862.3	40.27778	I.DAIEQPSRPTDKPLRLPLQ.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	4.2763	0.2971	2073.5	2073.362	2	662.9	41.17647	I.D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.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	4.4029	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
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	5.4851	0.3742	2519.63	2519.847	1	1532.8	41.666664	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	3	5.4458	0.4077	2387.3	2389.716	1	1593.5	42.5	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	2	3.2034	0.2222	2358.15	2360.716	4	312.1	40	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	3.2506	0.2887	1342.85	1342.624	2	347.7	65	D.KPLRLPLQDVY.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	5.6908	0.3514	2602.55	2602.006	1	1941.1	42.045452	L.LEAIDAIEQPSRPTDKPLRLPLQ.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	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
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	5.2719	0.3643	2979.56	2979.403	1	989.7	32	L.LEAIDAIEQPSRPTDKPLRLPLQDVY.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	3.5744	0.3357	1630.25	1629.875	1	571.6	65.38461	T.VIDAPGHRDFIKNM@.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	3.7084	0.3235	1604.37	1604.787	2	322.4	53.846157	V.T1V1I1D1A1P1G1H3R4D1F1I1K2N2.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	3.677	0.2888	1616.37	1613.875	1	602.2	65.38461	T.VIDAPGHRDFIKNM.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	3.7677	0.1897	1852.53	1851.139	1	475.4	56.666668	T.V1I1D1A1P1G1H3R4D1F1I1K2N2M1I1T1.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	4.626	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
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	3.2914	0.2702	2504.27	2505.82	1	534.9	45.238094	E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1.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	3.8468	0.2434	2450.48	2449.735	2	640.1	31.818182	T.VIVLNHPGQISAGYSPVLDCHTA.H
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	4.9638	0.3461	2491.43	2488.847	1	1287.2	40.476192	L.EAIDAIEQPSRPTDKPLRLPLQ.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	4.0906	0.2294	2552.96	2552.89	1	673.1	30.952381	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	4.0403	0.3252	2603.33	2605.952	1	1122.1	32.954548	E.A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1.Y
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	5.5184	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
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	6.3882	0.382	2502.83	2503.875	1	1071.5	38.095238	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	2	3.1988	0.1836	2503.69	2503.875	1	348.4	42.857143	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	5.5356	0.5025	2471.42	2473.875	1	1176.1	40.476192	L.LEAIDAIEQPSRPTDKPLRLPL.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	2	4.3309	0.3587	2865.81	2868.235	2	316.8	30.000002	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	6.2317	0.4111	3089.69	3092.563	1	1334.3	35.576923	T.LLEAIDAIEQPSRPTDKPLRLPLQDVY.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	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
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	3.6	0.4678	1736.89	1736.98	1	813	57.14286	V.T1V1I1D1A1P1G1H3R4D1F1I1K2N2M1.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	3	5.0318	0.3563	2388.11	2389.731	1	2385.2	47.5	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	3	5.1032	0.2993	2185.13	2187.522	1	1409.3	45.833336	A.I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.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	2	3.8734	0.1953	2194.37	2193.615	3	355.4	38.095238	G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1.F
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	3.3912	0.3654	1357.68	1358.624	1	349.3	65	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	4.0793	0.4266	2111.87	2111.529	2	467.4	44.736843	G.T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.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	3.6202	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.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.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	4.804	0.3314	2615.96	2618.035	1	1216.5	37.5	T.L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1.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	2	3.826	0.3899	2692.67	2694.051	1	418	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	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
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	4.8495	0.2993	2232.11	2231.6	1	1163.8	42.105263	E.AIDAIEQPSRPTDKPLRLPL.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	2	3.1582	0.1984	2604.39	2605.98	2	374.9	36.363636	K.T1L1L1E1A1I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1.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	4.6688	0.2268	3105.44	3107.577	1	653.9	28.846153	L.LEAIDAIEQPSRPTDKPLRLPLQDVYK.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	2.9894	0.1816	2438.59	2437.776	9	258	35.714287	K.KVGYNPKTVPFVPISGWNGDNM@.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	4.2842	0.478	2708.67	2710.051	1	699.8	47.826088	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M$I1E1.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	4.3868	0.4121	2340.17	2341.792	1	705.3	35.227272	G.G1I1G1T1V1P1V1G1R4V1E1T1G1V1I1K2P1G1M1V1V1T1F1.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	5.0067	0.3745	2867.93	2868.235	1	1046.4	33	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M1I1E1A1T1.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	4.3298	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
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	3.4033	0.191	1721.23	1723.022	2	407.8	56.666668	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1.W
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	3.1434	0.192	1357.47	1358.624	1	455.7	75	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	3	3.982	0.3582	2367.41	2366.723	1	758.2	36.842106	A.IEQPSRPTDKPLRLPLQDVY.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	4.2434	0.3998	2314.73	2317.583	1	461	45	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2.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	5.3449	0.3343	2884.52	2884.235	1	719.6	31	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M$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	3	4.0402	0.3504	2833.82	2836.235	1	1002.5	33	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	5.1548	0.3839	3279.65	3277.789	1	841.5	28.57143	L.LEAIDAIEQPSRPTDKPLRLPLQDVYKIG.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	3.1715	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
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	4.3145	0.1725	2087.03	2087.404	1	1044.4	45.588234	D.A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.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	2.9031	0.2846	1704.51	1704.022	2	374.5	56.666668	K.KVGYNPKTVPFVPISG.W
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	3.0198	0.2118	1558.99	1559.892	1	492.2	61.538464	K.KVGYNPKTVPFVPI.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	2.5329	0.1636	1576.62	1576.892	1	455.9	57.692307	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1.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	2.3416	0.2468	1558.43	1559.892	1	469	57.692307	K.KVGYNPKTVPFVPI.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	3.8822	0.3135	2464.43	2465.776	2	420.6	35.714287	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2N2G1D1N2M$.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	3	4.0451	0.2939	3002.84	3000.435	1	631.5	29	A.I1D1A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2D1V1Y1K2I1G1.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	3.8445	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
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	3.1986	0.2627	1990.65	1989.326	1	302.6	50	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	3.5142	0.1924	2086.63	2087.404	2	333.1	50	D.A1I1E1Q2P1S1R4P1T1D1K2P1L1R4L1P1L1Q2.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	4.4679	0.3805	2360.03	2360.716	1	1169.2	37.5	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	2	3.7718	0.3777	2420.33	2421.776	1	442.3	40.476192	K.KVGYNPKTVPFVPISGWNGDNM.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	4.6141	0.3818	1914.15	1911.235	1	1213.3	71.875	K.K2V1G1Y1N2P1K2T1V1P1F1V1P1I1S1G1W2.N
gi|6319597|ref|NP_009679.1|	YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	3.6916	0.2002	1992.39	1993.185	1	459.6	50	K.V1D1G1V1D1G1E1V1E1L1D1D1K2L1V1K2I1E1.Q
gi|6319597|ref|NP_009679.1|	YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the 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
gi|6319597|ref|NP_009679.1|	YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	3.2419	0.238	1314.41	1314.487	1	431.2	75	K.FRKDAPKVESH.L
gi|6319597|ref|NP_009679.1|	YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	3	5.9949	0.3533	1927.04	1927.156	1	2359.8	56.666668	V.K2L1D1D1D1V1V1K2E1Y1E1E1I1L1A1K2.I
gi|6319597|ref|NP_009679.1|	YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the 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
gi|6319597|ref|NP_009679.1|	YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	3.5304	0.3832	1910.11	1909.145	1	610.2	53.125	E.H3V1R4E1Y1V1P1S1V1I1E1P1S1F1G1I1G1.R

gi|6319597|ref|NP_009679.1|	YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	2	2.9402	0.2298	1335.29	1332.487	3	431.4	75	K.F1R4K2D1A1P1K2V1E1S1H3.L
gi|6319597|ref|NP_009679.1|	YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the 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
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; 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
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	2	5.44	0.4011	2589.27	2589.841	1	936.5	52.499996	F.K2W2F1G1W2P1G1L1E1I1P1D1D1E1K2D1Q2V1R4K2D1.L
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	2	3.4641	0.2911	2084.11	2085.22	3	224.6	50	L.F1H3Y1H3P1G1E1I1N2F1D1E1N2A1W2L1A1.Y
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	3	5.6977	0.264	2587.61	2589.841	1	1285.8	40	F.K2W2F1G1W2P1G1L1E1I1P1D1D1E1K2D1Q2V1R4K2D1.L
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	3	4.4479	0.3427	3093.56	3096.452	1	470.1	33.333336	K.W2F1G1W2P1G1L1E1I1P1D1D1E1K2D1Q2V1R4K2D1L1L1E1K2F1.N
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	2	4.3991	0.3622	1637.89	1638.69	1	544.2	66.66667	L.F1H3Y1H3P1G1E1I1N2F1D1E1N2.A
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	2	3.5909	0.2589	1897.27	1898.982	1	257.7	50	L.F1H3Y1H3P1G1E1I1N2F1D1E1N2A1W2.L
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	2	3.0248	0.2219	2558.43	2559.841	2	399.8	42.5	F.KWFGWPGLEIPDDEKDQVRKD.L
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; 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
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; 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
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; 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
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	2	4.493	0.3055	2560.37	2559.841	1	763.7	50	F.KWFGWPGLEIPDDEKDQVRKD.L
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	1	2.9071	0.2561	1375.53	1376.47	1	648.5	70	L.FHYHPGEINFD.E
gi|6319602|ref|NP_009684.1|	YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	1	3.3951	0.3505	1391.49	1392.47	1	567.2	65	L.F1H3Y1H3P1G1E1I1N2F1D1.E
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	4.9263	0.4066	2748.57	2749.645	1	672.7	47.727272	L.DEFYDRARDDADEDEEDPDTRSS.G
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.3045	0.2751	1292.19	1290.493	1	706.9	75	L.R4I1P1V1S1E1D1M1L1G1R4.I
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.4094	0.2555	1736.75	1734.067	1	695.3	60.714287	E.SLRIPVSEDMLGRIF.D
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	4.2312	0.3537	1753.87	1755.067	1	766.9	64.28571	E.S1L1R4I1P1V1S1E1D1M1L1G1R4I1F1.D
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.7106	0.2086	1853.91	1855.059	1	264.3	60.714287	A.R4E1E1V1P1G1R4R4G1Y1P1G1Y1M1Y1.T
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.4289	0.1815	1830.49	1831.059	1	262.8	57.14286	A.REEVPGRRGYPGYMY.T
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	3	4.431	0.3003	3229.37	3230.219	1	613.3	29.807693	L.D1E1F1Y1D1R4A1R4D1D1A1D1E1D1E1E1D1P1D1T1R4S1S1G1K2K2K2.D

gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	3	4.0841	0.2257	3189.62	3191.219	1	637.9	31.730768	L.DEFYDRARDDADEDEEDPDTRSSGKKK.D
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	4.0976	0.3331	1795.35	1794.899	1	324.6	60.714287	T.K2D1V1H3D1G1H3E1E1N2F1S1I1V1F1.A
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	2.9413	0.2408	1776.79	1773.899	1	228	53.571426	T.KDVHDGHEENFSIVF.A
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	3	4.7983	0.3677	1472.9	1473.731	1	2522.8	62.5	E.SLRIPVSEDMLGR.I
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	4.2679	0.3051	1492.97	1492.731	1	1056.2	75	E.S1L1R4I1P1V1S1E1D1M1L1G1R4.I
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.3509	0.2608	1473.69	1473.731	1	804.1	66.66667	E.SLRIPVSEDMLGR.I
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.0039	0.1634	1667.65	1667.883	1	254.2	57.692307	A.REEVPGRRGYPGYM.Y
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.5358	0.1573	1689.65	1690.883	2	252.6	53.846157	A.R4E1E1V1P1G1R4R4G1Y1P1G1Y1M1.Y
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.5637	0.2302	1749.33	1750.051	3	470	57.692307	L.EKVKFPRYNEIVNL.T
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.0481	0.2769	1923.11	1921.098	1	343.9	53.125	L.T1M1P1N2D1D1I1T1H3P1I1P1D1L1T1G1Y1.I
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	4.1523	0.3467	2491.67	2491.824	1	827.7	50	T.Q2I1P1I1L1T1M1P1N2D1D1I1T1H3P1I1P1D1L1T1G1Y1.I
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	2	3.9539	0.2959	2466.39	2465.824	1	694.7	47.61905	T.QIPILTMPNDDITHPIPDLTGY.I
gi|6319603|ref|NP_009685.1|	YBR127C	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 cytoplasm; Vma2p	3	4.3959	0.2059	1473.77	1473.731	1	2072.1	52.083332	E.SLRIPVSEDMLGR.I
gi|6319610|ref|NP_009691.1|	YBR133C	Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with 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.S1E1T1A1K2P1D1H3L1D1S1I1N2K2P1M1F1D1L1K2.S
gi|6319610|ref|NP_009691.1|	YBR133C	Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with 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.S1S1H3S1P1E1L1P1S1N2Y1D1Y1V1L1L1P1I1T1T1P1R4Y1K2E1I1V1G1Q2.V
gi|6319610|ref|NP_009691.1|	YBR133C	Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with 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.H3S1P1E1L1P1S1N2Y1D1Y1V1L1L1P1I1T1T1P1R4Y1K2E1I1V1G1Q2.V
gi|6319610|ref|NP_009691.1|	YBR133C	Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with 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.D1Y1V1L1L1P1I1T1T1P1R4Y1K2E1I1V1G1Q2.V
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	4.1039	0.3896	2121.13	2121.292	1	754.1	55.88235	L.N2W2K2P1V1D1I1P1D1T1L1D1D1F1G1G1F1Y1.G
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	3	4.6823	0.288	2646.62	2645.972	1	1589.9	40.476192	L.ILDEADRLLQDGHFDEFEKIIK.H
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	3	5.6108	0.2815	2605.31	2605.642	1	1094.1	37.5	E.S1S1K2L1T1D1P1S1E1D1V1D1E1D1V1D1E1D1V1L1K2E1N2.V
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	4.6601	0.3044	2604.09	2605.642	1	783.7	50	E.S1S1K2L1T1D1P1S1E1D1V1D1E1D1V1D1E1D1V1L1K2E1N2.V
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	4.8795	0.3422	2428.35	2429.485	1	790.6	52.499996	S.K2L1T1D1P1S1E1D1V1D1E1D1V1D1E1D1V1L1K2E1N2.V
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	3.7258	0.3114	1574.57	1576.731	1	913	70.83333	N.W2K2P1V1D1I1P1D1T1L1D1D1F1.G
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	4.1014	0.312	1958.67	1957.116	1	855.4	56.25	L.N2W2K2P1V1D1I1P1D1T1L1D1D1F1G1G1F1.Y
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	3.0727	0.2655	1936.59	1937.116	1	763.2	50	L.NWKPVDIPDTLDDFGGF.Y

gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	4.0662	0.348	2102.07	2100.292	1	674.1	50	L.NWKPVDIPDTLDDFGGFY.G
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	3.3595	0.2397	1840.45	1841.012	2	503.2	50	N.W2K2P1V1D1I1P1D1T1L1D1D1F1G1G1F1.Y
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	2	4.3637	0.3767	2006.29	2005.188	1	807.5	56.25	N.W2K2P1V1D1I1P1D1T1L1D1D1F1G1G1F1Y1.G
gi|6319618|ref|NP_009700.1|	YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for 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.I1S1L1V1I1P1P1K2G1Q2I1P1L1Y1Q2K2.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.F1K2D1A1E1D1N2E1V1I1K2F1.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.F1K2D1A1E1D1N2E1V1I1K2F1.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	3.3278	0.2486	1686.39	1685.045	1	430	53.571426	M.I1S1L1V1I1P1P1K2G1Q2I1P1L1Y1Q2.K
gi|6319635|ref|NP_009717.1|	YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	2	4.4153	0.3014	1833.55	1833.092	2	697.3	64.28571	V.PFLETEEKELRNIIT.I
gi|6319635|ref|NP_009717.1|	YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	2	4.0706	0.3124	2030.63	2029.341	1	664.7	56.25	I.PVPFLETEEKELRNIIT.I
gi|6319635|ref|NP_009717.1|	YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	2	3.7973	0.3529	2228.67	2229.579	1	460.8	50	H.SIPVPFLETEEKELRNIIT.I
gi|6319635|ref|NP_009717.1|	YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	2	4.3989	0.3027	2282.57	2281.604	1	317.4	44.444447	I.P1V1P1F1L1E1T1E1E1K2E1L1R4N2I1I1T1I1N2.N
gi|6319635|ref|NP_009717.1|	YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	2	4.2436	0.3089	2257.61	2256.604	1	434.6	47.22222	I.PVPFLETEEKELRNIITIN.N
gi|6319635|ref|NP_009717.1|	YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	2	3.0367	0.3484	1590.39	1589.792	1	171.6	62.5	L.QKELEDQHHVVVK.I
gi|6319635|ref|NP_009717.1|	YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	2	2.9947	0.2348	2059.21	2060.355	1	474.3	50	V.PFLETEEKELRNIITIN.N
gi|6319635|ref|NP_009717.1|	YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	2	3.387	0.2828	2254.21	2253.579	1	248.8	41.666664	H.S1I1P1V1P1F1L1E1T1E1E1K2E1L1R4N2I1I1T1.I
gi|6319636|ref|NP_009718.1|	YBR160W	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 specific substrates; Cdc28p	2	3.7384	0.1958	1407.43	1406.64	7	867.6	72.72727	L.W2Y1R4A1P1E1V1L1L1G1G1K2.Q
gi|6319636|ref|NP_009718.1|	YBR160W	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 specific substrates; Cdc28p	3	4.9115	0.2243	3001.22	3001.455	1	424.4	25	F.RVLGTPNEAIWPDIVYLPDFKPSFPQ.W
gi|6319636|ref|NP_009718.1|	YBR160W	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 specific substrates; Cdc28p	2	5.1629	0.4499	3033.61	3034.455	1	887.8	40	F.R4V1L1G1T1P1N2E1A1I1W2P1D1I1V1Y1L1P1D1F1K2P1S1F1P1Q2.W
gi|6319636|ref|NP_009718.1|	YBR160W	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 specific substrates; Cdc28p	2	4.593	0.3163	2999.71	3001.455	1	839.8	42	F.RVLGTPNEAIWPDIVYLPDFKPSFPQ.W
gi|6319636|ref|NP_009718.1|	YBR160W	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 specific substrates; Cdc28p	2	4.1193	0.3319	2658.35	2659.975	1	661.8	38.636364	L.G1T1P1N2E1A1I1W2P1D1I1V1Y1L1P1D1F1K2P1S1F1P1Q2.W
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	3.9569	0.4629	1742.75	1744.899	1	989.2	63.333332	N.SRDDPVVGPDQPYSIV.E
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	3.7747	0.3453	1716.23	1718.771	1	484.9	57.692307	K.D1N2K2E1Q2V1D1F1D1E1F1A1N2K2.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	1	2.9473	0.2509	1425.47	1426.554	9	209.6	50	T.R4E1F1D1E1V1Y1T1A1P1A1L1.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	3.2166	0.2937	1826.43	1827.003	1	1132.4	63.333332	T.REFDEVYTAPALGFPN.A
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	6.2713	0.2512	2273.39	2271.566	1	1936.5	50	K.D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1H3.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	4.8721	0.2689	2401.88	2401.74	1	736.9	32.894737	L.K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1H3.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	3.2943	0.1779	2262.17	2261.599	6	295.3	44.444447	L.K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1.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	4.3499	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.Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1H3.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.R4E1V1D1L1P1L1V1V1I1L1H3.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	3.5373	0.353	1402.95	1403.708	1	1142.2	77.27273	L.REVDLPLVVILH.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	5.1384	0.305	2653.43	2651.075	1	1477	39.285713	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	2	3.2975	0.3011	2214.41	2217.405	1	329.5	58.823532	K.L1H3L1K2D1N2K2E1Q2V1D1F1D1E1F1A1N2K2.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	3.2594	0.1886	2678.07	2680.075	2	402.1	35.714287	R.Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1H3.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	5.4477	0.4783	1964.63	1967.141	1	2148.4	80	K.K2F1D1K2D1E1K2A1T1H3P1E1G1W2P1R4.L
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	3.8508	0.3814	1509.14	1508.732	1	1021.9	52.272724	A.D1F1S1K2K2F1P1V1F1Y1G1R4.E
gi|6319655|ref|NP_009736.1|	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	1	3.9821	0.3168	1508.65	1508.732	1	279.5	59.090908	A.D1F1S1K2K2F1P1V1F1Y1G1R4.E
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	3.4729	0.1903	2512.35	2513.934	1	480.7	45	R.YLKDNELEELREVDLPLVVIL.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	4.4305	0.2786	1404.14	1403.708	1	2716.8	65.909096	L.REVDLPLVVILH.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	3.1638	0.1659	2650.87	2651.075	4	356.6	33.333336	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	2	4.1512	0.3155	2678.55	2680.075	1	781.3	47.61905	R.Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1H3.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	4.6	0.301	1420.55	1420.708	1	2632.4	65.909096	L.R4E1V1D1L1P1L1V1V1I1L1H3.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	4.5075	0.385	2149.25	2149.36	1	737.4	52.63158	L.G1V1P1N2G1S1L1P1D1H3P1P1T1V1K2N2P1S1F1Y1.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	3	3.984	0.231	2679.44	2680.075	1	1132.2	30.952381	R.Y1L1K2D1N2E1L1E1E1L1R4E1V1D1L1P1L1V1V1I1L1H3.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	4.2571	0.3769	1508.57	1508.732	1	994.8	52.272724	A.D1F1S1K2K2F1P1V1F1Y1G1R4.E
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	3.982	0.3401	1491.14	1491.732	1	742.7	50	A.DFSKKFPVFYGR.E
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	4.3872	0.2955	1510.29	1508.732	1	711.7	77.27273	A.D1F1S1K2K2F1P1V1F1Y1G1R4.E
gi|6319655|ref|NP_009736.1|	YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	1	2.5983	0.2334	1490.73	1491.732	1	245.7	54.545456	A.DFSKKFPVFYGR.E
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	4.1345	0.3479	1766.63	1764.899	1	979.3	63.333332	N.S1R4D1D1P1V1V1G1P1D1Q2P1Y1S1I1V1.E
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	3.5968	0.3168	1941.85	1942.141	1	460.8	56.666668	K.KFDKDEKATHPEGWPR.L
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	3.0442	0.3386	1260.54	1260.435	1	732	70	E.KHIDFAPTSPF.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	3.1182	0.2013	2274.63	2274.542	5	168.5	38.88889	A.ARDLLTRDEKDPKRLFEGN.A
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	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 (40S) 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
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	4.0695	0.3184	1608.21	1608.717	1	835.2	65.38461	L.D1S1E1K2H3I1D1F1A1P1T1S1P1F1.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	1	3.1047	0.3386	1274.62	1274.435	1	618.3	70	E.K2H3I1D1F1A1P1T1S1P1F1.G
gi|6319673|ref|NP_009755.1|	YBR196C	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression 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
gi|6319673|ref|NP_009755.1|	YBR196C	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation; Pgi1p	2	3.3293	0.2755	1715.17	1714.913	3	502.1	67.85714	N.H3F1T1Q2T1P1L1E1D1N2I1P1L1L1G1.G
gi|6319673|ref|NP_009755.1|	YBR196C	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression 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
gi|6319673|ref|NP_009755.1|	YBR196C	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation; Pgi1p	2	3.005	0.2896	1361.07	1363.526	1	457.9	63.636364	L.MVGKDEEQVKAE.G

gi|6319673|ref|NP_009755.1|	YBR196C	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of 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	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of 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
gi|6319673|ref|NP_009755.1|	YBR196C	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation; Pgi1p	2	3.8987	0.3371	1552.35	1551.745	1	1197.6	86.36364	F.DQYLHRFPAYLQ.Q
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	3.3959	0.3366	2517.09	2518.866	1	350	35.714287	N.SVPVKLGPFPKDEEFVKEIETE.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	3	3.8961	0.3168	2355.35	2355.656	1	704.3	39.473686	V.P1V1K2L1G1P1F1P1K2D1E1E1F1V1K2E1I1E1T1E1.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	3.5983	0.2349	2400.45	2401.74	9	295.5	47.368423	L.G1P1F1P1K2D1E1E1F1V1K2E1I1E1T1E1L1K2I1K2.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	3	5.0992	0.2683	2401.07	2401.74	2	843.1	36.842106	L.G1P1F1P1K2D1E1E1F1V1K2E1I1E1T1E1L1K2I1K2.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	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
gi|6319676|ref|NP_009758.1|	YBR199W	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr4p	3	4.87	0.2795	3368.24	3368.719	1	708.2	25	Y.T1F1L1N2D1E1E1F1T1D1E1F1K2D1G1I1K2S1I1L1P1K2D1R4V1V1E1F1.G
gi|6319676|ref|NP_009758.1|	YBR199W	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr4p	2	3.4851	0.3418	2165.23	2164.419	1	845.5	56.25	N.FEIVDLDFLRSEPYEKY.M
gi|6319676|ref|NP_009758.1|	YBR199W	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr4p	2	3.7497	0.3246	2067.35	2069.198	1	847.9	59.375	Y.T1F1L1N2D1E1E1F1T1D1E1F1K2D1G1I1K2.S
gi|6319679|ref|NP_009761.1|	YBR202W	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 promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	3.9495	0.1828	2457.01	2458.687	1	497.7	47.5	M.NDALREVVEDETELFPPNLTR.R
gi|6319679|ref|NP_009761.1|	YBR202W	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 promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	3.8077	0.3192	2486.41	2487.687	1	443.2	45	M.N2D1A1L1R4E1V1V1E1D1E1T1E1L1F1P1P1N2L1T1R4.R
gi|6319679|ref|NP_009761.1|	YBR202W	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 promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	3.3036	0.3198	2070.45	2073.369	1	720.6	47.058823	L.RLADMVDIDDVEEALRLV.R
gi|6319679|ref|NP_009761.1|	YBR202W	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 promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	4.0612	0.3597	2164.57	2162.404	1	793.5	52.941177	A.NRELNSVIIDLDDILQYQ.N
gi|6319679|ref|NP_009761.1|	YBR202W	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 promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	3.2989	0.2057	2333.65	2332.714	1	426.3	42.105263	N.NMPLPTKEIDYKDDVLDVIL.N
gi|6319679|ref|NP_009761.1|	YBR202W	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 promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	3.4154	0.1785	2701.17	2702.066	3	297.2	34.090908	A.I1D1N2N2M1P1L1P1T1K2E1I1D1Y1K2D1D1V1L1D1V1I1L1.N
gi|6319679|ref|NP_009761.1|	YBR202W	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 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
gi|6319679|ref|NP_009761.1|	YBR202W	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 promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	2	3.8348	0.3036	2772.47	2774.145	2	348.6	34.782608	R.A1I1D1N2N2M1P1L1P1T1K2E1I1D1Y1K2D1D1V1L1D1V1I1L1.N
gi|6319679|ref|NP_009761.1|	YBR202W	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 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.AIDNNMPLPTKEIDYKDDVLDVIL.N
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	1	2.4651	0.3012	1580.61	1581.766	1	270.7	50	L.SVSEYERTIPTLW.E
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	2.9284	0.2064	1545.25	1544.602	1	700.9	68.181816	D.A1Y1R4E1Y1F1D1Y1L1D1S1S1.G
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	1	2.8549	0.19	1529.49	1529.602	1	229.3	50	D.AYREYFDYLDSS.G
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	5.9037	0.409	2296.51	2297.578	1	1254.9	62.5	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	3.6567	0.2336	1709.49	1710.001	1	909.4	63.333332	Q.GVIHPVDDGKKEKGVM.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	3.3122	0.3453	1799.83	1800.934	1	430.6	53.571426	L.GFHHPDFTSCPIEQK.I
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	3.8325	0.4286	1819.33	1821.934	1	359.9	50	L.G1F1H3H3P1D1F1T1S1C1P1I1E1Q2K2.I
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	3.5455	0.2798	1700.19	1700.935	1	408.9	57.14286	K.AKYGTIPKDHWSIPS.W
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	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

gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	2.9507	0.3037	2820.49	2822.13	1	333.2	28	T.G1A1D1V1P1T1P1Y1A1K2E1L1E1D1F1A1F1P1D1T1P1T1I1V1K2A1.V
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.5786	0.2927	2597.49	2594.921	1	1122	47.727272	A.DVPTPYAKELEDFAFPDTPTIVK.A
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.3472	0.2878	2677.61	2679.004	1	377.2	34.782608	Q.HSQDFSPWYGSIPGLKVLVPYSAE.D
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.6009	0.2242	1345.65	1346.714	1	679.9	59.090908	A.ALKGLKPIVEFM.S
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	2.9121	0.3059	1644.65	1645.056	2	511	50	L.AVGAALKGLKPIVEFM.S
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.3916	0.3152	1359.65	1360.714	1	948.5	72.72727	A.A1L1K2G1L1K2P1I1V1E1F1M1.S
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.7723	0.2213	1346.71	1346.714	1	760.3	63.636364	A.ALKGLKPIVEFM.S
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.484	0.1604	1535.56	1536.635	7	125	50	E.ELDRDDDVFLIGE.E
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.6576	0.162	1193.57	1193.342	1	228.4	61.11111	R.RVVDTPITEY.G
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.9932	0.3222	2213.51	2213.473	1	726.9	47.22222	A.A1I1R4D1P1N2P1V1V1F1L1E1N2E1L1L1Y1G1E1.S
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	1	2.6493	0.1571	1162.59	1162.476	1	1053.3	72.22222	L.KGLKPIVEFM.S
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.2938	0.288	1346.51	1346.714	1	1067.8	72.72727	A.ALKGLKPIVEFM.S
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	2	3.5558	0.3464	1359.75	1360.714	1	1004.2	72.72727	A.A1L1K2G1L1K2P1I1V1E1F1M1.S
gi|6319698|ref|NP_009780.1|	YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an 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
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.6592	0.3783	1571.93	1572.857	2	653.6	60.714287	R.GGEKISPIELDGIML.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	1	2.9423	0.2855	1572.7	1572.857	2	515.7	50	R.GGEKISPIELDGIML.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.5997	0.4161	2043.79	2045.302	1	499.7	46.875	K.IGAPLNPNYKEKEFNFY.L
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.4347	0.4488	1955.87	1956.308	1	654.2	52.941177	L.INRGGEKISPIELDGIML.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.2569	0.3487	1749.53	1749.045	1	607.8	53.333336	N.R4G1G1E1K2I1S1P1I1E1L1D1G1I1M1L1.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.3924	0.2307	1790.35	1789.041	1	819.2	64.28571	F.HKLEKEFNAPVLEAY.A
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.6364	0.257	1650.57	1651.002	4	605	73.07692	Y.K2L1T1P1L1D1R4S1Y1V1V1M1P1L1.F
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	4.6768	0.3451	1613.85	1614.856	1	801.3	73.07692	K.F1V1N2T1N2P1V1K2F1P1G1F1A1R4.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.8554	0.3362	2224.11	2223.583	1	454.5	44.736843	K.E1L1I1N2R4G1G1E1K2I1S1P1I1E1L1D1G1I1M1L1.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.362	0.1703	2197.53	2198.583	1	438.3	44.736843	K.ELINRGGEKISPIELDGIML.S

gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	4.2473	0.3633	2385.61	2385.643	1	389.6	44.736843 M.D1A1K2I1G1A1P1L1N2P1N2Y1K2E1K2E1F1N2F1Y1.L
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	4.8774	0.3849	2358.81	2359.643	1	995.9	57.894737 M.DAKIGAPLNPNYKEKEFNFY.L
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.2079	0.1989	1977.99	1979.308	3	287.9	41.17647 L.I1N2R4G1G1E1K2I1S1P1I1E1L1D1G1I1M1L1.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	2.9209	0.2519	1809.55	1809.041	1	489.3	53.571426 F.H3K2L1E1K2E1F1N2A1P1V1L1E1A1Y1.A
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	3.4615	0.2235	1701.85	1702.935	1	684.3	64.28571 K.F1V1N2T1N2P1V1K2F1P1G1F1A1R4S1.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	2	4.4564	0.3943	1596.77	1594.856	1	1101.5	76.92308 K.FVNTNPVKFPGFAR.S
gi|6319699|ref|NP_009781.1|	YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral 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.I1G1A1P1L1N2P1N2Y1K2E1K2E1F1N2F1Y1.L
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	2	4.1816	0.2302	1987.03	1987.211	1	426.9	52.941177 E.A1N2S1P1R4P1V1I1S1D1P1L1D1E1I1D1I1L1.L
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	2	4.0725	0.3165	2566.39	2567.656	1	616.6	52.499996 A.K2E1Q2Q2D1E1I1E1G1E1E1L1A1E1S1E1R4N2K2Q2F1.E
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	2	4.8358	0.4168	2537.83	2537.656	1	1078.1	52.499996 A.KEQQDEIEGEELAESERNKQF.E
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	3	4.3558	0.3496	2608.73	2608.735	1	1250.9	40.476192 L.AKEQQDEIEGEELAESERNKQF.E
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	1	2.7498	0.3398	1261.73	1262.494	1	190	60.000004 L.RLPFSPPTTVF.I
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	1	2.7695	0.3445	1275.49	1276.494	2	156	55 L.R4L1P1F1S1P1P1T1T1V1F1.I
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	1	2.9938	0.2279	1487.7	1488.813	1	491.7	66.66667 Y.LLRLPFSPPTTVF.I
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	1	2.9607	0.1714	1505.66	1504.813	1	337.8	58.333332 Y.L1L1R4L1P1F1S1P1P1T1T1V1F1.I
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	2	2.9785	0.2841	1502.65	1504.813	1	465.9	66.66667 Y.L1L1R4L1P1F1S1P1P1T1T1V1F1.I
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	2	4.5997	0.4314	2271.55	2271.453	1	1267.1	58.823532 L.RNWQDVIYVTNPEEWSPH.V
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	2	3.5931	0.2368	1504.99	1504.813	1	395.4	62.5 Y.L1L1R4L1P1F1S1P1P1T1T1V1F1.I
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	1	2.8989	0.3211	1503.73	1504.813	1	295.6	54.166668 Y.L1L1R4L1P1F1S1P1P1T1T1V1F1.I
gi|6319724|ref|NP_009806.1|	YBR247C	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 nucleolus; Enp1p	1	2.8148	0.1546	1487.78	1488.813	1	327.9	54.166668 Y.LLRLPFSPPTTVF.I
gi|6319724|ref|NP_009806.1|	YBR247C	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 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|	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	3	5.4939	0.4017	2306.21	2307.613	1	977.9	45.833336 S.RNVEFAPPYLDDFTKIHPF.W
gi|6319728|ref|NP_009810.1|	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	2	3.2443	0.2999	2332.91	2333.613	1	469.1	41.666664 S.R4N2V1E1F1A1P1P1Y1L1D1D1F1T1K2I1H3P1F1.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	41.666664 S.R4N2V1E1F1A1P1P1Y1L1D1D1F1T1K2I1H3P1F1.W
gi|6319728|ref|NP_009810.1|	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	3	5.7573	0.3948	2306.96	2307.613	1	1179.5	50 S.RNVEFAPPYLDDFTKIHPF.W
gi|6319728|ref|NP_009810.1|	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	3	6.0847	0.2964	3213.02	3213.58	1	1359.5	31.896553 F.RWDQVQQPLPGEGNILPPGVSLPNDGGRKS.K
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 F.R4W2D1Q2V1Q2Q2P1L1P1G1E1G1N2I1L1P1P1G1V1S1L1P1N2D1G1G1R4K2S 1.K
gi|6319728|ref|NP_009810.1|	YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	3	4.7056	0.333	3125.9	3126.502	1	907.2	28.57143 F.RWDQVQQPLPGEGNILPPGVSLPNDGGRK.S
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	3.1243	0.2431	1641.67	1640.833	2	344	57.692307 K.A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.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	4.2079	0.4302	2404.59	2403.783	1	1215.1	50 F.AQFPLVGLPKATTPNVNDPIYF.L
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	3	3.822	0.1635	3417.41	3415.048	1	379.1	23.214285 I.D1I1V1K2P1I1L1P1I1L1P1E1V1E1L1P1F1E1K2L1P1F1D1D1K2I1V1Y1T1.I
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	3	4.9574	0.3166	3310.61	3312.943	1	538.9	27.777779 I.D1I1V1K2P1I1L1P1I1L1P1E1V1E1L1P1F1E1K2L1P1F1D1D1K2I1V1Y1.T
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	3	5.5991	0.3264	3494.75	3496.208	1	630.1	26.724138 L.IDIVKPILPILPEVELPFEKLPFDDKIVYT.I
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	3	5.8844	0.3141	3527.06	3529.208	1	510.2	25 L.I1D1I1V1K2P1I1L1P1I1L1P1E1V1E1L1P1F1E1K2L1P1F1D1D1K2I1V1Y1T1.I
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	3	4.7255	0.1793	3424.19	3427.103	1	673.7	25 L.I1D1I1V1K2P1I1L1P1I1L1P1E1V1E1L1P1F1E1K2L1P1F1D1D1K2I1V1Y1.T
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	3	5.0218	0.2751	3392.81	3395.103	1	503.5	24.107143 L.IDIVKPILPILPEVELPFEKLPFDDKIVY.T
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	3.467	0.3041	2016.39	2017.335	1	669.3	44.11765 V.GLPKATTPNVNDPIYFLR.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	3.9201	0.4321	2325.03	2326.744	1	824.6	52.499996	F.PLVGLPKATTPNVNDPIYFLR.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	3.6554	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
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	3	4.4646	0.3407	2354.33	2353.744	1	1582.2	41.25	F.P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.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	3.0555	0.1741	2354.05	2353.744	3	367.5	35	F.P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.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	3.4046	0.2856	2502.47	2501.921	1	652.2	45.238094	Q.F1P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.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	4.0349	0.2532	2672.71	2673.13	1	660.2	45.652176	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	4.5397	0.3865	2702.15	2704.13	1	834.3	50	F.A1Q2F1P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1L1R4.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	3	3.9358	0.3624	2602.61	2602.051	1	1356.2	39.772728	A.QFPLVGLPKATTPNVNDPIYFLR.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	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
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	4.3211	0.3893	2517.69	2516.943	1	929.6	47.727272	F.AQFPLVGLPKATTPNVNDPIYFL.R
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	3.3605	0.3126	2470.89	2471.864	1	412	40.476192	A.Q2F1P1L1V1G1L1P1K2A1T1T1P1N2V1N2D1P1I1Y1F1L1.R
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	3.0699	0.201	1819.83	1818.293	3	432	50	D.IVKPILPILPEVELPF.E
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	3.7927	0.222	1835.05	1835.293	2	570.5	53.333336	D.I1V1K2P1I1L1P1I1L1P1E1V1E1L1P1F1.E
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	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
gi|6319764|ref|NP_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	28.90625	L.L1E1R4T1P1N2I1D1N2E1E1L1V1N2E1E1Q2E1E1Q2E1L1L1E1E1E1N2N2R4M1N 2S1S1.F
gi|6319764|ref|NP_009846.1|	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	3	7.4142	0.4261	4003.13	4002.223	1	1969.1	31.25	Q.SLLERTPNIDNEELVNEEQEEQELLEEENNRMN.S
gi|6319764|ref|NP_009846.1|	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	3	9.0824	0.5641	4047.26	4049.223	1	2872	35.9375	Q.S1L1L1E1R4T1P1N2I1D1N2E1E1L1V1N2E1E1Q2E1E1Q2E1L1L1E1E1E1N2N2F 4M1N2.S
gi|6319764|ref|NP_009846.1|	YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	3	8.1961	0.5575	4222.7	4225.38	1	1660	28.676472	Q.S1L1L1E1R4T1P1N2I1D1N2E1E1L1V1N2E1E1Q2E1E1Q2E1L1L1E1E1E1N2N2F 4M1N2S1S1.F
gi|6319771|ref|NP_009853.1|	YBR294W	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates; Sul1p	1	3.1464	0.362	1419.48	1420.596	1	892.5	70	F.F1H3I1D1I1P1D1F1S1K2W2.D
gi|6319771|ref|NP_009853.1|	YBR294W	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate 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
gi|6319771|ref|NP_009853.1|	YBR294W	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates; Sul1p	1	3.1254	0.3415	1419.54	1420.596	1	870.1	70	F.F1H3I1D1I1P1D1F1S1K2W2.D
gi|6319771|ref|NP_009853.1|	YBR294W	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates; Sul1p	2	3.6948	0.2951	1423.29	1420.596	1	1442	85	F.F1H3I1D1I1P1D1F1S1K2W2.D
gi|6319771|ref|NP_009853.1|	YBR294W	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate 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
gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	2	4.4998	0.4174	1852.55	1852.057	1	989	62.5	H.ATRPPLPTLDTPSWNAN.S
gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	2	3.0938	0.3268	1780.03	1780.978	1	499.8	50	A.TRPPLPTLDTPSWNAN.S
gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	2	3.8483	0.4244	1804.21	1802.978	1	603.8	53.333336	A.T1R4P1P1L1P1T1L1D1T1P1S1W2N2A1N2.S
gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	1	2.403	0.1635	1549.63	1550.767	7	151	54.166668	Q.A1R4R4Q2I1E1D1L1V1P1V1Y1A1.V
gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	1	2.3675	0.1899	1530.74	1530.767	2	84.7	41.666664	Q.ARRQIEDLVPVYA.V
gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	1	3.0507	0.2224	1351.48	1352.475	1	372.8	60.000004	L.K2H3E1H3L1N2D1I1T1N2L1.T
gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	2	3.498	0.2048	1351.37	1352.475	1	778	85	L.K2H3E1H3L1N2D1I1T1N2L1.T
gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	2	4.788	0.4082	1873.69	1875.057	1	830	59.375	H.A1T1R4P1P1L1P1T1L1D1T1P1S1W2N2A1N2.S

gi|6319837|ref|NP_009918.1|	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	1	2.599	0.2996	1387.47	1388.61	7	116.9	55	A.RRQIEDLVPVY.A
gi|10383772|ref|NP_009911.2|	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway; Leu2p	2	3.2333	0.1627	1333.29	1332.53	1	748	75	L.Q2H3E1P1P1L1P1I1W2S1L1.D
gi|10383772|ref|NP_009911.2|	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway; Leu2p	2	3.5458	0.1566	1625.59	1624.875	1	651	57.14286	K.K2I1V1V1L1P1G1D1H3V1G1Q2E1I1T1.A
gi|10383772|ref|NP_009911.2|	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway; Leu2p	2	4.1479	0.4695	1781.61	1783.003	1	471.6	46.875	C.H3G1S1A1P1D1L1P1K2N2K2V1N2P1I1A1T1.I
gi|10383772|ref|NP_009911.2|	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway; Leu2p	2	4.2238	0.2529	1993.47	1993.235	1	834.7	55.263157	L.G1A1V1G1G1P1K2W2G1T1G1S1V1R4P1E1Q2G1L1L1.K
gi|10383772|ref|NP_009911.2|	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway; Leu2p	2	5.0335	0.4096	2335.33	2336.55	1	754.8	50	L.Y1E1P1C1H3G1S1A1P1D1L1P1K2N2K2V1N2P1I1A1T1.I
gi|10383772|ref|NP_009911.2|	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine 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	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway; Leu2p	1	2.5577	0.2839	1437.75	1438.695	2	491.4	50	L.V1K2N2P1T1H3L1N2G1I1I1I1T1.S
gi|10383772|ref|NP_009911.2|	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine 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
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, 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.KLSNPVLNAPFPEEYFEGL.T
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; 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
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; 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.F1V1G1Q2P1K2A1E1E1E1K2L1T1G1P1I1H3L1D1V1V1.K
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	2	4.0944	0.332	1902.63	1903.111	1	503.3	53.125	M.H3L1V1N2P1I1I1E1N2V1R4D1K2G1N2S1A1.L
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, 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
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; 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
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; 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
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; 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
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, 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
gi|10383761|ref|NP_009900.2|	YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	2	3.6468	0.3409	1847.65	1849.162	1	563.8	56.25	E.T1I1P1K2V1D1K2I1L1G1P1G1N2Q2F1V1T1.A
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	3.0238	0.2183	1570.13	1570.607	1	697.6	65.38461	D.AELADEEDAIHDEL.-
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	3.0133	0.1731	1585.95	1586.607	1	524.4	57.692307	D.A1E1L1A1D1E1E1D1A1I1H3D1E1L1.-
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	3	3.9854	0.2555	2730.47	2728.75	1	931.8	35.416664	A.QEKAAEEADADAELADEEDAIHDEL.-
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	3	4.9146	0.4248	3254.81	3254.236	1	752.8	28.57143	L.Y1E1E1A1Q2E1K2A1A1E1E1A1D1A1D1A1E1L1A1D1E1E1D1A1I1H3D1E1L1.-
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	3.3507	0.2192	2129.81	2130.346	1	665.9	50	T.ENQDLCMEHNIPGFPSLK.I
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	3.0599	0.2538	2882.73	2880.174	1	386.7	34.782608	Q.IDCTENQDLCMEHNIPGFPSLKIF.K
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	4.3387	0.4384	2391.67	2390.682	1	751	52.63158	T.ENQDLCMEHNIPGFPSLKIF.K
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	3.016	0.196	1648.35	1648.945	2	356.4	46.153847	C.M1E1H3N2I1P1G1F1P1S1L1K2I1F1.K
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	3.347	0.2509	1500.89	1499.753	4	365.8	62.5	M.EHNIPGFPSLKIF.K
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	1	2.9162	0.2426	1499.62	1499.753	1	255.8	58.333332	M.EHNIPGFPSLKIF.K

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	3.3609	0.2445	1633.49	1630.945	1	832.3	69.230774 C.MEHNIPGFPSLKIF.K
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	1	2.392	0.2417	1369.63	1370.637	1	478.3	68.181816 E.HNIPGFPSLKIF.K
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	3.0951	0.2242	1818.59	1818.931	1	660.8	57.692307 L.FYNDEEELEEYKPL.F
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	1	2.5044	0.1847	1153.56	1154.369	1	617.6	75 L.NMKEQFPLF.A
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	3.9405	0.376	2343.81	2343.33	1	418.3	45.238094 K.AAEEADADAELADEEDAIHDEL.-
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	3.4155	0.4049	2727.71	2728.75	1	525.6	39.583336 A.QEKAAEEADADAELADEEDAIHDEL.-
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	3.2914	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
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	3.4629	0.3497	2414.99	2416.682	1	460.9	39.473686 T.E1N2Q2D1L1C1M1E1H3N2I1P1G1F1P1S1L1K2I1F1.K
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	2.9572	0.2267	2034.03	2034.32	2	460.4	50 V.GKNHDEIVNDPKKDVLVL.Y
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	3.0044	0.2427	1386.97	1386.637	1	1184.7	77.27273 E.H3N2I1P1G1F1P1S1L1K2I1F1.K
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	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.E1H3K2D1S1P1D1F1R4F1P1M1D1I1V1F1G1E1Y1.W
gi|6319804|ref|NP_009884.1|	YCL045C	hypothetical protein; Ycl045cp	2	3.1959	0.3864	2331.51	2330.576	1	432.5	44.444447 Q.EHKDSPDFRFPMDIVFGEY.W
gi|6319804|ref|NP_009884.1|	YCL045C	hypothetical protein; Ycl045cp	1	2.5919	0.2192	1308.34	1309.467	6	309.3	65 L.KENQFSPGRVF.T
gi|6319804|ref|NP_009884.1|	YCL045C	hypothetical protein; Ycl045cp	2	4.0578	0.2903	2578.47	2580.019	1	714.6	45.238094 K.K2K2E1F1M1A1T1P1Y1T1P1V1I1P1I1N2D1N2F1I1I1T1.H
gi|6319804|ref|NP_009884.1|	YCL045C	hypothetical protein; Ycl045cp	1	2.5855	0.2112	1370.5	1371.495	1	244.2	59.090908 T.HFRNLLPGSDSQ.L
gi|6319804|ref|NP_009884.1|	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|	YCL045C	hypothetical protein; Ycl045cp	2	3.5176	0.3011	1505.79	1506.676	1	389.4	68.181816 Q.EHKDSPDFRFPM.D
gi|6319804|ref|NP_009884.1|	YCL045C	hypothetical protein; Ycl045cp	2	3.5535	0.2279	2570.83	2571.836	1	440.5	38.636364 T.H3F1R4N2L1L1P1G1S1D1S1Q2L1I1S1I1P1T1N2L1E1S1T1.S
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	2	3.9999	0.3188	1816.11	1818.053	2	1137.1	67.85714 K.I1T1E1K2P1E1L1I1N2D1I1L1L1E1C1.G
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	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	19.594595 S.H3M1P1S1L1I1E1K2P1E1R4G1Q2T1P1E1G1E1D1P1L1G1K2P1E1E1E1L1T1V1I 1P1E1F1G1G1A1D1.N
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	5.0161	0.4158	4060.61	4061.469	1	560.1	25 S.H3M1P1S1L1I1E1K2P1E1R4G1Q2T1P1E1G1E1D1P1L1G1K2P1E1E1E1L1T1V1I 1P1E1F1G1G1A1.D
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	1	2.6312	0.2741	1293.6	1294.58	1	691.3	65 N.KFPVIPEHTLL.V
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	1	3.3106	0.2577	1537.66	1538.843	1	515.4	58.333332 L.L1N2K2F1P1V1I1P1E1H3T1L1L1.V
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	2	3.2976	0.2728	1520.83	1521.843	7	696.2	62.5 L.LNKFPVIPEHTLL.V
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	4.2483	0.2727	3565.43	3563.94	1	488.7	27.34375 S.LIEKPERGQTPEGEDPLGKPEEELTVIPEFGGA.D
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	4.591	0.4279	4075.4	4077.469	1	399.7	20.833332 S.H3M$P1S1L1I1E1K2P1E1R4G1Q2T1P1E1G1E1D1P1L1G1K2P1E1E1E1L1T1V1I 1P1E1F1G1G1A1.D
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	3.3464	0.3769	2382.53	2383.712	2	288.8	32.5 K.V1Y1T1P1F1P1P1A1Q2L1P1R4K2V1D1L1E1I1E1S1G1.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	3.3539	0.3822	2211.97	2213.582	1	584.3	47.22222 K.VYTPFPPAQLPRKVDLEIE.S
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	3.069	0.2413	1803.95	1804.913	1	484.9	65.38461 H.NRDKPWDTDDIDKW.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	2.9342	0.2471	1712.41	1710.809	2	652	62.5 N.R4D1K2P1W2D1T1D1D1I1D1K2W2.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

gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	3.3689	0.1658	933.15	933.108	1	1379.8	92.85714	L.PDEVLTKM.N
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	1	2.5797	0.2931	1442.6	1443.648	1	288.9	58.333332	F.GVPTRFGNLPAQW.S
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	1	2.8827	0.2905	1461.5	1462.648	5	199.2	50	F.G1V1P1T1R4F1G1N2L1P1A1Q2W2.S
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	3.0667	0.286	2590.35	2590.89	1	527.1	38.636364	M.NAPQKPEDIPVATEKTLLEYDAF.L
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	3.2018	0.2513	1446.21	1443.648	1	513.9	62.5	F.GVPTRFGNLPAQW.S
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	3.3707	0.2734	1464.31	1462.648	1	785.1	75	F.G1V1P1T1R4F1G1N2L1P1A1Q2W2.S
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	4.5162	0.3549	1726.57	1724.984	1	1124.4	78.57143	F.L1F1G1V1P1T1R4F1G1N2L1P1A1Q2W2.S
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	4.047	0.3713	1703.61	1703.984	1	913.5	71.42857	F.LFGVPTRFGNLPAQW.S
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	4.1439	0.386	1637.89	1637.83	1	574.4	64.28571	M.NAPQKPEDIPVATEK.T
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	4.0729	0.3056	1680.51	1678.923	1	1217.2	73.07692	Y.R4V1E1E1T1L1P1D1E1V1L1T1K2M1.N
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	2	4.2212	0.2632	1530.45	1529.731	1	1515.3	79.16667	Y.RVEETLPDEVLTK.M
gi|6319849|ref|NP_009930.1|	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	1	3.1114	0.1743	1545.9	1546.731	7	257.3	54.166668	Y.R4V1E1E1T1L1P1D1E1V1L1T1K2.M
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	2	3.506	0.3026	1302.79	1300.538	7	538.5	72.72727	D.NLLDKVDSIIIG.G
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	2	3.7309	0.3678	1571.85	1572.888	1	1284.1	75	A.GFLLEKELKYFGK.A
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	1	2.4091	0.186	1166.56	1166.326	5	290.5	68.75	L.E1H3H3P1R4Y1V1V1L1.A
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	1	2.8399	0.1648	1385.57	1384.66	2	344.7	50	K.G1V1E1V1V1L1P1V1D1F1I1I1A1.D
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	1	2.9083	0.2145	1461.62	1462.687	1	638.6	62.5	R.V1D1F1N2V1P1L1D1G1K2K2I1T1.S
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	2	3.0202	0.2018	1587.47	1586.913	4	698.4	57.14286	K.A1K2G1V1E1V1V1L1P1V1D1F1I1I1A1.D
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	2	3.4822	0.3234	1683.97	1682.786	1	591.8	69.230774	A.S1H3L1G1R4P1N2G1E1R4N2E1K2Y1.S
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	2	3.1304	0.2159	1596.09	1594.708	4	360.9	70.83333	S.H3L1G1R4P1N2G1E1R4N2E1K2Y1.S
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	2	2.9517	0.2919	1727.77	1728.865	1	252.4	50	L.ASHLGRPNGERNEKY.S
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	2	3.8158	0.2998	1315.43	1314.538	6	663.3	77.27273	D.N2L1L1D1K2V1D1S1I1I1I1G1.G
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	1	2.6747	0.2709	1445.63	1446.687	1	460.8	58.333332	R.VDFNVPLDGKKIT.S
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	1	2.3214	0.255	1183.7	1183.433	1	534.6	75	F.LLEKELKYF.G
gi|10383781|ref|NP_009938.2|	YCR012W	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 in glycolysis and gluconeogenesis; Pgk1p	1	2.4135	0.2542	1149.59	1150.326	3	265.2	68.75	L.EHHPRYVVL.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	3.2181	0.2331	1700.17	1699.816	4	460.3	57.692307	N.AHYTYPDEWFPSVS.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	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	2	3.0681	0.2197	1317.79	1318.52	1	618.1	68.181816	E.SHGPLPWPWGAL.T
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	3.6987	0.3878	2138.19	2139.322	1	986.8	55.263157	N.N2W2T1P1G1E1A1S1D1T1P1P1L1P1P1H3A1T1P1K2.N
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	2.9757	0.3162	1676.27	1677.04	1	644.5	57.14286	K.YSIKEPIAPIVIHPV.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	3.5545	0.3209	1515.91	1513.864	1	806	73.07692	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	4.0647	0.2876	1529.63	1530.864	1	681.5	69.230774	Y.S1I1K2E1P1I1A1P1I1V1I1H3P1V1.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	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
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	3.035	0.3768	1674.51	1675.029	1	360.5	61.538464	K.EPIAPIVIHPVWRF.E
gi|10383792|ref|NP_009959.2|	YCR030C	Protein with a potential role in actin cytoskeletal organization; overexpression suppresses a pfy1 (profilin) null mutation; Syp1p	1	2.4521	0.2497	1530.86	1530.864	1	312.5	53.846157	Y.S1I1K2E1P1I1A1P1I1V1I1H3P1V1.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	3.4415	0.31	1513.15	1513.864	1	747.9	69.230774	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	3.0723	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 pfy1 (profilin) null mutation; Syp1p	2	4.2402	0.348	1719.33	1719.077	1	1119	71.42857	Y.S1I1K2E1P1I1A1P1I1V1I1H3P1V1W2.R
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; Fen1p	3	3.916	0.2964	1417.79	1417.564	1	747.5	52.499996	S.LWEHFDDVVTR.V
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; Fen1p	1	3.245	0.3495	1418.7	1417.564	1	653	65	S.LWEHFDDVVTR.V
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; Fen1p	3	3.8803	0.2313	2376.59	2375.649	1	1084.8	39.473686	S.LWEHFDDVVTRVTNGRFVPS.E
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; Fen1p	2	4.8304	0.4196	2347.65	2349.628	1	544.5	52.941177	L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1.F
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; Fen1p	2	3.5013	0.3227	2583.27	2583.908	4	171.2	36.842106	L.FERYPQLHDYLPTLERPFFN.I
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; Fen1p	2	3.2421	0.2653	2613.53	2613.908	1	215.5	39.473686	L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1F1N2.I
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; Fen1p	3	4.6717	0.3291	2612.15	2613.908	1	864.5	40.789474	L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1F1N2.I
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; Fen1p	3	4.3443	0.276	2586.11	2583.908	2	773.6	36.842106	L.FERYPQLHDYLPTLERPFFN.I
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; Fen1p	2	4.5277	0.4325	2814.67	2816.146	1	451.5	45.238094	L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1F1N2I1S1.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; Fen1p	3	4.7624	0.3015	2814.2	2816.146	1	1392.2	40.476192	L.F1E1R4Y1P1Q2L1H3D1Y1L1P1T1L1E1R4P1F1F1N2I1S1.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; Fen1p	2	3.8144	0.4101	2782.03	2784.146	1	556.1	47.61905	L.FERYPQLHDYLPTLERPFFNIS.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; Fen1p	3	3.8183	0.2041	2782.85	2784.146	5	447.7	26.190477	L.FERYPQLHDYLPTLERPFFNIS.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; Fen1p	2	3.0192	0.3018	2031.59	2032.306	1	364.3	50	Y.AAPLFERYPQLHDYLPT.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; 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; Fen1p	2	2.94	0.306	2071.25	2073.288	1	573.9	44.11765 A.VHLYFPILPHCGDCVGST.T
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; Fen1p	2	4.6516	0.4055	2322.53	2322.628	1	715.1	58.823532 L.FERYPQLHDYLPTLERPF.F
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; Fen1p	2	3.5195	0.3097	2174.27	2174.393	1	880.8	55.555557 A.VHLYFPILPHCGDCVGSTT.A
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; Fen1p	2	3.5793	0.2894	2093.97	2095.288	1	513.7	41.17647 A.V1H3L1Y1F1P1I1L1P1H3C1G1D1C1V1G1S1T1.T
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; Fen1p	2	3.0111	0.2592	1970.65	1972.183	1	282.1	43.75 A.VHLYFPILPHCGDCVGS.T
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; 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	32.5 L.A1A1S1E1K2E1E1E1E1M1E1N2K2F1A1P1P1P1K2K2S1E1P1T1I1I1S1P1K2P1F1.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.R4V1S1P1P1G1S1D1V1E1K2I1I1I1I1G1.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.I1V1R4G1S1D1P1D1T1T1W2L1I1I1S1P1N2.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.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	4.4504	0.2877	3633.26	3632.711	1	546.6	25	S.S1R4V1N2D1N2N2D1D1D1D1W2N2E1P1E1L1K2E1R4D1F1D1Q2A1P1L1K2P1N2.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	28.676472	N.S1I1P1A1P1K2Q2E1E1A1P1E1Q2A1P1E1E1E1I1E1E1E1A1E1E1A1A1P1Q2L1P1S1R4S1S1.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	2	4.7117	0.4172	2039.67	2041.376	1	406.5	50	S.K2S1P1A1P1V1S1K2K2E1P1V1K2T1P1S1P1A1P1A1.A
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	1	2.6039	0.4887	1422.5	1423.488	1	290.8	50	L.HDGPVIDEFFSC.D
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	1	2.6674	0.2973	1436.54	1437.488	3	290.9	50	L.H3D1G1P1V1I1D1E1F1F1S1C1.D
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	3.2814	0.314	1552.29	1551.647	1	719.1	62.5	A.L1H3D1G1P1V1I1D1E1F1F1S1C1.D
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	4.1602	0.328	2639.41	2640.967	1	430	40.476192	N.M1E1D1I1P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	3	4.9263	0.5003	2614.1	2615.967	1	1311	36.904762	N.MEDIPACKELPEVFFDPVIDLH.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	3	5.9574	0.3883	2642.93	2640.967	1	1446.4	39.285713	N.M1E1D1I1P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	4.1157	0.3138	2147.29	2148.411	1	882.7	52.941177	I.P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	3	4.0313	0.225	2872.46	2871.23	1	1075.5	32.608696	D.L1N2M1E1D1I1P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA 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

gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	3	3.9562	0.3384	3880.97	3882.291	1	219.6	22.65625	M.T1V1P1N2P1Y1D1V1D1L1N2M1E1D1I1P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	4.6408	0.3463	1815.67	1817.076	1	1845.9	82.14286	C.K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	4.3721	0.3395	1801.59	1799.076	1	1374.6	75	C.KELPEVFFDPVIDLH.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	1	2.4128	0.2349	1241.58	1242.423	3	154.1	68.75	F.NERPYFRLF.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	1	2.8171	0.2467	1257.5	1258.423	6	145.8	62.5	F.N2E1R4P1Y1F1R4L1F1.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	3	3.9323	0.2247	2657.69	2656.967	1	1170.5	33.333336	N.M$E1D1I1P1A1C1K2E1L1P1E1V1F1F1D1P1V1I1D1L1H3.S
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	3.0622	0.2302	1491.41	1490.773	1	467.8	63.636364	T.I1F1V1T1H3P1D1L1K2R4V1F1.Q
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	3.8432	0.1605	1750.89	1750.974	1	774.5	64.28571	Y.E1E1F1G1K2N2I1P1N2L1D1V1I1P1F1.A
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	3.1221	0.2818	1868.43	1869.128	1	398.2	53.333336	L.STKDEQAIDKKHLKNL.A
gi|10383811|ref|NP_010017.2|	YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	2	3.0843	0.2529	1472.41	1472.773	1	449.8	59.090908	T.IFVTHPDLKRVF.Q
gi|6320197|ref|NP_010277.1|	YDL007W	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 the core 20S particle; Rpt2p	2	5.8568	0.2532	2354.77	2355.612	1	845.3	58.333332	F.E1K2K2Q2E1E1E1K2K2Q2L1E1E1I1R4G1N2P1L1.S
gi|6320197|ref|NP_010277.1|	YDL007W	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 the core 20S particle; Rpt2p	2	4.5975	0.4091	1990.27	1990.218	1	1382.7	63.88889	A.GENAPSIVFIDEIDAIGTK.R
gi|6320197|ref|NP_010277.1|	YDL007W	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 the core 20S particle; Rpt2p	2	3.5867	0.177	2310.29	2309.587	1	402.8	38.88889	Q.E1I1K2E1S1V1E1L1P1L1T1H3P1E1L1Y1E1E1M1.G
gi|6320197|ref|NP_010277.1|	YDL007W	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 the core 20S particle; Rpt2p	2	5.4173	0.2783	2325.67	2326.612	1	677.6	52.77778	F.EKKQEEEKKQLEEIRGNPL.S
gi|6320197|ref|NP_010277.1|	YDL007W	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 the core 20S particle; Rpt2p	3	4.06	0.2105	2326.46	2326.612	1	907.8	40.27778	F.EKKQEEEKKQLEEIRGNPL.S
gi|6320197|ref|NP_010277.1|	YDL007W	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 the core 20S particle; Rpt2p	2	5.0948	0.2677	2325.79	2326.612	1	794.7	55.555557	F.EKKQEEEKKQLEEIRGNPL.S
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	3.1481	0.4106	1356.59	1357.506	1	556.5	62.5	S.HVSDVVGPEGVVY.A
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	3.5566	0.3957	1371.45	1372.506	1	463.6	58.333332	S.H3V1S1D1V1V1G1P1E1G1V1V1Y1.A
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	2	3.4345	0.2221	1331.61	1330.61	1	1346.1	77.27273	L.DELFIAPGKKVL.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	2	3.3134	0.2667	2058.21	2059.249	5	288.3	50	L.EQLTLEPYERDHCIVVG.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	2	4.3085	0.3971	1968.61	1968.214	1	666.3	55.88235	K.RISVEEPSKEDGVPPTKV.E
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	4.3563	0.2858	2285.42	2285.506	5	704.1	36.842106	K.R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1.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	2.6533	0.1583	1344.63	1345.582	6	567.1	62.5	M.GGLDELFIAPGKK.V
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	2	4.6915	0.2134	1575.43	1574.874	2	982.6	71.42857	M.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	2	3.7973	0.2928	1556.87	1557.874	1	979.8	71.42857	M.GGLDELFIAPGKKVL.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	1	3.5841	0.3017	1556.61	1557.874	1	883.9	60.714287	M.GGLDELFIAPGKKVL.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	2	3.1639	0.3421	1875.89	1875.277	1	528.4	50	A.GIM@GGLDELFIAPGKKVL.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	1	2.7299	0.1556	1447.55	1448.591	1	153.4	54.545456	V.E1F1S1H3R4P1G1R4E1L1I1S1.M
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	4.276	0.2799	2443.64	2445.693	1	709.7	35	K.R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4.V
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	2.5284	0.259	1526.63	1527.723	1	259.3	54.166668	A.VEFSHRPGRELIS.M

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	2.4023	0.2381	1579.68	1580.783	1	123.8	54.166668 V.E1F1S1H3R4P1G1R4E1L1I1S1M1.A
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	2.6584	0.3057	1378.51	1379.643	5	210.7	54.545456 K.KRPNIIPIIEDA.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	2	3.1836	0.37	1811.51	1812.027	1	697.5	56.25 R.ISVEEPSKEDGVPPTKV.E
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	2	4.4235	0.4511	2260.11	2260.506	1	1047	65.789474 R.ISVEEPSKEDGVPPTKVEYR.V
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	2	4.0209	0.2831	1346.33	1345.582	1	1275.5	70.83333 M.GGLDELFIAPGKK.V
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	2	2.9435	0.1501	1844.53	1845.031	1	361.9	46.42857 L.TLEPYERDHCIVVGR.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	1	3.7539	0.3036	1558.96	1557.874	1	882.2	57.14286 M.GGLDELFIAPGKKVL.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	1	3.8574	0.198	1577.01	1574.874	1	895.3	57.14286 M.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	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 of 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
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	2	4.1932	0.3297	2415.77	2416.693	1	443.9	45 K.RISVEEPSKEDGVPPTKVEYR.V
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	2	4.9708	0.3094	2445.53	2445.693	1	760	55 K.R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4.V
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	5.7125	0.4133	2444.99	2445.693	1	1081.2	41.25 K.R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4.V
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	2.2845	0.2496	1151.55	1152.299	1	214.2	66.66667 F.SHRPGRELIS.M
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	2.546	0.2747	1558.85	1559.783	1	173.4	58.333332 V.EFSHRPGRELISM.A
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	2	4.5502	0.4275	2059.59	2060.268	1	1296.9	70.588234 S.VEEPSKEDGVPPTKVEYR.V
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	2	4.6463	0.4182	2082.55	2083.268	1	798.1	61.764706 S.V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4.V
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	2	4.1612	0.1711	1358.73	1360.582	9	1005.8	62.5 M.G1G1L1D1E1L1F1I1A1P1G1K2K2.V
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	3.6941	0.2131	1575.78	1574.874	1	1018.9	60.714287 M.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	1	3.7963	0.2446	1559.26	1557.874	1	954.7	64.28571 M.GGLDELFIAPGKKVL.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	1	2.4559	0.2255	1227.58	1228.353	4	179.7	61.11111 V.EFSHRPGREL.I
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	2	3.98	0.2847	2416.61	2416.693	1	493.8	47.5 K.RISVEEPSKEDGVPPTKVEYR.V
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	2	4.7384	0.241	2447.27	2445.693	1	785.1	57.5 K.R4I1S1V1E1E1P1S1K2E1D1G1V1P1P1T1K2V1E1Y1R4.V
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	4.4733	0.3071	2416.52	2416.693	1	765	36.25 K.RISVEEPSKEDGVPPTKVEYR.V
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	2	3.3084	0.2561	1557.71	1557.874	2	496.1	53.571426 M.GGLDELFIAPGKKVL.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	1	2.6744	0.2331	1428.6	1428.591	1	213	63.636364 V.EFSHRPGRELIS.M
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	2.7233	0.2325	1547.65	1548.723	2	186.7	45.833336 A.V1E1F1S1H3R4P1G1R4E1L1I1S1.M
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	2.4528	0.1901	1169.3	1170.299	1	219.1	66.66667 F.S1H3R4P1G1R4E1L1I1S1.M
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	3.7422	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	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	3.1752	0.1996	1299.66	1300.57	1	621.9	70	S.K2K2P1T1L1D1D1V1L1K2K2.I
gi|6320185|ref|NP_010265.1|	YDL019C	Member of an oxysterol-binding protein family with seven members in S. cerevisiae; family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability; Osh2p	2	3.3857	0.3227	1609.79	1608.878	1	714.6	61.538464	K.R4V1A1K2P1F1N2P1L1L1G1E1T1F1.E
gi|6320185|ref|NP_010265.1|	YDL019C	Member of an oxysterol-binding protein family with seven members in S. cerevisiae; family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability; Osh2p	2	2.9827	0.26	1649.33	1647.754	2	324.5	58.333332	K.RRDHDLKDCGDIF.-
gi|6320185|ref|NP_010265.1|	YDL019C	Member of an oxysterol-binding protein family with seven members in S. cerevisiae; family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability; Osh2p	2	3.2882	0.2562	1596.99	1596.698	1	842.2	68.181816	T.WTESPRWDFWGE.S
gi|6320185|ref|NP_010265.1|	YDL019C	Member of an oxysterol-binding protein family with seven members in S. cerevisiae; 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.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	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.I1Q2R4V1G1L1G1E1I1I1R4F1.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	2	4.0799	0.2555	2075.73	2077.351	1	959.1	52.77778	Q.N2V1K2Y1L1P1G1I1T1L1P1D1N2L1V1A1N2P1D1.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	2	4.7787	0.4572	2944.75	2945.221	1	740.3	46	G.QERFEAPECLFQPGLVDVEQPGVGEL.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	2	2.9779	0.2482	1713.31	1713.887	2	417.2	57.14286	G.RAGENFPDYTFPSIV.G
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	4.2019	0.2875	2978.21	2977.221	1	1304.4	37	G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1.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	2	4.7574	0.4585	2977.59	2977.221	1	738.9	44	G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1.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	2	4.7593	0.414	2817.81	2817.091	1	607.5	45.833336	Q.ERFEAPECLFQPGLVDVEQPGVGEL.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	2	4.5605	0.4663	2846.29	2847.091	1	449.1	39.583336	Q.E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1.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	5.4247	0.3867	3091.46	3091.381	1	1160.4	36.53846	G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.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	2	4.6258	0.4388	3090.69	3091.381	1	635.4	38.46154	G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.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	2	4.0192	0.2423	3056.07	3058.381	1	586	36.53846	G.QERFEAPECLFQPGLVDVEQPGVGELL.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	1	2.7225	0.2521	1523.86	1522.739	1	676.1	53.571426	Q.PGLVDVEQPGVGELL.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	2	5.3952	0.4864	2959.29	2961.25	1	556.4	40	Q.E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.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	4.7011	0.2264	3058.73	3058.381	1	1075.7	34.615387	G.QERFEAPECLFQPGLVDVEQPGVGELL.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	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
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	5.5018	0.5628	2927.91	2930.25	1	858.7	46 Q.ERFEAPECLFQPGLVDVEQPGVGELL.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	2	3.6517	0.3882	3107.37	3109.427	1	259.1	26.923079 Q.E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1F1.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	2	4.0137	0.4024	3078.63	3077.427	1	488.4	34.615387 Q.ERFEAPECLFQPGLVDVEQPGVGELLF.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	2	4.7175	0.437	2948.49	2948.311	1	634.9	40 E.RFEAPECLFQPGLVDVEQPGVGELLF.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	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 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	4.8235	0.3154	3089.24	3091.381	1	971.7	32.692307 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.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	2	3.3954	0.3174	3090.55	3091.381	1	270.7	28.846153 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.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	2	4.7309	0.4767	2929.63	2930.25	1	596.6	40 Q.ERFEAPECLFQPGLVDVEQPGVGELL.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	2	4.9136	0.5023	2718.59	2716.975	1	605.8	45.652176 E.R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1.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	2	4.7449	0.466	2800.81	2801.135	1	1054.1	52.083332 E.RFEAPECLFQPGLVDVEQPGVGELL.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	2	5.2813	0.3732	2831.07	2831.135	1	725.5	45.833336 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	4.0367	0.2975	2831.15	2831.135	1	994.1	30.208334 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	4.4436	0.3636	2802.11	2801.135	1	1151.9	35.416664 E.RFEAPECLFQPGLVDVEQPGVGELL.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	4.5293	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
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	5.4073	0.4286	2275.91	2277.562	1	406.3	44.736843 G.R4A1G1E1N2F1P1D1Y1T1F1P1S1I1V1G1R4P1I1L1.R
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	5.3867	0.4711	2606.39	2606.944	1	336.8	28.40909 G.RAGENFPDYTFPSIVGRPILRAE.E
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	3.4091	0.3113	1966.37	1966.244	1	714.7	53.125 G.ENFPDYTFPSIVGRPIL.R
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	3.7485	0.3963	2023.25	2023.296	2	657.3	47.058823 A.GENFPDYTFPSIVGRPIL.R
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	4.016	0.2509	1987.07	1987.244	1	633.6	53.125 G.E1N2F1P1D1Y1T1F1P1S1I1V1G1R4P1I1L1.R
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	3.0697	0.1595	1734.97	1732.887	1	385.2	50 G.R4A1G1E1N2F1P1D1Y1T1F1P1S1I1V1.G
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	3.1139	0.3004	2701.87	2702.946	1	254.4	34.782608 G.QERFEAPECLFQPGLVDVEQPGVG.E
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	3.83	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 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	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
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	4.2876	0.1575	2799.89	2801.135	1	1124	34.375 E.RFEAPECLFQPGLVDVEQPGVGELL.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	2	4.6846	0.3552	3089.33	3091.381	1	482.8	34.615387 G.Q2E1R4F1E1A1P1E1C1L1F1Q2P1G1L1V1D1V1E1Q2P1G1V1G1E1L1L1.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	2	4.8475	0.3959	2800.75	2801.135	1	937.5	50 E.RFEAPECLFQPGLVDVEQPGVGELL.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	2	4.5942	0.3447	2249.57	2250.562	1	422.2	44.736843	G.RAGENFPDYTFPSIVGRPIL.R
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	3.2612	0.2041	1902.71	1903.29	1	608.3	53.333336	S.MYPGLPSRLEKELKQL.W
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	4.1846	0.3432	2437.22	2437.75	4	387.2	28.75	G.R4A1G1E1N2F1P1D1Y1T1F1P1S1I1V1G1R4P1I1L1R4.A
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	6.1673	0.4947	2640.77	2639.944	1	714.6	35.227272	G.R4A1G1E1N2F1P1D1Y1T1F1P1S1I1V1G1R4P1I1L1R4A1E1.E
gi|6320170|ref|NP_010249.1|	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; Gpr1p	2	4.1972	0.354	1910.37	1911.215	1	674.4	55.88235	Y.L1V1K2P1T1I1P1G1T1T1P1D1P1I1I1E1A1Q2.N
gi|6320170|ref|NP_010249.1|	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; Gpr1p	3	4.6231	0.2974	3465.53	3464.705	1	707.8	24.13793	Y.AMSEQPDLERNNPFDCENDITLNPSELVSK.Q
gi|6320170|ref|NP_010249.1|	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; Gpr1p	2	3.7753	0.3189	1949.51	1951.086	1	681.8	53.333336	N.N2Y1N2F1P1D1S1P1R4Q2G1G1Y1K2P1W2.S
gi|6320170|ref|NP_010249.1|	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; Gpr1p	2	3.1893	0.3825	1920.01	1920.277	1	335.6	53.125	H.HIPMLGGIDLDELNRLL.K
gi|6320170|ref|NP_010249.1|	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; Gpr1p	2	3.4913	0.2883	1890.51	1891.215	1	585	52.941177	Y.LVKPTIPGTTPDPIIEAQ.N
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	4.0496	0.3176	2218.93	2219.564	1	703.2	45.238094	T.A1K2I1G1P1D1V1V1I1G1P1N2V1T1I1G1D1G1V1R4I1T1.R
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	3.0402	0.2405	2191.89	2192.564	3	290	38.095238	T.AKIGPDVVIGPNVTIGDGVRIT.R
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	3.0263	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.L1Y1I1L1N2P1E1V1I1D1L1I1E1M$K2P1T1S1I1E1K2E1T1F1P1I1L1V1E1.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
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	3.0564	0.157	2019.63	2021.417	2	326.7	40.625	G.L1Y1I1L1N2P1E1V1I1D1L1I1E1M1K2P1T1.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	2	3.2148	0.2771	1545.03	1545.835	2	516.7	57.692307	H.KSISDNVPKEAIIM.-
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	3.3495	0.2367	2004.89	2002.417	2	580.1	50	G.LYILNPEVIDLIEMKPT.S
gi|6320143|ref|NP_010223.1|	YDL060W	Protein required for processing of 20S pre-rRNA 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	Protein required for processing of 20S pre-rRNA in the cytoplasm, associates with pre-40S ribosomal particles; Tsr1p	2	3.305	0.3422	1315.49	1316.502	1	746.9	85	N.RLVHIPDFGDF.Q
gi|6320143|ref|NP_010223.1|	YDL060W	Protein required for processing of 20S pre-rRNA in the cytoplasm, associates with pre-40S ribosomal particles; Tsr1p	3	4.1251	0.315	4264.31	4265.24	1	463.1	19.117647	E.Q2D1N2E1E1V1A1G1D1E1E1Y1D1I1E1D1N2E1G1F1E1E1L1S1P1E1E1E1E1R4 Q2L1R4E1F1.R
gi|6320143|ref|NP_010223.1|	YDL060W	Protein required for processing of 20S pre-rRNA in the cytoplasm, associates with 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; Idp1p	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; Idp1p	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; Idp1p	2	5.539	0.3703	2399.59	2399.742	1	689	57.894737	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	5.197	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.V1K2Q2P1V1V1E1L1D1G1D1E1M1T1R4I1I1W2.D
gi|6320128|ref|NP_010208.1|	YDL075W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; Rpl31ap	2	4.1448	0.1894	1857.55	1858.999	2	937.9	67.85714	S.R4K2R4N2E1E1E1D1A1K2N2P1L1F1S1.Y
gi|6320128|ref|NP_010208.1|	YDL075W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; Rpl31ap	2	4.817	0.2384	2021.65	2023.175	1	1175.8	66.66667	S.R4K2R4N2E1E1E1D1A1K2N2P1L1F1S1Y1.V
gi|6320128|ref|NP_010208.1|	YDL075W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; Rpl31ap	2	4.0034	0.3651	1748.83	1746.921	1	1127.8	80.769226	S.RKRNEEEDAKNPLF.S
gi|6320128|ref|NP_010208.1|	YDL075W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; Rpl31ap	2	4.1782	0.2187	1771.65	1770.921	1	1031.7	76.92308	S.R4K2R4N2E1E1E1D1A1K2N2P1L1F1.S
gi|6320128|ref|NP_010208.1|	YDL075W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; Rpl31ap	2	4.0244	0.2944	1996.63	1997.175	1	1160.9	66.66667	S.RKRNEEEDAKNPLFSY.V
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	2	4.1528	0.2708	1351.31	1348.466	1	794.1	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 hUAP56; Sub2p	2	3.9857	0.2555	1864.41	1865.072	1	1679.8	82.14286	F.VIDECDKVLEELDMR.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	2	4.6613	0.4372	2126.95	2126.352	1	1503.6	68.75	K.NFVIDECDKVLEELDMR.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	4.2848	0.2296	3046.64	3047.343	5	402.2	28.260868	K.N2F1V1I1D1E1C1D1K2V1L1E1E1L1D1M1R4R4D1V1Q2E1I1F1.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	4.121	0.2468	3359.27	3359.708	1	602.2	25	H.S1T1G1F1K2D1F1L1L1K2P1E1L1S1R4A1I1I1D1C1G1F1E1H3P1S1E1V1Q2.Q
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	4.3347	0.2765	3323.3	3322.708	1	400.3	24.107143	H.STGFKDFLLKPELSRAIIDCGFEHPSEVQ.Q
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	2	4.5386	0.2979	1883.59	1884.072	1	1245.6	71.42857	F.V1I1D1E1C1D1K2V1L1E1E1L1D1M1R4.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 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	3.3962	0.1679	1710.63	1708.884	1	735.9	69.230774	F.VIDECDKVLEELDM.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	4.1463	0.3267	2783	2783.063	2	791.9	35.714287	F.V1I1D1E1C1D1K2V1L1E1E1L1D1M1R4R4D1V1Q2E1I1F1.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	1	2.3855	0.3645	1122.4	1123.297	1	421.3	66.66667	L.KNKDTAPHIV.V
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	3.8716	0.3197	2034.31	2037.187	1	601.4	58.823532	E.G1D1G1P1S1Y1E1D1L1M1N2E1D1G1K2K2I1F1.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.K2R4V1E1Q2D1D1P1V1P1E1L1D1I1K2.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	2	3.529	0.2216	1288.27	1286.461	1	1250.5	80	F.S1H3E1V1K2L1P1A1W2G1F1.E
gi|6320103|ref|NP_010183.1|	YDL100C	ATPase, subunit of the GET complex; required for the retrieval of HDEL proteins from the Golgi to the ER in an ERD2 dependent fashion; involved in resistance to heat and metal stress; Get3p	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 GET complex; required for the retrieval of HDEL proteins from the Golgi to the ER in an ERD2 dependent fashion; involved in resistance to heat and metal stress; Get3p	2	3.9658	0.3577	1821.47	1820.006	1	735.8	69.230774	Q.KKYLDQIDELYEDF.H
gi|6320103|ref|NP_010183.1|	YDL100C	ATPase, subunit of the GET complex; required for the retrieval of HDEL proteins from the Golgi to the ER in an ERD2 dependent fashion; involved in resistance to heat and metal stress; Get3p	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 from the Golgi to the ER in an ERD2 dependent fashion; involved in resistance to heat and metal stress; Get3p	2	3.7133	0.3177	2155.67	2155.412	1	715.9	56.25	Q.KKYLDQIDELYEDFHVV.K
gi|6320103|ref|NP_010183.1|	YDL100C	ATPase, subunit of the GET complex; required for the retrieval of HDEL proteins 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 Npl4p 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 Npl4p 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 Npl4p 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 Npl4p 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 Npl4p 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.R4I1S1V1L1P1I1A1D1T1I1E1G1I1T1G1N2.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	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 Npl4p 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 Npl4p 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 Npl4p 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 Npl4p 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 Npl4p 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 Npl4p 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.G1D1L1V1T1I1H3P1C1P1D1I1K2Y1A1.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 Npl4p 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	35	T.W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1Q2Y1T1K2F1.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	20.588236	V.N2V1T1W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1Q2Y1T1K2F1G1.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	6.7615	0.5027	4052.15	4051.415	1	1487.2	28.787878	V.N2V1T1W2D1D1V1G1G1L1D1E1I1K2E1E1L1K2E1T1V1E1Y1P1V1L1H3P1D1Q2Y1T1K2F1.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	4.3807	0.4039	2156.85	2155.477	1	993.4	52.63158	A.T1R4I1S1V1L1P1I1A1D1T1I1E1G1I1T1G1N2L1F1.D
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	4.2339	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 Npl4p 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 Npl4p 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 Npl4p 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.G1R4F1D1R4E1V1D1I1G1I1P1D1A1T1G1R4L1.E
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	3.8129	0.2259	1989.05	1988.211	1	1093.4	44.11765	F.GRFDREVDIGIPDATGRL.E

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	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.006	0.3049	2358.53	2359.618	1	284.8	37.5	F.G1R4F1D1R4E1V1D1I1G1I1P1D1A1T1G1R4L1E1V1L1.R
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	1	3.0143	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 Npl4p 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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	1	2.8158	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	4.1853	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	7.4652	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	1	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.4625	0.2591	1647.57	1648.795	1	838.5	67.85714	F.D1R4E1V1D1I1G1I1P1D1A1T1G1R4L1.E
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	3.9146	0.2659	1626.85	1627.795	1	1220.8	78.57143	F.DREVDIGIPDATGRL.E
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	4.5403	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.3486	0.2672	1594.53	1595.815	1	646.4	57.692307	R.L1G1D1L1V1T1I1H3P1C1P1D1I1K2.Y
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	3.4218	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.2654	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.6834	0.265	1833.89	1832.07	1	894.6	56.666668	R.L1G1D1L1V1T1I1H3P1C1P1D1I1K2Y1A1.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	2	4.2172	0.3766	3056.23	3058.311	1	276.3	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.1809	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	3.1785	0.2658	2051.99	2053.372	3	324.8	36.11111	T.R4I1S1V1L1P1I1A1D1T1I1E1G1I1T1G1N2L1F1.D
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	5.6453	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	6.2993	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	4.5128	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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	3	5.2272	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 Npl4p 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 Npl4p 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 Npl4p 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 Npl4p 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.N2R4P1D1Q2I1D1P1A1I1L1R4P1G1R4L1D1Q2L1.I
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	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 Npl4p 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 Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	2	2.9797	0.2467	1481.71	1480.811	1	641.3	63.636364	E.MVELPLRHPQLF.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	5.0647	0.4741	2351.93	2351.522	1	1532.8	60.000004	A.R4A1L1D1D1F1G1V1D1Y1I1E1L1T1S1P1V1A1S1E1Q2.S
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	1	2.2954	0.1555	985.47	986.145	1	270.1	62.5	Y.K2T1V1D1K2I1G1V1N2.R
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	5.0547	0.4076	2593.83	2595.812	1	900	47.826088	E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3.V
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	5.2738	0.345	2782.59	2784.023	1	693.1	42	E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	3	4.6544	0.3617	3125.54	3126.358	1	760.2	29.464287	F.H3A1E1L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	3	4.4739	0.3258	2017.97	2016.264	1	909.8	51.5625	D.T1V1G1C1A1N2P1R4Q2V1Y1E1L1I1R4T1L1.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	4.5969	0.4345	1823.21	1824.821	1	1033.5	65.625	V.N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	1	2.9786	0.2398	1315.64	1316.488	7	317.2	65	Y.E1I1L1D1P1H3D1F1G1M1K2.R
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	1	3.133	0.3891	1581.56	1582.769	1	592.3	62.5	S.T1Y1E1I1L1D1P1H3D1F1G1M1K2.R
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	4.3809	0.2179	1568.79	1566.769	1	1503.1	83.33333	S.TYEILDPHDFGMK.R
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	5.7767	0.4359	2267.65	2267.404	1	1171.4	57.5	L.L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	3	5.0593	0.4342	2592.83	2595.812	1	933.4	33.695652	E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3.V
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	3.203	0.2252	1396.13	1396.516	1	762.3	75	Q.S1R4K2D1C1E1A1I1C1K2L1.G
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	3	4.3958	0.1987	1594.4	1594.836	5	915.4	52.083332	C.A1N2P1R4Q2V1Y1E1L1I1R4T1L1.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	1	2.5323	0.2246	1046.34	1047.067	1	430.4	68.75	H.F1H3N2D1T1G1C1A1I1.A
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	3.1526	0.2507	2078.35	2079.277	1	322.8	41.666664	S.T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1.N
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	3	5.4833	0.353	2784.89	2784.023	1	1074.6	32	E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	3.7559	0.3422	2782.09	2784.023	3	349.2	32	E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1N2G1H3V1S1.K
gi|6320071|ref|NP_010151.1|	YDL131W	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, Lys20p; Lys21p	2	3.739	0.3326	2278.95	2281.515	1	593.7	45	E.L1S1T1P1L1L1K2P1V1N2K2G1T1D1D1D1N2I1D1I1S1.N
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	1	2.3484	0.216	1276.56	1277.54	1	488.2	60.000004	R.GVENIERVVMM.K
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	2.9106	0.2224	1333.45	1332.453	1	650.4	80	W.SEDNDEKLIIR.C

gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	3.7729	0.3301	1719.51	1718.83	1	1454.6	78.57143	K.SLDAETEAEEDHMLK.K
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	3.669	0.2645	2056.75	2057.484	1	717	52.77778	W.VPDWDGVIPTPAIIKPKPL.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	4.3707	0.4848	2408.81	2406.873	1	1251.2	62.5	L.YWVPDWDGVIPTPAIIKPKPL.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	3	4.8179	0.2805	1958.93	1958.351	1	1262.6	42.647057	V.PDWDGVIPTPAIIKPKPL.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	3.0589	0.1857	1980.75	1979.351	1	575.9	50	V.P1D1W2D1G1V1I1P1T1P1A1I1I1K2P1K2P1L1.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	3.4446	0.3534	2865.63	2867.185	1	312.2	39.130436	M.KYDRKVPSPTGEYVKEPEWVLETD.G
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	2.9142	0.2508	2897.03	2898.185	1	316.2	34.782608	M.K2Y1D1R4K2V1P1S1P1T1G1E1Y1V1K2E1P1E1W2V1L1E1T1D1.G
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	4.108	0.3847	2518.09	2520.032	1	1072.8	54.761906	M.LYWVPDWDGVIPTPAIIKPKPL.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	4.4399	0.4303	2543.47	2546.032	1	847.9	52.380955	M.L1Y1W2V1P1D1W2D1G1V1I1P1T1P1A1I1I1K2P1K2P1L1.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	2.9673	0.3536	1511.15	1511.677	1	618.6	77.27273	L.RESFEDNVVRFL.N
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	4.6251	0.4253	2267.73	2267.697	1	793	57.894737	Y.W2V1P1D1W2D1G1V1I1P1T1P1A1I1I1K2P1K2P1L1.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	3.8178	0.4144	2242.47	2243.697	1	850.6	57.894737	Y.WVPDWDGVIPTPAIIKPKPL.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	2	4.2476	0.4517	2429.83	2431.873	1	903.1	55	L.Y1W2V1P1D1W2D1G1V1I1P1T1P1A1I1I1K2P1K2P1L1.W
gi|6320061|ref|NP_010141.1|	YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	3	4.1737	0.2333	2868.89	2867.185	1	990.6	35.869564	M.KYDRKVPSPTGEYVKEPEWVLETD.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	3.4403	0.2123	1950.43	1949.164	6	307.4	46.875	Q.F1Q2I1S1P1P1K2P1D1T1E1N2N2I1I1V1N2.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	4.404	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
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	2.9727	0.2469	1634.67	1636.855	3	523.9	54.166668	M.V1V1K2D1I1E1R4E1E1I1E1F1L1.S
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	4.1159	0.2837	1760.59	1760.982	1	1661.7	70	D.LVEEIDSDGSKIVRVT.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	4.4433	0.3646	1778.51	1780.982	1	1450.1	70	D.L1V1E1E1I1D1S1D1G1S1K2I1V1R4V1T1.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	3.267	0.3915	1441.35	1440.512	1	462.8	70.83333	K.HENGELNDGISVR.R
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	4.0827	0.3626	1837.33	1838.952	1	695.1	63.333332	L.R4S1K2H3E1N2G1E1L1N2D1G1I1S1V1R4.R
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	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
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	3.3634	0.3522	1988.51	1989.14	1	882.8	58.823532	T.Y1K2P1I1Y1E1D1T1P1S1V1S1D1P1L1T1G1S1.K
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	3.7948	0.3556	1969.51	1970.14	1	1080.1	64.70589	T.YKPIYEDTPSVSDPLTGS.K
gi|6320056|ref|NP_010136.1|	YDL145C	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early secretory pathway; Cop1p	1	2.8085	0.28	1295.61	1296.525	1	501.9	63.636364	W.A1S1F1H3P1T1L1P1L1I1V1S1.G
gi|6320056|ref|NP_010136.1|	YDL145C	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early secretory pathway; Cop1p	3	3.9031	0.2488	3444.14	3443.977	1	313.4	21.428572	I.FHPHQNLIISVGEDKTLRVWDLDKRTPVK.Q
gi|6320056|ref|NP_010136.1|	YDL145C	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early secretory pathway; Cop1p	1	2.3876	0.2075	1253.59	1254.503	6	330.7	50	L.V1I1H3P1R4E1V1I1L1Y1.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
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	3.615	0.3495	1464.25	1464.746	1	525.3	57.692307	L.V1I1L1P1K2Q2P1V1G1A1V1E1P1T1.S
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	3.3166	0.3242	1745.79	1746.967	1	838.4	64.28571	C.RTYIPSTPCELPAQL.G
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	4.0306	0.3193	2070.73	2071.245	1	1192.2	58.333332	A.TYKPIYEDTPSVSDPLTGS.K
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	3.2995	0.3267	1834.69	1835.166	1	440.1	53.333336	D.Q2I1L1P1Y1V1P1G1L1D1V1V1N2E1K2M1.N
gi|6320054|ref|NP_010134.1|	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	2	3.4561	0.3158	1915.45	1917.033	1	679.5	59.375	Q.K2T1Y1E1P1V1L1N2E1D1D1L1A1F1G1G1E1.A
gi|6320054|ref|NP_010134.1|	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	2	3.1529	0.1857	1291.59	1290.491	1	621.9	70	E.L1L1E1H3I1E1T1I1G1H3L1.I
gi|6320054|ref|NP_010134.1|	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	2	5.8495	0.4555	1956.57	1957.15	1	2087.1	78.125	W.SHNVDELLEHIETIGHL.I

gi|6320054|ref|NP_010134.1|	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	2	5.9873	0.3771	1982.99	1981.15	1	1865.9	78.125	W.S1H3N2V1D1E1L1L1E1H3I1E1T1I1G1H3L1.I
gi|6320054|ref|NP_010134.1|	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	4.4944	0.4394	1957.4	1957.15	1	1793.2	51.5625	W.SHNVDELLEHIETIGHL.I
gi|6320054|ref|NP_010134.1|	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	5.1722	0.3328	1980.2	1981.15	1	1905.6	53.125	W.S1H3N2V1D1E1L1L1E1H3I1E1T1I1G1H3L1.I
gi|6320054|ref|NP_010134.1|	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	2	2.9159	0.304	1618.53	1618.827	1	692.7	57.692307	N.VDELLEHIETIGHL.I
gi|6320054|ref|NP_010134.1|	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.SHNVDELLEHIETIGHL.I
gi|6320054|ref|NP_010134.1|	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	2	5.067	0.4196	1980.45	1981.15	1	2099.2	78.125	W.S1H3N2V1D1E1L1L1E1H3I1E1T1I1G1H3L1.I
gi|6320054|ref|NP_010134.1|	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	2	3.7958	0.3006	1959.05	1957.15	1	1204.3	65.625	W.SHNVDELLEHIETIGHL.I
gi|6320054|ref|NP_010134.1|	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	2	3.3791	0.3559	1732.85	1732.931	1	759.7	60.714287	H.NVDELLEHIETIGHL.I
gi|6320054|ref|NP_010134.1|	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	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
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	3	4.4729	0.2523	2651.6	2651.065	1	698.4	32.142857	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-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-18S rRNA; Nop14p	3	5.6297	0.3286	2681	2680.065	1	1598	41.666664	M.M1T1Q2P1K2K2N2P1M1E1P1K2T1D1L1D1K2E1Y1D1I1K2.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-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	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	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
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	3.4091	0.2186	1989.89	1991.362	4	506.3	53.125	S.T1V1W2K2S1L1P1A1F1N2E1I1I1L1P1I1Q2.Q
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	3	4.3159	0.3063	2649.35	2651.065	1	1043.1	36.904762	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-18S rRNA; Nop14p	3	4.7554	0.211	2813.06	2812.258	1	986.9	34.090908	L.M1M1T1Q2P1K2K2N2P1M1E1P1K2T1D1L1D1K2E1Y1D1I1K2.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 deadenylase 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
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	4.5359	0.2534	2225.61	2225.497	1	808.8	52.77778	A.L1N2I1P1K2K2D1T1R4P1Q2T1D1D1V1L1N2T1K2.G
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	2	4.4656	0.3982	2258.27	2257.456	1	663.2	50	A.TFKDELDKLYPIIEEGGSDS.A
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	2	4.3237	0.2381	2350.53	2351.535	1	1093.9	55	A.T1F1K2D1E1L1D1K2L1Y1P1I1I1E1E1G1G1S1D1S1A1.A

gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	2	3.9162	0.4303	2188.45	2191.378	1	639.3	52.77778	A.T1F1K2D1E1L1D1K2L1Y1P1I1I1E1E1G1G1S1D1.S
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	3	4.3488	0.2005	3083.03	3084.504	3	393.5	27.083334	L.N2F1E1L1L1P1E1P1P1V1E1R4A1K2D1N2P1W2P1Q2W2P1R4V1M1.R
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	3	3.8016	0.198	2171.12	2170.378	1	822.8	34.72222	A.TFKDELDKLYPIIEEGGSD.S
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	2	3.8881	0.2711	2193.69	2191.378	1	534	50	A.T1F1K2D1E1L1D1K2L1Y1P1I1I1E1E1G1G1S1D1.S
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	3	4.2404	0.3906	2194.22	2191.378	1	872.8	36.11111	A.T1F1K2D1E1L1D1K2L1Y1P1I1I1E1E1G1G1S1D1.S
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	2	3.7047	0.3091	2172.57	2170.378	1	461.1	47.22222	A.TFKDELDKLYPIIEEGGSD.S
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	2	4.7156	0.2335	1632.99	1632.91	1	992	79.16667	L.L1N2K2D1L1E1I1I1R4E1K2I1Q2.G
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	2	3.759	0.228	1575.13	1574.81	1	724.9	68.181816	A.K2D1N2P1W2P1Q2W2P1R4V1M1.R
gi|6320030|ref|NP_010110.1|	YDL171C	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 nitrogen source; Glt1p	2	3.0604	0.2789	1425.55	1422.594	1	1288.8	81.818184	L.D1L1D1L1D1I1P1E1M1G1K2Y1.A
gi|6320027|ref|NP_010107.1|	YDL174C	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane; Dld1p	2	3.0645	0.2036	2069.47	2070.228	2	406.7	46.666668	S.E1S1T1D1R4C1D1W2V1E1K2P1T1M1F1F1.K
gi|6320027|ref|NP_010107.1|	YDL174C	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane; Dld1p	3	3.8931	0.2622	1792.88	1793.159	1	899.3	44.642857	K.L1A1I1D1P1K2R4I1M1N2P1D1K2I1F1.K
gi|6320027|ref|NP_010107.1|	YDL174C	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane; Dld1p	2	4.1373	0.3879	1763.59	1764.843	3	394.7	57.14286	Q.A1G1L1P1W2E1D1L1N2D1Y1L1S1D1H3.G
gi|6320027|ref|NP_010107.1|	YDL174C	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane; Dld1p	2	3.8641	0.3234	1733.83	1732.869	1	891.2	67.85714	S.S1L1D1S1P1D1Y1L1H3D1P1V1K2I1D1.K
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	5.0647	0.4741	2351.93	2351.522	1	1532.8	60.000004	A.R4A1L1D1D1F1G1V1D1Y1I1E1L1T1S1P1V1A1S1E1Q2.S
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	1	2.2954	0.1555	985.47	986.145	1	270.1	62.5	Y.K2T1V1D1K2I1G1V1N2.R
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	3	4.4739	0.3258	2017.97	2016.264	1	909.8	51.5625	D.T1V1G1C1A1N2P1R4Q2V1Y1E1L1I1R4T1L1.K
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	3	4.5117	0.2585	4103.99	4105.437	2	418.1	19.444445	M.T1A1A1K2P1N2P1Y1A1A1K2P1G1D1Y1L1S1N2V1N2N2F1Q2L1I1D1S1T1L1R4E1G1E1Q2F1A1N2.A
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	3	4.944	0.3827	4175	4177.516	1	513.9	22.297297	M.T1A1A1K2P1N2P1Y1A1A1K2P1G1D1Y1L1S1N2V1N2N2F1Q2L1I1D1S1T1L1R4E1G1E1Q2F1A1N2A1.F
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	1	2.9786	0.2398	1315.64	1316.488	7	317.2	65	Y.E1I1L1D1P1H3D1F1G1M1K2.R
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	1	3.133	0.3891	1581.56	1582.769	1	592.3	62.5	S.T1Y1E1I1L1D1P1H3D1F1G1M1K2.R
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	4.3809	0.2179	1568.79	1566.769	1	1503.1	83.33333	S.TYEILDPHDFGMK.R
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	3.7068	0.3006	1899.67	1901.079	1	902.9	55.88235	M.T1A1A1K2P1N2P1Y1A1A1K2P1G1D1Y1L1S1N2.V
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	3.203	0.2252	1396.13	1396.516	1	762.3	75	Q.S1R4K2D1C1E1A1I1C1K2L1.G
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	3	4.3958	0.1987	1594.4	1594.836	5	915.4	52.083332	C.A1N2P1R4Q2V1Y1E1L1I1R4T1L1.K
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	4.3826	0.3172	2063.85	2065.324	1	935.5	61.11111	K.K2N2K2K2N2D1S1D1V1P1E1L1A1T1I1P1A1A1K2.R
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	1	2.5323	0.2246	1046.34	1047.067	1	430.4	68.75	H.F1H3N2D1T1G1C1A1I1.A
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	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-SceI), which is a site-specific endonuclease; Tfp1p	2	3.0537	0.3577	1790.77	1792.973	1	516.2	61.538464	Y.A1P1I1L1Y1E1N2D1H3F1F1D1Y1M1.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-SceI), 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-SceI), which is a site-specific endonuclease; Tfp1p	2	3.619	0.2613	2194.27	2193.353	1	515.7	44.444447	S.K2S1Y1P1I1S1E1G1P1E1R4A1N2E1L1V1E1S1Y1.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-SceI), 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-SceI), which is a site-specific endonuclease; Tfp1p	2	3.3035	0.2358	1831.65	1832.989	1	541.3	53.125	V.G1H3D1N2L1V1G1E1V1I1R4I1D1G1D1K2A1.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-SceI), which is a site-specific endonuclease; Tfp1p	2	3.2653	0.3512	1456.31	1456.596	1	853.9	70.83333	V.G1H3D1N2L1V1G1E1V1I1R4I1D1.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-SceI), 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-SceI), 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-SceI), which is a site-specific endonuclease; Tfp1p	1	3.6107	0.405	1534.7	1535.827	1	396.8	53.846157	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-SceI), which is a site-specific endonuclease; Tfp1p	1	3.095	0.2233	1552.59	1552.827	3	385.2	57.692307	L.G1F1L1K2D1G1V1K2N2I1P1S1F1L1.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-SceI), 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-SceI), 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-SceI), which is a site-specific endonuclease; Tfp1p	2	3.7859	0.3538	1551.81	1552.827	1	879.1	76.92308	L.G1F1L1K2D1G1V1K2N2I1P1S1F1L1.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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), which is a site-specific endonuclease; Tfp1p	2	3.184	0.3032	1710.29	1710.85	1	916.6	60.714287	S.K2S1Y1P1I1S1E1G1P1E1R4A1N2E1L1.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-SceI), 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-SceI), which is a site-specific endonuclease; Tfp1p	3	5.5368	0.3194	2966.21	2966.362	1	657.5	29.166666	A.I1K2E1E1S1Q2S1I1Y1I1P1R4G1I1D1T1P1A1L1D1R4T1I1K2W2.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-SceI), 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-SceI), which is a site-specific endonuclease; Tfp1p	2	3.2671	0.3479	1590.15	1590.779	1	298.8	58.333332	S.KFFEPSRGEKEVH.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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), 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-SceI), which is a site-specific endonuclease; Tfp1p	3	3.9842	0.2292	2590.61	2591.928	1	841.9	32.142857	E.S1Q2S1I1Y1I1P1R4G1I1D1T1P1A1L1D1R4T1I1K2W2Q2.F
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	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.I1K2L1P1L1I1P1D1Q2I1G1V1E1.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	2.7973	0.3147	1434.76	1435.747	3	620.7	54.166668	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	2	3.5995	0.2823	2620.95	2621.733	1	867	54.761906	Q.R4K2A1D1E1E1E1D1L1E1Y1G1D1V1P1D1E1F1L1D1P1L1.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	4.8295	0.3156	3011.69	3012.094	1	629	31.25	A.E1E1Q2R4K2A1D1E1E1E1D1L1E1Y1G1D1V1P1D1E1F1L1D1P1L1.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	2	3.6243	0.2893	1448.29	1450.747	1	873.8	75	Q.I1K2L1P1L1I1P1D1Q2I1G1V1E1.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	2	3.8689	0.3427	1438.71	1435.747	1	969.6	79.16667	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	3.2337	0.3331	1449.35	1450.747	1	939.8	62.5	Q.I1K2L1P1L1I1P1D1Q2I1G1V1E1.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	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
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	1	2.8651	0.3405	1503.66	1504.795	1	418.6	53.846157	L.K2L1G1E1V1I1T1T1I1P1T1I1G1F1.N
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	1	2.7106	0.225	1491.62	1489.795	1	409.4	53.846157	L.KLGEVITTIPTIGF.N
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	3.3511	0.1608	1488.93	1489.795	1	692.4	73.07692	L.KLGEVITTIPTIGF.N

gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	3.2282	0.3287	1831.93	1832.147	1	469	53.125	L.KLGEVITTIPTIGFNVE.T
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	3.0312	0.2094	1702.03	1703.022	2	670.3	61.538464	K.L1F1S1N2L1F1G1N2K2E1M1R4I1L1.M
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	3.3342	0.2786	1681.85	1683.022	1	891	69.230774	K.LFSNLFGNKEMRIL.M
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	3.6685	0.504	1601.39	1603.899	1	838.2	67.85714	L.KLGEVITTIPTIGFN.V
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	3.5276	0.3492	1623.05	1620.899	1	878.4	71.42857	L.K2L1G1E1V1I1T1T1I1P1T1I1G1F1N2.V
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	1	2.3069	0.33	1490.61	1489.795	1	364.6	50	L.KLGEVITTIPTIGF.N
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	3.322	0.3493	1503.55	1504.795	1	508.1	65.38461	L.K2L1G1E1V1I1T1T1I1P1T1I1G1F1.N
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	2.9872	0.3124	1849.87	1851.147	1	694.3	59.375	L.K2L1G1E1V1I1T1T1I1P1T1I1G1F1N2V1E1.T
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	2	3.2343	0.2374	1221.05	1221.503	1	735.4	77.77778	N.LFGNKEMRIL.M
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	1	2.963	0.2345	1235.48	1236.503	1	511.8	72.22222	N.L1F1G1N2K2E1M1R4I1L1.M
gi|6320009|ref|NP_010089.1|	YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	1	2.5032	0.2744	1220.6	1221.503	1	447.1	72.22222	N.LFGNKEMRIL.M
gi|6320003|ref|NP_010083.1|	YDL198C	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p	2	3.583	0.2316	1653.57	1654.789	1	790.6	69.230774	Q.N2R4N2F1D1N2P1E1S1G1L1R4I1V1.K
gi|6320003|ref|NP_010083.1|	YDL198C	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p	1	3.1217	0.2727	1530.56	1530.649	1	458.2	63.636364	K.H3Y1K2K2D1F1D1N2L1F1G1E1.K
gi|6320003|ref|NP_010083.1|	YDL198C	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p	2	3.056	0.3115	1514.39	1513.649	1	538.8	68.181816	K.HYKKDFDNLFGE.K
gi|6320003|ref|NP_010083.1|	YDL198C	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p	1	3.1471	0.3742	1529.5	1530.649	1	330.2	50	K.H3Y1K2K2D1F1D1N2L1F1G1E1.K
gi|6320003|ref|NP_010083.1|	YDL198C	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p	2	3.6222	0.2816	1531.15	1530.649	1	774.9	77.27273	K.H3Y1K2K2D1F1D1N2L1F1G1E1.K
gi|6320003|ref|NP_010083.1|	YDL198C	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p	2	5.3635	0.3969	1761.71	1762.929	1	1575.5	76.92308	K.H3Y1K2K2D1F1D1N2L1F1G1E1K2T1.G
gi|6319993|ref|NP_010073.1|	YDL208W	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing; Nhp2p	2	3.9767	0.3335	1982.31	1981.179	1	433.2	56.25	A.DVISHIPVLCEDHSVPY.I
gi|6319993|ref|NP_010073.1|	YDL208W	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing; Nhp2p	2	4.2772	0.2659	2011.57	2011.205	1	838.4	63.333332	N.K2K2K2D1G1K2N2K2E1E1E1Y1K2E1S1F1.N
gi|6319993|ref|NP_010073.1|	YDL208W	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing; Nhp2p	2	4.046	0.398	2002.95	2002.179	1	366.8	53.125	A.D1V1I1S1H3I1P1V1L1C1E1D1H3S1V1P1Y1.I
gi|6319993|ref|NP_010073.1|	YDL208W	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing; Nhp2p	2	3.2499	0.3739	1644.15	1644.782	6	297.2	50	M.GKDNKEHKESKESK.T
gi|6319993|ref|NP_010073.1|	YDL208W	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing; Nhp2p	2	4.5319	0.3351	1665.53	1666.782	1	751.9	73.07692	M.G1K2D1N2K2E1H3K2E1S1K2E1S1K2.T
gi|6319993|ref|NP_010073.1|	YDL208W	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing; Nhp2p	1	2.9004	0.1674	1185.72	1186.441	6	165.1	60.000004	L.R4K2G1E1K2G1L1V1V1I1A1.G
gi|6319993|ref|NP_010073.1|	YDL208W	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing; Nhp2p	2	3.4513	0.2336	1256.41	1256.534	1	488.1	75	K.NVKRGVKEVVK.A
gi|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	3.2281	0.2735	1526.56	1525.742	1	506.6	61.538464	F.KVIDVDGNPVIEVQ.Y
gi|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	2	4.8645	0.2967	1543.33	1542.742	1	1812.2	84.61539	F.K2V1I1D1V1D1G1N2P1V1I1E1V1Q2.Y
gi|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	2	3.6844	0.274	1528.29	1525.742	4	776	61.538464	F.KVIDVDGNPVIEVQ.Y
gi|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	2	3.3776	0.1576	1886.25	1883.34	7	251	46.875	S.A1M1V1L1T1K2M1K2E1I1A1E1A1K2I1G1K2.K
gi|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	3.4325	0.3744	1542.68	1542.742	1	470.4	57.692307	F.K2V1I1D1V1D1G1N2P1V1I1E1V1Q2.Y

gi|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	2	3.6766	0.2402	2758.99	2758.059	3	617.6	41.304348	Q.K2L1L1S1D1F1F1D1G1K2Q2L1E1K2S1I1N2P1D1E1A1V1A1Y1.G
gi|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	2	3.1598	0.2103	1513.83	1514.806	2	542.8	65.38461	F.G1I1V1V1P1R4N2T1T1V1P1T1I1K2.R
gi|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	2.5025	0.2185	1170.6	1171.385	2	144.1	62.5	S.EKERHVLIF.D
gi|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	2.6113	0.1561	1186.62	1186.385	1	165.1	62.5	S.E1K2E1R4H3V1L1I1F1.D
gi|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	2	4.4491	0.3621	1959.43	1960.169	1	600.9	66.66667	E.R4V1N2C1K2E1N2T1L1L1G1E1F1D1L1K2.N
gi|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	2	3.3444	0.3878	1246.55	1247.348	1	1195.1	81.818184	K.TGLDISDDARAL.R
gi|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	3.0524	0.2121	1526.82	1525.742	5	362.3	53.846157	F.KVIDVDGNPVIEVQ.Y
gi|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	3.3944	0.3766	1541.66	1542.742	1	397.9	53.846157	F.K2V1I1D1V1D1G1N2P1V1I1E1V1Q2.Y
gi|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	2	4.222	0.2809	1543.55	1542.742	1	1223	73.07692	F.K2V1I1D1V1D1G1N2P1V1I1E1V1Q2.Y
gi|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	2	3.1407	0.2532	1333.15	1330.466	1	1498.3	72.72727	A.G1E1P1V1L1E1A1I1F1E1V1D1.A
gi|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	2	3.7255	0.2748	1318.45	1318.466	1	1603.1	77.27273	A.GEPVLEAIFEVD.A
gi|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	3.3288	0.2619	1556.76	1557.784	1	783.8	61.538464	F.KSTLEPVEQVLKDA.K
gi|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	2.6019	0.2058	1273.63	1274.463	1	416.2	55.555557	K.S1E1K2E1R4H3V1L1I1F1.D
gi|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	3	4.1202	0.2155	2941.37	2943.297	1	731.6	31.25	E.R4V1N2C1K2E1N2T1L1L1G1E1F1D1L1K2N2I1P1MMP1A1G1E1.P
gi|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	2.6533	0.2733	1416.7	1417.567	1	292.9	65	K.KHEARQRLESY.V
gi|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	2	3.8543	0.2181	1528.07	1525.742	4	1111.1	69.230774	F.KVIDVDGNPVIEVQ.Y
gi|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	2	4.1052	0.256	1543.29	1542.742	1	999.4	73.07692	F.K2V1I1D1V1D1G1N2P1V1I1E1V1Q2.Y
gi|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	3.0743	0.3191	1526.68	1525.742	1	429.1	57.692307	F.KVIDVDGNPVIEVQ.Y
gi|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.K2V1I1D1V1D1G1N2P1V1I1E1V1Q2.Y
gi|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	2	3.3718	0.2902	1727.29	1726.898	1	728.3	65.38461	F.DDESVQKDMKTWPF.K
gi|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	2	4.2084	0.3019	1743.75	1744.898	1	669.7	61.538464	F.D1D1E1S1V1Q2K2D1M1K2T1W2P1F1.K
gi|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	3	5.8157	0.4356	3259.16	3260.588	1	1663.7	30.46875	F.DLGGGTFDVSLLHIAGGVYTVKSTSGNTHLGGQ.D
gi|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	2.6107	0.2113	1257.64	1258.463	7	347.4	55.555557	K.SEKERHVLIF.D

gi|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	2	2.9254	0.184	1795.51	1795.175	2	398.8	46.666668	D.M1F1G1I1V1V1P1R4N2T1T1V1P1T1I1K2.R
gi|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	2.3546	0.1689	1261.2	1262.348	3	335.9	50	K.T1G1L1D1I1S1D1D1A1R4A1L1.R
gi|6320204|ref|NP_010284.1|	YDR001C	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by Cdc28p; Nth1p	2	4.6244	0.2373	2117.63	2117.375	1	1061.3	62.5	L.Y1N2D1G1K2I1K2E1P1K2L1D1E1F1F1L1H3.D
gi|6320204|ref|NP_010284.1|	YDR001C	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by Cdc28p; Nth1p	2	3.6026	0.3689	2094.83	2094.375	1	705.3	50	L.YNDGKIKEPKLDEFFLH.D
gi|6320204|ref|NP_010284.1|	YDR001C	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by Cdc28p; Nth1p	3	4.8891	0.3904	2116.43	2117.375	1	742.9	42.1875	L.Y1N2D1G1K2I1K2E1P1K2L1D1E1F1F1L1H3.D
gi|6320204|ref|NP_010284.1|	YDR001C	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by Cdc28p; Nth1p	2	4.8495	0.2464	2118.57	2117.375	1	1046.4	59.375	L.Y1N2D1G1K2I1K2E1P1K2L1D1E1F1F1L1H3.D
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	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	21.428572	A.E1K2P1E1T1K2K2D1E1E1D1T1K2E1E1T1K2K2E1G1D1D1A1P1E1S1P1D1I1H3F1E1P1V1V1H3.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	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	5.0582	0.419	2454.01	2453.698	1	1035.5	50	M.S1S1E1D1K2K2P1V1V1D1K2K2E1E1A1A1P1K2P1P1S1S1A1.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	3.0384	0.3009	1825.05	1826.028	1	585.2	57.14286	D.AKEWKERGTGDCKFL.K
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	5.284	0.3733	2121.83	2123.351	1	1234.9	63.88889	C.A1N2H3I1I1A1P1E1Y1T1L1K2P1N2V1G1S1D1R4.S
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	3.9985	0.3175	2096.11	2096.351	1	627	47.22222	C.ANHIIAPEYTLKPNVGSDR.S
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	2.9696	0.287	1910.95	1911.168	1	427.8	53.125	N.HIIAPEYTLKPNVGSDR.S
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	4.1405	0.3633	1933.75	1935.168	1	1117.7	62.5	N.H3I1I1A1P1E1Y1T1L1K2P1N2V1G1S1D1R4.S
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	5.4172	0.4627	2662.85	2663.951	1	654.4	47.727272	C.A1N2H3I1I1A1P1E1Y1T1L1K2P1N2V1G1S1D1R4S1W2V1Y1.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	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 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	5.2339	0.3772	3969.32	3971.151	1	535.4	22.727274	A.E1K2P1E1T1K2K2D1E1E1D1T1K2E1E1T1K2K2E1G1D1D1A1P1E1S1P1D1I1H3F1E1P1V1.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	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
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	4.2838	0.4292	2122.37	2122.426	1	826.5	52.63158	E.DKKPVVDKKEEAAPKPPSSA.V
gi|6320214|ref|NP_010294.1|	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	1	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; Snq2p	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; Snq2p	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.K2A1D1V1I1Y1N2G1E1L1D1V1H3F1P1Y1L1.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

gi|6320214|ref|NP_010294.1|	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	2	3.7289	0.3136	1432.19	1430.545	1	939.1	81.818184	F.V1R4D1A1D1E1Q2G1I1H3I1R4.K
gi|6320214|ref|NP_010294.1|	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	2	4.4177	0.2784	1670.61	1670.872	1	968.4	80.769226	W.KDVCFTIPYEGGKR.M
gi|6320214|ref|NP_010294.1|	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	2	3.0962	0.2708	1493.15	1492.715	6	292.1	62.5	L.I1K2P1G1Y1E1N2K2V1P1R4T1A1.E
gi|6320214|ref|NP_010294.1|	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet 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	ABC transporter protein involved in multidrug resistance and resistance to singlet 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
gi|6320214|ref|NP_010294.1|	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	2	3.0715	0.2497	1182.29	1182.362	2	1099.7	87.5	T.LFEEFDRLL.L
gi|6320214|ref|NP_010294.1|	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	2	4.1784	0.352	1900.57	1901.095	1	946.6	60.000004	Y.K2A1D1V1I1Y1N2G1E1L1D1V1H3F1P1Y1.L
gi|6320214|ref|NP_010294.1|	YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	2	2.9319	0.1835	1296.15	1295.521	1	795.7	88.88889	T.LFEEFDRLLL.L
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	3.7674	0.3037	2419.77	2419.644	1	520.8	44.736843	S.EFDEELYKVIDGEDEKYLIA.T
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	4.1314	0.289	1885.59	1883.123	1	1017.9	64.28571	F.VITEPEKSWEEFEKM.I
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	4.2853	0.2383	2621.67	2619.882	1	1273.3	57.14286	Q.LSEFDEELYKVIDGEDEKYLIA.T
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	4.8859	0.4694	2142.49	2140.395	1	1164.5	55.88235	A.SVEIVDEIISDYKDWVKT.R
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	4.7799	0.4508	2124.83	2126.335	1	1169.5	62.5	Y.HSGEWFEKPQEQLPIHY.V
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	3.8962	0.3904	2225.47	2225.468	1	1317	61.764706	Y.HSGEWFEKPQEQLPIHYV.G
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	4.2263	0.3726	2443.93	2445.696	1	720	47.368423	Y.HSGEWFEKPQEQLPIHYVGY.S
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	3.1734	0.2159	1594.39	1593.866	1	676.4	70.83333	L.RKYIPGEPEFLPF.V
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	1	2.6316	0.1821	1592.64	1593.866	1	379.2	58.333332	L.RKYIPGEPEFLPF.V
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	3.0458	0.3334	1953.21	1952.211	1	406.8	50	S.VEIVDEIISDYKDWVK.T
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	3.1392	0.1786	1814.85	1811.983	1	785.6	57.14286	A.SVEIVDEIISDYKDW.V
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	5.0811	0.3723	2062.27	2059.29	1	2444.6	71.875	A.S1V1E1I1V1D1E1I1I1S1D1Y1K2D1W2V1K2.T
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	4.6321	0.3773	2042.03	2039.29	1	1878	65.625	A.SVEIVDEIISDYKDWVK.T
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	4.553	0.3711	2472.97	2473.696	1	604.3	44.736843	Y.H3S1G1E1W2F1E1K2P1Q2E1Q2L1P1I1H3Y1V1G1Y1.S
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	3.9944	0.3543	2160.05	2161.395	1	553.1	44.11765	A.S1V1E1I1V1D1E1I1I1S1D1Y1K2D1W2V1K2T1.R
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	3	4.076	0.2463	1902.26	1901.123	1	729.8	50	F.V1I1T1E1P1E1K2S1W2E1E1F1E1K2M1.I
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	3.8129	0.2602	2254.17	2255.406	1	817.3	50	S.E1F1D1E1E1L1Y1K2V1I1D1G1E1D1E1K2Y1L1.I
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	3	3.8139	0.2301	2257.55	2255.406	1	844	39.705883	S.E1F1D1E1E1L1Y1K2V1I1D1G1E1D1E1K2Y1L1.I

gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	4.4875	0.2412	2443.73	2441.644	1	1134.8	52.63158	S.E1F1D1E1E1L1Y1K2V1I1D1G1E1D1E1K2Y1L1I1A1.T
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	3	3.9518	0.1586	2774.21	2774.012	1	477.5	29.545454	A.Q2L1S1E1F1D1E1E1L1Y1K2V1I1D1G1E1D1E1K2Y1L1I1A1.T
gi|6320226|ref|NP_010306.1|	YDR023W	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; Ses1p	2	5.5439	0.4171	2151.37	2151.335	1	1355.2	65.625	Y.H3S1G1E1W2F1E1K2P1Q2E1Q2L1P1I1H3Y1.V
gi|6320226|ref|NP_010306.1|	YDR023W	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; 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 membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p	2	4.1029	0.3582	1951.59	1953.162	1	1082	61.11111	R.GGNEAIKINPPTGADFHIT.S
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	2.2551	0.2166	1090.56	1091.299	6	203.1	55	A.PKAPVASPRPA.A
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	2.6369	0.1938	1446.83	1445.702	7	215.8	45.833336	A.ATPNLSKDKKKKS.K
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	4.1176	0.3679	1620.49	1620.756	1	879.3	66.66667	R.G1G1N2E1A1I1K2I1N2P1P1T1G1A1D1F1.H
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	2.2093	0.2327	1172.65	1173.354	4	327.5	60.000004	A.IKINPPTGADF.H
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	4.6555	0.3505	1738.03	1738.897	1	1088.1	65.625	R.GGNEAIKINPPTGADFH.I
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	5.0976	0.395	1761.33	1760.897	1	797.7	59.375	R.G1G1N2E1A1I1K2I1N2P1P1T1G1A1D1F1H3.I
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	3	3.9656	0.2273	1978.13	1977.162	1	1026.8	40.27778	R.G1G1N2E1A1I1K2I1N2P1P1T1G1A1D1F1H3I1T1.S
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	3	4.1434	0.3002	1953.47	1953.162	1	1061.9	40.27778	R.GGNEAIKINPPTGADFHIT.S
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	4.7931	0.3886	1979.47	1977.162	1	858.5	55.555557	R.G1G1N2E1A1I1K2I1N2P1P1T1G1A1D1F1H3I1T1.S
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	3.0881	0.2573	1227.63	1228.465	2	725.4	70	A.S1N2L1G1W2I1P1V1K2A1K2.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.I1K2I1N2P1P1T1G1A1D1F1H3I1T1.S
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	3.8316	0.2952	1525.23	1524.76	1	721.8	65.38461	A.IKINPPTGADFHIT.S
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	2.7707	0.3181	1523.74	1524.76	1	357.2	46.153847	A.IKINPPTGADFHIT.S
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	2.8044	0.3612	1541.58	1542.76	1	440.4	50	A.I1K2I1N2P1P1T1G1A1D1F1H3I1T1.S
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	3.1891	0.2578	1699.45	1698.974	1	397.5	56.25	V.M1A1P1K2A1P1V1A1S1P1R4P1A1A1T1P1N2.L
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	3.2133	0.3435	1675.63	1676.974	1	466.9	50	V.MAPKAPVASPRPAATPN.L
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	2.9944	0.3375	1178.07	1178.377	1	540.2	72.72727	M.A1P1K2A1P1V1A1S1P1R4P1A1.A
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	2.5958	0.327	1292.63	1293.57	1	440.4	66.66667	V.MAPKAPVASPRPA.A
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	3.5806	0.4443	1177.68	1178.377	1	304.6	63.636364	M.A1P1K2A1P1V1A1S1P1R4P1A1.A
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	3.0152	0.4264	1162.81	1162.377	1	281.1	63.636364	M.APKAPVASPRPA.A
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	2.9649	0.2629	1324.41	1326.57	1	789.8	75	V.M$A1P1K2A1P1V1A1S1P1R4P1A1.A
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	2.6387	0.3074	1309.65	1310.57	1	353.9	62.5	V.M1A1P1K2A1P1V1A1S1P1R4P1A1.A

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	3.5845	0.3254	1901.55	1901.212	1	690.9	58.333332	V.M1A1P1K2A1P1V1A1S1P1R4P1A1A1T1P1N2L1S1.K
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	3.2788	0.3658	1879.53	1877.212	1	584.9	55.555557	V.MAPKAPVASPRPAATPNLS.K
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	3.1243	0.1847	2098.59	2099.313	1	300.4	46.875	Q.TSTQKEHPGYRQIFYSR.F
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	4.355	0.4007	1602.45	1601.756	1	828	63.333332	R.GGNEAIKINPPTGADF.H
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	2.5124	0.2169	1213.62	1213.465	9	362.1	60.000004	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	3.1754	0.2316	1213.59	1213.465	3	710.9	75	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	3.0994	0.2929	1312.35	1310.57	1	716.8	79.16667	V.M1A1P1K2A1P1V1A1S1P1R4P1A1.A
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	2.6719	0.3048	1310.54	1310.57	1	310.8	58.333332	V.M1A1P1K2A1P1V1A1S1P1R4P1A1.A
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	2.9249	0.1894	1211.15	1210.494	1	1561.9	88.88889	W.F1L1A1L1P1W2P1I1I1Q2.I
gi|6320255|ref|NP_010335.1|	YDR050C	Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is regulated by iron availability; transcription is controlled by activators Reb1p, Gcr1p, and Rap1p through binding sites in the 5' non-coding region; Tpi1p	2	3.2768	0.2027	1520.05	1518.753	1	417.6	66.66667	A.SLKPEFVDIINSR.N
gi|6320255|ref|NP_010335.1|	YDR050C	Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is regulated by iron availability; transcription is controlled by activators Reb1p, Gcr1p, and Rap1p through binding sites in the 5' non-coding region; Tpi1p	2	3.2035	0.2476	1502.95	1502.565	1	786.4	72.72727	R.S1Y1F1H3E1D1D1K2F1I1A1D1.K
gi|6320255|ref|NP_010335.1|	YDR050C	Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is 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.V1E1D1I1K2P1E1D1K2F1F1Y1Q2.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	2	4.1753	0.2292	2626.33	2627.798	1	503.9	40.476192	Y.D1K2P1W2Y1E1I1P1L1D1P1Q2V1G1Q2N2D1D1V1E1E1L1.S
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	3.5038	0.3076	1462.69	1463.625	1	704.6	68.181816	L.N2N2K2Y1I1C1E1P1P1L1S1L1.R
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	4.0392	0.3563	2295.45	2295.678	1	1308.9	57.5	R.SILKEPDLLLIDDPFLGLDPA.A
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	4.5354	0.3616	2316.93	2317.678	1	1303.2	57.5	R.S1I1L1K2E1P1D1L1L1L1I1D1D1P1F1L1G1L1D1P1A1.A
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	3.917	0.4094	2260.51	2259.598	1	799.4	50	L.K2E1P1D1L1L1L1I1D1D1P1F1L1G1L1D1P1A1A1I1A1.T
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	3.6088	0.2668	2549.33	2550.995	1	610.3	36.95652	R.SILKEPDLLLIDDPFLGLDPAAIA.T
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	5.8423	0.4415	2002.11	2001.281	1	1546.2	67.64706	L.K2E1P1D1L1L1L1I1D1D1P1F1L1G1L1D1P1A1.A
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	4.2067	0.3899	2237.57	2237.598	1	813.7	50	L.KEPDLLLIDDPFLGLDPAAIA.T
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	3.1731	0.3334	1887.91	1888.232	1	1049.1	66.66667	K.EHEIIKMPHLIELDGL.S
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	3.0553	0.1808	1736.03	1737.021	8	376.8	50	K.E1H3E1I1I1K2M1P1H3L1I1E1L1D1.G
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	5.0721	0.4083	1983.15	1982.281	1	1581.7	67.64706	L.KEPDLLLIDDPFLGLDPA.A
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	3.5605	0.1697	1743.73	1742.895	2	509.8	53.571426	L.R4L1I1S1P1G1E1Y1E1I1G1D1M1E1N2.-
gi|6320266|ref|NP_010346.1|	YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	2	3.9558	0.387	1496.63	1496.676	1	1164.5	66.66667	L.R4L1I1S1P1G1E1Y1E1I1G1D1M1.E
gi|6320267|ref|NP_010347.1|	YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	2	5.1714	0.3732	2471.15	2472.639	1	795.6	47.368423	A.N2Y1T1R4V1P1L1C1E1P1E1E1L1P1D1D1I1Q2K2E1.N
gi|6320267|ref|NP_010347.1|	YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	2	5.6323	0.367	2773.41	2774.966	1	930.4	43.18182	T.R4V1P1L1C1E1P1E1E1L1P1D1D1I1Q2K2E1N2E1Y1G1T1L1.D
gi|6320267|ref|NP_010347.1|	YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	2	5.3743	0.4395	2743.91	2745.966	1	1156.8	47.727272	T.RVPLCEPEELPDDIQKENEYGTL.D
gi|6320267|ref|NP_010347.1|	YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	2	4.9743	0.3393	3156.37	3157.351	1	821.5	38	A.N2Y1T1R4V1P1L1C1E1P1E1E1L1P1D1D1I1Q2K2E1N2E1Y1G1T1L1.D
gi|6320267|ref|NP_010347.1|	YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	2	4.8043	0.467	3121.99	3124.351	1	913.1	40	A.NYTRVPLCEPEELPDDIQKENEYGTL.D
gi|6320267|ref|NP_010347.1|	YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	2	3.3616	0.233	2089.11	2090.254	2	449.7	46.875	T.R4V1P1L1C1E1P1E1E1L1P1D1D1I1Q2K2E1.N
gi|6320267|ref|NP_010347.1|	YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	3	4.3798	0.2408	4161.65	4162.481	1	537.8	19.117647	T.R4V1P1L1C1E1P1E1E1L1P1D1D1I1Q2K2E1N2E1Y1G1T1L1D1S1P1G1H3L1Y1Q2V1K2S1R4.H
gi|6320267|ref|NP_010347.1|	YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	3	4.733	0.3847	3123.08	3124.351	1	1324.5	33	A.NYTRVPLCEPEELPDDIQKENEYGTL.D
gi|6320269|ref|NP_010349.1|	YDR064W	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosomal proteins; Rps13p	2	4.6696	0.3538	2086.59	2085.386	1	1254.9	70.588234	L.K2S1N2G1L1A1P1E1I1P1E1D1L1Y1Y1L1I1K2.K
gi|6320269|ref|NP_010349.1|	YDR064W	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosomal proteins; Rps13p	2	4.8217	0.1858	2066.87	2064.386	1	1101.2	67.64706	L.KSNGLAPEIPEDLYYLIK.K
gi|6320269|ref|NP_010349.1|	YDR064W	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosomal proteins; Rps13p	2	2.9816	0.1814	1543.27	1540.762	1	370.3	62.5	S.A1I1P1Y1S1R4N2A1P1A1W2F1K2.L
gi|6320269|ref|NP_010349.1|	YDR064W	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosomal proteins; Rps13p	1	2.743	0.2982	1409.42	1410.588	1	275.6	54.545456	S.A1I1P1Y1S1R4N2A1P1A1W2F1.K
gi|6320269|ref|NP_010349.1|	YDR064W	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosomal proteins; Rps13p	2	3.2132	0.2	1838.79	1841.053	1	763	56.666668	L.K2S1N2G1L1A1P1E1I1P1E1D1L1Y1Y1L1.I
gi|6320269|ref|NP_010349.1|	YDR064W	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 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.R4L1I1N2C1P1E1L1C1.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; Paa1p	2	3.5907	0.1661	1403.29	1401.602	1	829.2	77.27273	M.GTKIPHEYITIE.S
gi|6320291|ref|NP_010371.1|	YDR086C	Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum membrane, and of the Ssh1p complex (Ssh1p-Sbh2p-Sss1p); interacts with Ost4p and Wbp1p; Sss1p	2	4.0526	0.4894	1606.61	1608.791	1	1869.9	80.769226	L.VEAPVEFVREGTQF.L
gi|6320291|ref|NP_010371.1|	YDR086C	Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum membrane, and of the Ssh1p complex (Ssh1p-Sbh2p-Sss1p); interacts with Ost4p and Wbp1p; Sss1p	2	4.4689	0.3894	1721.51	1721.951	1	1430.5	78.57143	L.VEAPVEFVREGTQFL.A
gi|6320291|ref|NP_010371.1|	YDR086C	Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum membrane, and of the Ssh1p complex (Ssh1p-Sbh2p-Sss1p); interacts with Ost4p and Wbp1p; Sss1p	2	3.9173	0.3737	1741.99	1740.951	1	772.5	64.28571	L.V1E1A1P1V1E1F1V1R4E1G1T1Q2F1L1.A
gi|6320291|ref|NP_010371.1|	YDR086C	Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum membrane, and of the Ssh1p complex (Ssh1p-Sbh2p-Sss1p); 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 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	3.4558	0.3092	2713.57	2715.073	1	573.9	40.909092	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	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.C1I1I1K2I1P1G1S1T1P1K2D1E1P1K2A1L1.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	3	3.9904	0.3176	2744.9	2746.073	2	436.5	30.681818	A.S1V1T1N2R4E1E1E1L1D1K2V1T1D1V1I1E1R4E1L1I1L1L1.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	3	3.872	0.3034	3244.79	3245.718	8	244.9	24.074074	Y.YNLPLPEDMLDEDGLPLAVYPRNKIRTT.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	3.8981	0.2536	3044.87	3043.508	6	311.3	27.000002	Y.YNLPLPEDMLDEDGLPLAVYPRNKIR.T
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	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 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	4.7929	0.4019	3407.42	3408.894	1	288.3	25	V.YYNLPLPEDMLDEDGLPLAVYPRNKIRTT.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	2	4.5035	0.2121	1867.57	1868.19	1	577.4	59.375	S.CIIKIPGSTPKDEPKAL.L
gi|6320306|ref|NP_010386.1|	YDR101C	Protein associated with the ribosomal export complex; Arx1p	2	4.2462	0.4427	2467.75	2467.97	1	776.7	43.18182	T.MVIYPVDETKPILQPTGPLLGGK.A
gi|6320306|ref|NP_010386.1|	YDR101C	Protein associated with the ribosomal export complex; Arx1p	2	2.9626	0.362	1672.73	1672.021	1	554.9	50	T.LTLPGHELPLPKLGVS.A
gi|6320306|ref|NP_010386.1|	YDR101C	Protein associated with the ribosomal export complex; Arx1p	2	3.1815	0.2133	2230.77	2231.603	6	273.5	32.5	M.V1I1Y1P1V1D1E1T1K2P1I1L1Q2P1T1G1P1L1L1G1G1.K
gi|6320306|ref|NP_010386.1|	YDR101C	Protein associated with the ribosomal export complex; Arx1p	2	3.3108	0.2695	1692.59	1691.021	1	673.9	53.333336	T.L1T1L1P1G1H3E1L1P1L1P1K2L1G1V1S1.A
gi|6320308|ref|NP_010388.1|	YDR103W	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 signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p	2	3.4183	0.2275	2235.47	2237.602	1	422.7	42.105263	T.LSRTPNQIIELEKPSTLSPL.S
gi|6320308|ref|NP_010388.1|	YDR103W	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 signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p	2	3.2369	0.2566	1778.37	1776.088	9	363	50	Q.SRFPPYSPLLPPFGLS.Y
gi|6320308|ref|NP_010388.1|	YDR103W	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 signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p	2	3.978	0.3195	1796.23	1795.088	1	525.3	56.666668	Q.S1R4F1P1P1Y1S1P1L1L1P1P1F1G1L1S1.Y
gi|6320308|ref|NP_010388.1|	YDR103W	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 signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p	2	3.3918	0.3585	1690.63	1689.01	1	516.4	64.28571	Q.SRFPPYSPLLPPFGL.S
gi|6320308|ref|NP_010388.1|	YDR103W	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 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.S1P1S1V1E1K2E1L1T1D1E1E1I1L1Q2E1A1S1.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.S1P1S1V1E1K2E1L1T1D1E1E1I1L1Q2E1A1.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	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of 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
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	1	2.8428	0.2368	1555.54	1556.83	1	425.3	57.692307	A.K2V1P1I1L1G1N2D1I1I1H3V1G1Y1.N
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	4.1041	0.3447	1919.41	1920.13	1	1507.5	68.75	V.S1C1V1P1A1D1K2P1L1D1D1E1L1L1S1K2L1.E
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	3.0181	0.2227	1816.49	1814.052	2	493.6	56.666668	S.CVPADKPLDDELLSKL.E
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	3.333	0.2852	1831.85	1832.052	2	529.2	53.333336	S.C1V1P1A1D1K2P1L1D1D1E1L1L1S1K2L1.E
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	4.0115	0.2597	1752.13	1752.762	1	1138.5	75	L.Y1S1W2D1D1A1E1W2E1N2R4F1N2.Q
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	4.5508	0.172	1493.59	1492.654	1	1801.2	86.36364	Y.K2L1V1D1L1D1E1L1F1E1Q2Q2.H
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	4.5256	0.2985	1698.59	1697.882	1	2199.4	73.07692	L.GYKLVDLDELFEQQ.H
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	4.9965	0.1621	1714.61	1714.882	1	2294.6	76.92308	L.G1Y1K2L1V1D1L1D1E1L1F1E1Q2Q2.H
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	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
gi|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	3	3.9375	0.4127	3350.99	3352.561	1	292.2	22.413794	L.D1V1L1N2G1I1A1P1G1Y1V1D1Y1D1L1V1T1P1G1N2T1E1E1E1R4Y1A1N2A1R4 L
gi|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	4.7725	0.3583	2388.67	2391.543	1	852.9	50	F.N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi|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	4.4446	0.3365	2364.75	2366.543	1	757.6	50	F.NTHPGLEPIQEEEKPEIEEF.D
gi|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	2.9413	0.1517	2252.43	2252.439	3	399.2	41.666664	N.THPGLEPIQEEEKPEIEEF.D
gi|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	3.8192	0.2956	2708.27	2709.826	1	397.6	40.909092	F.N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1.G
gi|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	5.0035	0.3507	2592.71	2593.722	1	479.6	47.61905	N.T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1.G
gi|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	3.8726	0.3208	2567.85	2567.722	1	373.3	42.857143	N.THPGLEPIQEEEKPEIEEFDAE.G
gi|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	3.8726	0.3226	2971.35	2972.162	1	296.2	31.25	H.L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1.G
gi|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
gi|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	3	4.8211	0.2865	3626.75	3626.872	1	508	26.666668	F.NTHPGLEPIQEEEKPEIEEFDAEGEREARVF.T
gi|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	4.7152	0.3609	2652.67	2653.879	1	720.4	45.238094	H.L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi|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	3	4.318	0.3414	2837.21	2838.277	1	1510.9	35.227272	Y.RLLEDDETLEQFLRLPPEQILLR.W
gi|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	4.1296	0.3179	2793.43	2794.02	1	808.1	40.909092	A.H3L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi|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	3	5.4821	0.4106	2792.12	2794.02	1	2054.2	40.909092	A.H3L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi|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	3.8358	0.3015	2762.79	2764.02	1	634.2	36.363636	A.HLFNTHPGLEPIQEEEKPEIEEF.D
gi|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	3	5.5396	0.3949	4070.21	4071.349	1	601.8	25	A.H3L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1G1E1R4E1A 1R4V1F1.T
gi|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	3.7284	0.3026	1365.87	1366.675	1	1069.9	80	F.L1R4L1P1P1E1Q2I1L1L1R4.W
gi|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	3.3486	0.2799	1418.29	1417.561	1	701.7	68.181816	F.RAIDLDDKGWVE.K
gi|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	3	5.3061	0.383	3929.93	3931.208	1	335	24.21875	H.L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1G1E1R4E1A1F 4V1F1.T
gi|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	3	5.0139	0.375	3888.02	3887.208	1	420.5	26.5625	H.LFNTHPGLEPIQEEEKPEIEEFDAEGEREARVF.T
gi|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	3	4.6298	0.3823	3110.36	3112.303	1	855.2	29	A.H3L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1D1A1E1.G
gi|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	3	4.8514	0.377	3077.99	3079.303	1	1286.4	34	A.HLFNTHPGLEPIQEEEKPEIEEFDAE.G
gi|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	3	4.6725	0.3633	2763.08	2764.02	1	1650	39.772728	A.HLFNTHPGLEPIQEEEKPEIEEF.D
gi|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	4.3203	0.2654	2792.69	2794.02	1	628.3	38.636364	A.H3L1F1N2T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi|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	3.8053	0.1963	1262.33	1262.489	1	1062.9	85	S.LFDDLKDGLIL.L
gi|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	3.8721	0.2989	2276.55	2275.439	1	484.3	50	N.T1H3P1G1L1E1P1I1Q2E1E1E1K2P1E1I1E1E1F1.D
gi|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	3	4.8275	0.1793	1366.55	1366.675	4	1648.7	65	F.L1R4L1P1P1E1Q2I1L1L1R4.W

gi|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	3.1545	0.2452	1349.41	1348.675	1	942.9	75	F.LRLPPEQILLR.W
gi|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	3.7279	0.2722	1365.75	1366.675	1	1110.8	80	F.L1R4L1P1P1E1Q2I1L1L1R4.W
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	1	2.2862	0.1763	1367.61	1365.554	1	461.2	55	K.LTNLSMECRQL.K
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	3.2736	0.2866	1671.79	1669.795	1	735.1	66.66667	L.VDQIEYDETIRKC.N
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	3.7097	0.2807	1713.95	1714.926	2	805.7	60.714287	R.K2E1N2L1P1N2L1E1K2P1I1V1D1N2A1.S
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	3.8188	0.2365	1736.21	1734.916	1	874.3	61.538464	S.E1E1D1I1F1D1I1V1I1E1I1D1H3M1.I
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	3.5489	0.2438	1907.45	1907.131	1	967.4	63.333332	Q.RKYSELEKEVEQPSLA.Y
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	3.7354	0.26	1718.97	1718.916	1	864	57.692307	S.EEDIFDIVIEIDHM.I
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	3.8856	0.3487	1927.35	1929.131	1	398.3	53.333336	Q.R4K2Y1S1E1L1E1K2E1V1E1Q2P1S1L1A1.Y
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	3.0657	0.212	1697.37	1694.926	1	373	53.571426	R.KENLPNLEKPIVDNA.S
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	3.634	0.2306	1629.13	1626.977	1	765.6	73.07692	F.NLLKEPTIDFLLPL.T
gi|6320353|ref|NP_010434.1|	YDR150W	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 cortex; Num1p	2	4.0824	0.2433	1605.89	1606.857	1	960.2	70.83333	E.L1E1K2K2L1E1Q2P1S1L1E1Y1L1.V
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by 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
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	2	3.7553	0.3147	2949.49	2952.322	1	308.8	35.416664	K.N2Y1R4R4E1Q2D1V1P1L1I1V1P1V1V1N2P1E1H3L1D1I1V1A1Q2.K
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the 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
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by 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
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	2	4.1799	0.2542	2750.67	2750.112	3	243.6	36.363636	K.N2Y1R4R4E1Q2D1V1P1L1I1V1P1V1V1N2P1E1H3L1D1I1V1.A
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the 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
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	2	3.3715	0.1654	2437.81	2438.833	1	298.6	42.5	Y.RREQDVPLIVPVVNPEHLDIV.A
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	3	3.873	0.283	2637.89	2638.042	1	1155.5	36.363636	Y.RREQDVPLIVPVVNPEHLDIVAQ.K
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the 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
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	2	3.5109	0.323	2468.05	2469.833	1	408.3	45	Y.R4R4E1Q2D1V1P1L1I1V1P1V1V1N2P1E1H3L1D1I1V1.A
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the 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.NYRREQDVPLIVPVVNPEHLDIVAQ.K
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p 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
gi|6320362|ref|NP_010442.1|	YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by 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
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	3.2349	0.2283	1564.59	1564.664	4	429.4	62.5	M.DKLNDDEERLMDA.Q
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	4.1455	0.1667	2495.33	2495.71	5	1019.5	32.954548	S.N2D1Q2R4Q2D1A1A1D1G1I1T1P1P1P1K2Q2K2I1I1D1A1A1.I
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	4.1417	0.2973	2739.63	2740.969	1	965.7	52.380955	L.N2E1L1F1E1N2E1D1F1A1H3C1I1P1Y1K2E1A1I1R4I1T1.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	3.4269	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.D1F1A1H3C1I1P1Y1K2E1A1I1R4I1T1.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	31.666666 T.K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1E1K2T1E1E1K2S1E1L1P1K2V1E1D1L1.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	33.333336 T.K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1E1K2T1E1E1K2S1E1L1P1K2V1E1D1L1K2I1S1.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.D1T1N2K2E1E1R4N2D1G1K2T1I1E1V1G1.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.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	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	26.612906	K.E1E1E1K2S1A1E1T1K2E1P1T1K2E1P1T1K2V1E1E1P1V1K2K2E1E1K2P1V1Q2T1E1.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.V1V1D1I1E1V1P1M1E1Y1P1F1K2P1P1K2M1Q2.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.V1V1D1I1E1V1P1M1E1Y1P1F1K2P1P1K2M1Q2F1.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.V1V1D1I1E1V1P1M1E1Y1P1F1K2P1P1K2M1Q2F1.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.V1V1D1I1E1V1P1M1E1Y1P1F1K2P1P1K2M1Q2F1D1T1K2.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	2	3.1006	0.1582	1530.31	1530.724	2	402.6	72.72727	A.KEAEERTELRIR.A
gi|6320417|ref|NP_010497.1|	YDR211W	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; Gcd6p	2	4.3079	0.2815	1808.39	1807.007	1	1182.9	71.42857	Q.I1D1P1E1L1L1D1N2V1D1E1F1V1I1R4.N

gi|6320417|ref|NP_010497.1|	YDR211W	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; Gcd6p	2	4.3321	0.3593	2014.75	2017.212	1	549.1	50	F.N2V1K2I1D1D1N2M1D1L1D1R4N2T1K2I1S1.A
gi|6320417|ref|NP_010497.1|	YDR211W	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; Gcd6p	2	4.0692	0.2007	1987.53	1989.158	4	312.7	53.333336	W.W2D1N2V1S1T1D1P1R4Y1D1E1V1K2K2L1.T
gi|6320417|ref|NP_010497.1|	YDR211W	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; Gcd6p	1	2.2181	0.1646	1275.54	1276.453	1	400.1	61.11111	N.S1K2W2N2L1P1W2S1P1F1.K
gi|6320417|ref|NP_010497.1|	YDR211W	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; Gcd6p	1	2.6595	0.2158	1189.5	1188.375	4	296.4	62.5	S.K2W2N2L1P1W2S1P1F1.K
gi|6320417|ref|NP_010497.1|	YDR211W	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; Gcd6p	2	3.318	0.2315	1965.09	1966.158	1	488.9	60.000004	W.WDNVSTDPRYDEVKKL.T
gi|6320417|ref|NP_010497.1|	YDR211W	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; Gcd6p	1	2.4878	0.1787	1206.45	1206.401	2	436.7	66.66667	Q.S1F1D1K2P1D1L1I1L1F1.S
gi|6320417|ref|NP_010497.1|	YDR211W	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; Gcd6p	1	2.624	0.1621	1176.52	1175.375	8	278.8	62.5	S.KWNLPWSPF.K
gi|6320432|ref|NP_010512.1|	YDR226W	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence; Adk1p	2	4.7496	0.4208	2124.93	2125.339	1	897.1	55.88235	Y.H3K2I1F1N2P1P1K2E1D1M1K2D1D1V1T1G1E1.A
gi|6320432|ref|NP_010512.1|	YDR226W	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the 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	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence; Adk1p	2	4.268	0.3544	2102.79	2101.339	1	1126.1	61.764706	Y.HKIFNPPKEDMKDDVTGE.A
gi|6320438|ref|NP_010518.1|	YDR232W	5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic pathway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is regulated by Hap2p-Hap3p; Hem1p	1	2.6718	0.1777	1357.49	1357.596	3	285.2	54.166668	I.PNPSHIVPVLIGN.A
gi|6320438|ref|NP_010518.1|	YDR232W	5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic pathway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is regulated by Hap2p-Hap3p; Hem1p	2	3.4634	0.3115	1838.75	1837.216	1	692.8	52.941177	L.GIPVIPNPSHIVPVLIGN.A
gi|6320438|ref|NP_010518.1|	YDR232W	5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic pathway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is regulated by Hap2p-Hap3p; Hem1p	2	3.8659	0.3806	2218.61	2216.632	1	554.7	45	F.HELGIPVIPNPSHIVPVLIGN.A
gi|6320438|ref|NP_010518.1|	YDR232W	5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic pathway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is regulated by Hap2p-Hap3p; Hem1p	2	5.0909	0.4442	2244.53	2243.632	1	549.6	45	F.H3E1L1G1I1P1V1I1P1N2P1S1H3I1V1P1V1L1I1G1N2.A
gi|6320438|ref|NP_010518.1|	YDR232W	5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic pathway; an N-terminal signal sequence is required for localization to the 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
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	3.8715	0.1585	4710.14	4712.156	1	455.7	18.75	Q.VMPEVPQHEPSTTQEFNVDELSNELKKSTKNLQNELEKNNA.-
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	3.5245	0.3111	1742.53	1743.946	1	366.7	65.38461	A.C1E1K2T1K2P1Y1L1D1K2V1E1S1K2.L
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	5.2338	0.2595	2406.53	2404.694	1	2215.4	47.5	M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2.L
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	5.5071	0.4419	2402.25	2404.694	1	766.9	60.000004	M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2.L
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	5.6058	0.2782	2025.67	2025.346	1	1489.1	67.64706	K.T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2L1.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	5.4115	0.4017	2005.63	2003.346	1	1722.2	64.70589	K.TKPYLDKVESKLGPISNL.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	4.9201	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
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	2.9833	0.2569	1748.37	1749.106	1	716.4	60.714287	F.IKPHIDEALKQLPVF.Q
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	4.7455	0.3107	1969.83	1971.316	1	1202.4	68.75	F.I1K2P1H3I1D1E1A1L1K2Q2L1P1V1F1Q2A1.H
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	3.9983	0.3593	1952.77	1953.335	1	1384.1	68.75	A.GFIKPHIDEALKQLPVF.Q
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	4.2136	0.3085	1797.03	1797.025	1	1134.2	71.42857	M.ACEKTKPYLDKVESK.L
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	4.8135	0.3578	2377.81	2378.694	1	605.4	55	M.ACEKTKPYLDKVESKLGPISN.L
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	6.345	0.3351	2521.19	2518.854	1	2595.7	44.04762	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	5.7839	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; Rtn1p	2	3.2386	0.2744	1770.43	1769.106	2	717.4	60.714287	F.I1K2P1H3I1D1E1A1L1K2Q2L1P1V1F1.Q
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	3.8254	0.3264	1947.99	1948.316	1	573.1	50	F.IKPHIDEALKQLPVFQA.H

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	3.5253	0.2274	2081.53	2081.465	1	430.7	44.11765	A.GFIKPHIDEALKQLPVFQ.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	3.6194	0.2982	2104.75	2105.466	2	512.4	44.11765	A.G1F1I1K2P1H3I1D1E1A1L1K2Q2L1P1V1F1Q2.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	3.3043	0.225	1415.43	1416.646	1	863.4	72.72727	H.I1D1E1A1L1K2Q2L1P1V1F1Q2.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	3.2069	0.3057	1400.61	1401.646	1	873.1	72.72727	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	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
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	3.0583	0.2537	1471.37	1472.725	1	761	62.5	H.IDEALKQLPVFQA.H
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	3.0342	0.2444	1472.25	1472.725	2	783.5	70.83333	H.IDEALKQLPVFQA.H
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	4.0292	0.2487	1815.23	1816.025	2	791.2	60.714287	M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2.L
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	3.9149	0.2916	2517.41	2518.854	3	666.2	32.142857	M.A1C1E1K2T1K2P1Y1L1D1K2V1E1S1K2L1G1P1I1S1N2L1.V
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence 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
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence 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
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence 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
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence 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
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence 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
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP); Sec26p	2	4.3094	0.3872	2020.39	2021.244	1	1383.8	68.75	L.KDSCKNIEPIDTPISFR.Q
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.7889	0.3799	2042.33	2044.244	1	725	56.25	L.K2D1S1C1K2N2I1E1P1I1D1T1P1I1S1F1R4.Q
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.2615	0.2775	1965.67	1963.235	2	921	56.25	F.K2V1S1E1H3L1L1P1D1A1K2E1I1I1N2S1F1.I
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.4021	0.3284	1731.65	1730.956	1	574.6	50	T.AKPTGPVILPDGTYATE.S
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP); Sec26p	2	3.486	0.354	1494.25	1494.657	1	551	66.66667	A.LEKGSDEQKIDTM.K
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein 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.L1D1E1V1N2P1E1E1K2K2E1E1V1K2L1L1.E
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein 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
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence 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
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence 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
gi|6320444|ref|NP_010524.1|	YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence 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
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	3.3073	0.2739	2268.35	2266.589	1	151.9	47.22222	Q.E1L1R4F1P1S1P1T1P1I1Q2R4I1T1I1P1N2V1C1.N
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	3.085	0.222	2240.79	2239.589	2	131.5	38.88889	Q.ELRFPSPTPIQRITIPNVC.N
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	3.5133	0.2703	1983.61	1983.281	4	401.7	43.75	Y.A1D1N2D1E1D1K2F1K2K2L1K2P1I1V1A1K2.Y
gi|6320454|ref|NP_010534.1|	YDR248C	hypothetical protein; Ydr248cp	3	4.0187	0.1693	2814.95	2816.172	2	448.7	27.173912	F.K2D1I1Y1P1D1L1K2F1I1E1G1D1D1L1H3P1P1A1N2V1E1K2M1.T
gi|6320454|ref|NP_010534.1|	YDR248C	hypothetical protein; Ydr248cp	3	4.7583	0.3617	3085.04	3086.398	1	1314.1	35	L.I1H3E1F1K2D1I1Y1P1D1L1K2F1I1E1G1D1D1L1H3P1P1A1N2V1E1.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	L.I1H3E1F1K2D1I1Y1P1D1L1K2F1I1E1G1D1D1L1H3P1P1A1N2V1E1K2M1.T
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.T
gi|6320454|ref|NP_010534.1|	YDR248C	hypothetical protein; Ydr248cp	3	5.029	0.155	3055.16	3053.398	1	1153	32	L.IHEFKDIYPDLKFIEGDDLHPPANVE.K
gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	2	4.3206	0.4558	1513.33	1514.543	1	1660.2	83.33333	N.HEEGEVVEEEAEK.-
gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	1	2.6786	0.1945	1169.62	1170.414	2	288.2	70	S.R4L1I1G1A1P1P1G1Y1V1L1.S
gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	3	3.8244	0.1851	2152.01	2153.405	1	393.2	34.72222	A.R4D1G1K2L1D1P1V1I1G1R4D1E1E1I1A1R4A1I1.Q

gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	2	3.2853	0.2707	1528.11	1530.543	1	521.7	70.83333	N.H3E1E1G1E1V1V1E1E1E1A1E1K2.-
gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	2	4.3155	0.2951	2037.93	2037.188	1	1063.2	64.70589	L.VVLPNHEEGEVVEEEAEK.-
gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	2	3.0015	0.1624	2046.69	2046.337	2	403.8	41.17647	D.RFLPDKAIDLVDEACAVL.R
gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	2	3.2333	0.2565	2067.57	2068.337	1	536	41.17647	D.R4F1L1P1D1K2A1I1D1L1V1D1E1A1C1A1V1L1.R
gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	2	3.0253	0.2416	1722.59	1720.861	9	255.3	46.153847	L.A1E1F1L1F1D1D1E1S1N2V1I1R4F1.D
gi|6320464|ref|NP_010544.1|	YDR258C	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; Hsp78p	1	2.3983	0.1806	1156.71	1156.414	1	239.4	65	S.RLIGAPPGYVL.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	3.1581	0.389	1523.18	1524.671	1	486.8	50	Q.S1Q2F1P1Q2Y1P1S1S1V1G1T1P1L1.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	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
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	3.8051	0.2615	3160.94	3159.563	5	415.1	27.777779	A.DLPLPDLPPESPTEFPDPFKELPPINSR.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	2	3.3738	0.2476	1970.73	1969.211	5	292.1	50	T.V1N2G1K2P1V1R4Q2I1T1D1D1E1L1T1F1L1.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	3	4.5226	0.2302	3079.43	3078.431	1	877.8	26.85185	F.L1Q2N2S1N2L1G1G1I1I1P1T1V1N2G1K2P1V1R4Q2I1T1D1D1E1L1T1F1.L
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	3.8622	0.2008	3356.78	3358.711	7	529	21.551723	L.Q2N2S1N2L1G1G1I1I1P1T1V1N2G1K2P1V1R4Q2I1T1D1D1E1L1T1F1L1Y1N2.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	4.5812	0.355	3190.25	3192.563	1	474.4	29.62963	A.D1L1P1L1P1D1L1P1P1E1S1P1T1E1F1P1D1P1F1K2E1L1P1P1I1N2S1R4.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	7.1112	0.4427	4062.05	4059.479	1	641.5	26.428572	Q.N2T1E1E1S1I1I1A1D1L1P1L1P1D1L1P1P1E1S1P1T1E1F1P1D1P1F1K2E1L1P1 P1I1N2S1R4.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	5.0154	0.4341	4272.95	4274.725	1	659.8	22.297297	S.EQNTEESIIADLPLPDLPPESPTEFPDPFKELPPINSR.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	5.1094	0.4089	4319.63	4319.725	1	625.4	22.972973	S.E1Q2N2T1E1E1S1I1I1A1D1L1P1L1P1D1L1P1P1E1S1P1T1E1F1P1D1P1F1K2E L1P1P1I1N2S1R4.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	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	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN 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	TyB Gag-Pol 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
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	2.9487	0.2671	1114.25	1114.162	1	464.5	77.77778	V.PENPHHASPQ.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	3.0541	0.3064	1300.19	1300.358	1	562.6	72.72727	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	2	3.3357	0.2687	1618.95	1619.815	1	545.4	65.38461	N.GKPVRQITDDELTF.L
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	3.4098	0.3605	1569.64	1570.832	1	328.5	66.66667	K.E1E1L1Y1I1R4P1P1P1H3L1G1M1.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	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	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	2	4.046	0.3556	1823.55	1821.046	1	610	63.333332	K.VTNIIDRLNNNGIHIN.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	3.0524	0.1783	1946.43	1946.211	1	463	50	T.VNGKPVRQITDDELTFL.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	3.6501	0.3226	2131.73	2133.387	4	231.6	41.17647	T.V1N2G1K2P1V1R4Q2I1T1D1D1E1L1T1F1L1Y1.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	3.3502	0.2322	2031.45	2032.324	1	552	50	K.YVRPPPMLTSPNDFPNW.V
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	3.0176	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
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	3.7763	0.4273	1454.55	1452.569	1	684.8	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	2	3.6657	0.2597	1639.43	1638.815	1	532.4	65.38461	N.G1K2P1V1R4Q2I1T1D1D1E1L1T1F1.L
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	3.5816	0.3485	2010.55	2010.254	1	280.8	46.875	N.GKPVRQITDDELTFLYN.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	3.8879	0.3123	1919.39	1917.15	1	418	63.333332	N.G1K2P1V1R4Q2I1T1D1D1E1L1T1F1L1Y1.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	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
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	3.0122	0.228	1932.49	1933.198	5	289.1	50	K.E1E1L1Y1I1R4P1P1P1H3L1G1M1N2D1K2.L
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	4.0344	0.354	2120.45	2119.436	1	665.6	58.823532	Y.A1D1I1K2E1E1L1Y1I1R4P1P1P1H3L1G1M1N2.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	1	2.4076	0.2328	1499.7	1500.799	2	102	62.5	K.KYVRPPPMLTSPN.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	3.7562	0.2663	2283.77	2285.631	1	439.5	47.22222	K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2.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	3.2764	0.1884	2348.25	2347.436	1	183.3	44.444447	N.S1K2P1N2Y1R4R4N2P1S1D1E1K2N2D1S1R4S1Y1.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	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
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	3.2104	0.1561	2301.41	2301.631	1	318	47.22222	K.Y1V1R4P1P1P1M$L1T1S1P1N2D1F1P1N2W2V1K2.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	4.3463	0.2539	2120.63	2121.455	1	1101.1	61.764706	Y.V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2.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	4.7523	0.2835	2285.72	2285.631	1	1523.4	43.055553	K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2.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	4.1087	0.3232	2385.99	2387.736	1	624.8	52.63158	K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2T1.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	4.0267	0.3202	2550.39	2551.912	1	752.7	50	K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2T1Y1.I
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	2.2548	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
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	2.9832	0.2907	1854.39	1855.051	1	527.6	50	T.V1N2G1K2P1V1R4Q2I1T1D1D1E1L1T1F1.L
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	4.2505	0.2884	3433.82	3431.871	1	802.2	24.166666	F.LQNSNLGGIIPTVNGKPVRQITDDELTFLYN.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	3.3796	0.2321	1832.05	1833.051	1	508.4	50	T.VNGKPVRQITDDELTF.L
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	3.095	0.2077	1734.27	1732.974	1	526.8	60.714287	N.GKPVRQITDDELTFL.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	3.5687	0.2097	1750.17	1752.974	1	703.7	67.85714	N.G1K2P1V1R4Q2I1T1D1D1E1L1T1F1L1.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	3.4187	0.3188	1894.71	1896.15	1	277.3	53.333336	N.GKPVRQITDDELTFLY.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	3.3421	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
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	3.4273	0.2455	2094.63	2094.436	1	514.6	50	Y.ADIKEELYIRPPPHLGMN.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	4.4656	0.2993	2284.67	2285.631	1	733.2	61.11111	K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2.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	5.031	0.2793	2288.09	2285.631	1	1880.6	47.22222	K.Y1V1R4P1P1P1M1L1T1S1P1N2D1F1P1N2W2V1K2.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	4.113	0.3534	2259.73	2259.631	1	632	55.555557	K.YVRPPPMLTSPNDFPNWVK.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	5.3063	0.3193	2010.43	2012.088	1	2492.9	80	Y.IDQDELEIDEDEYKEK.V
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	3.5386	0.325	1666.29	1666.935	1	655.5	65.38461	K.EELYIRPPPHLGMN.D
gi|6320490|ref|NP_010570.1|	YDR284C	Diacylglycerol pyrophosphate (DGPP) phosphatase, zinc-regulated vacuolar membrane-associated lipid phosphatase, dephosphorylates DGPP to phosphatidate (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
gi|6320490|ref|NP_010570.1|	YDR284C	Diacylglycerol pyrophosphate (DGPP) phosphatase, zinc-regulated vacuolar membrane-associated lipid phosphatase, dephosphorylates DGPP to phosphatidate (PA) and Pi, then PA to diacylglycerol; involved in lipid signaling and cell metabolism; Dpp1p	2	3.6699	0.2473	1783.91	1785.136	1	615.6	60.714287	R.R4I1F1P1P1I1D1D1P1L1P1F1K2P1L1.M
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; Dpl1p	2	3.2539	0.2206	1496.69	1495.632	1	520.6	61.538464	A.PNFPHGIADDIEGL.G
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; Dpl1p	2	3.3524	0.3094	1672.55	1672.789	3	276.7	53.333336	G.S1A1P1N2F1P1H3G1I1A1D1D1I1E1G1L1.G
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; Dpl1p	1	2.462	0.2209	1200.49	1200.445	5	347.5	61.11111	N.G1W2Y1G1M1P1I1H3L1L1.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; Dpl1p	1	2.6456	0.2938	1180.48	1180.389	1	531.1	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; Dpl1p	2	3.0554	0.2345	1182.21	1180.389	2	964.1	83.33333	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; 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; Dpl1p	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; Dpl1p	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; Dpl1p	1	2.2096	0.2409	1186.84	1187.445	2	445.4	66.66667	N.GWYGMPIHLL.R
gi|6320503|ref|NP_010583.1|	YDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosyntheis; Sur2p	1	2.3874	0.1704	1583.79	1584.859	1	260.8	53.846157	L.RADLPRIIPDAAIY.Y
gi|6320503|ref|NP_010583.1|	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
gi|6320503|ref|NP_010583.1|	YDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosyntheis; Sur2p	1	2.2749	0.1557	1172.48	1172.358	7	167.1	50	L.T1H3R4E1Q2I1I1L1F1.T
gi|6320503|ref|NP_010583.1|	YDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosyntheis; Sur2p	2	3.515	0.2428	1968.51	1969.347	1	539.4	47.058823	N.LRPKESLLPEMSDGVLAL.V
gi|6320503|ref|NP_010583.1|	YDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosyntheis; Sur2p	2	3.4869	0.2931	1856.57	1857.079	1	156.7	57.14286	A.EKYRIHPSEEVAKRN.K
gi|6320503|ref|NP_010583.1|	YDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to 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
gi|6320503|ref|NP_010583.1|	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
gi|6320505|ref|NP_010585.1|	YDR299W	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to Brefeldin A; Bfr2p	2	3.3302	0.2336	1781.17	1782.771	1	748.4	61.538464	N.F1N2E1N2E1D1E1E1Q2H3A1R4I1E1.N
gi|6320505|ref|NP_010585.1|	YDR299W	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to Brefeldin A; Bfr2p	2	3.0579	0.2348	1768.31	1769.017	1	1166	66.66667	D.CANGRLPELISPVVKD.S
gi|6320505|ref|NP_010585.1|	YDR299W	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to Brefeldin A; Bfr2p	3	4.308	0.3056	3184.01	3184.451	1	918.3	28.703705	S.L1A1D1Q2I1S1D1I1A1I1K2P1V1N2K2D1F1D1I1E1D1E1E1N2A1S1L1F1.Q
gi|6320505|ref|NP_010585.1|	YDR299W	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to 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
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	3.8718	0.3103	2212.49	2211.587	1	800	58.333332	Y.I1E1N2V1K2T1D1S1R4N2M1P1V1K2E1V1I1I1V1.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.S1R4N2M1P1V1K2E1V1I1I1V1.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
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	4.2179	0.2007	1514.53	1514.824	1	1159.1	79.16667	D.SRNMPVKEVIIVE.S
gi|6320516|ref|NP_010596.1|	YDR310C	Transcriptional repressor required for mitotic repression of middle sporulation-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
gi|6320516|ref|NP_010596.1|	YDR310C	Transcriptional repressor required for mitotic repression of middle sporulation-specific genes; involved in telomere maintenance, regulated by the pachytene checkpoint; Sum1p	3	3.9769	0.2508	3847.82	3847.141	1	614.1	22.580645	Q.W2R4E1W2M1F1P1H3N2E1T1L1P1A1L1G1Q2D1G1I1N2E1D1N2L1N2E1T1I1D1N2M1.L
gi|6320516|ref|NP_010596.1|	YDR310C	Transcriptional repressor required for mitotic repression of middle sporulation-specific genes; involved in telomere maintenance, regulated by the pachytene checkpoint; Sum1p	2	5.3503	0.4202	2234.87	2234.476	1	1064.9	65	K.FHQIPSSPSNPVSQPAPVRTS.R
gi|6320516|ref|NP_010596.1|	YDR310C	Transcriptional repressor required for mitotic repression of middle sporulation-specific genes; involved in telomere maintenance, regulated by the pachytene checkpoint; Sum1p	1	2.5009	0.1818	1537.58	1536.682	5	219.3	50	V.N2L1K2S1A1S1N2Q2G1A1P1F1S1P1V1.N
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	2.4498	0.3406	1227.37	1228.446	1	494.8	66.66667	S.VQWRVPLGLC.F
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	2.63	0.1578	1308.52	1309.482	1	620	77.77778	L.MHDDQPFYKK.M
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	3.6679	0.2606	1282.23	1280.469	1	671.8	75	N.KVAPDHPFIQQ.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	3.5103	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
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	3.0808	0.2446	1329.11	1331.524	1	647.3	70	N.S1V1Q2W2R4V1P1L1G1L1C1.F
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	2.7114	0.2588	1316.9	1315.524	1	464.7	60.000004	N.SVQWRVPLGLC.F
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	3.3881	0.1985	1155.25	1155.385	1	957.6	83.33333	N.SVQWRVPLGL.N
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	3.4626	0.2637	1170.05	1170.385	1	969.7	83.33333	N.S1V1Q2W2R4V1P1L1G1L1.C
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	3.2605	0.2624	1940.31	1941.163	1	801.4	60.000004	K.NYSNSVQWRVPLGLCF.A
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	3.39	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
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	2.5102	0.3299	1243.74	1243.446	1	373.2	61.11111	S.V1Q2W2R4V1P1L1G1L1C1.F
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	2.9361	0.1536	1323.5	1324.482	1	819.9	77.77778	L.M1H3D1D1Q2P1F1Y1K2K2.M
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	3.1271	0.2703	1324.19	1324.482	2	1063.5	77.77778	L.M1H3D1D1Q2P1F1Y1K2K2.M
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	3.0054	0.2588	1279.98	1280.469	1	473.9	60.000004	N.KVAPDHPFIQQ.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	2.4139	0.304	1152.61	1152.338	1	456.3	66.66667	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	3.0195	0.2615	1493.47	1493.706	2	358	54.166668	K.VNKVAPDHPFIQQ.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	3.2032	0.2164	1327.39	1325.482	1	811.7	83.33333	L.M@HDDQPFYKK.M
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	3.7273	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
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	4.3966	0.3171	1513.61	1512.749	1	1578.1	87.5	S.K2V1N2K2V1A1P1D1H3P1F1I1Q2.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	2.2094	0.1855	1221.5	1222.387	7	235.1	55.555557	M.T1F1V1P1E1S1P1R4Y1L1.V
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	3.0225	0.1869	1195.09	1194.308	1	700.7	81.25	L.M1H3D1D1Q2P1F1Y1K2.K
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	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
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	2.9934	0.2829	1321.75	1324.482	3	989	77.77778	L.M1H3D1D1Q2P1F1Y1K2K2.M
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	2.8298	0.2752	1279.57	1280.469	1	559.6	65	N.KVAPDHPFIQQ.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	3.0746	0.2605	1494.29	1493.749	1	795.4	70.83333	S.KVNKVAPDHPFIQ.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	4.8127	0.3494	1641.79	1642.88	1	1113.4	76.92308	S.K2V1N2K2V1A1P1D1H3P1F1I1Q2Q2.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
gi|6320568|ref|NP_010648.1|	YDR361C	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 organization and vesicular transport; Bcp1p	2	2.9918	0.1605	1486.37	1484.837	1	1087.3	75	N.MPPEVVPPLYKIT.L
gi|6320568|ref|NP_010648.1|	YDR361C	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 organization and vesicular transport; Bcp1p	2	3.9118	0.3697	2223.49	2221.641	1	501.4	47.22222	L.S1E1R4L1I1N2M1P1P1E1V1V1P1P1L1Y1K2I1T1.L
gi|6320568|ref|NP_010648.1|	YDR361C	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 organization and vesicular transport; Bcp1p	2	3.1174	0.2619	1150.29	1150.309	3	641.3	75	N.H3L1S1D1Y1V1K2Y1L1.Q
gi|6320568|ref|NP_010648.1|	YDR361C	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 organization and vesicular transport; Bcp1p	2	4.3136	0.393	1544.49	1544.62	1	928.8	70.83333	D.F1D1F1F1G1G1N2P1E1V1D1F1H3.A
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	4.0112	0.3571	1948.37	1948.053	1	518.1	56.25	F.EDHDFAIDPTQPEFKGT.Q
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	4.6211	0.4125	1967.71	1969.053	1	736.6	56.25	F.E1D1H3D1F1A1I1D1P1T1Q2P1E1F1K2G1T1.Q
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	3.8947	0.2713	2322.43	2323.477	1	980.6	55.263157	K.EVFEDHDFAIDPTQPEFKGT.Q
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	3.7462	0.2738	2346.61	2347.477	1	385	39.473686	K.E1V1F1E1D1H3D1F1A1I1D1P1T1Q2P1E1F1K2G1T1.Q
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely 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	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	3.7825	0.2879	2015.45	2017.046	1	442.5	44.11765	A.L1E1G1G1N2E1K2S1S1E1D1K2E1E1T1T1I1E1.K
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	3	4.3134	0.2565	2583.8	2583.857	1	1036.6	36.25	K.ERIVEDTFTPDLEDPRFKEVF.E
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	4.137	0.3011	1870.71	1869.111	1	1086.2	75	E.R4M1Q2R4E1E1V1E1G1P1P1K2E1L1F1.Q
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely 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	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	4.0271	0.2346	1894.17	1894.956	3	823.8	60.000004	K.KETPNDEDEEVDMEIT.F
gi|6320573|ref|NP_010653.1|	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
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	3	5.6617	0.205	2350.13	2347.477	1	848.7	40.789474	K.E1V1F1E1D1H3D1F1A1I1D1P1T1Q2P1E1F1K2G1T1.Q
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	4.3992	0.352	2348.27	2347.477	1	684.3	50	K.E1V1F1E1D1H3D1F1A1I1D1P1T1Q2P1E1F1K2G1T1.Q
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely 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
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	3	4.7604	0.3029	1998.98	1999.094	1	1322.5	50	Q.N2N2R4E1L1E1D1F1D1K2Y1F1E1K2E1.A
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	2	4.927	0.392	1998.39	1999.094	1	1341.4	75	Q.N2N2R4E1L1E1D1F1D1K2Y1F1E1K2E1.A
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	3	4.5837	0.3289	3811.88	3811.088	1	623	23.387096	D.T1F1T1P1D1L1E1D1P1R4F1K2E1V1F1E1D1H3D1F1A1I1D1P1T1Q2P1E1F1K2G1T1.Q
gi|6320573|ref|NP_010653.1|	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely 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.L1G1E1R4I1K2P1V1V1V1I1N2.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.I1L1D1P1I1F1R4L1F1.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.R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1.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.R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1V1.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.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	3.2201	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.G1P1N2Y1V1P1G1K2K2D1D1L1F1I1K2.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$G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1.V
gi|6320593|ref|NP_010673.1|	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.6858	0.446	2089.93	2091.353	1	909.9	50	M.M@GRFVEPIDDCPAGNIIGL.V
gi|6320593|ref|NP_010673.1|	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	4.0833	0.4235	2198.87	2198.486	1	648	44.736843	M.M1G1R4F1V1E1P1I1D1D1C1P1A1G1N2I1I1G1L1V1.G
gi|6320593|ref|NP_010673.1|	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.9122	0.156	1293.77	1294.583	3	1135.5	88.88889	M.F1I1L1D1P1I1F1R4L1F1.T
gi|6320593|ref|NP_010673.1|	YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	2	3.2689	0.2141	1559.15	1558.88	1	527.5	72.72727	F.N2M$F1I1L1D1P1I1F1R4L1F1.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.GPNYVPGKKDDLFIK.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.N2M1F1I1L1D1P1I1F1R4L1F1.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
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	3	4.0565	0.2382	1985.75	1985.282	1	865.3	43.333332	V.S1I1E1E1K2N2R4Y1V1E1E1V1I1K2I1L1.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	2	4.3677	0.3828	2312.61	2313.356	1	578	52.380955	Q.EKHRPGDIENNAGSSPDSATTE.K
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	3	4.5831	0.2285	1964.81	1963.282	2	1393.2	55	V.SIEEKNRYVEEVIKIL.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	2	3.9554	0.3438	1782.41	1780.008	1	1378.7	71.42857	K.GTRVPQTPKDMAEYW.L
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	4.4145	0.4566	1798.75	1801.008	1	1547.7	71.42857	K.G1T1R4V1P1Q2T1P1K2D1M1A1E1Y1W2.L
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	3.0307	0.2232	2035.35	2037.298	1	404.2	50	K.GTRVPQTPKDM@AEYWLQ.S
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	3.6585	0.2608	1988.91	1988.335	1	541.8	56.25	K.GLRLLKPSKEEDTFQIL.K
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	3.3324	0.2535	2010.11	2011.335	1	374.2	46.875	K.G1L1R4L1L1K2P1S1K2E1E1D1T1F1Q2I1L1.K
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	4.3167	0.3436	1992.63	1993.146	1	842.8	55.88235	A.V1G1A1Y1P1G1N2D1Y1V1L1G1D1D1F1L1K2E1.S
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	3.256	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 Pdr1p, 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; Syf1p	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; Syf1p	2	3.4425	0.3099	2197.45	2199.505	1	610.5	47.058823	Q.SLKVPYPYIEDLEEIYLN.W
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	1	2.6504	0.2574	1032.45	1032.182	4	393.2	55.555557	K.KVGEDIAKAT.K
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.7758	0.2926	2564.57	2564.811	1	652.1	47.727272	R.VDFKNPHDIIEGINAGEIEIPEN.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	1	2.2064	0.2766	1524.52	1525.704	2	351.9	53.846157	D.FKNPHDIIEGINAG.E
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.0439	0.1705	2972.57	2973.19	1	209.9	32	V.G1C1R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1E1I1E1I1P1E1N2.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.7655	0.4088	1920.69	1921.113	1	1282.6	65.625	C.R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1.E
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.9466	0.2409	1898.91	1896.113	1	1303.7	65.625	C.RVDFKNPHDIIEGINAG.E
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.6854	0.1782	2298.47	2299.514	1	838.2	50	Q.SVGCRVDFKNPHDIIEGINAG.E
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.5681	0.3976	2272.73	2270.463	1	1094.8	55.263157	Q.S1V1G1C1R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1.G
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.9087	0.4478	1837.71	1839.061	1	1118	63.333332	C.RVDFKNPHDIIEGINA.G
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	1	2.4288	0.1862	961.67	962.197	7	396.1	55.555557	S.A1A1L1A1P1K2I1G1P1L1.G
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.2908	0.2044	1582.55	1583.741	4	438.5	53.846157	V.DFKNPHDIIEGINA.G
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.7711	0.3991	2464.65	2465.679	1	955.7	54.761906	V.DFKNPHDIIEGINAGEIEIPEN.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.4054	0.2639	2491.09	2493.679	1	375.6	38.095238	V.D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1E1I1E1I1P1E1N2.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.8864	0.3207	2379.31	2377.59	1	826.4	55	D.F1K2N2P1H3D1I1I1E1G1I1N2A1G1E1I1E1I1P1E1N2.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.1232	0.358	2350.65	2350.59	1	719.2	52.499996	D.FKNPHDIIEGINAGEIEIPEN.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.5404	0.3129	3158.97	3161.4	4	232.1	25.925926	Q.S1V1G1C1R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1E1I1E1I1P1E1N2.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.2052	0.1772	3122.79	3124.4	1	458.4	33.333336	Q.SVGCRVDFKNPHDIIEGINAGEIEIPEN.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.2542	0.2118	1527.39	1525.704	3	743.8	65.38461	D.FKNPHDIIEGINAG.E
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	1	3.0853	0.2929	1467.62	1468.652	1	597.4	62.5	D.FKNPHDIIEGINA.G
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	3	4.0125	0.2162	2972.87	2973.19	1	377	31	V.G1C1R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1E1I1E1I1P1E1N2.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.8616	0.1747	2720.65	2720.999	4	224	30.434782	C.RVDFKNPHDIIEGINAGEIEIPEN.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	3	3.8104	0.2509	3158.84	3161.4	2	340.9	25.925926	Q.S1V1G1C1R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1E1I1E1I1P1E1N2.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	3	3.8882	0.2706	3122.51	3124.4	1	513.5	32.407406	Q.SVGCRVDFKNPHDIIEGINAGEIEIPEN.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	3	4.4613	0.3418	2753.6	2753.999	1	585.5	39.130436	C.R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2A1G1E1I1E1I1P1E1N2.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.6203	0.2298	1789.37	1790.982	1	529.4	60.714287	C.R4V1D1F1K2N2P1H3D1I1I1E1G1I1N2.A
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	4.2064	0.4492	2056.51	2056.252	1	1266.8	64.70589	V.GCRVDFKNPHDIIEGINA.G
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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

gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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.-
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	2	3.8611	0.2889	1672.55	1674.878	1	1318.8	76.92308	C.R4V1D1F1K2N2P1H3D1I1I1E1G1I1.N
gi|6320625|ref|NP_010706.1|	YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity 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
gi|6320665|ref|NP_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
gi|6320665|ref|NP_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	2.9243	0.2901	1705.65	1704.889	2	546.7	53.846157	L.KDMESLDPDYYKSL.V
gi|6320665|ref|NP_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	3.4037	0.2239	1675.41	1673.921	2	727.7	69.230774	F.HLPSFDEDDLMKIL.S
gi|6320668|ref|NP_010748.1|	YDR460W	Subunit of TFIIH and nucleotide excision repair factor 3 complexes, involved in transcription initiation, required for nucleotide excision repair; ring finger protein similar to mammalian CAK and TFIIH subunit; Tfb3p	2	4.2711	0.2917	1669.25	1670.929	1	2013.4	91.66667	N.K2Y1L1E1E1V1E1D1I1I1Y1K2L1.D
gi|6320668|ref|NP_010748.1|	YDR460W	Subunit of TFIIH and nucleotide excision repair factor 3 complexes, involved in transcription initiation, required for nucleotide excision repair; ring finger protein similar to mammalian CAK and TFIIH subunit; Tfb3p	2	3.9331	0.2099	1655.17	1655.929	1	2126.1	87.5	N.KYLEEVEDIIYKL.D
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap 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	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap 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
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	2	3.7085	0.2664	2058.49	2059.277	5	271.2	46.875	T.E1T1F1E1Q2P1S1Q2R4E1E1A1K2K2V1V1K2.K
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	2	3.7563	0.2824	1904.43	1905.161	2	290.6	46.666668	E.TFEQPSQREEAKKVVK.K
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap 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	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap 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
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	1	2.4538	0.2406	932.69	932.186	3	373.3	71.42857	K.K2V1V1I1V1K2P1H3.D
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	2	4.0049	0.3944	1776.03	1777.033	1	664.5	66.66667	K.VVIVKPHDEGSKSHPF.G
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap 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	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap 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
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	2	2.9788	0.1822	1438.29	1436.695	5	223.1	62.5	K.KVVIVKPHDEGSK.S
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	2	3.2574	0.2652	1927.19	1929.161	7	334.3	50	E.T1F1E1Q2P1S1Q2R4E1E1A1K2K2V1V1K2.K
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap 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	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	3	4.0122	0.3048	1797.41	1799.033	1	625.3	41.666664	K.V1V1I1V1K2P1H3D1E1G1S1K2S1H3P1F1.G
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	2	2.9542	0.1756	1677.25	1677.855	1	587.8	61.538464	E.TFEQPSQREEAKKV.V
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	3	4.0916	0.2587	2192	2189.451	4	384.8	38.235294	T.E1T1F1E1Q2P1S1Q2R4E1E1A1K2K2V1V1K2K2.A
gi|6320679|ref|NP_010759.1|	YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap 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
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	3.1871	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.HVNDLPIDDILTL.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	3.5512	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
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	4.0938	0.2912	2800.77	2800.008	1	389.2	34.090908	L.FADNDIPFEIDRDEKEYPSLKEQ.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	3.3785	0.2496	2438.45	2439.587	2	449.7	44.736843	L.F1A1D1N2D1I1P1F1E1I1D1R4D1E1K2E1Y1P1S1L1.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	2	3.9284	0.3251	1522.79	1522.655	1	714.1	81.818184	D.RDEKEYPSLKEQ.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	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
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	3.1016	0.2357	1204.71	1205.298	1	872.5	88.88889	A.I1G1V1D1P1H3H3R4P1C1.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	3	4.66	0.2517	2828.42	2830.008	1	1025.1	35.227272	L.F1A1D1N2D1I1P1F1E1I1D1R4D1E1K2E1Y1P1S1L1K2E1Q2.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	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
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	3.7424	0.2552	1856.75	1857.009	1	673.2	60.000004	F.N2Q2H3V1N2D1L1P1I1D1D1I1L1T1L1D1.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
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	2.9646	0.1749	1495.27	1494.685	5	448.7	62.5	Q.H3V1N2D1L1P1I1D1D1I1L1T1L1.D
gi|6320691|ref|NP_010771.1|	YDR483W	Alpha1,2-mannosyltransferase of the Golgi 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.S1D1I1G1Y1H3H3P1P1Y1D1N2C1P1L1D1K2E1V1Y1.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	41.666664	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
gi|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
gi|6320691|ref|NP_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.SMDFIKKNPEYLDENNLM.S
gi|6320691|ref|NP_010771.1|	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	1	2.3038	0.1881	1211.54	1212.48	2	546.8	62.5	N.KKFPYPWVF.L
gi|6320691|ref|NP_010771.1|	YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	2	3.0011	0.3126	1439.65	1439.743	1	854.7	75	K.INKKFPYPWVF.L
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.S1M1D1F1I1K2K2N2P1E1Y1L1D1E1N2N2L1M1.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	2	3.274	0.1715	1453.41	1454.743	1	841.1	75	K.I1N2K2K2F1P1Y1P1W2V1F1.L
gi|6320703|ref|NP_010783.1|	YDR495C	Cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins, acidification of the vacuolar lumen, and assembly of the vacuolar H+-ATPase; Vps3p	2	3.4093	0.1877	2070.73	2072.178	1	545.3	53.125	T.S1C1E1E1S1E1I1D1N2I1E1D1Q2L1K2K2L1.A
gi|6320703|ref|NP_010783.1|	YDR495C	Cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins, acidification of the vacuolar lumen, and assembly of the vacuolar H+-ATPase; Vps3p	2	3.9107	0.3434	2050.57	2051.178	1	734.6	59.375	T.SCEESEIDNIEDQLKKL.A
gi|6320703|ref|NP_010783.1|	YDR495C	Cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins, acidification of the vacuolar lumen, and assembly of the vacuolar H+-ATPase; Vps3p	2	3.5216	0.2905	1830.61	1829.118	1	477.8	53.571426	K.N2Y1P1R4N2V1I1V1E1F1P1Y1I1I1A1.E
gi|6320706|ref|NP_010786.1|	YDR498C	Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-glycosylation in the Golgi but not in the ER; forms a complex with the cytosolic Tip20p; Sec20p	2	4.9148	0.3046	2858.27	2860.014	1	1195.6	47.826088	A.IANEHNDEEEEIEFEDLVNIIESK.V
gi|6320706|ref|NP_010786.1|	YDR498C	Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-glycosylation in the Golgi but not in the ER; forms a complex with the cytosolic Tip20p; Sec20p	2	4.4782	0.2607	2889.61	2890.014	1	649.3	43.47826	A.I1A1N2E1H3N2D1E1E1E1E1I1E1F1E1D1L1V1N2I1I1E1S1K2.V
gi|6320706|ref|NP_010786.1|	YDR498C	Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-glycosylation in the Golgi but not in the ER; forms a complex with the cytosolic Tip20p; Sec20p	2	4.84	0.4095	2673.77	2675.776	1	1124.1	54.761906	A.NEHNDEEEEIEFEDLVNIIESK.V
gi|6320706|ref|NP_010786.1|	YDR498C	Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-glycosylation in the Golgi but not in the ER; forms a complex with the cytosolic Tip20p; Sec20p	2	4.5753	0.3542	2561.79	2561.672	1	675.8	45	N.EHNDEEEEIEFEDLVNIIESK.V
gi|6320706|ref|NP_010786.1|	YDR498C	Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-glycosylation in the Golgi but not in the ER; forms a complex with the cytosolic Tip20p; Sec20p	3	4.5893	0.2114	2860.64	2860.014	1	884.9	34.782608	A.IANEHNDEEEEIEFEDLVNIIESK.V
gi|6320706|ref|NP_010786.1|	YDR498C	Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-glycosylation in the Golgi but not in the ER; forms a complex with the cytosolic Tip20p; Sec20p	2	3.2225	0.2829	2104.63	2105.089	1	930.6	56.25	A.NEHNDEEEEIEFEDLVN.I
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 Hsl1p; Gin4p	3	4.0218	0.3256	2498.18	2495.682	1	954.2	33.75	Q.K2G1E1F1E1M1P1S1D1D1E1I1S1R4E1A1Q2D1L1I1R4.K
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 Hsl1p; Gin4p	2	3.7836	0.2629	2326.31	2327.619	1	494.1	44.736843	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 Hsl1p; Gin4p	3	4.2216	0.2094	1819.82	1821.054	1	1033.9	50	L.V1E1R4G1P1L1P1E1H3E1A1I1R4F1F1.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 Hsl1p; Gin4p	2	3.6939	0.1929	1819.81	1821.054	1	543.6	50	L.V1E1R4G1P1L1P1E1H3E1A1I1R4F1F1.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 Hsl1p; Gin4p	2	3.4116	0.2954	1935.63	1935.214	1	683	53.333336	L.L1V1E1R4G1P1L1P1E1H3E1A1I1R4F1F1.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 Hsl1p; Gin4p	3	4.3772	0.2681	1935.32	1935.214	1	1954	51.666664	L.L1V1E1R4G1P1L1P1E1H3E1A1I1R4F1F1.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 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 Hsl1p; Gin4p	3	4.0581	0.3812	2162.51	2165.477	1	933.6	41.17647	F.N2L1L1V1E1R4G1P1L1P1E1H3E1A1I1R4F1F1.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 Hsl1p; 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 Hsl1p; Gin4p	2	4.222	0.3776	2326.73	2327.619	1	836.7	52.63158	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 Hsl1p; Gin4p	2	3.2728	0.2443	2298.43	2297.619	2	372.1	39.473686	T.DNLHLPILPPLNGDNELRKQ.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 Hsl1p; Gin4p	2	3.8492	0.3777	1797.89	1798.054	1	978.8	64.28571	L.VERGPLPEHEAIRFF.R
gi|6320726|ref|NP_010806.1|	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	2	3.3772	0.2067	1771.73	1768.964	1	412.2	50	L.SIHLPNTTEPILFDGN.V
gi|6320726|ref|NP_010806.1|	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	1	3.4856	0.2382	1551.57	1552.783	8	202.4	50	K.R4F1A1P1I1Y1E1E1I1A1N2V1L1.A
gi|6320726|ref|NP_010806.1|	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	2	3.5176	0.2784	1555.35	1552.783	1	291.6	70.83333	K.R4F1A1P1I1Y1E1E1I1A1N2V1L1.A
gi|6320726|ref|NP_010806.1|	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	3	4.053	0.313	3329	3329.836	1	688.2	29.62963	L.KYGLPQLPEEEYAKLEKPQPLDRDMIVQ.L
gi|6320726|ref|NP_010806.1|	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	2	3.5756	0.29	1776.43	1779.043	1	491.7	50	L.KYGLPQLPEEEYAKL.E
gi|6320726|ref|NP_010806.1|	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	2	3.6355	0.152	1798.11	1797.043	1	785.3	64.28571	L.K2Y1G1L1P1Q2L1P1E1E1E1Y1A1K2L1.E
gi|6320726|ref|NP_010806.1|	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	2	3.5658	0.2454	1535.37	1535.783	1	302.6	75	K.RFAPIYEEIANVL.A
gi|6320726|ref|NP_010806.1|	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	2	2.9386	0.2703	1752.21	1751.035	1	289.3	53.571426	H.SKRFAPIYEEIANVL.A
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	1	3.0222	0.4292	1386.65	1387.581	1	237.5	50	T.GEFILPDRHGVF.T
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	1	3.3171	0.3988	1404.55	1404.581	1	326.1	54.545456	T.G1E1F1I1L1P1D1R4H3G1V1F1.T
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	1	2.8831	0.2189	1347.67	1346.529	9	130.3	55	G.E1F1I1L1P1D1R4H3G1V1F1.T
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	2.9829	0.1912	1859.35	1857.098	4	337.3	50	Y.D1K2E1Q2R4L1F1D1N2I1I1V1F1P1T1.K
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	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 (OST) 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.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	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	2	3.5003	0.2948	2350.03	2349.654	2	209.7	34.210526	Y.D1K2E1Q2R4L1F1D1N2I1I1V1F1P1T1K2G1G1K2N2.L
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	2	5.0375	0.4044	2014.93	2016.169	1	884.8	52.941177	H.NDKVEDLVKNDDDIINGV.R
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	2	4.0156	0.3042	2171.53	2172.357	3	281.2	47.22222	H.NDKVEDLVKNDDDIINGVR.K
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	1	3.1044	0.1705	1380.78	1381.699	5	554.4	63.636364	Q.VSREVLEPILIL.L
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	1	2.6276	0.1636	1394.86	1396.699	5	510.2	63.636364	Q.V1S1R4E1V1L1E1P1I1L1I1L1.L
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	1	2.6989	0.2454	1509.83	1510.858	4	390.8	50	Q.V1S1R4E1V1L1E1P1I1L1I1L1L1.Q
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for 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

gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	2	3.1071	0.1626	1397.57	1395.726	1	853.2	77.27273	V.SREVLEPILILL.Q
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	2	3.4592	0.1521	1494.31	1494.858	1	1102.1	75	Q.VSREVLEPILILL.Q
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	1	3.2179	0.2193	1295.56	1296.566	4	638	70	V.S1R4E1V1L1E1P1I1L1I1L1.L
gi|6320824|ref|NP_010903.1|	YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	1	3.0339	0.1659	1282.73	1282.566	3	705.4	70	V.SREVLEPILIL.L
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	2	3.4083	0.1708	2003.27	2004.257	1	576.8	50	N.KIEIPTNEMESVEELIE.G
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	3	5.3746	0.2945	2581.31	2579.956	1	1275.1	43.18182	N.K2I1E1I1P1T1N2E1M1E1S1V1E1E1L1I1E1G1G1L1L1P1L1.L
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	2	3.7712	0.1986	2812.89	2810.219	1	766.2	41.666664	N.K2I1E1I1P1T1N2E1M1E1S1V1E1E1L1I1E1G1G1L1L1P1L1L1N2.S
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin 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.KIEIPTNEMESVEELIEGGLLPLLN.S
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	2	3.0428	0.2341	2782.13	2782.219	1	1013.9	43.75	N.KIEIPTNEMESVEELIEGGLLPLLN.S
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	2	3.4739	0.3282	1564.19	1564.751	1	321.5	62.5	S.G1H3K2I1D1K2E1N2P1Y1K2K2S1.I
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	3	4.9091	0.2751	2554.49	2554.956	1	964.2	42.045452	N.KIEIPTNEMESVEELIEGGLLPL.L
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	2	3.6318	0.2325	2780.91	2782.219	1	921.8	43.75	N.KIEIPTNEMESVEELIEGGLLPLLN.S
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	2	4.5562	0.3847	2148.05	2149.386	1	636.3	55.88235	C.SIRDKEIVMPEEHHGNEK.W
gi|6320813|ref|NP_010892.1|	YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	2	3.2846	0.2034	1660.11	1659.777	1	777.1	77.27273	C.C1N2H3K2D1F1P1F1W2Y1L1D1.R
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.2087	0.3558	1782.07	1779.988	1	425.2	60.000004	S.EDNLQLDGVDKIAVLH.G
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.8498	0.1578	1674.43	1672.873	1	788.2	67.85714	A.V1E1E1A1N2S1K2P1V1E1V1I1K2P1N2.G
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	2.9503	0.1774	1543.57	1540.723	1	565.6	70.83333	F.HCPLKDDAIETIK.M
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers 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.R4D1V1E1E1T1V1S1I1P1F1D1P1S1K2D1T1F1.D
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.0582	0.4572	2082.65	2083.259	1	824	64.70589	F.RDVEETVSIPFDPSKDTF.D
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.6191	0.3664	2764.79	2764.149	1	329.9	36	A.VEEANSKPVEVIKPNGLSEKKPADLA.S

gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.7582	0.3859	2795.57	2796.149	1	503.6	42 A.V1E1E1A1N2S1K2P1V1E1V1I1K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.5894	0.3038	2424.69	2424.8	1	674.6	50 E.SIKLRPSEDNLQLDGVDKIAVL.H
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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.H3C1P1L1K2D1D1A1I1E1T1I1K2M1L1.N
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	5.2104	0.4016	3557.87	3559.017	1	1085.9	29.032257 S.G1E1S1T1P1L1L1K2E1S1I1K2L1R4P1S1E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1H3.G
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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.SIKLRPSEDNLQLDGVDKIAVLH.G
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.696	0.4217	3108.11	3106.472	1	590.1	29 A.V1K2G1A1P1E1T1I1R4E1R4L1S1D1I1P1K2N2Y1D1E1I1Y1K2S1F1.T
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	3.9815	0.32	3070.4	3070.472	1	481	28 A.VKGAPETIRERLSDIPKNYDEIYKSF.T
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.8356	0.3426	1718.77	1716.944	1	1397.2	76.666664 L.VKLEDGDIVGDPMEKA.T
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	5.225	0.227	3578.27	3580.778	1	773.1	26.666668 A.G1K2S1D1D1N2Q2L1L1F1R4D1V1E1E1T1V1S1I1P1F1D1P1S1K2D1T1F1D1H3S1.K
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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

gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.0169	0.1712	2311.23	2311.641	2	441.3	40	E.SIKLRPSEDNLQLDGVDKIAV.L
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.8936	0.3918	1784.55	1785.075	1	1246	71.42857	F.HCPLKDDAIETIKML.N
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.5582	0.2874	1787.66	1785.075	1	2024.2	57.14286	F.HCPLKDDAIETIKML.N
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.0403	0.3893	2338.69	2339.694	1	586.4	47.368423	Y.KLEPREPQVDLEKEFAPSLL.N
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.8275	0.3367	2843.51	2843.166	1	492.7	39.130436	K.GAPETIRERLSDIPKNYDEIYKSF.T
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.6863	0.3478	2560.49	2561.941	1	467.5	38.636364	E.SIKLRPSEDNLQLDGVDKIAVLH.G
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	6.4952	0.4864	2560.49	2561.941	1	1769.2	48.863636	E.SIKLRPSEDNLQLDGVDKIAVLH.G
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.2157	0.3964	2593.81	2593.941	2	341.8	34.090908	E.S1I1K2L1R4P1S1E1D1N2L1Q2L1D1G1V1D1K2I1A1V1L1H3.G
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.7372	0.2805	2487.57	2488.803	4	435.2	39.473686	E.TIRERLSDIPKNYDEIYKSF.T
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.0314	0.2563	1387.71	1388.576	2	860.3	79.16667	L.VKLEDGDIVGDPM.E
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.8638	0.2384	1401.49	1402.576	1	863.8	79.16667	L.V1K2L1E1D1G1D1I1V1G1D1P1M1.E
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.653	0.3578	1544.03	1544.705	1	1430.2	83.33333	F.F1F1M1D1D1K2P1S1D1I1S1V1Q2.Q
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.172	0.3574	1529.51	1529.705	1	1380.8	83.33333	F.FFMDDKPSDISVQ.Q
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.9267	0.3492	1629.59	1630.812	1	556.1	57.692307	R.W2N2Q2P1Q2P1P1V1P1E1P1I1A1H3.L
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.0564	0.2946	2793.86	2796.149	1	1015.9	32	A.V1E1E1A1N2S1K2P1V1E1V1I1K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.5612	0.2755	1734.09	1734.944	1	730.6	60.000004	L.V1K2L1E1D1G1D1I1V1G1D1P1M1E1K2A1.T
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.0428	0.2035	1711.43	1710.822	3	309.7	50	T.V1S1I1P1F1D1P1S1K2D1T1F1D1H3S1.K
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.3568	0.3634	2109.49	2111.227	3	206	38.235294	Q.SKIDDLNRDDVESELTFN.G
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.7951	0.2649	2449.28	2449.567	1	1057.7	36.25	F.R4D1V1E1E1T1V1S1I1P1F1D1P1S1K2D1T1F1D1H3S1.K
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.4345	0.2859	2424.59	2422.567	1	950.4	33.75	F.RDVEETVSIPFDPSKDTFDHS.K
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.0834	0.27	1930.53	1931.045	1	707.4	56.666668	S.K2I1D1D1L1N2R4D1D1V1E1S1E1L1T1F1.N
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.0319	0.2476	2052.35	2053.279	1	244.3	39.473686	L.QVTPPEHKSDIPPPPDGGAL.A
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.9756	0.2344	2545.45	2545.826	1	341.9	42.5	T.E1I1Y1K2L1E1P1R4E1P1Q2V1D1L1E1K2E1F1A1P1S1.L
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.4806	0.1994	1558.49	1557.723	1	597.5	70.83333	F.H3C1P1L1K2D1D1A1I1E1T1I1K2.M
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	3.9777	0.1506	2363.3	2363.706	1	610.7	33.333336	A.N2S1K2P1V1E1V1I1K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	4.8324	0.3648	2362.65	2363.706	1	457.4	45.238094	A.N2S1K2P1V1E1V1I1K2P1N2G1L1S1E1K2K2P1A1D1L1A1.S
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.7069	0.4363	2112.51	2113.375	1	290.3	50	Y.KLEPREPQVDLEKEFAPS.L
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	2	3.4408	0.3336	2049.87	2051.361	1	539.9	46.875	L.K2R4L1Y1G1E1N2S1F1D1I1P1I1P1T1F1M1.E
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; 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

gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.2661	0.2965	2641.49	2639.911	1	637	32.142857	K.G1A1P1E1T1I1R4E1R4L1S1D1I1P1K2N2Y1D1E1I1Y1K2.S
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.1685	0.1881	2876.21	2876.166	1	574.5	29.347824	K.G1A1P1E1T1I1R4E1R4L1S1D1I1P1K2N2Y1D1E1I1Y1K2S1F1.T
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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.V1K2G1A1P1E1T1I1R4E1R4L1S1D1I1P1K2N2Y1.D
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to 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
gi|6320804|ref|NP_010883.1|	YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	3	4.5084	0.3473	2957.27	2958.296	1	511.9	29.166666	A.V1K2G1A1P1E1T1I1R4E1R4L1S1D1I1P1K2N2Y1D1E1I1Y1K2S1.F
gi|6320803|ref|NP_010882.1|	YEL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex 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
gi|6320803|ref|NP_010882.1|	YEL032W	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	7.7792	0.5303	3435.98	3438.387	1	1061.8	34.482758	A.N2Y1N2D1D1Q2D1D1A1D1E1R4D1L1L1G1D1D1D1G1D1D1L1E1K2E1K2K2A1 1.S
gi|6320803|ref|NP_010882.1|	YEL032W	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	5.2933	0.393	4226.21	4227.325	1	914.2	22.368422	L.AVGEDADINPEEHSNSGAGVENEGEDDEDHVFEKFNPLL.Q
gi|6320803|ref|NP_010882.1|	YEL032W	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	7.7099	0.5406	4273.67	4275.325	1	1466.3	25.657896	L.A1V1G1E1D1A1D1I1N2P1E1E1H3S1N2S1G1A1G1V1E1N2E1G1E1D1D1E1D1H V1F1E1K2F1N2P1L1L1.Q
gi|6320803|ref|NP_010882.1|	YEL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex 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
gi|6320803|ref|NP_010882.1|	YEL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex; Mcm3p	2	4.8418	0.4423	2017.19	2017.007	1	1209.2	62.5	A.G1V1E1N2E1G1E1D1D1E1D1H3V1F1E1K2F1.N
gi|6320803|ref|NP_010882.1|	YEL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex 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.S1I1D1V1I1L1D1D1D1L1V1D1K2T1K2P1G1D1R4V1N2V1V1.G
gi|6320803|ref|NP_010882.1|	YEL032W	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.S1I1D1V1I1L1D1D1D1L1V1D1K2T1K2P1G1D1R4V1N2V1V1.G
gi|6320803|ref|NP_010882.1|	YEL032W	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	4.3448	0.2734	2526.17	2526.847	1	887.9	34.090908	R.SIDVILDDDLVDKTKPGDRVNVV.G
gi|6320803|ref|NP_010882.1|	YEL032W	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	5.0958	0.2242	2913.29	2916.228	1	766.3	32	A.G1Q2L1P1R4S1I1D1V1I1L1D1D1D1L1V1D1K2T1K2P1G1D1R4V1N2.V
gi|6320803|ref|NP_010882.1|	YEL032W	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	4.0376	0.299	2879.9	2880.228	9	413.1	25	A.GQLPRSIDVILDDDLVDKTKPGDRVN.V
gi|6320803|ref|NP_010882.1|	YEL032W	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	6.1882	0.3065	3117.08	3116.493	1	1162.7	28.703705	A.G1Q2L1P1R4S1I1D1V1I1L1D1D1D1L1V1D1K2T1K2P1G1D1R4V1N2V1V1.G
gi|6320803|ref|NP_010882.1|	YEL032W	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	6.1066	0.2953	3078.44	3078.493	1	1352.8	31.48148	A.GQLPRSIDVILDDDLVDKTKPGDRVNVV.G
gi|6320803|ref|NP_010882.1|	YEL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex 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
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; 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.Q
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	3	4.1942	0.2472	2365.25	2363.52	1	999.7	36.904762	L.M1N2M1D1G1D1T1K2D1D1V1K2A1P1E1G1E1L1G1D1S1L1.Q
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	3	3.8517	0.2894	2231.57	2231.328	1	929.5	35	M.N2M1D1G1D1T1K2D1D1V1K2A1P1E1G1E1L1G1D1S1L1.Q
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	2	5.3857	0.5058	2230.41	2231.328	1	1134.5	55	M.N2M1D1G1D1T1K2D1D1V1K2A1P1E1G1E1L1G1D1S1L1.Q
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	1	2.686	0.1723	1126.58	1127.24	3	403.6	66.66667	K.KLEDLSPSTH.N
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; 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.K2L1E1D1L1S1P1S1T1H3.N
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	3	4.0392	0.2643	2338.58	2339.631	1	808.4	38.157894	K.K2L1E1D1L1S1P1S1T1H3N2M$E1V1P1V1V1K2R4N2.E
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	3	4.1086	0.2286	2339.93	2338.52	1	1836.2	42.857143	L.MNMDGDTKDDVKAPEGELGDSL.Q
gi|6320801|ref|NP_010880.1|	YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	2	5.5073	0.4427	2362.23	2363.52	1	1117.7	50	L.M1N2M1D1G1D1T1K2D1D1V1K2A1P1E1G1E1L1G1D1S1L1.Q
gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has 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
gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	4.5186	0.3585	1878.95	1877.149	1	593.3	64.28571	N.V1W2R4P1L1P1D1W2L1G1N2I1Q2P1Y1.D
gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	3.4293	0.3508	2632.45	2634.006	1	490.7	42.857143	Q.GIFKPYVPDFKNTPSVEFYDLR.N
gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	3.7075	0.3291	2661.55	2662.006	1	706.1	50	Q.G1I1F1K2P1Y1V1P1D1F1K2N2T1P1S1V1E1F1Y1D1L1R4.N
gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	3.5637	0.2214	1524.25	1524.643	1	779.4	77.27273	K.I1W2E1I1G1F1E1D1V1R4D1Q2.W
gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	2.9741	0.2791	1369.87	1370.566	4	538.9	60.000004	N.V1W2R4P1L1P1D1W2L1G1N2.I
gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	3.9023	0.3474	1854.35	1855.149	1	557	60.714287	N.VWRPLPDWLGNIQPY.D

gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	3.0089	0.1599	2249.25	2249.571	1	392.5	38.88889	Q.GIFKPYVPDFKNTPSVEFY.D
gi|6320799|ref|NP_010878.1|	YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	2	3.2001	0.2462	2270.97	2271.571	2	510	41.666664	Q.G1I1F1K2P1Y1V1P1D1F1K2N2T1P1S1V1E1F1Y1.D
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.5992	0.4191	2391.75	2393.674	1	1096.3	57.14286	N.A1S1I1P1K2T1P1E1D1I1S1I1L1P1V1N2D1E1P1G1Y1L1.Q
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	3.2342	0.3276	2196.75	2199.375	1	455.7	50	L.S1A1V1R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1.G
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.5525	0.4479	2355.79	2357.559	1	755.4	52.499996	L.S1A1V1R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1G1V1.S
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.4268	0.4801	2329.81	2330.559	1	1437.8	62.5	L.SAVRDHLEKDYPFPVVEGDGV.S
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	3.5939	0.3243	2503.67	2503.832	1	810.1	52.380955	A.VRDHLEKDYPFPVVEGDGVSIM.G
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.282	0.4575	2530.43	2531.832	1	494.4	40.476192	A.V1R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1G1V1S1I1M1.G
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.5894	0.4515	2405.57	2404.7	1	1041	52.499996	V.RDHLEKDYPFPVVEGDGVSIM.G
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.4211	0.417	2429.83	2431.7	1	503.5	42.5	V.R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1G1V1S1I1M1.G
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.568	0.3893	2690.59	2691.989	1	517.1	41.304348	L.S1A1V1R4D1H3L1E1K2D1Y1P1F1P1V1V1E1G1D1G1V1S1I1M1.G
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.5118	0.3887	2664.71	2661.989	1	582	41.304348	L.SAVRDHLEKDYPFPVVEGDGVSIM.G
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	3.7085	0.3664	2249.53	2248.512	1	735.2	47.368423	R.DHLEKDYPFPVVEGDGVSIM.G
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	3.1194	0.2231	1580.17	1580.868	1	858.6	66.66667	Q.I1V1F1E1P1T1F1P1I1N2E1K2M1.V
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	3.654	0.2995	2521.73	2523.805	1	303.8	34.090908	N.A1S1I1P1K2T1P1E1D1I1S1I1L1P1V1N2D1E1P1G1Y1L1Q2.D
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	3	4.419	0.2079	2526.11	2523.805	3	472.5	29.545454	N.A1S1I1P1K2T1P1E1D1I1S1I1L1P1V1N2D1E1P1G1Y1L1Q2.D
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.7234	0.3903	2449.55	2451.726	1	420.4	40.476192	A.S1I1P1K2T1P1E1D1I1S1I1L1P1V1N2D1E1P1G1Y1L1Q2.D
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	3.836	0.2951	2499.67	2497.805	1	626	47.727272	N.ASIPKTPEDISILPVNDEPGYLQ.D
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	3.7612	0.4068	2296.87	2298.595	1	471.7	42.5	A.SIPKTPEDISILPVNDEPGYL.Q
gi|6320793|ref|NP_010872.1|	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	2	4.9232	0.3845	2371.55	2369.674	1	827.3	52.380955	N.ASIPKTPEDISILPVNDEPGYL.Q
gi|6320784|ref|NP_010863.1|	YEL051W	Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis; Vma8p	2	3.4256	0.3009	2445.29	2447.462	1	489.2	45.238094	K.R4D1R4A1E1Q2D1A1S1E1V1A1A1D1E1E1P1Q2G1E1T1L1.V
gi|6320784|ref|NP_010863.1|	YEL051W	Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis; Vma8p	2	4.1064	0.3353	2416.49	2417.462	1	715.8	45.238094	K.RDRAEQDASEVAADEEPQGETL.V
gi|6320784|ref|NP_010863.1|	YEL051W	Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis; Vma8p	3	4.9268	0.2657	1965.47	1965.12	1	1194.1	48.214287	N.S1E1L1D1E1L1D1R4E1E1F1Y1R4L1K2.K
gi|6320784|ref|NP_010863.1|	YEL051W	Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the 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

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	3.1985	0.2111	1244.47	1244.395	2	462.2	72.22222	F.LHDHDHIFPL.D
gi|6320839|ref|NP_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.KNSPSDFNKPDLPELIQ.R
gi|6320839|ref|NP_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	3.5301	0.2725	2131.59	2132.331	1	1068.5	58.333332	F.IAPHLPVDLEAEDEAFTTY.R
gi|6320839|ref|NP_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	3.0818	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
gi|6320844|ref|NP_010923.1|	YER007C-A	hypothetical protein; Tma20p	3	5.5116	0.1924	2030.39	2028.397	1	1102	50	L.VKQYPKIEDVIDELIPK.K
gi|6320844|ref|NP_010923.1|	YER007C-A	hypothetical protein; Tma20p	3	5.0639	0.1683	2264.84	2267.649	2	1220.2	40.27778	L.V1K2Q2Y1P1K2I1E1D1V1I1D1E1L1I1P1K2K2S1.Q
gi|6320844|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	hypothetical protein; Tma20p	2	3.0214	0.1563	1821.05	1819.09	3	233.7	57.14286	K.Q2Y1P1K2I1E1D1V1I1D1E1L1I1P1K2.K
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.7206	0.2672	1731.41	1732.897	4	541.5	50	F.D1V1N2K2P1G1A1E1I1E1D1L1K2G1G1V1A1.G
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	4.8325	0.3564	4142.6	4145.439	1	465.4	20.714287	L.EEDGETEEEKRKREFEEGGGLPEQPLNPDFSKLNPL.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	4.8658	0.3872	4465.16	4467.756	1	576	21.052631	F.T1G1L1E1E1D1G1E1T1E1E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1N2P1L1.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	4.2523	0.1869	4315.43	4315.651	1	599.4	20.945946	T.GLEEDGETEEEKRKREFEEGGGLPEQPLNPDFSKLNPL.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.4733	0.2316	1441.53	1439.695	2	798.6	66.66667	F.KLGDEIEIRPGIV.T
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.013	0.2939	1835.93	1837.151	1	931.6	63.333332	V.F1K2L1G1D1E1I1E1I1R4P1G1I1V1T1K2.D
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.6006	0.2765	1712.39	1712.897	1	826.1	59.375	F.DVNKPGAEIEDLKGGVA.G
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	4.8537	0.3099	1713.26	1712.897	1	1261.1	50	F.DVNKPGAEIEDLKGGVA.G
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.5773	0.3098	1442.61	1444.641	1	780.1	66.66667	L.G1D1E1I1E1I1R4P1G1I1V1T1K2.D
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.8499	0.2944	1946.55	1947.152	1	1015.2	58.333332	R.SFDVNKPGAEIEDLKGGVA.G
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.5301	0.2702	1428.33	1427.641	1	702.5	66.66667	L.GDEIEIRPGIVTK.D
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.3117	0.1904	1967.21	1969.152	1	742.7	52.77778	R.S1F1D1V1N2K2P1G1A1E1I1E1D1L1K2G1G1V1A1.G
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	4.82	0.3617	4419.71	4416.756	1	703.4	23.026316	F.TGLEEDGETEEEKRKREFEEGGGLPEQPLNPDFSKLNPL.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.4262	0.2107	1498.55	1496.629	1	772.7	66.66667	R.HVSFVDCPGHDIL.M
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	4.5985	0.3934	1667.93	1668.974	1	1139.3	71.42857	F.KLGDEIEIRPGIVTK.D
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	2.9027	0.28	1626.59	1626.957	1	608.1	57.692307	K.TIPVPPRDFMISPR.L
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.6124	0.2776	1274.05	1273.355	1	652.4	80	V.S1F1V1D1C1P1G1H3D1I1L1.M
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	4.6766	0.2917	1533.95	1534.663	2	1376.6	73.07692	R.SFDVNKPGAEIEDL.K
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.7446	0.429	2125.61	2125.294	1	627.9	50	N.GNLEPVGEPDIVEETEVVAQ.E
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	4.7041	0.3742	1937.47	1937.203	1	1017.8	64.70589	G.GGLPEQPLNPDFSKLNPL.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.6517	0.2058	1241.91	1242.403	1	1302.6	80	F.K2L1G1D1E1I1E1I1R4P1G1.I
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	4.4816	0.2585	3864.23	3865.059	1	513.9	24.21875	L.E1E1D1G1E1T1E1E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1.N
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	5.4849	0.4245	4036.46	4037.271	1	688.8	25.735294	T.G1L1E1E1D1G1E1T1E1E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1.N
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	3.9123	0.3327	3991.13	3991.271	1	660.7	22.794117	T.GLEEDGETEEEKRKREFEEGGGLPEQPLNPDFSKL.N

gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	5.2932	0.3297	4190.96	4193.439	7	266.7	17.857143	L.E1E1D1G1E1T1E1E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1N2P1L1.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	5.3736	0.3808	4364.87	4365.651	1	940.1	22.972973	T.G1L1E1E1D1G1E1T1E1E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1N2P1L1.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	5.7324	0.4671	3066.08	3068.352	1	1254.2	34	E.E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1.N
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	5.1896	0.487	3029.36	3031.352	1	939.8	31	E.EEKRKREFEEGGGLPEQPLNPDFSKL.N
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	6.2829	0.4438	3398.3	3396.732	1	897.2	25.892857	E.E1E1K2R4K2R4E1F1E1E1G1G1G1L1P1E1Q2P1L1N2P1D1F1S1K2L1N2P1L1.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	3	5.0611	0.4301	3356.12	3355.732	4	628.7	24.107143	E.EEKRKREFEEGGGLPEQPLNPDFSKLNPL.S
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	4.0335	0.166	1887.41	1887.167	1	665.7	64.28571	Q.T1V1R4F1K2D1E1L1E1R4N2I1T1I1K2.L
gi|6320863|ref|NP_010942.1|	YER025W	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-Met; Gcd11p	2	3.44	0.2169	1862.47	1863.167	2	541.5	57.14286	Q.TVRFKDELERNITIK.L
gi|6320890|ref|NP_010969.1|	YER049W	hypothetical protein; Tpa1p	2	5.8479	0.4986	2489.25	2487.677	1	1354.4	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; Tpa1p	2	3.7852	0.2275	2065.89	2066.275	3	448.6	43.75	E.SNVLEDFEFPKDERNIL.S
gi|6320890|ref|NP_010969.1|	YER049W	hypothetical protein; Tpa1p	2	5.5057	0.4405	2732.59	2733.942	1	899	50	Q.G1W2Y1H3I1P1Q2V1G1E1E1G1Y1I1P1G1E1E1E1A1W2V1R4.N
gi|6320890|ref|NP_010969.1|	YER049W	hypothetical protein; Tpa1p	2	4.5709	0.4607	2701.89	2702.942	1	1074.4	52.272724	Q.GWYHIPQVGEEGYIPGEEEAWVR.N
gi|6320890|ref|NP_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.R4A1D1D1S1G1D1S1V1L1I1N2D1P1P1A1W2N2T1F1.N
gi|6320890|ref|NP_010969.1|	YER049W	hypothetical protein; Tpa1p	3	3.8577	0.2086	2486.9	2487.677	7	694.8	37.5	W.Y1H3I1P1Q2V1G1E1E1G1Y1I1P1G1E1E1E1A1W2V1R4.N
gi|6320890|ref|NP_010969.1|	YER049W	hypothetical protein; Tpa1p	2	5.7654	0.4667	2486.83	2487.677	1	1380.6	65	W.Y1H3I1P1Q2V1G1E1E1G1Y1I1P1G1E1E1E1A1W2V1R4.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; Tpa1p	3	4.9035	0.3191	2702.84	2702.942	1	928.6	39.772728	Q.GWYHIPQVGEEGYIPGEEEAWVR.N
gi|6320890|ref|NP_010969.1|	YER049W	hypothetical protein; Tpa1p	2	3.8468	0.3021	1839.55	1841.098	1	484.1	53.125	R.L1F1P1S1I1L1P1N2V1P1H3S1D1P1S1A1K2.L
gi|6320890|ref|NP_010969.1|	YER049W	hypothetical protein; Tpa1p	2	3.1744	0.3317	1818.89	1820.098	8	374.5	43.75	R.LFPSILPNVPHSDPSAK.L
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	5.4586	0.4276	2183.93	2185.478	1	1975.5	65.789474	F.G1G1T1S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	4.2309	0.376	2161.49	2160.478	1	1395.5	42.105263	F.GGTSVGKFPVQIVDDIVKHY.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	3.4905	0.2562	1944.03	1945.269	1	1075.1	62.5	T.SVGKFPVQIVDDIVKHY.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	5.9706	0.3571	1966.37	1967.269	1	2127.6	57.8125	T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	5.2121	0.3569	2184.47	2185.478	1	1054	38.157894	F.G1G1T1S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	4.114	0.3682	1721.55	1721.006	1	1263.3	76.92308	G.K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	4.9283	0.3642	1878.35	1879.191	1	1321.4	48.333332	S.V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; 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.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	4.2663	0.3424	1782.59	1782.093	1	1789.9	55	T.SVGKFPVQIVDDIVKH.Y
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	5.9198	0.3609	1805.12	1803.093	1	2335.8	63.333332	T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3.Y
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; 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.G1G1T1S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	3.9542	0.4123	1701.53	1702.006	1	1091.8	55.76923	G.KFPVQIVDDIVKHY.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	5.4368	0.3631	1720.28	1721.006	1	806.1	50	G.K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; 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
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	3.5527	0.2238	1781.13	1779.058	1	996.9	57.14286	V.G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	4.7456	0.4131	1944.62	1945.269	1	1246.8	48.4375	T.SVGKFPVQIVDDIVKHY.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	4.6431	0.3418	1965.83	1967.269	1	1429.2	68.75	T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; 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
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	4.1528	0.2264	1625.63	1624.773	1	1007.7	66.66667	Q.E1S1E1F1Q2D1I1I1E1V1I1R4Q2.D
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	3.3043	0.1973	1606.71	1606.773	1	1057.2	66.66667	Q.ESEFQDIIEVIRQ.D
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	4.237	0.4032	1615.1	1614.882	1	647.6	48.076923	V.G1K2F1P1V1Q2I1V1D1D1I1V1K2H3.Y
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	3.7301	0.392	1802.27	1803.093	1	706.5	53.333336	T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3.Y
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	5.7132	0.4253	1967.24	1967.269	1	1359.6	50	T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	4.3502	0.2559	1720.55	1721.006	1	700.1	48.076923	G.K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p 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
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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	3	5.1842	0.409	1776.35	1779.058	1	1234.4	58.928574	V.G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.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; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	2	4.6214	0.3593	1969.47	1967.269	1	1268.9	65.625	T.S1V1G1K2F1P1V1Q2I1V1D1D1I1V1K2H3Y1.S
gi|6320897|ref|NP_010976.1|	YER056C	Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine accumulation; Fcy2p	1	2.2119	0.224	1200.6	1201.365	7	323.7	60.000004	Q.DLEKRSPVIGS.S
gi|6320897|ref|NP_010976.1|	YER056C	Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) 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	Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) 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
gi|6320913|ref|NP_010992.1|	YER069W	Protein that is processed in the mitochondrion to yield acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase, which catalyze the 2nd and 3rd steps in arginine biosynthesis; enzymes form a complex with Arg2p; Arg5,6p	1	2.7426	0.2598	1162.47	1162.393	1	454.7	66.66667	Y.H3V1G1L1Y1P1I1V1L1H3.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
gi|6320924|ref|NP_011003.1|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	1	3.6545	0.2553	1452.63	1452.601	1	588.3	68.181816	Y.DLKEDITDFDKL.S
gi|6320924|ref|NP_011003.1|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.0153	0.2613	1399.61	1398.648	1	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|	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
gi|6320924|ref|NP_011003.1|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	1	2.4667	0.1983	1458.69	1459.642	2	185.9	54.545456	L.RIPYPLENENTL.S
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|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.9686	0.3565	1607.43	1607.732	1	1249.2	73.07692	L.MKDWDPLIEDGSSN.Q
gi|6320924|ref|NP_011003.1|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.8071	0.3585	1624.51	1624.732	1	1021.8	69.230774	L.M1K2D1W2D1P1L1I1E1D1G1S1S1N2.Q
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|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	1	3.9773	0.1714	1466.62	1466.601	1	600.4	63.636364	Y.D1L1K2E1D1I1T1D1F1D1K2L1.S
gi|6320924|ref|NP_011003.1|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.7111	0.179	1452.07	1452.601	2	1066.7	77.27273	Y.DLKEDITDFDKL.S
gi|6320924|ref|NP_011003.1|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	3.0052	0.2638	1395.99	1396.673	1	605.7	66.66667	A.KAPDGKILPPVFN.K
gi|6320924|ref|NP_011003.1|	YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	2	2.9594	0.2773	1978.15	1979.246	1	410.5	60.000004	Q.HQWEKKLNDNNPKLIT.A
gi|6320935|ref|NP_011014.1|	YER090W	Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis, forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp3p; Trp2p	2	3.9629	0.2468	1845.39	1845.082	3	730.7	53.125	T.I1K2T1G1P1T1E1G1I1E1T1D1P1L1E1I1L1.E
gi|6320935|ref|NP_011014.1|	YER090W	Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis, forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp3p; Trp2p	2	3.6231	0.2494	1826.57	1827.082	6	593.7	46.875	T.IKTGPTEGIETDPLEIL.E
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	3.8618	0.3566	1530.59	1531.663	1	951.2	69.230774	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	3.7284	0.3619	1550.17	1550.663	1	983.4	73.07692	L.S1R4I1I1E1N2S1E1G1N2V1E1L1A1.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	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.K2L1I1P1S1I1P1G1G1K2L1I1Q2.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.H3L1P1L1N2T1G1F1E1E1Y1N2P1I1F1E1L1I1M$.K
gi|6320956|ref|NP_011035.1|	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	2	3.7024	0.2821	2387.25	2389.706	4	507.6	42.105263	L.A1H3L1P1L1N2T1G1F1E1E1Y1N2P1I1F1E1L1I1M$.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.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	3.3842	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.H3E1E1Y1L1P1L1I1I1D1I1I1D1S1A1.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.F1H3E1E1Y1L1P1L1I1I1D1I1I1D1S1A1.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
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	3.956	0.416	1905.31	1906.143	1	608.5	59.375	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	4.0512	0.3361	2536.63	2537.783	1	312.2	38.636364	Q.ENKETVEPVVQDSEPKEVPAVVN.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	2	4.5555	0.3168	1734.95	1736.018	1	1127.4	67.85714	R.DKFLVITLPSPYDLN.G
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	4.1508	0.2245	1926.51	1927.143	1	497.5	56.25	N.E1K2E1V1P1A1E1P1E1T1Q2P1P1V1Q2V1K2.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	4.3432	0.1643	3170.54	3171.529	2	582.3	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	2	4.0268	0.2273	3169.97	3171.529	1	336.7	32.142857	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	2	4.9478	0.1531	2642.57	2643.956	1	475.2	39.130436	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	1	2.893	0.2162	1405.55	1406.666	5	336.2	59.090908	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	3.3699	0.2307	1750.63	1753.018	1	920.4	60.714287	R.D1K2F1L1V1I1T1L1P1S1P1Y1D1L1N2.G
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	4.2277	0.1983	2012.75	2013.323	1	1153.1	61.764706	R.D1K2F1L1V1I1T1L1P1S1P1Y1D1L1N2G1K2A1.V
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	4.7605	0.3106	1942.65	1941.244	1	881.2	65.625	R.D1K2F1L1V1I1T1L1P1S1P1Y1D1L1N2G1K2.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	3.742	0.2185	1396.35	1393.666	1	1672.5	81.818184	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	3.8366	0.3299	2726.43	2727.042	1	239.9	34.090908	L.T1E1E1P1A1A1D1F1K2C1R4D1K2F1L1V1I1T1L1P1S1P1Y1.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	3.8477	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.G1L1T1E1E1P1A1A1D1F1K2C1R4D1K2F1L1V1I1T1L1P1S1P1Y1.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	2	3.1259	0.2277	1729.65	1727.992	3	449.1	50	K.C1R4D1K2F1L1V1I1T1L1P1S1P1Y1.D
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	4.4845	0.3885	2976.33	2977.98	1	533.2	38	N.S1K2G1N2N2N2N2S1I1D1D1I1N2T1Q2P1D1E1F1N2D1F1L1N2D1T1.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	2.3724	0.2439	1591.34	1592.631	1	232.9	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	3.8512	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.S1I1F1I1K2Q2P1I1L1L1E1L1E1A1P1I1K2I1C1.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.G1S1K2P1G1Q2Q2V1D1L1E1E1N2E1I1R4Y1L1.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.W2S1D1P1D1K2D1I1V1G1W2.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	2	3.1669	0.1808	1399.31	1399.763	1	328.7	54.545456	K.ARSIFIKQPILL.E
gi|6320983|ref|NP_011062.1|	YER136W	GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p	2	3.7156	0.2178	1205.65	1204.416	1	930.7	80	L.G1P1I1E1E1K2F1M1G1I1A1.E
gi|6320983|ref|NP_011062.1|	YER136W	GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p	2	3.0051	0.1956	1952.97	1952.186	5	240.3	46.666668	Q.GLDLDKNTMDEVYYKF.G
gi|6320983|ref|NP_011062.1|	YER136W	GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p	2	3.065	0.1701	1617.29	1616.883	7	461.2	46.42857	Y.K2V1P1A1N2E1I1E1A1I1S1S1P1L1M1.G
gi|6320983|ref|NP_011062.1|	YER136W	GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p	2	3.6431	0.3089	1706.29	1706.934	1	557	67.85714	S.TIIETDKPHIELEPA.F
gi|6320983|ref|NP_011062.1|	YER136W	GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p	2	4.0523	0.3461	1725.39	1724.934	1	828.8	75	S.T1I1I1E1T1D1K2P1H3I1E1L1E1P1A1.F
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	4.9951	0.3267	1688.25	1686.788	1	1370.4	80.769226	A.K2M1E1N2I1N2F1N2E1D1G1E1I1N2.V
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	3.1568	0.2447	1143.13	1142.319	2	646.9	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	4.651	0.2872	1926.39	1927.173	2	739.9	64.28571	K.N2K2K2K2Q2E1L1T1E1E1Q2K2R4Q2L1.F
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	1	2.8777	0.1739	1271.39	1272.493	1	417.6	66.66667	L.K2H3L1N2P1G1Y1W2I1K2.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	1	2.6657	0.1794	1141.6	1142.319	1	522.6	68.75	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	3.9922	0.3056	2012.45	2013.056	1	337.5	53.333336	Y.H3V1N2C1C1N2P1E1L1D1N2G1W2D1I1F1.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	1	2.4537	0.2027	1510.71	1510.672	1	180.5	59.090908	Q.E1L1T1E1E1Q2K2R4Q2L1F1A1.K
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	3.8078	0.2556	1900.33	1901.151	1	458.9	50	K.K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1A1.K
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	4.4463	0.2581	1828.37	1829.072	1	717.1	65.38461	K.K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1.A
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	1	2.8586	0.2072	1143.64	1142.319	1	520.4	68.75	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	3.2037	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
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	1	2.64	0.2121	1128.57	1128.319	1	529.8	68.75	K.HLNPGYWIK.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	4.1839	0.3903	1900.85	1901.173	1	1014.9	71.42857	K.NKKKQELTEEQKRQL.F
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	5.79	0.3759	2029.61	2031.325	1	784.9	66.66667	K.K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1A1K2.M
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	4.9055	0.3165	2074.59	2075.35	1	1034.6	66.66667	K.N2K2K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1.A
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	3	4.4537	0.3015	2146.91	2147.429	1	908.2	45.3125	K.N2K2K2K2Q2E1L1T1E1E1Q2K2R4Q2L1F1A1.K
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	2.9981	0.1744	1143.15	1142.319	1	663.2	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	1	2.792	0.2262	1141.51	1142.319	1	520.2	68.75	K.H3L1N2P1G1Y1W2I1K2.N
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and 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
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	2	3.9117	0.455	1799.67	1799.145	1	493.4	50	K.G1I1D1I1K2P1I1P1L1D1D1P1V1K2F1L1.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	3	4.8548	0.2709	1930.28	1929.32	1	1334.2	45.3125	Q.K2G1I1D1I1K2P1I1P1L1D1D1P1V1K2F1L1.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	2	4.5507	0.4403	2260.85	2261.688	1	491.2	47.368423	N.S1I1Q2K2G1I1D1I1K2P1I1P1L1D1D1P1V1K2F1L1.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	3	4.2542	0.2217	2237.57	2237.688	1	873	35.526314	N.SIQKGIDIKPIPLDDPVKFL.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and 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	1929.32	1	539.7	50	Q.K2G1I1D1I1K2P1I1P1L1D1D1P1V1K2F1L1.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and 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
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	3	4.2135	0.327	2237.3	2237.688	2	837.7	34.210526	N.SIQKGIDIKPIPLDDPVKFL.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	2	4.196	0.4499	2236.55	2237.688	1	769.5	50	N.SIQKGIDIKPIPLDDPVKFL.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	3	4.4886	0.2964	1930.25	1929.32	1	1352.7	43.75	Q.K2G1I1D1I1K2P1I1P1L1D1D1P1V1K2F1L1.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and 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.S1I1Q2K2G1I1D1I1K2P1I1P1L1D1D1P1V1K2F1L1.K
gi|6320997|ref|NP_011076.1|	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and 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
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; 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
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; 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
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SILK complexes; Chd1p	2	4.5715	0.3186	2170.55	2171.452	1	1151.7	58.823532	Y.KADIDWDDIIPEEELKKL.Q
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; 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.H3F1N2S1P1D1S1N2D1F1V1F1L1L1.S
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; 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
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; 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
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SILK complexes; Chd1p	2	3.1375	0.1795	1654.85	1652.803	1	444.7	61.538464	D.HFNSPDSNDFVFLL.S
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SILK complexes; Chd1p	3	4.4219	0.2656	2449.22	2449.717	2	702.7	34.210526	T.DYKADIDWDDIIPEEELKKL.Q
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; 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
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; 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
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; 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
gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SILK complexes; Chd1p	2	3.3053	0.27	1504.37	1505.622	1	998.2	75	V.SKDTVEEEVLERA.R

gi|6321012|ref|NP_011091.1|	YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SILK complexes; Chd1p	2	3.7369	0.2438	1971.67	1972.199	3	868.6	56.666668	A.DIDWDDIIPEEELKKL.Q
gi|6321013|ref|NP_011092.1|	YER165W	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 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
gi|6321013|ref|NP_011092.1|	YER165W	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 control of poly(A) tail length, interacts with translation factor eIF-4G; Pab1p	2	2.9874	0.3849	2293.83	2295.659	1	551.4	45	Y.G1V1M1P1P1R4G1V1P1F1N2G1P1N2P1Q2Q2M1N2P1M1.G
gi|6321013|ref|NP_011092.1|	YER165W	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 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
gi|6321013|ref|NP_011092.1|	YER165W	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 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.N2L1D1D1S1V1D1D1E1K2L1E1E1E1F1A1P1Y1.G
gi|6321013|ref|NP_011092.1|	YER165W	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 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
gi|6321013|ref|NP_011092.1|	YER165W	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 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
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	5.295	0.3135	3367.67	3366.859	6	354.3	24.038462	V.Y1Y1N2M1P1L1P1K2D1M1I1D1E1E1G1N2P1I1M1Q2Y1P1R4N2K2I1R4.T
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	2	5.0717	0.3185	1872.51	1872.134	1	626.3	59.375	S.C1I1V1K2I1P1G1L1N2P1G1D1E1P1R4A1L1.L
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	4.7164	0.3495	2442.8	2441.595	1	1203.1	38.75	H.G1H3F1D1H3Y1P1P1G1Y1D1P1T1D1P1N2R4P1K2V1T1.K
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	4.4596	0.4559	3528.8	3530.069	7	298.2	22.321428	V.YYNMPLPKDMIDEEGNPIMQYPRNKIRTT.K
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	6.0678	0.4214	3570.74	3571.069	1	770.3	32.142857	V.Y1Y1N2M1P1L1P1K2D1M1I1D1E1E1G1N2P1I1M1Q2Y1P1R4N2K2I1R4T1T1.K
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	2	3.6777	0.3352	1976.09	1978.154	1	451	56.25	T.A1I1E1D1R4L1Q2D1G1V1P1D1C1I1E1L1L1.A
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	3.8382	0.3001	1712.12	1710.996	1	1379.9	50	C.I1V1K2I1P1G1L1N2P1G1D1E1P1R4A1L1.L
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	4.7771	0.3407	3057.92	3058.512	1	673.9	34.375	V.YYNMPLPKDMIDEEGNPIMQYPRNK.I
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	5.1501	0.3681	2647.22	2648.056	1	1003.5	39.285713	N.M1P1L1P1K2D1M1I1D1E1E1G1N2P1I1M1Q2Y1P1R4N2K2.I
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	2	4.1681	0.4065	2441.21	2441.595	2	475.1	42.5	H.G1H3F1D1H3Y1P1P1G1Y1D1P1T1D1P1N2R4P1K2V1T1.K
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	4.2106	0.2705	3162.98	3164.683	1	777.9	31	Y.YNMPLPKDMIDEEGNPIMQYPRNKIR.T
gi|6321014|ref|NP_011093.1|	YER166W	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; Dnf1p	3	4.7089	0.2606	3326.51	3327.859	2	318.1	25	V.YYNMPLPKDMIDEEGNPIMQYPRNKIR.T
gi|6321020|ref|NP_011099.1|	YER172C	RNA-dependent ATPase RNA helicase involved in the facilitation and disruption of snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs to activate the spliceosome for catalysis; Brr2p	2	3.4024	0.2573	2151.65	2150.404	1	572.4	52.941177	Q.GVWDVDNPLRQIPHFNNK.I
gi|6321020|ref|NP_011099.1|	YER172C	RNA-dependent ATPase RNA helicase involved in the facilitation and disruption of snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs to activate the spliceosome for catalysis; Brr2p	3	4.4521	0.2548	2415.8	2413.766	1	866.2	36.25	T.K2F1S1N2P1A1I1P1P1V1I1D1L1E1K2I1K2F1D1E1S1.S
gi|6321020|ref|NP_011099.1|	YER172C	RNA-dependent ATPase RNA helicase involved in the facilitation and disruption of snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs to activate the spliceosome for catalysis; Brr2p	3	4.6398	0.2438	2390.54	2388.766	1	904.4	35	T.KFSNPAIPPVIDLEKIKFDES.S
gi|6321020|ref|NP_011099.1|	YER172C	RNA-dependent ATPase RNA helicase involved in the facilitation and disruption of snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs to activate the spliceosome for catalysis; Brr2p	2	3.5458	0.4079	2178.03	2179.404	1	516.1	52.941177	Q.G1V1W2D1V1D1N2P1L1R4Q2I1P1H3F1N2N2K2.I
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	3.5023	0.2677	2388.13	2388.544	4	228.3	38.095238	T.DKKAPEDIEGSDTVQIELPESS.F
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	4.2712	0.358	2416.23	2413.544	1	785.5	47.61905	T.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1.F
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	3.791	0.235	3116.87	3117.301	1	755.5	38.88889	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	4.441	0.395	2912.79	2915.091	1	687.9	40	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	2	4.8901	0.2966	2941.47	2944.091	3	600	38	T.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.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	5.7628	0.411	2917.85	2915.091	1	1191.9	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	4.668	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.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.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.DKSARKYVDEQVELADAAPPPEAKLSIL.F
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.T1T1D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.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.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.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.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.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.T1T1D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.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.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.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.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1.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.D1K2K2A1P1E1D1I1E1G1S1D1T1V1Q2I1E1L1P1E1S1S1F1E1S1Y1.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.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	3.0632	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	66.66667	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	2	3.0842	0.172	2318.37	2318.594	5	204.3	38.88889	T.ETPTLRGRIPEDTWDFKKQ.G
gi|14318518|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; Vtc2p	2	3.1957	0.1876	1927.53	1926.136	1	576.8	66.66667	F.WLPDLETDIRQDPKQA.Y
gi|14318518|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; Vtc2p	2	3.4057	0.2105	1857.71	1858.953	3	483.4	50	A.G1R4D1L1E1R4L1E1E1D1F1S1E1I1Q2.N

gi|14318518|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; Vtc2p	3	4.4492	0.3728	2602.4	2604.783	1	758.5	33.75	R.WDDSDESKFVEELDKELEKVY.G
gi|14318518|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; Vtc2p	2	3.0232	0.3103	2630.55	2629.783	1	319.3	37.5	R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi|14318518|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; Vtc2p	3	4.9956	0.3098	2630.45	2629.783	1	1081.6	38.75	R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi|14318518|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; Vtc2p	3	4.3172	0.3458	3008.96	3008.34	1	595.2	31.52174	F.W2L1P1D1L1E1T1D1I1R4Q2D1P1K2Q2A1Y1E1E1E1K2K2K2L1.L
gi|14318518|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; Vtc2p	3	3.9237	0.1876	3252.44	3252.674	2	490.7	28	F.W2L1P1D1L1E1T1D1I1R4Q2D1P1K2Q2A1Y1E1E1E1K2K2K2L1L1K2.Q
gi|14318518|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; Vtc2p	2	3.9459	0.3201	1490.79	1492.731	1	1164.4	77.27273	K.H3D1K2L1Y1P1K2Y1P1S1V1K2.S
gi|14318518|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; Vtc2p	1	2.8738	0.3486	1474.65	1475.731	1	514.2	63.636364	K.HDKLYPKYPSVK.S
gi|14318518|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; Vtc2p	2	3.9494	0.333	1474.93	1475.731	1	1635.5	81.818184	K.HDKLYPKYPSVK.S
gi|14318518|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; Vtc2p	2	2.9969	0.2072	2086.75	2089.312	1	572	59.375	F.WLPDLETDIRQDPKQAY.E
gi|14318518|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; Vtc2p	2	3.2932	0.195	2417.63	2418.57	2	568	44.736843	W.DDSDESKFVEELDKELEKVY.G
gi|14318518|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; Vtc2p	2	3.754	0.317	2630.99	2629.783	1	632	45	R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi|14318518|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; Vtc2p	3	3.8164	0.2431	2606.51	2604.783	1	784	33.75	R.WDDSDESKFVEELDKELEKVY.G
gi|14318518|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; Vtc2p	2	3.5353	0.3716	2603.73	2604.783	2	365.3	40	R.WDDSDESKFVEELDKELEKVY.G
gi|14318518|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; Vtc2p	3	4.1943	0.3303	2627.42	2629.783	1	741.6	32.5	R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi|14318518|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; Vtc2p	2	3.0077	0.281	2628.79	2629.783	1	289.8	35	R.W2D1D1S1D1E1S1K2F1V1E1E1L1D1K2E1L1E1K2V1Y1.G
gi|14318518|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; Vtc2p	2	3.7909	0.3784	2604.17	2604.783	1	580.2	45	R.WDDSDESKFVEELDKELEKVY.G
gi|14318518|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; Vtc2p	3	4.728	0.265	2561.57	2561.91	1	663.2	31.818182	M.G1V1D1S1E1E1E1E1I1E1L1P1P1G1V1K2K2P1L1N2L1L1K2.N
gi|14318518|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; Vtc2p	3	3.8923	0.1735	3123.11	3122.5	2	506.6	28.125	F.W2L1P1D1L1E1T1D1I1R4Q2D1P1K2Q2A1Y1E1E1E1K2K2K2L1L1.K
gi|14318518|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; Vtc2p	1	2.8876	0.2547	1009.44	1010.228	1	356.9	78.57143	L.R4H3L1P1V1L1V1Y1.A
gi|14318514|ref|NP_116647.1|	YFL008W	Subunit of the multiprotein cohesin complex, essential protein involved in 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	3.4741	0.2923	1730.17	1728.853	1	592.1	57.692307	F.D1Y1V1S1D1H3L1D1A1I1Y1R4E1L1.T
gi|14318514|ref|NP_116647.1|	YFL008W	Subunit of the multiprotein cohesin complex, essential protein involved in 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	3.1187	0.3332	1979.75	1979.135	1	690.2	60.000004	K.T1F1D1Y1V1S1D1H3L1D1A1I1Y1R4E1L1.T
gi|14318514|ref|NP_116647.1|	YFL008W	Subunit of the multiprotein cohesin complex, essential protein involved in 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	3.4585	0.2808	1879.85	1877.029	1	690.5	60.714287	T.F1D1Y1V1S1D1H3L1D1A1I1Y1R4E1L1.T
gi|14318514|ref|NP_116647.1|	YFL008W	Subunit of the multiprotein cohesin complex, essential protein involved in 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

gi|14318514|ref|NP_116647.1|	YFL008W	Subunit of the multiprotein cohesin complex, essential protein involved in 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	4.0848	0.2809	1842.33	1842.102	1	968.2	71.42857	K.YHNDLIEKEIQPKIT.E
gi|14318504|ref|NP_116638.1|	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	2	3.5505	0.2804	1834.29	1835.02	1	293.3	53.571426	K.K2Y1H3P1D1I1N2K2E1P1D1A1E1K2K2.F
gi|14318504|ref|NP_116638.1|	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	2	3.3399	0.1965	2356.39	2357.572	3	202.1	41.666664	Q.K2Q2E1E1E1K2H3A1K2K2D1D1D1N2T1L1K2R4L1.E
gi|14318504|ref|NP_116638.1|	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	2	3.5137	0.3135	2846.91	2848.142	1	514.1	34.615387	T.VDLPHGLQDGDVVRIPGQGSYPDIAVE.A
gi|14318504|ref|NP_116638.1|	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	2	3.4791	0.3644	3161.91	3163.511	2	412.4	31.034481	K.TITVDLPHGLQDGDVVRIPGQGSYPDIAVE.A
gi|14318504|ref|NP_116638.1|	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	3	4.6942	0.2543	2326.88	2326.572	2	658.9	40.27778	Q.KQEEEKHAKKDDDNTLKRL.E
gi|14318504|ref|NP_116638.1|	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the 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
gi|14318504|ref|NP_116638.1|	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	2	3.6955	0.3384	1886.71	1888.044	1	807.8	52.941177	L.QDGDVVRIPGQGSYPDIA.V
gi|14318504|ref|NP_116638.1|	YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	2	4.0609	0.2407	1942.75	1941.194	1	410.9	56.666668	A.KKYHPDINKEPDAEKK.F
gi|14318501|ref|NP_116635.1|	YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes; Lpd1p	1	2.2409	0.1638	968.32	969.083	1	368.4	71.42857	K.EDHILDVK.N
gi|14318501|ref|NP_116635.1|	YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes; Lpd1p	2	3.1002	0.282	1266.47	1264.381	1	517.2	75	R.GRLVIDDQFNS.K
gi|14318501|ref|NP_116635.1|	YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes; Lpd1p	2	2.9448	0.3588	1528.83	1529.69	2	705.9	62.5	K.RNDDKNVVEIVVE.D
gi|14318501|ref|NP_116635.1|	YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes; Lpd1p	1	2.7102	0.2565	1528.71	1529.69	2	202.5	50	K.RNDDKNVVEIVVE.D
gi|14318501|ref|NP_116635.1|	YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes; Lpd1p	2	4.4618	0.2622	1802.25	1802.083	1	1528.3	71.42857	R.LVIDDQFNSKFPHIK.V
gi|14318501|ref|NP_116635.1|	YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes; Lpd1p	2	3.1678	0.2477	1657.67	1657.864	1	468.8	53.846157	A.KRNDDKNVVEIVVE.D
gi|14318501|ref|NP_116635.1|	YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of 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.G1R4L1V1I1D1D1Q2F1N2S1K2F1P1H3I1K2.V
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	2	4.1844	0.3602	2275.59	2277.514	2	535.5	44.736843	K.GHYTEGAELVDSVMDVIRRE.A
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	2	3.7738	0.3078	2725.63	2726.899	1	534.7	41.304348	K.G1H3Y1T1E1G1A1E1L1V1D1S1V1M1D1V1I1R4R4E1A1E1G1C1.D
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	2	3.4986	0.2188	2694.31	2694.899	6	280.4	30.434782	K.GHYTEGAELVDSVMDVIRREAEGC.D
gi|14318481|ref|NP_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
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	2	4.2825	0.2946	2305.77	2305.514	1	655.7	50	K.G1H3Y1T1E1G1A1E1L1V1D1S1V1M1D1V1I1R4R4E1.A
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	2	3.9469	0.3901	1512.41	1511.637	1	786.4	81.818184	T.YHGHDDIQKERL.N
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	2	3.7783	0.3883	1533.03	1532.637	1	880.4	86.36364	T.Y1H3G1H3D1D1I1Q2K2E1R4L1.N
gi|14318481|ref|NP_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
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	1	2.7761	0.1957	1012.57	1012.216	1	451.7	78.57143	-.M1R4E1I1I1H3I1S1.T
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	3	3.8381	0.2067	2756.57	2754.995	1	620.1	29.166666	E.GAELVDSVMDVIRREAEGCDSLQGF.Q
gi|14318481|ref|NP_116616.1|	YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	2	2.9274	0.1894	1193.25	1192.45	1	741.6	77.77778	A.VNLVPFPRLH.F
gi|14318481|ref|NP_116616.1|	YFL037W	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.F1W2E1T1I1C1G1E1H3G1L1D1F1.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.1264	0.2551	1578.29	1578.759	1	868.8	69.230774	S.SIEKSYELPDGQVI.T
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.8989	0.2537	1593.56	1594.759	1	723.8	57.692307	S.S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1.T
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.4338	0.332	1267.56	1268.471	1	325	65	D.LAGRDLTDYLM.K
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	2.9991	0.2786	2044.21	2045.232	2	385.8	44.444447	Q.S1S1S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.0594	0.3019	1535.5	1536.723	1	356.3	53.846157	E.K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.6767	0.3796	1791.71	1793.024	1	678.8	56.666668	S.SIEKSYELPDGQVITI.G
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.9143	0.325	1530.05	1530.573	1	1535	80.769226	M.G1Q2K2D1S1Y1V1G1D1E1A1Q2S1K2.R

gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.3064	0.4308	1385.52	1386.418	1	205.1	63.636364	Q.E1Y1D1E1S1G1P1S1I1V1H3H3.K
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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
gi|14318479|ref|NP_116614.1|	YFL039C	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.KQEYDESGPSIVHH.K
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.9974	0.3327	1377.6	1378.584	2	286.1	54.545456	L.R4V1A1P1E1E1H3P1V1L1L1T1.E
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.0652	0.3007	1275.59	1276.479	3	301.6	60.000004	L.R4V1A1P1E1E1H3P1V1L1L1.T
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	3	4.4611	0.3722	3244.91	3246.552	1	403.1	23.214285	Q.S1S1S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1N2E1R4F1R4A1P1E1A1L1.F
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	3	4.6001	0.2795	1783.46	1782.01	1	1131.1	51.923077	T.A1E1R4E1I1V1R4D1I1K2E1K2L1C1.Y
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.2759	0.3671	1473.73	1474.743	1	367.8	58.333332	E.LRVAPEEHPVLLT.E
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.2734	0.3323	1491.68	1492.743	1	481	62.5	E.L1R4V1A1P1E1E1H3P1V1L1L1T1.E
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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	Actin, structural protein involved in cell polarization, endocytosis, and other 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
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.8294	0.2876	1184.55	1185.368	2	215	61.11111	L.RYPIEHGIVT.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.6386	0.2865	1200.53	1200.368	4	189.9	55.555557	L.R4Y1P1I1E1H3G1I1V1T1.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.9402	0.2979	1398.64	1399.633	1	514.8	68.181816	L.TLRYPIEHGIVT.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.2998	0.3343	1416.66	1416.633	1	428.9	63.636364	L.T1L1R4Y1P1I1E1H3G1I1V1T1.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
gi|14318479|ref|NP_116614.1|	YFL039C	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.R4E1I1V1R4D1I1K2E1K2L1C1.Y
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.2007	0.1734	1399.59	1399.677	7	140.2	60.000004	E.REIVRDIKEKL.C
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.652	0.1612	1298.6	1299.472	4	233.2	60.000004	L.RYPIEHGIVTN.W
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.5133	0.2259	2092.65	2093.397	1	682.6	53.125	T.AEREIVRDIKEKLCYVA.L
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.1421	0.2806	1402.43	1401.692	3	662.1	68.181816	K.VKIIAPPERKYS.V
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	2.9554	0.2555	1461.75	1459.731	1	575	72.72727	K.IIAPPERKYSVW.I
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.0933	0.1626	2531.47	2530.934	1	207.6	32.5	T.EAPMNPKSNREKMTQIMFETF.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.0335	0.3316	1520.62	1520.723	1	291.6	46.153847	E.KSYELPDGQVITIG.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.0806	0.3462	1511.25	1512.573	1	489.1	65.38461	M.GQKDSYVGDEAQSK.R
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.3071	0.3772	1511.31	1511.654	1	1012.4	80	T.NWDDMEKIWHH.T
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.3335	0.2688	1529.77	1530.654	1	438.9	70	T.N2W2D1D1M1E1K2I1W2H3H3.T
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.1275	0.2424	1454.33	1454.725	1	584.7	72.72727	A.GRDLTDYLM@KIL.S
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.7056	0.2844	1202.73	1203.343	1	212.3	72.22222	G.NERFRAPEAL.F
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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	Actin, structural protein involved in cell polarization, endocytosis, and other 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
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	2.969	0.2062	1476.39	1476.731	3	475.1	68.181816	K.I1I1A1P1P1E1R4K2Y1S1V1W2.I
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.1177	0.2481	2153.39	2153.537	1	365.3	47.058823	T.EAPMNPKSNREKMTQIMF.E
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	3	4.172	0.3909	2089.07	2086.361	1	970.6	40.789474	A.GFAGDDAPRAVFPSIVGRPR.H
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.4109	0.2658	1236.57	1237.372	1	336.4	75	T.NWDDMEKIW.H
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.7191	0.233	1580.03	1578.759	1	823.7	73.07692	S.SIEKSYELPDGQVI.T

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
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	4.9296	0.2635	1869.31	1869.076	1	726.2	59.375	S.S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.5254	0.2104	1957.93	1957.154	1	821.3	55.88235	S.S1S1I1E1K2S1Y1E1L1P1D1G1Q2V1I1T1I1G1.N
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	3.0946	0.3196	1511.58	1511.654	1	433.6	70	T.NWDDMEKIWHH.T
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	1	2.9394	0.2494	1219.58	1220.343	1	237.3	72.22222	G.N2E1R4F1R4A1P1E1A1L1.F
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	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
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	2.9745	0.2065	1699.01	1700.976	6	396.4	50	T.TAEREIVRDIKEKL.C
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.8346	0.274	1922.29	1923.186	1	806.1	64.28571	T.AEREIVRDIKEKLCY.V
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	2.916	0.2963	1852.53	1852.107	1	346.7	69.230774	A.EREIVRDIKEKLCY.V
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	2	3.0346	0.2975	2023.83	2024.291	1	491.8	53.333336	T.TAEREIVRDIKEKLCY.V
gi|14318479|ref|NP_116614.1|	YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other 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	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport; Fet5p	2	3.2625	0.2422	1936.05	1937.026	1	551.8	57.14286	A.F1I1I1H3D1P1E1E1P1F1E1Y1D1H3E1.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
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	4.2002	0.41	2527.37	2527.77	1	786	55.263157	A.F1I1I1H3D1P1E1E1P1F1E1Y1D1H3E1R4V1I1T1L1.S
gi|14318477|ref|NP_116612.1|	YFL041W	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport; Fet5p	1	3.1268	0.3854	1435.56	1436.697	1	272.7	58.333332	K.GLPRQPEPLPKGF.T
gi|14318477|ref|NP_116612.1|	YFL041W	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport; Fet5p	1	3.1748	0.3286	1455.61	1454.697	2	229.6	54.166668	K.G1L1P1R4Q2P1E1P1L1P1K2G1F1.T
gi|14318477|ref|NP_116612.1|	YFL041W	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport; Fet5p	3	4.1422	0.157	2529.92	2527.77	2	792.2	31.578945	A.F1I1I1H3D1P1E1E1P1F1E1Y1D1H3E1R4V1I1T1L1.S
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	3.821	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	29.166666	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
gi|14318526|ref|NP_116659.1|	YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; 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
gi|14318526|ref|NP_116659.1|	YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; 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
gi|14318526|ref|NP_116659.1|	YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiquitination and degradation of proteasome substrates; Rpn11p	3	6.1164	0.2684	2274.71	2275.495	2	2049.3	51.47059	Y.S1K2R4I1E1E1E1K2E1L1T1E1E1E1L1K2T1R4.Y
gi|14318526|ref|NP_116659.1|	YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; 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
gi|14318526|ref|NP_116659.1|	YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; 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
gi|14318526|ref|NP_116659.1|	YFR004W	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.R4I1E1E1E1K2E1L1T1E1E1E1L1K2T1R4.Y
gi|14318526|ref|NP_116659.1|	YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; 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
gi|14318526|ref|NP_116659.1|	YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiquitination and degradation of proteasome substrates; Rpn11p	2	5.9526	0.2657	2274.59	2275.495	3	1324.6	61.764706	Y.S1K2R4I1E1E1E1K2E1L1T1E1E1E1L1K2T1R4.Y
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	3.3207	0.1619	1877.21	1876.999	3	431	57.14286	K.K2L1D1N2E1R4E1D1L1D1N2H3L1I1Q2.I
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	4.6528	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
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	4.8118	0.3335	3802.34	3804.333	1	885.7	27.419355	L.E1K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1K2F1P1E1C1D1K2L1S1P1P1I1I1Q2L 1.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	4.2482	0.3516	2262.13	2263.602	2	434.4	47.22222	K.K2L1E1K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1.K
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	4.8097	0.2884	3934.58	3934.507	1	667	23.4375	K.K2L1E1K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1K2F1P1E1C1D1K2L1S1P1P1I1 1Q2.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.K2F1P1E1C1D1K2L1S1P1P1I1I1Q2L1.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	25 L.E1K2L1P1V1L1E1P1P1E1Q2D1K2T1I1D1F1K2F1P1E1C1D1K2L1S1P1P1I1I1Q2L
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
gi|15530184|ref|NP_219497.1|	YFR024C-A	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 polymerization; Lsb3p	3	6.4361	0.4595	3934.1	3932.805	1	648.3	30.46875 F.N2Y1R4P1S1N2G1G1R4G1S1F1D1D1D1E1D1D1Y1Y1D1D1D1D1Y1Y1N2D1I1P1S1S1F1.S
gi|15530184|ref|NP_219497.1|	YFR024C-A	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 polymerization; Lsb3p	3	5.4341	0.2983	2911.04	2911.854	1	603.2	36.904762 S.R4N2R4W2A1D1D1E1Y1D1D1Y1D1D1D1Y1E1S1G1Y1R4R4.G
gi|15530184|ref|NP_219497.1|	YFR024C-A	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 polymerization; Lsb3p	2	3.9633	0.1995	2875.01	2875.854	1	288.3	38.095238 S.RNRWADDEYDDYDDDYESGYRR.G
gi|15530184|ref|NP_219497.1|	YFR024C-A	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 polymerization; Lsb3p	2	3.7626	0.1807	2910.33	2911.854	5	319.2	35.714287 S.R4N2R4W2A1D1D1E1Y1D1D1Y1D1D1D1Y1E1S1G1Y1R4R4.G
gi|14318551|ref|NP_116684.1|	YFR028C	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 substrates to effect a decrease in CDK/B-cyclin activity and mitotic exit; Cdc14p	2	3.1292	0.2907	1964.81	1964.143	1	696.8	46.875 Q.H3L1D1L1I1F1E1D1G1T1C1P1D1L1S1I1V1.K
gi|14318551|ref|NP_116684.1|	YFR028C	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 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.HLDLIFEDGTCPDLSIVK.N
gi|14318551|ref|NP_116684.1|	YFR028C	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 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.H3L1D1L1I1F1E1D1G1T1C1P1D1L1S1I1V1K2.N
gi|14318551|ref|NP_116684.1|	YFR028C	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 substrates to effect a decrease in CDK/B-cyclin activity and mitotic exit; Cdc14p	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	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	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	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	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	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	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	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	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	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	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	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	2	3.2015	0.2254	1690.63	1688.834	1	358	57.692307 G.H3N2P1D1E1N2K2T1R4V1R4L1P1S1.G
gi|14318555|ref|NP_116688.1|	YFR031C-A	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	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	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	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	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has 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
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	3.568	0.3061	1604.39	1604.759	1	420.1	61.538464 A.S1P1M1H3G1Q2N2P1D1I1Y1D1I1V1.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	1	2.7515	0.233	1357.6	1358.525	2	500.9	65 Q.F1F1D1I1N2P1K2P1D1I1H3.I
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	3.6958	0.265	1645.59	1646.884	1	1492.8	71.42857 L.LGYTPRVGIEEGINK.T
gi|6321437|ref|NP_011514.1|	YGL001C	C-3 sterol dehydrogenase, 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.Q2F1F1D1I1N2P1K2P1D1I1H3I1F1.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.F1F1D1I1N2P1K2P1D1I1H3I1F1.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

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	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	2	2.9146	0.1627	1606.31	1604.846	1	623.6	57.14286	A.G1I1F1G1P1G1D1R4Q2L1V1P1G1L1R4.Q
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	2	5.053	0.4455	2189.71	2189.349	1	1075.2	63.88889	G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
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	2	4.4081	0.4595	2165.61	2166.349	1	835.6	58.333332	G.EARPVPEEYLQTDPSYGLT.S
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	2	4.6052	0.3773	2248.45	2247.401	1	844	57.894737	A.G1E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
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	2	4.0936	0.2904	2333.79	2335.479	1	788.1	55	A.G1E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1S1.D
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	2	4.8799	0.349	2548.93	2547.913	1	593.4	50	N.T1A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1.Q
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	3	3.8542	0.2991	3074.42	3073.317	1	589.3	26.724138	N.IYNAERLGLGGGGDMPGSELADFVENADGF.A
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	2	4.6637	0.3595	2249.73	2247.597	1	467.6	50	V.VIRDGQLVEIPANEVVPGDIL.Q
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	2	4.5762	0.4451	2996.49	2997.176	1	1056	41.37931	Y.NAERLGLGGGGDMPGSELADFVENADGFAE.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	2	5.3676	0.4955	2828.47	2829.982	1	1182	50	Y.N2A1E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2	5.5138	0.4975	2796.39	2796.982	1	1598.3	55.555557	Y.NAERLGLGGGGDMPGSELADFVENADGF.A
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	2	3.6803	0.4193	1759.47	1760.811	1	932.3	64.28571	K.TVEEDHPIPEDVHEN.Y
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	2	5.3084	0.5001	2294.45	2295.381	1	1174.2	58.333332	K.TVEEDHPIPEDVHENYENK.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	2	4.4984	0.4098	2166.49	2167.207	1	690.2	55.88235	K.TVEEDHPIPEDVHENYEN.K
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	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	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	3.2265	0.2518	1418.55	1416.592	1	1033.6	78.57143	E.RLGLGGGGDMPGSEL.A
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	2	4.1385	0.3594	2036.51	2037.233	1	818.3	61.764706	E.ARPVPEEYLQTDPSYGLT.S
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	2	6.2826	0.4671	2222.25	2221.403	1	763.4	54.761906	A.ERLGLGGGGDMPGSELADFVEN.A
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	2	5.3432	0.3938	2446.41	2445.808	1	921.5	56.81818	T.A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1.Q
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	2	5.406	0.3477	2295.13	2292.482	1	618.3	43.18182	A.ERLGLGGGGDMPGSELADFVENA.D
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	2	4.723	0.3113	2589.91	2588.02	1	847.2	52.173912	A.VVIRDGQLVEIPANEVVPGDILQL.E
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	3	5.4401	0.2249	2620.94	2618.02	1	1211.1	35.869564	A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	3	4.2727	0.2074	2589.83	2588.02	1	919.7	36.95652	A.VVIRDGQLVEIPANEVVPGDILQL.E
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	2	3.7307	0.424	3031.41	3032.176	2	293.8	24.13793	Y.N2A1E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.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	2	4.1553	0.279	2811.85	2811.994	1	558.4	33.333336	A.ERLGLGGGGDMPGSELADFVENADGFAE.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	2	4.4259	0.467	2842.11	2843.994	1	514.3	31.48148	A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.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	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 cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	2	5.392	0.4153	2614.65	2611.799	1	1021.8	44	A.ERLGLGGGGDMPGSELADFVENADGF.A
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	3	4.5372	0.2913	2614.58	2611.799	1	2365.4	38	A.ERLGLGGGGDMPGSELADFVENADGF.A

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	2	5.3766	0.4611	2641.39	2641.799	1	644.5	44	A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2	3.2881	0.3161	3071.21	3073.317	1	435.5	32.75862	N.IYNAERLGLGGGGDMPGSELADFVENADGF.A
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	2	3.7432	0.3258	1505.73	1506.671	4	689	63.333332	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
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	2	4.0774	0.4926	1487.17	1487.671	1	593.4	63.333332	E.RLGLGGGGDMPGSELA.D
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	2	3.3583	0.3085	1251.39	1249.465	1	1314.5	85	Q.MADEKESLVVK.F
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	2	5.9924	0.5157	2421.85	2423.555	1	1640.8	63.15789	L.KTVEEDHPIPEDVHENYENK.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	3	5.1093	0.2774	2075.21	2075.161	1	697.2	40.625	L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1.E
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	2	3.2306	0.2368	1502.55	1502.674	4	374.1	62.5	V.VESPEGERIVCVK.G
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	3.5582	0.2529	1215.53	1216.34	1	315.2	72.22222	L.E1F1H3P1F1D1P1V1S1K2.K
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	3.3522	0.3862	1505.6	1506.671	1	290.5	53.333336	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
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	3.1361	0.4644	1486.66	1487.671	1	310.9	53.333336	E.RLGLGGGGDMPGSELA.D
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	2.9604	0.2949	1416.55	1416.592	5	285.8	53.571426	E.RLGLGGGGDMPGSEL.A
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	2	3.061	0.2348	1146.47	1146.37	1	585.8	77.77778	G.SIVDELKKTL.A
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	2	3.2313	0.1586	1160.51	1158.37	1	598.6	77.77778	G.S1I1V1D1E1L1K2K2T1L1.A
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	2	3.0281	0.3044	1505.81	1503.736	1	467.2	61.538464	G.SIVDELKKTLANTA.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	2	4.9853	0.1644	2618.49	2618.02	2	750.6	47.826088	A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	3	5.4371	0.3045	4057.97	4059.593	1	753.7	23.648647	T.A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1E1D1G1T1V1I1P1T1D1G1R4I1V1.T
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	3	5.0682	0.2951	2714.12	2713.878	1	1228.6	33.653847	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.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	2	5.2444	0.3944	2485.53	2482.684	1	2021.9	56.25	E.RLGLGGGGDMPGSELADFVENADGF.A
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	2.6785	0.2978	1569.65	1568.637	1	545.3	57.14286	M.PGSELADFVENADGF.A
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	2	5.2919	0.5343	2713.29	2713.878	1	1518.9	46.153847	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.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	2.7129	0.2811	1583.42	1584.637	3	279.6	46.42857	M.P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	3	5.1942	0.4124	2484.95	2482.684	1	1684.5	38.541664	E.RLGLGGGGDMPGSELADFVENADGF.A
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	3	6.7227	0.3985	2511.44	2511.684	1	2197.8	39.583336	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2	3.6276	0.4345	3153.41	3154.435	1	233.1	30.000002	E.RLGLGGGGDMPGSELADFVENADGFAEVFPQ.H
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	2.7683	0.1533	1429.54	1430.632	3	444.8	63.636364	K.V1L1E1F1H3P1F1D1P1V1S1K2.K
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	2	5.9946	0.4767	2512.29	2511.684	1	1841.4	56.25	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2	3.859	0.3615	2441.33	2441.749	1	346.4	35.714287	N.K2L1S1L1H3E1P1Y1T1V1E1G1V1S1P1D1D1L1M1L1T1A1.C
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	2	4.1995	0.4095	2417.55	2416.749	1	636.1	47.61905	N.KLSLHEPYTVEGVSPDDLMLTA.C
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	2	3.4294	0.239	1561.25	1560.806	3	571.6	62.5	K.V1L1E1F1H3P1F1D1P1V1S1K2K2.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	2	4.2271	0.4645	1754.61	1755.067	1	843.1	67.85714 K.SLKQYPKAKDALTKY.K
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	2	3.5338	0.2848	2759.65	2760.132	1	385.3	33.333336 L.TKNKLSLHEPYTVEGVSPDDLMLTA.C
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	2.291	0.273	1421.73	1422.671	3	113.4	55 T.SDEVLKRRKKY.G
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	2.9207	0.241	1201.59	1202.425	2	452.5	70 R.K2K2K2G1L1D1A1I1D1K2A1.F
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	3	4.2392	0.3021	3186.44	3185.614	1	587.3	27.777779 L.EFHPFDPVSKKVTAVVESPEGERIVCVK.G
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	2	3.2663	0.3358	1878.69	1879.117	2	610.4	50 R.DGQLVEIPANEVVPGDIL.Q
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	2.3272	0.2606	1023.34	1024.036	1	420.3	62.5 A.D1F1V1E1N2A1D1G1F1.A
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	2.3186	0.1882	1186.71	1185.469	1	449.4	61.11111 M.FFVGPIQFVM.E
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	2	3.0444	0.273	1372.41	1372.518	4	453.4	66.66667 L.EDGTVIPTDGRIV.T
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	2	3.1359	0.3633	1460.47	1461.579	1	806.3	66.66667 T.A1V1V1E1S1P1E1G1E1R4I1V1C1.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	2	4.1923	0.2678	1846.55	1844.029	1	644.6	65.625 L.QLEDGTVIPTDGRIVTE.D
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	2	4.2442	0.3984	1863.61	1865.029	1	666.9	65.625 L.Q2L1E1D1G1T1V1I1P1T1D1G1R4I1V1T1E1.D
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	2	4.5373	0.3846	1635.47	1632.808	1	685.1	71.42857 L.Q2L1E1D1G1T1V1I1P1T1D1G1R4I1V1.T
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	2	4.1802	0.2814	2690.03	2690.098	1	592.3	41.666664 T.A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	2	3.37	0.3231	1618.57	1616.786	1	639.2	50 A.ERLGLGGGGDMPGSELA.D
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	2	3.4466	0.1725	1563.41	1564.708	1	679.9	60.000004 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1.A
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	2	4.2741	0.3558	2279.51	2277.427	2	389.3	39.473686 G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1S1.D
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	2	4.0462	0.3767	1902.25	1901.052	1	663.1	52.77778 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1.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	2	6.3942	0.4206	2248.57	2247.403	1	729.1	52.380955 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2.A
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	2	4.6616	0.2926	2274.71	2273.597	1	505.6	50 V.V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1.Q
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	2	3.2806	0.1711	1842.59	1842.941	1	947.3	52.77778 L.G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2.A
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	2	4.4359	0.3068	2319.51	2319.482	1	439.6	38.636364 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1.D
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	2	6.1596	0.4726	2513.71	2511.684	1	2255.3	58.333332 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	3	4.3238	0.4133	2656.22	2657.799	1	1134.4	31 A.E1R4L1G1L1G1G1G1G1D1M$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
gi|6321430|ref|NP_011507.1|	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	2	5.4497	0.4729	2657.41	2657.799	1	1025	42 A.E1R4L1G1L1G1G1G1G1D1M$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2.6392	0.2081	1038.58	1038.293	2	455.3	62.5 F.FVGPIQFVM.E
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	2	6.1747	0.4699	2642.75	2641.799	1	1351.2	48 A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2	4.3092	0.2731	1969.47	1969.267	1	760.3	58.823532 G.Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	2	6.4014	0.4927	2239.37	2237.337	1	1758.3	59.090908 L.G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2	6.2003	0.5011	2214.45	2213.337	1	1627.8	56.81818 L.GLGGGGDMPGSELADFVENADGF.A

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	2	4.7356	0.3215	2348.65	2346.729	1	1084.7	61.904762	A.VVIRDGQLVEIPANEVVPGDIL.Q
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	2	3.2233	0.2216	1196.23	1196.469	1	1185.3	83.33333	M.F1F1V1G1P1I1Q2F1V1M1.E
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	2.2302	0.1735	1195.57	1196.469	1	457.2	61.11111	M.F1F1V1G1P1I1Q2F1V1M1.E
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	2	3.2639	0.3472	1518.09	1519.674	2	300.9	62.5	V.V1E1S1P1E1G1E1R4I1V1C1V1K2.G
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	3	6.2375	0.4112	2320.88	2321.381	1	2223.1	48.61111	K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.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	2.7079	0.4037	1302.74	1303.433	4	230.2	53.846157	E.RLGLGGGGDMPGSE.L
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	2.5913	0.3176	1318.47	1320.433	8	222	53.846157	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1.L
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	2	3.8429	0.4462	1603.93	1602.759	1	537.6	59.375	E.RLGLGGGGDMPGSELAD.F
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	2	5.9716	0.4285	2262.69	2263.403	1	1226.9	54.761906	A.E1R4L1G1L1G1G1G1G1D1M$P1G1S1E1L1A1D1F1V1E1N2.A
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	2	3.6759	0.1819	2403.13	2403.728	2	312.9	35.714287	V.V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2.L
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	2	3.4081	0.3673	2034.09	2035.305	1	635.8	58.333332	I.RDGQLVEIPANEVVPGDIL.Q
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	2	5.2241	0.3724	2306.55	2305.455	1	1185.4	52.272724	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1.G
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	2	3.6691	0.3941	2302.63	2303.595	1	684.2	50	I.R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	2	5.2285	0.3773	2628.57	2627.799	1	591.1	40	A.ERLGLGGGGDM@PGSELADFVENADGF.A
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	2.6301	0.2685	1368.56	1368.495	1	493.1	59.090908	A.GLSDWVDFGVIC.G
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	2	4.4887	0.3164	2516.89	2517.887	1	593.5	43.18182	V.V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	2	3.9549	0.3374	2064.87	2065.126	1	662.1	42.5	L.G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2	4.227	0.3604	2614.69	2611.799	1	876.3	40	A.ERLGLGGGGDMPGSELADFVENADGF.A
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	2	4.9937	0.3288	2588.77	2588.02	1	810.2	50	A.VVIRDGQLVEIPANEVVPGDILQL.E
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	2.492	0.2502	1364.78	1365.569	5	302.9	45.833336	I.PANEVVPGDILQL.E
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	2.9994	0.2341	1381.93	1380.569	1	479.4	58.333332	I.P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	3	5.5851	0.2271	2616.5	2618.02	1	1108.7	41.304348	A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	3	4.5814	0.2899	2587.22	2588.02	7	568.8	30.434782	A.VVIRDGQLVEIPANEVVPGDILQL.E
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	2	5.2071	0.4869	1752.53	1749.936	1	1226	73.52941	E.RLGLGGGGDMPGSELADF.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	2	5.4743	0.156	2619.55	2618.02	1	887.8	50	A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	2	6.2073	0.5407	1772.33	1770.936	1	1629.2	79.411766	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1.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	2	4.365	0.4127	1509.33	1506.671	2	840.6	70	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
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	2	4.6288	0.3274	2057.71	2059.233	1	993.8	64.70589	E.A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
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	2	3.3152	0.2371	1419.17	1416.592	1	925.1	75	E.RLGLGGGGDMPGSEL.A
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	2	4.0031	0.298	1717.89	1717.028	2	855.7	56.25	A.A1D1I1V1F1L1A1P1G1L1S1A1I1I1D1A1L1.K

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	2	3.6757	0.3078	1701.45	1700.028	1	1128.7	65.625	A.ADIVFLAPGLSAIIDAL.K
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	2	4.0582	0.4519	1487.29	1487.671	1	950.2	70	E.RLGLGGGGDMPGSELA.D
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	2	3.5315	0.2311	1432.45	1434.592	1	935.9	75	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1.A
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	2	3.1349	0.1695	1035.17	1033.086	2	771.2	87.5	L.AVDKHYGDQ.T
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	2	3.2496	0.2156	1045.71	1046.086	3	773.9	87.5	L.A1V1D1K2H3Y1G1D1Q2.T
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	2	3.906	0.3139	1319.13	1318.427	2	618	70.83333	M.T1G1D1G1V1N2D1A1P1S1L1K2K2.A
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	2.6697	0.287	1248.52	1249.465	3	509.4	60.000004	Q.MADEKESLVVK.F
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	2.5267	0.1938	1392.58	1392.596	1	107.7	59.090908	N.Q2M1A1D1E1K2E1S1L1V1V1K2.F
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	2	3.2045	0.2932	1966.45	1966.028	1	428.5	53.333336	E.EDHPIPEDVHENYENK.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	2	3.3159	0.3604	1988.09	1989.028	1	544.4	60.000004	E.E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.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	2	4.5526	0.3475	2218.31	2219.276	1	1287.6	61.764706	T.V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.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	2	5.6678	0.475	2074.23	2075.161	1	1382.6	65.625	L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1.E
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	2	5.0485	0.5013	2051.07	2052.161	1	1617.7	68.75	L.KTVEEDHPIPEDVHENY.E
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	2	4.2838	0.4266	2492.91	2493.592	1	628.2	47.5	K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2V1A1.E
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	2.355	0.1638	1032.57	1033.21	2	371.5	68.75	G.SIVDELKKT.L
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	3.3552	0.3543	1203.54	1203.34	2	315.8	72.22222	L.EFHPFDPVSK.K
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	3.3367	0.4155	1505.66	1506.671	1	355.8	56.666668	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
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	2.9072	0.2169	1417.65	1416.592	2	320.3	57.14286	E.RLGLGGGGDMPGSEL.A
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	3.6008	0.5161	1488.84	1487.671	1	353.4	56.666668	E.RLGLGGGGDMPGSELA.D
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	2	3.1088	0.3375	1934.47	1936.128	1	554.7	53.125	E.ARPVPEEYLQTDPSYGL.T
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	2	4.2196	0.2764	1956.43	1957.128	1	703.6	59.375	E.A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1.T
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	2	5.436	0.525	1786.23	1786.936	1	1312.8	79.411766	E.R4L1G1L1G1G1G1G1D1M$P1G1S1E1L1A1D1F1.V
gi|6321430|ref|NP_011507.1|	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	2	5.9524	0.5347	2134.57	2133.288	1	2242.2	72.5	E.R4L1G1L1G1G1G1G1D1M$P1G1S1E1L1A1D1F1V1E1N2.A
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	2	5.6933	0.4896	2107.57	2108.288	1	1623	70	E.RLGLGGGGDM@PGSELADFVEN.A
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	2	3.4484	0.4294	1863.49	1865.069	1	512.8	47.22222	E.RLGLGGGGDM@PGSELADFV.E
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	2	6.5195	0.4779	2117.37	2117.288	1	1322.9	67.5	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2.A
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	2	5.9348	0.4672	2091.55	2092.288	1	1671.5	77.5	E.RLGLGGGGDMPGSELADFVEN.A
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	2	6.2265	0.3511	2003.01	2001.184	1	836	65.789474	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1.N
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	2	4.6024	0.3585	1979.53	1978.184	1	760.1	63.15789	E.RLGLGGGGDMPGSELADFVE.N
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	2	3.5831	0.3588	2496.73	2494.681	1	409.9	40.476192	L.EDGTVIPTDGRIVTEDCFLQID.Q

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	2	3.3435	0.2815	2523.17	2520.681	1	266.6	35.714287 L.E1D1G1T1V1I1P1T1D1G1R4I1V1T1E1D1C1F1L1Q2I1D1.Q
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	2	4.1058	0.1649	2172.23	2173.464	1	699.4	52.63158 V.I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1.Q
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	2	3.6566	0.2748	1849.15	1849.069	1	435.4	50 E.RLGLGGGGDMPGSELADFV.E
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	2	4.901	0.4663	1868.45	1871.069	1	1324.4	72.22222 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1.E
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	2	4.2275	0.2659	2148.45	2148.464	1	795.4	57.894737 V.IRDGQLVEIPANEVVPGDIL.Q
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	2	4.8872	0.4233	2280.45	2278.455	1	695	43.18182 E.RLGLGGGGDMPGSELADFVENAD.G
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	3	4.2546	0.3264	2186.87	2189.367	2	773.8	30.952381 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1.D
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	2	4.1647	0.3815	2696.71	2698.878	1	495.6	30.769232 E.RLGLGGGGDM@PGSELADFVENADGFAE.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	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	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	4.1984	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 cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	2	3.2968	0.3602	2582.11	2583.763	1	268.3	28 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1.E
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	3	5.9485	0.3954	2713.91	2713.878	1	1362.5	35.576923 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.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	3	4.4571	0.4071	2681.96	2682.878	1	1205.5	33.653847 E.RLGLGGGGDMPGSELADFVENADGFAE.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	3	4.4412	0.3383	4244.12	4242.814	1	452.6	17.948719 T.AVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGRIVTE.D
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	2	5.2951	0.5394	2715.89	2713.878	1	1353.1	44.230766 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.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	2	5.8468	0.4298	2189.33	2189.367	1	1432.6	61.904762 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1.D
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	2	5.6226	0.4634	2527.51	2527.684	1	1510.7	52.083332 E.R4L1G1L1G1G1G1G1D1M$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	2	5.565	0.381	2484.97	2482.684	1	2298.6	60.416668 E.RLGLGGGGDMPGSELADFVENADGF.A
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	2	3.0423	0.2745	1247.91	1248.323	2	325.9	70 E.S1L1A1V1D1K2H3Y1G1D1Q2.T
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	2	6.1799	0.4322	2451.39	2451.555	1	2246.9	65.789474 L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.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	2	4.5391	0.347	2195.51	2194.276	1	1613.8	67.64706 T.VEEDHPIPEDVHENYENK.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	2	5.2568	0.3814	2323.27	2321.381	1	1058.5	52.77778 K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.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	3	5.5737	0.4735	2293.28	2295.381	1	2179.7	48.61111 K.TVEEDHPIPEDVHENYENK.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	2	3.3125	0.3257	1604.39	1601.807	1	572.2	57.692307 A.VVESPEGERIVCVK.G
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	2.9138	0.1685	1345.62	1346.514	7	244.9	60.000004 L.E1F1H3P1F1D1P1V1S1K2K2.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	2	4.5266	0.4292	1690.73	1691.885	1	1045.1	64.28571 T.A1V1V1E1S1P1E1G1E1R4I1V1C1V1K2.G
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	2	4.0493	0.4455	1670.83	1672.885	1	1471.2	71.42857 T.AVVESPEGERIVCVK.G
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	2	3.7301	0.4181	1772.43	1773.99	1	1069	60.000004 V.TAVVESPEGERIVCVK.G
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	2	4.3877	0.3833	1792.55	1793.99	1	1140.3	60.000004 V.T1A1V1V1E1S1P1E1G1E1R4I1V1C1V1K2.G
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	2	4.2	0.3389	2809.75	2809.946	1	484.6	41.304348 K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2V1A1E1L1A1.S

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	2.6246	0.1557	1415.34	1415.632	4	434.6	63.636364 K.VLEFHPFDPVSK.K
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	2	3.938	0.3039	1430.99	1430.632	1	860.3	77.27273 K.V1L1E1F1H3P1F1D1P1V1S1K2.K
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	2	3.017	0.1868	1987.45	1987.155	1	411.2	50 A.R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
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	2	4.3142	0.4077	2206.55	2205.367	1	921.9	52.380955 E.R4L1G1L1G1G1G1G1D1M$P1G1S1E1L1A1D1F1V1E1N2A1.D
gi|6321430|ref|NP_011507.1|	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	2	3.805	0.4006	2180.01	2179.367	1	494.8	38.095238 E.RLGLGGGGDM@PGSELADFVENA.D
gi|6321430|ref|NP_011507.1|	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	2	5.3931	0.4716	2164.97	2163.367	1	1385.1	64.28571 E.RLGLGGGGDMPGSELADFVENA.D
gi|6321430|ref|NP_011507.1|	YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	3	5.2648	0.4704	2524.73	2527.684	1	1955.8	37.5 E.R4L1G1L1G1G1G1G1D1M$P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
gi|6321430|ref|NP_011507.1|	YGL008C	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	3.0929	0.3199	2658.07	2659.098	2	499.5	39.583336 T.AVVIRDGQLVEIPANEVVPGDILQL.E
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	2	3.0213	0.1711	2906.43	2908.307	1	371.2	32.692307 A.N2T1A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	3	4.8472	0.3926	2498.93	2498.684	1	1876.2	37.5 E.RLGLGGGGDM@PGSELADFVENADGF.A
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	2	4.0695	0.3156	2793.13	2792.203	1	563	40 N.T1A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1.E
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	3	5.2305	0.2943	4219.22	4219.735	1	818.7	22.368422 A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1E1D1G1T1V1I1P1T1D1G1R4I1V1T1E1.D
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	3	4.8383	0.4035	4173.65	4171.735	1	1087.4	24.342104 A.VVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGRIVTE.D
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	2.2223	0.1956	1211.72	1210.274	1	436.2	60.000004 E.L1A1D1F1V1E1N2A1D1G1F1.A
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	3	4.4574	0.3109	4114.94	4113.698	1	494.8	23.026316 N.TAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGRIV.T
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	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 cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	3	6.7465	0.3552	2511.8	2511.684	1	2552.9	42.708336 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1.A
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	3	6.1231	0.3847	3988.7	3987.514	1	760.8	24.305555 A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1E1D1G1T1V1I1P1T1D1G1R4I1V1.T
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	3	4.4591	0.3189	4280.03	4277.802	1	860.9	22.435898 A.N2T1A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1E1D1G1T1V1I1P1T1D1G1R4I1V1.T
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	2	4.3472	0.4003	3190.87	3190.435	1	467.5	35 E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1V1F1P1Q2.H
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	3	5.8191	0.416	3152.99	3154.435	1	545.2	30.833334 E.RLGLGGGGDMPGSELADFVENADGFAEVFPQ.H
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	2	3.2735	0.1645	1467.97	1466.754	5	339.3	63.636364 F.D1R4L1M1N2G1K2P1M1K2E1K2.K
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	3	6.0632	0.3211	2451.86	2451.555	1	3717.4	57.894737 L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.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	2	3.1231	0.3239	1192.53	1191.413	1	1279.6	80 K.GLDAIDKAFLK.S
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	3	4.5097	0.349	4162.88	4161.698	1	963.1	23.684212 N.T1A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1E1D1G1T1V1I1P1T1D1G1R4I1V1.T
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	3	5.1408	0.4037	3941.69	3941.514	1	711.1	25 A.VVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGRIV.T
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	2	3.5927	0.214	1335.93	1334.587	1	840.5	81.818184 K.K2G1L1D1A1I1D1K2A1F1L1K2.S
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	2	3.0849	0.2825	1319.65	1319.587	1	995.7	81.818184 K.KGLDAIDKAFLK.S
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	2	3.3824	0.21	1559.89	1560.806	1	559.4	62.5 K.V1L1E1F1H3P1F1D1P1V1S1K2K2.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	2	2.9106	0.2372	2330.21	2327.704	1	247.6	33.333336 A.A1D1I1V1F1L1A1P1G1L1S1A1I1I1D1A1L1K2T1S1R4Q2.I

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	3.051	0.2285	1559.54	1560.806	1	425.9	58.333332	K.V1L1E1F1H3P1F1D1P1V1S1K2K2.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	2	3.2274	0.269	1543.47	1543.806	1	855.7	70.83333	K.VLEFHPFDPVSKK.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	2.8486	0.272	1542.65	1543.806	1	568.2	62.5	K.VLEFHPFDPVSKK.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	3	5.0042	0.2417	2888.06	2888.179	1	1264.9	32.692307	Q.T1F1S1S1S1T1V1K2R4G1E1G1F1M1V1V1T1A1T1G1D1N2T1F1V1G1R4.A
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	2	3.4516	0.2304	1627.31	1624.905	1	1164	70.83333	Q.I1S1L1T1E1N2W2L1I1F1I1T1R4.A
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	2.5571	0.1598	1062.58	1063.285	8	408.7	68.75	K.SLKQYPKAK.D
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	3	4.202	0.1648	2851.85	2853.179	1	1032.5	30.769232	Q.TFSSSTVKRGEGFMVVTATGDNTFVGR.A
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	2	3.7098	0.3389	2177.37	2175.459	1	371.5	44.736843	T.R4A1A1G1P1F1W2S1S1I1P1S1W2Q2L1A1G1A1V1F1.A
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	2	3.0764	0.3088	2108.53	2109.451	1	275.5	37.5	A.A1R4S1A1A1D1I1V1F1L1A1P1G1L1S1A1I1I1D1A1L1.K
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	3	4.8557	0.3957	2346.47	2343.663	1	1568	38.095238	S.TVKRGEGFMVVTATGDNTFVGR.A
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	2	4.478	0.3769	2343.59	2343.663	1	469.1	45.238094	S.TVKRGEGFMVVTATGDNTFVGR.A
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	2.7192	0.1748	1241.64	1242.393	1	431	66.66667	R.K2R4G1E1G1H3W2E1I1L1.G
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	3	6.0346	0.4266	2373.71	2373.663	1	2008.5	40.476192	S.T1V1K2R4G1E1G1F1M1V1V1T1A1T1G1D1N2T1F1V1G1R4.A
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	3	5.5935	0.4078	2517.11	2517.82	1	1818.2	40.217392	S.T1V1K2R4G1E1G1F1M1V1V1T1A1T1G1D1N2T1F1V1G1R4A1A1.A
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	3	4.4035	0.2963	2484.53	2485.82	1	1737.7	41.304348	S.TVKRGEGFMVVTATGDNTFVGRAA.A
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	2	3.1142	0.2755	1762.49	1761.127	1	403.4	43.75	L.R4Y1T1L1G1I1T1I1I1G1V1P1V1G1L1P1A1.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	2	3.6767	0.3196	2013.39	2014.373	1	610.1	42.105263	A.RSAADIVFLAPGLSAIIDAL.K
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	2	3.4395	0.379	2038.81	2037.373	1	514.4	42.105263	A.R4S1A1A1D1I1V1F1L1A1P1G1L1S1A1I1I1D1A1L1.K
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	2	3.0517	0.3433	1555.53	1556.863	1	627.8	79.16667	L.M1N2G1K2P1M1K2E1K2K2S1T1R4.S
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	2	3.608	0.1537	1574.73	1575.928	1	637.9	75	F.DRLMNGKPMKEKK.S
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	2	3.749	0.2348	1506.17	1506.671	2	740.9	63.333332	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
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	2	3.6337	0.3797	1488.37	1487.671	1	572.5	63.333332	E.RLGLGGGGDMPGSELA.D
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	2	3.0246	0.2108	1973.83	1973.084	4	273.3	43.75	A.G1E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1.G
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	2.7347	0.1609	1403.54	1404.52	1	264.2	59.090908	A.G1E1A1R4P1V1P1E1E1Y1L1Q2.T
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	2.6209	0.3179	1387.58	1388.52	1	392.7	68.181816	A.GEARPVPEEYLQ.T
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	2.8051	0.2079	1331.65	1331.468	4	184.8	60.000004	G.EARPVPEEYLQ.T
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	2.3873	0.236	1273.56	1274.389	3	189.3	55	A.G1E1A1R4P1V1P1E1E1Y1L1.Q
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	2	2.9718	0.1747	1275.45	1274.389	2	533.9	70	A.G1E1A1R4P1V1P1E1E1Y1L1.Q
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	2.2622	0.1667	1202.46	1203.337	2	213.3	61.11111	G.EARPVPEEYL.Q
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	2	3.5237	0.2125	1614.97	1614.852	1	608.3	67.85714	T.A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2.E

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	2	3.4799	0.3942	2008.09	2009.136	1	714.5	55.88235	A.GEARPVPEEYLQTDPSYG.L
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	2	3.2647	0.2619	1971.75	1973.084	1	330.5	46.875	G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1.L
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	2	4.0932	0.3271	1912.33	1915.033	1	803.9	63.333332	G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1.G
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	3	4.2059	0.3298	2189.72	2189.349	1	708.5	37.5	G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
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	2	4.6328	0.3743	2123.31	2122.296	1	797.9	58.333332	A.GEARPVPEEYLQTDPSYGL.T
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	2	5.1899	0.3925	2087.97	2087.244	1	970.3	61.764706	G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1.T
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	2	3.8295	0.3419	2028.15	2029.322	1	505	52.77778	A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1.D
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	2	4.3919	0.412	2224.73	2223.401	1	769.1	55.263157	A.GEARPVPEEYLQTDPSYGLT.S
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	2	3.6553	0.1688	2030.63	2029.248	1	1100.6	58.333332	R.D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2.L
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	2	5.1626	0.4324	2189.27	2189.349	1	996.7	61.11111	G.E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1T1.S
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	2	3.6726	0.3306	1782.21	1780.811	1	638.4	53.571426	K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2.Y
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	2	2.9231	0.3649	1593.53	1594.634	1	721	66.66667	E.EDHPIPEDVHENY.E
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	2	4.4543	0.4292	2191.25	2191.207	1	1412.3	64.70589	K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2.K
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	2	4.3909	0.4159	1924.09	1923.987	1	1062.2	63.333332	K.TVEEDHPIPEDVHENY.E
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	2	4.751	0.432	1945.27	1944.987	1	859.7	56.666668	K.T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1.E
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	3.135	0.1944	1345.54	1346.468	5	131.2	50	G.E1A1R4P1V1P1E1E1Y1L1Q2.T
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	2	2.9633	0.1577	1441.61	1442.64	5	325.7	58.333332	V.V1I1R4D1G1Q2L1V1E1I1P1A1N2.E
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	2	3.7195	0.1787	1672.85	1672.888	4	523	67.85714	A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1.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	2	3.9197	0.2988	1635.61	1636.786	1	957.5	62.5	A.E1R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1.D
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	2	4.8077	0.4506	2064.83	2065.244	1	1255	67.64706	G.EARPVPEEYLQTDPSYGL.T
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	2	3.3769	0.3602	2003.87	2005.322	1	389	50	A.VVIRDGQLVEIPANEVVPG.D
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	2	5.5414	0.3939	2420.25	2417.808	1	1137.7	61.363636	T.AVVIRDGQLVEIPANEVVPGDIL.Q
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	2	5.4073	0.427	2373.45	2373.729	1	889.1	57.14286	A.V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1.Q
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	2	3.8161	0.3862	2520.15	2518.913	1	529.4	45.652176	N.TAVVIRDGQLVEIPANEVVPGDIL.Q
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	3.118	0.223	1261.44	1262.465	1	687.9	70	Q.M1A1D1E1K2E1S1L1V1V1K2.F
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	2.7229	0.258	1248.39	1249.465	1	607.5	65	Q.MADEKESLVVK.F
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	2	3.8879	0.3118	1909.53	1910.985	1	885.3	60.000004	L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2.Y
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	2	4.9021	0.2629	1508.45	1508.7	1	1323.2	87.5	L.N2Q2M1A1D1E1K2E1S1L1V1V1K2.F
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	3	6.0691	0.3926	2451.65	2451.555	1	2268.6	46.05263	L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2.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	3	5.3803	0.3683	2422.79	2423.555	1	2073.7	46.05263	L.KTVEEDHPIPEDVHENYENK.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	2	5.7719	0.4294	2073.47	2075.161	1	1479.1	65.625	L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1.E
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	2	3.649	0.2395	2623.19	2623.766	1	281.1	35.714287	L.K2T1V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1E1N2K2V1A1.E
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	2	3.6473	0.3335	1842.07	1842.882	1	756.5	57.14286	T.V1E1E1D1H3P1I1P1E1D1V1H3E1N2Y1.E
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	2	3.1426	0.4158	1302.73	1303.433	1	684	76.92308	E.RLGLGGGGDMPGSE.L
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	2.8753	0.3638	1302.36	1303.433	1	238.4	53.846157	E.RLGLGGGGDMPGSE.L
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	3.0808	0.184	1417.57	1418.593	2	400.5	59.090908	Y.D1N2A1P1Y1S1P1K2P1V1K2W2.N
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	3.0087	0.2655	1402.55	1402.593	1	395.6	59.090908	Y.DNAPYSPKPVKW.N
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	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	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	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
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	3.4927	0.5199	1486.67	1487.671	1	262.6	50	E.RLGLGGGGDMPGSELA.D
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	2	3.981	0.3279	2057.89	2059.305	1	515.8	52.77778	I.R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1.Q
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	3	4.4905	0.2225	4292.42	4291.814	1	505.6	19.23077	T.A1V1V1I1R4D1G1Q2L1V1E1I1P1A1N2E1V1V1P1G1D1I1L1Q2L1E1D1G1T1V1I1P1T1D1G1R4I1V1T1E1.D
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	2	4.5537	0.4609	2683.33	2682.878	1	1385.7	46.153847	E.RLGLGGGGDMPGSELADFVENADGFAE.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	3	4.9779	0.3772	2712.11	2713.878	1	1294.6	33.653847	E.R4L1G1L1G1G1G1G1D1M1P1G1S1E1L1A1D1F1V1E1N2A1D1G1F1A1E1.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	2	4.5428	0.4464	2422.35	2423.555	1	1085.3	60.526318	L.KTVEEDHPIPEDVHENYENK.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	3.1453	0.2153	1332.55	1331.514	2	281.5	65	L.EFHPFDPVSKK.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	2	2.9311	0.2511	1402.17	1402.593	9	497.1	63.636364	Y.DNAPYSPKPVKW.N
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	2	4.2542	0.3642	1769.95	1769.007	1	1009.2	71.42857	A.I1A1Y1D1N2A1P1Y1S1P1K2P1V1K2W2.N
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	2	3.6587	0.3016	1428.37	1430.632	1	697.9	72.72727	K.V1L1E1F1H3P1F1D1P1V1S1K2.K
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	2	3.0859	0.1583	1873.31	1871.056	1	390.3	50	F.G1W2W2S1E1N2W2T1D1I1V1T1V1V1R4.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	2	3.4791	0.2776	1409.55	1406.668	1	873.8	75	S.LTENWLIFITR.A
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	3.1081	0.1543	1559.57	1560.806	2	447.9	58.333332	K.V1L1E1F1H3P1F1D1P1V1S1K2K2.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	2.7446	0.2994	1542.63	1543.806	1	590.9	62.5	K.VLEFHPFDPVSKK.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	2	3.7002	0.2806	1546.53	1543.806	1	887.3	75	K.VLEFHPFDPVSKK.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	3	4.6149	0.3304	2453.93	2454.856	2	794.5	32.142857	A.V1V1E1S1P1E1G1E1R4I1V1C1V1K2G1A1P1L1F1V1L1K2.T
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	2.3987	0.2291	1195.54	1196.469	1	626.6	66.66667	M.F1F1V1G1P1I1Q2F1V1M1.E
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	2	2.9276	0.295	1195.43	1196.469	1	1037.7	77.77778	M.F1F1V1G1P1I1Q2F1V1M1.E
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	2	4.7997	0.4109	2145.47	2145.296	1	735.9	58.333332	A.G1E1A1R4P1V1P1E1E1Y1L1Q2T1D1P1S1Y1G1L1.T
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	2.2839	0.2518	1460.45	1461.579	3	349.7	45.833336	T.A1V1V1E1S1P1E1G1E1R4I1V1C1.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	2	3.1325	0.2034	1308.63	1308.567	1	460.8	80	N.G1K2P1M1K2E1K2K2S1T1R4.S
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	2.3646	0.2336	1441.68	1442.671	2	109	55	T.S1D1E1V1L1K2R4R4K2K2Y1.G
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	2	3.445	0.3481	1499.95	1501.77	1	956.7	69.230774	A.ASRKKKGLDAIDKA.F
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	2.9528	0.3282	1500.76	1501.77	1	350	53.846157	A.ASRKKKGLDAIDKA.F
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	2.7935	0.1745	1520.69	1522.77	2	403.3	57.692307	A.A1S1R4K2K2K2G1L1D1A1I1D1K2A1.F
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	2.6021	0.3043	1594.85	1592.882	5	96.9	45.833336	T.SDEVLKRRKKYGL.N
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	2	4.1725	0.3064	2208.75	2209.533	1	452.4	52.941177	Y.D1N2A1P1Y1S1P1K2P1V1K2W2N2L1P1R4L1W2.G
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	3	4.6894	0.3981	2206.7	2209.533	1	809.6	41.17647	Y.D1N2A1P1Y1S1P1K2P1V1K2W2N2L1P1R4L1W2.G
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	2	3.645	0.3729	2181.53	2182.533	1	479.9	52.941177	Y.DNAPYSPKPVKWNLPRLW.G
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	3	3.8872	0.2787	2180.63	2182.533	1	687.2	39.705883	Y.DNAPYSPKPVKWNLPRLW.G
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	2	3.1813	0.3078	2371.27	2373.709	1	295.8	44.444447	A.Y1D1N2A1P1Y1S1P1K2P1V1K2W2N2L1P1R4L1W2.G
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	3	3.8148	0.2454	2373.02	2373.709	1	558.7	40.27778	A.Y1D1N2A1P1Y1S1P1K2P1V1K2W2N2L1P1R4L1W2.G
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	2	4.0888	0.2085	1730.09	1729.974	1	729.6	67.85714	Q.GEEKKSKQPVNFLPQ.G
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	2	3.4601	0.3542	1968.75	1970.189	1	588.3	46.875	Q.GKWLKPNEIEYEFGGTT.G
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	2	3.0689	0.2238	1989.63	1991.189	1	379.4	40.625	Q.G1K2W2L1K2P1N2E1I1E1Y1E1F1G1G1T1T1.G
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	2	3.2942	0.3303	1209.37	1208.406	1	598.9	81.25	F.F1E1V1R4L1P1W2F1T1.L
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	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) sterol reductase, catalyzes the final step in ergosterol 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
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	2	2.9387	0.2031	1323.87	1325.615	1	1023.3	86.36364	F.MGAPLNPRWGIL.D
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	2	4.0371	0.1621	1750.67	1750.974	1	546.1	57.14286	Q.G1E1E1K2K2S1K2Q2P1V1N2F1L1P1Q2.G
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	2	3.2321	0.2355	1489.45	1490.791	2	447.8	66.66667	F.F1M1G1A1P1L1N2P1R4W2G1I1L1.D
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	2	3.3418	0.2731	1475.27	1472.791	1	476.3	70.83333	F.FMGAPLNPRWGIL.D
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	2	3.3813	0.1831	1865.83	1867.154	1	413.2	60.000004	Q.M1S1G1D1K2T1G1R4K2T1F1P1F1L1P1Y1.Q
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	2	4.0675	0.2775	1844.91	1846.154	1	494.6	60.000004	Q.MSGDKTGRKTFPFLPY.Q
gi|6321425|ref|NP_011502.1|	YGL013C	Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of multidrug resistance genes; Pdr1p	3	5.2023	0.1587	3486.47	3483.829	8	402.1	25	S.NIDDSKINCLLPKNFRDVGFLDNRDFIEN.V
gi|6321425|ref|NP_011502.1|	YGL013C	Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of multidrug resistance genes; Pdr1p	3	5.6455	0.3092	1971.41	1971.188	1	1833.9	48.333332	V.G1F1L1D1N2R4D1F1I1E1N2V1H3L1V1R4.R
gi|6321425|ref|NP_011502.1|	YGL013C	Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of multidrug resistance genes; Pdr1p	3	4.959	0.2342	1946.87	1945.188	1	1409.1	45	V.GFLDNRDFIENVHLVR.R
gi|6321424|ref|NP_011501.1|	YGL014W	Member of the PUF protein family, which is defined by the presence of Pumilio homology domains that confer RNA binding activity; preferentially binds mRNAs encoding nucleolar ribosomal RNA-processing factors; Puf4p	2	3.4688	0.3143	1899.81	1899.202	1	766.9	63.333332	F.HILPPQQNTPPPPWLY.S
gi|6321424|ref|NP_011501.1|	YGL014W	Member of the PUF protein family, which is defined by the presence of Pumilio homology domains that confer RNA binding activity; preferentially binds mRNAs encoding nucleolar ribosomal RNA-processing factors; Puf4p	2	3.619	0.3182	1920.37	1921.202	1	702.8	56.666668	F.H3I1L1P1P1Q2Q2N2T1P1P1P1P1W2L1Y1.S
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	3.1259	0.2593	1707.03	1706.808	1	493.7	62.5	L.D1E1F1D1E1N2H3K2H3P1I1R4F1.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	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
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	3.1795	0.3742	2256.53	2257.444	1	366.8	41.17647	E.I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1G1D1F1.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	3.8328	0.3832	2515.43	2517.734	1	940	50	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	2	3.099	0.471	1336.63	1338.565	3	321.9	63.636364	S.A1I1G1P1H3P1Y1P1T1L1V1R4.T
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	3.0357	0.1979	1415.39	1413.719	4	528.6	66.66667	Q.ARNEGVTVPIILM.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	4.6792	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.K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.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
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	2.6625	0.2296	1051.38	1052.164	4	345.4	55.555557	G.S1A1I1G1P1H3P1Y1P1T1.L
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	2.208	0.3116	963.44	964.086	1	416.7	62.5	S.A1I1G1P1H3P1Y1P1T1.L
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	3.7036	0.3478	2065.41	2065.243	1	429.5	53.333336	K.E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.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	3.3083	0.2803	2039.57	2040.243	1	388.5	53.333336	K.EILDEFDENHKHPIRF.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	1	3.5271	0.3036	1351.56	1352.648	1	344.3	68.181816	A.E1V1L1P1K2L1G1P1K2I1G1W2.D
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	3.1591	0.2598	1336.6	1337.648	1	325.4	68.181816	A.EVLPKLGPKIGW.D
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	3.2736	0.3268	1910.63	1911.127	1	602.1	57.14286	E.ILDEFDENHKHPIRF.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	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
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	5.0405	0.463	2193.63	2195.417	1	1467.3	65.625	K.K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.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	4.4255	0.363	2167.77	2168.417	1	1095.6	62.5	K.KEILDEFDENHKHPIRF.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	4.3081	0.4277	2509.22	2509.827	3	549.6	30.263159	A.NVKKEILDEFDENHKHPIRF.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	5.1722	0.3787	2543.42	2541.827	1	2499.5	48.684208	A.N2V1K2K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.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	5.1802	0.3634	2540.71	2541.827	1	1233.4	57.894737	A.N2V1K2K2E1I1L1D1E1F1D1E1N2H3K2H3P1I1R4F1.G
gi|6321407|ref|NP_011484.1|	YGL031C	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 but may be required for normal translation rate; Rpl24ap	1	2.4168	0.2218	1289.65	1290.478	1	237.6	77.77778	K.E1R4R4S1L1K2P1E1V1R4.K
gi|6321407|ref|NP_011484.1|	YGL031C	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 but may be required for normal translation rate; Rpl24ap	1	2.497	0.2831	1166.69	1166.382	1	305.8	72.22222	A.K2I1Y1P1G1R4G1T1L1F1.V
gi|6321407|ref|NP_011484.1|	YGL031C	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 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
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	3.3242	0.1951	1774.39	1775.052	2	251.5	50	L.T1V1P1K2G1E1E1L1I1N2P1I1S1D1L1M1.Q
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	2.9343	0.184	2034.51	2035.342	4	412.5	41.666664	L.G1S1L1T1V1P1K2G1E1E1L1I1N2P1I1S1D1L1M1.Q
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	5.0026	0.4158	3056.39	3058.456	1	614.7	32	T.V1L1L1D1Y1T1R4P1I1S1D1D1P1E1V1I1N2K2V1K2E1E1L1K2A1H3.N
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	3.9899	0.3473	2422.57	2423.577	1	330	42.5	Y.T1Y1H3S1P1R4P1G1D1D1S1T1Q2E1G1I1L1W2P1V1H3.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	2	4.3695	0.3293	2582.51	2584.716	1	556.4	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	4.2105	0.3027	2552.41	2553.716	1	703.2	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	3	4.9997	0.4122	2586.65	2584.716	1	755.8	32.142857	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	3	4.1487	0.4661	2552.66	2553.716	1	1071.7	36.904762	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	3	3.9326	0.3107	2088.23	2088.365	1	672.1	45.588234	T.VLLDYTRPISDDPEVINK.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	4.1742	0.1581	2113.71	2111.365	1	658.1	58.823532	T.V1L1L1D1Y1T1R4P1I1S1D1D1P1E1V1I1N2K2.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	3	4.4701	0.4981	2392.58	2393.577	1	953.7	35	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	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.T1V1P1K2G1E1E1L1I1N2P1I1S1D1L1.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	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 associated with the mitochondrial nucleoid; putative mitochondrial ribosomal protein with similarity to E. coli L7/L12 ribosomal protein; required for normal respiratory growth; Mnp1p	2	3.4169	0.2998	2064.63	2065.291	1	345.5	50	T.TTTAPSHKDDVRPVDPKIS.K
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.8165	0.3206	1425.93	1425.622	2	1106.5	75	L.SIDDLIHEIITVG.P
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.7334	0.1697	1679.36	1678.88	1	1262.7	53.571426	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	4.5013	0.4571	1476.83	1476.642	1	1874.8	83.33333	I.D1D1L1I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.6253	0.2736	1660.7	1659.88	1	978.6	50	L.SIDDLIHEIITVGPH.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	4.1165	0.4118	1462.31	1459.642	1	1708.4	79.16667	I.DDLIHEIITVGPH.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.5253	0.3629	1016.31	1016.146	1	1290.5	93.75	I.H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.4359	0.2985	1003.33	1003.146	1	1302.6	93.75	I.HEIITVGPH.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	3.9432	0.2414	1573.46	1572.801	2	1162.8	53.846157	S.IDDLIHEIITVGPH.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	4.5195	0.3942	1662.45	1659.88	1	1718.8	75	L.SIDDLIHEIITVGPH.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.3973	0.2841	1129.81	1130.305	1	1196.4	88.88889	L.I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.8698	0.2077	1591.28	1590.801	1	1669.9	57.692307	S.I1D1D1L1I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	4.1948	0.3563	1359.61	1360.553	1	1466.8	81.818184	D.D1L1I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.9536	0.2592	1344.45	1344.553	1	1674.4	86.36364	D.DLIHEIITVGPH.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	4.9026	0.4363	1678.23	1678.88	1	1655.6	67.85714	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	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 Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	2.9824	0.1821	1791.91	1793.039	1	615.4	53.333336	I.L1S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.5	0.311	1957.76	1957.23	1	1210.8	48.4375	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2.Q
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.8666	0.384	2277.23	2275.544	1	1427.1	38.157894	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2Q2A1N2.N
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.1256	0.3475	2064.02	2063.361	1	942.9	41.17647	L.SIDDLIHEIITVGPHFKQ.A
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.3352	0.2576	2087.39	2087.361	1	736.4	39.705883	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2Q2.A
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.6858	0.3451	2064.59	2063.361	1	903.4	50	L.SIDDLIHEIITVGPHFKQ.A

gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.6919	0.2721	2273.77	2275.544	1	918.9	50	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2Q2A1N2.N
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	6.1684	0.4683	2157.81	2159.44	1	1569	61.11111	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2Q2A1.N
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	6.3176	0.3907	2159.9	2159.44	1	1931.7	51.38889	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2Q2A1.N
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	3.8923	0.2851	1957.22	1957.202	1	1118	43.75	I.D1D1L1I1H3E1I1I1T1V1G1P1H3F1K2Q2A1.N
gi|6321362|ref|NP_011439.1|	YGL076C	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 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
gi|6321362|ref|NP_011439.1|	YGL076C	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 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
gi|6321362|ref|NP_011439.1|	YGL076C	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 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
gi|6321362|ref|NP_011439.1|	YGL076C	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 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
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	4.8379	0.5189	1659.81	1659.88	1	1846.7	75	L.SIDDLIHEIITVGPH.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	5.2487	0.4896	1676.31	1678.88	1	1790.9	75	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.5815	0.1787	1679	1678.88	2	786	48.214287	L.S1I1D1D1L1I1H3E1I1I1T1V1G1P1H3.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	3	4.3871	0.2391	1660.25	1659.88	2	1464.9	50	L.SIDDLIHEIITVGPH.F
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.0791	0.3431	2135.67	2134.44	3	445.1	36.11111	L.SIDDLIHEIITVGPHFKQA.N
gi|6321362|ref|NP_011439.1|	YGL076C	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 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
gi|6321362|ref|NP_011439.1|	YGL076C	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 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
gi|6321362|ref|NP_011439.1|	YGL076C	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 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
gi|6321362|ref|NP_011439.1|	YGL076C	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 C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	2	3.1571	0.4018	1658.05	1659.88	1	847.2	53.571426	L.SIDDLIHEIITVGPH.F
gi|6321360|ref|NP_011437.1|	YGL078C	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.G1F1E1E1D1I1K2N2I1I1R4E1T1.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.9298	0.2782	1580.53	1582.736	1	1281.8	75	K.G1F1E1E1D1I1K2N2I1I1R4E1T1.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	3	4.525	0.3017	3821.06	3823.199	1	894.3	27.272728	Q.SEALTSLPQSDIDEYFKENEIAVEDSLDLALRPL.L
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	3	3.9846	0.2955	1935.92	1935.185	1	1540.5	50	M.LEKGFEEDIKNIIRET.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.821	0.3234	2231.99	2233.43	1	628.7	47.22222	M.L1E1K2G1F1E1E1D1I1K2N2I1I1R4E1T1D1A1S1.K
gi|6321360|ref|NP_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.G1F1E1E1D1I1K2N2I1I1R4E1T1D1A1S1K2R4Q2.T
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.3944	0.2811	2491.19	2492.792	1	470.8	42.5	M.LEKGFEEDIKNIIRETDASKR.Q
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	3	5.7082	0.311	2843.99	2844.19	1	475.2	33.695652	H.K2K2E1K2K2G1E1K2E1V1E1V1P1E1K2E1S1E1K2K2P1E1P1T1.S
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	2.9732	0.2619	2346.13	2345.475	1	518.4	50	Q.SDIDEYFKENEIAVEDSLDL.A
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in 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	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	1	2.7767	0.2542	1581.7	1582.736	3	361.7	50	K.G1F1E1E1D1I1K2N2I1I1R4E1T1.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.5305	0.3014	1563.63	1564.736	1	1258.2	70.83333	K.GFEEDIKNIIRET.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	3	4.1447	0.2697	2583.53	2583.842	2	632.5	32.142857	K.E1K2K2G1E1K2E1V1E1V1P1E1K2E1S1E1K2K2P1E1P1T1.S
gi|6321360|ref|NP_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
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.5143	0.3162	1470.11	1472.725	1	921.5	77.27273	K.RKVVDEEVIEKK.K
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	3	4.6352	0.2089	2841.74	2842.173	1	657.8	31.25	K.KEKKGEKEVEVPEKESEKKPEPTSA.V
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	4.4212	0.2959	2544.19	2545.91	1	625	47.5	M.T1K2E1E1I1A1D1K2K2R4K2V1V1D1E1E1V1I1E1K2K2.K
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	3	4.7691	0.191	2544.32	2545.91	1	834.5	37.5	M.T1K2E1E1I1A1D1K2K2R4K2V1V1D1E1E1V1I1E1K2K2.K
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	3	7.0119	0.3557	2813	2812.19	1	2224.9	40.217392	H.KKEKKGEKEVEVPEKESEKKPEPT.S
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	1	2.5126	0.2739	1226.7	1226.505	2	556.5	65	S.KFPKPTPIQAV.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
gi|6321360|ref|NP_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.GFEEDIKNIIRET.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	1	2.9166	0.205	1581.67	1582.736	1	371.9	54.166668	K.G1F1E1E1D1I1K2N2I1I1R4E1T1.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	4.0232	0.2658	1581.65	1582.736	1	1403.3	75	K.G1F1E1E1D1I1K2N2I1I1R4E1T1.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.9554	0.3023	1563.69	1564.736	1	1350.4	75	K.GFEEDIKNIIRET.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	4.3844	0.454	1702.37	1704.964	1	1467.9	76.92308	M.LEKGFEEDIKNIIR.E
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	5.6219	0.4241	1954.69	1957.185	1	1932.4	73.333336	M.L1E1K2G1F1E1E1D1I1K2N2I1I1R4E1T1.D
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	3.7464	0.199	1490.39	1490.725	1	785.5	77.27273	K.R4K2V1V1D1E1E1V1I1E1K2K2.K
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in 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 ATP-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
gi|6321360|ref|NP_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
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	4.8934	0.3762	2545.65	2545.91	1	1033.2	57.5	M.T1K2E1E1I1A1D1K2K2R4K2V1V1D1E1E1V1I1E1K2K2.K
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	4.2148	0.2518	2515.69	2515.91	1	753.4	52.499996	M.TKEEIADKKRKVVDEEVIEKK.K
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	1	2.7293	0.2079	1067.64	1068.293	1	576.2	75	S.K2F1P1K2P1T1P1I1Q2.A
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	1	2.6492	0.2311	1056.61	1056.293	6	459.6	68.75	S.KFPKPTPIQ.A
gi|6321360|ref|NP_011437.1|	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	2	4.1119	0.3011	1945.59	1945.291	1	538.9	60.000004	F.F1K2D1V1D1L1T1K2K2P1K2K2I1T1F1D1.-
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	4.6594	0.3546	1937.35	1937.166	2	658.3	55.88235	C.G1V1S1E1D1V1E1D1G1A1L1V1T1K2P1K2R4L1.A
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	3.8781	0.214	1912.77	1914.166	1	704.5	55.88235	C.GVSEDVEDGALVTKPKRL.A
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	3.1193	0.2302	2054.57	2053.362	1	360	47.058823	Q.L1A1P1G1K2D1H3I1L1F1L1D1E1E1G1M1V1F1.A
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	3.4141	0.3036	1918.27	1919.202	1	545.5	59.375	L.APGKDHILFLDEEGMVF.A
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	3.6918	0.4301	1739.81	1739.762	3	472	53.571426	K.LSDEDAEKRADEMDD.-
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	3.368	0.1869	1624.13	1622.757	1	813.4	69.230774	L.G1P1F1E1D1D1T1E1V1P1T1R4I1K2.N
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	3.402	0.3279	1766.61	1766.989	1	503.6	60.714287	F.EVGIPKDNLPEYTYK.D
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	4.3671	0.3551	1578.49	1578.811	1	1386.2	76.92308	A.KIPRESFPPLAEGH.K
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	2	4.2305	0.2664	1597.83	1598.811	1	1613.6	80.769226	A.K2I1P1R4E1S1F1P1P1L1A1E1G1H3.K
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for 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
gi|6321341|ref|NP_011418.1|	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by 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	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the release of Nmd3p 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	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the 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
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	3.0869	0.2644	1668.87	1668.711	3	484.9	46.666668	Q.T1K2S1R4D1E1G1G1N2G1D1I1P1T1A1Q2.E
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	3.606	0.2529	2203.55	2201.607	3	290.3	40	S.K2A1P1N2E1P1L1L1P1P1L1P1G1Q2P1P1L1I1N2I1G1.L
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	3.758	0.3235	2314.41	2315.767	2	297.2	38.095238	S.K2A1P1N2E1P1L1L1P1P1L1P1G1Q2P1P1L1I1N2I1G1L1.V
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	3.1834	0.2209	1590.65	1590.733	1	614	62.5	Y.N2A1A1E1D1L1D1R4D1F1F1K2M1.N
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	3.5036	0.4149	2092.57	2093.474	1	603.4	44.736843	L.SKAPNEPLLPPLPGQPPLIN.I
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	3.2261	0.2895	2026.61	2029.396	1	506.1	50	S.K2A1P1N2E1P1L1L1P1P1L1P1G1Q2P1P1L1I1N2.I

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	3.3992	0.3139	2004.21	2006.396	1	374.1	41.666664	S.KAPNEPLLPPLPGQPPLIN.I
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	2	3.4221	0.1643	2300.65	2301.653	2	317.4	41.17647	N.L1D1K2L1W2T1L1I1P1E1D1K2R4D1Q2Y1L1K2.S
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	2	3.0526	0.2242	1387.65	1388.681	1	653.8	80	H.F1W2K2P1V1L1N2L1D1K2L1.W
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	2	2.9492	0.2095	1374.45	1373.681	1	624.1	75	H.FWKPVLNLDKL.W
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	2	3.0868	0.2168	1207.75	1208.49	7	874.5	80	K.G1R4I1P1N2V1P1V1I1V1K2.A
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	1	2.5446	0.2674	1248.73	1249.542	2	336.8	59.090908	L.GKGRIPNVPVIV.K
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	1	2.8527	0.2813	1265.76	1266.542	4	334.9	59.090908	L.G1K2G1R4I1P1N2V1P1V1I1V1.K
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	2	3.8382	0.3109	1826.37	1827.072	1	597.6	65.38461	L.W2T1L1I1P1E1D1K2R4D1Q2Y1L1K2.S
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	1	2.2167	0.1587	1132.54	1132.348	2	595.8	68.75	H.FWKPVLNLD.K
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	2	3.5322	0.3326	1914.35	1915.15	1	676	57.14286	L.W2T1L1I1P1E1D1K2R4D1Q2Y1L1K2S1.A
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	2	3.3826	0.2976	1806.57	1806.072	1	735.9	69.230774	L.WTLIPEDKRDQYLK.S
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	3	4.4661	0.1561	1388.9	1388.681	5	1197.8	67.5	H.F1W2K2P1V1L1N2L1D1K2L1.W
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	1	2.2002	0.179	1372.57	1373.681	1	734.5	70	H.FWKPVLNLDKL.W
gi|6321335|ref|NP_011412.1|	YGL103W	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 mutate to cycloheximide resistance; Rpl28p	2	3.1902	0.2312	1395.87	1396.716	1	831.9	62.5	L.G1K2G1R4I1P1N2V1P1V1I1V1K2.A
gi|6321333|ref|NP_011410.1|	YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	3	4.7763	0.3326	3022.94	3022.252	1	690.5	29.807693	C.G1S1N2D1D1K2V1E1F1V1E1P1P1K2D1S1K2A1G1D1K2V1F1F1E1G1F1.G
gi|6321333|ref|NP_011410.1|	YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization 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
gi|6321333|ref|NP_011410.1|	YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization 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
gi|6321333|ref|NP_011410.1|	YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	2	4.9571	0.4314	2425.45	2425.69	1	1035	55.263157	N.D1G1L1E1V1I1F1K2D1E1E1E1K2D1H3P1V1R4K2L1.T
gi|6321333|ref|NP_011410.1|	YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization 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
gi|6321333|ref|NP_011410.1|	YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization 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
gi|6321333|ref|NP_011410.1|	YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	3	4.8982	0.3601	2397.2	2397.69	1	1657.7	40.789474	N.DGLEVIFKDEEEKDHPVRKL.T
gi|6321333|ref|NP_011410.1|	YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	2	3.2836	0.2553	2357.47	2355.673	4	186.6	40.476192	N.H3D1L1D1L1P1H3E1V1I1E1K2K2K2K2A1P1A1G1G1A1A1.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
gi|6321331|ref|NP_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
gi|6321331|ref|NP_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
gi|6321331|ref|NP_011408.1|	YGL107C	Mitochondrial protein required for sporulation; Rmd9p	2	3.5432	0.1781	2217.35	2216.597	1	896.9	50	A.ESFFDKIINDEMPYKIIL.Q
gi|6321331|ref|NP_011408.1|	YGL107C	Mitochondrial protein required for sporulation; Rmd9p	2	3.4453	0.2889	1418.47	1417.643	1	610.3	70.83333	N.SLKDISDDILIGK.V
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	3.3725	0.2495	1743.67	1743.025	1	470.9	53.571426	L.I1N2E1P1L1P1Q2V1P1R4L1P1T1F1T1.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	2	3.4798	0.4288	1950.59	1950.119	1	551.4	63.333332	K.GEKVTDEDKEKLLERC.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	4.0658	0.2474	3014.12	3016.348	1	663.6	27.083334	Y.L1D1E1E1E1V1D1F1D1R4L1I1N2E1P1L1P1Q2V1P1R4L1P1T1F1.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	5.2013	0.3975	3280.97	3282.629	1	857.7	30.769232	Y.Y1L1D1E1E1E1V1D1F1D1R4L1I1N2E1P1L1P1Q2V1P1R4L1P1T1F1T1.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	4.9675	0.3902	3446.81	3446.805	1	1109.1	31.48148	V.Y1Y1L1D1E1E1E1V1D1F1D1R4L1I1N2E1P1L1P1Q2V1P1R4L1P1T1F1T1.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	4.404	0.348	3408.77	3408.832	1	718	25.925926	S.VYYLDEEEVDFDRLINEPLPQVPRLPTF.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	5.4297	0.284	3526.01	3524.875	1	1076.6	27.67857	Y.Y1L1D1E1E1E1V1D1F1D1R4L1I1N2E1P1L1P1Q2V1P1R4L1P1T1F1T1T1H3.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.Y1Y1L1D1E1E1E1V1D1F1D1R4L1I1N2E1P1L1P1Q2V1P1R4L1P1T1F1T1T1H3.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	41.666664	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	2	3.4169	0.2993	2234.97	2235.594	9	271.7	36.11111	A.IIQNPNLNDIRVSQPPFIR.G
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	3.4195	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
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	3.6764	0.2474	1606.29	1606.755	1	785.7	61.538464	F.L1T1G1E1D1E1I1E1D1A1V1R4K2I1.S
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	3.4712	0.344	1586.71	1588.755	1	835.9	61.538464	F.LTGEDEIEDAVRKI.S
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	3.3218	0.4022	1734.65	1735.94	1	850.2	60.714287	L.SKQHPLPSEEPLVHH.D
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	3.2806	0.3295	1674.19	1675.833	1	442	53.571426	F.LTGEDEIEDAVRKIS.L
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	3	4.0249	0.2997	2107.76	2107.331	1	824.8	44.11765	A.EELSKQHPLPSEEPLVHH.D
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	3.7584	0.339	2106.39	2107.331	1	419.9	47.058823	A.EELSKQHPLPSEEPLVHH.D
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	3	5.7557	0.4209	2754.95	2755.016	1	1262.7	34.782608	A.EELSKQHPLPSEEPLVHHDAGEFK.G
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	3.4631	0.206	2482.93	2483.819	1	269	40	Q.R4Y1F1N2D1A1P1L1L1A1V1P1G1R4T1Y1P1V1E1L1Y1.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	3.3198	0.1797	2454.03	2455.819	1	305.8	42.5	Q.RYFNDAPLLAVPGRTYPVELY.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	3.071	0.3511	1761.57	1758.94	1	307.2	53.571426	L.S1K2Q2H3P1L1P1S1E1E1P1L1V1H3H3.D
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	3.6805	0.3699	2156.61	2159.455	1	802.2	55.555557	Y.F1N2D1A1P1L1L1A1V1P1G1R4T1Y1P1V1E1L1Y1.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	3.4066	0.2494	1383.13	1382.529	7	383.4	63.636364	T.V1K2D1N2Q2D1V1L1I1H3P1S1.T
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	1	2.2834	0.2557	1203.43	1204.313	4	350.7	55	F.A1H3P1D1G1D1H3I1T1L1L1.N
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	3.2696	0.3201	1169.77	1170.355	1	1069.7	83.33333	K.K2L1G1I1D1D1L1V1H3F1.D
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	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.Q2I1I1D1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.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	20.454546	E.I1F1L1H3S1L1P1V1K2E1F1Q2I1I1D1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.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.I1D1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.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.I1I1D1T1L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.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. coli S5 and rat S2 ribosomal proteins; Rps2p	2	4.3325	0.3243	2072.85	2075.452	1	613.3	58.823532	T.L1L1P1G1L1Q2D1E1V1M1N2I1K2P1V1Q2K2Q2.T
gi|6321303|ref|NP_011380.1|	YGL135W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp	2	4.9649	0.4107	1794.65	1796.958	1	1905.5	76.666664	A.G1K2F1P1T1P1V1S1H3N2D1D1L1Y1G1K2.V
gi|6321303|ref|NP_011380.1|	YGL135W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp	2	4.0703	0.3907	1774.91	1775.958	1	1179.7	70	A.GKFPTPVSHNDDLYGK.V
gi|6321303|ref|NP_011380.1|	YGL135W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp	2	4.5818	0.3675	1977.07	1976.196	1	525.4	58.823532	A.GKFPTPVSHNDDLYGKVT.D
gi|6321303|ref|NP_011380.1|	YGL135W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp	2	4.872	0.4386	2001.53	1999.196	1	471.4	55.88235	A.G1K2F1P1T1P1V1S1H3N2D1D1L1Y1G1K2V1T1.D
gi|6321303|ref|NP_011380.1|	YGL135W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp	2	4.8205	0.4013	1875.17	1875.091	1	1476.1	68.75	A.GKFPTPVSHNDDLYGKV.T
gi|6321303|ref|NP_011380.1|	YGL135W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp	2	4.6807	0.309	1895.75	1897.091	1	1576.7	68.75	A.G1K2F1P1T1P1V1S1H3N2D1D1L1Y1G1K2V1.T
gi|6321303|ref|NP_011380.1|	YGL135W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp	3	3.9467	0.2502	1999.49	1999.211	9	363.8	36.764706	S.K2A1G1K2F1P1T1P1V1S1H3N2D1D1L1Y1G1K2.V
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	2	3.8119	0.3514	1956.63	1957.188	1	455.6	52.941177	E.EAIENVLPNVEGKDSLTK.I
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	1	2.3417	0.309	1309.77	1308.607	1	456.8	59.090908	F.AVFHPTLPIIIS.G
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	3	4.02	0.164	2788.07	2788.083	1	851.6	32.291664	L.T1L1R4G1E1I1E1E1A1I1E1N2V1L1P1N2V1E1G1K2D1S1L1T1K2.I
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	2	4.4536	0.4564	2019.63	2021.261	1	1197.2	62.5	R.S1D1R4V1K2G1I1D1F1H3P1T1E1P1W2V1L1.T
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	2	3.2554	0.285	2354.61	2354.63	1	268.1	44.736843	F.SNRSDRVKGIDFHPTEPWVL.T
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	3	4.9053	0.4856	4136.6	4139.254	1	548	25	N.SEAVEAEKKEEEAPQQQQSEQQPEQGEAVPEPVEEES.-
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	3	5.5636	0.5593	4251.26	4253.358	1	766.4	26.35135	S.NSEAVEAEKKEEEAPQQQQSEQQPEQGEAVPEPVEEES.-
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	1	2.9204	0.1773	1425.63	1426.6	2	484	59.090908	K.G1I1D1F1H3P1T1E1P1W2V1L1.T
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	1	2.5769	0.3	1249.58	1250.528	1	349.5	55	A.V1F1H3P1T1L1P1I1I1I1S1.G
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	1	2.9395	0.359	1236.74	1237.528	1	371.6	55	A.VFHPTLPIIIS.G
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	2	3.0415	0.2185	1784.73	1784.969	1	665.5	60.714287	R.SDRVKGIDFHPTEPW.V
gi|6321301|ref|NP_011378.1|	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	2	3.6055	0.282	1997.69	1997.261	1	1383.9	68.75	R.SDRVKGIDFHPTEPWVL.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; Flc3p	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; Flc3p	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
gi|6321299|ref|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

gi|6321289|ref|NP_011365.1|	YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	2	3.8569	0.3726	1984.19	1985.331	1	780.8	55.88235	K.KGIPVEDFPKTGLFPEPL.N
gi|6321289|ref|NP_011365.1|	YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	2	4.2893	0.1598	2002.69	2005.331	1	1096.6	61.764706	K.K2G1I1P1V1E1D1F1P1K2T1G1L1F1P1E1P1L1.N
gi|6321289|ref|NP_011365.1|	YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	2	3.4078	0.2835	2340.43	2341.712	1	442.1	50	K.KGIPVEDFPKTGLFPEPLNKN.F
gi|6321289|ref|NP_011365.1|	YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	2	3.5143	0.3014	2230.01	2227.608	2	571.7	44.736843	K.KGIPVEDFPKTGLFPEPLNK.N
gi|6321289|ref|NP_011365.1|	YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	2	3.7423	0.3226	2250.55	2251.608	1	584.6	44.736843	K.K2G1I1P1V1E1D1F1P1K2T1G1L1F1P1E1P1L1N2K2.N
gi|6321289|ref|NP_011365.1|	YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	3	4.0897	0.2659	2367.05	2367.712	2	883.9	32.5	K.K2G1I1P1V1E1D1F1P1K2T1G1L1F1P1E1P1L1N2K2N2.F
gi|6321289|ref|NP_011365.1|	YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	2	3.1846	0.2481	1875.05	1875.157	3	343.2	40.625	K.G1I1P1V1E1D1F1P1K2T1G1L1F1P1E1P1L1.N
gi|6321289|ref|NP_011365.1|	YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	3	4.1009	0.305	2226.44	2227.608	1	1013.6	39.473686	K.KGIPVEDFPKTGLFPEPLNK.N
gi|6321285|ref|NP_011362.1|	YGL153W	Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p	2	3.5222	0.3558	1778.19	1779.025	1	308.3	60.000004	M.K2E1P1K2K2D1G1I1V1G1D1E1V1S1K2K2.I
gi|6321285|ref|NP_011362.1|	YGL153W	Peroxisomal membrane protein that is a central component of the peroxisomal 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.M1K2E1P1K2K2D1G1I1V1G1D1E1V1S1K2K2.I
gi|6321285|ref|NP_011362.1|	YGL153W	Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p	2	4.1553	0.2424	1888.31	1889.218	1	393	56.25	A.MKEPKKDGIVGDEVSKK.I
gi|6321285|ref|NP_011362.1|	YGL153W	Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p	3	4.0491	0.2486	1910.96	1911.218	6	511.2	40.625	A.M1K2E1P1K2K2D1G1I1V1G1D1E1V1S1K2K2.I
gi|6321285|ref|NP_011362.1|	YGL153W	Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p	3	4.3174	0.3336	1890.14	1889.218	1	805	43.75	A.MKEPKKDGIVGDEVSKK.I
gi|6321285|ref|NP_011362.1|	YGL153W	Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p	2	3.5665	0.3763	2232.73	2234.595	1	619.7	52.941177	Y.EAMPPTLPHRDWKDYFVM.A
gi|6321285|ref|NP_011362.1|	YGL153W	Peroxisomal membrane protein that is a central component of the peroxisomal 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
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
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
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	24.242424	S.K2V1E1D1D1R4E1K2T1T1E1N2D1S1P1N2K2E1E1K2S1G1N2D1D1G1L1I1K2P1 V1I1T1N2.T
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
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.I1M1M1D1P1V1R4V1I1I1G1H3.K
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	3.9866	0.2882	2177.11	2176.428	1	983.9	60.526318	L.SKVGNDIPVLEDLFPDTSTK.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	4.3378	0.4025	2189.59	2191.439	1	1849.6	69.44444	L.A1K2G1L1D1Q2D1I1E1F1D1L1S1K2P1F1T1P1F1.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	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) 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	20	L.Q2E1K2L1S1P1D1L1P1D1E1E1I1P1T1L1E1L1P1K2D1L1D1M1K2D1H3L1E1F1L1.K
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
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.K2V1G1N2D1I1P1V1L1E1D1L1F1P1D1T1S1T1K2.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.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	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 Gcn20p; 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
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	3.1211	0.2748	1413.56	1414.627	2	459.5	58.333332	L.G1K2P1I1E1D1L1D1K2I1I1S1A1.G
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	2.8206	0.2832	1398.61	1399.627	6	409.3	54.166668	L.GKPIEDLDKIISA.G
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	3.0639	0.3135	1599.55	1599.865	1	605	53.571426	F.SLGKPIEDLDKIISA.G
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	2.7986	0.2022	1472.52	1470.809	1	313.5	54.166668	K.K2S1D1V1I1F1P1I1L1I1P1T1L1.L
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	3.0811	0.2627	1456.57	1456.809	1	644.6	70.83333	K.KSDVIFPILIPTL.L
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	2.7736	0.2517	1457.7	1456.809	2	281.3	50	K.KSDVIFPILIPTL.L
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	3.8402	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.V1I1E1I1L1P1N2I1L1K2N2L1G1D1A1V1P1E1V1R4D1A1.T
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	3.3857	0.2543	2624.65	2625.999	2	390.8	36.363636	L.G1A1L1V1E1R4L1G1E1E1Q2F1P1D1L1I1P1R4L1L1D1T1L1.S
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	3	4.7944	0.2242	2595.26	2595.999	1	1362.3	39.772728	L.GALVERLGEEQFPDLIPRLLDTL.S
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	2.9661	0.2172	2810.33	2812.181	1	367.9	30.434782	F.V1V1N2D1E1L1L1K2S1L1F1P1L1F1N2Q2D1D1S1G1L1R4L1F1.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	2	3.8699	0.3601	2283.03	2281.784	1	793.9	55	K.KSDVIFPILIPTLLAPPIDAF.R
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	3.6251	0.2778	2247.19	2247.47	1	441.6	44.444447	S.N2T1D1T1T1L1E1D1L1T1K2L1I1D1E1I1F1K2N2.I
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	3.3834	0.2344	1495.57	1496.719	1	834.9	77.27273	A.V1L1E1R4L1P1N2F1F1D1K2T1.V
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	3.9495	0.1802	1817.59	1819.107	1	714.9	67.85714	E.R4L1G1E1E1Q2F1P1D1L1I1P1R4L1L1.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	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
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	4.0442	0.3203	2312.13	2312.544	1	475.6	52.63158	L.NWEDISPVLEKGTRESHVSK.R
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	2.4574	0.1572	1287.42	1288.521	1	422.6	61.11111	L.F1Y1K2K2P1E1F1I1G1F1.S
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	4.0586	0.2615	1413.58	1414.673	1	735.4	68.181816	E.K2A1K2P1L1E1P1I1L1D1Q2F1.G
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	3.5393	0.3085	1400.27	1399.673	1	922.3	72.72727	E.KAKPLEPILDQF.G
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	3.8093	0.252	1399.69	1399.673	1	679.4	63.636364	E.KAKPLEPILDQF.G
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	3.0324	0.2492	1573.64	1574.902	1	426.3	57.692307	M.S1K2K2S1D1V1I1F1P1I1L1I1P1T1.L
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	2.9201	0.1696	1414.39	1414.673	2	744.4	68.181816	E.K2A1K2P1L1E1P1I1L1D1Q2F1.G
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	3.9275	0.1998	1354.49	1354.649	3	1196.7	75	S.K2I1L1I1E1I1P1L1T1H3Y1.E

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	3.6926	0.2369	1340.55	1340.649	2	1241	80 S.KILIEIPLTHY.E
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	2.574	0.3313	1557.88	1558.902	1	421.9	57.692307 M.SKKSDVIFPILIPT.L
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	3.2493	0.2933	1353.51	1354.649	1	861.7	75 S.K2I1L1I1E1I1P1L1T1H3Y1.E
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	4.1466	0.1887	1689.31	1689.061	4	546.6	60.714287 M.S1K2K2S1D1V1I1F1P1I1L1I1P1T1L1.L
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	3.4727	0.2163	1672.41	1672.061	4	549.4	60.714287 M.SKKSDVIFPILIPTL.L
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	3.1147	0.2127	1471.19	1470.809	1	680.2	70.83333 K.K2S1D1V1I1F1P1I1L1I1P1T1L1.L
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	3.1013	0.336	1398.71	1399.627	1	483.8	62.5 L.GKPIEDLDKIISA.G
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	3	3.9481	0.1728	2026.43	2025.356	1	2492.4	51.5625 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	1	2.2485	0.1928	1518.72	1518.795	1	261.3	59.090908 Q.ELFYKKPEFIGF.S
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	3.0893	0.3036	1720.25	1717.962	1	527.3	61.538464 S.HNSNLFEEYIPKLL.V
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	3.0057	0.2936	1285.91	1288.521	1	932.1	77.77778 L.F1Y1K2K2P1E1F1I1G1F1.S
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	3.1722	0.2988	1397.07	1399.673	1	817.2	68.181816 E.KAKPLEPILDQF.G
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	3.705	0.3163	1398.59	1399.673	1	921.1	72.72727 E.KAKPLEPILDQF.G
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	3.8013	0.2047	1413.72	1414.673	1	636.4	63.636364 E.K2A1K2P1L1E1P1I1L1D1Q2F1.G
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	4.6377	0.283	1673.65	1674.963	1	1469.3	76.92308 Y.K2E1K2A1K2P1L1E1P1I1L1D1Q2F1.G
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	3.9184	0.2897	1821.31	1820.139	1	949.3	67.85714 F.YKEKAKPLEPILDQF.G
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	3.71	0.1716	1298.47	1299.597	3	690.9	80 L.KKVDKPTLEKL.V
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	3.4415	0.3212	1546.37	1544.761	2	663	66.66667 L.G1E1E1Q2F1P1D1L1I1P1R4L1L1.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	0.2248	1079.49	1077.275	1	704.3	81.25 F.CLEIGLKPF.L
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	2.8979	0.1627	1544.68	1544.761	8	279.7	45.833336 L.G1E1E1Q2F1P1D1L1I1P1R4L1L1.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	3.1541	0.2657	1600.51	1599.865	1	447.9	57.14286 F.SLGKPIEDLDKIISA.G
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	4.6487	0.2325	1817.73	1819.107	1	632.6	64.28571 E.R4L1G1E1E1Q2F1P1D1L1I1P1R4L1L1.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	4.0612	0.3307	1798.95	1797.107	1	778.4	71.42857 E.RLGEEQFPDLIPRLL.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	3	4.597	0.1554	1819.22	1819.107	3	824.6	48.214287 E.R4L1G1E1E1Q2F1P1D1L1I1P1R4L1L1.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	3.6643	0.2749	1400.45	1399.673	1	1444	86.36364 E.KAKPLEPILDQF.G
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	3.5995	0.1576	1413.71	1414.673	1	869.1	72.72727 E.K2A1K2P1L1E1P1I1L1D1Q2F1.G
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	4.0511	0.2482	1413.51	1414.673	1	790.6	68.181816 E.K2A1K2P1L1E1P1I1L1D1Q2F1.G
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	3.9343	0.3593	1398.69	1399.673	1	906	72.72727 E.KAKPLEPILDQF.G
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	4.3572	0.2756	1656.51	1656.963	1	1593.5	76.92308 Y.KEKAKPLEPILDQF.G
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	3.0876	0.2523	1533.47	1531.839	1	461.6	70.83333 L.LLEGEKRSPFVKK.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	4.1548	0.4341	1986.35	1987.315	1	1156.7	60.000004 N.F1Y1K2E1K2A1K2P1L1E1P1I1L1D1Q2F1.G
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	3.0823	0.3092	1966.13	1967.315	1	674.2	63.333332 N.FYKEKAKPLEPILDQF.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	3.966	0.3978	2494.31	2495.748	1	326.9	42.857143 Y.QKETTDIFFPPDATNDFPIAVQ.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	1	3.369	0.1787	1174.55	1173.395	1	462.6	77.77778 L.EKIILEPSPF.N
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	4.3392	0.2323	1961.65	1963.219	1	906.8	59.375 L.E1K2I1I1L1E1P1S1P1F1N2E1N2V1A1L1Q2.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	3.5383	0.2981	1858.59	1860.121	3	731.3	56.666668 F.L1K2D1A1N2L1E1D1Q2L1P1L1V1I1V1C1.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	3.063	0.1949	1962.41	1963.089	1	430.3	53.333336 N.N2S1P1E1K2F1L1K2E1N2D1Q2Y1D1T1L1.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	1	3.1193	0.1937	1549.66	1550.867	1	845.7	64.28571 L.K2N2I1Q2A1P1P1G1A1I1S1P1I1L1L1.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	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.S1K2S1D1N2L1P1L1I1K2P1F1.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.S1K2S1D1N2L1P1L1I1K2P1F1.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.K2E1E1T1I1E1L1A1R4P1V1L1Q2.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.L1K2E1D1K2L1E1C1S1E1E1L1G1D1I1V1K2P1F1D1T1T1L1A1L1A1C1Y1L1.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.R4E1I1E1R4I1V1K2D1N2N2V1Y1D1P1E1R4V1K2N2F1.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.S1K2S1D1N2L1P1L1I1K2P1F1.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	3.2825	0.2578	1550.39	1550.867	1	1826.3	82.14286	L.K2N2I1Q2A1P1P1G1A1I1S1P1I1L1L1.Y
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	1	2.3204	0.2266	1387.47	1388.519	1	506.1	65	M.KSLQDDPYQFF.L
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	2	3.1782	0.2341	1925.75	1927.23	3	581.2	50	A.K2L1S1D1K2I1E1N2K2I1D1D1V1K2F1L1.K
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	2	3.9969	0.3434	1907.95	1906.23	1	1006.2	63.333332	A.KLSDKIENKIDDVKFL.K
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	2	2.9719	0.2768	1656.61	1656.876	1	622	61.538464	V.QIPLDETEPPRFLT.N
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	2	4.1296	0.2453	1942.65	1942.176	1	793.8	59.375	L.ADTVQIPLDETEPPRFL.T
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA 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

gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	1	2.7458	0.1719	1500.91	1502.841	4	298.1	62.5	Q.T1I1I1L1P1I1Y1G1R4P1V1P1F1.H
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	3	3.8176	0.2589	1502.42	1502.841	1	1232.9	56.25	Q.T1I1I1L1P1I1Y1G1R4P1V1P1F1.H
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	2	4.0281	0.3827	1488.11	1486.841	1	903.4	75	Q.TIILPIYGRPVPF.H
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	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 heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	2	3.9595	0.273	1870.25	1871.097	2	640.5	60.000004	A.DTVQIPLDETEPPRFL.T
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	2	3.182	0.1599	1962.45	1963.176	1	355.1	40.625	L.A1D1T1V1Q2I1P1L1D1E1T1E1P1P1R4F1L1.T
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	1	3.1659	0.1954	1582.8	1583.872	4	189.2	46.153847	A.TKVPSKPDRNSKIL.R
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	3	4.358	0.2889	3154.04	3155.492	1	543.7	30.555555	N.NEEEDNNKKKSSPATKVPSKPDRNSKIL.R
gi|6321231|ref|NP_011308.1|	YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA 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
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	3.7721	0.3934	1742.05	1742.977	1	950.5	73.07692	N.AKGDWLPWERIAHY.N
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	4.0204	0.3832	1763.57	1764.977	1	921.7	73.07692	N.A1K2G1D1W2L1P1W2E1R4I1A1H3Y1.N
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	3.2582	0.2113	2238.51	2237.569	1	586	47.22222	M.GLIPNAKGDWLPWERIAHY.N
gi|6321206|ref|NP_011283.1|	YGL231C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; Ygl231cp	1	2.3231	0.2948	1387.66	1388.584	5	250.4	50	D.W2L1P1W2E1R4I1A1H3Y1.N
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	3.6302	0.3779	1914.71	1916.048	1	689.6	60.000004	L.KNDYVDLDNLEEISTF.G
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	4.0714	0.413	1980.65	1981.337	1	746.6	55.88235	F.I1K2T1D1S1S1I1F1P1D1L1V1P1V1L1G1I1F1.Q
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	3.3348	0.2928	3172.75	3174.4	1	214.6	28	N.V1T1L1R4E1E1D1V1E1L1F1E1D1D1P1I1E1Y1I1R4R4D1L1E1G1S1.D
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	3.1099	0.2454	1430.49	1428.703	1	571.4	70	A.V1T1R4I1P1K2Y1F1E1I1F1.N
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	4.4688	0.4465	2143.71	2143.312	1	884.3	55.88235	A.NLKNDYVDLDNLEEISTF.G
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	3.397	0.1554	2164.81	2165.312	1	281.7	41.17647	A.N2L1K2N2D1Y1V1D1L1D1N2L1E1E1I1S1T1F1.G
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	3.0536	0.2751	3138.55	3139.4	1	228.8	28	N.VTLREEDVELFEDDPIEYIRRDLEGS.D
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	3.7387	0.2953	1515.19	1513.687	7	653.1	62.5	S.EKPFDPLPEIDVN.N
gi|6321198|ref|NP_011276.1|	YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	2	3.4845	0.2315	1667.21	1664.84	1	798.8	65.38461	S.I1A1D1S1D1F1P1D1R4W2P1T1L1L1.S
gi|6321196|ref|NP_011273.1|	YGL241W	Karyopherin, responsible for nuclear import of Spt15p, histones H2A and H2B, and Nap1p; amino terminus shows similarity to those of other importins, particularly Cse1p; localization is primarily nuclear; Kap114p	2	2.9194	0.3314	2020.17	2020.293	1	390.5	43.75	F.LKKKPNDGFLPDEINQY.L
gi|6321196|ref|NP_011273.1|	YGL241W	Karyopherin, responsible for nuclear import of Spt15p, histones H2A and H2B, and Nap1p; amino terminus shows similarity to those of other importins, particularly Cse1p; localization is primarily nuclear; Kap114p	2	4.5454	0.3606	2042.67	2043.293	1	602	53.125	F.L1K2K2K2P1N2D1G1F1L1P1D1E1I1N2Q2Y1.L
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.4057	0.2498	1599.93	1598.707	4	283.6	57.692307	F.T1E1E1M1K2N2G1T1E1E1G1L1K2N2.C
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.5545	0.2064	2692.45	2694.863	1	931.8	45.454548	F.DDTNPSKEKEEFQDSILEDLDLL.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	4.9535	0.2674	2723.03	2721.863	1	1112.7	40.909092	F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.3881	0.2709	2720.47	2721.863	1	430.5	38.636364	F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	4.3741	0.2706	2692.07	2694.863	1	1100.9	40.909092	F.DDTNPSKEKEEFQDSILEDLDLL.G

gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.011	0.2785	2839.97	2842.039	2	413.3	34.782608 R.FDDTNPSKEKEEFQDSILEDLDLL.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	4.9311	0.3563	2479.76	2477.773	1	599.1	36.842106 Q.W2M1V1D1K2D1L1V1G1N2W2D1D1P1R4F1P1T1V1R4.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	5.1085	0.2568	2719.22	2721.863	1	1346.9	43.18182 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	4.2135	0.3345	2724.31	2721.863	1	508.6	40.909092 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	4.0967	0.3482	2312.41	2313.48	1	777	55.555557 L.ITKDRLEEDESFEDFLTPQ.T
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.5463	0.3792	2500.55	2501.755	1	562	40.476192 Y.K2D1I1V1V1D1K2D1D1A1D1V1I1N2V1D1E1E1V1T1L1M1.D
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.4452	0.1656	2695.25	2694.863	1	604	43.18182 F.DDTNPSKEKEEFQDSILEDLDLL.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	3.989	0.178	3257.63	3258.546	3	492.2	25 L.I1I1R4F1D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	4.8896	0.464	1855.27	1854.017	1	744.7	70 T.Y1D1F1C1V1P1I1V1D1A1I1E1G1V1T1H3.A
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.9885	0.3403	1873.43	1874.953	1	497.5	64.28571 D.R4L1E1E1D1E1S1F1E1D1F1L1T1P1Q2.T
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.9411	0.3487	1855.41	1855.953	1	606.4	67.85714 D.RLEEDESFEDFLTPQ.T
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.412	0.1999	1376.39	1378.574	1	1390.8	90 Q.W2M1V1D1K2D1L1V1G1N2W2.D
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	4.1673	0.2788	2376.41	2377.455	2	310.4	39.473686 F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1.D
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	4.5755	0.3168	2351.91	2353.455	1	950	52.63158 F.DDTNPSKEKEEFQDSILEDL.D
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	5.0757	0.3337	1828.52	1828.029	2	1749	51.666664 A.DTKDVVPVDLVDFDHL.I
gi|37362649|ref|NP_011269.2|	YGL245W	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; 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 (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; Gus1p	2	3.2127	0.2725	2041.65	2042.293	1	471.9	47.058823 A.DTKDVVPVDLVDFDHLIT.K
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.2155	0.1743	2064.57	2063.293	1	677	50 A.D1T1K2D1V1V1P1V1D1L1V1D1F1D1H3L1I1T1.K
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.0151	0.2055	1166.21	1165.332	2	728.9	77.77778 K.LNLEGDFKKT.K
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.3465	0.264	1875.43	1873.968	1	382.2	53.571426 L.ITKDRLEEDESFEDF.L
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.5988	0.1939	2525.51	2525.632	4	360.7	35 R.F1D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1.D
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	4.3268	0.3626	1828.53	1828.029	1	1130.5	73.333336 A.DTKDVVPVDLVDFDHL.I
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.9713	0.2591	2693.01	2694.863	1	892.8	45.454548 F.DDTNPSKEKEEFQDSILEDLDLL.G

gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.7434	0.2676	2719.65	2721.863	1	587.1	40.909092	F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	4.9671	0.2802	2844.65	2842.039	1	1039.2	36.95652	R.FDDTNPSKEKEEFQDSILEDLDLL.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	5.3001	0.2423	2872.28	2870.039	1	1351.5	36.95652	R.F1D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	5.1059	0.2745	2723.12	2721.863	1	832.6	38.636364	F.D1D1T1N2P1S1K2E1K2E1E1F1Q2D1S1I1L1E1D1L1D1L1L1.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.7556	0.2518	2251.37	2249.477	1	587.3	47.22222	N.PSKEKEEFQDSILEDLDLL.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	3.4875	0.2875	1251.07	1251.515	1	829.3	80	F.NKKVIDPIAPR.H
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	3	5.11	0.209	2696.75	2694.863	2	1043.7	36.363636	F.DDTNPSKEKEEFQDSILEDLDLL.G
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	1	2.2541	0.1614	1250.65	1251.515	4	258.9	60.000004	F.NKKVIDPIAPR.H
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	4.7844	0.2934	1848.35	1847.029	1	954.2	66.66667	A.D1T1K2D1V1V1P1V1D1L1V1D1F1D1H3L1.I
gi|37362649|ref|NP_011269.2|	YGL245W	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; Gus1p	2	4.1526	0.3973	1838.41	1836.017	1	547.8	63.333332	T.YDFCVPIVDAIEGVTH.A
gi|6321184|ref|NP_011261.1|	YGL253W	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; 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	2	5.4264	0.443	2341.41	2340.419	1	1691.4	63.88889	A.RIEEDPFENLEDTDDLFQN.E
gi|6321184|ref|NP_011261.1|	YGL253W	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; 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	2	6.2893	0.4134	2366.47	2365.419	1	1640.3	66.66667	A.R4I1E1E1D1P1F1E1N2L1E1D1T1D1D1L1F1Q2N2.E
gi|6321184|ref|NP_011261.1|	YGL253W	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; 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	2	4.2932	0.4761	2929.49	2932.026	1	830.6	45.652176	A.R4I1E1E1D1P1F1E1N2L1E1D1T1D1D1L1F1Q2N2E1F1G1I1N2.T
gi|6321184|ref|NP_011261.1|	YGL253W	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; 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	2	4.3893	0.3992	2643.69	2643.711	1	1352.3	55	A.R4I1E1E1D1P1F1E1N2L1E1D1T1D1D1L1F1Q2N2E1F1.G
gi|6321184|ref|NP_011261.1|	YGL253W	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; 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	2	4.051	0.3825	2900.25	2901.026	1	1085.5	45.652176	A.RIEEDPFENLEDTDDLFQNEFGIN.T
gi|6321184|ref|NP_011261.1|	YGL253W	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; 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.E1K2E1G1I1I1K2P1I1S1K2H3.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
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	3.3722	0.278	1545.67	1542.788	1	558.8	72.72727	E.K2Y1D1R4I1L1K2E1V1P1T1Y1.R
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	3.2879	0.2309	2671.37	2672.07	1	391.6	42.5	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	2	3.1784	0.2396	2640.73	2642.07	1	341.4	37.5	A.VILDQEKYDRILKEVPTYRYV.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	3.2371	0.2306	1967.53	1967.284	1	348.7	57.14286	E.K2Y1D1R4I1L1K2E1V1P1T1Y1R4Y1V1.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	3.5058	0.2765	1381.21	1379.643	1	512.5	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	3	4.5966	0.1642	2342.6	2343.619	1	781.1	42.647057	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	2	3.6807	0.3148	2341.89	2343.619	1	251.3	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	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.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	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	3	4.1323	0.3472	2639.99	2642.07	6	541.7	28.75	A.VILDQEKYDRILKEVPTYRYV.S
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	2	3.1083	0.1963	1493.41	1491.745	1	1012.9	72.72727	L.LYRVENPEIVQM.F
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	2	4.0015	0.3834	1768.27	1766.865	1	766.3	62.5	Q.LSGNPILGDGKSDNQNH.A
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	2	3.0169	0.2088	2347.71	2348.59	1	364.5	41.666664	L.CVYDRDKPITDVLYPIGCY.N
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	2	2.9656	0.2172	1563.73	1564.698	2	451.7	68.181816	L.REIIREDDQFSR.V
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	2.6272	0.2875	1170.4	1171.257	1	505.4	66.66667	L.HYGHPDFINA.T
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	2.3429	0.2088	1212.63	1213.422	2	207.5	66.66667	L.TPHYAERILL.S
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	2.8608	0.2275	1377.63	1378.586	1	503	60.000004	L.YRVENPEIVQM.F
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	2.8873	0.2571	1393.45	1394.586	3	470.9	60.000004	L.Y1R4V1E1N2P1E1I1V1Q2M1.F
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	2	3.9674	0.4052	1926.27	1926.143	1	798.1	66.66667	Y.DRDKPITDVLYPIGCY.N
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	2	4.2798	0.4519	1947.33	1946.143	1	649	63.333332	Y.D1R4D1K2P1I1T1D1V1L1Y1P1I1G1C1Y1.N
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	2.9719	0.3987	1429.28	1430.612	1	505.3	70	Q.LHPVEWDCFVK.D
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	3.0722	0.3968	1445.4	1445.612	1	618.2	65	Q.L1H3P1V1E1W2D1C1F1V1K2.D
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	3.0987	0.3196	1299.85	1300.417	1	560.5	65	K.L1H3Y1G1H3P1D1F1I1N2A1.T
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	3.5637	0.2957	1401.5	1402.522	1	617.7	68.181816	K.L1H3Y1G1H3P1D1F1I1N2A1T1.F
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	2.8802	0.3853	1284.67	1284.417	1	767.1	70	K.LHYGHPDFINA.T
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	2	3.2833	0.2581	1585.79	1586.698	1	513.8	72.72727	L.R4E1I1I1R4E1D1D1Q2F1S1R4.V
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	3	4.2841	0.2523	2292.56	2289.614	1	1248.9	45.833336	V.M1E1D1G1T1R4L1I1D1L1P1A1E1E1R4Y1L1K2L1.G
gi|6321469|ref|NP_011546.1|	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	1	2.2789	0.2659	1063.52	1064.236	1	434.8	78.57143	A.H3W2Q2A1P1L1L1W2.F
gi|6321471|ref|NP_011548.1|	YGR034W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA; Rpl26bp	1	2.3302	0.1872	1337.7	1337.565	1	286.1	60.000004	L.HLDKDRKALIQ.R
gi|6321471|ref|NP_011548.1|	YGR034W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA; Rpl26bp	2	3.6219	0.1889	1354.29	1356.565	2	438	70	L.H3L1D1K2D1R4K2A1L1I1Q2.R
gi|6321471|ref|NP_011548.1|	YGR034W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA; Rpl26bp	2	3.0937	0.3168	1651.09	1651.95	1	267.9	61.538464	K.ALPIRRDDEVLVVR.G
gi|6321471|ref|NP_011548.1|	YGR034W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA; Rpl26bp	1	2.8709	0.2524	1208.74	1209.434	1	452.3	72.22222	K.LHLDKDRKAL.I
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	2	4.6232	0.4846	2747.25	2747.908	1	720.9	47.61905	M.Y1H3D1P1S1D1E1P1E1Y1P1P1L1N2L1D1D1E1F1W2K2L1.D
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	2	4.3132	0.4508	2721.69	2720.908	1	1058.5	54.761906	M.YHDPSDEPEYPPLNLDDEFWKL.D
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	3	4.7886	0.3071	2722.46	2720.908	1	1182.3	36.904762	M.YHDPSDEPEYPPLNLDDEFWKL.D
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	3	4.1145	0.2791	2852.45	2852.101	1	906.7	34.090908	A.MYHDPSDEPEYPPLNLDDEFWKL.D
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	2	3.0723	0.3143	1953.35	1952.325	1	360.5	50	A.NLPMRPPLPWETVWSK.T
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	3	5.2794	0.2341	2749.64	2747.908	1	1341.3	40.476192	M.Y1H3D1P1S1D1E1P1E1Y1P1P1L1N2L1D1D1E1F1W2K2L1.D
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	2	4.5208	0.4788	2746.39	2747.908	1	826.1	52.380955	M.Y1H3D1P1S1D1E1P1E1Y1P1P1L1N2L1D1D1E1F1W2K2L1.D
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	2	3.0116	0.1908	1569.19	1568.859	1	315.5	54.166668	A.N2L1P1M1R4P1P1L1P1W2E1T1V1.W
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	2	3.08	0.2672	1736.07	1735.097	1	579.6	57.14286	Y.IANLPMRPPLPWETV.W
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	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	2	3.7661	0.3184	1945.67	1943.31	1	601.5	60.000004 Y.I1A1N2L1P1M1R4P1P1L1P1W2E1T1V1W2.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	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	2	3.3937	0.3657	1618.35	1618.855	1	433.1	53.846157 H.V1T1V1R4G1P1K2A1E1E1I1L1E1R4.G
gi|6321522|ref|NP_011599.1|	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	3	4.5689	0.1534	1416.65	1416.618	1	1660.4	56.81818 T.V1R4G1P1K2A1E1E1I1L1E1R4.G
gi|6321522|ref|NP_011599.1|	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	2	3.068	0.1937	1789.71	1791.067	2	490.2	53.333336 H.V1T1V1R4G1P1K2A1E1E1I1L1E1R4G1L1.K
gi|6321522|ref|NP_011599.1|	YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	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 Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	1	2.419	0.2086	1209.55	1210.415	2	548.8	60.000004 L.GIKYDPSIGIF.G
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	5.618	0.4142	2216.27	2217.201	1	1171.6	61.11111 E.P1E1Q2E1E1E1G1A1V1E1E1H3E1Q2V1G1H3Q2Q2.S
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	5.6185	0.4481	2189.31	2190.201	1	1210.1	66.66667 E.PEQEEEGAVEEHEQVGHQQ.S
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	3	4.4581	0.369	2500.22	2500.855	1	1881.6	46.25 L.KYKDPQSPKIEVLEQELVRAE.A
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	3	4.3913	0.291	2531	2529.855	2	690.6	32.5 L.K2Y1K2D1P1Q2S1P1K2I1E1V1L1E1Q2E1L1V1R4A1E1.A
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	4.2993	0.3682	2500.33	2500.855	1	637.4	55 L.KYKDPQSPKIEVLEQELVRAE.A
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	3.9387	0.2374	2528.59	2529.855	1	701	55 L.K2Y1K2D1P1Q2S1P1K2I1E1V1L1E1Q2E1L1V1R4A1E1.A
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	2.9642	0.1923	1737.95	1738.789	1	581	58.333332 S.E1L1D1D1Q2F1I1D1R4Y1D1Q2Y1.R
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	4.7574	0.397	1650.43	1649.706	1	1242.7	64.28571 W.GLENDDDVSDITDKL.G
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	4.9604	0.4026	1665.59	1666.706	1	1970.6	75 W.G1L1E1N2D1D1D1V1S1D1I1T1D1K2L1.G
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	3.3997	0.3015	1722.25	1720.789	1	733.2	62.5 S.ELDDQFIDRYDQY.R
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	4.1663	0.3952	2034.55	2036.116	1	972.1	56.666668 Y.EVSELDDQFIDRYDQY.R
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	1	2.8611	0.1754	1431.63	1432.645	6	482	63.636364 K.Y1K2D1P1Q2S1P1K2I1E1V1L1.E

gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	1	3.6638	0.2835	1561.78	1562.819	1	663.3	66.66667	L.K2Y1K2D1P1Q2S1P1K2I1E1V1L1.E
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	3.3673	0.1616	1544.97	1545.819	1	640.9	70.83333	L.KYKDPQSPKIEVL.E
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	1	3.3529	0.2138	1545.82	1545.819	1	533.7	58.333332	L.KYKDPQSPKIEVL.E
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	3.427	0.1941	1658.75	1658.979	4	582.3	61.538464	Y.LKYKDPQSPKIEVL.E
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	4.9953	0.4064	1830.27	1830.999	1	846.2	62.5	L.L1E1L1L1D1D1S1P1V1T1P1G1E1T1R4P1A1.Y
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	2	4.7872	0.4783	1810.43	1810.999	1	1122.8	68.75	L.LELLDDSPVTPGETRPA.Y
gi|6321523|ref|NP_011600.1|	YGR086C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	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.D1L1V1K2P1E1D1D1I1R4D1T1F1E1T1S1.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.K2S1F1D1D1L1Y1K2I1I1F1.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	2	2.9835	0.294	1364.51	1364.686	4	447.1	65	L.LTMPKELFEKK.D
gi|6321534|ref|NP_011611.1|	YGR097W	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p	3	4.6834	0.3009	3035.27	3036.32	2	490	25.925926	F.L1T1D1I1D1E1T1T1N2T1I1T1D1P1F1T1T1A1P1R4G1P1K2K2A1Q2P1A1.Q
gi|6321534|ref|NP_011611.1|	YGR097W	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p	2	3.3438	0.3183	2931.83	2934.304	1	185.7	29.166666	K.E1F1I1L1P1E1T1D1E1R4S1P1Y1F1I1N2V1P1I1P1K2A1Q2P1T1.S
gi|6321534|ref|NP_011611.1|	YGR097W	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p	3	4.713	0.3161	3001.49	3001.32	3	510.7	25.925926	F.LTDIDETTNTITDPFTTAPRGPKKAQPA.Q
gi|6321534|ref|NP_011611.1|	YGR097W	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p	2	3.3056	0.3358	1760.33	1758.974	1	582.2	57.14286	Q.HGIISKPPAFEWDNF.V
gi|6321534|ref|NP_011611.1|	YGR097W	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p	2	3.1308	0.3077	1712.35	1712.882	1	388	61.538464	F.I1L1P1E1T1D1E1R4S1P1Y1F1I1N2.V
gi|6321534|ref|NP_011611.1|	YGR097W	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p	2	3.379	0.3042	1970.17	1971.201	1	458.4	43.75	H.G1I1I1S1K2P1P1A1F1E1W2D1N2F1V1T1Q2.H
gi|6321534|ref|NP_011611.1|	YGR097W	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p	2	3.9692	0.3561	2355.77	2355.617	1	568.9	44.736843	Q.E1L1Q2H3G1I1I1S1K2P1P1A1F1E1W2D1N2F1V1T1.Q
gi|6321537|ref|NP_011614.1|	YGR100W	Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p, Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function; Mdr1p	2	3.6369	0.2591	2023.91	2021.188	1	665.1	55.88235	K.YKLPANENILEDTNAEVS.F
gi|6321537|ref|NP_011614.1|	YGR100W	Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p, Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function; Mdr1p	2	3.9872	0.3753	1890.81	1892.208	1	576.5	50	N.AALDPTHPKVIDLPTFR.M
gi|6321537|ref|NP_011614.1|	YGR100W	Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p, 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

gi|6321537|ref|NP_011614.1|	YGR100W	Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p, Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function; Mdr1p	2	3.1206	0.2151	1841.99	1843.13	1	567.3	53.333336	A.A1L1D1P1T1H3P1K2V1I1D1L1P1T1F1R4.M
gi|6321537|ref|NP_011614.1|	YGR100W	Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p, Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function; Mdr1p	2	4.2468	0.1802	2206.25	2206.455	1	659.8	55.555557	M.NQIELPTGVTIDEEKYKVE.Q
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit biogenesis; constituent of several different pre-ribosomal particles; Nop7p	3	4.9747	0.1998	2331.02	2330.548	1	1417.6	39.473686	R.QEDSLLKLDPTEIEEDVKVE.S
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit biogenesis; constituent of several different pre-ribosomal particles; Nop7p	3	4.9274	0.2547	4522.4	4523.524	1	633.4	22.222223	L.N2A1D1E1A1N2T1D1E1T1E1K2E1E1E1Q2E1K2K2Q2E1K2E1Q2E1K2E1Q2N2E1 E1T1E1L1D1T1F1.E
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	3.429	0.1684	2732.15	2731.929	6	306.5	36.363636	L.E1S1R4Q2E1D1S1L1L1K2L1D1P1T1E1I1E1E1D1V1K2V1E1.S
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	3.4169	0.29	2264.41	2265.464	3	294.2	41.666664	K.E1R4Y1P1S1F1P1D1A1I1R4D1I1D1D1A1L1N2M1.L
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit 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
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	4.8058	0.4135	1819.29	1820.101	1	1427	80	A.NKYLPGEALPPHLSPW.G
gi|6321540|ref|NP_011617.1|	YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit biogenesis; constituent of several different pre-ribosomal particles; Nop7p	2	5.2126	0.4405	1841.35	1841.101	1	1486.1	76.666664	A.N2K2Y1L1P1G1E1A1L1P1P1H3L1S1P1W2.G
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	2	3.2456	0.1907	1479.55	1479.67	1	670	68.181816	Q.DIYDLEDLKKNL.M
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	2	3.3178	0.311	2464.31	2465.569	1	303.1	36.11111	S.W2N2E1K2R4Q2K2Y1E1D1L1E1H3D1Q2L1D1S1T1.R
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	3	6.7143	0.4254	4436.72	4437.422	1	1429.8	25.657896	F.GDGHDYDWALEIENEELENGNDNNEAEEEEIDEETGAIK.S
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	3	7.7503	0.504	4484.84	4485.422	1	2360	28.947369	F.G1D1G1H3D1Y1D1W2A1L1E1I1E1N2E1E1L1E1N2G1N2D1N2N2E1A1E1E1E1E1 I1D1E1E1T1G1A1I1K2.S
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome 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	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	3	4.0351	0.2083	2863.58	2866.14	1	837.7	33.695652	Y.K2I1V1D1N2P1F1D1K2T1N2P1E1K2F1E1D1T1L1D1N2I1I1Q2.S
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome 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	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	2	3.5636	0.1934	1626.49	1626.847	1	1999.6	79.16667	Q.KYNDLDQIIVEYL.Q
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome 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	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	3	4.0128	0.2321	3135.02	3132.148	1	700.5	27.083334	L.DELDDFIEDDEFSDEDDETRQRRIQ.E
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome 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	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	2	3.6072	0.2334	2833.87	2835.14	2	499.2	36.95652	Y.KIVDNPFDKTNPEKFEDTLDNIIQ.S
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome 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	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	2	3.8922	0.2834	2434.69	2435.569	1	576.6	50	S.WNEKRQKYEDLEHDQLDST.R
gi|6321552|ref|NP_011631.1|	YGR116W	Essential protein that interacts with histones and is involved in nucleosome 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	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	3	3.9505	0.3635	2233.1	2233.489	1	863.7	34.210526	Q.HQIHPPVDHPSSKPVEVIES.I
gi|6321563|ref|NP_011640.1|	YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine 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	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine 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
gi|6321563|ref|NP_011640.1|	YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine 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	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine 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
gi|6321563|ref|NP_011640.1|	YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine 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	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine 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
gi|6321563|ref|NP_011640.1|	YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	2.9105	0.2585	2470.37	2471.688	1	285.9	47.368423	F.D1T1T1D1E1P1D1V1K2P1Y1L1P1E1E1I1L1W2R4Q2.K
gi|6321563|ref|NP_011640.1|	YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine 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
gi|6321563|ref|NP_011640.1|	YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway; Asn2p	3	4.5582	0.1842	2169.68	2169.524	1	1070	45.588234	C.M1N2I1D1P1N2E1K2M1I1K2P1K2E1G1R4I1E1.K
gi|6321563|ref|NP_011640.1|	YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine 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
gi|6321563|ref|NP_011640.1|	YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway; Asn2p	2	4.4193	0.1649	1508.39	1508.773	9	1253.2	77.27273	A.R4V1P1F1L1D1K2D1F1L1Q2L1.C
gi|6321595|ref|NP_011672.1|	YGR156W	Pta1p Interacting protein; Pti1p	2	3.0277	0.1958	1491.29	1492.871	8	540.2	54.166668	N.L1S1K2I1P1P1L1Q2L1I1E1I1I1.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
gi|6321596|ref|NP_011673.1|	YGR157W	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	4.2997	0.3259	2034.97	2033.28	1	817.4	59.375 N.T1T1T1P1E1L1F1E1K2D1L1T1E1F1L1T1K2.V
gi|6321596|ref|NP_011673.1|	YGR157W	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	4.2966	0.4255	2228.73	2228.527	1	1348.3	55.88235 L.NWKMPIELYNGDDWIGLY.K
gi|6321596|ref|NP_011673.1|	YGR157W	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	4.4009	0.4824	2135.51	2135.423	1	973.8	56.25 N.W2K2M1P1I1E1L1Y1N2G1D1D1W2I1G1L1Y1.K
gi|6321596|ref|NP_011673.1|	YGR157W	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	3.1608	0.2573	1207.33	1206.434	1	647.5	75 L.N2W2K2M1P1I1E1L1Y1.N
gi|6321596|ref|NP_011673.1|	YGR157W	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	3.1787	0.2223	1195.23	1194.434	1	870.6	87.5 L.NWKMPIELY.N
gi|6321596|ref|NP_011673.1|	YGR157W	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis; Cho2p	2	5.4345	0.4652	2249.77	2251.527	1	1599.9	58.823532 L.N2W2K2M1P1I1E1L1Y1N2G1D1D1W2I1G1L1Y1.K
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	1	2.7987	0.2702	1310.67	1311.437	4	229.9	60.000004 F.NADRDAIFELF.A
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	1	2.6706	0.1727	1325.59	1326.437	1	290.1	65 F.N2A1D1R4D1A1I1F1E1L1F1.A
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.1309	0.1767	1336.23	1334.488	2	459	72.22222 S.W2S1I1D1D1E1W2L1K2K2.E
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	4.2671	0.4575	2246.53	2244.509	1	530.6	47.368423 W.SIDDEWLKKEFEHIGGVIGA.R
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	4.0411	0.3192	1825.49	1824.046	1	1165.7	70 V.SVRIPTHPETEQPKGF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	4.1713	0.3019	1849.53	1847.046	1	982.1	63.333332 V.S1V1R4I1P1T1H3P1E1T1E1Q2P1K2G1F1.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	4.8883	0.4	2403.29	2400.696	1	1322.1	52.499996 W.SIDDEWLKKEFEHIGGVIGAR.V
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	3	4.036	0.2503	1824.65	1824.046	3	715.3	45 V.SVRIPTHPETEQPKGF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.5538	0.3253	2173.77	2173.43	1	580.3	50 W.SIDDEWLKKEFEHIGGVIG.A
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	3	4.2413	0.262	1637.27	1637.836	1	1394.8	57.692307 V.RIPTHPETEQPKGF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	3	3.8846	0.2165	2938.07	2939.196	1	312	29 K.EIDGRPINCDM@STSKPAGNNDRAKKF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.5031	0.3136	1823.43	1824.046	1	732.2	56.666668 V.SVRIPTHPETEQPKGF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.1938	0.2844	1636.63	1637.836	1	723.4	65.38461 V.RIPTHPETEQPKGF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.2586	0.2399	1322.21	1320.488	1	811.5	88.88889 S.WSIDDEWLKK.E
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.6149	0.3623	2196.37	2197.43	1	409.4	41.666664 W.S1I1D1D1E1W2L1K2K2E1F1E1H3I1G1G1V1I1G1.A
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	4.1724	0.3469	2138.63	2139.378	1	485.2	50 W.S1I1D1D1E1W2L1K2K2E1F1E1H3I1G1G1V1I1.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.8086	0.3956	2117.11	2116.378	1	361.5	44.11765 W.SIDDEWLKKEFEHIGGVI.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.9828	0.3478	2267.35	2269.509	1	634	42.105263 W.S1I1D1D1E1W2L1K2K2E1F1E1H3I1G1G1V1I1G1A1.R
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	3	4.2671	0.2776	1637.24	1637.836	1	1147.1	53.846157 V.RIPTHPETEQPKGF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	3	4.1814	0.3107	1822.52	1824.046	2	959.7	48.333332 V.SVRIPTHPETEQPKGF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.2931	0.293	1637.45	1637.836	1	603.4	65.38461 V.RIPTHPETEQPKGF.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.6109	0.3575	1657.79	1658.836	1	778.5	69.230774 V.R4I1P1T1H3P1E1T1E1Q2P1K2G1F1.G
gi|6321599|ref|NP_011675.1|	YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	2	3.8656	0.3617	1822.85	1824.046	1	921.9	63.333332 V.SVRIPTHPETEQPKGF.G
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	1	2.3728	0.2738	1368.62	1369.514	1	359.8	54.545456 L.KDATPIEDVFSF.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	4.6854	0.3477	2372.21	2372.502	1	1036.1	57.14286 E.SAPVPPSEQVKEETEVAETEQS.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	4.2886	0.2958	2397.61	2397.502	1	720.5	47.61905 E.S1A1P1V1P1P1S1E1Q2V1K2E1E1T1E1V1A1E1T1E1Q2S1.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	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	39.166668	K.T1K2P1A1E1E1K2S1A1E1P1E1V1K2Q2E1T1P1A1E1E1G1E1Q2G1E1K2G1Q2I1K2.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.Q2K2E1R4E1E1K2T1E1G1K2E1N2K2E1V1P1V1Q2E1E1T1K2S1A1I1E1.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	5.1479	0.3484	3430.91	3430.751	1	431	25	K.KQQKEREEKTEGKENKEVPVQEETKSAIE.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.K2D1A1T1P1I1E1D1V1F1S1F1.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	1	2.7447	0.3437	1381.61	1382.514	1	583.9	68.181816	L.K2D1A1T1P1I1E1D1V1F1S1F1.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

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	3.6831	0.2495	2017.43	2017.24	1	450.3	52.941177	L.S1T1K2G1Y1P1H3E1P1P1L1L1E1E1I1G1I1N2.F
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	3.7661	0.3818	1847.31	1845.059	1	939.4	60.000004	K.G1Y1P1H3E1P1P1L1L1E1E1I1G1I1N2F1.D
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	3.2748	0.2214	1697.93	1696.882	2	337.5	50	K.G1Y1P1H3E1P1P1L1L1E1E1I1G1I1N2.F
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	3.4393	0.297	1824.67	1826.059	1	1388.7	66.66667	K.GYPHEPPLLEEIGINF.D
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	3.8087	0.2889	1995.11	1995.24	1	501.4	44.11765	L.STKGYPHEPPLLEEIGIN.F
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	4.2327	0.4165	2143.13	2142.416	1	1079.4	58.333332	L.STKGYPHEPPLLEEIGINF.D
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	4.2072	0.4555	2165.43	2165.416	1	919.6	52.77778	L.S1T1K2G1Y1P1H3E1P1P1L1L1E1E1I1G1I1N2F1.D
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	2.9754	0.1566	1403.23	1400.821	2	711.6	54.545456	H.I1I1T1K2T1K2M$V1L1I1P1I1.R
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	1	2.3634	0.2448	1116.77	1117.481	3	374.6	75	T.KMVLIPIRF.G
gi|6321612|ref|NP_011689.1|	YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; 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.V1R4D1D1Q2C1T1I1D1D1F1I1D1V1I1N2E1Q2.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.V1R4D1D1Q2C1T1I1D1D1F1I1D1V1I1N2E1Q2H3R4N2Y1.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.R4A1S1L1E1K2E1L1E1N2V1G1I1R4.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
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	3.8965	0.3255	2025.77	2027.239	3	358.4	52.941177	L.KDLVKDGNDKVLEDSTIH.I
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	2.9064	0.2307	1992.61	1993.221	1	462.4	53.125	K.KIGDLDFSDREKVLDEL.L
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	3.3066	0.1617	2013.93	2015.221	2	347.5	50	K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1.L
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	3	4.051	0.3318	2410.88	2409.645	4	415.2	31.578945	K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1Y1.H
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	3	4.5019	0.322	2522.27	2521.786	1	811.6	38.75	K.KIGDLDFSDREKVLDELLDYH.F
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	3.4063	0.305	2546.85	2549.786	1	586.7	45	K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1Y1H3.F
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	4.3478	0.3286	2520.55	2521.786	1	1001.3	55	K.KIGDLDFSDREKVLDELLDYH.F
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	2.9595	0.1949	2826.35	2828.078	2	262.8	31.818182	K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1Y1H3F1E1.R
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	3.0173	0.2781	2797.59	2798.078	1	373.8	36.363636	K.KIGDLDFSDREKVLDELLDYHFE.R
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays 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

gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; 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
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; 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
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	3	4.9349	0.3893	3083.81	3082.44	1	842.1	27.083334	K.KIGDLDFSDREKVLDELLDYHFERK.S
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	3.3607	0.3211	1661.43	1659.842	1	876.5	67.85714	F.RKELHPDHVPTVGSS.F
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	3.1311	0.1766	2633.11	2634.066	4	348.5	34.090908	W.MIKDVQPFIPKSLRPSFDEAVSQ.G
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	4.3182	0.4063	2386.65	2384.645	1	384	50	K.KIGDLDFSDREKVLDELLDY.H
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	3	5.5372	0.2989	2295.26	2295.572	1	2019.3	43.421055	L.K2D1L1V1K2D1G1N2D1K2V1L1E1D1S1T1I1H3I1K2.D
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	4.6105	0.3188	2267.09	2268.572	1	997.9	55.263157	L.KDLVKDGNDKVLEDSTIHIK.D
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	3	4.1938	0.4046	2795.36	2798.078	1	832.3	32.954548	K.KIGDLDFSDREKVLDELLDYHFE.R
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	4.1663	0.3001	1694.15	1694.833	4	516.8	57.14286	L.K2D1L1V1K2D1G1N2D1K2V1L1E1D1S1.T
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	3.5475	0.3013	2245.67	2245.469	1	407.1	44.444447	K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1.Y
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	4.1517	0.3273	2407.73	2409.645	2	383.3	44.736843	K.K2I1G1D1L1D1F1S1D1R4E1K2V1L1D1E1L1L1D1Y1.H
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	4.0817	0.3211	1918.59	1917.167	1	517.5	56.25	E.KLKDLVKDGNDKVLEDS.T
gi|6321614|ref|NP_011691.1|	YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	4.1901	0.2205	1940.73	1939.167	2	428.4	53.125	E.K2L1K2D1L1V1K2D1G1N2D1K2V1L1E1D1S1.T
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	6.238	0.4952	4230.08	4230.582	1	1336.6	30.000002	A.S1A1K2D1S1E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I P1A1I1I1C1.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	5.3845	0.4691	4187.9	4187.582	1	715.8	25	A.SAKDSEIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	6.7544	0.4816	4140.65	4142.504	1	1282.5	28.676472	S.A1K2D1S1E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I1P A1I1I1C1.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	5.4061	0.2254	4027.01	4029.425	1	1675.2	28.787878	A.KDSEIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	5.4103	0.487	4098.65	4100.504	1	998.7	26.470589	S.AKDSEIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human 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
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	4.8777	0.3518	3900.77	3901.251	1	916.2	25.78125	K.DSEIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	5.2919	0.3766	3938.21	3940.251	1	988.6	27.34375	K.D1S1E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I1P1A1I1 1C1.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	4.1093	0.2394	3713.6	3714.046	1	534	25	S.AKDSEIDEEDMFNLPDELQLLPEDKERDPIPA.I
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	6.5124	0.4602	3754.1	3753.046	1	1576.1	30.645163	S.A1K2D1S1E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I1P A1.I
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	5.8102	0.4151	4068.95	4070.425	1	1527.7	31.060606	A.K2D1S1E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I1P1A I1I1C1.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	3.8805	0.2576	3734.54	3736.084	2	503.9	20.833332	S.E1I1D1E1E1D1M1F1N2L1P1D1E1L1Q2L1L1P1E1D1K2E1R4D1P1I1P1A1I1I1C1 C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	4.7264	0.3059	3700.1	3699.084	1	600.3	23.333334	S.EIDEEDMFNLPDELQLLPEDKERDPIPAIIC.C
gi|6321626|ref|NP_011703.1|	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	3	4.5007	0.3347	3516.65	3514.793	1	733	27.586206	K.DSEIDEEDMFNLPDELQLLPEDKERDPIPA.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	2	3.4521	0.3697	1710.25	1708.967	1	724.7	60.000004	L.AKVINDAFGIEEGLMT.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	2.3528	0.2078	1211.58	1212.42	1	367.2	55	A.L1S1R4P1N2V1E1V1V1A1L1.N
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	3.325	0.2093	1594.69	1595.79	1	899.2	69.230774	M.GVNEEKYTSDLKIV.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	3.6141	0.3794	1682.41	1680.074	1	616.6	56.666668	K.KVVITAPSSTAPMFVM.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	3.392	0.2919	1695.59	1697.074	1	907.8	60.000004	K.K2V1V1I1T1A1P1S1S1T1A1P1M1F1V1M1.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	3.9968	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.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	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.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	4.0822	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.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	4.0112	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.K2E1T1T1Y1D1E1I1K2K2V1V1K2.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.K2E1T1T1Y1D1E1I1K2K2V1V1K2A1.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	2	3.6718	0.2825	2128.55	2129.286	1	398.3	47.22222	A.T1Q2K2T1V1D1G1P1S1H3K2D1W2R4G1G1R4T1A1.S
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	2	3.7192	0.3257	1374.35	1374.533	1	1725.7	80	N.SKYFDPIFEDL.V
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	2	3.5935	0.2102	1704.49	1702.93	1	690	65.38461	N.S1K2Y1F1D1P1I1F1E1D1L1V1T1L1.S
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	3	4.3206	0.1981	2029.88	2029.344	4	1350.3	48.4375	S.SVRPVEKNLPEKNEYIL.A
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	2	3.1324	0.3739	2212.61	2213.582	1	333.7	41.666664	S.SVRPVEKNLPEKNEYILAL.N
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	2	4.346	0.3423	2053.13	2053.344	1	519	59.375	S.S1V1R4P1V1E1K2N2L1P1E1K2N2E1Y1I1L1.A
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	2	4.2022	0.2737	2030.53	2029.344	1	668.2	62.5	S.SVRPVEKNLPEKNEYIL.A
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	1	2.3449	0.1712	1373.66	1374.533	1	724	60.000004	N.SKYFDPIFEDL.V
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	2	3.5412	0.2353	1690.63	1687.93	1	619	61.538464	N.SKYFDPIFEDLVTL.S
gi|6321632|ref|NP_011709.1|	YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	2	4.2346	0.2921	2028.59	2029.344	1	571.2	59.375	S.SVRPVEKNLPEKNEYIL.A
gi|6321637|ref|NP_011714.1|	YGR198W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; YGR198W is an essential gene; Ygr198wp	2	3.8723	0.2688	2317.71	2317.637	1	345.7	45	M.P1N2S1N2V1R4I1P1P1T1V1P1S1K2I1I1D1V1V1D1Q2.A
gi|6321637|ref|NP_011714.1|	YGR198W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; YGR198W is an essential gene; Ygr198wp	2	3.8648	0.307	2291.47	2289.637	1	340.8	45	M.PNSNVRIPPTVPSKIIDVVDQ.A
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	1	3.1107	0.3802	1411.55	1412.64	1	519.7	54.166668	L.K2L1L1T1P1V1P1S1D1I1D1I1S1.R
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	1	2.7603	0.397	1397.79	1398.64	1	515.4	58.333332	L.KLLTPVPSDIDIS.R
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	1	3.2487	0.1608	1371.59	1372.562	1	217.6	54.166668	G.R4S1D1I1V1G1S1P1V1A1E1L1L1.K
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	1	2.9195	0.2564	1355.64	1356.562	2	245	58.333332	G.RSDIVGSPVAELL.K
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	4.5309	0.2724	1782.39	1780.926	1	876.3	64.28571	Q.K2T1N2P1D1D1L1T1P1E1E1I1N2K2F1.A
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single 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

gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	4.9327	0.4608	1930.65	1931.136	1	986.1	58.333332 L.K2S1H3G1G1A1P1D1V1K2P1G1Q2P1L1P1S1A1Y1.T
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	3.0696	0.1597	1374.29	1372.562	2	621.2	66.66667 G.R4S1D1I1V1G1S1P1V1A1E1L1L1.K
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	3.6995	0.317	2273.11	2273.599	4	526.5	42.105263 H.G1I1I1V1Q2L1P1L1P1A1H3L1D1E1D1R4I1T1S1R4.V
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	3.5691	0.2712	2244.11	2244.599	1	923	50 H.GIIVQLPLPAHLDEDRITSR.V
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	3	4.342	0.2596	3492.41	3492.833	1	500.3	22.413794 R.Y1V1D1Q2L1N2E1D1P1H3T1H3G1I1I1V1Q2L1P1L1P1A1H3L1D1E1D1R4I1T1.S
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	4.0758	0.2881	1486.41	1486.724	1	839.4	73.07692 A.N2V1R4Q2P1S1L1G1P1T1L1G1V1K2.G
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	4.4235	0.4125	1469.63	1466.724	1	969.8	76.92308 A.NVRQPSLGPTLGVK.G
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	4.0206	0.2704	1696.25	1694.881	1	1430.3	68.75 L.K2S1H3G1G1A1P1D1V1K2P1G1Q2P1L1P1S1.A
gi|6321643|ref|NP_011720.1|	YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	2	3.9079	0.4607	1675.71	1672.881	1	1131.2	62.5 L.KSHGGAPDVKPGQPLPS.A
gi|6321650|ref|NP_011727.1|	YGR211W	Essential protein with two zinc fingers, present in the nucleus of growing cells but relocates to the cytoplasm in starved cells via a process mediated by Cpr1p; binds to translation elongation factor eEF-1 (Tef1p); Zpr1p	2	3.9711	0.4022	1807.27	1806.999	1	645.4	61.538464 N.S1W2I1E1Y1K2P1G1E1P1Q2H3K2W2.S
gi|6321650|ref|NP_011727.1|	YGR211W	Essential protein with two zinc fingers, present in the nucleus of growing cells but 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	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from 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
gi|6321657|ref|NP_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
gi|6321657|ref|NP_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	66.66667 K.DFTEYPEHRVEFY.K
gi|6321657|ref|NP_011734.1|	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus; Crm1p	2	3.3806	0.283	1751.43	1750.846	1	711.9	70.83333 K.D1F1T1E1Y1P1E1H3R4V1E1F1Y1.K
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	4.0639	0.2909	1571.41	1570.753	1	998.5	75 H.L1T1L1D1D1I1D1E1K2I1I1H3Q2.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.S1I1Q2P1I1F1T1R4D1G1P1L1K2L1N2D1E1T1L1H3I1L1.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.SIQPIFTRDGPLKLNDETLHIL.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	3.607	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.K2E1L1E1H3R4D1D1M1I1H3Y1E1P1F1G1P1K2.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	3.9121	0.3097	2187.93	2188.457	1	206.9	53.125	M.LEEQVKCNPNRPIYWIQ.S
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	3.0076	0.277	1956.17	1957.067	9	215.3	38.235294	H.GEKVPTVEHEDDSAAVIC.V
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	5.2227	0.4965	1977.17	1978.067	1	527.9	61.764706	H.G1E1K2V1P1T1V1E1H3E1D1D1S1A1A1V1I1C1.V
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	3.4725	0.2414	1358.41	1358.64	2	376.6	80	L.E1N2K2I1I1R4M1P1L1V1E1.S
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	4.2369	0.3513	1746.43	1744.94	1	1143.9	70	T.TVKDDGSELLPVSDRL.N
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	2.9408	0.2831	1908.57	1906.078	1	653.6	53.333336	Y.S1A1L1E1R4I1C1E1M1V1D1Y1I1D1A1T1.A
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	3.5232	0.3911	1698.13	1700.858	2	315	61.538464	F.R4H3E1W2P1S1L1V1D1E1L1V1A1E1.G
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	3.5824	0.346	1680.19	1680.858	1	307	57.692307	F.RHEWPSLVDELVAE.G
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	3.4861	0.2309	1419.57	1420.535	1	1056.6	80	N.L1W2E1N2E1T1N2V1E1L1R4.K
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	3.8047	0.2401	1408.37	1407.518	1	1128.7	80	H.G1K2W2Q2D1E1L1K2E1V1C1.Q
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	5.3357	0.34	1763.55	1764.94	1	1089.2	70	T.T1V1K2D1D1G1S1E1L1L1P1V1S1D1R4L1.N
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	3.3375	0.2368	1538.35	1537.648	1	1112.3	81.818184	H.G1K2W2Q2D1E1L1K2E1V1C1Q2.R
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	1	2.2415	0.227	1379.92	1381.531	5	272.2	60.000004	F.RHEWPSLVDEL.V
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	3.9696	0.2346	1397.73	1398.531	1	1209.5	85	F.R4H3E1W2P1S1L1V1D1E1L1.V
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	5.123	0.2324	1921.67	1923.257	1	1374.8	66.66667	T.D1L1N2K2I1V1E1K2F1P1K2Q2A1E1K2L1.S
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	2	4.5214	0.2925	1901.51	1901.257	1	1226.5	66.66667	T.DLNKIVEKFPKQAEKL.S
gi|6321679|ref|NP_011756.1|	YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	3	4.5484	0.2015	2087.09	2087.292	1	997.3	42.1875	L.K2E1N2F1R4H3D1K2G1E1N2R4N2G1K2L1L1.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	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 phosphoenolpyruvate 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.T1A1E1E1A1L1D1L1I1V1D1A1I1K2.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	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
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	4.2894	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.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	3.515	0.2068	2723.73	2724.045	1	307.2	34.782608	D.GKYDLDFKNPNSDKSKWLTGPQLA.D
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	4.9062	0.3197	2628.41	2625.889	1	574.6	55	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	1	2.5545	0.277	1463.68	1463.76	1	497	62.5	S.KSKTSPYVLPVPF.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	3.8589	0.171	1796.11	1797.101	1	608.1	53.333336	L.S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2.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	3.0769	0.335	1576.88	1576.919	1	535.6	57.692307	S.KSKTSPYVLPVPFL.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	3.3651	0.3136	2493.03	2493.697	1	352	42.105263	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	6.2507	0.3046	3149.75	3148.568	1	1039.9	30.000002	L.A1D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L1.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	4.7384	0.3059	3074.57	3076.489	1	673.7	25.862068	A.D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L1.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	1	3.6069	0.2722	1515.7	1516.717	1	1095.5	61.538464	Q.T1A1E1E1A1L1D1L1I1V1D1A1I1K2.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	1	3.0555	0.3415	1500.72	1501.717	1	878.2	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	3.7107	0.4756	1712.83	1710.75	1	839.9	61.538464	V.SIEDPFAEDDWEAW.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	1	2.2309	0.1512	1248.54	1248.508	6	441.4	65	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	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-phosphoglycerate to phosphoenolpyruvate 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.T1A1E1E1A1L1D1L1I1V1D1A1I1K2.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	44.444447	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.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	4.2537	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.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	4.0003	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	19.166666	M.K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2S1H3F1F1K2T1A1G1I1Q2I1.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	4.719	0.2578	2466.5	2467.697	1	662.7	40.789474	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	6.1698	0.4314	2611.85	2609.859	1	1238.2	40	E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2.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	4.919	0.4962	2607.63	2609.859	1	662.6	50	E.F1F1K2D1G1K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2.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	4.667	0.4151	2582.75	2580.859	1	664	50	E.FFKDGKYDLDFKNPNSDKSKW.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	3.6595	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.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	5.2083	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
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	3.8124	0.281	3205.01	3206.538	1	413.2	24.038462	S.EFFKDGKYDLDFKNPNSDKSKWLTGPQ.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	4.136	0.212	2613.92	2614.889	1	565	35	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	6.6877	0.5112	2569.37	2569.807	1	2556.4	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	6.3575	0.4843	2538.95	2539.807	1	2386.3	42.857143	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	4.9616	0.4011	2538.53	2539.807	1	1181.6	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	3	6.3468	0.4113	2513.45	2511.755	1	2487.3	46.25	G.K2Y1D1L1D1F1K2N2P1N2S1D1K2S1K2W2L1T1G1P1Q2.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	4.5111	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.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	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	1	2.4227	0.2081	1378.46	1378.484	2	351.3	54.545456	K.HSDPNDPLSWPL.V
gi|6321700|ref|NP_011777.1|	YGR261C	Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline phosphatase to the vacuole via the alternate pathway; exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p	2	4.7687	0.2643	1738.21	1738.83	1	621	70	T.E1V1G1E1T1G1N2D1I1R4E1G1A1E1L1K2.D
gi|6321700|ref|NP_011777.1|	YGR261C	Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline phosphatase to the vacuole via the alternate pathway; exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p	1	2.3169	0.1586	1402.78	1403.578	5	196.3	54.545456	L.RFAENDPNLTLL.S
gi|6321700|ref|NP_011777.1|	YGR261C	Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline phosphatase to the vacuole via the alternate pathway; exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p	3	4.7304	0.2852	4086.98	4088.393	1	803.6	24.264706	S.SEGSPRSCPLPDKYNEIEYPSYEVVNDPDLDLFLQ.S
gi|6321700|ref|NP_011777.1|	YGR261C	Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline phosphatase to the vacuole via the alternate pathway; exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p	3	5.3579	0.3139	4129.28	4130.393	1	1033.4	25.735294	S.S1E1G1S1P1R4S1C1P1L1P1D1K2Y1N2E1I1E1Y1P1S1Y1E1V1V1N2D1P1D1L1D1L1F1L1Q2.S
gi|6321700|ref|NP_011777.1|	YGR261C	Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline phosphatase to the vacuole via the alternate pathway; exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p	2	3.1477	0.2147	2302.49	2303.493	1	363.8	44.444447	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.R4N2W2S1D1I1I1P1I1E1N2L1.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.R4I1I1E1E1P1T1K2D1V1R4L1I1F1.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.H3F1D1L1E1T1D1E1D1A1V1P1I1F1A1K2.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	2	3.9116	0.2077	2543.81	2544.822	2	639.6	47.5	M.SEEKEKENTRIIEEPTKDVRL.I
gi|6321706|ref|NP_011783.1|	YGR267C	GTP-cyclohydrolase I, catalyzes the first step in the folic acid biosynthetic pathway; 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	41.666664	Y.T1L1N2P1P1V1E1R4D1G1F1S1W2P1S1V1G1T1R4.Q
gi|6321706|ref|NP_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
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	4.326	0.319	2504.43	2505.59	1	990.4	52.63158	L.S1Q2D1R4N2D1W2D1D1I1F1E1E1F1K2D1I1S1F1A1.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	3.4369	0.2449	1505.85	1505.751	1	866.5	72.72727	Q.KQELEKELLDFL.G
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	4.059	0.2548	1793.33	1795.04	1	609.1	57.14286	S.K2I1S1L1P1D1F1D1D1E1L1K2K2V1Q2.K
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	3.805	0.1755	2364.51	2363.737	1	875.2	47.368423	E.ELQFSLINDALGLRYDMVHK.L
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	3.794	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
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	3.625	0.1991	1517.27	1516.648	2	564.9	66.66667	M.LKDRDGPEDLEKT.S
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	5.0736	0.4959	2474.61	2474.596	1	1572.7	55	C.SFEWEDYELNDAIEEAKGEAK.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	4.3591	0.1592	3000.35	3002.367	1	522.4	32.692307	Q.S1L1L1E1A1P1E1D1D1P1N2Q2M1I1E1M1K2P1S1P1G1F1D1P1K2L1A1.L
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	3.3407	0.2696	2296.89	2297.344	2	285.9	38.88889	C.S1F1E1W2E1D1Y1E1L1N2D1A1I1E1E1A1K2G1E1.A
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	3.3729	0.3136	1724.21	1724.926	1	652.1	65.38461	S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1.M
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	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
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	4.0109	0.3653	1857.53	1857.118	1	597.7	60.714287	S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1.G
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	3.0262	0.2505	2638.69	2640	1	352.5	45.238094	S.YRKPEMTPPESWPSMGEIIFEN.V
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	3.3259	0.2024	2667.07	2668	8	197.1	38.095238	S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1G1E1I1I1F1E1N2.V
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	4.4277	0.2736	2421.39	2421.781	1	732.2	52.63158	S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1G1E1I1I1F1.E
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	3.7766	0.4121	2737.75	2739.133	1	674.1	43.18182	S.YRKPEMTPPESWPSMGEIIFENV.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	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
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	4.356	0.2919	2257.67	2257.592	8	602	40.27778	H.SKKIPEVPQTDDERKIYPL.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	2	3.0622	0.2485	1240.61	1242.536	3	716.1	70	F.A1Y1R4P1G1L1P1I1V1L1K2.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	3	4.1508	0.315	2999.54	3001.398	1	768.5	30.208334	S.YRKPEMTPPESWPSMGEIIFENVDF.A
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	4.3575	0.3915	2170.19	2170.514	1	571	38.235294	S.KKIPEVPQTDDERKIYPL.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	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
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	3.0088	0.2355	1227.75	1226.295	1	1213.2	88.88889	Q.TRIVEEFGDC.T
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	4.4988	0.374	2063.77	2065.34	1	611.4	59.375	K.K2I1P1E1V1P1Q2T1D1D1E1R4K2I1Y1P1L1.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	2	4.0937	0.3894	2041.01	2042.34	1	536.1	56.25	K.KIPEVPQTDDERKIYPL.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	2	3.1291	0.2305	1488.71	1489.801	1	1003.4	70.83333	V.DFAYRPGLPIVLK.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	3.135	0.2006	1588.51	1588.933	4	431.2	53.846157	N.VDFAYRPGLPIVLK.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	3.5113	0.3215	2550.39	2551.897	1	592.3	45	S.Y1R4K2P1E1M1T1P1P1E1S1W2P1S1M1G1E1I1I1F1E1.N
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p	1	2.3217	0.2502	1396.47	1397.484	1	285.6	55	H.TWSEFERIEAE.K
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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	4.6503	0.4181	2186.31	2187.3	1	958.8	61.11111	N.V1K2T1V1D1E1S1N2V1D1P1D1E1L1L1F1D1T1E1.L
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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	3.2707	0.1588	1658.03	1658.762	1	572.7	70.83333	H.T1W2S1E1F1E1R4I1E1A1E1K2N2.V
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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	3.0264	0.2397	2094.13	2095.282	3	344.3	47.058823	C.D1F1V1A1D1V1P1P1P1K2K2G1T1D1Y1D1F1Y1.E
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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	3.4917	0.2864	1641.43	1639.762	1	361	62.5	H.TWSEFERIEAEKN.V
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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	3.2798	0.2836	1398.15	1397.484	1	1000.1	80	H.TWSEFERIEAE.K
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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	3.3753	0.3628	1819.91	1820.991	1	569.1	56.666668	N.VKTVDESNVDPDELLF.D
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb 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	3.9391	0.3644	2037.91	2037.185	1	1123.2	64.70589	N.VKTVDESNVDPDELLFDT.E
gi|6321724|ref|NP_011801.1|	YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain 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
gi|6321784|ref|NP_011860.1|	YHL003C	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lac1p; Lag1p	2	3.4881	0.2373	1649.33	1648.915	1	733.1	70.83333	M.Y1R4T1Y1P1V1I1T1N2P1F1L1F1.K
gi|6321784|ref|NP_011860.1|	YHL003C	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lac1p; Lag1p	2	2.9705	0.233	1758.91	1760.089	1	434.7	53.846157	M.YRTYPVITNPFLFK.I
gi|6321782|ref|NP_011859.1|	YHL004W	Mitochondrial ribosomal protein of the small subunit; Mrp4p	2	3.3579	0.2852	1793.23	1793.039	1	547.4	60.714287	H.K2D1I1F1Y1P1P1L1P1E1N2I1T1V1E1.S
gi|6321782|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
gi|6321772|ref|NP_011848.1|	YHL015W	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. coli S10 and rat S20 ribosomal proteins; Rps20p	2	3.1861	0.3178	1561.71	1562.834	1	514.4	62.5	H.K2R4Y1I1D1L1E1A1P1V1Q2I1V1.K
gi|6321772|ref|NP_011848.1|	YHL015W	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. coli S10 and rat S20 ribosomal proteins; Rps20p	1	3.5675	0.3716	1561.68	1562.834	1	497	58.333332	H.K2R4Y1I1D1L1E1A1P1V1Q2I1V1.K
gi|6321772|ref|NP_011848.1|	YHL015W	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. 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
gi|6321772|ref|NP_011848.1|	YHL015W	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. coli S10 and rat S20 ribosomal proteins; Rps20p	2	3.3203	0.2801	1544.73	1544.834	1	628.3	70.83333	H.KRYIDLEAPVQIV.K
gi|6321772|ref|NP_011848.1|	YHL015W	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. 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
gi|6321772|ref|NP_011848.1|	YHL015W	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. 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
gi|6321766|ref|NP_011842.1|	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	3.046	0.2102	2592.85	2592.998	5	280	31.818182	Y.ANKDLPLHTDLPFLENVPGFQIL.Q

gi|6321766|ref|NP_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
gi|6321766|ref|NP_011842.1|	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	3.9771	0.2358	2401.45	2401.724	1	415.6	42.5	H.YANKDLPLHTDLPFLENVPGF.Q
gi|6321766|ref|NP_011842.1|	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	4.1017	0.3619	2755.05	2756.174	1	705.6	41.304348	H.YANKDLPLHTDLPFLENVPGFQIL.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.Q
gi|6321766|ref|NP_011842.1|	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	4.3351	0.3053	2409.63	2407.815	1	956	57.5	N.KDLPLHTDLPFLENVPGFQIL.Q
gi|6321766|ref|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	72.72727	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
gi|6321766|ref|NP_011842.1|	YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	2	3.6412	0.3439	2528.25	2529.855	1	625.7	40.476192	H.YANKDLPLHTDLPFLENVPGFQ.I
gi|6321764|ref|NP_011840.1|	YHL023C	Protein required for sporulation; Rmd11p	2	3.276	0.1584	1360.25	1359.695	1	1275.8	77.27273	S.KFPSLPSLPIFL.S
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
gi|6321764|ref|NP_011840.1|	YHL023C	Protein required for sporulation; Rmd11p	3	3.9664	0.1776	2159.21	2161.489	1	973.4	36.764706	Q.N2E1F1E1K2M1P1N2F1K2L1Q2P1V1L1R4G1S1.Y
gi|6321753|ref|NP_011829.1|	YHL034C	Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p	3	6.4183	0.3851	2822.21	2819.893	1	1569.4	39.130436	D.V1A1V1I1R4P1E1N2D1E1E1E1I1E1Q2E1T1G1S1E1E1K2Q2E1.-
gi|6321753|ref|NP_011829.1|	YHL034C	Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p	2	5.8338	0.4376	2618.57	2618.681	1	2231	61.904762	A.VIRPENDEEEIEQETGSEEKQE.-
gi|6321753|ref|NP_011829.1|	YHL034C	Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p	2	6.234	0.3802	2645.51	2647.681	1	2025.2	59.523808	A.V1I1R4P1E1N2D1E1E1E1I1E1Q2E1T1G1S1E1E1K2Q2E1.-
gi|6321753|ref|NP_011829.1|	YHL034C	Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p	2	4.1488	0.309	2788.47	2788.893	1	922.7	45.652176	D.VAVIRPENDEEEIEQETGSEEKQE.-
gi|6321753|ref|NP_011829.1|	YHL034C	Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p	2	5.4252	0.3805	2340.69	2341.616	1	908.9	61.11111	L.V1K2F1P1T1K2I1D1F1D1N2I1K2E1N2Y1D1T1K2.V
gi|6321753|ref|NP_011829.1|	YHL034C	Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p	2	3.8039	0.3079	2103.49	2104.146	1	454.4	44.11765	A.VIRPENDEEEIEQETGSE.E
gi|6321753|ref|NP_011829.1|	YHL034C	Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p	2	3.0111	0.3386	1451.97	1452.604	1	508.7	58.333332	F.GDEVSVEIPIKEH.T
gi|6321748|ref|NP_011824.1|	YHL039W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Yhl039wp	2	3.8381	0.4184	2068.79	2069.409	1	671.3	52.941177	N.EKFSPKPDQALIRVPETL.L
gi|6321748|ref|NP_011824.1|	YHL039W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Yhl039wp	2	4.7381	0.4095	2307.81	2309.645	1	581.4	52.63158	F.V1N2E1K2F1S1P1K2P1D1Q2A1L1I1R4V1P1E1T1L1.L
gi|6321748|ref|NP_011824.1|	YHL039W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Yhl039wp	3	3.937	0.2986	2283.35	2282.645	2	1253.7	39.473686	F.VNEKFSPKPDQALIRVPETL.L
gi|6321748|ref|NP_011824.1|	YHL039W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Yhl039wp	2	4.5049	0.301	2281.97	2282.645	1	803.8	55.263157	F.VNEKFSPKPDQALIRVPETL.L
gi|6321748|ref|NP_011824.1|	YHL039W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Yhl039wp	2	3.115	0.2049	2281.97	2282.645	1	275.4	39.473686	F.VNEKFSPKPDQALIRVPETL.L
gi|6321748|ref|NP_011824.1|	YHL039W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Yhl039wp	3	4.6475	0.3534	2306.75	2309.645	1	959.4	36.842106	F.V1N2E1K2F1S1P1K2P1D1Q2A1L1I1R4V1P1E1T1L1.L
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; Arn1p	2	3.9598	0.3859	1985.77	1985.213	1	598.5	56.666668	K.D1N2D1P1I1L1D1W2F1E1K2L1P1S1K2F1.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; Arn1p	3	4.6521	0.343	2093.45	2093.387	1	1616.1	43.75	T.KDNDPILDWFEKLPSKF.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; Arn1p	3	5.0469	0.3661	2114.99	2115.387	1	1013	42.1875	T.K2D1N2D1P1I1L1D1W2F1E1K2L1P1S1K2F1.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; Arn1p	3	5.5645	0.4295	3311.48	3310.596	1	1906.3	37.5	E.Y1I1E1D1G1E1Y1V1D1T1K2D1N2D1P1I1L1D1W2F1E1K2L1P1S1K2F1.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; Arn1p	3	5.4854	0.3397	3280.7	3278.596	1	892.7	27.884615	E.YIEDGEYVDTKDNDPILDWFEKLPSKF.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; Arn1p	2	4.329	0.4725	1962.29	1965.213	1	955.3	63.333332	K.DNDPILDWFEKLPSKF.T
gi|6321790|ref|NP_011866.1|	YHR003C	Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	2	3.2618	0.261	1390.97	1388.592	1	1209.1	80	R.L1K2F1Y1D1S1I1L1E1T1F1.Q
gi|6321790|ref|NP_011866.1|	YHR003C	Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	2	2.9868	0.2164	1627.75	1628.82	1	724.9	62.5	A.V1Y1S1E1E1V1L1D1F1I1E1R4L1.F
gi|6321790|ref|NP_011866.1|	YHR003C	Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	2	3.3992	0.1984	1628.41	1625.862	1	982.1	66.66667	Y.SEEVLDFIERLFK.E
gi|6321790|ref|NP_011866.1|	YHR003C	Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	2	3.1709	0.1527	1671.87	1672.995	1	625.9	64.28571	E.A1L1R4H3L1P1E1L1G1T1M1P1G1I1F1.G
gi|6321790|ref|NP_011866.1|	YHR003C	Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	2	3.6433	0.3978	2152.51	2152.519	2	381.6	38.88889	A.VRDEALRHLPELGTMPGIF.G
gi|6321790|ref|NP_011866.1|	YHR003C	Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	2	3.2992	0.3699	1655.59	1652.995	1	699.7	64.28571	E.ALRHLPELGTMPGIF.G
gi|6321792|ref|NP_011868.1|	YHR005C	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	2	3.0198	0.256	1678.33	1679.738	1	560.9	57.14286	S.NVKSDTDRDAETVTQ.N
gi|6321792|ref|NP_011868.1|	YHR005C	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	2	3.5348	0.2352	1699.89	1700.738	1	515.5	57.14286	S.N2V1K2S1D1T1D1R4D1A1E1T1V1T1Q2.N
gi|6321792|ref|NP_011868.1|	YHR005C	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	1	2.6062	0.2306	1314.5	1314.569	2	416.6	66.66667	K.WFKDTPFILF.L
gi|6321792|ref|NP_011868.1|	YHR005C	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	2	3.1492	0.1743	1326.55	1326.569	1	793.5	83.33333	K.W2F1K2D1T1P1F1I1L1F1.L
gi|6321792|ref|NP_011868.1|	YHR005C	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	2	3.1488	0.1766	1309.33	1308.567	1	1023.7	83.33333	S.K2W2F1K2D1T1P1F1I1L1.F
gi|6321792|ref|NP_011868.1|	YHR005C	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	2	2.9374	0.1534	1937.69	1939.22	3	299.6	46.666668	K.S1M1P1I1R4K2Y1F1P1D1Y1Q2G1R4V1G1.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	3.5271	0.3143	1296.03	1296.596	1	793.1	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.E1F1F1E1E1C1Q2K2K2Y1G1D1I1F1.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; Erg11p	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
gi|6321796|ref|NP_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.KVTLPDLKWDF.G
gi|6321796|ref|NP_011872.1|	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2p	2	3.3756	0.1852	2378.51	2378.73	3	419.4	37.5	T.KVTLPDLKWDFGALEPYISGQ.I
gi|6321796|ref|NP_011872.1|	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2p	2	3.8503	0.2551	2192.13	2193.547	1	645.2	50	T.KVTLPDLKWDFGALEPYIS.G
gi|6321796|ref|NP_011872.1|	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2p	1	2.8556	0.3187	1361.77	1362.612	1	667.4	70	T.KVTLPDLKWDF.G
gi|6321796|ref|NP_011872.1|	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2p	2	3.6735	0.3208	1361.89	1362.612	1	1629.6	90	T.KVTLPDLKWDF.G
gi|6321796|ref|NP_011872.1|	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2p	2	3.0961	0.179	1101.29	1100.346	1	1366.3	87.5	T.KVTLPDLKW.D
gi|6321796|ref|NP_011872.1|	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; 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
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	4.6637	0.3957	1910.67	1911.146	1	1158.2	63.333332	L.E1A1R4I1P1E1I1L1E1E1M1Q2G1D1L1F1.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	3.4624	0.2939	1606.41	1606.788	1	525.8	70.83333	S.R4V1L1E1K2E1K2D1H3V1E1G1F1.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	4.5315	0.3344	2940.41	2940.953	1	497.1	25.961538	K.SSDKDATTDGKNDDEEEEKEAGIVDEL.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	5.7354	0.362	2042.43	2041.068	1	1560.5	70.588234	D.G1K2N2D1D1E1E1E1E1K2E1A1G1I1V1D1E1L1.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.E1L1N2L1T1G1P1K2V1P1E1D1I1Y1K2S1H3.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	28.448275	E.Q2V1N2E1P1T1K2N2E1E1A1E1I1E1V1D1E1M1E1V1D1A1E1G1E1E1V1E1V1K2.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.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	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	31.666666	Q.S1Q2I1S1P1E1K2Q2T1P1N2K2K2D1K2K2K2E1E1E1E1Q2L1S1E1E1D1A1K2L1K2.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	NADP-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	NADP-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	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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
gi|6321832|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.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.1988	0.3766	2594.61	2593.97	1	612.4	43.18182	L.D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.1509	0.3101	2476.49	2477.881	1	449	38.095238	D.P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.2109	0.2681	2568.19	2568.97	1	223.6	34.090908	L.DPETIFDLKPLDPTVKVPFPTPT.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	3	5.289	0.3288	3097.52	3098.549	1	896.4	35.185184	F.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T1I1G1.A
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.3995	0.2933	2750.93	2752.197	3	308	33.333336	D.P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T1I1G1.A
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.5019	0.2931	3099.13	3098.549	1	351	33.333336	F.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T1I1G1.A
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.1749	0.35	3170.71	3170.628	3	244.4	28.57143	F.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T1I1G1A1.A
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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
gi|6321832|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.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.2901	0.3724	2799.19	2796.233	1	581.2	41.666664	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	3.1845	0.2751	2453.37	2453.881	1	266.6	30.952381	D.PETIFDLKPLDPTVKVPFPTPT.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	3	4.0231	0.2485	3780.38	3783.118	1	754.1	25	L.S1A1A1G1A1I1R4L1G1K2L1G1E1A1D1D1G1A1G1T1T1D1E1D1Y1M1A1W2K2D1S1I1L1E1V1L1.K
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.3065	0.3273	1869.57	1867.115	2	336	53.333336	A.ETNLPVHYDLNGPRKL.F
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.2424	0.2737	2199.61	2199.474	1	169.4	50	A.ETNLPVHYDLNGPRKLFAN.Y
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.963	0.399	2168.47	2169.394	1	467.3	44.444447	H.Y1L1P1S1H3Q2L1N2R4N2A1D1G1I1Q2L1G1P1F1.D
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.3862	0.1808	1435.51	1434.592	1	1297.4	75	Q.L1N2R4N2A1D1G1I1Q2L1G1P1F1.D
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	1	2.9291	0.3486	1572.68	1573.789	1	530.2	54.166668	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	3.8477	0.3239	1647.43	1644.868	1	584.6	65.38461	L.AVWPSNPLEKVEQF.L
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.5411	0.3726	1573.19	1573.85	1	847.5	69.230774	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	3.8334	0.3467	1886.89	1885.208	1	626.9	56.25	F.D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.7242	0.172	2077.47	2077.364	5	504.1	47.058823	F.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2.V
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	3	4.929	0.4333	2708.33	2708.129	1	852	34.782608	N.L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	4.9644	0.2801	2823.29	2824.233	1	483.8	37.5	F.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.T
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.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.T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1.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
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	3	3.963	0.2765	2928.02	2926.338	2	509.3	28	F.N2L1D1P1E1T1I1F1D1L1K2P1L1D1P1T1V1K2V1P1F1P1T1P1T1T1.I

gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.6395	0.4487	2039.29	2039.291	1	372.3	50 A.E1T1N2L1P1V1H3Y1D1L1N2G1P1R4K2L1F1.A
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated 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
gi|6321832|ref|NP_011908.1|	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	2	3.4844	0.3694	2014.53	2014.291	1	393.8	53.125 A.ETNLPVHYDLNGPRKLF.A
gi|6321843|ref|NP_011919.1|	YHR052W	Essential protein that interacts with proteasome components and has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles; Cic1p	2	3.0963	0.1673	1831.97	1831.971	2	316.4	57.14286 K.NLLEDDEEELKKDLQ.L
gi|6321843|ref|NP_011919.1|	YHR052W	Essential protein that interacts with proteasome components and has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles; Cic1p	2	5.2564	0.2404	1588.53	1589.737	3	1264.7	79.16667 N.LLEDDEEELKKDL.Q
gi|6321843|ref|NP_011919.1|	YHR052W	Essential protein that interacts with proteasome components and has a potential role 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	Essential protein that interacts with proteasome components and has a potential role 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.K2D1K2I1E1E1T1H3E1D1D1M1V1T1I1D1.G
gi|6321843|ref|NP_011919.1|	YHR052W	Essential protein that interacts with proteasome components and has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles; Cic1p	2	2.9231	0.2792	2038.69	2039.401	5	266.8	41.17647 K.S1T1P1V1S1T1P1S1K2E1K2K2K2V1I1E1K2K2.S
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	1	2.5995	0.2556	1524.7	1525.783	1	824.2	61.538464 A.KAELDPLDIDAVLL.T
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	2	4.6754	0.4275	2397.57	2398.635	1	1732.5	54.761906 A.YINPKNDVDVIANPDGERAIPS.A
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	3	7.4273	0.5089	3167.9	3166.596	1	1497.3	34.82143 S.D1Y1D1A1D1E1L1A1E1A1L1Q2P1V1I1V1N2T1P1H3L1K2K2P1I1G1L1I1G1.A
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	1	2.8538	0.1784	1461.72	1462.732	1	195.5	54.545456 Q.L1I1R4N2P1K2N2T1I1I1N2F1.R
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	2	4.1804	0.3101	2235.63	2235.459	1	893.7	52.499996 Y.INPKNDVDVIANPDGERAIPS.A
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	3	6.3259	0.5474	3130.61	3131.596	1	1799.3	35.714287 S.DYDADELAEALQPVIVNTPHLKKPIGLIG.A
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	2	3.0492	0.2187	1442.95	1443.732	3	502.9	59.090908 Q.LIRNPKNTIINF.R
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	2	4.7744	0.4253	2260.69	2263.459	1	905.8	50 Y.I1N2P1K2N2D1V1D1V1I1A1N2P1D1G1E1R4A1I1P1S1.A
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	2	4.917	0.3588	2425.89	2427.635	1	1843.2	57.14286 A.Y1I1N2P1K2N2D1V1D1V1I1A1N2P1D1G1E1R4A1I1P1S1.A
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	2	3.3711	0.271	1721.71	1722.994	4	179.6	53.846157 L.Q2Q2L1I1R4N2P1K2N2T1I1I1N2F1.R
gi|37362658|ref|NP_011931.2|	YHR064C	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; Ssz1p	2	3.7708	0.2842	1571.09	1571.863	2	462.6	66.66667 Q.QLIRNPKNTIINF.R
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	4.0277	0.1641	2219.69	2218.53	1	555.1	52.77778 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	4.0471	0.1731	2244.53	2243.53	1	689.1	58.333332 M.D1E1A1D1R4L1L1D1M1E1F1G1P1V1L1D1R4I1L1.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	3.9216	0.3234	2216.78	2218.53	1	898.2	40.27778 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	3.3432	0.1949	2451.15	2448.855	1	567.5	45 L.VMDEADRLLDMEFGPVLDRIL.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	4.0931	0.2465	2474.99	2475.855	8	1208.9	38.75 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	3.5889	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	Lanosterol synthase, an essential enzyme that catalyzes the cyclization of squalene 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
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	2	3.356	0.2785	1923.35	1924.213	1	1065.4	67.85714	S.C1A1I1E1Y1P1S1Y1R4F1L1F1P1I1K2.A
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	2	3.4961	0.2545	1905.11	1905.213	1	571.5	57.14286	S.CAIEYPSYRFLFPIK.A
gi|6321870|ref|NP_011946.1|	YHR079C	Serine-threonine kinase and endoribonuclease; transmembrane protein that initiates the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p	1	3.8493	0.3746	1559.52	1560.864	1	242.7	65.38461	A.R4W2V1S1P1T1F1P1G1I1I1V1G1L1.F
gi|6321870|ref|NP_011946.1|	YHR079C	Serine-threonine kinase and endoribonuclease; transmembrane protein that initiates the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p	2	4.4124	0.3949	1933.47	1933.314	1	405.8	53.125	L.SKIGFMPEKEIPIVESK.S
gi|6321870|ref|NP_011946.1|	YHR079C	Serine-threonine kinase and endoribonuclease; transmembrane protein that initiates the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p	2	3.5082	0.3532	1559.75	1560.864	1	917.4	69.230774	A.R4W2V1S1P1T1F1P1G1I1I1V1G1L1.F
gi|6321870|ref|NP_011946.1|	YHR079C	Serine-threonine kinase and endoribonuclease; transmembrane protein that initiates the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p	2	3.6302	0.251	1864.83	1865.235	1	887.2	60.000004	S.K2I1G1F1M1P1E1K2E1I1P1I1V1E1S1K2.S
gi|6321870|ref|NP_011946.1|	YHR079C	Serine-threonine kinase and endoribonuclease; transmembrane protein that initiates the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p	2	2.982	0.3995	1542.27	1542.864	1	1349.4	76.92308	A.RWVSPTFPGIIVGL.F
gi|6321870|ref|NP_011946.1|	YHR079C	Serine-threonine kinase and endoribonuclease; transmembrane protein that initiates the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p	2	3.825	0.3306	1560.35	1560.864	1	939.7	69.230774	A.R4W2V1S1P1T1F1P1G1I1I1V1G1L1.F
gi|6321880|ref|NP_011956.1|	YHR088W	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p	2	4.2193	0.3798	2095.09	2097.254	1	816.8	59.375	E.T1I1N2K2E1V1E1G1D1E1D1D1L1M1R4Y1F1.N
gi|6321880|ref|NP_011956.1|	YHR088W	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p	3	5.255	0.423	2769.95	2767.954	1	1104	34.523808	T.R4V1Y1D1E1T1I1N2K2E1V1E1G1D1E1D1D1L1M1R4Y1F1.N
gi|6321880|ref|NP_011956.1|	YHR088W	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p	2	3.7455	0.2694	2766.89	2767.954	1	531.7	42.857143	T.R4V1Y1D1E1T1I1N2K2E1V1E1G1D1E1D1D1L1M1R4Y1F1.N
gi|6321880|ref|NP_011956.1|	YHR088W	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p	3	4.4292	0.2367	1714.64	1714.974	1	779.9	53.846157	L.T1F1I1H3L1P1E1G1P1T1F1Y1F1K2.L
gi|6321880|ref|NP_011956.1|	YHR088W	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, 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	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p	2	4.2997	0.2176	1713.79	1714.974	1	481	65.38461	L.T1F1I1H3L1P1E1G1P1T1F1Y1F1K2.L
gi|6321880|ref|NP_011956.1|	YHR088W	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p	2	3.3583	0.2938	2318.17	2319.458	1	388.8	47.22222	Y.DETINKEVEGDEDDLMRYF.N
gi|6321880|ref|NP_011956.1|	YHR088W	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent 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.D1E1T1I1N2K2E1V1E1G1D1E1D1D1L1M1R4Y1F1.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
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	3.258	0.3458	1441.23	1440.725	1	1195.5	77.27273	N.TKIPYFNAPIYL.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	2	4.7546	0.3155	2128.83	2126.46	1	522.3	58.823532	R.SINTKIPYFNAPIYLENK.T
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	3.7443	0.1504	1712.55	1711.014	2	894.8	73.07692	T.KIPYFNAPIYLENK.T
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	5.6138	0.3403	2019.13	2019.286	1	1479.5	71.875	R.S1I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1E1N2.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	5.1016	0.3628	1999.97	1998.286	1	1385.6	65.625	R.SINTKIPYFNAPIYLEN.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	4.2578	0.3684	1886.71	1884.182	1	1088.3	66.66667	R.SINTKIPYFNAPIYLE.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	3.4056	0.205	1482.19	1482.736	1	797.2	72.72727	T.K2I1P1Y1F1N2A1P1I1Y1L1E1.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	3.2631	0.2866	1455.61	1454.725	1	988.4	77.27273	N.T1K2I1P1Y1F1N2A1P1I1Y1L1.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	2.6751	0.1928	1440.17	1440.725	1	716.9	68.181816	N.TKIPYFNAPIYL.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	2	3.3653	0.292	1442.91	1440.725	2	801.9	68.181816	N.TKIPYFNAPIYL.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	2	4.3605	0.2969	2147.65	2149.46	1	506.6	58.823532	R.S1I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1E1N2K2.T
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	3	3.937	0.3091	2063.54	2061.382	1	1014.1	43.75	S.I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1E1N2K2.T
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	3.1488	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
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	4.459	0.4252	1772.99	1773.067	1	1017.6	67.85714	R.S1I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1.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	2	3.7351	0.4213	1753.37	1755.067	1	905.6	64.28571	R.SINTKIPYFNAPIYL.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	3.1975	0.2846	1468.57	1468.736	3	619.9	63.636364	T.KIPYFNAPIYLE.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	3.1332	0.2774	1583.35	1584.841	1	766.7	62.5	N.T1K2I1P1Y1F1N2A1P1I1Y1L1E1.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	3.5394	0.2591	1353.25	1352.62	1	1203.5	85	T.K2I1P1Y1F1N2A1P1I1Y1L1.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	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
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	3.2414	0.3617	1796.21	1797.104	1	548.9	50	S.INTKIPYFNAPIYLE.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	3.1136	0.2055	1683.75	1684.988	1	771.2	61.538464	S.I1N2T1K2I1P1Y1F1N2A1P1I1Y1L1.E
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	1	2.4498	0.3406	1227.37	1228.446	1	494.8	66.66667	S.VQWRVPLGLC.F
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	3	4.2947	0.3285	3257.15	3256.573	1	718.4	27.777779	A.SWVPVSKRGADYNADDLMHDDQPFYKSL.F
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	1	2.7881	0.3567	1330.77	1331.524	1	483.9	60.000004	N.S1V1Q2W2R4V1P1L1G1L1C1.F
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.0808	0.2446	1329.11	1331.524	1	647.3	70	N.S1V1Q2W2R4V1P1L1G1L1C1.F
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	1	2.7114	0.2588	1316.9	1315.524	1	464.7	60.000004	N.SVQWRVPLGLC.F
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.3881	0.1985	1155.25	1155.385	1	957.6	83.33333	N.SVQWRVPLGL.N
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.4626	0.2637	1170.05	1170.385	1	969.7	83.33333	N.S1V1Q2W2R4V1P1L1G1L1.C
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.2605	0.2624	1940.31	1941.163	1	801.4	60.000004	K.NYSNSVQWRVPLGLCF.A
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.8048	0.405	1228.33	1228.446	1	1426	94.44444	S.VQWRVPLGLC.F
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	1	2.5102	0.3299	1243.74	1243.446	1	373.2	61.11111	S.V1Q2W2R4V1P1L1G1L1C1.F
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.1667	0.1661	2299.39	2299.41	1	538	47.22222	K.R4G1A1D1Y1N2A1D1D1L1M1H3D1D1Q2P1F1Y1K2.S
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.7689	0.4607	1759.37	1759.968	1	908.7	69.230774	A.KVNKCPPDHPYIQY.E
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.2771	0.2994	1513.89	1512.634	1	938.4	68.181816	D.D1L1M1H3D1D1Q2P1F1Y1K2S1.L
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.0225	0.1869	1195.09	1194.308	1	700.7	81.25	L.M1H3D1D1Q2P1F1Y1K2.K
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.7522	0.1897	1533.67	1534.653	1	823.8	75	T.R4L1W2P1N2G1Q2D1Q2P1S1S1K2.G
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	1	2.3207	0.1759	1419.75	1418.558	1	329.5	55	N.KCPPDHPYIQY.E
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.7342	0.2666	1595.97	1596.792	1	851.1	70.83333	A.KVNKCPPDHPYIQ.Y
gi|6321886|ref|NP_011962.1|	YHR094C	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 is limiting; Hxt1p	2	3.2607	0.3043	1779.61	1779.968	1	486.9	57.692307	A.K2V1N2K2C1P1P1D1H3P1Y1I1Q2Y1.E
gi|6321886|ref|NP_011962.1|	YHR094C	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 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	3	3.9959	0.207	2033.12	2033.213	3	562.2	38.333332	L.S1H3N2P1R4Y1K2E1E1E1N2A1L1K2K2Y1.F
gi|6321906|ref|NP_011982.1|	YHR114W	SH3 domain protein implicated in the regulation of actin polymerization, able to recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p	2	4.1429	0.3036	2007.91	2009.199	1	728.8	58.823532	Y.V1Q2K2D1D1D1E1I1T1I1T1P1G1D1K2I1S1L1.V
gi|6321906|ref|NP_011982.1|	YHR114W	SH3 domain protein implicated in the regulation of actin polymerization, able to recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p	2	3.2827	0.4267	2364.29	2364.619	1	194.6	44.736843	Q.DFVYKPSPVWHDDEKFAVPS.S
gi|6321906|ref|NP_011982.1|	YHR114W	SH3 domain protein implicated in the regulation of actin polymerization, able to recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p	2	4.8505	0.2589	1761.35	1760.936	1	1731.4	70	Q.KDDDEITITPGDKISL.V
gi|6321906|ref|NP_011982.1|	YHR114W	SH3 domain protein implicated in the regulation of actin polymerization, able to recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p	2	3.2204	0.2734	2123.93	2125.354	1	233	52.941177	F.V1Y1K2P1S1P1V1W2H3D1D1E1K2F1A1V1P1S1.S
gi|6321906|ref|NP_011982.1|	YHR114W	SH3 domain protein implicated in the regulation of actin polymerization, able to 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	46.666668 N.E1T1K2L1K2F1P1T1L1P1E1V1P1T1F1F1.A
gi|6321924|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
gi|6321924|ref|NP_012000.1|	YHR132C	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required for normal cell wall assembly; Ecm14p	2	4.604	0.3316	2405.81	2405.715	1	757.4	55.263157 K.K2E1T1K2Y1L1D1D1L1D1F1L1V1I1P1V1F1N2P1D1.G
gi|6321924|ref|NP_012000.1|	YHR132C	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required for normal cell wall assembly; Ecm14p	2	3.0697	0.2927	2602.11	2602.943	2	318.7	33.333336 K.KETKYLDDLDFLVIPVFNPDGY.A
gi|6321924|ref|NP_012000.1|	YHR132C	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required for normal cell wall assembly; Ecm14p	2	4.1053	0.3672	2382.63	2382.715	1	580.8	50 K.KETKYLDDLDFLVIPVFNPD.G
gi|6321924|ref|NP_012000.1|	YHR132C	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required 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	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; Nsg1p	2	4.6197	0.4016	1833.67	1832.124	1	1418	70 K.NKIVAEPDMVPDWAVF.G
gi|6321925|ref|NP_012001.1|	YHR133C	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; Nsg1p	2	4.4893	0.3191	1380.85	1379.686	1	1499.9	87.5 T.KKEAALPPLGNKL.G
gi|6321925|ref|NP_012001.1|	YHR133C	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; Nsg1p	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	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting 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.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	3.5842	0.1778	2432.47	2431.699	2	339.8	50 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	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.D1L1I1Y1R4D1I1K2P1D1N2F1L1I1G1R4P1G1Q2P1D1A1N2.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.D1L1I1Y1R4D1I1K2P1D1N2F1L1I1G1R4P1G1Q2P1D1A1N2.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.V1I1D1L1L1G1P1S1L1E1D1L1F1D1W2C1G1R4K2F1.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.R4D1I1K2P1D1N2F1L1I1G1R4P1G1Q2P1D1A1N2.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.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	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.V1I1D1L1L1G1P1S1L1E1D1L1F1D1W2C1G1R4.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.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	4.3614	0.371	1903.99	1904.22	1	413.5	56.666668	L.KAPNNKQKYEKIGEKK.R
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.G1I1I1G1G1P1G1P1V1L1V1P1N2P1G1E1I1K2.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.Q2S1N2G1I1I1G1G1P1G1P1V1L1V1P1N2P1G1E1I1K2.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	45	T.QSNGIIGGPGPVLVPNPGEIK.E
gi|6321940|ref|NP_012016.1|	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	5.2321	0.4119	2346.51	2347.651	1	531.1	43.18182	T.Q2S1N2G1I1I1G1G1P1G1P1V1L1V1P1N2P1G1E1I1K2E1F1.T
gi|6321940|ref|NP_012016.1|	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	3.5823	0.2097	1738.55	1736.945	1	743.6	64.28571	K.A1K2K2D1E1E1V1F1T1L1D1P1I1V1N2.K
gi|6321940|ref|NP_012016.1|	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	2	5.1124	0.2402	1716.47	1715.046	1	1114.2	64.70589	N.GIIGGPGPVLVPNPGEIK.E
gi|6321940|ref|NP_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
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	3.0795	0.214	1515.62	1516.717	2	645.5	57.692307	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	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.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	2	2.9072	0.221	1250.37	1248.508	4	586.9	75	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	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	77.77778	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
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	2.9865	0.2872	1791.55	1793.141	2	614.9	53.333336	K.S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1.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	4.0486	0.2616	1702.73	1705.063	1	899.2	64.28571	S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1.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	4.0117	0.3204	1686.97	1688.063	1	792.8	64.28571	S.KTSPYVLPVPFLNVL.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	3.7602	0.3372	1380.29	1380.562	1	409.1	75	M.RDEDKSKWMGK.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	3.7392	0.2675	1697.29	1697.921	1	427.5	65.38461	L.EMRDEDKSKWMGKG.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	4.4164	0.2647	1659.97	1660.87	1	587	75	L.E1M1R4D1E1D1K2S1K2W2M1G1K2.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	3.7374	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
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	4.5047	0.3397	2969.53	2970.251	1	374.2	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	2	4.4603	0.4167	2938.53	2939.251	1	451.8	39.130436	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	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
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	4.468	0.386	2447.67	2448.694	1	591.1	52.63158	F.FKDGKYDLDFKNPESDKSKW.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	4.4323	0.1757	2845.37	2846.226	1	581.3	29.807693	L.A1D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1.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	3.244	0.2076	2296.31	2295.621	4	378.5	35.714287	S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1.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	5.4397	0.3309	2236.41	2237.569	1	1776.9	60.000004	S.K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1.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	4.043	0.3319	2613.53	2614.889	1	422.7	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	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.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	4.8109	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
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	5.7952	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 glycolysis 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.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	2.5545	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	30.000002	L.A1D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L1.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	25.862068	A.D1L1S1K2S1K2T1S1P1Y1V1L1P1V1P1F1L1N2V1L1N2G1G1S1H3A1G1G1A1L1.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	3.6069	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
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	2.3595	0.1623	1360.59	1361.667	4	444.2	59.090908	S.KTSPYVLPVPFL.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	4.744	0.3745	1501.41	1501.717	1	2279.1	80.769226	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	5.0579	0.2969	1514.75	1516.717	1	2284.9	84.61539	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	3	5.2894	0.3515	2364.89	2363.522	1	1119.6	44.444447	K.R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.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	2.996	0.1585	1471.81	1472.644	1	403.2	70	L.E1M1R4D1E1D1K2S1K2W2M1.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	2.9905	0.2143	1273.23	1273.429	2	725.2	75	L.LRIEEELGDKA.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	2.5924	0.2351	1287.43	1288.429	6	204.3	55	L.L1R4I1E1E1E1L1G1D1K2A1.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	2.4704	0.2491	1272.52	1273.429	8	223.6	55	L.LRIEEELGDKA.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	4.766	0.4775	2339.57	2339.522	1	903.3	43.055553	K.RYPIVSIEDPFAEDDWEAW.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	5.9392	0.3854	2362.09	2363.522	1	882.3	52.77778	K.R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2.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	4.0629	0.3628	1639.77	1640.87	1	463.3	66.66667	L.EMRDEDKSKWMGK.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	5.013	0.3992	2326.43	2327.517	1	628.6	52.77778	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	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
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	4.3851	0.4905	2514.13	2515.782	1	827.6	52.499996	F.KDGKYDLDFKNPESDKSKWLT.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	4.9037	0.4123	2541.91	2543.782	1	770.9	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	5.3112	0.3815	2193.56	2195.414	1	1247.4	42.647057	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	4.2156	0.3455	2170.73	2171.414	1	887.9	52.941177	D.GKYDLDFKNPESDKSKWL.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	5.0011	0.3846	2475.79	2475.694	1	770.1	52.63158	F.F1K2D1G1K2Y1D1L1D1F1K2N2P1E1S1D1K2S1K2W2.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	4.4404	0.3026	2690.73	2691.959	1	512.9	42.857143	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	2	4.2362	0.3683	2662.07	2662.959	1	364.4	42.857143	F.FKDGKYDLDFKNPESDKSKWLT.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	4.3058	0.2431	2665.16	2662.959	1	744.7	34.523808	F.FKDGKYDLDFKNPESDKSKWLT.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	4.0784	0.2714	2596.58	2595.871	1	1301.3	38.75	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	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
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	5.3024	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.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	4.2537	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.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	4.0003	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	19.166666	M.K2R4Y1P1I1V1S1I1E1D1P1F1A1E1D1D1W2E1A1W2S1H3F1F1K2T1A1G1I1Q2I1.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.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	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; Eno2p	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

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	4.7856	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.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	3	4.5596	0.2617	2625.08	2625.889	1	628.9	35	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	4.2446	0.3172	2598.83	2598.889	1	360.7	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	2	3.0634	0.2207	1690.57	1691.023	1	607.3	60.714287	S.KSKTSPYVLPVPFLN.V
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.8127	0.1962	1475.37	1474.698	1	795	70.83333	F.D1D1V1D1G1K2P1L1V1E1K2I1M1.D

gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.4875	0.3747	1762.33	1764.97	1	532.9	53.333336	F.D1D1V1D1G1K2P1L1V1E1K2I1M1D1T1A1.G
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	5.2902	0.2985	3036.77	3037.44	1	1251.7	35.576923	S.KVLPGPEVPKDAVKDREQFVDDLEQAL.Y
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.4564	0.2315	3070.61	3072.44	5	386.1	28.846153	S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1L1.Y
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.3497	0.2772	2646.47	2647.793	1	327.6	30.000002	S.G1V1S1G1G1E1E1G1A1R4Y1G1P1S1L1M1P1G1G1S1E1E1A1W2P1H3.I
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	4.707	0.4091	2332.85	2334.547	1	814.1	57.894737	F.R4V1L1P1E1C1A1S1D1N2L1P1V1D1K2D1I1H3I1N2.W
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.2214	0.25	2827.47	2828.106	1	316.8	35.416664	K.V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1.L
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	6.2206	0.4175	2910.68	2912.112	1	955.4	33.333336	L.L1E1K2G1D1I1I1I1D1G1G1N2S1H3F1P1D1S1N2R4R4Y1E1E1L1.K
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.4146	0.2404	2958.53	2958.28	9	340.3	30.000002	S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1.L
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	4.1599	0.2549	3073.88	3072.44	1	627.2	27.884615	S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1L1.Y
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.9361	0.3475	2922.83	2924.28	1	463.3	34	S.KVLPGPEVPKDAVKDREQFVDDLEQA.L
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	5.882	0.4334	2957.3	2958.28	1	1480	36	S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1.L
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	4.4042	0.4926	1877.03	1878.179	1	717.7	65.625	S.KVLPGPEVPKDAVKDRE.Q
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	4.1027	0.1985	3260.12	3260.634	1	430.8	26.85185	L.LEKGDIIIDGGNSHFPDSNRRYEELKKK.G
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	4.4706	0.2061	2852.9	2853.202	1	1496.7	37.5	S.KVLPGPEVPKDAVKDREQFVDDLEQ.A
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	2.9447	0.1838	2923.21	2924.28	9	330.2	30.000002	S.KVLPGPEVPKDAVKDREQFVDDLEQA.L
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	5.2671	0.3435	2922.41	2924.28	4	622.2	29	S.KVLPGPEVPKDAVKDREQFVDDLEQA.L
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.2328	0.1553	2883.67	2886.202	4	353	31.25	S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2.A
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	4.7859	0.4013	2884.76	2886.202	1	1038.6	33.333336	S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2.A
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	2	3.5652	0.3316	2623.91	2625.955	1	387.5	38.636364	S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1.E
gi|6321977|ref|NP_012053.1|	YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	3	5.5293	0.392	2960.42	2958.28	1	867.8	34	S.K2V1L1P1G1P1E1V1P1K2D1A1V1K2D1R4E1Q2F1V1D1D1L1E1Q2A1.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	1	2.925	0.2218	1250.45	1250.394	1	457.4	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	3.182	0.1993	2135.57	2137.345	1	425.4	47.058823	L.D1T1I1E1D1D1M1S1I1E1H3D1L1K2I1D1L1L1.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	3.6724	0.345	2633.75	2635.065	2	370.7	38.095238	F.MEEMYQDKLPPNVKPNETPIFL.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	4.2945	0.2972	2660.29	2662.065	1	406.9	40.476192	F.M1E1E1M1Y1Q2D1K2L1P1P1N2V1K2P1N2E1T1P1I1F1L1.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	4.5556	0.3593	2245.61	2245.642	1	701.8	55.555557	E.MYQDKLPPNVKPNETPIFL.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	3	3.9962	0.1771	2903.21	2904.119	1	597.1	29.545454	K.VKERSRYDDELVPTQQEEEYKFN.M
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	3.1595	0.1685	2481.59	2483.771	1	879.1	47.5	L.R4A1L1D1T1I1E1D1D1M1S1I1E1H3D1L1K2I1D1L1L1.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	3	4.4714	0.2073	1719.68	1719.031	4	897.8	50	H.KLKPEYQEVIKEIT.E
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	4.0409	0.3484	2267.53	2267.623	1	492.1	61.11111	M.Y1Q2D1K2L1P1P1N2V1K2P1N2E1T1P1I1F1L1K2.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	3.2372	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.K2L1K2P1E1Y1Q2E1V1I1K2E1I1T1E1K2M1.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.K2L1P1P1N2V1K2P1N2E1T1P1I1F1L1.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	3.4612	0.3623	1709.57	1708.054	1	400.7	53.571426	D.KLPPNVKPNETPIFL.K
gi|6321997|ref|NP_012073.1|	YHR203C	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has 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	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has similarity to rat S4 ribosomal protein; Rps4bp	1	2.6893	0.2608	1317.04	1315.642	1	344.7	60.000004	H.KLRESLPLIVF.L
gi|6321997|ref|NP_012073.1|	YHR203C	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has similarity to rat S4 ribosomal protein; Rps4bp	2	3.9034	0.4305	1375.23	1375.434	1	778	70.83333	L.S1G1C1Y1A1P1R4P1S1A1G1P1H3.K
gi|6321997|ref|NP_012073.1|	YHR203C	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has similarity to rat S4 ribosomal protein; Rps4bp	1	2.9112	0.2271	1329.79	1330.642	2	356.8	60.000004	H.K2L1R4E1S1L1P1L1I1V1F1.L
gi|6321997|ref|NP_012073.1|	YHR203C	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has similarity to rat S4 ribosomal protein; Rps4bp	3	4.844	0.3033	1394.24	1394.576	1	3840.1	77.27273	E.RHDGGFDLVHIK.D
gi|6322000|ref|NP_012076.1|	YHR206W	Nuclear response regulator and transcription factor, part of a branched two-component signaling system; required for optimal induction of heat-shock genes in response to oxidative stress; involved in osmoregulation; Skn7p	2	4.0246	0.3497	1599.45	1599.748	1	688.9	72.72727	Q.SWEFQHPEFRVH.Y
gi|6322000|ref|NP_012076.1|	YHR206W	Nuclear response regulator and transcription factor, part of a branched two-component signaling system; required for optimal induction of heat-shock genes in response to oxidative stress; involved in osmoregulation; Skn7p	2	2.9466	0.348	1621.81	1620.748	1	364.7	54.545456	Q.S1W2E1F1Q2H3P1E1F1R4V1H3.Y
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	3.3179	0.2579	1359.37	1356.564	1	988.2	77.27273	A.VVSPIKEIGWNN.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	2.9471	0.2053	1445.51	1444.643	4	522.5	62.5	A.A1V1V1S1P1I1K2E1I1G1W2N2N2.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	3.3704	0.3561	1409.31	1409.533	1	623	72.72727	S.A1A1R4I1C1L1P1T1F1E1S1E1.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	3.677	0.2376	2483.97	2485.674	3	242.7	41.666664	A.R4D1K2L1D1P1Q2E1W2D1I1N2E1R4Y1Y1T1I1T1.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	4.0378	0.2679	2456.53	2456.674	1	285.8	44.444447	A.RDKLDPQEWDINERYYTIT.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	3	4.3978	0.3699	3120.41	3121.481	1	597.9	31.48148	A.V1V1S1P1I1K2E1I1G1W2N2N2E1D1I1H3V1P1L1L1P1G1E1Q2C1G1A1L1.T
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	3.7371	0.2761	3120.79	3121.481	1	275	27.777779	A.V1V1S1P1I1K2E1I1G1W2N2N2E1D1I1H3V1P1L1L1P1G1E1Q2C1G1A1L1.T
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	1	2.4314	0.2151	1383.62	1384.629	1	543.3	54.166668	K.K2E1L1V1T1A1P1L1D1G1T1I1L1.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	3	4.8311	0.4316	3085.43	3086.481	1	615.7	32.407406	A.VVSPIKEIGWNNEDIHVPLLPGEQCGAL.T
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	3.4672	0.2953	3120.37	3121.481	1	239.7	27.777779	A.V1V1S1P1I1K2E1I1G1W2N2N2E1D1I1H3V1P1L1L1P1G1E1Q2C1G1A1L1.T
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	3	4.897	0.2874	3123.74	3121.481	1	701.2	33.333336	A.V1V1S1P1I1K2E1I1G1W2N2N2E1D1I1H3V1P1L1L1P1G1E1Q2C1G1A1L1.T

gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	3.5458	0.2236	2526.43	2527.753	2	223.4	39.473686 L.ARDKLDPQEWDINERYYTIT.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	2	3.4653	0.3816	1374.27	1372.564	1	1317.8	81.818184 A.V1V1S1P1I1K2E1I1G1W2N2N2.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	1	2.4434	0.1876	1371.43	1372.564	2	222.3	54.545456 A.V1V1S1P1I1K2E1I1G1W2N2N2.E
gi|6322002|ref|NP_012078.1|	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine 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.E1E1E1E1S1K2L1A1P1I1S1T1P1E1V1P1K2K2K2I1K2.T
gi|6322180|ref|NP_012255.1|	YIL010W	Nuclear thiol peroxidase which functions as an alkyl-hydroperoxide reductase during 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	Nuclear thiol peroxidase which functions as an alkyl-hydroperoxide reductase during 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	Nuclear thiol peroxidase which functions as an alkyl-hydroperoxide reductase during post-diauxic growth; Dot5p	3	3.9263	0.2994	2406.47	2407.772	1	381	40 L.E1E1E1E1S1K2L1A1P1I1S1T1P1E1V1P1K2K2K2I1K2.T
gi|6322163|ref|NP_012238.1|	YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	2	3.3408	0.1541	2290.25	2291.426	5	215.4	36.842106 Q.L1E1R4V1A1D1E1D1A1N2L1N2D1L1P1E1T1G1F1F1.E
gi|6322163|ref|NP_012238.1|	YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	2	3.8825	0.4056	2264.53	2266.426	1	680.8	55.263157 Q.LERVADEDANLNDLPETGFF.E
gi|6322163|ref|NP_012238.1|	YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	2	3.3804	0.1873	1678.15	1676.82	1	827.2	65.38461 L.GRDYPIEVDEELLQ.L
gi|6322163|ref|NP_012238.1|	YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	2	3.3418	0.2446	1934.47	1937.156	2	330.7	40 L.GRDYPIEVDEELLQLF.L
gi|6322163|ref|NP_012238.1|	YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	2	3.7013	0.2218	1696.23	1694.82	4	779.3	65.38461 L.G1R4D1Y1P1I1E1V1D1E1E1L1L1Q2.L
gi|6322163|ref|NP_012238.1|	YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	2	3.6659	0.2589	1397.25	1396.67	1	792.2	75 R.VIKEKFDEFIK.T
gi|6322163|ref|NP_012238.1|	YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	2	4.22	0.3323	2534.11	2531.888	1	584.3	45 L.F1K2K2I1V1D1D1T1I1M1E1N2P1E1P1N2K2K2N2I1Q2.K
gi|6322163|ref|NP_012238.1|	YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	2	4.0184	0.2582	2502.53	2502.888	1	627.6	47.5 L.FKKIVDDTIMENPEPNKKNIQ.K
gi|6322159|ref|NP_012234.1|	YIL030C	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation; Ssm4p	3	5.0853	0.4095	3727.37	3728.838	1	705.2	25.80645 T.L1D1E1H3A1V1D1E1N2E1V1E1E1V1E1H3D1I1P1E1R4D1I1N2N2A1P1V1N2N2I1N2.N
gi|6322159|ref|NP_012234.1|	YIL030C	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation; Ssm4p	3	4.8781	0.3055	3899.63	3899.047	1	356.1	21.969696 Q.NTLDEHAVDENEVEEVEHDIPERDINNAPVNNIN.N
gi|6322159|ref|NP_012234.1|	YIL030C	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation; Ssm4p	3	5.0889	0.3712	3633.08	3633.919	1	519.7	25 Q.QNAINRPNAPVFIPPPAQNRAGNVDQDEQDFGAA.V
gi|6322159|ref|NP_012234.1|	YIL030C	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation; Ssm4p	2	3.1101	0.1815	1613.23	1613.981	1	1125.5	69.230774 M.FVPVTKDDKLLKPL.D
gi|6322159|ref|NP_012234.1|	YIL030C	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation; Ssm4p	3	4.2934	0.2961	3733.85	3733.051	1	442.6	25.735294 Q.QNAINRPNAPVFIPPPAQNRAGNVDQDEQDFGAAV.G
gi|6322159|ref|NP_012234.1|	YIL030C	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation; Ssm4p	2	4.0155	0.3659	1541.55	1542.732	1	841	69.230774 M.M1L1D1G1S1S1P1Y1P1G1D1F1L1K2.S
gi|6322159|ref|NP_012234.1|	YIL030C	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 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	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation; Ssm4p	3	4.9056	0.4192	3612.44	3614.678	1	688.2	25.833332 L.D1E1H3A1V1D1E1N2E1V1E1E1V1E1H3D1I1P1E1R4D1I1N2N2A1P1V1N2N2I1N2.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.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	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.Y1E1I1T1L1P1R4E1F1Y1D1M1D1.Q
gi|6322148|ref|NP_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
gi|6322148|ref|NP_012223.1|	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles; Gvp36p	2	4.3596	0.3304	2340.19	2341.468	1	879.5	52.499996 N.S1F1A1E1E1P1E1A1K2P1E1V1A1E1E1E1K2P1Q2T1A1.I
gi|6322148|ref|NP_012223.1|	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi 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	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles; Gvp36p	2	4.6041	0.2618	2532.77	2533.813	1	873.1	52.499996 T.D1I1S1Q2L1P1R4E1Y1T1E1L1E1D1K2V1D1T1I1K2L1.I
gi|6322148|ref|NP_012223.1|	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles; Gvp36p	3	4.4947	0.1945	2280.41	2278.565	1	1130.5	43.055553 I.SQLPREYTELEDKVDTIKL.I
gi|6322148|ref|NP_012223.1|	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles; Gvp36p	3	5.5928	0.2148	2509.31	2506.813	6	1089.6	35 T.DISQLPREYTELEDKVDTIKL.I
gi|6322148|ref|NP_012223.1|	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles; Gvp36p	2	4.3644	0.2231	2531.63	2533.813	4	494.5	42.5 T.D1I1S1Q2L1P1R4E1Y1T1E1L1E1D1K2V1D1T1I1K2L1.I
gi|6322148|ref|NP_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.D1I1S1Q2L1P1R4E1Y1T1E1L1E1D1K2V1D1T1I1K2L1.I
gi|6322148|ref|NP_012223.1|	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles; Gvp36p	2	4.3608	0.2675	2533.69	2533.813	1	609.6	45 T.D1I1S1Q2L1P1R4E1Y1T1E1L1E1D1K2V1D1T1I1K2L1.I
gi|6322148|ref|NP_012223.1|	YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi 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
gi|6322146|ref|NP_012221.1|	YIL043C	cytochrome b reductase; Cbr1p	2	3.048	0.243	1521.57	1520.71	1	530.7	60.714287 F.G1L1P1H3A1D1D1V1L1G1L1P1I1G1Q2.H
gi|6322146|ref|NP_012221.1|	YIL043C	cytochrome b reductase; Cbr1p	2	4.368	0.4317	1661.45	1660.852	1	1413.9	73.333336 F.G1L1P1H3A1D1D1V1L1G1L1P1I1G1Q2H3.I
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
gi|6322146|ref|NP_012221.1|	YIL043C	cytochrome b reductase; Cbr1p	1	3.1929	0.417	1520.54	1520.71	2	215.8	42.857143 F.G1L1P1H3A1D1D1V1L1G1L1P1I1G1Q2.H
gi|6322146|ref|NP_012221.1|	YIL043C	cytochrome b reductase; Cbr1p	2	3.1828	0.3466	1639.17	1639.852	1	904	63.333332 F.GLPHADDVLGLPIGQH.I
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	3	5.875	0.3765	4125.8	4124.476	1	522.1	22.142857 K.F1A1P1D1F1A1D1E1E1Y1V1N2K2L1E1G1E1I1P1E1K2Y1G1E1H3S1I1E1V1P1G1A1V1K2L1C1.N
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	1	2.2379	0.158	926.32	925.993	1	116.9	64.28571 K.N2H3E1S1I1R4V1G1.E
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	3.9669	0.3871	2084.85	2085.302	1	361.8	50 Y.L1K2G1R4N2G1L1G1F1P1I1N2E1Q2D1P1S1K2S1.K
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	4.2314	0.4163	2056.77	2058.302	1	723	63.88889 Y.LKGRNGLGFPINEQDPSKS.K
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	4.4344	0.2855	1654.55	1656.891	1	1168.1	73.07692 N.D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2.G
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	4.2492	0.2665	1830.43	1831.047	1	661.9	56.666668 A.N2D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2G1.R
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	3.2412	0.393	1712.35	1714.943	2	227.4	57.14286 N.D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2G1.R
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	5.4071	0.4017	1852.59	1851.017	1	1893.8	82.14286 E.T1D1E1V1E1L1I1F1D1D1Y1L1Y1A1K2.D
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	4.3728	0.3627	1837.81	1835.017	1	1986.8	82.14286 E.TDEVELIFDDYLYAK.D
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	4.3948	0.2554	1845.75	1845.074	1	742.3	63.333332 T.A1N2D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2.G
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	2	4.0476	0.3628	1774.43	1772.995	1	794.7	67.85714 A.N2D1V1K2Q2G1K2P1H3P1E1P1Y1L1K2.G
gi|6322136|ref|NP_012211.1|	YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol 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

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	4.3271	0.3787	1531.51	1529.739	1	1232.1	79.16667	T.RELVYHGPPFSNL.D
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	3.8829	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.S1L1P1E1D1E1L1I1E1K2I1K2D1V1H3.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.S1A1I1D1V1L1D1P1L1T1K2D1P1V1D1F1V1R4Q2.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.CTHDQIESEIENIFNFL.Q
gi|14318437|ref|NP_116578.1|	YIL078W	Threonyl-tRNA synthetase, essential cytoplasmic protein; Ths1p	2	4.4276	0.229	2134.85	2132.251	1	881.7	59.375	F.C1T1H3D1Q2I1E1S1E1I1E1N2I1F1N2F1L1.Q
gi|14318437|ref|NP_116578.1|	YIL078W	Threonyl-tRNA synthetase, essential cytoplasmic protein; Ths1p	2	2.9681	0.2577	1734.37	1735.811	6	213.6	50	F.CTHDQIESEIENIF.N
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.354	0.2195	1938.67	1940.108	1	641.6	44.444447	N.V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.5973	0.4371	2288.45	2289.516	1	815.2	47.727272	S.ANVGPEIVIGEPCHGSAPDIAGK.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	2.9573	0.2401	2561.53	2561.984	2	211.7	31.25	L.T1I1G1L1I1P1G1D1G1I1G1K2E1V1I1P1A1G1K2Q2V1L1E1N2L1.N
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for 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
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.5101	0.2617	2222.73	2220.496	1	566.5	44.444447	F.REPQCFDVIVAPNLYGDIL.S
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	5.2742	0.3944	1908.73	1909.26	1	1424.2	71.875	V.K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1R4.E
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.1086	0.1947	2180.57	2181.533	1	486.4	50	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for 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	23.648647	L.G1V1V1P1S1A1N2V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1G1K2G1I1A1N2P1I1A1T1I1R4.S
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	3	4.8009	0.3074	2178.83	2181.533	1	1757.1	46.05263	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.0179	0.2992	2365.73	2366.825	1	415.1	42.857143	F.ANVRPVKSVEGEKGKPIDMVIV.R
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.423	0.2246	1644.75	1646.863	1	667	67.85714	F.Q2E1T1G1K2A1L1P1D1E1T1V1K2V1L1.K
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.686	0.3548	1742.95	1741.917	1	593	53.125	E.I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1G1K2.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	5.6162	0.4749	2129.07	2128.334	1	1384.9	60.000004	N.V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1G1K2.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.9697	0.4761	2103.49	2104.334	1	800.5	55	N.VGPEIVIGEPCHGSAPDIAGK.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.6526	0.4846	2243.19	2244.438	1	586.7	42.857143	A.N2V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1G1K2.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.7443	0.4349	2217.71	2218.438	1	529.9	40.476192	A.NVGPEIVIGEPCHGSAPDIAGK.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for 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

gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	3	3.8665	0.3782	1885.73	1886.26	1	1119.6	42.1875	V.KSVEGEKGKPIDMVIVR.E
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	3	5.0447	0.2884	2181.14	2181.533	1	1723.4	46.05263	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.3957	0.2179	2179.93	2181.533	1	424.9	47.368423	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.5496	0.2217	2107.79	2109.454	2	403.4	44.444447	A.N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.4625	0.3164	2395.13	2395.825	1	557.4	47.61905	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1.R
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.3189	0.2628	1554.17	1553.691	3	432.7	53.571426	E.I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.3992	0.4258	2032.25	2033.212	1	675.5	47.368423	A.NVGPEIVIGEPCHGSAPDIA.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.2541	0.4656	2128.11	2128.29	1	849.2	50	S.A1N2V1G1P1E1I1V1I1G1E1P1C1H3G1S1A1P1D1I1A1.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.9165	0.3679	2103.57	2104.29	1	667	45	S.ANVGPEIVIGEPCHGSAPDIA.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.9164	0.2817	1267.67	1268.513	1	691.7	70.83333	S.L1T1I1G1L1I1P1G1D1G1I1G1K2.E
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	1	3.5906	0.39	1268.65	1268.513	1	478.7	66.66667	S.L1T1I1G1L1I1P1G1D1G1I1G1K2.E
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	2.9776	0.3247	1652.11	1650.956	2	289.7	53.125	L.TIGLIPGDGIGKEVIPA.G
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.2447	0.2597	1568.27	1569.678	1	718.4	66.66667	L.SQSDGLFREICKE.V
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.6608	0.2719	1747.81	1749.073	3	250.3	50	V.K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1.R
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	3	4.4504	0.299	1909.31	1909.26	1	890.7	42.1875	V.K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1R4.E
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.4739	0.2173	2079.99	2081.4	1	552.6	55.555557	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1.V
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.0392	0.2447	2179.85	2181.533	1	561.5	50	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	3	5.1202	0.3234	2178.68	2181.533	1	1331	46.05263	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.1776	0.3274	2152.49	2154.533	1	630.7	52.63158	F.ANVRPVKSVEGEKGKPIDMV.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.0982	0.1909	1948.43	1949.208	1	313.8	47.058823	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1.M
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	3	4.0195	0.2182	2109.56	2109.454	2	535.1	37.5	A.N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	3.1195	0.3066	2083.01	2083.454	1	417.9	47.22222	A.NVRPVKSVEGEKGKPIDMV.I
gi|6322097|ref|NP_012172.1|	YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	2	4.5248	0.3947	2554.77	2556.012	1	418.9	43.18182	F.A1N2V1R4P1V1K2S1V1E1G1E1K2G1K2P1I1D1M1V1I1V1R4.E
gi|6322086|ref|NP_012161.1|	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	3	4.632	0.385	3312.26	3310.754	1	959.1	36.53846	N.VDPQFEWDNFISRDPNFLLPNLPMRTF.K
gi|6322086|ref|NP_012161.1|	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	2	3.4895	0.176	2032.61	2032.411	7	396.6	53.125	F.ISRDPNFLLPNLPMRTF.K
gi|6322086|ref|NP_012161.1|	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	2	3.8831	0.1579	1629.27	1627.942	1	1264.5	76.92308	F.ISRDPNFLLPNLPM.R
gi|6322086|ref|NP_012161.1|	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	3	5.6883	0.4482	3481.01	3480.858	1	720.5	27.777779	F.N2V1D1P1Q2F1E1W2D1N2F1I1S1R4D1P1N2F1L1L1P1N2L1P1M$R4T1F1.K
gi|6322086|ref|NP_012161.1|	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	3	4.3104	0.3197	3443.36	3440.858	1	1073.5	32.407406	F.NVDPQFEWDNFISRDPNFLLPNLPM@RTF.K

gi|6322086|ref|NP_012161.1|	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	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 Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	3	4.7194	0.3333	3349.37	3348.754	1	547.9	28.846153	N.V1D1P1Q2F1E1W2D1N2F1I1S1R4D1P1N2F1L1L1P1N2L1P1M1R4T1F1.K
gi|6322086|ref|NP_012161.1|	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	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 Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	2	3.463	0.2161	2492.41	2493.816	1	343.6	42.105263	Q.F1E1W2D1N2F1I1S1R4D1P1N2F1L1L1P1N2L1P1M1.R
gi|6322086|ref|NP_012161.1|	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	2	3.3337	0.1855	2465.85	2466.816	1	435.7	47.368423	Q.FEWDNFISRDPNFLLPNLPM.R
gi|6322083|ref|NP_012158.1|	YIL108W	Putative metalloprotease; Yil108wp	2	3.0876	0.1802	2218.15	2216.414	1	417.2	50	N.S1T1G1A1S1P1P1I1F1P1K2E1E1C1T1W2N2R4L1.D
gi|6322083|ref|NP_012158.1|	YIL108W	Putative metalloprotease; Yil108wp	3	4.5239	0.2807	2237.99	2239.528	1	781.3	38.88889	K.T1V1Q2V1Q2H3P1Q2L1P1P1I1T1Y1P1I1H3N2Q2.F
gi|6322083|ref|NP_012158.1|	YIL108W	Putative metalloprotease; Yil108wp	2	4.9313	0.4218	2238.47	2239.528	1	815.8	52.77778	K.T1V1Q2V1Q2H3P1Q2L1P1P1I1T1Y1P1I1H3N2Q2.F
gi|6322083|ref|NP_012158.1|	YIL108W	Putative metalloprotease; Yil108wp	2	3.6205	0.2451	2202.27	2203.513	1	541.1	44.11765	Q.V1Q2H3P1Q2L1P1P1I1T1Y1P1I1H3N2Q2F1F1.K
gi|6322083|ref|NP_012158.1|	YIL108W	Putative metalloprotease; Yil108wp	2	3.1926	0.2552	1906.43	1907.16	1	521.5	50	Q.V1Q2H3P1Q2L1P1P1I1T1Y1P1I1H3N2Q2.F
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	3.605	0.219	2186.37	2187.376	1	425.6	50	Y.Q2H3L1Y1D1D1I1D1P1P1P1L1N2E1D1G1L1I1V1.R
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	3.8209	0.3672	2326.59	2326.555	1	241.9	36.842106	Y.FKIPLDSENNEESADQINMM.D
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	3.6807	0.3314	1830.37	1831.081	1	546.3	63.333332	H.FYPGFSGKNPNDIVKF.S
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	3.8046	0.4023	2178.33	2179.378	1	424.4	47.22222	F.KIPLDSENNEESADQINMM.D
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	3.1645	0.2089	2350.55	2351.555	1	362.2	39.473686	Y.F1K2I1P1L1D1S1E1N2N2E1E1S1A1D1Q2I1N2M1M1.D
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	3	4.1436	0.3114	2323.04	2320.564	1	777.3	46.05263	Y.QHLYDDIDPPPLNEDGLIVR.C
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	3.4252	0.351	2222.01	2223.458	1	397.4	50	G.Q2T1H3F1Y1P1G1F1S1G1K2N2P1N2D1I1V1K2F1.S
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	3.161	0.3564	2197.69	2197.458	1	341	50	G.QTHFYPGFSGKNPNDIVKF.S
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	4.61	0.4688	2201.33	2203.378	1	1142	61.11111	F.K2I1P1L1D1S1E1N2N2E1E1S1A1D1Q2I1N2M1M1.D
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	3.0054	0.158	970.01	970.205	1	886.7	92.85714	L.L1T1K2I1P1Q2I1F1.Q
gi|6322082|ref|NP_012157.1|	YIL109C	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; Sec24p	2	4.6898	0.511	1848.19	1851.081	1	528.9	63.333332	H.F1Y1P1G1F1S1G1K2N2P1N2D1I1V1K2F1.S
gi|6322077|ref|NP_012152.1|	YIL114C	Putative mitochondrial porin (voltage-dependent anion channel), related to Por1p but not required for mitochondrial membrane permeability or mitochondrial osmotic stability; Por2p	1	3.3795	0.2348	1408.54	1408.559	2	292	70	L.FNRDFFHTNPL.S
gi|6322077|ref|NP_012152.1|	YIL114C	Putative mitochondrial porin (voltage-dependent anion channel), related to Por1p but not required for mitochondrial membrane permeability or mitochondrial osmotic stability; Por2p	2	3.0883	0.1853	1427.61	1426.559	3	491.7	70	L.F1N2R4D1F1F1H3T1N2P1L1.S
gi|6322077|ref|NP_012152.1|	YIL114C	Putative mitochondrial porin (voltage-dependent anion channel), related to Por1p but not required for mitochondrial membrane permeability or mitochondrial osmotic stability; Por2p	1	2.9671	0.2375	1425.58	1426.559	1	162.2	70	L.F1N2R4D1F1F1H3T1N2P1L1.S
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	2	3.1835	0.2989	2006.47	2007.114	1	636.6	53.125	T.S1S1I1I1R4E1N2D1F1E1D1E1L1A1E1S1M1.Q
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	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.S1Y1L1N2R4A1P1I1L1V1L1P1T1.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

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	2	3.3725	0.2066	1476.07	1474.756	2	555.5	70.83333	K.S1Y1L1N2R4A1P1I1L1V1L1P1T1.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	2	4.3178	0.2347	1788.01	1788.933	3	333.5	60.714287	R.S1K2L1L1E1E1H3D1N2D1L1N2L1V1Q2.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	3	3.8381	0.2991	2046.8	2047.253	7	402.6	29.411766	R.T1E1S1V1K2P1E1P1E1I1T1A1P1P1H3S1R4F1.S
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	3	4.0847	0.2672	1900.34	1903.111	1	1073.4	43.75	E.S1V1K2P1E1P1E1I1T1A1P1P1H3S1R4F1S1.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	2	3.9691	0.3944	1813.01	1815.032	1	1103	73.333336	E.S1V1K2P1E1P1E1I1T1A1P1P1H3S1R4F1.S
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	2	4.0109	0.3573	1904.09	1903.111	1	1138.1	68.75	E.S1V1K2P1E1P1E1I1T1A1P1P1H3S1R4F1S1.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	2	3.9547	0.3318	1734.11	1735.076	3	599.6	50	K.S1Y1L1N2R4A1P1I1L1V1L1P1T1V1R4.K
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	3	4.3189	0.1618	1734.8	1735.076	4	1092.4	50	K.S1Y1L1N2R4A1P1I1L1V1L1P1T1V1R4.K
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	2.7616	0.2513	1343.49	1344.437	4	393.5	55	S.L1H3L1D1N2P1D1Y1E1T1L1.E
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	2	4.0159	0.3386	1830.13	1830.958	1	1197.1	71.42857	S.I1I1R4E1N2D1F1E1D1E1L1A1E1S1M1.Q
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	2	3.8584	0.3172	1917.25	1919.036	1	701.5	50	S.S1I1I1R4E1N2D1F1E1D1E1L1A1E1S1M1.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.K2L1D1I1S1K2P1E1E1I1V1T1F1.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	2	4.3531	0.2196	1520.39	1519.778	1	1326.2	79.16667	Y.KLDISKPEEIVTF.S
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	4.5465	0.3422	2125.65	2124.281	1	1654.8	71.875	L.RDSLNSYPNLEEIVWCQ.E
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	3.7302	0.3418	2236.23	2237.44	1	639.9	50	Q.LRDSLNSYPNLEEIVWCQ.E
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	5.0315	0.4001	1996.45	1996.15	1	1139.8	70	L.RDSLNSYPNLEEIVWC.Q
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	2.9816	0.186	1836.79	1836.011	1	532.7	57.14286	L.RDSLNSYPNLEEIVW.C
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	4.5339	0.4899	2436.45	2436.65	1	781.7	47.368423	F.AQLRDSLNSYPNLEEIVWCQ.E
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	3.1592	0.2546	2260.61	2262.44	3	402.6	41.17647	Q.L1R4D1S1L1N2S1Y1P1N2L1E1E1I1V1W2C1Q2.E
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	3.1764	0.4363	2023.45	2024.114	1	617.8	50	L.SLPHGYDGQGPEHSSGRLE.R
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	5.0714	0.461	1728.71	1726.97	1	1723.7	82.14286	Q.WIIEDIEHGKSIGTK.E
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	3	4.1519	0.2605	1789.22	1788.057	1	1358.4	45	K.HDLDKEINLGPGILPR.F
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	4.5378	0.4275	1790.55	1788.057	1	963.8	63.333332	K.HDLDKEINLGPGILPR.F
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	4.4313	0.3598	2659.49	2660.04	1	991.2	45.652176	F.KSPKELATEILPHEPTNVPESTLK.E
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	3	4.7847	0.3608	2659.49	2660.04	1	1033.8	32.608696	F.KSPKELATEILPHEPTNVPESTLK.E
gi|6322066|ref|NP_012141.1|	YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	2	5.4951	0.4317	2002.31	2003.309	1	2112.6	67.64706	F.SKHDLDKEINLGPGILPR.F
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	3.9545	0.4405	2637.39	2638.761	1	615	47.61905	L.HGEEVQPITDEEREKTDYYEVA.H

gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	4.5043	0.2797	2667.43	2667.761	1	369.8	40.476192	L.H3G1E1E1V1Q2P1I1T1D1E1E1R4E1K2T1D1Y1Y1E1V1A1.H
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	3.3067	0.2903	2720.13	2721.944	1	520.9	36.95652	C.N2H3P1F1V1F1D1E1V1E1G1V1V1N2P1S1R4G1N2S1D1L1L1F1.R
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	3	4.0873	0.2092	2555.39	2556.836	2	463.9	34.090908	T.TVLENNDGKRAEEKPESKSPAKK.T
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	3	5.0873	0.4319	2666.45	2667.761	1	907.4	35.714287	L.H3G1E1E1V1Q2P1I1T1D1E1E1R4E1K2T1D1Y1Y1E1V1A1.H
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	4.1861	0.3368	2666.93	2667.761	1	328.8	38.095238	L.H3G1E1E1V1Q2P1I1T1D1E1E1R4E1K2T1D1Y1Y1E1V1A1.H
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	4.1378	0.2951	1778.69	1779.99	1	1709.2	73.07692	N.SIIDFIKERQSEQW.S
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	4.6602	0.3774	1802.35	1800.99	1	1763.5	76.92308	N.S1I1I1D1F1I1K2E1R4Q2S1E1Q2W2.S
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	5.6612	0.4645	2209.59	2210.563	1	1171.8	67.64706	L.K2K2E1V1E1K2D1L1P1D1K2V1E1K2V1I1K2C1.K
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	5.1896	0.4111	2186.27	2186.563	1	840.8	58.823532	L.KKEVEKDLPDKVEKVIKC.K
gi|6322065|ref|NP_012140.1|	YIL126W	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; Sth1p	2	3.6107	0.3031	1739.61	1739.931	1	617.8	57.14286	Q.AHHNIPYLRDSPFTA.A
gi|6322058|ref|NP_012133.1|	YIL133C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Bp, E. coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p; Rpl16ap	2	3.6656	0.2879	1950.85	1951.319	1	516.8	53.125	F.EGIPPPYDKKKRVVVPQ.A
gi|6322058|ref|NP_012133.1|	YIL133C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Bp, E. coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p; Rpl16ap	2	3.5485	0.2719	1974.69	1975.319	1	446.7	50	F.E1G1I1P1P1P1Y1D1K2K2K2R4V1V1V1P1Q2.A
gi|6322058|ref|NP_012133.1|	YIL133C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Bp, E. coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p; Rpl16ap	1	2.2041	0.2832	1104.4	1104.257	2	148.8	62.5	F.NKTRGPFHF.R
gi|6322058|ref|NP_012133.1|	YIL133C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Bp, E. coli L13 and rat L13a ribosomal 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|	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; Tma108p	3	4.4302	0.2094	3281.03	3280.671	2	560.8	24.107143	L.STEEKDQLEDVPYQVPLFGVLPDGKMDTK.N
gi|6322054|ref|NP_012129.1|	YIL137C	Putative metalloprotease; Tma108p	3	5.7339	0.2927	2964.86	2966.303	1	1643.5	36	L.S1T1E1E1K2D1Q2L1E1D1V1P1Y1Q2V1P1L1F1G1V1L1P1D1G1K2M1.D
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	3	4.5742	0.3329	3312.98	3314.671	1	1021.9	29.464287	L.S1T1E1E1K2D1Q2L1E1D1V1P1Y1Q2V1P1L1F1G1V1L1P1D1G1K2M1D1T1K2.N
gi|6322049|ref|NP_012124.1|	YIL142W	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required 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	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required 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
gi|6322049|ref|NP_012124.1|	YIL142W	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.K2L1G1E1C1D1V1I1E1E1I1M1L1G1E1Q2P1F1L1K2F1.S
gi|6322049|ref|NP_012124.1|	YIL142W	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct2p	2	5.5037	0.3547	2499.45	2496.887	1	1807.1	55	C.KLGECDVIEEIMLGEQPFLKF.S
gi|6322049|ref|NP_012124.1|	YIL142W	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required 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
gi|6322049|ref|NP_012124.1|	YIL142W	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required 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.K2L1G1E1C1D1V1I1E1E1I1M$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
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	5.4625	0.4352	2109.51	2109.176	1	1373.2	61.11111	Q.T1H3S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1.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	2	4.4038	0.2943	2210.57	2211.396	1	775.9	57.894737	H.S1D1D1E1D1L1P1A1V1S1P1Y1P1N2E1K2A1L1V1K2.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	5.6023	0.3487	2453.63	2453.642	1	2238.4	61.904762	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	3.0926	0.2327	1669.43	1668.8	1	487.9	64.28571	T.S1R4G1G1P1F1D1E1I1P1Q2A1D1I1F1.I
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	2.4565	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.K2W2D1I1K2E1T1S1R4G1G1P1F1D1E1I1P1Q2A1D1I1F1.I
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.G1R4C1G1S1G1A1I1D1L1L1H3K2V1G1I1P1D1A1N2I1L1.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	41.666664	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.H3K2V1G1I1P1D1A1N2I1L1.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.L1H3K2V1G1I1P1D1A1N2I1L1.K
gi|6322228|ref|NP_012303.1|	YIR037W	Thiol peroxidase that functions as a hydroperoxide receptor to sense intracellular hydroperoxide levels and transduce a redox signal to the Yap1p transcription factor; Hyr1p	2	3.5374	0.3246	1690.79	1687.936	1	844.9	64.28571	L.APVDKKGQPFPFDQL.K
gi|6322228|ref|NP_012303.1|	YIR037W	Thiol peroxidase that functions as a hydroperoxide receptor to sense intracellular 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	L.A1P1V1D1K2K2G1Q2P1F1P1F1D1Q2L1.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	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for 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
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	5.1381	0.4473	2017.59	2018.318	1	691.4	57.894737	C.GATPLPRLGAPTPEELGLVE.T
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	5.4409	0.449	2039.69	2041.318	1	885.3	63.15789	C.G1A1T1P1L1P1R4L1G1A1P1T1P1E1E1L1G1L1V1E1.T
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	4.0067	0.3522	2026.45	2027.21	3	413.6	46.875	E.SDEGVKDIREENIYDML.A
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	4.0753	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
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	4.8625	0.2812	2348.53	2349.473	1	686.2	52.63158	Y.DDLKTELEDNLSKNNGQWTQ.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	4.8634	0.2853	2543.17	2541.649	1	703.5	50	S.Y1D1D1L1K2T1E1L1E1D1N2L1S1K2N2N2G1Q2W2T1Q2.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	3.3241	0.1871	1914.73	1912.017	2	340.1	50	S.YDDLKTELEDNLSKNN.G
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	3.0139	0.1569	2122.85	2121.2	2	342.3	47.058823	S.Y1D1D1L1K2T1E1L1E1D1N2L1S1K2N2N2G1Q2.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	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.DDLKTELEDNLSKNNGQWTQELETDFLESL.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	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
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	3.7406	0.1908	1990.47	1989.114	1	662.2	60.000004	M.VREDNFDGVDRTHKNW.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	2	3.6648	0.1652	2147.37	2149.307	1	540.8	50	T.M1V1R4E1D1N2F1D1G1V1D1R4T1H3K2N2W2.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	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.D1I1G1V1D1W2P1F1K2Q2L1.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; Vtc4p	2	4.5364	0.3938	1701.59	1702.874	1	784	65.38461	Q.T1Q2L1G1Q2E1P1P1E1W2V1R4E1L1.V
gi|27808709|ref|NP_012515.2|	YJL019W	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-like chaperone Jem1p and with centrin homolog Cdc31p; Mps3p	2	3.1928	0.3332	1916.47	1918.114	1	765.1	67.85714	N.KQEIWEEITNRLETQ.Q
gi|27808709|ref|NP_012515.2|	YJL019W	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-like chaperone Jem1p and with centrin homolog Cdc31p; Mps3p	2	3.8576	0.3228	2262.13	2263.52	1	315.2	39.473686	L.N2H3L1T1S1P1T1W2R4Q2G1S1G1V1Q2P1I1E1L1L1.T
gi|27808709|ref|NP_012515.2|	YJL019W	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-like chaperone Jem1p and with centrin homolog Cdc31p; Mps3p	2	3.5865	0.3581	1891.71	1893.115	1	664.4	56.25	L.T1S1P1T1W2R4Q2G1S1G1V1Q2P1I1E1L1L1.T
gi|27808709|ref|NP_012515.2|	YJL019W	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-like chaperone Jem1p and with centrin homolog Cdc31p; Mps3p	2	4.0306	0.3598	2233.51	2234.52	1	325.2	42.105263	L.NHLTSPTWRQGSGVQPIELL.T
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	3.6425	0.191	2968.77	2969.052	1	251.1	31.25	K.NEPYTETEEAEENEKTEPKPEFTPE.T
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	3.9469	0.3442	1822.51	1823.081	1	591.5	60.000004	Q.I1V1S1E1F1K2D1E1V1I1Q2P1I1G1A1R4.T
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	3	5.3474	0.3751	4547.21	4548.797	1	913.1	24.324326	N.KNEPYTETEEAEENEKTEPKPEFTPETEHNEEPQMELL.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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	3	3.8535	0.2028	2676.2	2673.798	1	527.2	30.681818	G.N2N2E1S1E1N2V1N2S1G1E1K2I1Y1P1Q2E1P1P1I1S1H3R4.T
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	3.5539	0.2601	1616.79	1617.802	1	652.6	57.692307	L.ALPKHNEVEEHVKS.S
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	4.0004	0.2396	1789.35	1789.051	1	895.2	67.85714	L.K2E1N2E1K2K2I1V1P1E1P1I1N2R4A1.Q
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	4.3284	0.3321	2905.53	2905.295	1	622	41.304348	Q.HKEKEEEEPEQLQELPRAIPVMPF.V
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	3.875	0.329	1893.71	1894.181	1	683.5	56.666668	L.KENEKKIVPEPINRAQ.V
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	3.4545	0.3849	1639.23	1638.802	1	559.6	61.538464	L.A1L1P1K2H3N2E1V1E1E1H3V1K2S1.S
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	3	4.112	0.2093	3020.96	3021.996	2	429.4	32.291664	H.EDREGDNDEEKEEEDSEENRRAALR.E
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	3	4.4306	0.3171	3060.89	3061.996	2	408	31.25	H.E1D1R4E1G1D1N2D1E1E1K2E1E1E1D1S1E1E1N2R4R4A1A1L1R4.E
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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	3	4.6256	0.2588	4419.44	4420.623	1	612	21.527777	K.NEPYTETEEAEENEKTEPKPEFTPETEHNEEPQMELL.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 Myo5p; localized predominantly to cortical actin patches; Bbc1p	2	4.6289	0.231	1766.19	1766.051	1	965.6	60.714287	L.KENEKKIVPEPINRA.Q
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 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 Myo5p; 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.E1M1E1K2E1E1P1L1L1N2E1D1K2E1R4T1V1L1F1P1I1K2Y1H3.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.K2N2K2P1D1P1A1I1V1E1K2I1V1T1E1.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.L1K2E1M1E1K2E1E1P1L1L1N2E1D1K2E1R4T1V1L1F1P1I1K2Y1H3.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.E1D1K2E1R4T1V1L1F1P1I1K2Y1H3.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 subunits; Rnr2p	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, Vps51p-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.N2F1L1D1K2V1I1D1I1I1T1T1N2.F
gi|6322431|ref|NP_012505.1|	YJL029C	Component of the GARP (Golgi-associated retrograde protein) complex, Vps51p-Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting; Vps53p	2	3.3671	0.2118	1505.89	1506.739	3	838.1	70.83333	W.NFLDKVIDIITTN.F
gi|6322431|ref|NP_012505.1|	YJL029C	Component of the GARP (Golgi-associated retrograde protein) complex, Vps51p-Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting; Vps53p	2	3.0339	0.3833	1553.91	1552.9	1	682.8	65.38461	N.TIRLLQPVPPFSLA.G
gi|6322431|ref|NP_012505.1|	YJL029C	Component of the GARP (Golgi-associated retrograde protein) complex, Vps51p-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.K2F1F1K2D1L1P1I1S1D1P1T1L1K2.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.D1Y1S1H3G1H3N2P1S1N2S1V1D1D1D1I1I1E1V1E1E1P1Q2T1L1.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	33.333336	V.D1Y1S1H3G1H3N2P1S1N2S1V1D1D1D1I1I1E1V1E1E1P1Q2T1L1E1D1L1E1S1L1.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	2	4.4823	0.2633	1648.83	1649.971	1	1232.6	84.61539	A.KFFKDLPISDPTLK.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	3.9832	0.3173	2309.51	2309.405	1	822.4	47.5	H.GHNPSNSVDDDIIEVEEPQTL.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	5.6442	0.4013	2554.01	2552.976	1	1165.5	39.772728	M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	4.0183	0.3311	2553.35	2552.976	1	461.1	43.18182	M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	4.034	0.2948	2583.59	2581.976	1	453.7	43.18182	M.Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	7.3158	0.4058	2715.41	2714.169	1	1644.6	42.391304	T.M1Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.296	0.1958	2186.49	2187.552	3	387	42.105263	D.S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E

gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	4.9496	0.3964	2552.99	2552.976	4	611.8	30.681818	M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.5429	0.2624	2554.17	2552.976	1	554.2	45.454548	M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	5.8069	0.4133	2579.99	2581.976	1	1252.6	40.909092	M.Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	4.4368	0.3606	2684.15	2684.169	1	611.4	27.173912	T.MYIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.6063	0.2388	2684.75	2684.169	1	357.3	36.95652	T.MYIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	3.9316	0.2526	2784.5	2785.274	2	663.6	26.041666	N.TMYIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	4.9964	0.3846	3485.63	3485.925	1	1098.9	28.333334	M.YIDSPVNLLKPFNPTLPEGIRPAEEGEKSIC.A
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.1331	0.2885	1650.59	1650.962	1	815.7	60.714287	L.LKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.9082	0.3138	2161.27	2161.552	2	470.1	50	D.SPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	3.8139	0.2661	2159.78	2161.552	5	667.4	32.894737	D.SPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.9581	0.2966	1638.17	1637.854	1	1360.5	83.33333	Y.SRKHDLHEDMKQL.K
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	2.9479	0.2001	2078.65	2079.147	1	343.8	50	K.K2D1F1D1G1I1E1V1E1D1E1E1N2V1K2E1Y1.H
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	4.122	0.1835	1394.97	1394.627	2	1611.4	90	M.K2I1E1D1E1D1F1L1K2L1M1.K
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	4.092	0.2205	2417.45	2417.8	1	610.4	45.238094	Y.I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	5.0878	0.331	2420	2417.8	1	1229.4	41.666664	Y.I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	4.1226	0.3368	2580.23	2581.976	1	477.3	40.909092	M.Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.6432	0.2699	2552.69	2552.976	1	405.5	40.909092	M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	3.904	0.2321	2728.88	2730.169	1	622.8	26.086956	T.M$Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	6.4274	0.3679	2584.31	2581.976	1	1054.6	38.636364	M.Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	4.864	0.3458	2552.3	2552.976	1	753.2	34.090908	M.YIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	4.4956	0.3838	2681.63	2684.169	1	1208.8	32.608696	T.MYIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.5725	0.2959	2712.25	2714.169	1	359.2	36.95652	T.M1Y1I1D1S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	2.9052	0.2229	2683.43	2684.169	1	300.7	32.608696	T.MYIDSPVNLLKPFNPTLPEGIRPA.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	4.013	0.3321	1673.51	1670.962	1	807.6	64.28571	L.L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	2	3.3956	0.3565	1783.69	1785.121	1	481.7	56.666668	N.L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.E
gi|6322411|ref|NP_012485.1|	YJL050W	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 rRNA; Mtr4p	3	4.7198	0.2381	2188.37	2187.552	1	885.4	40.789474	D.S1P1V1N2L1L1K2P1F1N2P1T1L1P1E1G1I1R4P1A1.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.C1L1A1P1L1A1K2V1I1N2D1A1F1G1I1E1E1G1L1M1T1.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	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	Putative protein of unknown function, identified based on comparison to related yeast species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Yjl062w-ap	3	3.8405	0.3588	2614.91	2615.889	1	564	32.954548	F.L1H3K2D1N2D1F1A1D1V1P1I1P1P1I1D1P1Q2E1L1E1A1L1.K
gi|13129172|ref|NP_076894.1|	YJL062W-A	Putative protein of unknown function, identified based on comparison to related yeast species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Yjl062w-ap	2	4.2957	0.2849	2615.51	2615.889	1	598.5	40.909092	F.L1H3K2D1N2D1F1A1D1V1P1I1P1P1I1D1P1Q2E1L1E1A1L1.K
gi|13129172|ref|NP_076894.1|	YJL062W-A	Putative protein of unknown function, identified based on comparison to related yeast species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Yjl062w-ap	2	3.1558	0.3923	2472.71	2474.729	1	389	40.476192	L.HKDNDFADVPIPPIDPQELEAL.K
gi|13129172|ref|NP_076894.1|	YJL062W-A	Putative protein of unknown function, identified based on comparison to related yeast species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Yjl062w-ap	2	3.2083	0.1935	2763.57	2764.066	1	546.2	36.95652	H.F1L1H3K2D1N2D1F1A1D1V1P1I1P1P1I1D1P1Q2E1L1E1A1L1.K
gi|13129172|ref|NP_076894.1|	YJL062W-A	Putative protein of unknown function, identified based on comparison to related yeast species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Yjl062w-ap	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	Putative protein of unknown function, identified based on comparison to related yeast species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Yjl062w-ap	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 stretches; Mpm1p	2	3.277	0.3627	1928.29	1931.196	1	702.7	70	K.LRDIDEYDNPLLPLPF.N
gi|6322395|ref|NP_012469.1|	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	2	4.1133	0.3542	1953.37	1951.196	1	605.7	63.333332	K.L1R4D1I1D1E1Y1D1N2P1L1L1P1L1P1F1.N
gi|6322395|ref|NP_012469.1|	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	2	2.9724	0.2437	1694.51	1693.095	2	313.3	53.571426	S.K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1.E
gi|6322395|ref|NP_012469.1|	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	2	3.7173	0.3447	2376.71	2377.827	1	543	45	S.KAIPPLPQLDFLLPLEEIKSD.K
gi|6322395|ref|NP_012469.1|	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic 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
gi|6322395|ref|NP_012469.1|	YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	2	4.3507	0.4445	2398.89	2401.827	1	640.5	55	S.K2A1I1P1P1L1P1Q2L1D1F1L1L1P1L1E1E1I1K2S1D1.K
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	3.275	0.2269	1484.49	1484.779	1	503.4	70.83333	Q.LSITKPELSRIVQ.S
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	1	2.4848	0.1532	1483.67	1484.779	6	145.4	50	Q.LSITKPELSRIVQ.S
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	3.4258	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
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	3.6019	0.2759	2414.61	2414.811	1	608.5	45	A.ADVIINVPRKSDKVNDVVYIR.G
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	3	3.8828	0.3187	2998.88	2999.391	1	579.1	28.703705	A.ATAEEHPQLEKKPTPLPSLKDLPSLGSN.A
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	3.8092	0.3676	1788.23	1789.088	1	908.1	64.28571	N.VPRKSDKVNDVVYIR.G
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	3.6336	0.2284	1586.75	1587.819	3	633.4	62.5	F.INFPRDNEIVTIR.G
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	3.9863	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.N2I1T1D1I1E1E1Y1T1R4G1P1E1F1W2I1S1P1D1T1P1L1K2F1P1L1.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	2	3.2559	0.2819	2123.49	2125.441	1	704.2	52.941177	Y.T1R4G1P1E1F1W2I1S1P1D1T1P1L1K2F1P1L1.N
gi|6322363|ref|NP_012437.1|	YJL098W	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p	3	5.2136	0.4093	3354.38	3356.229	1	788.8	26.724138	N.DRSELKENEDDNTGDADDEVEDDTNQVESA.N
gi|6322363|ref|NP_012437.1|	YJL098W	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p	3	6.6721	0.5078	3394.79	3394.229	1	1766.1	36.206894	N.D1R4S1E1L1K2E1N2E1D1D1N2T1G1D1A1D1D1E1V1E1D1D1T1N2Q2V1E1S1A1.N
gi|6322363|ref|NP_012437.1|	YJL098W	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p	2	4.3083	0.2123	1520.33	1520.812	1	885.9	81.818184	N.R4F1L1L1D1D1L1L1I1N2I1R4.L
gi|6322363|ref|NP_012437.1|	YJL098W	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p	2	4.426	0.3099	1502.65	1501.812	2	913.2	81.818184	N.RFLLDDLLINIR.L
gi|6322363|ref|NP_012437.1|	YJL098W	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p	3	4.058	0.2456	3000.8	3002.236	5	386.3	28	T.R4L1N2F1N2P1D1S1D1A1T1E1Q2V1P1G1E1V1N2R4D1H3K2I1P1L1.K
gi|6322363|ref|NP_012437.1|	YJL098W	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p	3	4.1454	0.3047	3637.04	3638.721	1	472.9	31.034481	N.M1N2N2E1E1Q2H3S1L1M1P1D1F1N2N2G1D1F1K2D1E1E1D1E1N2P1F1E1P1Q2.Y
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	4.8217	0.2415	2160.14	2160.452	1	1378.8	45.3125	V.PDMHLRDELVEELPRYF.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	3.8546	0.2014	2342.29	2343.637	1	364.7	44.444447	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	3.7483	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.V1K2E1I1G1F1P1V1I1V1R4.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.H3V1I1K2G1P1A1E1L1K2.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.H3R4T1I1T1L1P1G1L1I1N2.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	54.166668	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.I1Y1S1D1L1P1Q2Q2E1R4D1T1I1M1K2.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.V1K2K2D1E1L1T1L1E1G1I1K2Q2F1.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.R4A1I1M1P1I1I1E1G1H3D1V1L1A1Q2.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.S1D1L1P1Q2Q2E1R4D1T1I1M1K2E1F1.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.R4A1I1M1P1I1I1E1G1H3.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
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	3.8484	0.2036	1377.87	1378.482	1	1519.6	80 F.D1D1M1E1L1D1E1N2L1L1R4.G
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	3.1771	0.3838	1437.62	1438.665	1	338.5	58.333332 T.L1L1R4E1L1E1P1A1P1L1S1P1S1.S
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	3.4511	0.2727	1438.45	1438.665	1	902.5	66.66667 T.L1L1R4E1L1E1P1A1P1L1S1P1S1.S
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	3.8099	0.3503	2168.47	2167.343	1	542.1	52.77778 S.K2N2G1D1D1Y1I1I1P1E1T1E1L1G1H3I1D1I1T1.L
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	3	4.2167	0.3294	2941.64	2939.214	1	894.3	32 L.SNAVRIPTVVQDKNPNPADDPDFYKH.F
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	3.1095	0.357	1437.84	1438.665	2	286.5	50 T.L1L1R4E1L1E1P1A1P1L1S1P1S1.S
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	5.0007	0.3986	2254.43	2255.421	1	643.5	52.63158 L.S1K2N2G1D1D1Y1I1I1P1E1T1E1L1G1H3I1D1I1T1.L
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen 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	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen 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.S1K2N2G1D1D1Y1I1I1P1E1T1E1L1G1H3I1D1.I
gi|6322289|ref|NP_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.R4E1L1E1P1A1P1L1S1P1S1S1G1P1V1W2D1I1L1.A
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	4.2847	0.4208	2289.65	2290.665	1	791.3	50 T.LLRELEPAPLSPSSGPVWDIL.A
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	4.3405	0.3611	2230.81	2231.421	1	592.8	50 L.SKNGDDYIIPETELGHIDIT.L
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	3.4886	0.3129	2974.43	2976.214	1	396.5	34 L.S1N2A1V1R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3.F
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	3	5.5713	0.3883	3125.69	3124.39	1	561.9	26.923079 L.S1N2A1V1R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3F1.Y
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen 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	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen 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	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	4.5663	0.4423	2308.85	2309.507	1	483.3	52.77778 W.K2F1P1P1P1F1S1G1H3Y1D1P1E1T1D1F1V1W2G1R4.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.K2F1P1P1P1F1S1G1H3Y1D1P1E1T1D1F1V1W2G1R4.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
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	4.1548	0.2594	1535.47	1536.667	1	990.6	79.16667 L.Y1T1W2E1G1S1D1P1D1L1K2P1L1.L
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	2.8141	0.2543	1209.5	1210.346	1	236.8	65 L.R4E1L1E1P1A1P1L1S1P1S1.S
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	2.6859	0.2028	1199.61	1200.381	4	162.9	55 L.S1N2A1V1R4I1P1T1V1V1Q2.D
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	2.8307	0.3024	1367.49	1368.502	1	567.4	63.636364 A.T1P1I1N2A1E1K2G1Y1V1D1F1.E
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	3.1658	0.3253	1423.27	1422.665	1	969.3	70.83333 T.LLRELEPAPLSPS.S
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	3.2567	0.374	1437.6	1438.665	1	378	54.166668 T.L1L1R4E1L1E1P1A1P1L1S1P1S1.S
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	4.9685	0.3673	2037.79	2039.157	1	1337.7	67.64706 L.S1K2N2G1D1D1Y1I1I1P1E1T1E1L1G1H3I1D1.I
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	3.8825	0.2945	1953.71	1951.078	1	736.1	68.75 S.K2N2G1D1D1Y1I1I1P1E1T1E1L1G1H3I1D1.I
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen 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
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	3	4.4153	0.2724	2036.48	2039.157	1	732.8	39.705883 L.S1K2N2G1D1D1Y1I1I1P1E1T1E1L1G1H3I1D1.I
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	4.672	0.4207	2387.33	2387.743	1	771.9	52.380955 T.L1L1R4E1L1E1P1A1P1L1S1P1S1S1G1P1V1W2D1I1L1A1.G
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	3.9813	0.3552	2444.53	2445.795	1	726	50 T.L1L1R4E1L1E1P1A1P1L1S1P1S1S1G1P1V1W2D1I1L1A1G1.T
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	3.725	0.2914	2791.59	2792.191	1	388.5	34 T.L1L1R4E1L1E1P1A1P1L1S1P1S1S1G1P1V1W2D1I1L1A1G1T1I1Q2.D
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	3	4.2046	0.287	2975.93	2976.214	1	690.9	28 L.S1N2A1V1R4I1P1T1V1V1Q2D1K2N2P1N2P1A1D1D1P1D1F1Y1K2H3.F
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	2	3.9506	0.4024	2091.37	2091.268	1	348.8	56.25 W.K2F1P1P1P1F1S1G1H3Y1D1P1E1T1D1F1V1W2.G
gi|6322289|ref|NP_012363.1|	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen 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.E1Y1I1D1D1H3R4S1G1K2I1V1V1Q2.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	3.6166	0.4364	1956.69	1959.131	1	388.8	63.333332	G.E1F1E1Y1I1D1D1H3R4S1G1K2I1V1V1Q2.L
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	1	2.9813	0.2799	1437.71	1436.663	1	464.7	59.090908	N.KYPEIDDIVMVN.V
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.7815	0.2304	1438.47	1436.663	1	772.8	77.27273	N.KYPEIDDIVMVN.V
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	4.6963	0.4135	2888.75	2891.201	1	1504.9	36.458336	L.SIIDETVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.6975	0.3146	2918.71	2920.201	1	275.4	33.333336	L.S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.8781	0.3465	1424.51	1423.606	1	602.3	75	F.SYEGIDAIKDALK.S
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	4.1521	0.365	2233.85	2232.495	1	725.9	38.88889	T.VWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	5.5547	0.4216	2918.93	2920.201	1	1459.8	35.416664	L.S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.1395	0.4086	3132.03	3132.535	1	534.2	38.46154	F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.4806	0.4707	3163.05	3164.535	1	325.9	32.692307	F.K2L1S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	4.8607	0.2238	3131.45	3132.535	2	895.5	25.961538	F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	2.9756	0.2421	1510.89	1509.786	1	718.8	68.181816	E.KFQIPLEELYKT.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.5798	0.3629	1437.99	1438.606	2	893.1	62.5	F.S1Y1E1G1I1D1A1I1K2D1A1L1K2.S
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	3.9277	0.2849	2833.97	2832.123	1	871.7	31.52174	S.I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.7781	0.3888	2231.87	2232.495	1	559.5	44.444447	T.VWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	4.6483	0.4096	2230.13	2232.495	1	1173.8	48.61111	T.VWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.2126	0.2523	3131.29	3132.535	1	272.7	30.769232	F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	1	2.5694	0.2705	1510.87	1509.786	1	476.8	59.090908	E.KFQIPLEELYKT.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.9123	0.3042	1523.93	1524.786	1	1731	90.909096	E.K2F1Q2I1P1L1E1E1L1Y1K2T1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	1	2.9131	0.2762	1523.67	1524.786	1	560.6	59.090908	E.K2F1Q2I1P1L1E1E1L1Y1K2T1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.0473	0.17	1638.07	1638.945	2	645.3	58.333332	E.K2F1Q2I1P1L1E1E1L1Y1K2T1I1.A
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	5.7707	0.3908	3131.78	3132.535	1	1599.3	33.653847	F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	4.7004	0.2534	3164.33	3164.535	1	1141.2	27.884615	F.K2L1S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.6666	0.3799	2421.29	2421.669	1	487.6	45	S.I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1.K
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.4003	0.3477	2508.51	2509.747	4	292.4	40.476192	L.S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1.K
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.9654	0.3196	1698.03	1696.882	1	899.9	65.38461	Y.E1N2K2Y1P1E1I1D1D1I1V1M1V1N2.V
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.323	0.2102	1583.23	1580.779	1	1047.2	70.83333	Y.E1N2K2Y1P1E1I1D1D1I1V1M1V1.N
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.7437	0.2452	1451.29	1450.663	2	844.4	81.818184	N.K2Y1P1E1I1D1D1I1V1M1V1N2.V

gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.6344	0.2751	1965.93	1967.149	1	796.8	62.5 W.E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.3844	0.2764	2255.29	2255.495	1	800.3	55.555557 T.V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.7541	0.3448	2230.89	2232.495	1	1358.4	69.44444 T.VWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.4424	0.3652	2334.47	2333.6	1	737	55.263157 E.TVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	5.142	0.4512	2356.49	2357.6	1	1123.7	63.15789 E.T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.0651	0.2446	2486.49	2487.715	1	538.3	47.5 D.E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	4.8405	0.4525	2801.54	2804.123	1	905.7	33.695652 S.IIDETVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.6961	0.2823	2832.89	2832.123	1	383.9	39.130436 S.I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.1784	0.2739	2919.63	2920.201	4	220.7	29.166666 L.S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.737	0.32	2888.91	2891.201	1	365.7	37.5 L.SIIDETVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	5.6156	0.4451	2917.67	2920.201	1	1172.4	32.291664 L.S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	4.0176	0.3182	2726.45	2727.081	4	478.5	39.130436 F.KLSIIDETVWEGIEPPSKDVLDEL.K
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.8089	0.2454	2751.89	2754.081	4	474.2	36.95652 F.K2L1S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1.K
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	5.4763	0.3031	3134.09	3132.535	1	1561.7	33.653847 F.KLSIIDETVWEGIEPPSKDVLDELKNY.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	3	4.3979	0.2367	3164.18	3164.535	1	768.3	25 F.K2L1S1I1I1D1E1T1V1W2E1G1I1E1P1P1S1K2D1V1L1D1E1L1K2N2Y1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.975	0.1515	1424.45	1422.681	1	1111.8	85 E.K2F1Q2I1P1L1E1E1L1Y1K2.T
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	1	3.1056	0.2176	1408.5	1408.681	1	612.8	65 E.KFQIPLEELYK.T
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	1	2.9102	0.2119	1524.55	1524.786	5	381	50 E.K2F1Q2I1P1L1E1E1L1Y1K2T1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	1	2.9754	0.2528	1510.66	1509.786	1	445.8	54.545456 E.KFQIPLEELYKT.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.8944	0.2837	1525.49	1524.786	1	1360.3	86.36364 E.K2F1Q2I1P1L1E1E1L1Y1K2T1.I
gi|6322466|ref|NP_012540.1|	YJR007W	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 inhibiting the exchange of GDP for GTP; Sui2p	2	3.6626	0.3631	2484.39	2485.747	1	398.3	42.857143 L.SIIDETVWEGIEPPSKDVLDEL.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	3.3256	0.4149	1495.79	1497.651	1	884.2	75 F.QERDPANLPWASL.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	2.5591	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
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	3.325	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.K2V1V1I1T1A1P1S1S1T1A1P1M1F1V1M1.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.C1L1A1P1L1A1K2V1I1N2D1A1F1G1I1E1E1G1L1M1T1.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.V1R4V1A1I1N2G1F1G1R4I1G1.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.TFQERDPANLPWASL.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	4.6167	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.K2E1T1T1Y1D1E1I1K2K2V1V1K2A1.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
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	3.5713	0.1893	1667.15	1666.695	2	232.5	66.66667 K.Q2F1T1E1E1E1R4E1D1V1V1E1H3.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	5.2135	0.488	2330.39	2331.336	1	1395.8	57.894737 Q.F1T1E1E1E1R4E1D1V1V1E1H3A1C1P1G1P1G1S1C1.G
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	3.2112	0.3511	2460.51	2461.467	1	376	45 K.Q2F1T1E1E1E1R4E1D1V1V1E1H3A1C1P1G1P1G1S1C1.G
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	3.7331	0.3674	2434.57	2434.467	1	682.9	50 K.QFTEEEREDVVEHACPGPGSC.G
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	3.5401	0.1727	1369.61	1368.66	4	410.4	63.636364 M.ELGILPRDILTK.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	3.8024	0.2605	1501.85	1499.852	1	1203.1	75 T.MELGILPRDILTK.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	4.4431	0.3368	1645.85	1646.968	1	2007.5	84.61539 T.M1E1L1G1I1L1P1R4D1I1L1T1K2E1.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	3.4999	0.199	1838.39	1839.116	2	690.6	53.125 R.Y1E1G1P1R4G1A1P1G1M1P1E1M1L1K2P1S1.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	4.6935	0.3106	1768.21	1769.104	1	703.7	66.66667 A.K2K2A1P1S1L1P1E1G1Q2E1I1I1K2P1L1.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	3.455	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; Ilv3p	2	3.0367	0.3173	1459.87	1460.717	1	448.2	58.333332	F.KKEDFKKPQVGVG.S
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	1	2.3161	0.2576	1503.71	1503.782	1	302.3	50	A.GIPPAPKGVPQIEVT.F
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	1	2.3896	0.2488	1285.65	1286.472	1	562.6	63.636364	F.T1K2E1G1E1R4L1V1G1I1P1A1.K
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	3	4.0198	0.2876	1555.46	1554.833	9	689.2	50	F.TKEGERLVGIPAKR.Q
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	2	3.0987	0.2584	1682.01	1682.964	1	426.4	53.571426	F.TKEGERLVGIPAKRQ.A
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	2	3.1014	0.2489	1192.23	1190.385	4	256.1	65	A.EAYLGKPVKNA.V
gi|6322505|ref|NP_012579.1|	YJR045C	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; 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 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; Ssc1p	2	4.001	0.2113	2458.41	2459.764	2	361.7	38.636364	M.E1G1K2V1P1K2I1I1E1N2A1E1G1S1R4T1T1P1S1V1V1A1F1.T
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	3	3.9075	0.1861	3896.18	3898.492	7	225.7	20.945946	A.TKDAGQIVGLNVLRVVNEPTAAALAYGLEKSDSKVVAV.F
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	2	3.9728	0.3772	1522.35	1522.67	1	1496.1	83.33333	F.KTETGIDLENDRM.A
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	2	3.4839	0.1671	1538.01	1540.67	1	1018.3	83.33333	F.K2T1E1T1G1I1D1L1E1N2D1R4M1.A
gi|6322505|ref|NP_012579.1|	YJR045C	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; Ssc1p	2	2.9558	0.2366	1270.57	1270.472	1	463.3	68.181816	F.TKEGERLVGIPA.K
gi|6322524|ref|NP_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
gi|6322524|ref|NP_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	3.7474	0.3986	2221.33	2221.549	6	277.8	32.5	T.S1L1G1P1R4G1L1D1K2I1L1I1S1P1D1G1E1I1T1I1T1.N
gi|6322524|ref|NP_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	3.2978	0.3087	2196.85	2196.549	1	386.7	37.5	T.SLGPRGLDKILISPDGEITIT.N
gi|6322524|ref|NP_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	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	2	3.9768	0.2053	1448.29	1450.619	1	279.8	70	Q.R4E1K2E1L1R4E1I1E1A1R4.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	4.1304	0.3124	1968.19	1967.238	1	838.5	66.66667	L.A1D1K2I1Y1Y1L1P1V1T1P1E1Y1I1T1Y1.I
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	1	2.4692	0.1613	1453.36	1454.712	1	506.2	58.333332	M.N2F1H3V1P1L1P1P1S1G1I1L1F1.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	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
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	1	3.0618	0.2498	1409.64	1410.682	1	551	68.181816	Y.I1I1E1L1E1R4P1D1A1I1L1L1.T
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	1	2.9532	0.2741	1453.68	1454.712	1	585.2	58.333332	M.N2F1H3V1P1L1P1P1S1G1I1L1F1.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	2	2.9996	0.2805	1601.63	1602.905	8	339.8	50	T.M$N2F1H3V1P1L1P1P1S1G1I1L1F1.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	2	2.9854	0.2419	1439.01	1438.712	5	323	58.333332	M.NFHVPLPPSGILF.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	2	3.4751	0.3463	1454.21	1454.712	1	491.5	70.83333	M.N2F1H3V1P1L1P1P1S1G1I1L1F1.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	2	4.1574	0.4037	1588.01	1586.905	1	1311.7	76.92308	T.M1N2F1H3V1P1L1P1P1S1G1I1L1F1.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	2	2.9731	0.1933	1568.85	1569.905	1	635.9	57.692307	T.MNFHVPLPPSGILF.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	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	2	3.0402	0.164	1302.43	1302.56	4	685	75 S.K2V1N2Y1P1V1L1I1R4P1S1.Y
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	4.1973	0.358	2430.61	2430.628	1	798.2	57.5 L.SETKLPPVLEDEIDDETFHKS.R
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	4.575	0.3549	2455.21	2455.628	1	793.2	55 L.S1E1T1K2L1P1P1V1L1E1D1E1I1D1D1E1T1F1H3K2S1.R
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	1	3.3965	0.2074	1447.67	1447.72	1	814.9	68.181816 K.TILDHPNIPWKL.I
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	1	3.8536	0.3668	1463.65	1464.72	1	921.1	68.181816 K.T1I1L1D1H3P1N2I1P1W2K2L1.I
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	3.4388	0.1812	1448.43	1447.72	1	1000.2	81.818184 K.TILDHPNIPWKL.I
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	1	3.0194	0.2994	1450.6	1450.693	1	470.2	54.545456 L.D1H3P1N2I1P1W2K2L1I1I1S1.G
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	1	3.2596	0.3405	1432.63	1433.693	1	705.9	63.636364 L.DHPNIPWKLIIS.G
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	3.092	0.228	1338.19	1336.621	1	1190.1	88.88889 F.I1K2Y1D1L1F1P1K2I1W2.H
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	2.9257	0.2027	1781.35	1781.117	1	399	50 K.T1I1L1D1H3P1N2I1P1W2K2L1I1I1S1.G
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	3	4.167	0.3556	2429.21	2430.628	1	886	40 L.SETKLPPVLEDEIDDETFHKS.R
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	4.8475	0.4935	2113.87	2113.329	1	561.8	61.764706 T.KLPPVLEDEIDDETFHKS.R
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	3.7066	0.2959	2097.85	2097.234	2	412.3	44.11765 L.S1E1T1K2L1P1P1V1L1E1D1E1I1D1D1E1T1F1.H
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	3.4501	0.2543	2078.53	2078.234	1	658.7	52.941177 L.SETKLPPVLEDEIDDETF.H
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	5.3918	0.3749	2134.45	2135.329	1	496.3	64.70589 T.K2L1P1P1V1L1E1D1E1I1D1D1E1T1F1H3K2S1.R
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	1	3.332	0.2911	1446.59	1447.72	1	1019.8	68.181816 K.TILDHPNIPWKL.I
gi|6322577|ref|NP_012651.1|	YJR117W	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 processing; contains multiple transmembrane spans; Ste24p	2	3.0103	0.1601	1448.91	1447.72	1	995.5	81.818184 K.TILDHPNIPWKL.I
gi|6322577|ref|NP_012651.1|	YJR117W	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 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; Ilm1p	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.A1I1R4E1E1K2N2E1E1F1K2R4L1.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	18.243242 K.T1E1T1T1E1I1I1E1I1I1N2D1E1E1N2D1D1E1D1G1K2D1N2D1D1N2N2E1K2G1N2D1D1S1D1A1K2K2.-
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	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	2	3.7261	0.2835	1662.15	1662.886	1	702.9	66.66667 N.AIREEKNEEFKRL.N
gi|6322582|ref|NP_012656.1|	YJR122W	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins; Caf17p	2	3.9682	0.3151	1959.25	1960.196	1	943.3	56.666668 Q.FPNLPKDIENPWFDNL.L
gi|6322582|ref|NP_012656.1|	YJR122W	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins; Caf17p	2	4.8235	0.2365	1983.53	1981.196	1	1322.3	73.333336 Q.F1P1N2L1P1K2D1I1E1N2P1W2F1D1N2L1.L
gi|6322592|ref|NP_012666.1|	YJR132W	Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta homolog; Nmd5p	3	5.1885	0.2279	4292.63	4295.397	1	512.8	19.285715 S.G1F1E1E1D1T1K2W2D1E1N2F1L1D1V1G1D1D1D1E1N2D1D1E1G1D1L1T1E1K2Y1L1E1L1I1K2.N
gi|6322592|ref|NP_012666.1|	YJR132W	Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta homolog; Nmd5p	1	2.5791	0.266	1457.67	1458.675	1	249.3	50 L.RHLTPADQELFM.G
gi|6322592|ref|NP_012666.1|	YJR132W	Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta homolog; Nmd5p	3	4.4669	0.3699	4252.31	4253.397	1	761.8	21.428572 S.GFEEDTKWDENFLDVGDDDENDDEGDLTEKYLELIK.N
gi|6322592|ref|NP_012666.1|	YJR132W	Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta 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 homodimers 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	Protein involved in mitochondrial genome maintenance; component of the mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p	3	6.7996	0.444	3551.75	3553.177	1	1886.2	37.068966	K.VQKDLIEPLDPKDIEIKPDGLIYLPEIKYR.R
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	4.5955	0.2029	2229.23	2229.541	1	1422.1	47.22222	K.V1Q2K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1.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	2	5.0894	0.1889	2228.99	2229.541	1	1099.2	61.11111	K.V1Q2K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1.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	2	3.3985	0.1664	2000.59	1999.278	1	673.8	59.375	Q.K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1.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	4.2909	0.2779	3264.14	3266.813	1	574.1	25.925926	K.V1Q2K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1G1L1I1Y1L1P1E1I1K2.Y
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	6.5767	0.3103	3235.25	3233.813	1	2012.5	37.962963	K.VQKDLIEPLDPKDIEIKPDGLIYLPEIK.Y
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	5.3779	0.374	3006.92	3006.55	1	2600.7	40	Q.KDLIEPLDPKDIEIKPDGLIYLPEIK.Y
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	3.3311	0.2594	3005.27	3006.55	1	266.8	30.000002	Q.KDLIEPLDPKDIEIKPDGLIYLPEIK.Y
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	6.6163	0.4206	3035.39	3036.55	1	2436.1	41	Q.K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1G1L1I1Y1L1P1E1I1K2.Y
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	7.1167	0.4335	3589.88	3591.177	1	1932.6	37.931034	K.V1Q2K2D1L1I1E1P1L1D1P1K2D1I1E1I1K2P1D1G1L1I1Y1L1P1E1I1K2Y1R4.R
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	3.8709	0.2334	3324.47	3325.913	1	517.3	23.148148	Q.KDLIEPLDPKDIEIKPDGLIYLPEIKYR.R
gi|6322608|ref|NP_012682.1|	YJR148W	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase; Bat2p	1	2.4314	0.2151	1383.62	1384.629	1	543.3	54.166668	K.K2E1L1V1T1A1P1L1D1G1T1I1L1.E
gi|6322608|ref|NP_012682.1|	YJR148W	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase; Bat2p	2	3.9975	0.2642	1384.29	1384.629	1	961	70.83333	K.K2E1L1V1T1A1P1L1D1G1T1I1L1.E
gi|6322608|ref|NP_012682.1|	YJR148W	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase; Bat2p	2	3.3479	0.2444	1903.25	1904.136	1	640.5	56.666668	S.AQRICLPTFDPEELIT.L
gi|6322608|ref|NP_012682.1|	YJR148W	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase; Bat2p	2	4.0931	0.2958	2038.35	2038.296	1	575.9	53.125	S.A1Q2R4I1C1L1P1T1F1D1P1E1E1L1I1T1L1.I
gi|6322608|ref|NP_012682.1|	YJR148W	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase; Bat2p	2	4.5097	0.3999	2017.67	2017.296	1	532	53.125	S.AQRICLPTFDPEELITL.I
gi|6322852|ref|NP_012925.1|	YKL001C	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine 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	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism; Met14p	1	2.3994	0.236	1277.62	1278.467	5	110	50	Y.E1A1P1K2A1P1E1L1H3L1R4.T
gi|6322852|ref|NP_012925.1|	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
gi|6322852|ref|NP_012925.1|	YKL001C	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism; Met14p	3	4.5746	0.3782	1541.51	1540.759	1	1440	60.416668	A.P1Y1E1A1P1K2A1P1E1L1H3L1R4.T
gi|6322852|ref|NP_012925.1|	YKL001C	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine 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	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism; Met14p	2	4.1256	0.3982	1698.17	1700.916	1	592.8	60.714287	I.S1A1P1Y1E1A1P1K2A1P1E1L1H3L1R4.T
gi|6322852|ref|NP_012925.1|	YKL001C	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism; Met14p	2	4.4298	0.3398	1611.79	1612.838	1	845.3	73.07692	S.A1P1Y1E1A1P1K2A1P1E1L1H3L1R4.T
gi|6322852|ref|NP_012925.1|	YKL001C	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism; Met14p	2	3.1044	0.2568	1666.51	1664.842	1	524.9	66.66667	T.W2H3P1N2L1T1Y1D1E1R4K2A1L1.R
gi|6322848|ref|NP_012921.1|	YKL005C	Negative regulator of transcription elongation, contains a TFIIS-like domain and a PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably binds RNA polymerase II large subunit; Bye1p	2	4.8211	0.2773	2457.41	2455.813	1	668.5	50	K.TRYEKDFYIVPSKGGEIPEIL.K
gi|6322848|ref|NP_012921.1|	YKL005C	Negative regulator of transcription elongation, contains a TFIIS-like domain and a PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably binds RNA polymerase II large subunit; Bye1p	2	5.1814	0.3727	2480.55	2481.813	1	835.7	57.5	K.T1R4Y1E1K2D1F1Y1I1V1P1S1K2G1G1E1I1P1E1I1L1.K
gi|6322848|ref|NP_012921.1|	YKL005C	Negative regulator of transcription elongation, contains a TFIIS-like domain and a PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably binds RNA polymerase II large subunit; Bye1p	3	6.7108	0.4209	3224.63	3224.464	1	919.6	36	A.K2S1D1T1A1E1N2E1M1P1T1R4K2D1F1E1S1E1K2E1H3K2L1R4Y1N2.A
gi|6322848|ref|NP_012921.1|	YKL005C	Negative regulator of transcription elongation, contains a TFIIS-like domain and a 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.KSDTAENEMPTRKDFESEKEHKLRYN.A
gi|6322842|ref|NP_012915.1|	YKL010C	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 ubiquitin fusion proteins; Ufd4p	1	2.8845	0.2764	1416.64	1417.651	1	491.7	62.5	L.GQHPVGRTLPEIL.S
gi|6322842|ref|NP_012915.1|	YKL010C	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 ubiquitin fusion proteins; Ufd4p	2	3.7503	0.1695	1965.35	1965.963	1	1291.7	63.333332	S.STEADREEEENCLDHM.R
gi|6322842|ref|NP_012915.1|	YKL010C	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 ubiquitin fusion proteins; Ufd4p	2	3.3699	0.2551	2054.67	2055.158	2	465.6	46.875	L.E1N2P1S1T1P1D1K2T1E1E1D1W2K2G1I1W2.S
gi|6322842|ref|NP_012915.1|	YKL010C	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 ubiquitin fusion proteins; Ufd4p	2	3.0254	0.1544	1479.61	1478.775	7	387.8	57.692307	Q.F1L1T1G1S1P1K2L1P1I1G1G1F1K2.S
gi|6322842|ref|NP_012915.1|	YKL010C	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 ubiquitin fusion proteins; Ufd4p	2	2.9633	0.2385	2032.33	2033.158	2	437.6	43.75	L.ENPSTPDKTEEDWKGIW.S
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	3.0485	0.1831	1690.45	1690.936	1	779.1	69.230774	N.E1F1H3T1R4I1P1D1L1P1I1F1V1S1.T
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	2.979	0.3197	1950.55	1951.341	4	318.6	43.75	Y.F1D1F1S1L1P1I1L1P1R4L1L1V1P1S1K2S1.E
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	3.6618	0.4394	1495.93	1496.75	1	624.7	75	F.HTRIPDLPIFVST.L
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	2.9439	0.2408	1053.29	1053.333	5	664.4	75	Q.LTNPILRLL.K

gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	3.4034	0.2868	1690.59	1690.875	1	369.4	46.42857	K.S1R4L1P1Q2D1D1I1L1N2N2I1G1T1L1.R
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	5.2012	0.4154	2158.47	2159.305	1	2059.9	70.588234	W.E1F1I1K2D1E1E1E1E1I1L1E1A1I1G1D1T1R4.L
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	3.5009	0.353	1674.09	1671.936	1	456.9	61.538464	N.EFHTRIPDLPIFVS.T
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	3.0381	0.3227	1514.85	1514.75	1	346.9	62.5	F.H3T1R4I1P1D1L1P1I1F1V1S1T1.L
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	2.9631	0.3498	1396.01	1395.644	1	370.7	72.72727	F.HTRIPDLPIFVS.T
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	3.1565	0.2368	1206.45	1205.442	1	497.3	77.77778	Y.FDFSLPILPR.L
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	5.6854	0.3223	2139.79	2137.305	1	1984.8	70.588234	W.EFIKDEEEEILEAIGDTR.L
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	3.1756	0.3037	1732.33	1733.089	3	258.1	42.857143	Y.F1D1F1S1L1P1I1L1P1R4L1L1V1P1S1.K
gi|6322838|ref|NP_012911.1|	YKL014C	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 biogenesis of the 60S ribosomal subunit; Urb1p	2	3.2554	0.2792	1414.03	1412.644	1	316.6	68.181816	F.H3T1R4I1P1D1L1P1I1F1V1S1.T
gi|6322833|ref|NP_012906.1|	YKL019W	Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase 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
gi|6322833|ref|NP_012906.1|	YKL019W	Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase 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
gi|6322833|ref|NP_012906.1|	YKL019W	Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor; Ram2p	2	3.2255	0.2494	1363.71	1361.535	2	809.4	80	N.KELDWLDEVTL.N
gi|6322833|ref|NP_012906.1|	YKL019W	Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor; Ram2p	2	3.3245	0.2355	1374.85	1374.535	1	897.3	80	N.K2E1L1D1W2L1D1E1V1T1L1.N
gi|6322833|ref|NP_012906.1|	YKL019W	Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor; Ram2p	2	3.8365	0.309	2678.67	2678.955	1	401.6	42.857143	Y.D1Y1S1D1V1K2P1L1P1I1E1T1D1L1Q2D1E1L1C1R4I1M1.Y
gi|6322833|ref|NP_012906.1|	YKL019W	Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor; Ram2p	2	3.1182	0.2838	2651.89	2651.955	1	531.9	45.238094	Y.DYSDVKPLPIETDLQDELCRIM.Y
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	3.3686	0.3153	2542.55	2543.858	1	381.4	40.476192	L.S1L1D1I1P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1.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	3	4.7875	0.1946	3009.08	3012.049	4	407.9	28.125	C.E1E1L1F1E1K2V1E1E1N2E1K2Q2E1D1D1D1D1K2E1D1I1S1P1A1.F
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	4.9192	0.3785	3583.1	3583.657	1	758.8	26.785713	H.F1Y1P1C1E1E1L1F1E1K2V1E1E1N2E1K2Q2E1D1D1D1D1K2E1D1I1S1P1A1.F
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	5.0356	0.4695	2627.42	2629.938	1	903.2	40.476192	L.D1I1P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1H3F1.Q
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	4.0514	0.2081	2543.3	2543.858	1	561.1	35.714287	L.S1L1D1I1P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1.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.S1L1D1I1P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1.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.D1I1P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1H3F1Q2.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.S1L1D1I1P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1H3F1Q2.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
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	3.3805	0.3241	2629.43	2629.938	1	543.5	45.238094	L.D1I1P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1H3F1.Q
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	4.8339	0.3578	2960.3	2962.307	1	833.5	31.25	L.S1L1D1I1P1N2Q2K2E1N2D1A1A1K2T1P1H3F1M1P1I1F1H3F1Q2.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	4.6074	0.4267	2598.74	2598.938	1	882.3	41.666664	L.DIPNQKENDAAKTPHFMPIFHF.Q
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	3.4742	0.3428	2798.71	2799.176	1	416	39.130436	L.SLDIPNQKENDAAKTPHFMPIFHF.Q
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	3	4.6774	0.3459	4507.49	4509.266	1	557.9	23.571428	L.N2K2E1E1E1E1E1E1E1E1E1E1D1E1E1E1E1E1E1E1E1M1E1D1V1M1D1D1N2D1 E1T1A1R4E1N2.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	3	7.6343	0.4992	4351.07	4352.162	1	2432.5	30.882353	N.KEEEEEEEEEEDEEEEEEEEMEDVMDDNDETAREN.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	3	8.0651	0.5832	4464.89	4466.266	1	3761.2	32.857143	L.NKEEEEEEEEEEDEEEEEEEEMEDVMDDNDETAREN.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	3	7.526	0.4655	4579.43	4579.425	1	1386.2	25	K.LNKEEEEEEEEEEDEEEEEEEEMEDVMDDNDETAREN.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	3	6.7481	0.3484	4622.12	4623.425	1	1449.5	25.694445	K.L1N2K2E1E1E1E1E1E1E1E1E1E1D1E1E1E1E1E1E1E1E1M1E1D1V1M1D1D1N 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	3	8.6648	0.5778	4390.76	4393.162	1	2936.3	32.352943	N.K2E1E1E1E1E1E1E1E1E1D1E1E1E1E1E1E1E1M1E1D1V1M1D1D1N2D1E1T1A1R4E1N2.A
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	3	5.6986	0.4112	2602.64	2601.791	1	1065.4	40.476192	T.R4E1N2T1F1Q2K2P1Y1S1D1E1E1V1T1K2T1P1V1G1S1R4.A
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	3.2438	0.1537	2593.79	2593.905	2	573.7	42.857143	R.FRKPEGVFLDITEPDSIECRLA.T
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	3.5254	0.2641	1657.39	1655.761	1	1713.5	80.769226	Y.RYELPSFNDDIQGT.G
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	3.1055	0.2551	1674.23	1674.761	2	699	57.692307	Y.R4Y1E1L1P1S1F1N2D1D1I1Q2G1T1.G
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	3.2447	0.3504	1387.35	1387.703	1	1011.5	77.27273	H.IKELVPIIYTPT.E
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	3.0245	0.3028	2010.53	2013.215	1	424.3	50	L.REGDSRPGLLPGLDTITNT.S
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	3.239	0.2714	2568.91	2569.791	3	207.5	35.714287	T.RENTFQKPYSDEEVTKTPVGSR.A
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	4.4748	0.4312	2407.85	2409.667	1	554.8	50	R.FRKPEGVFLDITEPDSIECR.L
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	2.9379	0.1615	1209.41	1209.466	1	847.9	87.5	Q.MWEPVYRPM.I
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	2	2.9351	0.279	2656.49	2657.863	1	176.2	34.782608	E.QEQVPGGAPGETVKVPRDFDECLQ.W
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	3	5.6625	0.329	2569.19	2569.791	1	1114.7	39.285713	T.RENTFQKPYSDEEVTKTPVGSR.A
gi|6322823|ref|NP_012896.1|	YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	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-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	4.4603	0.4378	2066.43	2067.269	1	1273.4	67.64706	Y.K2D1S1L1L1P1V1P1T1E1Y1D1S1P1L1D1A1W2.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	2	4.1499	0.3856	2787.73	2788.085	1	783.2	41.666664	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.S1D1G1H3K2I1D1I1P1N2G1S1I1L1.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-Glc 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-Glc 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	2	4.1885	0.287	1969.53	1969.183	1	660.1	60.000004	L.E1W2D1K2I1K2S1P1N2P1D1E1V1V1K2Y1.E
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	3	4.2592	0.3106	2928.32	2928.993	1	592.3	30.000002	T.GGEEDGVNNENADKEDLYTKPEQVYN.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	3	4.4103	0.3289	2960.42	2961.993	1	918	33	T.G1G1E1E1D1G1V1N2N2E1N2A1D1K2E1D1L1Y1T1K2P1E1Q2V1Y1N2.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	3.6422	0.2856	2959.83	2961.993	1	232.7	34	T.G1G1E1E1D1G1V1N2N2E1N2A1D1K2E1D1L1Y1T1K2P1E1Q2V1Y1N2.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	3.7029	0.3743	2928.39	2928.993	1	196.1	32	T.GGEEDGVNNENADKEDLYTKPEQVYN.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	3	4.1609	0.1782	2814.26	2814.89	6	490.8	29.166666	T.GGEEDGVNNENADKEDLYTKPEQVY.N

gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	3	4.0529	0.2982	3189.68	3191.302	2	331.2	23.148148	T.GGEEDGVNNENADKEDLYTKPEQVYNVY.K
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	4.8257	0.3692	2056.37	2057.178	1	426.4	59.375	N.ENADKEDLYTKPEQVYN.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	3.5129	0.1855	2342.55	2343.486	3	190.1	36.11111	N.E1N2A1D1K2E1D1L1Y1T1K2P1E1Q2V1Y1N2V1Y1.K
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	4.9303	0.3624	2103.31	2101.382	1	763.6	47.22222	K.DYIMSPVGNPEGPEKPNKK.F
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	1	2.7208	0.2333	989.44	990.151	1	291.9	68.75	Y.K2A1L1H3P1I1S1P1N2.F
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	1	2.5443	0.2047	976.46	977.151	5	299.4	68.75	Y.KALHPISPN.F
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	4.4598	0.3627	2078.97	2079.178	3	216.6	46.875	N.E1N2A1D1K2E1D1L1Y1T1K2P1E1Q2V1Y1N2.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	4.0454	0.4631	1725.77	1725.942	1	730.7	63.333332	M.SPVGNPEGPEKPNKKF.F
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	4.3902	0.4862	1745.51	1746.942	1	1135.2	70	M.S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2F1.F
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	4.6217	0.317	2254.07	2255.556	1	1008.2	55.263157	K.K2D1Y1I1M1S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2.F
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	2.9738	0.1511	2794.85	2796.128	3	182.6	28.260868	K.D1Y1I1M1S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2F1F1D1P1R4.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	3.1157	0.2806	2762.19	2764.128	1	366.3	36.95652	K.DYIMSPVGNPEGPEKPNKKFFDPR.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	2.9106	0.2646	3085.01	3084.474	5	110.4	26	K.D1Y1I1M1S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2F1F1D1P1R4V1W2.V
gi|6322790|ref|NP_012863.1|	YKL060C	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; 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	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; Fba1p	2	3.9681	0.4153	1578.53	1578.765	1	830	71.42857	M.SPVGNPEGPEKPNKK.F
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	3	3.9808	0.2519	2012.15	2011.207	1	825.2	39.705883	M.S1P1V1G1N2P1E1G1P1E1K2P1N2K2K2F1F1D1.P
gi|6322790|ref|NP_012863.1|	YKL060C	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; Fba1p	2	3.0918	0.3517	2242.77	2241.511	1	254.1	47.368423	M.SPVGNPEGPEKPNKKFFDPR.V
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	3.9391	0.3316	1643.89	1644.934	1	738	60.714287	D.S1L1L1D1I1V1K2P1I1N2D1A1V1T1K2.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	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.F1E1T1E1F1A1D1T1I1D1N2V1R4E1E1F1K2K2I1K2Q2P1A1.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	2	3.1722	0.2733	1963.75	1964.188	1	334.7	50	K.RLPGYGKDDPNGIERIY.G
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	3.2357	0.1884	1893.61	1892.223	1	585.3	60.000004	N.AYRTLPINNMPVPEYL.E
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	3.6496	0.2935	1429.29	1426.612	1	673.5	72.72727	L.HDIVKPEDFVLN.S
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	5.4576	0.4521	2306.47	2307.619	1	1060.2	63.88889	N.A1Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1E1N2F1.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	1	3.1055	0.1598	1561.61	1562.702	1	538.6	62.5	K.S1L1K2S1D1F1E1K2S1Y1E1T1L1.S
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	1	2.5778	0.3297	1546.63	1547.702	1	447.3	58.333332	K.SLKSDFEKSYETL.S
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	4.7052	0.2542	1646.29	1644.85	1	795.8	69.230774	R.S1L1H3D1I1V1K2P1E1D1F1V1L1N2.S
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	4.7488	0.3344	2086.37	2087.364	1	654.9	59.375	Y.R4T1L1P1I1N2N2M$P1V1P1E1Y1L1E1N2F1.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	5.2461	0.4698	2046.47	2048.364	1	986.3	68.75	Y.RTLPINNMPVPEYLENF.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	3	4.6928	0.3721	3615.02	3617.015	1	425	25	N.D1F1I1L1I1S1L1P1Q2N2A1Q2P1V1T1A1P1G1S1K2T1D1S1W2F1N2E1T1L1I1G1G1R4.A
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	1	3.453	0.1861	1387.71	1387.703	6	605.5	63.636364	F.KLDKSIKDLITL.I
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	4.945	0.4356	2323.19	2323.619	1	919.2	58.333332	N.A1Y1R4T1L1P1I1N2N2M$P1V1P1E1Y1L1E1N2F1.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	5.4989	0.3574	2071.23	2071.364	1	1194.3	68.75	Y.R4T1L1P1I1N2N2M1P1V1P1E1Y1L1E1N2F1.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	5.1886	0.4511	2284.97	2282.619	1	1764	75	N.AYRTLPINNMPVPEYLENF.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	4.3349	0.2607	1627.55	1626.85	1	838.1	73.07692	R.SLHDIVKPEDFVLN.S
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	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	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the 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

gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	2.9736	0.2517	2212.99	2211.54	1	537.3	47.058823	A.YRTLPINNMPVPEYLENF.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	3.969	0.2224	1387.57	1387.703	1	1031.6	81.818184	F.KLDKSIKDLITL.I
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	1	2.8572	0.1711	1205.44	1206.416	2	728.4	66.66667	S.D1F1K2I1P1E1F1K2I1G1.S
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	1	2.5978	0.1774	1193.54	1194.416	6	574.2	61.11111	S.DFKIPEFKIG.S
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	3.2529	0.2502	1913.71	1913.223	2	445	56.666668	N.A1Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1.E
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	4.6711	0.4999	2298.39	2298.619	1	1453.2	66.66667	N.AYRTLPINNM@PVPEYLENF.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	4.7031	0.3719	2285.55	2282.619	1	1192.9	66.66667	N.AYRTLPINNMPVPEYLENF.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	3	4.6468	0.3248	2306.48	2307.619	1	696.6	37.5	N.A1Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1E1N2F1.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	3	4.6015	0.3174	2283.17	2282.619	1	1517.8	48.61111	N.AYRTLPINNMPVPEYLENF.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	2	5.5646	0.4129	2308.59	2307.619	1	1074.7	63.88889	N.A1Y1R4T1L1P1I1N2N2M1P1V1P1E1Y1L1E1N2F1.Q
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	1	3.1693	0.1957	1439.82	1440.685	1	283.9	65	A.A1R4E1K2K2F1I1P1R4E1F1.N
gi|6322770|ref|NP_012843.1|	YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	1	2.9677	0.2223	1421.74	1421.685	1	250.6	60.000004	A.AREKKFIPREF.N
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
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.5258	0.2472	1826.23	1826.967	3	276.3	53.571426	T.K2L1D1P1T1K2E1E1D1K2E1F1V1N2N2.M
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	5.0461	0.3967	2330.39	2331.556	1	614.2	52.77778	Y.EYTKLDPTKEEDKEFVNNM.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.I1V1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.6392	0.2193	1317.5	1318.501	3	135.2	65	Q.V1A1D1E1K2E1R4A1R4L1L1.G
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	3.9767	0.3157	2862.89	2864.285	1	409.9	24	K.I1V1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi|6322769|ref|NP_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
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.0479	0.1706	1373.57	1370.594	1	796.6	77.77778	T.FVLDDWKRKY.S
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.3893	0.1854	1389.43	1386.594	1	1074.3	88.88889	T.F1V1L1D1D1W2K2R4K2Y1.S
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	L.D1V1K2I1V1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2G1L1 .K
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	4.0081	0.2396	3344.06	3346.891	2	538.6	21.666666	L.DVKIVDLEQSSEFASLFPLKQAPAFLGPKGL.K
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.8198	0.4514	2244.37	2243.632	1	697.1	52.499996	S.S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2G1L1.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
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.2137	0.1646	2756.69	2756.063	7	298.5	33.333336	T.F1V1L1D1D1W2K2R4K2Y1S1N2D1D1T1R4P1V1A1L1P1W2.F
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	5.4341	0.4594	1861.59	1863.056	1	2000.6	78.125	W.D1K2P1V1V1V1N2G1E1D1K2E1I1V1D1G1K2.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
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	5.1084	0.3868	1958.59	1959.16	1	731.4	60.000004	T.K2L1D1P1T1K2E1E1D1K2E1F1V1N2N2M1.W
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.4274	0.268	1475.37	1474.741	1	716.7	65.38461	V.A1A1S1P1I1V1K2T1P1F1A1E1V1K2.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.I1V1D1L1E1Q2S1S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	4.6998	0.4029	3001.55	3004.496	1	1093	33.333336	K.IVDLEQSSEFASLFPLKQAPAFLGPKGL.K
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.0818	0.4387	1883.07	1884.097	1	668.9	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
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.6356	0.3392	1907.91	1907.097	1	395.4	58.823532	S.K2A1E1K2K2K2D1E1A1K2P1A1D1D1A1A1P1A1.K
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	1	2.4315	0.1741	1385.59	1386.594	1	486.2	66.66667	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	41.666664	S.S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2.G
gi|6322769|ref|NP_012842.1|	YKL081W	Translation 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	3.2307	0.3474	1703.71	1701.963	2	726.3	53.333336	A.DDAAPAKKPKHPLEAL.G
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	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|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	4.0589	0.3001	2724.77	2723.063	1	665.9	35.714287	T.FVLDDWKRKYSNDDTRPVALPW.F
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	5.25	0.3707	2470.63	2471.79	1	870.1	45.454548	K.K2D1E1A1K2P1A1D1D1A1A1P1A1K2K2P1K2H3P1L1E1A1L1.G
gi|6322769|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	Translation elongation factor EF-1 gamma; Tef4p	1	2.7281	0.1813	1427.3	1428.473	1	404.5	61.11111	W.F1W2E1H3Y1N2P1E1E1Y1.S
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.0523	0.2687	2222.13	2223.364	1	667.2	55.88235	Y.E1Y1T1K2L1D1P1T1K2E1E1D1K2E1F1V1N2N2.M
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.505	0.1927	2199.49	2200.364	1	308.7	50	Y.EYTKLDPTKEEDKEFVNN.M
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.7208	0.3049	2147.17	2147.373	1	733.4	53.125	T.K2L1D1P1T1K2E1E1D1K2E1F1V1N2N2M1W2.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	Translation elongation factor EF-1 gamma; Tef4p	1	3.7008	0.3163	1473.69	1474.741	1	657.7	61.538464	V.A1A1S1P1I1V1K2T1P1F1A1E1V1K2.L
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	53.846157	V.AASPIVKTPFAEVK.L
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	4.358	0.3602	2406.67	2407.665	1	543.2	44.444447	T.K2L1D1P1T1K2E1E1D1K2E1F1V1N2N2M1W2A1W2.D
gi|6322769|ref|NP_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.SPIVKTPFAEVK.L
gi|6322769|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	72.72727	S.KAEKKKDEAKPA.D
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.K2A1E1K2K2K2D1E1A1K2P1A1.D
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	3	3.9037	0.2929	2037.44	2037.271	4	473.9	30.555555	S.K2A1E1K2K2K2D1E1A1K2P1A1D1D1A1A1P1A1K2.K
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.0449	0.1687	1722.39	1722.963	3	520.5	50	A.D1D1A1A1P1A1K2K2P1K2H3P1L1E1A1L1.G
gi|6322769|ref|NP_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.S1E1F1A1S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2G1L1.K
gi|6322769|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.L1T1Y1T1P1P1K2K2Q2K2A1E1K2P1K2A1E1.K
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.3929	0.1959	1529.85	1527.893	1	830.2	73.07692	S.LFPLKQAPAFLGPK.G
gi|6322769|ref|NP_012842.1|	YKL081W	Translation elongation factor EF-1 gamma; Tef4p	2	3.6971	0.3363	1802.43	1805.183	1	706	56.25	A.S1L1F1P1L1K2Q2A1P1A1F1L1G1P1K2G1L1.K
gi|6322765|ref|NP_012838.1|	YKL085W	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and 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
gi|6322765|ref|NP_012838.1|	YKL085W	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and 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
gi|6322765|ref|NP_012838.1|	YKL085W	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and 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
gi|6322765|ref|NP_012838.1|	YKL085W	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and 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	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p	2	3.1145	0.3003	1563.81	1562.763	1	595.7	53.571426	L.GPDGIEKIHPIGELS.S
gi|6322762|ref|NP_012835.1|	YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2	2.9146	0.2067	1787.45	1787.139	1	402.5	43.333332	S.V1M1R4D1W2S1P1L1T1P1V1L1I1A1P1A1.M
gi|6322762|ref|NP_012835.1|	YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2	3.5387	0.3747	1782.65	1785.067	1	559.4	64.28571	N.S1I1V1H3M1P1G1D1F1I1Y1F1N2P1K2.S
gi|6322762|ref|NP_012835.1|	YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2	3.507	0.3515	2056.43	2059.366	1	293.5	41.17647	N.K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q
gi|6322762|ref|NP_012835.1|	YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2	4.3109	0.3099	2036.69	2037.366	1	798.7	61.764706	N.KEVITAPTGPRVPFTEFF.Q
gi|6322762|ref|NP_012835.1|	YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2	3.3226	0.2884	1768.75	1766.067	1	681.7	67.85714	N.SIVHMPGDFIYFNPK.S
gi|6322762|ref|NP_012835.1|	YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2	2.9752	0.1909	1681.35	1680.885	1	290	45.833336	F.T1V1P1E1V1E1R4L1P1Y1H3R4Y1.S
gi|6322762|ref|NP_012835.1|	YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2	4.7176	0.2681	2175.19	2175.47	1	934.9	58.333332	K.N2K2E1V1I1T1A1P1T1G1P1R4V1P1F1T1E1F1F1.Q
gi|6322762|ref|NP_012835.1|	YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	2	3.7043	0.3526	2150.33	2151.47	1	601.4	47.22222	K.NKEVITAPTGPRVPFTEFF.Q
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	3.5963	0.154	1708.31	1706.977	1	560.3	57.692307	L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1.D
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	3.8344	0.2881	2690.39	2689.823	1	463.1	38.095238	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	3.9997	0.4113	2660.87	2662.823	1	438.3	38.095238	S.NFDEEFTREKPIDSVVDEYLSE.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	3.0329	0.2087	2697.69	2699.163	1	378.1	30.434782	K.ILQEPLVFPDGFDRDAKDLLIGLL.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	3.1419	0.1642	2240.59	2239.597	8	317.7	36.842106	E.P1L1V1F1P1D1G1F1D1R4D1A1K2D1L1L1I1G1L1L1.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	3.8362	0.3267	2700.8	2699.163	2	430.4	30.434782	K.ILQEPLVFPDGFDRDAKDLLIGLL.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	3.6511	0.3028	2115.97	2117.372	2	477.7	53.125	L.D1V1V1Y1R4D1L1K2P1E1N2I1L1L1D1Y1Q2.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	3.7575	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.VFPDGFDRDAKDLLIGLL.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	3.6942	0.3432	2024.93	2027.321	1	629	47.058823	L.V1F1P1D1G1F1D1R4D1A1K2D1L1L1I1G1L1L1.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.I1L1Q2E1P1L1V1F1P1D1G1F1D1R4D1A1K2D1L1L1I1G1L1L1.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.I1L1Q2E1P1L1V1F1P1D1G1F1D1R4D1A1K2D1L1L1I1G1L1L1.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	3	4.26	0.3182	2692.19	2689.823	1	1026.2	35.714287	S.N2F1D1E1E1F1T1R4E1K2P1I1D1S1V1V1D1E1Y1L1S1E1.S
gi|6322722|ref|NP_012795.1|	YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	2	3.7511	0.308	2288.33	2289.489	1	795.4	52.63158	Q.N2W2H3P1L1P1D1F1G1G1L1H3P1D1P1N2L1T1Y1A1.R
gi|6322722|ref|NP_012795.1|	YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	2	2.9576	0.3419	2260.65	2262.489	1	668.3	44.736843	Q.NWHPLPDFGGLHPDPNLTYA.R
gi|6322722|ref|NP_012795.1|	YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	2	3.0708	0.1724	2150.43	2148.385	3	296.5	36.11111	N.WHPLPDFGGLHPDPNLTYA.R
gi|6322722|ref|NP_012795.1|	YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	2	4.3697	0.4401	2217.61	2217.41	1	726.6	50	Q.N2W2H3P1L1P1D1F1G1G1L1H3P1D1P1N2L1T1Y1.A
gi|6322722|ref|NP_012795.1|	YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	2	3.6606	0.3126	2172.33	2173.385	1	437.1	41.666664	N.W2H3P1L1P1D1F1G1G1L1H3P1D1P1N2L1T1Y1A1.R
gi|6322722|ref|NP_012795.1|	YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	2	4.396	0.3221	2100.39	2101.306	1	594.6	52.941177	N.W2H3P1L1P1D1F1G1G1L1H3P1D1P1N2L1T1Y1.A
gi|6322722|ref|NP_012795.1|	YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	2	3.2985	0.304	2191.49	2191.41	1	628.3	47.22222	Q.NWHPLPDFGGLHPDPNLTY.A
gi|6322722|ref|NP_012795.1|	YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	2	4.2	0.4248	2075.91	2077.306	1	581.1	55.88235	N.WHPLPDFGGLHPDPNLTY.A
gi|6322720|ref|NP_012793.1|	YKL129C	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p	2	3.6159	0.2427	2268.79	2269.563	5	164.7	34.210526	N.G1I1T1D1K2N2K2D1Q2L1Q2K2D1L1I1E1L1I1G1T1.T
gi|6322720|ref|NP_012793.1|	YKL129C	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p	2	3.6085	0.2053	1830.43	1830.089	1	821	63.333332	K.NKDQLQKDLIELIGTT.T
gi|6322720|ref|NP_012793.1|	YKL129C	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p	1	3.4674	0.427	1207.54	1208.406	1	299.5	72.22222	K.NRLEVPPHVF.A
gi|6322720|ref|NP_012793.1|	YKL129C	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p	1	3.688	0.2438	1223.61	1224.406	1	346.4	77.77778	K.N2R4L1E1V1P1P1H3V1F1.A
gi|6322720|ref|NP_012793.1|	YKL129C	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p	1	2.718	0.1886	1317.56	1318.521	1	289.9	66.66667	Q.IKNERNFHIF.Y
gi|6322720|ref|NP_012793.1|	YKL129C	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect 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	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p	2	3.6641	0.3224	2343.75	2344.668	1	335.5	37.5	N.GITDKNKDQLQKDLIELIGTT.T
gi|6322720|ref|NP_012793.1|	YKL129C	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has 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.LFDWIVDRV.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|	YKL143W	Protein required for growth at low temperature; Ltv1p	1	3.4427	0.3	1580.67	1580.824	2	498.3	57.692307	Q.HLKPIGLDPENSIF.I
gi|6322706|ref|NP_012779.1|	YKL143W	Protein required for growth at low temperature; Ltv1p	2	3.0962	0.1594	1983.87	1985.158	2	567.1	50	M.LDDFLDNYELESGGRKL.A
gi|6322706|ref|NP_012779.1|	YKL143W	Protein required for growth at low temperature; Ltv1p	3	4.4343	0.2207	3793.25	3794.765	7	467.3	20.689655	E.A1K2D1E1D1E1F1E1D1E1F1D1E1W2D1I1D1N2V1E1N2F1E1D1E1N2Y1V1K2E1M
gi|6322706|ref|NP_012779.1|	YKL143W	Protein required for growth at low temperature; Ltv1p	2	3.7023	0.2703	1596.85	1598.824	1	661.3	65.38461	Q.H3L1K2P1I1G1L1D1P1E1N2S1I1F1.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.K2Q2T1E1N2D1L1K2D1I1E1A1R4.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.K2Y1N2I1E1L1P1L1P1P1R4I1D1P1S1V1T1.M
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	4.6378	0.3893	1705.21	1704.976	1	813.5	73.07692	L.R4E1V1V1E1L1P1L1L1S1P1E1R4F1.A
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	4.4046	0.4428	1685.27	1684.976	1	860.7	69.230774	L.REVVELPLLSPERF.A
gi|6322699|ref|NP_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.SPKDQGELIGIL.N
gi|6322699|ref|NP_012772.1|	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.8534	0.2524	1571.83	1572.798	1	1331.3	75	G.DDKWIDLPISKIE.E
gi|6322699|ref|NP_012772.1|	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; 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	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.548	0.2235	1452.21	1452.579	1	965.3	86.36364	A.H3H3I1V1E1N2P1N2D1K2T1K2.V
gi|6322699|ref|NP_012772.1|	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
gi|6322699|ref|NP_012772.1|	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.6439	0.2135	1645.27	1645.815	3	492.2	69.230774	A.HHIVENPNDKTKVN.L
gi|6322699|ref|NP_012772.1|	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.4602	0.1725	1761.95	1758.975	2	397.7	60.714287	A.HHIVENPNDKTKVNL.L
gi|6322699|ref|NP_012772.1|	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.0582	0.3729	2075.67	2077.388	1	499.4	47.22222	K.FVTPKGSNVVRPYTPVSDL.S
gi|6322699|ref|NP_012772.1|	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol 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
gi|6322699|ref|NP_012772.1|	YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	2	3.303	0.2017	1588.67	1588.798	1	927.9	66.66667	G.D1D1K2W2I1D1L1P1I1S1K2I1E1.E
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.6647	0.3365	1620.19	1620.797	1	643.1	61.538464	Y.K2Y1V1D1P1N2V1L1P1E1T1E1S1L1.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.6501	0.3613	1947.73	1949.164	1	516.5	53.333336	L.V1F1E1L1D1E1N2L1K2P1S1K2P1S1Y1Y1.L
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.6675	0.1644	1929.33	1930.164	1	646.4	60.000004	L.VFELDENLKPSKPSYY.L
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.8875	0.3349	2226.37	2225.417	1	636.5	58.333332	K.GDERYKYVDPNVLPETESL.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	4.9447	0.3632	2596.47	2597.8	1	465.4	42.857143	F.S1Q2K2G1D1E1R4Y1K2Y1V1D1P1N2V1L1P1E1T1E1S1L1.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	4.8872	0.3913	2035.67	2037.418	1	725.3	56.25	L.A1L1V1I1D1R4L1L1P1Y1W2Q2D1V1I1A1K2.D
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.0333	0.2055	2013.69	2014.418	1	517.2	40.625	L.ALVIDRLLPYWQDVIAK.D
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	1	2.9042	0.2521	1573.64	1574.746	1	192.8	53.846157	Y.R4R4S1F1D1V1P1P1P1P1I1D1A1S1.S
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	4.2658	0.4094	1605.39	1604.797	1	677.5	61.538464	Y.KYVDPNVLPETESL.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.2925	0.1597	1699.71	1700.855	1	327.5	57.692307	F.E1L1D1E1N2L1K2P1S1K2P1S1Y1Y1.L

gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	4.033	0.2992	2282.51	2280.493	1	677	52.63158	F.ELDENLKPSKPSYYLDPEAA.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.4412	0.2805	2305.49	2303.493	1	533.2	44.736843	F.E1L1D1E1N2L1K2P1S1K2P1S1Y1Y1L1D1P1E1A1A1.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	2.9227	0.2086	1922.71	1923.13	1	528.7	53.125	D.ENLKPSKPSYYLDPEAA.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.3999	0.2341	1621.55	1620.813	1	923.3	65.38461	L.V1F1E1L1D1E1N2L1K2P1S1K2P1S1.Y
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.7737	0.3254	2248.37	2249.417	1	423.6	50	K.G1D1E1R4Y1K2Y1V1D1P1N2V1L1P1E1T1E1S1L1.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.2206	0.2333	2525.69	2526.802	1	223.4	38.095238	L.VFELDENLKPSKPSYYLDPEAA.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.6672	0.3536	2549.73	2551.802	2	209.3	38.095238	L.V1F1E1L1D1E1N2L1K2P1S1K2P1S1Y1Y1L1D1P1E1A1A1.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	3.5904	0.2919	2567.87	2568.8	1	395.6	42.857143	F.SQKGDERYKYVDPNVLPETESL.A
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	4.1921	0.3795	1858.03	1856.957	1	791.1	64.28571	R.H3G1Q2S1E1W2N2E1K2N2L1F1T1G1W2.V
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	2	4.1742	0.4246	1698.27	1696.816	1	1474.1	80.769226	H.GQSEWNEKNLFTGW.V
gi|6322697|ref|NP_012770.1|	YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	1	2.6185	0.2278	1309.47	1310.44	1	356.3	61.11111	E.W2N2E1K2N2L1F1T1G1W2.V
gi|9755335|ref|NP_012765.2|	YKL157W	Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p	2	3.2899	0.2542	1430.03	1427.594	1	1087.1	72.72727	R.SKTIELEDPTFF.K
gi|9755335|ref|NP_012765.2|	YKL157W	Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p	2	3.0454	0.3827	1612.63	1612.779	1	509.1	62.5	L.HYDLTVEPDFKTF.K
gi|9755335|ref|NP_012765.2|	YKL157W	Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p	2	3.0655	0.1766	1801.43	1799.975	3	331.6	53.571426	L.SERSKTIELEDPTFF.K
gi|9755335|ref|NP_012765.2|	YKL157W	Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p	1	2.4398	0.2498	1163.59	1164.396	2	111	68.75	K.NFRIPVRVY.A
gi|9755335|ref|NP_012765.2|	YKL157W	Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis 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	2	5.0984	0.3271	1955.31	1957.044	1	1565.4	75	S.Q2F1D1R4Y1P1E1E1E1F1N2Y1G1I1Q2.G
gi|6322676|ref|NP_012749.1|	YKL172W	Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p	2	4.2728	0.3706	2642.41	2642.749	1	822.8	45.238094	T.SETNTDEHIKDIYDDTERELAF.Y
gi|6322676|ref|NP_012749.1|	YKL172W	Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p	2	3.7956	0.3321	2590.35	2589.731	1	620.8	42.5	E.TNTDEHIKDIYDDTERELAFY.K
gi|6322676|ref|NP_012749.1|	YKL172W	Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p	2	4.1249	0.3215	2805.83	2805.925	1	687.6	36.363636	T.SETNTDEHIKDIYDDTERELAFY.K
gi|6322676|ref|NP_012749.1|	YKL172W	Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p	2	3.2537	0.2383	2426.09	2426.555	1	460.9	44.736843	E.TNTDEHIKDIYDDTERELAF.Y
gi|6322671|ref|NP_012743.1|	YKL178C	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; Ste3p	2	4.21	0.315	1994.69	1994.203	1	1330.5	71.875	Y.LFADKETDDILDEIDLK.E
gi|6322671|ref|NP_012743.1|	YKL178C	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; Ste3p	2	4.2537	0.2754	1735.65	1733.867	1	1743.9	75	F.ADKETDDILDEIDLK.E
gi|6322671|ref|NP_012743.1|	YKL178C	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; Ste3p	2	5.0806	0.2985	1562.07	1562.7	1	1766.5	87.5	D.K2E1T1D1D1I1L1D1E1I1D1L1K2.E

gi|6322671|ref|NP_012743.1|	YKL178C	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; Ste3p	1	4.1188	0.2617	1546.79	1547.7	1	990.1	70.83333	D.KETDDILDEIDLK.E
gi|6322671|ref|NP_012743.1|	YKL178C	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; Ste3p	2	5.1856	0.2751	1749.77	1750.867	1	2106.5	78.57143	F.A1D1K2E1T1D1D1I1L1D1E1I1D1L1K2.E
gi|6322671|ref|NP_012743.1|	YKL178C	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; Ste3p	2	4.089	0.298	1547.73	1547.7	1	1446.8	83.33333	D.KETDDILDEIDLK.E
gi|6322671|ref|NP_012743.1|	YKL178C	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; Ste3p	2	5.4155	0.2872	2012.49	2013.203	1	2287.9	75	Y.L1F1A1D1K2E1T1D1D1I1L1D1E1I1D1L1K2.E
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.0686	0.1783	1918.51	1919.036	2	446.6	50	R.S1K2E1W2F1Q2L1D1D1E1D1F1D1L1L1.N
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	4.1805	0.3337	2141.87	2143.369	1	678	62.5	L.W2I1D1E1P1F1N2L1D1F1D1P1R4D1V1I1K2.G
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.5782	0.2574	2119.65	2120.369	1	456.7	53.125	L.WIDEPFNLDFDPRDVIK.G
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	3	4.0778	0.165	2333.3	2331.595	1	594.8	40.27778	L.W2I1D1E1P1F1N2L1D1F1D1P1R4D1V1I1K2G1K2.D
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.3209	0.3209	2329.59	2331.595	2	336.6	44.444447	L.W2I1D1E1P1F1N2L1D1F1D1P1R4D1V1I1K2G1K2.D
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	4.6435	0.3173	2076.49	2079.224	1	974.3	63.333332	L.R4S1K2E1W2F1Q2L1D1D1E1D1F1D1L1L1.N
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	1	3.1707	0.3441	1526.61	1525.829	4	222.1	50	L.I1G1R4P1P1L1L1V1P1G1M1T1P1C1.T
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.2578	0.3739	1923.23	1923.301	1	429	50	F.GPIKVELPTKETVEIGIV.D
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.8595	0.3507	2252.39	2252.616	1	474.2	44.736843	K.C1F1G1P1I1K2V1E1L1P1T1K2E1T1V1E1I1G1I1V1.D
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.1811	0.2523	2045.15	2045.339	1	763.1	60.000004	M.L1W2K2E1F1D1E1T1I1F1N2L1P1K2N2K2.L
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.8263	0.3631	2248.47	2247.64	1	407.9	52.77778	W.KEFDETIFNLPKNKLVPTL.E
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	4.5227	0.4317	2270.69	2271.64	1	359.4	52.77778	W.K2E1F1D1E1T1I1F1N2L1P1K2N2K2L1V1P1T1L1.E
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	3	4.5389	0.3007	2459.12	2459.853	1	533	36.842106	L.W2K2E1F1D1E1T1I1F1N2L1P1K2N2K2L1V1P1T1L1.E
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.521	0.3147	2432.59	2433.853	1	495.5	50	L.WKEFDETIFNLPKNKLVPTL.E
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.4224	0.2501	1823.87	1822.025	1	1270.2	64.28571	T.GSEPIKEIIDNWEKY.E
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.3676	0.3493	2303.89	2305.595	1	500.6	55.555557	L.WIDEPFNLDFDPRDVIKGK.D
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.473	0.2969	2055.23	2057.224	1	881.9	60.000004	L.RSKEWFQLDDEDFDLL.N
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	2.919	0.2031	2154.43	2154.474	8	234.7	43.75	S.E1R4I1V1D1C1I1I1R4L1P1V1K2W2E1T1T1.T
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	3	4.0396	0.2419	2434.97	2433.853	1	527.6	34.210526	L.WKEFDETIFNLPKNKLVPTL.E
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	2.964	0.1857	1356.29	1356.651	1	695.3	70	C.IIRLPVKWETT.T
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.5513	0.1811	1957.97	1955.097	4	370.8	50	L.E1W2L1E1N2P1S1N2T1P1D1K2D1Y1L1L1.S
gi|6322666|ref|NP_012739.1|	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	2	3.0164	0.2375	1372.21	1372.651	3	343.6	60.000004	C.I1I1R4L1P1V1K2W2E1T1T1.T
gi|6322639|ref|NP_012712.1|	YKL210W	Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and essential for viability; Uba1p	2	4.1202	0.3408	2613.55	2614.828	1	587.2	45.238094	F.KLEPVDFEKDDDTNHHIEFITA.C
gi|6322639|ref|NP_012712.1|	YKL210W	Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and essential for viability; Uba1p	2	3.0933	0.1865	2150.29	2149.299	1	403.1	41.17647	D.K2V1G1P1E1T1E1E1I1F1N2D1S1F1W2E1S1L1.D
gi|6322639|ref|NP_012712.1|	YKL210W	Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and essential for viability; Uba1p	2	3.1185	0.2941	2007.31	2005.083	1	269.2	35.294117	F.T1P1N2A1N2L1K2I1Q2V1N2D1D1D1P1D1P1N2.A
gi|6322639|ref|NP_012712.1|	YKL210W	Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and essential for viability; Uba1p	2	3.0215	0.2243	1432.71	1432.749	2	340.6	72.72727	F.TEVKVPRKISFK.S
gi|6322637|ref|NP_012710.1|	YKL212W	Lipid phosphoinositide phosphatase of the ER and Golgi, involved in protein 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 Sla1p; 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.G1V1D1S1L1D1P1F1D1Q2I1K2D1S1D1I1R4.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.P1F1D1Q2I1K2D1S1D1I1R4T1I1.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.K2N2G1V1D1S1L1D1P1F1D1Q2I1K2D1S1D1I1R4.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	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	3.3053	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.KVPVGDQPPDIERQIKDML.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	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.K2V1P1V1G1D1Q2P1P1D1I1E1R4Q2.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.E1R4K2E1L1D1E1I1A1P1V1P1D1A1F1V1P1I1I1K2.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
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	3.5659	0.4108	2175.03	2175.554	1	386.1	41.666664	E.R4K2E1L1D1E1I1A1P1V1P1D1A1F1V1P1I1I1K2.I
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	3.3946	0.2995	1871.91	1870.081	1	1139.5	70	Q.AMEDLPEEEITDHKVL.S
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	3.229	0.1687	1888.45	1889.082	1	737.2	60.000004	Q.A1M1E1D1L1P1E1E1E1I1T1D1H3K2V1L1.S

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	3.5908	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.E1G1C1D1I1L1D1E1K2V1L1P1K2.F
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	3.5747	0.2398	2649.65	2649.888	2	370.8	35.714287	F.N2S1V1D1I1P1Y1E1L1T1P1E1E1Q2K2D1K2D1L1L1Q2F1.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	6.0816	0.5499	2343.89	2345.574	1	1124.9	59.523808	K.K2E1E1L1G1V1E1N2P1L1D1G1I1A1T1S1P1V1H3E1I1A1.Y
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	3.0102	0.2234	1845.33	1846.149	1	770.8	56.666668	W.KLEGMDGLPESKEWLL.R
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	3.4268	0.3037	2621.63	2622.888	1	436.2	35.714287	F.NSVDIPYELTPEEQKDKDLLQF.A
gi|6322876|ref|NP_012949.1|	YKR024C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp7p	2	3.4185	0.1935	2147.91	2149.379	1	685.4	50	L.P1G1E1E1E1K2Y1M1D1Y1I1Q2P1Y1H3P1M1.G
gi|6322876|ref|NP_012949.1|	YKR024C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in 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 ATP-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
gi|6322876|ref|NP_012949.1|	YKR024C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp7p	2	4.1061	0.3159	2637.77	2640.033	1	908.2	45	L.L1F1L1L1P1G1E1E1E1K2Y1M1D1Y1I1Q2P1Y1H3P1M1.G
gi|6322892|ref|NP_012965.1|	YKR039W	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source; Gap1p	2	5.3579	0.4123	2076.47	2077.379	1	781.9	70.588234	F.K2R4V1K2P1I1E1V1D1P1N2L1S1E1A1E1K2V1.A
gi|6322892|ref|NP_012965.1|	YKR039W	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source; Gap1p	1	2.7348	0.1696	1264.56	1264.44	8	324.8	61.11111	L.A1E1Q2R4F1L1P1E1I1F1.S
gi|6322892|ref|NP_012965.1|	YKR039W	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source; Gap1p	2	3.0001	0.241	2098.65	2099.227	1	227.7	41.17647	S.S1Y1E1K2N2N2P1D1N2L1K2H3N2G1I1T1I1D1.S
gi|6322892|ref|NP_012965.1|	YKR039W	General amino acid permease; localization to the plasma membrane is regulated by 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	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source; Gap1p	2	3.876	0.2721	2305.59	2303.582	1	571.1	55.555557	A.E1K2M1D1I1D1T1G1R4R4E1V1D1L1D1L1L1K2Q2.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
gi|6322892|ref|NP_012965.1|	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.K2R4V1K2P1I1E1V1D1P1N2L1S1E1A1E1.K
gi|6322892|ref|NP_012965.1|	YKR039W	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source; Gap1p	2	3.1418	0.1915	1993.69	1995.249	1	857.4	65.625	S.F1K2R4V1K2P1I1E1V1D1P1N2L1S1E1A1E1.K
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of 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
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	2	3.5629	0.2377	2467.55	2467.786	3	255.3	40	L.E1Y1L1Q2D1I1G1L1E1Y1L1T1D1G1R4P1G1F1K2L1L1.F
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	2	5.0735	0.3023	3093.95	3094.194	1	668.6	36.53846	L.N2E1T1E1L1L1V1D1E1E1E1K2A1Q2N2D1S1E1E1E1Q2V1K2G1I1P1S1.F
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of 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
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	3	4.0718	0.3494	3393.2	3394.584	1	312.4	25	L.NETELLVDEEEKAQNDSEEEQVKGIPSFW.L
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	3	4.4133	0.4403	3645.53	3646.848	1	281.2	21.666666	L.N2E1T1E1L1L1V1D1E1E1E1K2A1Q2N2D1S1E1E1E1Q2V1K2G1I1P1S1F1W2L1T1.A
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	2	2.9174	0.1848	1279.19	1278.488	1	944	80	R.TIEKITPIESF.F
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the 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
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	2	5.9949	0.2827	2191.29	2190.236	1	1259.1	64.70589	Q.NEDQDEELEEDLEERLAL.D
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	3	4.0651	0.2319	2708.48	2706.788	1	1084.3	34.090908	L.NETELLVDEEEKAQNDSEEEQVK.G
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the 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
gi|6322901|ref|NP_012974.1|	YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the 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
gi|6322922|ref|NP_012995.1|	YKR069W	S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in sulfate assimilation, methionine metabolism, and siroheme biosynthesis; Met1p	1	3.0698	0.218	1511.44	1512.762	2	422.9	53.846157	F.K2D1H3G1Y1I1P1V1V1L1P1G1I1S1.S
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
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	4.1483	0.3937	2127.83	2129.485	1	1000.1	58.333332	L.L1K2W2V1P1E1V1V1E1E1I1G1S1R4P1P1G1V1L1.V
gi|6322923|ref|NP_012996.1|	YKR070W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein 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
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	3.0627	0.1842	1540.99	1541.698	7	441	58.333332	S.LDQESIEHDLKLT.S

gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	3.3327	0.1955	1709.65	1708.863	1	749.1	69.230774	N.AIREEIYEEISQVE.T
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	3.5809	0.3721	1767.55	1768.883	1	564.1	57.692307	N.NLYDDNHLDWNHVL.C
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	4.5774	0.3441	2486.71	2485.773	1	909.6	50	K.R4V1F1D1E1E1L1P1K2N2N2D1F1P1L1P1S1V1D1L1L1.C
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	2.9105	0.2329	1924.39	1923.127	1	1185	63.333332	N.AIREEIYEEISQVETL.N
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	3.7871	0.4004	1707.87	1707.835	3	259.9	53.571426	K.ENEETNSKPEVGFVK.S
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	3.5945	0.2234	1962.19	1963.151	1	1323.5	73.333336	C.FYDGILEEGEKTIRYE.L
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	4.3501	0.2677	2458.09	2458.773	1	1075.2	50	K.RVFDEELPKNNDFPLPSVDLL.C
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	3.7065	0.1803	1759.45	1760.951	1	387	63.333332	A.L1N2P1N2D1Q2D1E1T1G1G1L1I1I1I1K2.G
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	3.5966	0.2074	1811.73	1812.03	1	489.2	50	L.ALNPNDQDETGGLIIIK.G
gi|6322935|ref|NP_013008.1|	YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	2	4.0435	0.2177	1981.23	1983.151	1	1561.8	76.666664	C.F1Y1D1G1I1L1E1E1G1E1K2T1I1R4Y1E1.L
gi|6322939|ref|NP_013012.1|	YKR086W	RNA helicase in the DEAH-box family involved in the second catalytic step of splicing, exhibits ATP-dependent RNA unwinding activity; Prp16p	2	3.8562	0.2659	1901.39	1901.141	6	279.1	43.75	F.F1G1N2A1P1Q2F1T1I1P1G1R4T1F1P1V1Q2.T
gi|6322939|ref|NP_013012.1|	YKR086W	RNA helicase in the DEAH-box family involved in the second catalytic step of splicing, exhibits ATP-dependent RNA unwinding activity; Prp16p	2	3.463	0.2806	1878.37	1878.141	1	512	53.125	F.FGNAPQFTIPGRTFPVQ.T
gi|6322939|ref|NP_013012.1|	YKR086W	RNA helicase in the DEAH-box family involved in the second catalytic step of splicing, exhibits ATP-dependent RNA unwinding activity; Prp16p	2	3.2938	0.2715	2052.93	2053.4	1	461.6	44.11765	V.P1E1P1L1S1E1L1P1E1E1A1K2L1L1P1V1I1R4.N
gi|6322939|ref|NP_013012.1|	YKR086W	RNA helicase in the DEAH-box family involved in the second catalytic step of 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
gi|6322946|ref|NP_013019.1|	YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	4.446	0.4298	2946.69	2944.063	1	675	37.5	T.ERYNLSPSPEDEDFEGPTEEEMQTL.R
gi|6322946|ref|NP_013019.1|	YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is 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
gi|6322946|ref|NP_013019.1|	YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is 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
gi|6322946|ref|NP_013019.1|	YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is 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
gi|6322946|ref|NP_013019.1|	YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	3.4807	0.2373	1268.31	1267.597	1	967.5	88.88889	L.IIFIPIFEKF.V
gi|6322946|ref|NP_013019.1|	YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is 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
gi|6322946|ref|NP_013019.1|	YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is 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
gi|6322946|ref|NP_013019.1|	YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	2	4.4592	0.3065	2485.69	2486.792	1	717.7	55.263157	S.VHPEKNYPWNDKFVDEIKRA.L
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	5.3853	0.5393	2338.55	2339.475	1	833.6	57.5	N.SPLIEEDDNSVNPHDEVTKIS.G
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	6.5495	0.4779	2364.51	2365.475	1	1033.8	60.000004	N.S1P1L1I1E1E1D1D1N2S1V1N2P1H3D1E1V1T1K2I1S1.G
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	5.1638	0.3614	2338.97	2339.475	1	1181.6	38.75	N.SPLIEEDDNSVNPHDEVTKIS.G
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	4.5961	0.3747	2895.65	2898.037	1	533.2	38	N.N2I1S1P1N2S1P1L1I1E1E1D1D1N2S1V1N2P1H3D1E1V1T1K2I1S1.G
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	5.9093	0.2939	3162.77	3161.365	1	957.7	37.5	F.S1L1G1D1I1D1D1L1E1N2A1E1P1P1L1T1E1R4E1E1L1E1C1E1L1I1K2.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.F1Y1D1F1D1D1I1K2R4E1I1E1N2E1T1A1.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	3	4.5814	0.2499	2919.08	2918.218	1	1179.2	35.227272 N.K2T1V1E1E1S1L1D1K2E1E1D1Y1F1R4K2H3P1V1Y1R4T1I1.S
gi|6323021|ref|NP_013093.1|	YLL008W	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p	2	3.3261	0.1704	2518.53	2515.784	1	529.7	47.5 L.VMDEADRMLEEGFQDELNEIM.G
gi|6323021|ref|NP_013093.1|	YLL008W	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p	1	2.462	0.3074	1196.51	1197.416	3	406.4	66.66667 F.K2N2L1E1V1P1V1L1I1C1.T
gi|6323021|ref|NP_013093.1|	YLL008W	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p	2	3.7396	0.3698	1632.03	1630.721	1	991.3	73.07692 D.F1Y1A1P1E1T1E1G1D1E1A1K2K2Q2.M
gi|6323021|ref|NP_013093.1|	YLL008W	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p	2	4.0446	0.2472	2163.01	2160.38	1	898.3	55.88235 M.NDTIEDILVEEKEEKEIL.R
gi|6323021|ref|NP_013093.1|	YLL008W	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p	2	4.3576	0.3837	2022.71	2023.025	1	810.1	58.823532 K.K2V1S1E1G1D1N2L1D1E1D1V1H3E1D1L1D1A1.G
gi|6323021|ref|NP_013093.1|	YLL008W	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p	2	4.8226	0.2086	2180.27	2181.38	1	863.3	55.88235 M.N2D1T1I1E1D1I1L1V1E1E1K2E1E1K2E1I1L1.R
gi|6323021|ref|NP_013093.1|	YLL008W	Nucleolar DEAD-box protein required for ribosome assembly and function, including 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.K2A1I1E1T1I1P1I1E1K2L1P1F1I1L1S1.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.Q2E1N2P1Y1I1Y1Y1P1T1P1N2P1I1P1V1K2M1P1K2D1E1K2T1F1.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.K2A1I1E1T1I1P1I1E1K2L1P1F1I1L1.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

gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	4.4621	0.3493	1867.63	1869.137	1	755.7	56.25	N.L1V1R4I1P1Q2Q2Q2P1A1P1A1E1I1T1P1S1.Y
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	4.9039	0.4133	1983.89	1985.241	1	945.6	61.764706	R.N2L1V1R4I1P1Q2Q2Q2P1A1P1A1E1I1T1P1S1.Y
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	4.1678	0.4821	1845.55	1846.137	1	981.8	65.625	N.LVRIPQQQPAPAEITPS.Y
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	4.1026	0.351	1515.59	1512.703	1	685.3	75	L.LFDEVEKAHPDVL.T
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	1	3.3089	0.4321	1511.45	1512.703	1	750.2	70.83333	L.LFDEVEKAHPDVL.T
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.4214	0.2782	2416.47	2415.539	9	224.9	40	K.GKSRDENVPEEAEECLEVLPN.H
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	3	4.4327	0.2901	2156.12	2157.335	2	851.8	41.17647	A.V1A1R4D1S1K2P1E1E1L1D1S1K2E1R4Q2L1Q2.L
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	1	2.6952	0.2749	1589.28	1590.786	1	173.8	50	Y.R4R4L1P1D1S1A1L1D1L1V1D1I1S1.C
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.3975	0.3826	2182.89	2185.419	1	354.9	50	Q.A1R4Q2G1K2L1D1P1V1I1G1R4E1E1E1I1R4S1T1.I
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.2312	0.257	2055.95	2055.174	1	317.9	56.666668	L.RQRYNEEKHGHEELTQ.A
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.3573	0.2273	2084.39	2085.174	1	182.8	43.333332	L.R4Q2R4Y1N2E1E1K2H3G1H3E1E1L1T1Q2.A
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.6266	0.1709	2158.11	2157.335	1	340.8	47.058823	A.V1A1R4D1S1K2P1E1E1L1D1S1K2E1R4Q2L1Q2.L
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.1795	0.2592	2154.65	2155.419	1	310.6	44.444447	Q.ARQGKLDPVIGREEEIRST.I
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.759	0.3105	2127.67	2129.335	1	710.6	58.823532	A.VARDSKPEELDSKERQLQ.L
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.1782	0.3935	1475.29	1475.644	1	704.2	68.181816	K.YKGDFEERFKGV.L
gi|6323002|ref|NP_013074.1|	YLL026W	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 arsenite; involved in [PSI+] propagation; Hsp104p	2	3.5622	0.2983	1575.75	1576.798	1	774.9	62.5	S.DHQHPQLQPIHIL.A
gi|6323000|ref|NP_013072.1|	YLL028W	Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH; phosphorylation enhances activity and sorting to the plasma membrane; Tpo1p	2	3.7862	0.4147	1227.41	1226.345	1	688.6	80	H.A1A1H3E1D1V1E1L1S1I1K2.D
gi|6323000|ref|NP_013072.1|	YLL028W	Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH; 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
gi|6323000|ref|NP_013072.1|	YLL028W	Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH; phosphorylation enhances activity and sorting to the plasma membrane; Tpo1p	1	3.0144	0.1903	1081.51	1082.188	1	638.8	75	A.H3E1D1V1E1L1S1I1K2.D
gi|6323000|ref|NP_013072.1|	YLL028W	Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH; phosphorylation enhances activity and sorting to the plasma membrane; Tpo1p	1	2.6814	0.2239	1069.52	1070.188	1	610.3	75	A.HEDVELSIK.D
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	3	3.9798	0.3255	3723.11	3725.153	1	533	21.774193	K.GKVELVPVEENLVDSIWPDFETLPERPCNDLL.L
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	3	5.3011	0.3874	3761.75	3764.153	1	720.5	25	K.G1K2V1E1L1V1P1V1E1E1N2L1V1D1S1I1W2P1D1F1E1T1L1P1E1R4P1C1N2D1L 1L1.L
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	3	4.6367	0.303	3841.19	3838.312	1	928.4	25.78125	K.GKVELVPVEENLVDSIWPDFETLPERPCNDLLL.L
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	3	5.2977	0.2251	3993.68	3992.472	1	799	24.242424	K.G1K2V1E1L1V1P1V1E1E1N2L1V1D1S1I1W2P1D1F1E1T1L1P1E1R4P1C1N2D1L 1L1L1L1.K
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	3	4.9794	0.2468	3948.89	3951.472	1	1136.3	26.51515	K.GKVELVPVEENLVDSIWPDFETLPERPCNDLLLL.K
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	3	5.6803	0.451	3875.36	3878.312	1	825.5	25.78125	K.G1K2V1E1L1V1P1V1E1E1N2L1V1D1S1I1W2P1D1F1E1T1L1P1E1R4P1C1N2D1L 1L1L1.L
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	2	3.186	0.231	1245.99	1245.548	1	729.2	70	L.KIGIDPKLITF.N
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	2	4.3861	0.3778	1718.83	1719.95	1	906.4	69.230774	T.IHLTKPTKEEMDNY.T
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	2	3.2518	0.1882	1557.19	1556.754	2	446.1	57.692307	K.G1K2V1E1L1V1P1V1E1E1N2L1V1D1.S

gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	2	3.4398	0.2988	2429.99	2429.741	4	210.7	31.578945	D.SIWPDFETLPERPCNDLLLL.K
gi|6322999|ref|NP_013071.1|	YLL029W	hypothetical protein; Yll029wp	2	4.5272	0.2686	2454.51	2454.741	1	457	44.736843	D.S1I1W2P1D1F1E1T1L1P1E1R4P1C1N2D1L1L1L1L1.K
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	4.3776	0.2308	1917.91	1916.265	1	1330.8	80	S.LFIELPNTEEKLDIIK.T
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	4.6181	0.2449	2131.65	2130.53	1	841.9	58.823532	S.LFIELPNTEEKLDIIKTL.T
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.9108	0.2826	2204.33	2204.419	1	329.5	55.88235	A.G1R4F1D1R4E1I1C1L1N2V1P1N2E1V1S1R4L1.H
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	3	3.8686	0.2445	2202.95	2204.419	1	593.4	36.764706	A.G1R4F1D1R4E1I1C1L1N2V1P1N2E1V1S1R4L1.H
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.208	0.404	1713.75	1713.073	1	493.6	61.538464	A.IVQPIKRPELYEKV.G
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	2.9643	0.2549	2015.79	2017.37	1	338.4	46.875	L.FIELPNTEEKLDIIKTL.T
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	4.3293	0.2624	2150.41	2151.53	1	993.3	64.70589	S.L1F1I1E1L1P1N2T1E1E1K2L1D1I1I1K2T1L1.T
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.0797	0.2046	1650.23	1648.859	2	624.2	57.14286	T.AKREGFATVPDVTWA.N
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.8877	0.2699	1493.25	1490.83	1	1221.7	75	Q.L1M1E1L1I1G1L1P1I1L1H3P1E1.I
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.3079	0.3061	1505.49	1506.814	1	924.1	75	M.E1L1I1G1L1P1I1L1H3P1E1I1F1.L
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.8491	0.2802	1464.37	1464.613	1	1197.6	77.27273	M.L1K2D1V1I1E1S1E1L1E1E1F1.G
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.7584	0.363	1492.35	1491.814	1	539.4	62.5	M.ELIGLPILHPEIF.L
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	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	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.2977	0.2343	1639.75	1639.006	1	954.2	69.230774	L.M1E1L1I1G1L1P1I1L1H3P1E1I1F1.L
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	4.5077	0.3142	1750.73	1753.166	1	830.2	67.85714	Q.L1M1E1L1I1G1L1P1I1L1H3P1E1I1F1.L
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	2.9678	0.2195	1377.39	1376.698	1	599.3	72.72727	E.L1I1G1L1P1I1L1H3P1E1I1F1.L
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	2	3.4561	0.2993	1736.53	1736.166	1	640.3	57.14286	Q.LMELIGLPILHPEIF.L
gi|6322994|ref|NP_013066.1|	YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large 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.N2I1T1D1E1N2S1G1E1S1G1G1K2G1E1I1K2.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.A1P1I1I1Q2F1P1K2L1V1G1T1Q2.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
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	3.3952	0.2026	1570.99	1569.92	1	1131.6	75	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	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.Q2A1P1L1I1I1L1P1L1D1P1H3D1W2D1T1P1C1A1I1I1D1A1.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.A1P1L1I1I1L1P1L1D1P1H3D1W2D1T1P1C1A1I1I1D1A1.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, vacuolar 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	Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport; 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
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	1	3.1736	0.3639	1473.47	1474.703	1	337.6	63.636364	L.FRFLEPETGHIK.I
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	1	3.4957	0.1524	1491.59	1492.703	2	363.3	68.181816	L.F1R4F1L1E1P1E1T1G1H3I1K2.I
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	3.2256	0.2212	2280.99	2281.527	1	508.5	41.666664	M.NRFSKDIEAIDQELTPYIQ.G
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	3.4331	0.2425	1491.87	1492.703	1	928	77.27273	L.F1R4F1L1E1P1E1T1G1H3I1K2.I
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	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
gi|6323048|ref|NP_013120.1|	YLR020C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; involved in sterol metabolism; Yeh2p	3	4.2143	0.2228	2122.85	2123.435	1	803.3	44.11765	F.K2S1R4L1N2D1G1V1E1E1V1K2R4E1P1I1L1L1.L
gi|6323048|ref|NP_013120.1|	YLR020C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; involved in sterol metabolism; Yeh2p	2	4.1627	0.4132	1559.11	1558.808	1	1282.1	79.16667	L.W2A1H3D1V1I1D1R4I1G1K2P1M1.I
gi|6323048|ref|NP_013120.1|	YLR020C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; involved in sterol metabolism; Yeh2p	2	3.8681	0.2581	1870.65	1869.183	1	696.9	53.333336	K.G1A1E1K2I1F1P1D1K2K2T1W2F1P1I1A1.K
gi|6323048|ref|NP_013120.1|	YLR020C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; 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	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; involved in sterol metabolism; Yeh2p	2	3.8402	0.3076	1851.87	1849.183	2	472.6	46.666668	K.GAEKIFPDKKTWFPIA.K
gi|6323048|ref|NP_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
gi|6323068|ref|NP_013140.1|	YLR039C	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 rRNA and ribosomal protein genes; Ric1p	3	4.2696	0.2994	1921.34	1921.18	4	1090	43.333332	L.T1L1L1D1N2I1E1K2I1I1D1V1I1R4D1E1.I
gi|6323068|ref|NP_013140.1|	YLR039C	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 rRNA and ribosomal protein genes; Ric1p	3	3.9805	0.181	1900.97	1900.18	1	1155.9	43.333332	L.TLLDNIEKIIDVIRDE.I
gi|6323068|ref|NP_013140.1|	YLR039C	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 rRNA and ribosomal protein genes; Ric1p	2	3.1551	0.2853	1902.75	1900.18	1	577.4	46.666668	L.TLLDNIEKIIDVIRDE.I
gi|6323068|ref|NP_013140.1|	YLR039C	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 rRNA and ribosomal protein genes; Ric1p	2	3.3555	0.3332	1920.65	1921.18	1	574.6	50	L.T1L1L1D1N2I1E1K2I1I1D1V1I1R4D1E1.I
gi|6323068|ref|NP_013140.1|	YLR039C	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 rRNA and ribosomal protein genes; Ric1p	2	3.2187	0.3374	1418.31	1418.74	1	877.6	77.27273	K.MHLWPVSPPQLL.R
gi|6323068|ref|NP_013140.1|	YLR039C	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 rRNA and ribosomal protein genes; Ric1p	2	3.9437	0.2313	1435.13	1434.74	1	996.5	77.27273	K.M1H3L1W2P1V1S1P1P1Q2L1L1.R
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	2	3.5853	0.3377	2097.67	2099.386	1	411.3	44.444447	S.LKPNDAESEKEVIDTILAL.V
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	2	4.0872	0.2744	2120.21	2121.386	1	617.8	50	S.L1K2P1N2D1A1E1S1E1K2E1V1I1D1T1I1L1A1L1.V
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	3	3.8832	0.2236	2901.2	2902.257	1	678.4	29	L.Q2T1P1I1D1M1S1L1K2P1N2D1A1E1S1E1K2E1V1I1D1T1I1L1A1L1.V
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	3	3.8818	0.1932	3462.86	3464.976	3	556.6	23.275862	Q.DKSFNDNSKIRMIEIMLPVFDAPQNLVEQA.K
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	2	5.0955	0.2497	2800.07	2800.315	1	714.7	45.833336	T.Y1V1T1Q2R4P1V1Y1L1G1L1P1A1N2L1V1D1L1N2V1P1A1K2L1L1.Q
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, 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

gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	2	3.2227	0.2958	1493.79	1494.787	1	936.5	65.38461	L.P1A1N2L1V1D1L1N2V1P1A1K2L1L1.Q
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	2	4.7443	0.4561	2766.15	2768.315	1	896.3	52.083332	T.YVTQRPVYLGLPANLVDLNVPAKLL.Q
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, 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
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	3	3.9658	0.1611	3542.36	3541.186	1	711.5	24.193548	T.YVTQRPVYLGLPANLVDLNVPAKLLQTPIDMS.L
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	2	3.3538	0.1506	1664.03	1662.832	1	550.3	60.714287	N.D1A1E1S1E1K2E1V1I1D1T1I1L1A1L1.V
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, 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
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, 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
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	2	3.5986	0.2871	1764.35	1763.907	1	1158.1	60.000004	M.GKGSIDEQHPRYGGVY.V
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, 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
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	1	2.8047	0.2093	1323.33	1324.592	4	391	63.636364	A.N2L1V1D1L1N2V1P1A1K2L1L1.Q
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	1	2.5481	0.1989	1308.55	1309.592	5	459.7	68.181816	A.NLVDLNVPAKLL.Q
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, 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
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, 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
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	1	2.9512	0.1902	1005.49	1006.209	1	583.6	75	E.K2L1I1H3G1P1K2A1Q2.Y
gi|6323073|ref|NP_013145.1|	YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	1	2.6835	0.3279	991.55	992.209	1	585.4	75	E.KLIHGPKAQ.Y
gi|6323074|ref|NP_013146.1|	YLR045C	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome alignment; interacts with spindle pole body component Spc72p; Stu2p	2	4.0808	0.4044	2503.55	2504.901	1	821	50	S.MLPEETILDKLPKDFQERITS.S
gi|6323074|ref|NP_013146.1|	YLR045C	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome alignment; interacts with spindle pole body component Spc72p; Stu2p	2	3.2277	0.2611	2503.97	2504.901	1	427.8	37.5	F.SMLPEETILDKLPKDFQERIT.S
gi|6323074|ref|NP_013146.1|	YLR045C	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome alignment; interacts with spindle pole body component Spc72p; Stu2p	2	3.9703	0.3078	2708.97	2708.058	1	585.5	38.636364	F.S1M1L1P1E1E1T1I1L1D1K2L1P1K2D1F1Q2E1R4I1T1S1S1.K
gi|6323074|ref|NP_013146.1|	YLR045C	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome 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
gi|6323074|ref|NP_013146.1|	YLR045C	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome alignment; interacts with spindle pole body component Spc72p; Stu2p	2	3.8563	0.2236	1493.29	1492.669	1	1037.8	70.83333	T.GNNSDLLEEILFK.K
gi|6323074|ref|NP_013146.1|	YLR045C	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome 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
gi|6323077|ref|NP_013149.1|	YLR048W	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0 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
gi|6323077|ref|NP_013149.1|	YLR048W	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0 gene reduces growth rate, deletion of both genes is lethal; Rps0bp	2	4.0294	0.432	1809.55	1810.915	1	1465.6	78.57143	Y.FYRNPEEVEQVAEEA.A
gi|6323077|ref|NP_013149.1|	YLR048W	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0 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
gi|6323077|ref|NP_013149.1|	YLR048W	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0 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
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	1	2.5273	0.2774	1160.58	1160.276	1	453.8	61.11111	H.S1F1H3P1V1D1G1F1L1Q2.S
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	3	4.2364	0.1549	2721.65	2721.854	1	505.4	31.818182	F.IKEVEGDDNDRIYENDPNTKKNN.-
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	2	3.6815	0.3602	2754.47	2755.854	5	162.5	34.090908	F.I1K2E1V1E1G1D1D1N2D1R4I1Y1E1N2D1P1N2T1K2K2N2N2.-
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	2	3.4622	0.2126	2721.21	2721.854	1	273	38.636364	F.IKEVEGDDNDRIYENDPNTKKNN.-
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	2	4.8983	0.4176	2392.35	2393.472	1	438.7	50	F.I1K2E1V1E1G1D1D1N2D1R4I1Y1E1N2D1P1N2T1K2.K

gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	2	3.3848	0.2049	1990.33	1991.176	3	290.4	46.666668	S.Y1R4R4P1D1D1S1L1F1D1P1K2L1R4D1A1.K
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	2	3.2433	0.2198	2720.77	2721.854	9	175.9	31.818182	F.IKEVEGDDNDRIYENDPNTKKNN.-
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	3	4.1832	0.1913	2758.31	2755.854	1	446.6	30.681818	F.I1K2E1V1E1G1D1D1N2D1R4I1Y1E1N2D1P1N2T1K2K2N2N2.-
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	2	3.1224	0.2724	1964.53	1965.176	1	454.4	53.333336	S.YRRPDDSLFDPKLRDA.K
gi|6323085|ref|NP_013157.1|	YLR056W	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 on non-fermentable carbon sources; Erg3p	2	3.3494	0.2211	1616.61	1615.833	1	560.8	66.66667	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
gi|6323087|ref|NP_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
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.2771	0.3357	908.13	908.049	1	575.1	77.77778	V.P1G1G1V1R4I1G1A1P1A1.M
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	1	2.6265	0.3114	1178.65	1178.42	1	444.9	54.166668	S.ALVPGGVRIGAPA.M
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	1	2.5914	0.2516	1281.65	1282.498	1	380	53.846157	K.S1A1L1V1P1G1G1V1R4I1G1A1P1A1.M
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.9623	0.2872	1606.33	1606.773	1	1382.1	80.769226	Y.RVNPETGIIDYDTL.E
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; 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
gi|6323087|ref|NP_013159.1|	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
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.6474	0.3846	1689.77	1690.845	1	2033.9	80.769226	D.P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.4299	0.2482	2003.33	2003.127	1	570.9	68.75	V.DTDPEVDSIIKDEIERQ.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.5983	0.375	2026.61	2025.127	1	613.1	68.75	V.D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.0318	0.3129	1910.67	1909.039	1	453.8	66.66667	D.T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	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
gi|6323087|ref|NP_013159.1|	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
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	1	2.6691	0.2058	1305.47	1306.436	3	434.4	60.000004	R.G1M1G1E1E1D1F1H3R4I1V1.Q
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	1	2.5209	0.2183	1290.51	1290.436	2	331	55	R.GMGEEDFHRIV.Q
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	5.7792	0.4595	2466.63	2467.638	1	798.5	60.000004	T.S1H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	3	6.3412	0.4441	2467.37	2467.638	1	1883.9	51.25	T.S1H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	3	4.1934	0.2164	1671.89	1671.845	1	830.6	44.230766	D.PEVDSIIKDEIERQ.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; 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
gi|6323087|ref|NP_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.HLVDTDPEVDSIIKDEIERQ.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.5883	0.2348	2380.25	2379.672	1	727.9	45	R.SINPKTGKEVLYDLENPINFS.V
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.9287	0.3174	2403.05	2405.672	1	526	40	R.S1I1N2P1K2T1G1K2E1V1L1Y1D1L1E1N2P1I1N2F1S1.V
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.4578	0.2295	2292.55	2292.594	1	517.9	39.473686	R.SINPKTGKEVLYDLENPINF.S
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; 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	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.0475	0.2952	1889.55	1890.19	1	604.8	56.25	R.GVRSINPKTGKEVLYDL.E
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; 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
gi|6323087|ref|NP_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.L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	4.8094	0.3757	1626.15	1624.773	1	1107.3	73.07692	Y.R4V1N2P1E1T1G1I1I1D1Y1D1T1L1.E
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	5.1332	0.3531	2466.17	2467.638	1	886.1	62.5	T.S1H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	3	5.1252	0.5211	2436.92	2439.638	1	1405.7	47.5	T.SHLVDTDPEVDSIIKDEIERQ.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	5.2882	0.4617	2379.01	2379.56	1	742.8	57.894737	S.H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.1275	0.1909	2351.31	2352.56	1	524.2	50	S.HLVDTDPEVDSIIKDEIERQ.K

gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	3	4.363	0.3845	2465.72	2467.638	1	690.2	36.25 T.S1H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	1	2.7425	0.2619	1576.53	1577.818	1	463	50 R.SINPKTGKEVLYDL.E
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	3	5.9027	0.4021	2381.63	2379.56	1	1017.9	42.105263 S.H3L1V1D1T1D1P1E1V1D1S1I1I1K2D1E1I1E1R4Q2.K
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.7923	0.4455	1864.27	1863.167	1	722.5	60.526318 N.SIPGDKSALVPGGVRIGAPA.M
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.5271	0.3454	1886.29	1887.167	1	684.2	57.894737 N.S1I1P1G1D1K2S1A1L1V1P1G1G1V1R4I1G1A1P1A1.M
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.9939	0.325	1912.47	1913.19	1	461.6	56.25 R.G1V1R4S1I1N2P1K2T1G1K2E1V1L1Y1D1L1.E
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	3	4.43	0.3842	2691.32	2692.044	1	882.3	31.52174 R.GVRSINPKTGKEVLYDLENPINFS.V
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	2	3.7049	0.3378	1909.49	1907.056	1	724.8	60.000004 E.S1F1P1Y1R4V1N2P1E1T1G1I1I1D1Y1D1.T
gi|6323087|ref|NP_013159.1|	YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	1	2.3153	0.2073	896.42	897.062	4	343.9	71.42857 Q.KHSIDLIA.S
gi|6323089|ref|NP_013161.1|	YLR060W	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 similar; Frs1p	2	3.3967	0.4401	1968.25	1971.133	1	426.8	50 Y.WIEEDDSVKTYFPGRGA.K
gi|6323089|ref|NP_013161.1|	YLR060W	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 similar; Frs1p	3	4.2917	0.2432	2306.24	2304.649	1	1397.1	44.736843 Q.SKEDKDILHVDIPVTRPDIL.H
gi|6323089|ref|NP_013161.1|	YLR060W	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 similar; Frs1p	2	4.9325	0.4017	2304.09	2304.649	1	1267.7	55.263157 Q.SKEDKDILHVDIPVTRPDIL.H
gi|6323089|ref|NP_013161.1|	YLR060W	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 similar; Frs1p	2	3.3847	0.2219	1353.79	1354.679	2	859.4	68.181816 A.NFIAKPLPINKV.S
gi|6323089|ref|NP_013161.1|	YLR060W	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 similar; Frs1p	1	3.6602	0.4435	1595.6	1596.925	1	628	65.38461 Y.VHIIEDSPVFPVIM.D
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	1	3.1498	0.2347	1457.47	1458.57	1	196.9	65 L.ENNIREFPEYF.A
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 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
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	2	2.9729	0.3164	1716.31	1715.86	2	314.8	50 K.GSLENNIREFPEYF.A
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	2	3.8475	0.2312	1734.33	1734.86	1	588.7	69.230774 K.G1S1L1E1N2N2I1R4E1F1P1E1Y1F1.A
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	2	2.9388	0.2768	1860.71	1858.017	1	502.5	50 K.GSLENNIREFPEYFAA.Q
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	1	2.5206	0.1688	1214.6	1215.351	5	204.2	62.5 N.NIREFPEYF.A
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 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
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	2	3.1513	0.2343	1865.49	1865.034	1	617.8	60.714287 K.K2G1S1L1E1N2N2I1R4E1F1P1E1Y1F1.A
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	2	3.0003	0.288	1058.33	1058.227	2	380.4	75 N.R4A1V1P1D1S1K2I1R4.I
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	2	3.5533	0.2231	1043.41	1042.227	1	483.4	81.25 N.RAVPDSKIR.I
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 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
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 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
gi|6323104|ref|NP_013176.1|	YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	2	3.9889	0.4509	2056.81	2059.286	1	693	53.125 L.SKKGSLENNIREFPEYF.A
gi|6323112|ref|NP_013184.1|	YLR083C	Protein whose 24kDa cleavage product is found in endosome-enriched membrane fractions, predicted to be a transmembrane protein; Emp70p	2	4.743	0.3494	2024.91	2026.216	1	958	63.333332 R.F1H3F1C1Q2P1E1K2V1E1K2Q2P1E1S1L1.G
gi|6323112|ref|NP_013184.1|	YLR083C	Protein whose 24kDa cleavage product is found in endosome-enriched membrane 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
gi|6323112|ref|NP_013184.1|	YLR083C	Protein whose 24kDa cleavage product is found in endosome-enriched membrane fractions, predicted to be a transmembrane protein; Emp70p	2	3.7031	0.2864	1924.65	1925.015	1	621.5	50 N.ELNLDDDFQEDSGWKL.N
gi|6323118|ref|NP_013190.1|	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.4308	0.2113	1786.21	1784.917	1	518.1	57.14286 K.RDEGEISYPEDIFLT.A
gi|6323118|ref|NP_013190.1|	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.4516	0.2528	1854.81	1855.996	1	346	46.666668 K.RDEGEISYPEDIFLTA.G
gi|6323118|ref|NP_013190.1|	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_013190.1|	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.9824	0.393	1708.13	1708.837	1	980.2	64.28571 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
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
gi|6323118|ref|NP_013190.1|	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.5879	0.3652	1576.79	1577.645	1	795.7	69.230774	M.VRPPVEGEESFESD.Q
gi|6323118|ref|NP_013190.1|	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	2.9955	0.2071	2075.59	2074.394	1	322.4	41.17647	F.CRGPETGVLIPIPQYPLY.T
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
gi|6323118|ref|NP_013190.1|	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.4981	0.2974	1453.53	1452.78	1	1027.8	72.72727	M.YLFPKIDLPFKA.V
gi|6323118|ref|NP_013190.1|	YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	2	3.3289	0.1928	1534.53	1532.867	1	566.8	70.83333	Y.L1F1P1K2I1D1L1P1F1K2A1V1Q2.E
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	3	4.2564	0.2214	1640.69	1641.094	2	879.4	51.923077	F.T1L1V1D1M1P1K2I1L1P1I1R4I1L1.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	2	3.0872	0.2342	1521.61	1521.988	2	608.5	62.5	T.LVDMPKILPIRIL.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	1	2.9067	0.2993	1520.68	1521.988	3	229.8	54.166668	T.LVDMPKILPIRIL.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	2	3.8944	0.282	1641.21	1641.094	1	760.7	65.38461	F.T1L1V1D1M1P1K2I1L1P1I1R4I1L1.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	2	3.6467	0.2559	1625.87	1623.094	1	906.4	69.230774	F.TLVDMPKILPIRIL.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	3	4.3045	0.1648	1789.73	1789.27	2	735	41.07143	C.F1T1L1V1D1M1P1K2I1L1P1I1R4I1L1.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	3	3.9507	0.2077	1769.93	1770.27	1	1136.2	50	C.FTLVDMPKILPIRIL.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	2	3.7618	0.2738	1642.65	1641.094	2	545.1	57.692307	F.T1L1V1D1M1P1K2I1L1P1I1R4I1L1.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	3	3.8477	0.23	1640.03	1641.094	2	548.2	44.230766	F.T1L1V1D1M1P1K2I1L1P1I1R4I1L1.S
gi|9755337|ref|NP_013194.2|	YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	2	2.935	0.202	1538.55	1538.988	1	632.4	58.333332	T.L1V1D1M1P1K2I1L1P1I1R4I1L1.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	3.7634	0.3941	2100.97	2101.225	1	755.1	52.77778	Q.K2V1I1G1D1G1I1E1S1I1S1E1T1D1D1N2W2L1S1.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	4.9974	0.4269	2078.27	2079.225	1	879.8	58.333332	Q.KVIGDGIESISETDDNWLS.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	3.0885	0.1834	2149.71	2150.304	3	275.4	42.105263	Q.KVIGDGIESISETDDNWLSA.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	5.5294	0.4391	2141.45	2141.339	1	1405.5	67.64706	T.NEKDISSPENLDDIYFKL.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	2.9777	0.1776	1972.79	1974.181	3	374.9	43.333332	L.NRLLDDNRELFIPETQ.E
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	3.4477	0.3475	1466.39	1466.68	1	408.8	72.72727	Q.E1V1V1H3P1H3P1D1F1L1L1F1.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	3	4.0955	0.207	2165.36	2165.373	2	719.8	37.5	L.H3F1D1D1I1P1Q2D1E1L1E1I1I1L1R4E1R4.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	1	3.3318	0.3553	1467.54	1466.68	1	236	59.090908	Q.E1V1V1H3P1H3P1D1F1L1L1F1.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	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	3.4947	0.3876	1853.39	1853.008	1	814.2	64.28571	L.ITVRHPLSEFTNDYC.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	3	4.0379	0.3434	1907.27	1907.257	1	997.8	40	S.R4L1L1E1D1L1K2D1L1A1N2P1I1V1K2F1.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	3.1506	0.2066	1451.33	1450.68	1	480	72.72727	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-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	1	3.4613	0.3336	1450.54	1450.68	1	310.5	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-Ipi1p-Ipi3p), 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.L1L1I1E1D1I1F1G1K2F1.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.S1L1P1H3R4D1P1I1P1F1.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 Pep5p 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
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	4.0417	0.2515	1617.53	1614.839	1	2075.8	85.71429	K.KIVDEGLNGVDLVSR.I
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	2.9774	0.2089	1515.85	1516.638	5	359.6	58.333332	Q.H3F1Y1N2S1Q2P1G1K2G1Y1V1T1.D
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	1	2.2675	0.213	1285.72	1286.441	7	518.1	54.545456	K.K2I1V1D1E1G1L1N2G1V1D1L1.V
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	4.2132	0.387	1632.55	1634.839	1	668.6	71.42857	K.K2I1V1D1E1G1L1N2G1V1D1L1V1S1R4.I
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	3	3.994	0.4134	2291.66	2293.5	1	1042.8	34.210526	N.A1T1E1G1D1A1E1H3I1T1P1D1N2L1R4R4E1L1I1L1.Q
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.408	0.3239	2152.31	2153.321	1	560	47.058823	L.G1S1V1G1E1P1I1S1P1D1L1W2E1W2Y1H3E1K2.V
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.4333	0.1943	1865.37	1863.158	2	578.9	53.125	K.K2I1V1D1E1G1L1N2G1V1D1L1V1S1R4I1L1.V
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.2468	0.2871	1919.59	1921.3	1	651.6	55.88235	K.K2G1D1T1V1A1I1Y1L1P1M1I1P1E1A1V1I1A1.M

gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	3	4.1353	0.3379	1588.55	1588.676	1	1517.9	50	D.G1A1G1R4D1H3D1G1Y1Y1W2I1R4.G
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	4.4319	0.3695	2675.11	2673.887	1	242.4	38.636364	L.G1S1V1G1E1P1I1S1P1D1L1W2E1W2Y1H3E1K2V1G1N2K2N2.C
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.0254	0.256	2223.65	2225.658	1	721.6	45	W.G1V1K2K2G1D1T1V1A1I1Y1L1P1M$I1P1E1A1V1I1A1.M
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under 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	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.3072	0.2278	2187.53	2186.658	4	331.6	35	W.GVKKGDTVAIYLPMIPEAVIA.M
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.5349	0.4267	1657.87	1658.769	1	569.4	68.181816	S.V1W2N2H3H3D1R4Y1M1D1T1Y1.L
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.0822	0.4091	1604.99	1605.703	1	642.6	70.83333	F.ESTPAYPDYGRYW.R
gi|6323182|ref|NP_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
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.3682	0.2889	1493.19	1492.588	1	421.7	68.181816	E.S1T1P1A1Y1P1D1Y1G1R4Y1W2.R
gi|6323182|ref|NP_013254.1|	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	2	3.6943	0.2097	1500.95	1500.695	1	1258.4	81.818184	Q.S1I1N2E1P1E1K2F1F1D1K2M1.A
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.2988	0.1672	1479.45	1478.627	1	1187.5	70.83333	H.D1A1L1K2D1E1K2D1L1G1R4S1L1.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.2515	0.2524	1461.43	1460.627	1	1238.3	70.83333	H.DALKDEKDLGRSL.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	3	4.6562	0.3802	2447.81	2448.687	1	1109.6	40	S.SQETKETEEEPKKAKEDSLIK.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), 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.SGHYTPIPAGSSPLKRDL.K
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), 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	60.000004	C.IMERDLYPRRW.G
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.4021	0.2332	1891.95	1893.115	1	753.5	63.333332	V.R4L1H3D1A1L1K2D1E1K2D1L1G1R4S1L1.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.2359	0.2891	1810.07	1810.063	6	596.2	53.125	S.GHYTPIPAGSSPLKRDL.K
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	3	4.1632	0.4011	1775	1775.011	1	915.5	45	G.H3Y1T1P1I1P1A1G1S1S1P1L1K2R4D1L1.K
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	1	2.724	0.2049	1459.48	1460.627	1	735.5	70.83333	H.DALKDEKDLGRSL.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.3906	0.2055	1460.01	1460.627	1	1111.6	66.66667	H.DALKDEKDLGRSL.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	4.6948	0.2071	2256.83	2257.478	1	580.2	55.555557	Q.E1T1K2E1T1E1E1E1P1K2K2A1K2E1D1S1L1I1K2.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	4.5961	0.2733	2449.85	2448.687	1	896.7	60.000004	S.SQETKETEEEPKKAKEDSLIK.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.7188	0.3198	1530.07	1530.69	1	442.7	70.83333	R.L1H3D1A1L1K2D1E1K2D1L1G1R4.S
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	1	2.803	0.151	1183.52	1184.28	1	321.3	62.5	L.R4Y1E1E1G1I1E1L1Y1.D
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	3.3888	0.3591	1732.61	1732.928	1	1595.6	71.42857	R.L1H3D1A1L1K2D1E1K2D1L1G1R4S1L1.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	1	2.7602	0.3409	1583.76	1584.812	1	355.2	54.166668	N.L1I1E1F1D1N2K2R4N2L1G1V1F1.W
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	2	4.4217	0.388	1710.61	1710.928	1	1834.7	75	R.LHDALKDEKDLGRSL.E
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	1	2.3669	0.2252	1367.54	1368.545	1	294.4	59.090908	A.G1S1S1P1L1K2R4D1L1K2S1Y1.I
gi|6323204|ref|NP_013276.1|	YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), 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.H3Y1T1P1I1P1A1G1S1S1P1L1K2R4D1L1K2S1Y1.I
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.7148	0.4241	1676.31	1677.685	1	480	53.571426	T.S1E1S1V1G1E1G1H3P1D1K2I1C1D1Q2.V
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.7015	0.3229	1733.49	1732.767	1	1160.7	76.666664	Q.G1V1H3E1E1K2D1L1E1D1I1G1A1G1D1Q2.G
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.089	0.462	2387.35	2387.495	1	780.2	47.61905	E.SVGEGHPDKICDQVSDAILDAC.L
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.0473	0.3412	2210.39	2211.498	1	505.2	41.666664	S.D1E1E1I1I1D1I1I1S1K2N2F1D1L1R4P1G1V1L1.V
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.1969	0.286	2155.81	2155.467	1	431.1	41.666664	K.R4V1Q2V1Q2F1S1Y1A1I1G1I1A1E1P1L1S1L1H3.V

gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to 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
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.7575	0.2798	1719.75	1719.031	1	592.2	57.14286	L.V1K2E1L1D1L1A1R4P1I1Y1L1P1T1A1.S
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.2309	0.2371	2678.67	2680.093	2	317.5	33.333336	E.I1I1E1K2V1I1P1R4D1M1L1D1E1N2T1K2Y1F1I1Q2P1S1.G
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.3797	0.2976	1506.35	1506.679	1	1768.2	87.5	A.T1K2S1D1E1E1I1I1D1I1I1S1K2.N
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	3	4.3148	0.302	2316.23	2317.655	1	1067.2	36.842106	L.V1K2E1L1D1L1A1R4P1I1Y1L1P1T1A1S1Y1G1H3F1.T
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.6649	0.3785	1711.95	1712.767	1	663.3	60.000004	Q.GVHEEKDLEDIGAGDQ.G
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	5.1172	0.3848	2544.57	2543.61	1	471.3	40.909092	S.E1S1V1G1E1G1H3P1D1K2I1C1D1Q2V1S1D1A1I1L1D1A1C1.L
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.4564	0.46	2411.65	2413.495	1	708.3	42.857143	E.S1V1G1E1G1H3P1D1K2I1C1D1Q2V1S1D1A1I1L1D1A1C1.L
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to 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	L.V1K2E1L1D1L1A1R4P1I1Y1L1P1T1.A
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.5184	0.2701	1628.59	1628.952	1	1023.3	73.07692	L.VKELDLARPIYLPT.A
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.2286	0.4543	2189.83	2191.485	1	764.2	50	K.V1I1P1R4D1M1L1D1E1N2T1K2Y1F1I1Q2P1S1.G
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	3	3.8801	0.1943	3250.73	3251.684	1	726.3	24.107143	K.VIPRDMLDENTKYFIQPSGRFVIGGPQGD.A
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.276	0.3588	2168.33	2167.485	1	765.4	52.941177	K.VIPRDMLDENTKYFIQPS.G
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.2502	0.4477	2050.31	2051.328	1	586.8	58.823532	K.I1V1R4D1T1I1K2K2I1G1Y1D1D1S1A1K2G1F1.D
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	3	4.7725	0.3571	3634.97	3637.08	1	639.2	24.21875	K.V1I1P1R4D1M1L1D1E1N2T1K2Y1F1I1Q2P1S1G1R4F1V1I1G1G1P1Q2G1D1A1G1L1T1.G
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	3	3.8741	0.2723	3082.43	3079.544	1	521.2	26.923079	K.VIPRDMLDENTKYFIQPSGRFVIGGPQ.G
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	3	5.0862	0.3191	3116.03	3116.544	2	667.5	26.923079	K.V1I1P1R4D1M1L1D1E1N2T1K2Y1F1I1Q2P1S1G1R4F1V1I1G1G1P1Q2.G
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	4.4042	0.2048	1404.01	1404.574	1	1574.3	86.36364	T.K2S1D1E1E1I1I1D1I1I1S1K2.N
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.6097	0.2416	1490.57	1491.679	2	774.6	62.5	A.TKSDEEIIDIISK.N
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.734	0.2533	1762.73	1761	1	790.8	61.538464	K.V1I1P1R4D1M1L1D1E1N2T1K2Y1F1.I
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	3	4.764	0.3407	2380.16	2379.723	1	900.5	38.88889	S.E1I1I1E1K2V1I1P1R4D1M1L1D1E1N2T1K2Y1F1.I
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	2	3.2648	0.1882	2378.43	2379.723	1	357.6	47.22222	S.E1I1I1E1K2V1I1P1R4D1M1L1D1E1N2T1K2Y1F1.I
gi|6323209|ref|NP_013281.1|	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to 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.I1I1E1K2V1I1P1R4D1M1L1D1E1N2T1K2Y1F1.I
gi|6323216|ref|NP_013288.1|	YLR187W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Caf120p and Skg4p; Skg3p	3	5.4594	0.4034	3563.24	3560.939	1	619.4	27.586206	F.D1K2S1E1E1E1P1Q2E1T1N2L1F1I1M1P1E1K2H3Q2G1V1P1G1Y1D1T1I1I1R4F1.L
gi|6323216|ref|NP_013288.1|	YLR187W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Caf120p and Skg4p; Skg3p	3	4.0929	0.3183	3520.4	3520.939	1	602.5	26.724138	F.DKSEEPQETNLFIMPEKHQGVPGYDTIIRF.L
gi|6323216|ref|NP_013288.1|	YLR187W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Caf120p and Skg4p; Skg3p	2	4.8307	0.349	2126.37	2127.459	1	616.9	52.941177	F.I1M1P1E1K2H3Q2G1V1P1G1Y1D1T1I1I1R4F1.L
gi|6323216|ref|NP_013288.1|	YLR187W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Caf120p and Skg4p; Skg3p	2	4.088	0.3841	2102.43	2102.459	1	1267.2	67.64706	F.IMPEKHQGVPGYDTIIRF.L
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	2	3.4329	0.2519	1954.59	1953.268	1	568.5	50	L.K2I1P1L1P1N2I1I1E1I1D1D1Q2P1I1V1N2.K
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	2	3.5537	0.259	2083.79	2083.442	1	592	47.058823	L.K2I1P1L1P1N2I1I1E1I1D1D1Q2P1I1V1N2K2.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	2	2.9621	0.2346	1524.47	1524.668	9	405.7	57.692307	K.EDGIKTAISAIYNE.L
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	2	3.1098	0.2706	1931.69	1932.268	2	455.5	43.75	L.KIPLPNIIEIDDQPIVN.K
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	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
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	4.9463	0.2787	2083.37	2083.442	1	1014.5	44.11765 L.K2I1P1L1P1N2I1I1E1I1D1D1Q2P1I1V1N2K2.A
gi|6323224|ref|NP_013296.1|	YLR195C	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p	3	6.7971	0.4947	3902.99	3905.369	1	1752.8	31.060606 W.R4T1Q2P1V1K2D1F1D1E1K2V1V1E1E1G1P1I1D1K2P1K2T1P1E1D1I1S1D1K2P1L1P1L1.L
gi|6323224|ref|NP_013296.1|	YLR195C	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p	3	5.279	0.3854	3863.12	3862.369	1	1423.1	28.030304 W.RTQPVKDFDEKVVEEGPIDKPKTPEDISDKPLPL.L
gi|6323224|ref|NP_013296.1|	YLR195C	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p	2	3.3689	0.3255	1512.63	1511.715	1	610.5	72.72727 L.KKEDIDQVFELF.K
gi|6323224|ref|NP_013296.1|	YLR195C	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p	3	6.6519	0.4636	4105.49	4107.607	1	1245.1	26.428572 W.R4T1Q2P1V1K2D1F1D1E1K2V1V1E1E1G1P1I1D1K2P1K2T1P1E1D1I1S1D1K2P1L1P1L1L1S1.S
gi|6323224|ref|NP_013296.1|	YLR195C	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p	3	6.1029	0.526	4061.15	4062.607	1	1416.6	27.857143 W.RTQPVKDFDEKVVEEGPIDKPKTPEDISDKPLPLLS.S
gi|6323224|ref|NP_013296.1|	YLR195C	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p	2	3.5016	0.2056	1655.77	1655.847	2	619.4	53.571426 L.FLDDLKFGPGDGFLN.F
gi|6323224|ref|NP_013296.1|	YLR195C	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of 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.K2K2E1D1I1D1Q2V1F1E1L1F1.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.K2D1Q2L1D1I1D1D1D1L1K2E1Y1N2L1E1.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	3	5.349	0.2683	3305.96	3305.449	1	1625.1	34.25926 K.FHEGEKGEDPYISLPNQEDSQEEKQELQ.V
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	4.4102	0.3197	1557.97	1558.772	1	1336.1	71.42857 V.A1P1N2L1S1E1L1I1G1E1V1I1G1A1R4.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	3.549	0.2638	1857.59	1857.033	1	1010.3	64.28571 S.IKEEFPYVDCISNEL.A
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	4.007	0.3894	1540.07	1539.772	1	890.4	64.28571 V.APNLSELIGEVIGAR.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	3.8065	0.2418	1659.69	1658.905	1	782.7	63.333332 T.V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1R4.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	3.4457	0.3229	1528.15	1528.733	1	759.6	65.38461 K.M1H3T1V1A1P1N2L1S1E1L1I1G1E1.V
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	4.3461	0.1539	1722.57	1720.963	1	521.6	56.25 M.HTVAPNLSELIGEVIGA.R
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	4.6586	0.4514	1739.83	1740.963	1	848.2	62.5 M.H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1.R
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	4.1607	0.3969	1871.53	1873.156	1	724.1	52.941177 K.M1H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1.R
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	5.6579	0.4963	1875.95	1877.151	1	1847.7	82.35294 M.HTVAPNLSELIGEVIGAR.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	3.3152	0.3521	1885.29	1883.123	1	334.1	46.666668 W.H3F1P1E1L1A1K2L1V1P1D1N2Y1T1F1A1.K
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	3	3.8942	0.1867	1877.75	1877.151	2	997.4	39.705883 M.HTVAPNLSELIGEVIGAR.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	3	3.9198	0.3021	2033.03	2033.343	1	817.3	37.5 K.M1H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1R4.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	4.12	0.3938	2022.61	2024.343	1	806	58.333332 K.M@HTVAPNLSELIGEVIGAR.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	4.1871	0.3867	2008.55	2008.343	1	949.8	61.11111 K.MHTVAPNLSELIGEVIGAR.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	1	2.7953	0.2011	1206.65	1207.415	1	383.3	70 L.KTKGNTPKYGL.I
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	3.1763	0.2777	1207.33	1207.415	1	444.3	75 L.KTKGNTPKYGL.I
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	2.9346	0.214	1258.45	1257.473	1	1072.9	77.27273 N.LSELIGEVIGAR.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	3	3.8655	0.2773	2556.23	2553.838	2	621.2	33.75 S.IKEEFPYVDCISNELAQDLIR.G
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	3	4.4535	0.3539	2680.52	2681.957	3	325	29.545454 M.ELYNKDKPAAEVEETKEKESSKK.R

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
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	3	5.0588	0.3363	3536.66	3536.927	3	648.8	24.166666	L.AISDKNLGPSIKEEFPYVDCISNELAQDLIR.G
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	4.3911	0.2214	2275.93	2276.506	1	547.4	55.263157	Y.NKDKPAAEVEETKEKESSKK.R
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	3	4.508	0.2317	2278.25	2276.506	1	857.6	39.473686	Y.NKDKPAAEVEETKEKESSKK.R
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	3	4.8885	0.2761	2303.45	2303.506	1	929.6	40.789474	Y.N2K2D1K2P1A1A1E1V1E1E1T1K2E1K2E1S1S1K2K2.R
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	5.3285	0.4803	1898.79	1901.151	1	1680.3	79.411766	M.H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1R4.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	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
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	3	4.4496	0.2766	2031.32	2033.343	2	798.4	37.5	K.M1H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1R4.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	3.2884	0.2887	2035.27	2033.343	1	666.5	50	K.M1H3T1V1A1P1N2L1S1E1L1I1G1E1V1I1G1A1R4.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	3	4.8389	0.3747	2432.36	2432.693	1	972.4	41.25	Y.NKDKPAAEVEETKEKESSKKR.K
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	3	4.5541	0.3973	2462.18	2463.693	1	798.2	40	Y.N2K2D1K2P1A1A1E1V1E1E1T1K2E1K2E1S1S1K2K2R4.K
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	2.6482	0.3336	1207.84	1207.415	1	347.4	65	L.KTKGNTPKYGL.I
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	4.4094	0.2594	1273.43	1272.473	1	1575.7	90.909096	N.L1S1E1L1I1G1E1V1I1G1A1R4.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	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	2	4.0761	0.247	2192.97	2193.281	1	615.9	53.125	T.Q2R4D1L1N2Y1Y1D1Y1L1D1E1L1S1D1T1F1.K
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	4.6907	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	2	4.211	0.2837	2334.75	2335.726	1	833	50	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	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
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	3.2085	0.2214	1738.39	1738.833	3	616.1	54.166668	T.Q2R4D1L1N2Y1Y1D1Y1L1D1E1L1.S
gi|6323249|ref|NP_013321.1|	YLR220W	Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p	2	3.8907	0.1973	2112.73	2110.372	1	942.6	52.941177	N.SNLINREIEDILLEINPN.F
gi|6323249|ref|NP_013321.1|	YLR220W	Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p	3	4.579	0.1534	2046.86	2047.294	4	1273.3	43.75	S.N2L1I1N2R4E1I1E1D1I1L1L1E1I1N2P1N2.F
gi|6323249|ref|NP_013321.1|	YLR220W	Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p	2	3.2088	0.2364	2615.51	2617.831	1	479.9	40.476192	N.S1N2L1I1N2R4E1I1E1D1I1L1L1E1I1N2P1N2F1S1D1E1.T
gi|6323249|ref|NP_013321.1|	YLR220W	Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p	3	4.0315	0.211	2135.78	2135.372	2	774.8	41.17647	N.S1N2L1I1N2R4E1I1E1D1I1L1L1E1I1N2P1N2.F
gi|6323249|ref|NP_013321.1|	YLR220W	Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p	3	4.8156	0.1702	2109.89	2110.372	3	1406.5	44.11765	N.SNLINREIEDILLEINPN.F
gi|6323249|ref|NP_013321.1|	YLR220W	Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p	2	4.2026	0.213	2021.65	2023.294	1	1394	68.75	S.NLINREIEDILLEINPN.F
gi|6323249|ref|NP_013321.1|	YLR220W	Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 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.S1N2L1I1N2R4E1I1E1D1I1L1L1E1I1N2P1N2.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	41.666664	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	L.ATNSPSLRIIPVPDLSGPEASLPLDVEIY.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-18S rRNA; Utp13p	2	3.413	0.3069	2158.63	2159.531	1	448.2	45	N.SPSLRIIPVPDLSGPEASLPL.D
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	3.2789	0.1545	1727.61	1726.952	1	517.6	64.28571	C.F1S1V1I1S1P1P1S1F1E1N2V1K2E1K2.W
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	4.4471	0.2854	2383.43	2383.671	1	1324.1	60.526318	F.S1V1I1S1P1P1S1F1E1N2V1K2E1K2W2F1P1E1V1H3.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
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	3.1903	0.2862	2056.07	2058.301	1	389.9	46.875	I.SPPSFENVKEKWFPEVH.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	2.4771	0.4293	1432.45	1433.582	1	523	50	H.HHCPGVPCLVVGT.Q
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	4.0238	0.3579	2502.97	2504.847	1	844.3	50	C.FSVISPPSFENVKEKWFPEVH.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	3.417	0.3358	2270.73	2270.593	2	391.9	38.88889	S.VISPPSFENVKEKWFPEVH.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	3.0455	0.2897	2268.61	2268.574	1	461.3	50	C.FSVISPPSFENVKEKWFPE.V
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	4.4305	0.3521	2357.31	2357.671	1	1099.2	55.263157	F.SVISPPSFENVKEKWFPEVH.H
gi|6323269|ref|NP_013341.1|	YLR240W	Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-phosphate; forms membrane-associated signal transduction complex with Vps15p to 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
gi|6323269|ref|NP_013341.1|	YLR240W	Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-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
gi|6323269|ref|NP_013341.1|	YLR240W	Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-phosphate; forms membrane-associated signal transduction complex with Vps15p to regulate protein sorting; similar to p110 subunit of mammalian PI 3-kinase; Vps34p	3	3.8565	0.4456	2362.64	2364.851	1	594.7	35	L.GQDPKPFPPLMKLPPQIIEAF.G
gi|6323273|ref|NP_013345.1|	YLR244C	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p	3	4.9388	0.3926	3335.09	3336.695	1	817.9	29.464287	A.S1Y1P1L1T1P1R4R4Y1V1P1E1D1I1P1K2P1D1W2A1A1N2G1L1P1V1S1E1Q2.R
gi|6323273|ref|NP_013345.1|	YLR244C	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p	2	3.0305	0.2651	2286.27	2285.521	1	627.2	50	L.HNAKDGLEGAYDPFPKFKYS.G
gi|6323273|ref|NP_013345.1|	YLR244C	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p	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 aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p	3	3.9816	0.2253	3368.84	3368.773	1	536	25.862068	K.ASYPLTPRRYVPEDIPKPDWAANGLPVSEQ.R
gi|6323273|ref|NP_013345.1|	YLR244C	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p	3	5.4451	0.4246	3408.77	3408.773	1	831.6	30.172413	K.A1S1Y1P1L1T1P1R4R4Y1V1P1E1D1I1P1K2P1D1W2A1A1N2G1L1P1V1S1E1Q2.R
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	4.3822	0.321	2751.21	2751.694	1	1544.8	56.521736	R.A1V1D1N2I1P1V1G1P1N2F1D1D1E1E1D1E1G1E1D1L1C1N2C1.E
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	3.2674	0.2591	2578.55	2579.482	1	563	40.476192	V.D1N2I1P1V1G1P1N2F1D1D1E1E1D1E1G1E1D1L1C1N2C1.E

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	4.6414	0.3669	2725.69	2724.694	1	1444.1	54.347824	R.AVDNIPVGPNFDDEEDEGEDLCNC.E
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	4.1627	0.3214	2751.65	2751.694	1	656	28.260868	R.A1V1D1N2I1P1V1G1P1N2F1D1D1E1E1D1E1G1E1D1L1C1N2C1.E
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	2.9428	0.2104	1413.93	1413.657	1	848.1	62.5	L.VEDPQVIAPFLGK.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	2	3.1005	0.1627	1528.23	1526.702	3	407.1	58.333332	L.E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	1	2.707	0.1831	1526.54	1526.702	2	186.3	50	L.E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	1	2.6248	0.4071	1511.8	1512.702	1	217.7	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	1	2.5495	0.2238	1154.6	1155.342	2	202	61.11111	D.NAWIPRGELV.E
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	1	2.3814	0.1552	1533.52	1531.744	6	211.5	45.833336	M.C1K2L1V1E1D1P1Q2V1I1A1P1F1.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	2	3.4562	0.2689	1588.09	1588.627	1	390.6	61.538464	T.VYVEHDIDGTHSDT.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	2.9149	0.2055	1972.33	1974.008	1	260.3	46.666668	T.Q2E1E1C1R4T1V1Y1V1E1H3D1I1D1G1T1.H
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	3.343	0.2872	2393.43	2394.457	1	235.5	42.105263	N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3D1.I
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	2.9994	0.2209	2752.69	2753.862	1	262.7	32.608696	N.GQVDGFPTQEECRTVYVEHDIDGT.H
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	4.4384	0.2661	1783.63	1784.93	1	653.5	67.85714	A.T1E1T1V1D1N2K2D1I1E1R4F1I1P1S1.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	2	3.6326	0.2925	1890.45	1891.043	1	774.9	60.000004	A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1.F
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	5.3876	0.2997	1991.69	1991.133	1	992.5	45.3125	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	2	2.9907	0.221	1702.71	1703.955	1	1038.3	64.28571	M.C1K2L1V1E1D1P1Q2V1I1A1P1F1L1G1.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	3.7488	0.2104	2566.59	2567.802	1	507.5	40.476192	Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2.T
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	3.9986	0.3777	2542.63	2542.802	1	433.3	42.857143	Y.EELSNTDLEFKFPEPGYLEGVK.T
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	3.5763	0.3222	1972.27	1970.229	1	709.7	56.25	T.DLEFKFPEPGYLEGVKT.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	3	4.0707	0.2652	2671.28	2669.907	1	614.8	28.40909	Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1.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	4.2697	0.3456	2668.65	2669.907	1	607.3	38.636364	Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1.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	4.1479	0.3933	2642.05	2643.907	1	1220.8	52.272724	Y.EELSNTDLEFKFPEPGYLEGVKT.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	3.9068	0.3909	1645.41	1645.903	1	579.7	61.538464	M.C1K2L1V1E1D1P1Q2V1I1A1P1F1L1.G
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	5.1533	0.2577	2440.41	2437.628	1	787.1	47.5	Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	3.2218	0.1875	1040.63	1042.181	5	679.3	87.5	L.L1K2D1E1T1V1A1P1R4.F
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	3.1597	0.3028	1158.63	1156.341	1	1097.3	94.44444	E.L1L1K2D1E1T1V1A1P1R4.F
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	1	3.0821	0.2765	1155.55	1156.341	1	455.9	72.22222	E.L1L1K2D1E1T1V1A1P1R4.F
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	1	3.9122	0.2011	1499.35	1500.606	1	783.9	68.181816	E.K2K2E1D1E1E1D1K2F1D1A1M1.G
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	1	3.7413	0.3133	1484.44	1485.606	1	907.8	72.72727	E.KKEDEEDKFDAM.G
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	4.8424	0.2028	2255.9	2253.452	1	998.9	39.473686	E.K2K2E1D1E1E1D1K2F1D1A1M$G1N2K2I1A1G1G1K2.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	2.9805	0.2562	2441.39	2442.587	1	374.1	42.5	M.R4A1I1A1N2G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1.V
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	3.1925	0.2383	2672.17	2672.835	1	360.4	36.363636	M.R4A1I1A1N2G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1.H
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	3.5123	0.3095	1572.33	1569.714	1	1258.6	75	N.IIEHDVPEHFFGE.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	2	5.0977	0.358	1992.23	1991.133	1	801.7	62.5	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	2	2.9449	0.237	1401.55	1400.662	1	501.1	68.181816	L.R4M1P1E1L1I1P1V1L1S1E1T1.M
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	1	3.2635	0.3374	1399.62	1400.662	8	171.1	50	L.R4M1P1E1L1I1P1V1L1S1E1T1.M
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	1	2.9244	0.2498	1384.65	1385.662	2	189.8	54.545456	L.RMPELIPVLSET.M
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	3.1349	0.2494	1386.47	1385.662	1	635.6	72.72727	L.RMPELIPVLSET.M
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	3.5608	0.1993	1899.59	1899.089	3	439.6	50	A.T1E1T1V1D1N2K2D1I1E1R4F1I1P1S1L1.I
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	3.0039	0.3009	2190.07	2190.458	1	514.4	47.22222	K.ATETVDNKDIERFIPSLIQ.C
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	3.9743	0.2502	2120.61	2119.379	1	612.9	58.823532	A.TETVDNKDIERFIPSLIQ.C
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	3.9502	0.2058	2039.81	2041.274	1	796.2	59.375	T.E1T1V1D1N2K2D1I1E1R4F1I1P1S1L1I1Q2.C
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	3.0636	0.2834	1515.67	1516.854	1	525.4	66.66667	L.RMPELIPVLSETM.W
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	1	2.9932	0.2347	1515.55	1516.854	2	165.9	50	L.RMPELIPVLSETM.W
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	2.932	0.3078	1534.81	1532.854	1	486.7	62.5	L.R4M1P1E1L1I1P1V1L1S1E1T1M1.W
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	4.3622	0.3101	2175.77	2177.371	1	659.9	50	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1A1.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	3.1671	0.2133	2202.53	2202.387	1	854.8	52.77778	A.SFLNGNIIEHDVPEHFFGE.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	2	5.0813	0.3928	2226.41	2227.387	1	1126.1	58.333332	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	2	4.9984	0.4284	2341.31	2341.547	1	1185.3	60.526318	A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	3.3367	0.2136	1553.31	1551.706	3	692.9	72.72727	L.T1R4K2E1I1E1E1H3C1S1M1L1.G
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	2.968	0.2418	1534.29	1533.706	1	645.3	68.181816	L.TRKEIEEHCSML.G
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	2.9924	0.1889	1076.91	1077.309	1	900.2	87.5	E.AIKDKLIEF.G
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	1	3.4394	0.2793	1570.71	1569.714	2	732.9	58.333332	N.IIEHDVPEHFFGE.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	1	3.0196	0.2206	1571.57	1569.714	1	530.8	58.333332	I.IEHDVPEHFFGEL.A
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	3.4052	0.2155	2152.61	2152.371	1	519	44.444447	F.LNGNIIEHDVPEHFFGELA.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	3.2999	0.286	1587.49	1586.714	1	711.7	66.66667	I.I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	4.6923	0.4244	1873.75	1875.029	1	1514.1	73.333336	N.G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	1	2.5996	0.2569	1589.42	1586.714	1	211.6	50	I.I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	4.195	0.4202	1856.33	1854.029	1	1309.9	70	N.GNIIEHDVPEHFFGEL.A
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	3.3789	0.2616	2575.01	2572.044	2	437.3	36.363636	S.AVIIDNMCKLVEDPQVIAPFLGK.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	2	3.6007	0.3082	2184.27	2182.367	1	405.9	47.22222	Q.GAGPRIEKKEDEEDKFDAM@.G
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	5.1136	0.2807	2189.09	2191.367	1	955.9	38.88889	Q.G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
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	4.3458	0.3348	2192.41	2191.367	1	864.8	55.555557	Q.G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
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	3.7979	0.2591	2378.39	2379.55	2	421.7	42.5	S.G1Q2G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
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	3.2667	0.1894	1413.87	1412.573	1	1078.6	72.72727	N.A1W2I1P1R4G1E1L1V1E1S1H3.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	1	3.1869	0.17	1357.57	1358.566	2	591.5	63.636364	L.K2E1F1E1G1G1V1I1I1I1T1H3.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	1	2.3292	0.1658	1516.56	1517.681	2	333.5	50	S.HLDKTPSEYIQW.R
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	3.8077	0.3155	2346.59	2345.632	1	749.3	50	T.K2A1T1E1T1V1D1N2K2D1I1E1R4F1I1P1S1L1I1Q2.C
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	3.6718	0.1867	1358.41	1358.566	1	1256.1	77.27273	L.K2E1F1E1G1G1V1I1I1I1T1H3.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	3.9027	0.311	2057.43	2057.478	1	597.9	50	L.V1E1D1P1Q2V1I1A1P1F1L1G1K2L1L1P1G1L1K2.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	5.2232	0.4288	1947.43	1949.065	1	825.8	67.64706	L.R4R4V1G1N2V1G1E1D1D1A1I1P1E1V1S1H3A1.G
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	4.7367	0.3718	1544.39	1544.804	1	2112.3	76.92308	K.A1L1K2E1F1E1G1G1V1I1I1I1T1H3.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	1	3.0962	0.25	1543.57	1544.804	2	516.5	53.846157	K.A1L1K2E1F1E1G1G1V1I1I1I1T1H3.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	1	2.656	0.1847	1532.55	1533.706	2	501.4	68.181816	L.TRKEIEEHCSML.G
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	1	2.7098	0.2134	1342.55	1343.566	1	613	68.181816	L.KEFEGGVIIITH.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	1	3.2964	0.2932	1527.66	1527.804	1	192.1	61.538464	K.ALKEFEGGVIIITH.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	3.8715	0.4189	2224.59	2225.599	1	701.6	55.555557	L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
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	3.741	0.392	2200.61	2199.599	1	769.2	55.555557	L.QVVNELLKDETVAPRFKIV.V
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	4.4982	0.3895	2222.87	2225.599	1	1430.3	45.833336	L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
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	3.5073	0.2166	2324.69	2325.731	1	545.4	44.736843	L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1V1.E
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	4.5435	0.4283	2311.77	2312.758	1	1147.8	57.894737	T.LQVVNELLKDETVAPRFKIV.V
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	4.265	0.2891	2314.91	2312.758	1	1318	42.105263	T.LQVVNELLKDETVAPRFKIV.V
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	5.2032	0.3986	3440.12	3439.931	1	814.7	27.586206	Y.EELSNTDLEFKFPEPGYLEGVKTKQKAIVK.V
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	5.3439	0.3477	3685.88	3685.332	1	619.7	23.4375	M.VDAAKDQVALRMPELIPVLSETMWDTKKEVKAA.A
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	5.0462	0.303	3475.73	3476.931	1	663	25.862068	Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1K2Q2K2A1I1V1K2.V
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	4.0849	0.3077	2060.33	2061.254	1	842.5	60.000004	E.S1H3L1D1K2T1P1S1E1Y1I1Q2W2R4F1Q2.T
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	3.0137	0.2215	2063.73	2065.286	1	583.4	53.125	A.G1T1W2Q2R4P1H3L1I1V1L1D1E1P1T1N2Y1.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	6.1023	0.3919	2705.06	2704.189	1	1654.6	44.31818	L.R4M1P1E1L1I1P1V1L1S1E1T1M1W2D1T1K2K2E1V1K2A1A1.A
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	4.477	0.2945	2294.73	2295.503	1	677.1	47.5	L.K2T1L1R4R4V1G1N2V1G1E1D1D1A1I1P1E1V1S1H3A1.G
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	3.9428	0.2781	2263.89	2264.503	1	560.3	45	L.KTLRRVGNVGEDDAIPEVSHA.G

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	4.755	0.3484	1762.21	1763.056	1	1445.8	73.333336 L.S1K2A1L1K2E1F1E1G1G1V1I1I1I1T1H3.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	4.6176	0.4018	1743.85	1743.056	1	1478	73.333336 L.SKALKEFEGGVIIITH.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	1	2.8636	0.2224	1319.73	1320.58	8	321.2	60.000004 A.GTWQRPHLIVL.D
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	3.6013	0.306	2675.89	2674.189	1	465.2	43.18182 L.RMPELIPVLSETMWDTKKEVKAA.A
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	3.7724	0.2696	3016.49	3018.338	1	360.2	38 A.G1T1W2Q2R4P1H3L1I1V1L1D1E1P1T1N2Y1L1D1R4D1S1L1G1A1L1.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	3	4.4345	0.2377	2924.27	2924.286	3	533.8	28.125 G.TWQRPHLIVLDEPTNYLDRDSLGAL.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	3	6.5806	0.2702	3017.15	3018.338	3	831.6	33 A.G1T1W2Q2R4P1H3L1I1V1L1D1E1P1T1N2Y1L1D1R4D1S1L1G1A1L1.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	3.4611	0.2628	1678.55	1679.781	1	429.9	53.571426 L.DEPTNYLDRDSLGAL.A
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	4.626	0.4225	1695.61	1694.888	1	1343.4	78.57143 Q.CIADPTEVPETVHLL.G
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	4.5478	0.4389	1714.33	1711.888	1	1326.9	78.57143 Q.C1I1A1D1P1T1E1V1P1E1T1V1H3L1L1.G
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	4.3493	0.2221	1428.87	1428.657	1	1557.9	79.16667 L.V1E1D1P1Q2V1I1A1P1F1L1G1K2.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	2	3.3028	0.3442	1512.47	1512.702	1	535.5	66.66667 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	1	3.0562	0.2676	1525.73	1526.702	1	254.5	58.333332 L.E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	3.8018	0.2051	1987.07	1989.229	1	629.2	53.125 T.D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1.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	5.0302	0.2994	2062.53	2063.237	1	1370.7	64.70589 L.S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	4.0748	0.4661	1886.57	1887.998	1	1047.5	68.75 T.VYVEHDIDGTHSDTSVL.D
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	1	2.8141	0.2168	1299.55	1300.458	2	191.5	55 D.N2A1W2I1P1R4G1E1L1V1E1.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	1	2.7311	0.2645	1283.69	1284.458	1	193.8	60.000004 D.NAWIPRGELVE.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	3.3602	0.1623	2596.05	2596.679	1	347.7	40.476192 Q.V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3D1I1D1G1T1.H
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	3.5503	0.2884	2783.45	2784.862	1	324.3	34.782608 N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3D1I1D1G1T1.H
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	3.7981	0.3385	1249.01	1248.41	1	989.3	85 F.K2F1P1E1P1G1Y1L1E1G1V1.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	1	2.4913	0.264	1247.54	1248.41	1	653.5	65 F.K2F1P1E1P1G1Y1L1E1G1V1.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	3.9119	0.3016	1533.25	1531.744	1	838.9	79.16667 M.C1K2L1V1E1D1P1Q2V1I1A1P1F1.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	2	3.5558	0.3503	1515.81	1516.744	1	728.9	75 M.CKLVEDPQVIAPF.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	4.5966	0.3498	2106.38	2105.292	1	658.4	41.17647 F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	1	2.7151	0.2189	1285.59	1286.456	1	131	55 N.E1L1L1K2D1E1T1V1A1P1R4.F
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	3.1132	0.3676	1841.35	1843.877	1	644.8	57.14286 Q.E1E1C1R4T1V1Y1V1E1H3D1I1D1G1T1.H
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	4.539	0.4547	2276.69	2278.368	1	647.9	55.555557 N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3.D
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	4.0564	0.3781	2250.77	2252.368	1	755.8	55.555557 N.GQVDGFPTQEECRTVYVEH.D
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	3.0483	0.221	1684.19	1682.825	1	225.5	57.692307 T.E1T1V1D1N2K2D1I1E1R4F1I1P1S1.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	2	4.1854	0.267	1765.47	1764.93	1	631	67.85714	A.TETVDNKDIERFIPS.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	2	4.6365	0.3691	1988.27	1991.133	1	779	59.375	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	4.7213	0.2239	1989.5	1991.133	1	956.4	43.75	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	2	2.9748	0.1829	1398.55	1400.662	3	455.4	63.636364	L.R4M1P1E1L1I1P1V1L1S1E1T1.M
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	1	3.2987	0.2581	1399.62	1400.662	1	173.2	50	L.R4M1P1E1L1I1P1V1L1S1E1T1.M
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	4.487	0.3281	2273.27	2272.516	1	1110	55.263157	L.SNTDLEFKFPEPGYLEGVKT.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	3	5.2464	0.3379	2274.02	2272.516	1	2987.3	50	L.SNTDLEFKFPEPGYLEGVKT.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	4.1227	0.2707	2141.65	2143.379	1	730.2	61.764706	A.T1E1T1V1D1N2K2D1I1E1R4F1I1P1S1L1I1Q2.C
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	3.1993	0.1739	2214.47	2215.458	1	423.5	44.444447	K.A1T1E1T1V1D1N2K2D1I1E1R4F1I1P1S1L1I1Q2.C
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	3.4459	0.3757	1855.57	1857.978	1	393.4	57.14286	S.H3D1S1V1F1L1D1N2V1C1E1Y1I1I1N2.Y
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	3.7641	0.3516	1837.57	1838.978	1	450.9	57.14286	S.HDSVFLDNVCEYIIN.Y
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	1	2.2403	0.2163	1167.56	1168.441	3	249.2	66.66667	L.R4M1P1E1L1I1P1V1L1S1.E
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	3.3243	0.2986	2038.29	2039.215	1	553.2	46.875	T.ISHDSVFLDNVCEYIIN.Y
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	5.631	0.4255	2104.47	2105.292	1	534.1	50	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	4.6867	0.3097	2674.83	2673.882	1	668.1	40.909092	K.A1Y1E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	3.7183	0.3757	2647.27	2648.882	1	697.6	43.18182	K.AYEELSNTDLEFKFPEPGYLEGV.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	1	3.0065	0.2887	1155.76	1156.341	1	459.7	72.22222	E.L1L1K2D1E1T1V1A1P1R4.F
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	1	2.9913	0.3435	1141.59	1142.341	2	388.1	66.66667	E.LLKDETVAPR.F
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	3.6412	0.2763	1743.57	1744.881	3	715	61.538464	R.I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
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	4.8287	0.4009	3041.93	3043.092	7	368.5	24	Q.V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3D1I1D1G1T1H3S1D1T1.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	1	3.3161	0.3823	1568.54	1569.714	1	760.2	58.333332	N.IIEHDVPEHFFGE.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	4.8303	0.3875	3531.86	3533.645	1	576.4	25.833332	N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1H3D1I1D1G1T1H3S1D1T1S1V1L1.D
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	3.749	0.4003	1685.77	1682.873	1	857.9	65.38461	N.IIEHDVPEHFFGEL.A
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	4.6004	0.3744	1815.83	1816.977	1	883.7	60.714287	G.N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	4.3208	0.3996	1967.35	1968.133	1	1187.5	62.5	L.NGNIIEHDVPEHFFGEL.A
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	3.402	0.2531	2171.25	2171.411	7	377.8	38.88889	L.SNTDLEFKFPEPGYLEGVK.T
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	3.8321	0.2523	2171.78	2171.411	1	2421.7	44.444447	L.SNTDLEFKFPEPGYLEGVK.T
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	4.2141	0.2594	2296.21	2295.516	1	637.2	42.105263	L.S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1K2T1.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	3	5.3788	0.399	2612.6	2615.044	1	1282.9	35.227272	S.A1V1I1I1D1N2M$C1K2L1V1E1D1P1Q2V1I1A1P1F1L1G1K2.L
gi|6323278|ref|NP_013350.1|	YLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	2	3.4571	0.2893	2613.87	2615.044	1	417.6	38.636364	S.A1V1I1I1D1N2M$C1K2L1V1E1D1P1Q2V1I1A1P1F1L1G1K2.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	2	3.6544	0.2574	2207.51	2207.367	1	508	50	Q.G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M$.G
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	1	2.7286	0.162	1435.37	1434.546	1	212.8	59.090908	E.S1H3L1D1K2T1P1S1E1Y1I1Q2.W
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	4.117	0.3045	1921.35	1922.065	1	786.4	61.764706	L.RRVGNVGEDDAIPEVSHA.G
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	2.9837	0.252	1323.41	1323.494	5	824.5	75	A.WIPRGELVESH.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	1	2.4705	0.2023	1341.59	1340.494	1	209.9	65	A.W2I1P1R4G1E1L1V1E1S1H3.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	3.1263	0.2396	1395.99	1394.573	1	1082.8	77.27273	N.AWIPRGELVESH.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	1	3.2311	0.2185	1530.57	1528.677	1	289.7	58.333332	D.N2A1W2I1P1R4G1E1L1V1E1S1H3.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	3.6325	0.2055	1964.55	1964.183	3	299.5	53.125	T.KATETVDNKDIERFIPS.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	2	4.3709	0.3546	1623.95	1622.759	1	1128.5	79.16667	E.S1H3L1D1K2T1P1S1E1Y1I1Q2W2.R
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	5.9538	0.3204	1835.53	1834.129	1	905.6	56.666668	M.C1K2L1V1E1D1P1Q2V1I1A1P1F1L1G1K2.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	4.3175	0.2369	1816.88	1815.129	1	2521.9	61.666668	M.CKLVEDPQVIAPFLGK.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	2	3.6682	0.3298	2167.19	2166.367	1	645.9	52.77778	Q.GAGPRIEKKEDEEDKFDAM.G
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	4.0392	0.3364	2193.39	2191.367	1	669.6	52.77778	Q.G1A1G1P1R4I1E1K2K2E1D1E1E1D1K2F1D1A1M1.G
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	1	2.2047	0.3196	1322.58	1323.494	8	136	50	A.WIPRGELVESH.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	3.9129	0.3337	2011.01	2011.307	1	418.6	50	L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2.I
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	2.9008	0.2703	1533.69	1534.681	1	738.5	72.72727	S.H3L1D1K2T1P1S1E1Y1I1Q2W2.R
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	4.332	0.2047	1359.81	1358.566	1	1881.9	90.909096	L.K2E1F1E1G1G1V1I1I1I1T1H3.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	4.1052	0.1653	1345.83	1343.566	1	1709.8	86.36364	L.KEFEGGVIIITH.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	1	2.6013	0.1563	1532.59	1533.706	1	501.2	68.181816	L.TRKEIEEHCSML.G
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	1	2.7011	0.2539	1357.97	1358.566	1	688.9	63.636364	L.K2E1F1E1G1G1V1I1I1I1T1H3.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	3	4.1881	0.3091	2225.51	2225.599	2	847.1	36.11111	L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
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	3.7598	0.3919	2224.85	2225.599	1	585.7	47.22222	L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
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	4.3525	0.2916	1459.39	1456.725	1	1274.4	70.83333	A.LKEFEGGVIIITH.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	4.0431	0.2432	1472.33	1472.725	1	1993.7	83.33333	A.L1K2E1F1E1G1G1V1I1I1I1T1H3.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	3.9192	0.2302	1528.45	1527.804	1	1544.4	65.38461	K.ALKEFEGGVIIITH.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	4.1406	0.3421	2034.01	2035.224	1	777.7	58.333332	T.LRRVGNVGEDDAIPEVSHA.G
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	5.9733	0.5677	3199.94	3202.243	1	1145.8	30.769232	F.R4K2R4A1V1D1N2I1P1V1G1P1N2F1D1D1E1E1D1E1G1E1D1L1C1N2C1.E
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	5.3395	0.476	3165.95	3165.243	1	1299.8	30.769232	F.RKRAVDNIPVGPNFDDEEDEGEDLCNC.E
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	3.2633	0.2839	3165.71	3165.243	1	406	32.692307	F.RKRAVDNIPVGPNFDDEEDEGEDLCNC.E
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	4.349	0.3001	2338.22	2339.758	1	684.4	36.842106	T.L1Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V

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	1	2.312	0.1564	1207.93	1206.425	7	345	60.000004	L.KEFEGGVIIIT.H
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	3.0513	0.2936	1519.69	1519.787	1	469.7	63.636364	K.KAKDILDEFRKR.A
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	4.7315	0.3843	1741.31	1741.956	1	1100.9	71.42857	T.NMEFQYPGTSKPQIT.D
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	5.1054	0.2756	1758.53	1760.956	1	909.1	67.85714	T.N2M1E1F1Q2Y1P1G1T1S1K2P1Q2I1T1.D
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	3.6783	0.4515	2114.31	2115.227	1	606.8	52.941177	N.GQVDGFPTQEECRTVYVE.H
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	4.2349	0.5456	2136.33	2138.227	1	703.6	55.88235	N.G1Q2V1D1G1F1P1T1Q2E1E1C1R4T1V1Y1V1E1.H
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	3.5449	0.1644	1600.45	1599.781	7	567.5	57.692307	A.IGADLIDERIIDQQ.A
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	1	3.7761	0.1718	1597.42	1598.766	2	1128.4	70.83333	T.D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
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	5.1753	0.4054	1974.99	1975.159	1	1431.5	65.625	S.N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	1	3.8041	0.2464	1467.54	1468.65	5	843.3	63.636364	T.D1L1E1F1K2F1P1E1P1G1Y1L1.E
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	5.1159	0.2575	1759.01	1756.95	1	1210.2	71.42857	T.D1L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	3.5059	0.3429	1494.29	1494.616	1	866.6	73.07692	M.R4A1I1A1N2G1Q2V1D1G1F1P1T1Q2.E
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	3.3462	0.276	1363.79	1364.486	1	357.6	62.5	M.R4A1I1A1N2G1Q2V1D1G1F1P1T1.Q
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	3.6501	0.2522	1396.29	1394.54	1	1593	90	H.L1D1K2T1P1S1E1Y1I1Q2W2.R
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	4.129	0.2255	1617.83	1618.781	1	932.9	69.230774	A.I1G1A1D1L1I1D1E1R4I1I1D1Q2Q2.A
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	1	3.1833	0.1563	1367.59	1368.518	2	323.5	70	L.E1F1K2F1P1E1P1G1Y1L1E1.G
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	2.9395	0.1818	1370.47	1368.518	2	845.2	80	L.E1F1K2F1P1E1P1G1Y1L1E1.G
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	1	3.4145	0.3491	1527.54	1526.702	1	219.1	54.166668	L.E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	3.7605	0.3338	1512.31	1512.702	1	945.9	79.16667	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	3.0686	0.1929	2239.15	2240.58	1	451.9	47.22222	A.V1I1I1D1N2M$C1K2L1V1E1D1P1Q2V1I1A1P1F1.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	2	3.1077	0.1701	2217.57	2218.58	2	449.8	44.444447	A.VIIDNM@CKLVEDPQVIAPF.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	2	5.1821	0.3471	1815.89	1816.975	1	1580.1	75	S.N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
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	3.9338	0.2927	1758.01	1757.937	1	840.2	64.28571	L.SNTDLEFKFPEPGYL.E
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	4.2836	0.164	1687.53	1686.859	1	1213.8	73.07692	S.N2T1D1L1E1F1K2F1P1E1P1G1Y1L1.E
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	3.2179	0.176	1569.67	1570.755	1	880.2	70.83333	N.T1D1L1E1F1K2F1P1E1P1G1Y1L1.E
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	1	3.6292	0.2908	1584.71	1584.766	1	966.5	66.66667	T.DLEFKFPEPGYLE.G
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	5.07	0.2938	2043.35	2043.237	1	1273.8	61.764706	L.SNTDLEFKFPEPGYLEGV.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	4.7483	0.3332	1957.83	1956.159	1	1090.7	62.5	S.NTDLEFKFPEPGYLEGV.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	3.3891	0.2426	1382.09	1380.54	1	1272.8	80	H.LDKTPSEYIQW.R
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	3.2159	0.1618	1298.53	1300.458	4	752.6	70	D.N2A1W2I1P1R4G1E1L1V1E1.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	1	2.9498	0.2769	1355.59	1356.518	1	293.8	65	L.EFKFPEPGYLE.G
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	1	3.1632	0.2715	1237.61	1238.402	1	412.9	77.77778	L.E1F1K2F1P1E1P1G1Y1L1.E
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	1	2.8915	0.2469	1227.5	1227.402	1	310.2	66.66667	L.EFKFPEPGYL.E
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	2.9214	0.2123	1240.39	1238.402	6	555.6	83.33333	L.E1F1K2F1P1E1P1G1Y1L1.E
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	4.6107	0.3792	1992.25	1991.133	1	827.7	59.375	L.N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	3.2062	0.2066	1738.41	1740.95	3	551.4	50	T.DLEFKFPEPGYLEGV.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	3.4421	0.3418	1518.13	1516.606	1	732.9	81.818184	E.K2K2E1D1E1E1D1K2F1D1A1M$.G
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	4.2736	0.2081	1501.91	1500.606	1	1367.5	86.36364	E.K2K2E1D1E1E1D1K2F1D1A1M1.G
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	1	4.0822	0.2279	1499.47	1500.606	1	924.4	72.72727	E.K2K2E1D1E1E1D1K2F1D1A1M1.G
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	1	3.8048	0.1594	1487.52	1485.606	1	866	72.72727	E.KKEDEEDKFDAM.G
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	4.1188	0.338	1487.25	1485.606	1	893.7	77.27273	E.KKEDEEDKFDAM.G
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	4.1474	0.3256	1419.37	1418.546	1	959.2	77.27273	E.SHLDKTPSEYIQ.W
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	1	2.7655	0.3606	1418.65	1418.546	1	405	59.090908	E.SHLDKTPSEYIQ.W
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	1	2.3969	0.1601	1235.42	1236.37	1	490.9	61.11111	N.IIEHDVPEHF.F
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	1	2.817	0.2495	1249.52	1250.37	1	569.1	66.66667	N.I1I1E1H3D1V1P1E1H3F1.F
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	1	2.8339	0.1756	1299.43	1300.458	3	234	60.000004	D.N2A1W2I1P1R4G1E1L1V1E1.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	1	3.404	0.3889	1568.58	1569.714	1	1171.1	70.83333	N.IIEHDVPEHFFGE.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	1	3.0048	0.1787	1552.48	1552.709	2	373.1	45.833336	E.T1V1D1N2K2D1I1E1R4F1I1P1S1.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	1	2.6213	0.1685	1534.64	1534.709	1	448.7	50	E.TVDNKDIERFIPS.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	2	3.8067	0.2613	1248.43	1248.41	1	971.6	85	F.K2F1P1E1P1G1Y1L1E1G1V1.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	1	2.6706	0.2103	1247.49	1248.41	1	576.5	65	F.K2F1P1E1P1G1Y1L1E1G1V1.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	1	2.9343	0.3574	1471.48	1472.554	1	248.9	59.090908	I.E1H3D1V1P1E1H3F1F1G1E1L1.A
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	1	2.3859	0.213	1455.48	1456.554	2	182	50	I.EHDVPEHFFGEL.A
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	4.9798	0.4358	1875.37	1876.973	1	793.8	60.000004	L.N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	2	4.5318	0.4088	1758.57	1760.869	1	1291.7	67.85714	N.G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	2	4.3028	0.3415	1854.31	1854.973	1	638.5	53.333336	L.NGNIIEHDVPEHFFGE.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	2	3.8096	0.3937	1530.63	1531.744	1	818.2	79.16667	M.C1K2L1V1E1D1P1Q2V1I1A1P1F1.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	2	4.9849	0.4456	1988.61	1991.133	1	755.2	59.375	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	4.3082	0.2989	1991.27	1991.133	1	1168.2	45.3125	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	2	4.0937	0.3427	1798.21	1796.977	1	877.2	60.714287	G.NIIEHDVPEHFFGEL.A

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	3.2812	0.2407	1803.57	1802.965	1	530	53.571426	F.L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1.G
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	3.101	0.2963	1628.57	1629.903	1	614.7	61.538464	M.CKLVEDPQVIAPFL.G
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	1	2.5721	0.2341	1339.44	1340.561	1	848.9	65	D.LEFKFPEPGYL.E
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	4.8588	0.4288	2136.81	2139.309	1	813.7	55.88235	S.F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	2	3.7699	0.1691	1639.39	1640.861	2	963.5	65.38461	D.L1E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	3.5572	0.374	1624.41	1625.861	4	591.8	50	D.LEFKFPEPGYLEGV.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	4.5896	0.4083	2298.33	2299.466	1	485	42.105263	V.A1S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1.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	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, 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	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
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	3.1622	0.235	2230.33	2228.469	1	675.5	47.22222	S.FLNGNIIEHDVPEHFFGEL.A
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	4.105	0.4478	2250.65	2253.469	1	691.9	50	S.F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	4.2874	0.2942	1938.79	1939.261	1	817.5	70	L.R4M1P1E1L1I1P1V1L1S1E1T1M1W2D1T1.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	3.6091	0.2617	1918.13	1919.261	1	619.7	60.000004	L.RMPELIPVLSETMWDT.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	4.2356	0.3802	2411.77	2413.626	1	479.4	40	V.A1S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	4.7906	0.4817	2340.61	2341.547	1	692.1	50	A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	4.2585	0.1909	1434.17	1434.546	1	1143.4	77.27273	E.S1H3L1D1K2T1P1S1E1Y1I1Q2.W
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	1	3.3171	0.158	1434.38	1434.546	1	422	59.090908	E.S1H3L1D1K2T1P1S1E1Y1I1Q2.W
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	3.0237	0.1933	939.27	939.23	1	1103.9	93.75	F.LGKLLPGLK.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	3.4925	0.1697	1530.25	1528.677	1	1363.7	75	D.N2A1W2I1P1R4G1E1L1V1E1S1H3.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	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, 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	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
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	1	3.9981	0.3949	1585.51	1586.714	1	917.7	62.5	N.I1I1E1H3D1V1P1E1H3F1F1G1E1.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	2	4.9578	0.4177	1814.49	1815.129	1	1937.9	80	M.CKLVEDPQVIAPFLGK.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	2	3.7275	0.3353	1781.53	1781.965	2	411.8	50	F.LNGNIIEHDVPEHFF.G
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	4.9474	0.4352	2080.55	2081.292	1	725.9	55.88235	F.LNGNIIEHDVPEHFFGEL.A
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	3.9546	0.3473	2317.45	2315.547	1	663.9	47.368423	A.SFLNGNIIEHDVPEHFFGEL.A
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	4.5539	0.3043	2343.38	2341.547	1	808.3	40.789474	A.S1F1L1N2G1N2I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	3.3544	0.2247	1321.55	1322.551	7	494.5	65	T.M1W2D1T1K2K2E1V1K2A1A1.A

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	3.1353	0.2659	1532.57	1533.706	1	669.5	68.181816	L.TRKEIEEHCSML.G
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	1	2.6195	0.189	1550.53	1551.706	1	368.9	59.090908	L.T1R4K2E1I1E1E1H3C1S1M1L1.G
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	3.4272	0.2449	1345.63	1343.566	1	1109.6	77.27273	L.KEFEGGVIIITH.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	5.0531	0.4664	2069.09	2069.435	1	1266.4	65.625	L.R4M1P1E1L1I1P1V1L1S1E1T1M1W2D1T1K2.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	4.4948	0.4918	2045.57	2047.435	1	1326.7	68.75	L.RMPELIPVLSETMWDTK.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	3	3.9736	0.2619	2261.06	2261.66	1	681.7	32.5	L.V1E1D1P1Q2V1I1A1P1F1L1G1K2L1L1P1G1L1K2S1N2.F
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	3.8517	0.2126	2035.55	2035.478	4	535.6	36.11111	L.VEDPQVIAPFLGKLLPGLK.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	1	2.5763	0.1677	1532.63	1533.706	1	427	63.636364	L.TRKEIEEHCSML.G
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	3.8028	0.2544	1411.53	1410.613	1	776.1	75	K.A1K2D1I1L1D1E1F1R4K2R4.A
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	3.8459	0.2512	2224.58	2225.599	1	789.1	37.5	L.Q2V1V1N2E1L1L1K2D1E1T1V1A1P1R4F1K2I1V1.V
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	3.7698	0.174	1359.55	1358.566	1	1484.5	86.36364	L.K2E1F1E1G1G1V1I1I1I1T1H3.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	3.3795	0.2241	1529.81	1527.804	1	640.5	53.846157	K.ALKEFEGGVIIITH.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	3.2245	0.2344	1190.65	1191.383	1	235	77.77778	T.E1F1V1K2K2C1P1A1A1K2.A
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	3.3532	0.1721	1545.85	1544.804	2	543.9	53.846157	K.A1L1K2E1F1E1G1G1V1I1I1I1T1H3.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	1	3.0776	0.2195	1357.69	1358.566	1	738.6	68.181816	L.K2E1F1E1G1G1V1I1I1I1T1H3.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	4.5699	0.2149	1598.21	1598.766	1	1433.4	83.33333	T.D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
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	3.3489	0.1741	1406.71	1404.663	1	681.9	66.66667	K.A1L1K2E1F1E1G1G1V1I1I1I1T1.H
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	1	2.4833	0.2033	1141.71	1141.359	7	120	61.11111	F.KIEGTPRRIA.G
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	1	2.2336	0.3267	1025.87	1026.308	1	521.1	61.11111	F.LGKLLPGLKS.N
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	1	2.7682	0.154	940.65	939.23	1	753.7	75	F.LGKLLPGLK.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	3.9669	0.3549	1798.75	1799.975	1	1561.6	71.42857	S.NTDLEFKFPEPGYLE.G
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	4.579	0.2556	2278.15	2279.443	1	1040.9	50	Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
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	4.0902	0.2279	2148.09	2149.328	1	1176.4	58.823532	Y.E1E1L1S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1.E
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	3.5214	0.3059	1840.57	1842.055	1	1013.5	60.000004	N.TDLEFKFPEPGYLEGV.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	4.4222	0.2906	1605.49	1604.828	1	1143	75	F.L1H3E1K2K2A1K2D1I1L1D1E1F1.R
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	1	3.2122	0.2032	1585.69	1586.828	1	819.1	66.66667	F.LHEKKAKDILDEF.R
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	3.2851	0.3733	1569.19	1569.714	1	1024.5	70.83333	N.IIEHDVPEHFFGE.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	2	4.1031	0.3404	1702.59	1700.873	1	850.2	65.38461	N.I1I1E1H3D1V1P1E1H3F1F1G1E1L1.A
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	1	2.7034	0.2352	1201.48	1202.298	1	487.3	61.11111	H.D1V1P1E1H3F1F1G1E1L1.A
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	3.8663	0.1665	1525.73	1526.702	1	785.2	75	L.E1F1K2F1P1E1P1G1Y1L1E1G1V1.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	3.7536	0.3001	1904.39	1905.053	1	601.7	50	L.S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1E1.G
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	2.9986	0.3371	1669.79	1670.859	1	823.3	61.538464	S.NTDLEFKFPEPGYL.E
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	3.821	0.3621	1455.25	1455.65	1	1303.9	86.36364	T.DLEFKFPEPGYL.E
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	4.0937	0.3325	2129.07	2129.328	1	876.2	52.941177	Y.EELSNTDLEFKFPEPGYL.E
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	4.9843	0.469	1966.75	1968.133	1	961.7	62.5	F.LNGNIIEHDVPEHFFGE.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	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
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	3.9927	0.2408	1774.37	1774.937	2	790.2	60.714287	L.S1N2T1D1L1E1F1K2F1P1E1P1G1Y1L1.E
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	3.9008	0.2863	1583.63	1584.766	1	1346.2	79.16667	T.DLEFKFPEPGYLE.G
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	1	3.368	0.2715	1455.54	1455.65	1	1073.7	72.72727	T.DLEFKFPEPGYL.E
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	4.4699	0.3792	2416.27	2414.628	1	622.8	42.5	Y.EELSNTDLEFKFPEPGYLEGV.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	3	5.3332	0.2629	2980.7	2981.338	1	1035.9	33	A.GTWQRPHLIVLDEPTNYLDRDSLGAL.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	3	6.6071	0.2612	3020.12	3018.338	1	1255.3	35	A.G1T1W2Q2R4P1H3L1I1V1L1D1E1P1T1N2Y1L1D1R4D1S1L1G1A1L1.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	4.8932	0.4288	1723.37	1724.836	1	1603.3	84.61539	Q.H3D1E1S1E1K2I1D1N2E1M1A1K2R4.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	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
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	5.2893	0.453	2236.61	2237.367	1	977.5	61.764706	E.L1L1H3H3E1H3E1I1E1H3E1E1E1I1Q2R4G1A1.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	3.1783	0.2036	2777.31	2777.926	2	175.9	35	L.S1W2E1E1W2H3M1D1H3E1H3Q2L1K2D1Y1T1P1E1T1F1.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	3.9082	0.3497	1980.29	1981.048	1	895.1	66.66667	L.HHEHEIEHEEEIQRGA.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	3.9509	0.3037	1868.05	1868.907	1	392.5	53.571426	H.H3E1H3E1I1E1H3E1E1E1I1Q2R4G1A1.S
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 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.-
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	4.1727	0.453	1511.53	1511.718	1	1003.2	76.666664	T.RAAVEEGILPGGGTAL.V
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 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
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.0843	0.3306	1538.61	1539.642	2	260.4	62.5	G.EKKDRYDDALNAT.R
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 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
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.1078	0.2783	1418.45	1418.636	1	424.2	77.27273	D.NFDQKLGVDIIR.K
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 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
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	3	3.8531	0.3218	1617.65	1617.889	1	833.1	51.923077	D.NFDQKLGVDIIRKA.I

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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.7412	0.1703	1329.81	1329.666	2	1597.1	85	S.KVEFEKPLLLL.S
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	4.6693	0.4063	2040.93	2042.257	1	454.9	52.77778	L.NGSGPKEAIQERIEQIKGS.I
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	4.0679	0.2428	1617.07	1617.889	1	1159.6	73.07692	D.NFDQKLGVDIIRKA.I
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.4778	0.1585	1637.73	1638.889	1	704.2	65.38461	D.N2F1D1Q2K2L1G1V1D1I1I1R4K2A1.I
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	3	5.1285	0.4033	2640.62	2643.059	1	1677	37.5	S.RVLDEVVVDNFDQKLGVDIIRKA.I
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 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.FITDPKSSKVEFEKPLLLL.S
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.1047	0.1765	2227.41	2227.643	2	285	41.666664	Y.F1I1T1D1P1K2S1S1K2V1E1F1E1K2P1L1L1L1L1.S
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	4.2231	0.3243	1806.61	1807.023	1	478.6	56.666668	S.G1P1K2E1A1I1Q2E1R4I1E1Q2I1K2G1S1.I
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	4.762	0.4283	1786.75	1789.081	1	1656.6	76.666664	K.G1R4N2V1L1I1E1Q2P1F1G1P1P1K2I1T1.K
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.0118	0.2521	1506.35	1506.609	1	899.2	70.83333	K.LIDEYGDDFAKGY.D
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	1	2.982	0.3021	1510.69	1511.718	2	224.9	46.666668	T.RAAVEEGILPGGGTAL.V
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.7702	0.2435	1617.55	1617.889	1	832.1	73.07692	D.NFDQKLGVDIIRKA.I
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.9007	0.1878	1953.27	1953.153	1	375.6	50	N.G1S1G1P1K2E1A1I1Q2E1R4I1E1Q2I1K2G1S1.I
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 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	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; Hsp60p	2	4.9384	0.3599	1766.17	1767.081	1	1251.4	70	K.GRNVLIEQPFGPPKIT.K
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	3	5.0625	0.1843	1766.72	1767.081	1	2320.5	58.333332	K.GRNVLIEQPFGPPKIT.K
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	3	4.0346	0.2748	2324.39	2324.683	1	532.5	35.714287	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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	1	2.57	0.2037	1214.48	1215.302	2	607.1	72.22222	G.KLIDEYGDDF.A
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.9149	0.3923	1552.61	1553.842	1	1107.4	65.38461	R.NVLIEQPFGPPKIT.K
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.1348	0.2038	1342.49	1340.605	4	788.3	68.181816	V.LIEQPFGPPKIT.K
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 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	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; Hsp60p	1	3.4636	0.1831	1216.5	1216.506	1	749.6	77.77778	S.KVEFEKPLLL.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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.4244	0.1943	1565.37	1566.81	1	1034.4	70.83333	D.N2F1D1Q2K2L1G1V1D1I1I1R4K2.A
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 protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	2	3.1418	0.1945	1944.53	1945.186	2	460.9	44.444447	C.AVKAPGFGDNRKNTIGDIA.V
gi|6323294|ref|NP_013366.1|	YLR264W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp and has similarity to rat S28 ribosomal protein; Rps28bp	1	2.7159	0.1674	1585.63	1586.841	7	237.9	50	R.N2V1K2G1P1V1R4E1N2D1I1L1V1L1.M
gi|6323294|ref|NP_013366.1|	YLR264W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp 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
gi|6323294|ref|NP_013366.1|	YLR264W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp and has similarity to rat S28 ribosomal protein; Rps28bp	1	3.2964	0.3406	1582.58	1583.93	6	276.9	46.153847	N.VKGPVRENDILVLM.E
gi|6323294|ref|NP_013366.1|	YLR264W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp and has similarity to rat S28 ribosomal protein; Rps28bp	2	3.0256	0.2271	1602.51	1602.93	6	270.6	57.692307	N.V1K2G1P1V1R4E1N2D1I1L1V1L1M1.E
gi|6323294|ref|NP_013366.1|	YLR264W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp 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
gi|6323294|ref|NP_013366.1|	YLR264W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp and has similarity to rat S28 ribosomal protein; Rps28bp	1	2.7506	0.2088	1565.85	1566.841	2	236.3	50	R.NVKGPVRENDILVL.M
gi|6323315|ref|NP_013387.1|	YLR285W	Putative nicotinamide N-methyltransferase, has a role in rDNA silencing and in lifespan determination; Nnt1p	2	3.501	0.3449	1966.33	1967.197	1	564.1	46.875	A.G1L1F1E1E1P1E1D1F1L1P1P1P1P1K2P1H3.F
gi|6323322|ref|NP_013394.1|	YLR291C	Beta 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; Gcd7p	2	5.815	0.4779	2043.19	2042.294	1	2027.2	73.52941	Q.GIKDLIDEIKNIDEGIQQ.I
gi|6323322|ref|NP_013394.1|	YLR291C	Beta 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; Gcd7p	2	2.9273	0.2775	1947.75	1949.154	1	335.4	46.42857	A.R4W2N2H3V1N2D1L1I1E1Q2I1R4D1L1.G
gi|6323322|ref|NP_013394.1|	YLR291C	Beta 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; Gcd7p	2	3.992	0.3192	1914.93	1914.163	1	1044.1	65.625	Q.GIKDLIDEIKNIDEGIQ.Q
gi|6323322|ref|NP_013394.1|	YLR291C	Beta 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; Gcd7p	2	5.7045	0.3029	2062.45	2065.294	1	1975.6	73.52941	Q.G1I1K2D1L1I1D1E1I1K2N2I1D1E1G1I1Q2Q2.I
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	2.2593	0.1698	1080.59	1081.259	7	334.1	64.28571	Y.NFEKPFLW.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	3.7679	0.1912	1445.51	1445.617	1	1025.5	75	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	1	2.6546	0.1984	1459.53	1460.617	1	494.2	60.000004	K.S1N2Y1N2F1E1K2P1F1L1W2.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	2.7099	0.2092	1444.64	1445.617	1	608.3	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	4.5251	0.2422	1463.29	1460.617	1	1320.6	85	K.S1N2Y1N2F1E1K2P1F1L1W2.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	2.9734	0.2461	1245.47	1244.435	1	757.1	81.25	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, 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
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	3.8095	0.2523	1422.51	1420.665	2	193.4	68.181816	C.G1N2K2V1D1V1K2E1R4K2V1K2.A
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	3.4696	0.1926	1661.85	1662.87	1	835.6	62.5	S.A1K2S1N2Y1N2F1E1K2P1F1L1W2.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	3.5358	0.2521	1775.63	1777.029	1	709.4	57.692307	S.A1K2S1N2Y1N2F1E1K2P1F1L1W2L1.A
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	4.1846	0.273	1719.73	1720.963	2	401.2	60.000004	A.R4K2L1A1G1N2P1Q2L1E1F1V1A1S1P1A1.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	4.117	0.1828	1448.23	1445.617	1	1355	85	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	1	2.6073	0.1544	1459.44	1460.617	1	581.1	65	K.S1N2Y1N2F1E1K2P1F1L1W2.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	4.1252	0.1511	1461.41	1460.617	1	1194.6	80	K.S1N2Y1N2F1E1K2P1F1L1W2.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	2.8908	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, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	1	2.3143	0.1824	1255.63	1256.435	4	309.3	62.5	N.Y1N2F1E1K2P1F1L1W2.L
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid 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
gi|6323333|ref|NP_013406.1|	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
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	3.0554	0.1527	1612.03	1610.789	1	876.1	57.692307	S.V1G1I1E1F1I1D1D1I1I1A1D1F1Q2.Q
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	6.7599	0.5014	3839.87	3841.233	1	1767.2	30.303032	T.T1I1G1G1I1I1V1D1S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1H3G1T1.I
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	4.2051	0.4314	2975.79	2976.247	1	595.7	39.583336	S.G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1H3G1T1.I
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	4.9241	0.4446	2676.65	2675.949	1	704.4	35.714287	S.G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1.H
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid 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	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid 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 homoserine-O-acetyl serine sulfhydrylase, 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
gi|6323333|ref|NP_013406.1|	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
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	5.3034	0.3226	2909.09	2910.139	1	1033.1	35.869564	E.A1R4F1V1E1G1D1N2P1E1E1F1E1K2V1F1D1E1R4T1K2A1V1Y1.L
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	5.3078	0.4331	3269.27	3266.619	1	617.8	28.703705	G.G1I1I1V1D1S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1.H
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	6.0938	0.3312	3541.04	3540.935	1	970.4	30.000002	T.T1I1G1G1I1I1V1D1S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1.H
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	3.9685	0.1821	3182.06	3180.414	1	702.5	28.846153	V.D1S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1E1G1Y1H3G1T1.I
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	4.0049	0.2164	3190.7	3188.592	1	582	26.85185	T.T1I1G1G1I1I1V1D1S1G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1.E
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	1	2.9366	0.262	1341.59	1342.538	4	401.1	54.545456	H.K2H3G1I1P1V1V1V1D1N2T1F1.G
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid 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	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	2	4.4336	0.2763	2322.29	2323.605	1	385.5	44.444447	S.G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2F1S1Q2P1A1.E
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid 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
gi|6323333|ref|NP_013406.1|	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
gi|6323333|ref|NP_013406.1|	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	F.G1V1K2D1L1P1N2A1D1K2E1T1D1P1F1K2L1S1.G
gi|6323333|ref|NP_013406.1|	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	3	4.0753	0.1569	2574.53	2573.752	1	738.5	33.75	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	4.2919	0.2421	1786.35	1787.025	2	1113.7	69.230774	S.G1K2F1P1W2K2D1Y1P1E1K2F1P1Q2.F
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.1605	0.2808	1704.69	1705.862	1	1183.4	73.07692	A.DYDKINPDDRIDIL.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.0098	0.1878	1724.35	1724.862	1	1590.6	76.92308	A.D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.8194	0.1839	1458.81	1460.73	3	622.8	66.66667	W.D1G1K2D1A1K2D1M1P1I1L1I1K2.A
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	3	4.3116	0.3004	4041.26	4041.47	1	576.6	20	A.DKDAEYDEVVEIDLNTLEPYINGPFTPDLATPVSKM.K

gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	3	5.4514	0.2541	2405.99	2405.616	5	760.3	34.210526	L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.8206	0.4117	2402.89	2405.616	2	719	44.736843	L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.4049	0.2852	1873.35	1874.058	1	651.7	56.666668	N.PADYDKINPDDRIDIL.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.2108	0.2351	1807.69	1809.038	1	583.6	60.000004	Q.V1G1G1E1K2D1L1K2R4A1I1D1L1N2K2E1.V
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.1022	0.3007	2682.67	2682.023	1	417.3	43.47826	L.TDKLKDKDGNEFMLKPPHGDGLPQ.R
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	2.9592	0.2466	1737.91	1736.001	8	264.7	46.42857	K.YNMGFWKPGSGIIHQ.I
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.1972	0.2894	1609.61	1607.87	1	485.7	57.692307	K.YNMGFWKPGSGIIH.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.4367	0.1615	1343.55	1344.528	1	336.2	54.545456	M.G1F1W2K2P1G1S1G1I1I1H3Q2.I
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.8249	0.2455	1926.47	1925.998	1	940.8	56.25	L.SADKDAEYDEVVEIDLN.T
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.2845	0.2647	1653.21	1652.752	3	882.1	65.38461	D.KDAEYDEVVEIDLN.T
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.509	0.2589	1681.71	1682.84	1	688.7	60.714287	N.T1Y1Q2A1P1P1A1D1R4S1T1V1E1V1K2.V
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.2666	0.2546	1662.23	1662.84	1	800.4	64.28571	N.TYQAPPADRSTVEVK.V
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	3	3.978	0.2719	1444.43	1444.73	5	737	50	W.DGKDAKDMPILIK.A
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.4736	0.2072	1183.22	1183.352	1	402.9	72.22222	R.EHAALEPRFL.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.8588	0.3771	2405.81	2405.616	1	653.9	44.736843	L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.06	0.2208	1441.79	1440.744	1	372.6	57.692307	L.GLAELAPGKPVTMR.V
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	2.9479	0.1739	1247.47	1246.495	1	523.7	72.72727	A.GLPQVAKPVTVH.C
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.1919	0.1861	1786.37	1786.038	1	685.1	60.000004	Q.VGGEKDLKRAIDLNKE.V
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.7497	0.257	2049.01	2048.347	2	431.9	47.058823	Q.VGGEKDLKRAIDLNKEVY.D
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.2981	0.2473	1213.53	1214.398	4	248.9	50	M.G1F1W2K2P1G1S1G1I1I1H3.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	3	4.2158	0.1751	3059.63	3058.439	1	1215.8	33.653847	L.TDKLKDKDGNEFMLKPPHGDGLPQRGY.D
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.5928	0.3249	1857.25	1856.234	1	926.3	66.66667	F.KPWDGKDAKDMPILIK.A
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.5356	0.1875	1326.78	1327.528	1	455.1	63.636364	M.GFWKPGSGIIHQ.I
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.7229	0.3275	1330.65	1330.59	1	831.4	68.181816	N.MGFWKPGSGIIH.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.2548	0.387	1344.69	1346.59	1	1140.9	77.27273	N.M1G1F1W2K2P1G1S1G1I1I1H3.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.6022	0.2549	1345.33	1346.59	1	775.9	68.181816	N.M1G1F1W2K2P1G1S1G1I1I1H3.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.2807	0.225	1610.85	1611.656	1	722.7	61.538464	S.ADKDAEYDEVVEID.L
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.2883	0.2685	1207.42	1208.313	1	345.3	61.11111	T.IERDGQLETF.K
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.9035	0.2995	1283.76	1284.557	1	716.4	66.66667	L.GLAELAPGKPVTM.R
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.2529	0.3557	1286.33	1284.557	1	776.1	70.83333	L.GLAELAPGKPVTM.R

gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.7617	0.369	1690.33	1688.979	1	562.9	53.333336	Y.INGPFTPDLATPVSKM.K
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.6616	0.3863	1413.45	1414.514	1	177.5	59.090908	G.EYKGVPDTARDY.R
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.6936	0.2419	2117.35	2116.335	1	689.4	50	F.KNPADYDKINPDDRIDIL.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.5424	0.3618	2377.81	2377.616	1	777.6	47.368423	L.NFKNPADYDKINPDDRIDIL.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	4.6127	0.3804	2404.45	2405.616	1	623.4	42.105263	L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	3	5.2306	0.2956	2406.29	2405.616	1	1143.4	39.473686	L.N2F1K2N2P1A1D1Y1D1K2I1N2P1D1D1R4I1D1I1L1.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.2281	0.275	1141.49	1142.346	1	581.9	72.22222	G.FWKPGSGIIH.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.0872	0.2509	1327.49	1327.528	1	566.5	68.181816	M.GFWKPGSGIIHQ.I
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.6153	0.2022	1425.66	1426.618	1	389.9	68.181816	S.SREHAALEPRFL.G
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently 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.MGFWKPGSGIIHQ.I
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.6499	0.3516	1476.03	1476.721	1	707.6	66.66667	N.M1G1F1W2K2P1G1S1G1I1I1H3Q2.I
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.6884	0.3351	1457.48	1458.721	1	481.9	58.333332	N.MGFWKPGSGIIHQ.I
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.3416	0.4651	1330.29	1330.59	1	1167.4	81.818184	N.MGFWKPGSGIIH.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.1771	0.348	1344.63	1346.59	1	848.3	72.72727	N.M1G1F1W2K2P1G1S1G1I1I1H3.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.0049	0.3975	1444.17	1444.694	1	574.7	62.5	Y.NMGFWKPGSGIIH.Q
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	1	2.8093	0.2294	1535.68	1535.746	1	291.2	53.846157	M.LKPPHGDGLPQRGY.D
gi|6323335|ref|NP_013407.1|	YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	2	3.8158	0.2559	1690.35	1688.938	1	542.2	60.714287	F.M1L1K2P1P1H3G1D1G1L1P1Q2R4G1Y1.D
gi|6323354|ref|NP_013425.1|	YLR321C	Subunit of the RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; essential gene required for cell cycle progression; 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
gi|6323354|ref|NP_013425.1|	YLR321C	Subunit of the RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; essential gene required for cell cycle progression; phosphorylated in the G1 phase of the cell cycle; Snf5p paralog; Sfh1p	2	3.7127	0.2529	1986.39	1987.138	1	811.3	64.28571	C.NLQDRFFEDNFQWNL.N
gi|6323354|ref|NP_013425.1|	YLR321C	Subunit of the RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; essential gene required for cell cycle progression; phosphorylated in the G1 phase of the cell cycle; Snf5p paralog; Sfh1p	2	3.0745	0.2469	1759.15	1759.875	1	946.3	79.16667	C.NLQDRFFEDNFQW.N
gi|6323356|ref|NP_013428.1|	YLR324W	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p; Pex30p	2	3.1323	0.1933	2530.63	2530.666	1	771.5	52.499996	L.SYERTPWTDEFLNEAPSPENF.H
gi|6323356|ref|NP_013428.1|	YLR324W	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p; Pex30p	3	4.1962	0.1643	3602.3	3599.821	1	633.9	25.862068	L.SYERTPWTDEFLNEAPSPENFHLPEETNTM@.V
gi|6323356|ref|NP_013428.1|	YLR324W	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p; Pex30p	3	5.8113	0.3792	3582.8	3583.821	1	2332.4	37.068966	L.SYERTPWTDEFLNEAPSPENFHLPEETNTM.V
gi|6323356|ref|NP_013428.1|	YLR324W	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p; Pex30p	2	2.96	0.2013	1629.59	1630.841	1	307.5	58.333332	T.WKKPSKEDSFSKY.T
gi|6323356|ref|NP_013428.1|	YLR324W	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p; Pex30p	2	4.1238	0.2965	2557.35	2557.666	1	596.9	50	L.S1Y1E1R4T1P1W2T1D1E1F1L1N2E1A1P1S1P1E1N2F1.H
gi|6323356|ref|NP_013428.1|	YLR324W	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number; partially functionally redundant with Pex31p; genetic 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
gi|6323360|ref|NP_013432.1|	YLR328W	Nicotinic acid mononucleotide adenylyltransferase, involved in NAD(+) salvage 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	Nicotinic acid mononucleotide adenylyltransferase, involved in NAD(+) salvage pathway; Nma1p	3	4.3015	0.1913	2906.93	2904.247	2	532.1	28	T.R4A1P1D1F1K2P1P1S1A1D1E1E1L1I1P1P1P1D1P1E1S1K2I1P1K2.S

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
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
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	3.3455	0.2191	2813.69	2814.931	1	470.2	34	S.VAVEPSNEDVKPEEKGSEAEDDINNV.S
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	3.8106	0.389	2122.09	2123.111	1	476.3	52.77778	Q.KSEDTDTHSNEQADNGFVQ.T
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	3.2078	0.237	2371.95	2373.66	1	393.2	37.5	T.T1Q2D1H3H3V1I1E1F1P1T1V1L1L1P1E1N2V1K2A1G1.S
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	4.0856	0.3825	1902.45	1903.01	1	1060.7	58.823532	L.KSEPVGTPNIEENKADSS.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	3	3.942	0.1871	3094.55	3094.166	1	546.8	27.777779	V.A1V1E1P1S1N2E1D1V1K2P1E1E1K2G1S1E1A1E1D1D1I1N2N2V1S1K2E1.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	3	4.093	0.2284	3032.72	3030.183	1	480.5	28.703705	S.VAVEPSNEDVKPEEKGSEAEDDINNVSK.E
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
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
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	4.2041	0.3357	3159.37	3159.298	1	464.1	30.357143	S.VAVEPSNEDVKPEEKGSEAEDDINNVSKE.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	4.2895	0.3867	3194.17	3194.298	1	331.1	28.57143	S.V1A1V1E1P1S1N2E1D1V1K2P1E1E1K2G1S1E1A1E1D1D1I1N2N2V1S1K2E1.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	3.017	0.1661	1645.85	1646.883	9	530.5	65.38461	Q.DHHVIEFPTVLLPE.N
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	3.6665	0.262	1664.27	1664.883	2	506.1	69.230774	Q.D1H3H3V1I1E1F1P1T1V1L1L1P1E1.N
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	2.8253	0.2887	1188.92	1189.36	3	237.8	66.66667	K.HNNIPIVRPE.W
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	4.0974	0.3199	2115.57	2116.425	1	1408.6	63.88889	Q.DHHVIEFPTVLLPENVKAG.S
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
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
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	2.5469	0.1892	1404.68	1405.681	2	387.3	54.166668	Y.GTHKPESPVLKIV.N
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	3.8516	0.2379	1724.87	1724.895	1	401.8	70.83333	Q.N2L1E1E1E1K2K2Q2R4N2H3F1K2.S
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	4.0329	0.3465	2041.31	2043.236	4	291.1	50	Q.V1S1Q2N2L1E1E1E1K2K2Q2R4N2H3F1K2.S
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	3.2693	0.2103	1422.93	1424.651	1	752.7	66.66667	C.L1G1P1L1D1P1L1K2E1I1S1D1L1.Q
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	4.4643	0.3697	1687.69	1685.922	1	1182	71.42857	T.V1C1L1G1P1L1D1P1L1K2E1I1S1D1L1.Q
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
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
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	2.6348	0.2616	1424.75	1424.651	2	499.2	54.166668	C.L1G1P1L1D1P1L1K2E1I1S1D1L1.Q
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	2.4435	0.267	1409.83	1410.651	5	426.3	50	C.LGPLDPLKEISDL.Q
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	4.0037	0.3207	1671.19	1669.922	1	1000.4	75	T.VCLGPLDPLKEISDL.Q
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	4.4808	0.3217	1583.41	1584.649	1	1589.3	87.5	R.H3Q2E1E1D1I1E1L1E1A1E1P1K2.D
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	4.3237	0.3515	2675.96	2677.723	1	648.6	31.52174	S.N2E1D1V1K2P1E1E1K2G1S1E1A1E1D1D1I1N2N2V1S1K2E1A1.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	3.1486	0.1729	1207.41	1206.36	1	871.1	83.33333	K.H3N2N2I1P1I1V1R4P1E1.W
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
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
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	3.4388	0.2616	1614.21	1613.854	2	239.8	57.692307	L.EKYGTHKPESPVLK.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	2	3.5196	0.1661	1827.63	1826.146	2	320.7	50	L.EKYGTHKPESPVLKIV.N
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	4.2774	0.3958	2056.31	2057.263	1	439.2	60.000004	Q.N2L1E1E1E1K2K2Q2R4N2H3F1K2S1I1Q2.A
gi|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; Sgd1p	3	3.89	0.2072	2384.09	2381.65	1	775.1	40.789474	S.K2I1S1I1E1D1D1L1L1D1D1I1P1D1W2N2I1I1A1R4.Q
gi|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; Sgd1p	2	6.5944	0.3954	2379.61	2381.65	1	1677.9	63.15789	S.K2I1S1I1E1D1D1L1L1D1D1I1P1D1W2N2I1I1A1R4.Q
gi|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; 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	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	2	3.2868	0.188	1658.57	1658.933	1	676.6	60.714287	Q.K2T1D1G1I1R4I1P1G1V1I1L1D1E1L1.K
gi|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; 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	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	2	3.1988	0.2132	1930.29	1929.111	1	293.8	60.714287	F.LHHYEEEMENILKDQ.Q

gi|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; Sgd1p	2	4.5844	0.32	2026.37	2027.238	1	1313.2	78.125	S.IEDDLLDDIPDWNIIAR.Q
gi|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; Sgd1p	2	3.7356	0.2964	2201.41	2199.463	1	765.8	55.555557	S.KISIEDDLLDDIPDWNIIA.R
gi|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; Sgd1p	2	2.9818	0.1631	2220.63	2221.463	3	468	44.444447	S.K2I1S1I1E1D1D1L1L1D1D1I1P1D1W2N2I1I1A1.R
gi|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; Sgd1p	2	6.6846	0.4178	2382.73	2381.65	1	2100.3	71.05263	S.K2I1S1I1E1D1D1L1L1D1D1I1P1D1W2N2I1I1A1R4.Q
gi|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; Sgd1p	3	3.9588	0.2122	2381.21	2381.65	1	963.8	43.421055	S.K2I1S1I1E1D1D1L1L1D1D1I1P1D1W2N2I1I1A1R4.Q
gi|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; Sgd1p	2	3.6339	0.2092	1950.71	1951.111	1	1280.6	71.42857	F.L1H3H3Y1E1E1E1M1E1N2I1L1K2D1Q2.Q
gi|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; Sgd1p	2	5.3393	0.3772	2049.23	2049.238	1	1129.3	75	S.I1E1D1D1L1L1D1D1I1P1D1W2N2I1I1A1R4.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
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	5.1054	0.4507	2283.79	2285.465	1	1425.6	70.588234	Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.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	4.3076	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
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	4.0152	0.3694	2536.61	2537.719	1	1118.3	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	3.5401	0.3953	2579.91	2581.798	1	390.1	45	A.ASYHYPEIEDLVDRIENPEKY.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	4.0231	0.3308	2610.86	2609.798	1	494.8	30.000002	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	2	5.2698	0.3906	2513.53	2510.719	1	2032.3	65.789474	A.SYHYPEIEDLVDRIENPEKY.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	3.5866	0.3936	2564.73	2565.799	1	913.7	50	S.YHYPEIEDLVDRIENPEKYAA.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	3.6725	0.3404	2752.41	2753.956	1	608.5	43.18182	A.S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1A1.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	4.3005	0.362	2287.46	2285.465	1	498.8	41.17647	Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.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	3.5393	0.3606	1440.73	1440.645	1	325.3	66.66667	A.RAGAVAPEDIWVR.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	3.8236	0.2182	1547.75	1548.792	1	469.7	75	F.L1S1D1L1P1D1F1E1K2L1L1P1F1.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	2	3.6238	0.4404	1617.55	1618.781	1	860.7	65.38461	S.SILDITDEELVSHF.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	2	3.0723	0.4276	1460.33	1460.645	1	479.1	58.333332	A.R4A1G1A1V1A1P1E1D1I1W2V1R4.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
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	4.4419	0.3945	2282.97	2285.465	1	1198.6	61.764706	Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.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	4.9649	0.3102	2448.41	2449.641	1	1441.5	58.333332	S.Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.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	4.1255	0.3992	2580.21	2581.798	1	914.8	50	A.ASYHYPEIEDLVDRIENPEKY.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	5.1613	0.3448	2608.87	2609.798	1	829.7	50	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	2	3.5254	0.3157	2402.01	2402.623	1	800.3	44.736843	Y.HYPEIEDLVDRIENPEKYAA.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	3.0643	0.3266	2499.65	2501.701	1	497.2	40	Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1A1.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	5.5721	0.4462	2535.69	2537.719	1	2207.6	68.42105	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	3	4.2352	0.3047	2446.82	2449.641	1	840.8	47.22222	S.Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1.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	3.3519	0.3049	2357.73	2357.544	1	698.2	47.22222	Y.H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1.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	3.9644	0.2729	2473.75	2473.701	5	390.1	37.5	Y.HYPEIEDLVDRIENPEKYAAA.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	5.179	0.4408	2612.03	2609.798	1	810.3	33.75	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	4.2276	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 P0 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

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	4.4958	0.4081	2592.49	2593.799	1	918.5	52.499996	S.Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1.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	4.9545	0.2194	2682.47	2681.877	1	1352.1	52.380955	A.S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A1A1.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	4.3093	0.2956	2636.87	2636.877	1	1071	47.61905	S.YHYPEIEDLVDRIENPEKYAAA.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	3.2467	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
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	4.3397	0.2543	3677.81	3679.084	1	871.7	25.833332	N.Y1K2D1L1L1A1V1A1I1A1A1S1Y1H3Y1P1E1I1E1D1L1V1D1R4I1E1N2P1E1K2Y1A
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	2.7419	0.3156	1265.48	1266.35	1	614.5	61.11111	A.SYHYPEIEDL.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	2	3.1435	0.2156	1559.35	1556.815	1	785.2	67.85714	S.L1A1I1G1Y1P1T1L1P1S1V1G1H3T1L1.I
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	3.3375	0.2493	1537.31	1534.792	2	532.4	79.16667	F.LSDLPDFEKLLPF.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	3.1083	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
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	2.9656	0.2172	1563.73	1564.698	2	451.7	68.181816	L.REIIREDDQFSR.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	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.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	3	4.3288	0.2286	2427.29	2427.821	1	1213.4	38.157894	I.V1L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1.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	2.6272	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
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	4.6935	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.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	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 Gsc2p; 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
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	2.6203	0.2324	1537.69	1538.957	2	154.3	62.5	C.QLPLIIIPKIDKF.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	2.3769	0.2213	1553.69	1554.957	1	184.9	62.5	C.Q2L1P1L1I1I1I1P1K2I1D1K2F1.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.Q2L1P1L1I1I1P1K2I1D1K2F1.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.GTKLIELPLEERYLRL.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	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.L1H3Y1G1H3P1D1F1I1N2A1T1.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.I1Y1D1R4N2K2P1K2T1D1V1L1V1P1I1G1C1.Y
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	4.1491	0.334	2589.89	2591.933	1	426.5	42.5	Q.R4Q2E1P1M1P1E1G1D1F1L1N2R4V1I1T1P1I1Y1H3F1.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	4.255	0.3802	1875.95	1876.129	1	793.2	63.333332	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 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.I1Y1D1R4N2K2P1K2T1D1V1L1V1P1I1G1C1Y1.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	3.9069	0.2296	2340.51	2337.603	1	662.6	55.555557	M.C1I1Y1D1R4N2K2P1K2T1D1V1L1V1P1I1G1C1Y1.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	3.4865	0.2789	2310.83	2312.603	1	828	58.333332	M.CIYDRNKPKTDVLVPIGCY.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	3	3.8688	0.2056	2719.37	2722.064	1	536.9	30.952381	Q.Q2R4Q2E1P1M1P1E1G1D1F1L1N2R4V1I1T1P1I1Y1H3F1.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	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.Q2L1P1L1I1I1I1P1K2I1D1.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.Q2L1P1L1I1I1I1P1K2I1D1.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.R4E1I1I1R4E1D1D1Q2F1S1R4.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.L1E1D1G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1G1.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	41.666664	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	4.1787	0.2103	2326.11	2327.688	1	399.4	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	3.7368	0.3732	2300.57	2301.688	1	408.6	52.77778	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	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.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	4.5161	0.3856	1897.21	1898.129	1	606.1	66.66667	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.Q2L1P1L1I1I1I1P1K2I1D1K2F1.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.G1T1K2L1I1E1L1P1L1E1E1R4Y1L1R4L1.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	2	3.3409	0.2301	1526.31	1524.732	2	647.3	66.66667	A.D1I1E1L1P1H3G1A1W2P1E1L1M1.K
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.9575	0.3173	1526.79	1526.715	1	721	75	N.A1L1K2P1V1F1Q2D1L1Y1E1S1T1.K
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.5649	0.4046	1513.29	1511.715	1	516.8	62.5	N.ALKPVFQDLYEST.K
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	1	2.3951	0.1954	1454.47	1454.636	1	405.5	50	A.L1K2P1V1F1Q2D1L1Y1E1S1T1.K
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	1	2.8807	0.2498	1377.54	1378.584	3	425.9	65	K.L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.9832	0.3282	2118.45	2117.448	2	568.5	50	L.D1W2Y1P1I1F1K2N2A1L1K2P1V1F1Q2D1L1.Y
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	2.9939	0.1813	1479.49	1476.713	1	649.4	75	L.THVEPPKDLDVIL.V
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.5989	0.2916	2754.95	2757.047	1	363.7	42.857143	L.EFNSQPDYREKLEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	4.1793	0.3222	2303.57	2303.687	1	1052.9	55.555557	G.A1L1D1W2Y1P1I1F1K2N2A1L1K2P1V1F1Q2D1L1.Y
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	6.3486	0.4266	2788.88	2790.047	1	1548.2	41.666664	L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	5.3748	0.2824	2756.9	2757.047	3	711.7	33.333336	L.EFNSQPDYREKLEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.3043	0.2584	2789.39	2790.047	1	223.7	33.333336	L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	4.3185	0.2872	2397.44	2395.651	1	970.8	38.88889	N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-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

gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.9315	0.1821	2392.73	2395.651	1	640	55.555557	N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.4115	0.3112	1247.99	1248.397	1	892	80	F.S1H3G1F1S1P1V1F1K2D1L1.T
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.0447	0.3076	1773.95	1771.11	6	291.5	50	T.HVEPPKDLDVILVAPK.G
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.3914	0.2896	1327.83	1326.542	1	608.4	77.27273	L.RDNGLNVIIGVR.K
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	4.0892	0.3124	1553.05	1553.805	1	553.9	65.38461	L.NLRDNGLNVIIGVR.K
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	4.0599	0.1916	1576.53	1576.805	1	601.2	65.38461	L.N2L1R4D1N2G1L1N2V1I1I1G1V1R4.K
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	5.5681	0.4716	2257.35	2257.585	1	1282.8	60.000004	L.T1H3V1E1P1P1K2D1L1D1V1I1L1V1A1P1K2G1S1G1R4.T
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.0749	0.1838	940.37	941.162	1	1433.1	87.5	N.GLNVIIGVR.K
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.7619	0.2832	1364.37	1362.584	1	1390.4	85	K.LEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	4.9956	0.3019	2303.27	2303.687	1	1064.7	44.444447	G.A1L1D1W2Y1P1I1F1K2N2A1L1K2P1V1F1Q2D1L1.Y
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.5059	0.2187	2756.63	2757.047	1	354.4	40.476192	L.EFNSQPDYREKLEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.681	0.3181	2788.49	2790.047	1	231.3	35.714287	L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	6.0797	0.3371	2790.23	2790.047	1	1802.6	44.04762	L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	4.5229	0.4567	1894.47	1893.215	1	837.1	65.625	L.T1H3V1E1P1P1K2D1L1D1V1I1L1V1A1P1K2.G
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	4.8854	0.4037	2014.89	2016.345	1	1195.5	63.88889	L.THVEPPKDLDVILVAPKGS.G
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	4.271	0.3385	1871.69	1872.215	1	972.3	68.75	L.THVEPPKDLDVILVAPK.G
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.6334	0.172	2394.47	2395.651	1	571.3	55.555557	N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	4.1271	0.3421	2398.25	2395.651	1	1568.3	43.055553	N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	4.6146	0.4578	1872.53	1872.215	1	1262.1	46.875	L.THVEPPKDLDVILVAPK.G
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	5.4879	0.409	2231.05	2229.585	1	1627.8	67.5	L.THVEPPKDLDVILVAPKGSGR.T
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	1	2.7328	0.2649	1445.62	1446.646	1	350.9	54.166668	A.AIEDGWVPGKNLF.T
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.4716	0.2939	1446.33	1446.646	1	866.1	75	A.AIEDGWVPGKNLF.T
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.6256	0.2796	1463.89	1462.646	1	639.8	66.66667	A.A1I1E1D1G1W2V1P1G1K2N2L1F1.T
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	1	2.8829	0.2048	1267.55	1267.47	8	433.5	66.66667	G.ALDWYPIFKN.A
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.7655	0.3744	1267.31	1267.47	1	1449.2	83.33333	G.ALDWYPIFKN.A
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.3963	0.151	1282.05	1280.47	3	1175.4	77.77778	G.A1L1D1W2Y1P1I1F1K2N2.A
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	1	2.8313	0.2523	1361.51	1362.584	3	436	65	K.LEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.3258	0.1956	1197.07	1194.416	1	1234.7	88.88889	N.ALKPVFQDLY.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.0872	0.2388	2510.71	2511.751	1	340	50	L.EFNSQPDYREKLEKELDTIR.N
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	4.632	0.408	2770.85	2773.047	1	1005.3	39.285713	L.EFNSQPDYREKLEKELDTIRNM@.E

gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	5.0863	0.2338	2805.11	2806.047	1	2056.6	40.476192	L.E1F1N2S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M$.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.7058	0.3275	2756.03	2757.047	1	326.8	40.476192	L.EFNSQPDYREKLEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	5.4844	0.2584	2759.15	2757.047	1	1096.3	36.904762	L.EFNSQPDYREKLEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	4.2042	0.3435	2364.91	2366.651	1	728.5	58.333332	N.SQPDYREKLEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	5.0797	0.4186	2478.65	2480.755	1	1916.2	42.105263	F.NSQPDYREKLEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	1	3.0202	0.3233	1233.65	1234.397	3	749	70	F.SHGFSPVFKDL.T
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	1	3.3236	0.261	1247.48	1248.397	2	871.6	70	F.S1H3G1F1S1P1V1F1K2D1L1.T
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	3.8571	0.214	2394.39	2395.651	1	736.5	58.333332	N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	4.1548	0.1871	2395.55	2395.651	1	1099.1	38.88889	N.S1Q2P1D1Y1R4E1K2L1E1K2E1L1D1T1I1R4N2M1.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	3	3.8477	0.2289	2366.81	2366.651	1	1195.5	38.88889	N.SQPDYREKLEKELDTIRNM.E
gi|6323387|ref|NP_013459.1|	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	2	2.9842	0.2091	2359.21	2356.725	3	314.6	33.333336	L.SDAAQSETWPAIKPLLTKGKTL.Y
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) 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 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	2	3.9519	0.3428	2966.59	2966.303	1	632.3	37.5	N.L1K2E1K2Y1P1Q2L1V1Y1P1D1L1G1P1L1P1D1E1P1G1Y1E1E1F1.Q
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	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 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	2	3.9167	0.3247	1649.99	1649.841	1	2083.5	80.769226	S.RYNIPTIIDDLTSQ.A
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	2	4.4729	0.2804	1668.99	1668.841	1	1348.2	69.230774	S.R4Y1N2I1P1T1I1I1D1D1L1T1S1Q2.A
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	2	3.6365	0.4237	1907.17	1907.149	1	688.4	55.555557	H.DRVPEPTMGSPDAPPLVGA.V
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	2	3.0589	0.3882	1929.49	1929.149	1	436.6	50	H.D1R4V1P1E1P1T1M1G1S1P1D1A1P1P1L1V1G1A1.V
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	2	4.0537	0.2684	2446.61	2446.54	1	851.7	50	K.DKDDDGLEPDVENEKESLPGPF.V
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	3	4.5953	0.2782	2585.57	2585.893	1	891.2	35.714287	T.D1M1D1I1D1N2P1K2D1A1D1F1P1D1L1I1R4K2P1L1I1N2.I
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	2	3.7811	0.3359	2555.71	2556.893	2	384.8	40.476192	T.DMDIDNPKDADFPDLIRKPLIN.I
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	3	5.1274	0.2767	4215.53	4216.391	1	543.3	22.222223	L.EYEEVEETMEDVTGKDKDDDGLEPDVENEKESLPGPF.V
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	3	4.9931	0.3881	2966.57	2966.303	1	960	30.208334	N.L1K2E1K2Y1P1Q2L1V1Y1P1D1L1G1P1L1P1D1E1P1G1Y1E1E1F1.Q
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	3	5.3038	0.2963	2938.52	2938.303	1	1743.2	38.541664	N.LKEKYPQLVYPDLGPLPDEPGYEEF.Q
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	2	4.2956	0.3335	2938.39	2938.303	1	615.1	37.5	N.LKEKYPQLVYPDLGPLPDEPGYEEF.Q
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	3	4.3134	0.231	3434.48	3435.898	1	743.3	28.57143	N.LKEKYPQLVYPDLGPLPDEPGYEEFQQKL.R
gi|6323389|ref|NP_013461.1|	YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	3	4.3106	0.2007	2672.69	2673.007	1	1063.5	35.227272	W.KACLPEEIRDLDEATIPVNGRKF.F
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	1	2.9639	0.2908	1454.56	1454.623	1	455.7	58.333332	K.V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	1	2.9483	0.2555	1440.53	1438.623	1	511.7	62.5	K.VHVPSIENPFGIE.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.5491	0.3061	1439.91	1438.623	1	635	75	K.VHVPSIENPFGIE.L

gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.6658	0.3283	1453.79	1454.623	1	754.3	79.16667 K.V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.7882	0.3543	2378.49	2377.595	1	239.6	38.88889 K.V1F1E1Y1F1S1G1Y1P1A1E1Q2F1E1F1I1H3N2K2.T
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	1	3.3691	0.2717	1566.64	1566.797	1	919.4	65.38461 L.KVHVPSIENPFGIE.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	4.0967	0.3799	1586.65	1584.797	1	986.4	76.92308 L.K2V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	1	3.8731	0.3317	1583.62	1584.797	1	924.9	65.38461 L.K2V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	2.9393	0.1898	1698.65	1698.957	1	841	64.28571 F.L1K2V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.0485	0.2347	2334.91	2335.701	1	597.1	47.368423 K.V1H3V1P1S1I1E1N2P1F1G1I1E1L1W2P1I1F1S1K2.V
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.8706	0.3891	1439.19	1438.623	1	619.3	75 K.VHVPSIENPFGIE.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	1	2.6237	0.336	1438.64	1438.623	1	416.5	54.166668 K.VHVPSIENPFGIE.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	1	2.4897	0.2193	1453.71	1454.623	2	475.9	58.333332 K.V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.7832	0.2925	1568.59	1566.797	1	909.6	76.92308 L.KVHVPSIENPFGIE.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.5937	0.4348	1677.97	1679.957	1	879.5	67.85714 F.LKVHVPSIENPFGIE.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.1544	0.2447	1569.15	1566.797	1	965	76.92308 L.KVHVPSIENPFGIE.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	1	3.4195	0.3496	1583.49	1584.797	1	736.6	57.692307 L.K2V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	1	3.2788	0.2713	1566.72	1566.797	1	763	57.692307 L.KVHVPSIENPFGIE.L
gi|6323404|ref|NP_013476.1|	YLR372W	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; Sur4p	2	3.7826	0.4055	1587.39	1584.797	1	832.4	76.92308 L.K2V1H3V1P1S1I1E1N2P1F1G1I1E1.L
gi|6323411|ref|NP_013482.1|	YLR378C	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 ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	2	3.3718	0.2379	1881.71	1882.213	1	591.4	56.666668 L.PEVIAPERKVPYNQKL.I
gi|6323411|ref|NP_013482.1|	YLR378C	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 ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	2	4.0589	0.3613	1905.81	1905.213	3	529.5	53.333336 L.P1E1V1I1A1P1E1R4K2V1P1Y1N2Q2K2L1.I
gi|6323411|ref|NP_013482.1|	YLR378C	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 ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	2	4.3796	0.3925	2385.71	2385.743	1	642.7	50 F.E1S1F1L1P1E1V1I1A1P1E1R4K2V1P1Y1N2Q2K2L1.I
gi|6323411|ref|NP_013482.1|	YLR378C	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 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
gi|6323411|ref|NP_013482.1|	YLR378C	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 ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	2	3.0675	0.298	1063.93	1064.356	1	1209.2	93.75 Q.IGIYPIKLF.Y
gi|6323411|ref|NP_013482.1|	YLR378C	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 ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	2	3.8954	0.3077	2244.93	2245.583	1	455.3	47.22222 F.ESFLPEVIAPERKVPYNQK.L
gi|6323411|ref|NP_013482.1|	YLR378C	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 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
gi|6323411|ref|NP_013482.1|	YLR378C	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 ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	2	3.5355	0.3784	2357.39	2358.743	1	377.3	39.473686 F.ESFLPEVIAPERKVPYNQKL.I
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	3.5475	0.3137	1925.45	1924.123	1	682.7	63.333332 T.AQWIEHQPLNDPAYIQ.L
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	3	3.8743	0.2633	3109.25	3110.246	1	693.4	28.846153 Q.Y1I1P1R4Y1L1G1G1E1N2D1N2D1L1D1H3Y1T1P1P1D1G1S1L1D1V1H3.L
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	3.0802	0.2545	1655.35	1655.983	8	324.6	54.166668 A.PWIFNPIWNIIKN.W
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	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
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	3.928	0.3172	1946.53	1947.123	1	650.3	56.666668	T.A1Q2W2I1E1H3Q2P1L1N2D1P1A1Y1I1Q2.L
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	3.02	0.181	1550.23	1549.721	1	830.9	77.27273	M.IEKEREELVEQF.L
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	3.0852	0.1853	1258.45	1258.549	3	1136.7	83.33333	W.IFNPIWNIIK.N
gi|42742289|ref|NP_013493.2|	YLR389C	Metalloprotease involved, with homolog Axl1p, 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 Axl1p, 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 Axl1p, 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 Axl1p, 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 Axl1p, 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 Axl1p, in N-terminal processing of pro-a-factor to the mature form; member of the insulin-degrading enzyme family; Ste23p	2	3.3212	0.2842	1565.29	1566.886	1	708.8	62.5	T.L1F1V1A1P1V1R4Q2P1M1K2D1F1.E
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	1	3.0127	0.334	1593.67	1594.894	1	538.6	57.692307	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	3.54	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.H3N2R4Q2F1L1E1N2I1F1D1P1G1L1P1N2E1A1I1A1D1E1L1.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
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	2	4.0266	0.3363	1734.77	1734.933	1	320.7	60.714287	L.L1R4E1G1K2E1A1P1P1Q2F1A1W2P1S1.K
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	2	3.4592	0.3902	1715.71	1713.933	1	716.9	64.28571	L.LREGKEAPPQFAWPS.K
gi|6323445|ref|NP_013517.1|	YLR413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; Ylr413wp	1	3.3893	0.315	1439.77	1438.707	2	285.2	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	3.332	0.2782	1440.39	1438.707	1	449.6	77.27273	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	3.3359	0.3651	1780.47	1780.932	1	427.2	53.571426	S.RIIEEHESPIDAEKN.F
gi|6323445|ref|NP_013517.1|	YLR413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; Ylr413wp	2	3.5733	0.284	2698.21	2699.94	1	233.3	34.090908	L.N2I1G1K2D1D1L1H3L1D1G1E1L1Q2D1R4Q2H3M1Y1V1P1A1.V
gi|6323445|ref|NP_013517.1|	YLR413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; Ylr413wp	2	3.7881	0.3927	2664.11	2665.94	1	520.4	45.454548	L.NIGKDDLHLDGELQDRQHMYVPA.V
gi|6323445|ref|NP_013517.1|	YLR413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; Ylr413wp	2	3.0873	0.36	1438.35	1438.707	1	443	72.72727	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	1	3.7358	0.2998	1452.7	1452.707	1	317.1	68.181816	E.E1K2T1K2L1S1P1V1F1E1L1F1.A
gi|6323445|ref|NP_013517.1|	YLR413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; Ylr413wp	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; Ylr413wp	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|	YLR421C	Subunit of the 19S regulatory particle of the 26S proteasome lid; Rpn13p	3	4.2784	0.2715	2733.41	2732.944	1	615.1	29.545454	C.E1Y1N2E1D1S1R4L1C1T1P1I1P1V1Q2G1E1I1E1I1K2P1N2.E
gi|6323453|ref|NP_013525.1|	YLR421C	Subunit of the 19S regulatory particle of the 26S proteasome lid; Rpn13p	3	5.3685	0.4354	4025	4026.272	1	859.1	27.34375	C.E1Y1N2E1D1S1R4L1C1T1P1I1P1V1Q2G1E1I1E1I1K2P1N2E1E1E1E1L1G1F1W 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|	YLR421C	Subunit of the 19S regulatory particle of the 26S proteasome lid; Rpn13p	2	3.7928	0.2768	1551.63	1552.781	2	735.5	61.538464	C.T1P1I1P1V1Q2G1E1I1E1I1K2P1N2.E
gi|6323453|ref|NP_013525.1|	YLR421C	Subunit of the 19S regulatory particle of the 26S proteasome lid; Rpn13p	2	3.2567	0.3067	1770.15	1770.905	6	482.6	50	E.I1K2P1N2E1E1E1E1L1G1F1W2D1F1.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; Crn1p	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
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	3.5907	0.3651	2103.73	2103.447	1	499.6	47.22222	F.A1V1I1P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4.G
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	4.8361	0.3606	2081.33	2079.447	1	1069	58.333332	F.AVIPIEEVGKAPDQVPLFR.G
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	4.8739	0.4074	2526.51	2527.821	1	197.8	40	L.E1E1K2K2E1Q2P1K2V1E1K2P1I1S1E1S1E1K2E1V1K2.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	4.4423	0.3773	2628.71	2627.952	1	390	47.61905	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	5.3018	0.3776	3964.16	3965.218	1	564.9	26.470589	A.T1D1R4K2Q2E1Q2S1L1P1Q2E1E1K2S1S1E1K2T1K2S1P1E1Q2E1K2S1A1T1P1 P1S1S1I1T1.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	4.477	0.2263	2912.95	2914.28	1	252.6	37.5	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	3	4.7362	0.3281	3143.72	3144.391	1	669.8	28.846153	F.F1V1P1R4R4S1E1E1F1Q2E1D1I1Y1P1D1A1P1S1N2K2P1A1L1T1A1E1.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	4.0665	0.3054	3107.67	3108.391	1	437.8	36.53846	F.FVPRRSEEFQEDIYPDAPSNKPALTAE.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	3.9588	0.215	2103.29	2103.429	1	1373	45.833336	V.IPIEEVGKAPDQVPLFRGH.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	4.303	0.2268	2129.09	2129.429	1	1182.7	44.444447	V.I1P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.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	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
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	5.5688	0.4281	2274.57	2273.64	1	1419.8	60.000004	F.AVIPIEEVGKAPDQVPLFRGH.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	6.2348	0.4031	3949.76	3949.445	1	1000.7	27.205881	Q.ETALEEKKEQPKVEKPISESEKEVKQEAPKSPSPL.K
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	3.968	0.3794	2090.51	2091.285	2	494.8	50	Y.KFHDHVDEDGEPIDIKPV.K
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	4.1514	0.2967	2694.65	2693.932	1	709.6	45.454548	F.FVPRRSEEFQEDIYPDAPSNKPA.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	4.3072	0.1515	2908.55	2908.197	1	746.5	32.291664	F.FVPRRSEEFQEDIYPDAPSNKPALT.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	4.4044	0.2268	2943.61	2942.197	1	486	37.5	F.F1V1P1R4R4S1E1E1F1Q2E1D1I1Y1P1D1A1P1S1N2K2P1A1L1T1.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	3.7651	0.1667	2910.69	2908.197	1	508	37.5	F.FVPRRSEEFQEDIYPDAPSNKPALT.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	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.A1V1I1P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.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	3.6892	0.3718	2104.03	2103.429	1	564	38.88889	V.IPIEEVGKAPDQVPLFRGH.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	4.257	0.4052	1778.73	1779.993	1	1088.2	66.66667	I.EEVGKAPDQVPLFRGH.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	5.7241	0.3159	1989.02	1990.269	1	1894.6	52.941177	I.PIEEVGKAPDQVPLFRGH.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	5.9677	0.4496	3534.71	3534.986	1	819.9	26.666668	L.EEKKEQPKVEKPISESEKEVKQEAPKSPSPL.K
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	4.35	0.4044	1990.83	1990.269	1	1752.1	67.64706	I.PIEEVGKAPDQVPLFRGH.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	4.1793	0.3614	2012.59	2015.269	1	523.1	58.823532	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	3.6648	0.1757	2420.99	2420.817	1	880.9	45.238094	A.FAVIPIEEVGKAPDQVPLFRGH.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	5.3382	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
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	4.4241	0.4024	2739.77	2740.128	1	284.2	45.652176	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	4.5916	0.2876	2349.65	2349.733	1	774.7	52.499996	K.KDRTPKVEPSKELKPEPVSIA.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	4.9169	0.3146	2377.13	2377.733	1	582.6	47.5	K.K2D1R4T1P1K2V1E1P1S1K2E1L1K2P1E1P1V1S1I1A1.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	3.6564	0.3044	2105.31	2106.47	3	433.4	47.22222	D.RTPKVEPSKELKPEPVSIA.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	3.6411	0.3789	2582.35	2580.9	1	545.8	45.238094	Y.KFHDHVDEDGEPIDIKPVKFLT.G
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	6.5359	0.4151	2507.84	2507.795	1	2459	45	Y.K2F1H3D1H3V1D1E1D1G1E1P1I1D1I1K2P1V1K2F1L1.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	5.1781	0.3992	2481.81	2479.795	1	991.9	52.499996	Y.KFHDHVDEDGEPIDIKPVKFL.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	4.3901	0.3864	2068.43	2067.303	1	1290.2	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	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
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	3.2168	0.406	1736.83	1737.91	1	1042.5	73.333336	W.NIREEKIVSEGPAHTG.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	4.3698	0.2603	2114.27	2115.285	1	862.2	55.88235	Y.K2F1H3D1H3V1D1E1D1G1E1P1I1D1I1K2P1V1.K
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	4.247	0.2467	2907.74	2908.197	1	647.3	30.208334	F.FVPRRSEEFQEDIYPDAPSNKPALT.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	3.6586	0.1741	2908.47	2908.197	3	300.6	29.166666	F.FVPRRSEEFQEDIYPDAPSNKPALT.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	3	4.0005	0.4264	2270.66	2273.64	1	803.8	41.25	F.AVIPIEEVGKAPDQVPLFRGH.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	4.7906	0.2806	2942.27	2942.197	1	598.2	28.125	F.F1V1P1R4R4S1E1E1F1Q2E1D1I1Y1P1D1A1P1S1N2K2P1A1L1T1.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	3	3.8933	0.1729	2980.7	2979.276	1	837.8	30.000002	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	3.9494	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
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	4.9724	0.3958	3820.22	3821.317	1	622.4	25.757576 L.EEKKEQPKVEKPISESEKEVKQEAPKSPSPLKSA.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	5.6072	0.4541	3147.98	3148.581	1	910.3	30.555555 K.KEQPKVEKPISESEKEVKQEAPKSPSPL.K
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	5.3324	0.2596	2481.02	2479.795	1	755	35 Y.KFHDHVDEDGEPIDIKPVKFL.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	4.8756	0.2776	2709.59	2708.128	4	437.2	29.347824 T.ETKKDRTPKVEPSKELKPEPVSIA.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	3.8104	0.2837	1774.85	1776.083	1	622.8	56.25 F.AVIPIEEVGKAPDQVPL.F
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	4.2065	0.2308	2626.58	2627.952	1	696.8	34.523808 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	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.V1I1P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4.G
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	4.687	0.359	2276.42	2273.64	1	806.1	41.25 F.AVIPIEEVGKAPDQVPLFRGH.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	4.7256	0.4354	2298.71	2301.64	1	720.7	41.25 F.A1V1I1P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.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	5.5369	0.5164	2301.29	2301.64	1	1344.8	55 F.A1V1I1P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.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	3.9415	0.2885	3451.43	3448.841	2	429.8	17.96875 I.A1V1N2W2N2A1S1G1G1G1A1F1A1V1I1P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.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	6.0876	0.4549	3572.81	3574.986	1	804.2	28.333334 L.E1E1K2K2E1Q2P1K2V1E1K2P1I1S1E1S1E1K2E1V1K2Q2E1A1P1K2S1P1S1P1L1.K
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	4.3002	0.3414	3016.43	3014.276	1	558.6	26 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	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.V1I1P1I1E1E1V1G1K2A1P1D1Q2V1P1L1F1R4G1H3.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
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	5.3626	0.4649	2272.65	2273.64	1	1568.4	60.000004 F.AVIPIEEVGKAPDQVPLFRGH.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	4.7625	0.4447	2478.55	2479.795	1	823	50 Y.KFHDHVDEDGEPIDIKPVKFL.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	4.0094	0.2274	2480.12	2479.795	9	392.9	28.75 Y.KFHDHVDEDGEPIDIKPVKFL.T
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	4.5867	0.4008	1773.71	1772.99	1	784.7	70 S.D1I1D1P1D1L1K2S1D1L1L1P1N2I1G1K2.L
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	3.4591	0.2121	1948.13	1949.147	2	431.4	47.058823 Q.S1S1D1I1D1P1D1L1K2S1D1L1L1P1N2I1G1K2.L
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	4.1856	0.3252	2241.65	2240.602	1	481.1	52.63158 S.DIDPDLKSDLLPNIGKLYPL.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	4.5247	0.3089	1754.49	1752.946	1	481	73.07692 A.E1E1L1D1D1M1N2I1E1I1I1R4N2K2.L
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	1	2.2306	0.1502	1310.68	1310.449	2	400.4	66.66667 Y.KAYLEDFYNF.V
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	4.7855	0.3582	2439.53	2439.758	1	451.5	45.238094 Q.S1S1D1I1D1P1D1L1K2S1D1L1L1P1N2I1G1K2L1Y1P1L1.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	3.9169	0.3029	2417.67	2414.758	1	478.3	45.238094 Q.SSDIDPDLKSDLLPNIGKLYPL.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	4.6652	0.4014	2328.73	2327.68	1	544.6	52.499996 S.SDIDPDLKSDLLPNIGKLYPL.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	4.0464	0.2432	2262.33	2263.602	1	396.6	47.368423 S.D1I1D1P1D1L1K2S1D1L1L1P1N2I1G1K2L1Y1P1L1.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	3.3276	0.337	1916.37	1917.265	5	353.9	46.875 D.P1D1L1K2S1D1L1L1P1N2I1G1K2L1Y1P1L1.A

gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	1	2.652	0.2675	1195.5	1196.349	1	499	72.22222	T.IHDRDKGEIL.Q
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	1	3.2882	0.352	1353.64	1354.506	4	367.2	59.090908	T.GTIHDRDKGEIL.Q
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	1	2.7826	0.1783	1211.59	1212.349	1	502.7	66.66667	T.I1H3D1R4D1K2G1E1I1L1.Q
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	3.7532	0.244	1732.47	1732.946	1	369	57.692307	A.EELDDMNIEIIRNK.L
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	3.7522	0.3673	1578.61	1579.706	1	637.2	70.83333	F.LETGNLEDHFYQL.E
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	3.1568	0.284	1442.55	1443.726	5	346.6	58.333332	K.SDLLPNIGKLYPL.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	2	3.7036	0.2614	1458.31	1458.726	2	359.6	62.5	K.S1D1L1L1P1N2I1G1K2L1Y1P1L1.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	1	2.2274	0.2689	1442.55	1443.726	1	365.6	50	K.SDLLPNIGKLYPL.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	1	2.3342	0.2526	1372.59	1372.506	4	293.8	54.545456	T.G1T1I1H3D1R4D1K2G1E1I1L1.Q
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	1	2.3192	0.1707	1253.66	1254.56	2	376.7	65	D.L1L1P1N2I1G1K2L1Y1P1L1.A
gi|6323480|ref|NP_013552.1|	YLR447C	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; Vma6p	1	2.5827	0.2154	1241.77	1241.56	1	432.4	65	D.LLPNIGKLYPL.A
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	3.2203	0.156	2011.37	2011.22	1	446.1	50	T.M1A1A1I1D1P1E1P1F1D1D1D1K2K2P1S1T1L1.R
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	2.9496	0.2798	1642.67	1643.88	1	803.4	66.66667	Y.GKQALPGIPANSELTF.D
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	3.8804	0.3464	1904.49	1905.205	1	1117.1	55.88235	K.LLEGGIIIEDRVTGKGPH.A
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	3.4264	0.3659	2671.73	2672.14	1	618.2	41.304348	Y.SLNVEPYSPTPALNFKIPVTIRIT.M
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	1	2.2842	0.2425	1497.7	1498.768	3	100.2	46.153847	M.AVGGERRIVIPAPY.A
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	1	2.4959	0.2456	1517.59	1518.768	6	105.4	46.153847	M.A1V1G1G1E1R4R4I1V1I1P1A1P1Y1.A
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	4.619	0.3862	1876.91	1878.139	1	527.4	55.88235	L.EGGIIIEDRVTGKGPHAK.K
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) 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 (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	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 peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	3.8128	0.2754	1729.49	1730.015	1	1180.2	75	E.KVKDSEESKPKPKTK.L
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	3.9626	0.3553	1990.65	1991.298	1	664.8	52.77778	L.LEGGIIIEDRVTGKGPHAK.K
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	4.3532	0.4252	1876.75	1878.139	1	622.5	58.823532	L.EGGIIIEDRVTGKGPHAK.K
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	3	4.5996	0.4533	1877.48	1878.139	1	955.9	42.647057	L.EGGIIIEDRVTGKGPHAK.K
gi|6323482|ref|NP_013554.1|	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	2	3.5076	0.2522	1903.53	1903.139	1	486.9	58.823532	L.E1G1G1I1I1I1E1D1R4V1T1G1K2G1P1H3A1K2.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	3.1809	0.2139	1916.17	1917.023	1	426.1	57.14286	T.D1K2Y1D1E1N2N2P1E1H3R4K2I1A1Y1.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	3.4251	0.2238	1887.51	1888.969	4	226.5	57.14286	Y.L1R4N2W2D1G1R4T1D1K2D1A1E1E1R4.R
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	3.5166	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-methyltransferase, 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-methyltransferase, 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-methyltransferase, 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-methyltransferase, 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	1	2.7693	0.2001	947.58	947.166	1	500	75 Y.KVLKPGGTF.A
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	3	4.4013	0.2826	2738.87	2738.03	1	692.5	34.375 L.R4K2I1F1E1P1G1D1H3V1T1V1I1N2G1E1H3Q2G1D1A1G1L1V1L1.M
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	2	5.0943	0.2563	1848.65	1849.32	1	1351.4	66.66667 Q.K2L1L1I1P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	2	3.7691	0.2972	1977.93	1979.451	1	423.8	56.25 S.Q2K2L1L1I1P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	3	4.6269	0.1846	1955.15	1957.451	1	2283.9	50 S.QKLLIPVQELPLLLKPN.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	3	4.7496	0.2051	1982.12	1979.451	1	1605.7	45.3125 S.Q2K2L1L1I1P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	3	4.6226	0.1739	1831.04	1829.32	1	2792.9	58.333332 Q.KLLIPVQELPLLLKPN.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	2	3.6054	0.317	1958.75	1957.451	1	418.2	53.125 S.QKLLIPVQELPLLLKPN.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	2	4.5295	0.4244	2106.47	2105.307	1	891.2	58.823532 L.R4K2I1F1E1P1G1D1H3V1T1V1I1N2G1E1H3Q2.G
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	2	2.9261	0.3205	1627.33	1625.868	1	497.7	73.07692 L.RKIFEPGDHVTVIN.G
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	3	4.9526	0.1555	1978.1	1979.451	1	2439	50 S.Q2K2L1L1I1P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	2	3.5099	0.2905	1976.87	1979.451	1	402.2	53.125 S.Q2K2L1L1I1P1V1Q2E1L1P1L1L1L1K2P1N2.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	2	3.5648	0.3553	1955.85	1957.451	1	792.9	68.75 S.QKLLIPVQELPLLLKPN.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	3	4.9955	0.3042	1960.37	1957.451	2	1493.3	43.75 S.QKLLIPVQELPLLLKPN.K
gi|6323632|ref|NP_013703.1|	YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA 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 heterotrimeric complex with Erp1, Erp2p, 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.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	1	3.147	0.1735	1577.68	1576.698	5	347.6	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	3.8031	0.2943	1827.63	1824.979	1	1161.6	71.42857 R.RVEEITDEIVDELTY.L
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	5.084	0.4505	2064.97	2066.313	1	1979.4	78.125 R.RVEEITDEIVDELTYLK.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	4.1587	0.3293	1940.61	1938.139	1	640.9	60.000004 R.RVEEITDEIVDELTYL.K
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	3.7542	0.2989	1616.63	1617.756	1	1382.8	82.14286 L.SRAIELDIESGAEAR.D
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	3.4637	0.3305	1638.91	1638.756	1	1081.7	67.85714 L.S1R4A1I1E1L1D1I1E1S1G1A1E1A1R4.D
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	4.8984	0.3549	1955.49	1957.139	1	1246.5	63.333332 R.R4V1E1E1I1T1D1E1I1V1D1E1L1T1Y1L1.K
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	3.7315	0.3289	1356.39	1354.633	4	385.9	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	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.R4V1E1E1I1T1D1E1I1V1D1E1L1T1Y1L1K2.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.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	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	2	3.41	0.2009	1371.17	1370.633	3	376.1	70	N.E1K2L1K2P1I1E1V1E1L1R4.R
gi|41629688|ref|NP_013695.2|	YML017W	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 in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p	2	2.909	0.1782	2440.75	2441.766	6	258.1	36.842106	D.L1P1P1R4F1S1N2F1D1I1E1D1L1F1Q2A1K2F1T1K2.F
gi|41629688|ref|NP_013695.2|	YML017W	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 in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p	3	4.1461	0.2844	2207.6	2207.445	1	919.1	44.736843	L.KKQTPTEEESHSATPTPKPL.S
gi|41629688|ref|NP_013695.2|	YML017W	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 in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p	2	5.396	0.484	2206.47	2207.445	1	833.5	57.894737	L.KKQTPTEEESHSATPTPKPL.S
gi|41629688|ref|NP_013695.2|	YML017W	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 in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p	2	4.9283	0.4457	2232.81	2233.445	1	695.2	57.894737	L.K2K2Q2T1P1T1E1E1E1S1H3S1A1T1P1T1P1K2P1L1.S
gi|41629688|ref|NP_013695.2|	YML017W	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 in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p	2	5.1355	0.4498	2206.41	2207.445	1	1113.4	60.526318	L.KKQTPTEEESHSATPTPKPL.S
gi|6323619|ref|NP_013690.1|	YML022W	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p	2	3.069	0.194	1203.33	1203.467	3	638.1	70	R.SKLNAPVFTLL.N
gi|6323619|ref|NP_013690.1|	YML022W	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p	2	3.7439	0.25	1663.95	1662.885	1	615.2	61.538464	A.LHQYPNFPSEGILF.E
gi|6323619|ref|NP_013690.1|	YML022W	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p	2	3.4548	0.3337	1693.33	1693.943	1	769.4	65.38461	F.EDFLPIFRNPGLFQ.K
gi|6323619|ref|NP_013690.1|	YML022W	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p	2	3.4283	0.2353	1584.25	1582.812	1	691	70.83333	F.E1D1F1L1P1I1F1R4N2P1G1L1F1.Q
gi|6323619|ref|NP_013690.1|	YML022W	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; 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	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	4.6422	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.AWTNIPRKEGGLGPINIPLL.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	3.7566	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
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	4.3149	0.4242	2178.75	2180.425	1	722.3	67.64706	D.KVKFDPPDFDENNLFRPT.D
gi|6323607|ref|NP_013679.1|	YML034W	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p	2	3.8139	0.3358	2503.51	2503.595	1	459	47.5	Q.ELQEEVNEQLEHENGSEFDVK.Q
gi|6323607|ref|NP_013679.1|	YML034W	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p	2	4.5016	0.4668	1945.67	1944.158	1	621.9	60.000004	T.RIETPQLPTEKDVEKC.E
gi|6323607|ref|NP_013679.1|	YML034W	Protein with a putative role in sister chromatid segregation, potentially phosphorylated 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 putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p	3	4.2277	0.2876	3091.7	3090.397	1	615.7	28.846153	Q.K2E1V1P1S1T1I1L1V1P1E1V1E1Q2Q2E1P1S1Q2S1E1R4T1P1S1L1F1.S
gi|6323607|ref|NP_013679.1|	YML034W	Protein with a putative role in sister chromatid segregation, potentially 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
gi|6323607|ref|NP_013679.1|	YML034W	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p	3	4.4983	0.2713	3897.98	3899.321	1	853.2	25	S.F1A1D1K2L1P1Q2K2E1V1P1S1T1I1L1V1P1E1V1E1Q2Q2E1P1S1Q2S1E1R4T1P1S1L1F1.S
gi|6323607|ref|NP_013679.1|	YML034W	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p	2	3.12	0.2167	2186.05	2187.519	1	336.6	44.444447	D.K2L1P1Q2K2E1V1P1S1T1I1L1V1P1E1V1E1Q2Q2.E
gi|6323607|ref|NP_013679.1|	YML034W	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p	3	6.5766	0.3919	3561.44	3562.978	1	1097.1	30.000002	D.K2L1P1Q2K2E1V1P1S1T1I1L1V1P1E1V1E1Q2Q2E1P1S1Q2S1E1R4T1P1S1L1F1.S
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	4.7377	0.3016	2989.61	2990.213	2	503.9	28	Q.N2D1D1Q2N2P1K2N2K2P1G1W2V1V1Y1P1P1P1P1K2P1S1Y1N2S1D1.T
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	5.2039	0.3361	2954.12	2955.213	1	1019.8	36	Q.NDDQNPKNKPGWVVYPPPPKPSYNSD.T
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	4.0908	0.2269	2506.22	2505.766	1	1135.3	36.904762	Q.N2D1D1Q2N2P1K2N2K2P1G1W2V1V1Y1P1P1P1P1K2P1S1.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	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
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	2	4.0177	0.3256	2792.65	2793.888	1	452.5	43.18182	M.F1H3Y1E1A1D1N2E1E1N2L1E1E1L1N2D1S1K2P1L1I1D1Q2.L
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	1	2.2845	0.1971	1191.45	1190.345	2	412.8	62.5	F.H3E1K2E1P1V1K2F1Y1.K
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	1	2.8985	0.2946	1436.68	1437.681	1	637.1	65	S.IFHEKEPVKFY.K
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	1	3.1982	0.2311	1451.58	1452.681	1	651.7	70	S.I1F1H3E1K2E1P1V1K2F1Y1.K
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	2	2.967	0.2281	1436.77	1437.681	1	925.1	75	S.IFHEKEPVKFY.K

gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose 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
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	2	3.4215	0.2901	1511.15	1511.73	1	1154.2	75	K.KILEEYDGDIGKM.N
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	2	3.5603	0.1959	1453.27	1452.681	1	966.7	75	S.I1F1H3E1K2E1P1V1K2F1Y1.K
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	1	2.8736	0.3288	1436.79	1437.681	1	674.1	70	S.IFHEKEPVKFY.K
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	2	3.2585	0.2955	1436.75	1437.681	1	976.7	75	S.IFHEKEPVKFY.K
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	3	3.8798	0.1973	1437.95	1437.681	1	1937	67.5	S.IFHEKEPVKFY.K
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	2	3.0494	0.2429	1436.69	1437.681	1	1020.9	75	S.IFHEKEPVKFY.K
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain 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
gi|6323593|ref|NP_013664.1|	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	2	3.5903	0.176	1452.25	1452.681	1	1131	80	S.I1F1H3E1K2E1P1V1K2F1Y1.K
gi|6323583|ref|NP_013655.1|	YML057W	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-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.W2A1D1P1I1E1E1Y1D1E1V1L1D1K2D1L1T1E1E1D1I1V1N2S1K2.T
gi|6323583|ref|NP_013655.1|	YML057W	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-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
gi|6323583|ref|NP_013655.1|	YML057W	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-response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	2	4.3672	0.4553	3109.79	3110.326	1	903.9	44	L.L1W2A1D1P1I1E1E1Y1D1E1V1L1D1K2D1L1T1E1E1D1I1V1N2S1K2.T
gi|6323583|ref|NP_013655.1|	YML057W	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-response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	3	6.072	0.5007	3110.33	3110.326	1	746.6	37	L.L1W2A1D1P1I1E1E1Y1D1E1V1L1D1K2D1L1T1E1E1D1I1V1N2S1K2.T
gi|6323583|ref|NP_013655.1|	YML057W	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-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
gi|6323583|ref|NP_013655.1|	YML057W	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-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
gi|6323583|ref|NP_013655.1|	YML057W	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-response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	2	5.6163	0.426	2995.09	2996.166	1	690.5	50	L.W2A1D1P1I1E1E1Y1D1E1V1L1D1K2D1L1T1E1E1D1I1V1N2S1K2.T
gi|6323583|ref|NP_013655.1|	YML057W	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-response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	2	5.0703	0.4528	2965.99	2967.166	1	776.3	52.083332	L.WADPIEEYDEVLDKDLTEEDIVNSK.T
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,	2	3.5296	0.1596	1744.41	1742.995	1	453.5	60.714287	K.T1L1D1P1V1W2N2E1D1A1K2I1P1I1L1.S
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,	3	4.0786	0.2806	3070.07	3071.998	1	373.2	25.961538	K.KEDENEDTTEKEEDENEESSQTDVGIA.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,	2	3.8633	0.4072	1931.71	1933.122	1	473.4	50	D.K2N2G1Q2V1P1P1V1P1E1V1P1Q2E1Y1T1Q2.-
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,	2	3.2597	0.2973	1909.89	1911.122	1	444	50	D.KNGQVPPVPEVPQEYTQ.-
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,	2	4.0427	0.3357	2630.27	2631.875	1	621.5	40.909092	K.I1N2Y1G1K2D1K2N2G1Q2V1P1P1V1P1E1V1P1Q2E1Y1T1Q2.-
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,	2	5.3691	0.459	2072.49	2073.291	1	778.9	68.75	H.W2F1P1V1K2E1D1K2S1E1E1K2A1V1E1R4A1.E
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,	2	4.342	0.4135	2601.61	2601.875	1	503.1	40.909092	K.INYGKDKNGQVPPVPEVPQEYTQ.-
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,	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,	2	4.5047	0.3827	1595.79	1593.78	1	1046.3	84.61539	F.HEEEKKKVGGNLPQ.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,	3	4.3454	0.437	2784.47	2785.216	8	266	26.086956	K.TLDPVWNEDAKIPILSRSKNQVIF.N
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,	2	3.5254	0.2207	1854.51	1854.116	1	924.4	70	T.LFHEEEKKKVGGNLPQ.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,	2	5.5545	0.4118	2212.49	2213.432	1	2053.3	76.47059	L.H3W2F1P1V1K2E1D1K2S1E1E1K2A1V1E1R4A1.E
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,	3	4.4069	0.3384	2215.94	2213.432	1	1055.4	44.11765	L.H3W2F1P1V1K2E1D1K2S1E1E1K2A1V1E1R4A1.E
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,	3	5.1041	0.3311	2952.23	2954.454	1	1436.9	35.576923	Q.GSFNPEYIKPSFDIVKGGITDKPMKIA.S
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,	2	3.2298	0.1958	1712.37	1712.103	1	736.5	53.846157	F.LSKFWVIYMPVLSQ.Q
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,	2	4.0107	0.2839	1384.47	1382.544	1	507.5	85	L.K2L1K2D1H3E1H3K2V1T1E1.S
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,	3	5.11	0.3836	2329.64	2327.591	1	933.6	43.055553	S.L1H3W2F1P1V1K2E1D1K2S1E1E1K2A1V1E1R4A1.E
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,	2	4.9026	0.4036	2048.87	2049.291	1	1360.5	68.75	H.WFPVKEDKSEEKAVERA.E
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,	2	3	0.2815	1178.99	1179.448	1	1041.6	85	S.VKLGDGHLIVK.I
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,	2	3.1545	0.252	1364.53	1364.544	1	296.2	80	L.KLKDHEHKVTE.S
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,	2	3.6235	0.1908	1548.47	1548.785	1	498.4	63.636364	N.VKNPRWNETKYL.L
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,	2	4.3911	0.3861	1740.33	1740.957	1	616.9	67.85714	L.FHEEEKKKVGGNLPQ.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,	2	4.4776	0.4061	1793.43	1792.998	1	1070.3	73.07692	S.L1H3W2F1P1V1K2E1D1K2S1E1E1K2.A
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,	2	4.1069	0.3602	1773.27	1772.998	1	1331.7	73.07692	S.LHWFPVKEDKSEEK.A
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,	2	3.6755	0.2513	2075.35	2075.35	1	216.7	44.11765	F.H3E1E1E1K2K2K2V1G1G1N2L1P1Q2K2V1I1N2.Q
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,	2	5.3171	0.4063	2204.55	2205.481	1	742.7	58.333332	F.H3E1E1E1K2K2K2V1G1G1N2L1P1Q2K2V1I1N2Q2.Q
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,	2	4.8371	0.4291	2174.83	2176.481	1	1017.2	58.333332	F.HEEEKKKVGGNLPQKVINQ.Q
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,	2	3.5786	0.3068	1569.47	1568.785	1	437.3	59.090908	N.V1K2N2P1R4W2N2E1T1K2Y1L1.L
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	3.5448	0.2331	1593.39	1592.805	3	515.7	65.38461	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	2	4.1516	0.4013	1722.41	1722.979	1	1156.4	64.28571	Q.K2A1P1K2W2Y1P1S1E1D1V1A1A1L1K2.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	3.6274	0.1922	1591.58	1592.805	1	870.9	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 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 Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	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 Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	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 Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	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 Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	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 Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	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 5.8S rRNA; Rpl6ap	1	3.3788	0.3715	1574.62	1575.805	1	862.1	57.692307	Q.KAPKWYPSEDVAAL.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.0516	0.2038	1610.73	1610.952	1	488.9	53.571426	Y.TPVPAIDVTMPITVR.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.3143	0.4035	1627.63	1628.952	1	833.3	67.85714	Y.T1P1V1P1A1I1D1V1T1M1P1I1T1V1R4.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	6.7076	0.2002	4060.28	4060.936	1	1166.2	28.125	E.E1V1Q2E1E1D1E1E1D1N2D1G1E1E1E1Q2E1E1E1E1E1E1E1Q2K2E1E1V1K2P1E1P1K2.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	2.9496	0.2798	1642.67	1643.88	1	803.4	66.66667	Y.GKQALPGIPANSELTF.D
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	6.4861	0.2626	4364.09	4364.363	1	367.8	20	E.EVQEEDEEDNDGEEEQEEEEEEEQKEEVKPEPKKSK.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	6.1679	0.4177	4235.21	4236.189	1	599.8	23.529411	E.EVQEEDEEDNDGEEEQEEEEEEEQKEEVKPEPKKS.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	5.5149	0.3531	4277.81	4279.189	1	516.7	22.058825	E.E1V1Q2E1E1D1E1E1D1N2D1G1E1E1E1Q2E1E1E1E1E1E1E1Q2K2E1E1V1K2P1E1P1K2K2S1.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	6.0563	0.3041	4491.2	4492.537	1	340.5	20.13889	E.EVQEEDEEDNDGEEEQEEEEEEEQKEEVKPEPKKSKK.E
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	5.1321	0.2586	4538.09	4539.537	7	210.5	18.055555	E.E1V1Q2E1E1D1E1E1D1N2D1G1E1E1E1Q2E1E1E1E1E1E1E1Q2K2E1E1V1K2P1E1P1K2K2S1K2K2.E
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	6.4377	0.2121	4021.67	4020.936	1	828.1	25.78125	E.EVQEEDEEDNDGEEEQEEEEEEEQKEEVKPEPK.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.4448	0.2816	1879.41	1879.043	1	443.6	52.941177	L.E1G1G1I1V1I1E1D1R4T1I1G1D1G1P1Q2A1K2.R
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	5.7356	0.2733	4668.08	4669.652	1	406.5	18.918919	E.E1V1Q2E1E1D1E1E1D1N2D1G1E1E1E1Q2E1E1E1E1E1E1E1Q2K2E1E1V1K2P1E1P1K2K2S1K2K2E1.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	6.6331	0.2901	4407.95	4409.363	1	531.1	22.142857	E.E1V1Q2E1E1D1E1E1D1N2D1G1E1E1E1Q2E1E1E1E1E1E1E1Q2K2E1E1V1K2P1E1P1K2K2S1K2.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.7285	0.3114	2094.69	2093.335	3	319.3	42.105263	K.V1L1E1G1G1I1V1I1E1D1R4T1I1G1D1G1P1Q2A1K2.R
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.4263	0.455	2067.15	2068.335	1	619.7	55.263157	K.VLEGGIVIEDRTIGDGPQAK.R
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	6.0867	0.2815	4620.02	4621.652	1	451.5	20.27027	E.EVQEEDEEDNDGEEEQEEEEEEEQKEEVKPEPKKSKKE.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.3805	0.3293	2311.13	2311.587	1	954.4	52.380955	K.S1K2V1L1E1G1G1I1V1I1E1D1R4T1I1G1D1G1P1Q2A1K2.R
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.2636	0.1637	1458.27	1457.667	1	317.8	66.66667	K.KDLEEGPTKPKSK.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.2233	0.322	1884.43	1883.133	1	355.9	56.666668	V.E1F1K2K2D1L1E1E1G1P1T1K2P1K2S1K2.K
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	1	2.357	0.1619	1285.78	1285.532	5	126.1	55	G.GERRIIIPAPY.A
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	1	2.5149	0.1596	1528.75	1528.795	3	128.1	46.153847	M.SVGGERRIIIPAPY.A
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.6618	0.3938	1861.81	1862.133	4	211.8	46.666668	V.EFKKDLEEGPTKPKSK.K

gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	2.9055	0.2	2119.21	2119.423	1	256.7	44.11765	V.EFKKDLEEGPTKPKSKKE.Q
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.0075	0.4155	2212.57	2213.597	1	824.6	57.894737	L.NVEPYTPVPAIDVTMPITVR.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.7806	0.2268	2325.35	2326.756	1	1248.1	52.499996	S.LNVEPYTPVPAIDVTMPITVR.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.2609	0.4312	2412.49	2413.835	1	907.1	50	Y.SLNVEPYTPVPAIDVTMPITVR.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.2194	0.3258	2237.41	2237.597	5	346.9	36.842106	L.N2V1E1P1Y1T1P1V1P1A1I1D1V1T1M1P1I1T1V1R4.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.1114	0.3825	2350.47	2351.756	1	566	40	S.L1N2V1E1P1Y1T1P1V1P1A1I1D1V1T1M1P1I1T1V1R4.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.492	0.4841	2438.65	2439.835	1	1026.1	52.380955	Y.S1L1N2V1E1P1Y1T1P1V1P1A1I1D1V1T1M1P1I1T1V1R4.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.5648	0.3402	2246.13	2248.191	1	400.4	41.666664	K.RNPDFEDDDFLGGDFDEDE.I
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.8743	0.3484	1778.05	1778.783	1	603	57.14286	K.R4N2P1D1F1E1D1D1D1F1L1G1G1D1F1.D
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	4.1569	0.421	1855.19	1856.043	1	846	64.70589	L.EGGIVIEDRTIGDGPQAK.R
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; 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.EFKKDLEEGPTKPK.S
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.3479	0.245	1667.55	1664.881	1	404.7	65.38461	V.E1F1K2K2D1L1E1E1G1P1T1K2P1K2.S
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	3	4.2519	0.2544	1874.66	1874.188	1	1352.7	50	K.KVEFKKDLEEGPTKPK.S
gi|6323566|ref|NP_013637.1|	YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	2	3.6919	0.3499	2270.95	2270.463	8	168.7	38.88889	L.RIIKRNPDFEDDDFLGGDF.D
gi|6323562|ref|NP_013633.1|	YML078W	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; involved in protein refolding after import into mitochondria; Cpr3p	1	2.598	0.1955	1285.56	1286.535	2	341.3	66.66667	F.H3R4I1I1P1D1F1M1I1Q2.G
gi|6323562|ref|NP_013633.1|	YML078W	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; involved in protein refolding after import into mitochondria; Cpr3p	2	3.5197	0.3988	1668.71	1671.013	1	893.9	73.07692	K.GVPFHRIIPDFMIQ.G
gi|6323562|ref|NP_013633.1|	YML078W	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; involved in protein refolding after import into mitochondria; Cpr3p	2	3.0847	0.2129	1269.93	1270.535	1	1194	88.88889	F.HRIIPDFMIQ.G
gi|6323562|ref|NP_013633.1|	YML078W	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; involved in protein refolding after import into mitochondria; Cpr3p	2	3.3188	0.2866	1288.37	1286.535	1	1146.3	83.33333	F.H3R4I1I1P1D1F1M1I1Q2.G
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	3	4.7671	0.3302	2755.76	2755.928	4	314.6	27.000002	L.E1H3G1I1K2P1D1G1H3L1E1D1G1L1S1K2P1K2G1G1E1E1G1F1S1T1.F
gi|6323554|ref|NP_013625.1|	YML085C	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	L.E1H3G1I1K2P1D1G1H3L1E1D1G1L1S1K2P1K2G1G1E1E1G1F1S1T1.F
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	3	4.2862	0.2608	1900.37	1901.166	1	604.9	40	H.Y1T1V1G1R4E1I1L1G1D1V1L1D1R4I1R4.K
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	3	4.2392	0.3872	1874.48	1876.166	1	678.2	41.666664	H.YTVGREILGDVLDRIR.K
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	2	3.5897	0.3424	2869.55	2870.105	1	313.4	38.46154	L.EHGIKPDGHLEDGLSKPKGGEEGFSTF.F
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which 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	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	3	6.3242	0.3575	3069.02	3070.342	1	1665.9	34.82143	Y.SLEHGIKPDGHLEDGLSKPKGGEEGFSTF.F
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	2	4.0278	0.4519	2014.59	2015.233	1	417.9	58.333332	L.EHGIKPDGHLEDGLSKPKG.G
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which 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 (Tub2p) 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
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	2	3.6707	0.2361	2903.73	2904.105	1	140.8	30.769232	L.E1H3G1I1K2P1D1G1H3L1E1D1G1L1S1K2P1K2G1G1E1E1G1F1S1T1F1.F
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	2	4.1558	0.3235	1981.87	1983.181	1	315.6	50	L.E1H3G1I1K2P1D1G1H3L1E1D1G1L1S1K2P1K2.G
gi|6323554|ref|NP_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.LVPYPRIHFPL.V
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	2	3.302	0.424	1182.53	1181.334	1	714.5	75	D.GHLEDGLSKPK.G
gi|6323554|ref|NP_013625.1|	YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	2	4.0415	0.3597	1957.55	1958.181	2	265.7	52.941177	L.EHGIKPDGHLEDGLSKPK.G
gi|6323553|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
gi|6323553|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	3.5121	0.304	1657.85	1654.99	1	748.3	61.538464	S.TKIYAPLTPFVEKF.V
gi|6323553|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	3.6599	0.1778	1258.81	1260.523	7	1025.3	75	A.T1I1R4V1V1P1G1F1N2I1K2.S
gi|6323553|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

gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the 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
gi|6323531|ref|NP_013602.1|	YML105C	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.P1R4L1E1E1I1D1D1F1N2D1I1D1D1L1D1M1E1L1A1.E
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	4.5142	0.3463	2062.65	2063.268	1	1165.9	62.5	E.S1L1R4E1I1P1Y1G1P1D1F1D1N2I1E1F1K2.K
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the 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
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	4.2217	0.257	2380.31	2379.554	1	832.1	42.105263	M.PRLEEIDDFNDIDDLDMELA.E
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	3	4.3624	0.278	3569.96	3572.92	1	858.9	21.666666	M.PRLEEIDDFNDIDDLDMELAELDPSLRTPIA.P
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	4.6153	0.3624	1840.35	1841.03	1	1739.4	82.14286	L.REIPYGPDFDNIEFK.K
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	3	4.2658	0.3825	1841.18	1841.03	1	1546.1	48.214287	L.REIPYGPDFDNIEFK.K
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	5.2034	0.3443	1861.37	1861.03	1	2102.9	82.14286	L.R4E1I1P1Y1G1P1D1F1D1N2I1E1F1K2.K
gi|6323531|ref|NP_013602.1|	YML105C	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.S1L1R4E1I1P1Y1G1P1D1F1D1N2I1E1F1K2.K
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	2	5.1458	0.3386	2062.13	2063.268	1	1657.1	68.75	E.S1L1R4E1I1P1Y1G1P1D1F1D1N2I1E1F1K2.K
gi|6323531|ref|NP_013602.1|	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the 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
gi|6323526|ref|NP_013597.1|	YML110C	2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase, involved in ubiquinone (Coenzyme Q) biosynthesis; located in mitochondria; Coq5p	2	3.92	0.3834	2062.29	2063.161	1	771.9	58.823532	L.V1S1N2G1E1K2L1E1E1I1D1S1D1S1K2D1I1Y1.T
gi|6323526|ref|NP_013597.1|	YML110C	2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase, involved in 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-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase, involved 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
gi|6323521|ref|NP_013592.1|	YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	2	4.5477	0.3855	3084.57	3085.255	1	983.2	41.666664	Y.KTIDLEDEEYYDYDFEDIDPEVISK.F
gi|6323521|ref|NP_013592.1|	YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is 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
gi|6323521|ref|NP_013592.1|	YML115C	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.SSENYKTIDLEDEEYYDYDFEDIDPEVISK.F
gi|6323521|ref|NP_013592.1|	YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is 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	Component of the mannan polymerase I; forms a complex with Mnn9p, which is involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	3	4.0478	0.2257	3259.13	3260.432	3	452	24	Y.K2T1I1D1L1E1D1E1E1Y1Y1D1Y1D1F1E1D1I1D1P1E1V1I1S1K2F1.D
gi|6323521|ref|NP_013592.1|	YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	3	4.8047	0.349	3234.38	3232.432	1	1010	36	Y.KTIDLEDEEYYDYDFEDIDPEVISKF.D
gi|6323521|ref|NP_013592.1|	YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is 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	Component of the mannan polymerase I; forms a complex with Mnn9p, which is 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
gi|6323521|ref|NP_013592.1|	YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is involved in in mannan synthesis; mutants are vanadate-resistant; Van1p	2	3.9507	0.3639	2955.45	2957.081	1	915.6	43.47826	Y.KTIDLEDEEYYDYDFEDIDPEVIS.K
gi|6323521|ref|NP_013592.1|	YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is 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
gi|6323512|ref|NP_013583.1|	YML123C	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; 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
gi|6323512|ref|NP_013583.1|	YML123C	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; 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
gi|6323512|ref|NP_013583.1|	YML123C	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; 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
gi|6323512|ref|NP_013583.1|	YML123C	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; 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
gi|6323512|ref|NP_013583.1|	YML123C	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; 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
gi|6323512|ref|NP_013583.1|	YML123C	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; 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
gi|6323512|ref|NP_013583.1|	YML123C	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; exit from the ER during maturation requires Pho86p; Pho84p	2	3.2785	0.3385	1792.43	1792.985	7	319.4	50	N.D1F1A1H3I1E1D1P1L1E1R4R4R4L1.A
gi|6323511|ref|NP_013582.1|	YML124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	3	4.4121	0.1741	1991.18	1989.186	1	1584.1	51.666664	H.Y1T1V1G1R4E1I1V1D1E1V1E1E1R4I1R4.K
gi|6323511|ref|NP_013582.1|	YML124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which 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.E1H3G1I1K2E1D1G1H3L1E1D1G1L1S1K2P1K2.G
gi|6323511|ref|NP_013582.1|	YML124C	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	44.11765	H.YTVGREIVDEVEERIRKM.A
gi|6323511|ref|NP_013582.1|	YML124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	2	3.9058	0.4332	1989.79	1990.18	1	479	50	L.EHGIKEDGHLEDGLSKPK.G
gi|6323511|ref|NP_013582.1|	YML124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which 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
gi|6323511|ref|NP_013582.1|	YML124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	2	3.302	0.424	1182.53	1181.334	1	714.5	75	D.GHLEDGLSKPK.G
gi|6323511|ref|NP_013582.1|	YML124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	3	4.3135	0.3244	2786.69	2787.927	5	376.1	27.000002	L.E1H3G1I1K2E1D1G1H3L1E1D1G1L1S1K2P1K2G1G1E1E1G1F1S1T1.F
gi|6323511|ref|NP_013582.1|	YML124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which 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
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	4.8013	0.3104	3023.87	3026.256	1	1922.5	38.541664	Y.A1N2E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2.V

gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein 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
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	3.3508	0.301	2837.57	2838.074	1	372.2	38.636364	N.E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2.V
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	4.2522	0.3439	3189.73	3190.432	1	534	36	L.Y1A1N2E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2.V
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	4.1676	0.3115	2682.37	2680.943	1	393.1	45.238094	N.ETENDILLKDELDEMAEKYPHF.Q
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	5.8048	0.3815	3031.04	3029.302	1	2254.8	39.583336	L.YANETENDILLKDELDEMAEKYPHF.Q
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein 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
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	6.0108	0.2203	3431.51	3430.706	1	1403.6	32.407406	L.Y1A1N2E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2V1H3.Y
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	3.657	0.3453	2311.55	2313.537	1	504.5	50	T.K2D1Q2M1N2R4Y1L1P1E1Y1S1E1D1N2R4L1L1.I
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	2.9595	0.2651	1298.43	1297.5	1	577.5	70	V.RVPIDGKQEVR.Y
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	3.1171	0.3019	1395.83	1396.633	2	356.2	59.090908	A.VRVPIDGKQEVR.Y
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein 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
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	3.634	0.4361	2807.67	2809.074	1	397.8	38.636364	N.ETENDILLKDELDEMAEKYPHFQ.V
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	4.5705	0.2802	2840.24	2838.074	1	917.5	32.954548	N.E1T1E1N2D1I1L1L1K2D1E1L1D1E1M1A1E1K2Y1P1H3F1Q2.V
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	4.4931	0.2969	3156.97	3157.432	1	784.4	40	L.YANETENDILLKDELDEMAEKYPHFQ.V
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	4.0828	0.1547	2683.82	2680.943	7	639.3	28.57143	N.ETENDILLKDELDEMAEKYPHF.Q
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein 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
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	5.0186	0.3222	3392.69	3393.706	1	734.4	26.85185	L.YANETENDILLKDELDEMAEKYPHFQVH.Y
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	3	3.8057	0.3653	3042.98	3045.347	1	1249.9	35.416664	N.ETENDILLKDELDEMAEKYPHFQVH.Y
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	1	3.2297	0.2832	1567.54	1568.783	1	397.9	61.538464	T.N2I1L1D1E1P1V1H3G1I1Y1I1P1A1.A
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	1	2.8204	0.321	1550.48	1551.783	2	266	50	T.NILDEPVHGIYIPA.A
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein 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
gi|6323510|ref|NP_013581.1|	YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	2.9049	0.1946	1566.19	1566.844	1	510.2	61.538464	H.VAVRVPIDGKQEVR.Y
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	1	3.1592	0.2749	1577.61	1578.688	1	299	57.692307	L.N2A1I1N2E1N2I1R4D1D1L1S1A1L1.L
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	1	3.0515	0.2945	1557.65	1558.688	1	246.8	53.846157	L.NAINENIRDDLSAL.L
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	4.1982	0.275	1561.51	1558.688	1	709.9	65.38461	L.NAINENIRDDLSAL.L
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	1	2.3045	0.2428	1320.57	1320.488	1	611.6	65	K.TGKWEPNLDLF.M
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	1	2.5467	0.2535	1528.44	1529.742	3	367.6	54.545456	W.KIQPYLPEFSFC.D
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding 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
gi|6323505|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
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	4.3081	0.3204	1899.41	1900.193	1	1119.8	75	K.ALWKIQPYLPEFSFC.D
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	4.2007	0.3482	1917.13	1918.193	1	636.6	60.714287	K.A1L1W2K2I1Q2P1Y1L1P1E1F1S1F1C1.D

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
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	1	2.9731	0.2312	1450.67	1448.662	2	466.4	59.090908 T.KTGKWEPNLDLF.M
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	4.4681	0.3987	1734.67	1731.955	1	1433.3	83.33333 L.W2K2I1Q2P1Y1L1P1E1F1S1F1C1.D
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	2	4.2979	0.234	1717.51	1715.955	1	1403.8	83.33333 L.WKIQPYLPEFSFC.D
gi|6323505|ref|NP_013576.1|	YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.5419	0.2792	2336.73	2338.536	1	845.1	52.63158 A.ALDTTPERNFNDEFQAIKDL.T
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	2.9951	0.2076	1658.09	1657.991	6	414.4	57.14286 L.KDLSKDVPVFLVPSL.V
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.5804	0.28	2151.99	2154.298	1	739.4	52.941177 L.DTTPERNFNDEFQAIKDL.T
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.4228	0.2326	2177.61	2179.298	3	438.1	41.17647 L.D1T1T1P1E1R4N2F1N2D1E1F1Q2A1I1K2D1L1.T
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	3	4.089	0.2601	3747.05	3745.045	6	236.4	20.833332 R.SKQEEKDEKSDPEEKKNTFKDVTDEEKLKFN.E
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.8685	0.2459	1792.53	1791.028	1	674.3	67.85714 L.S1F1A1P1Y1N2P1V1P1P1F1Y1R4S1K2.G
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	3	6.1252	0.3603	3516.11	3516.835	1	840.2	32.75862 F.S1S1L1P1L1G1P1I1K2E1R4S1K2Q2E1E1K2D1E1K2S1D1P1E1E1K2K2N2T1F1.K
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.2282	0.2648	1882.19	1881.048	1	488.1	56.666668 N.YNADPKPEPVDEFYPV.N
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	2	3.1417	0.2869	1897.29	1899.048	4	415.2	53.333336 N.Y1N2A1D1P1K2P1E1P1V1D1E1F1Y1P1V1.N
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and 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
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	3	4.8699	0.2465	3784.64	3787.045	1	423	25 R.S1K2Q2E1E1K2D1E1K2S1D1P1E1E1K2K2N2T1F1K2D1V1T1D1E1E1K2L1K2F1N2.E
gi|6323654|ref|NP_013725.1|	YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	3	4.5306	0.3837	2307.86	2309.405	1	735	39.705883 A.R4Q2N2F1D1N2I1E1E1T1G1N2R4Y1P1H3R4Q2.T
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	2.9912	0.1982	1942.37	1944.061	1	348.3	56.666668 A.LHDPEVYENPDEFIPE.R
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.4773	0.1964	1962.27	1963.061	6	252.9	50 A.L1H3D1P1E1V1Y1E1N2P1D1E1F1I1P1E1.R
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.3001	0.2094	1902.75	1901.123	1	572.3	50 R.N2N2D1M1S1T1E1L1N2L1D1L1I1E1K2M1.K
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.9419	0.2958	2286.29	2286.462	1	948.8	55.88235 A.LHDPEVYENPDEFIPERW.V
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.8131	0.2227	2309.83	2311.462	1	767.6	52.941177 A.L1H3D1P1E1V1Y1E1N2P1D1E1F1I1P1E1R4W2.V
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.1136	0.29	2517.57	2514.71	1	571.3	44.736843 A.LHDPEVYENPDEFIPERWVE.G

gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.0799	0.4186	2657.47	2658.84	1	589.8	45.238094	A.LHDPEVYENPDEFIPERWVEGS.K
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	4.5935	0.3401	2686.83	2687.84	1	830.3	47.61905	A.L1H3D1P1E1V1Y1E1N2P1D1E1F1I1P1E1R4W2V1E1G1S1.K
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.495	0.3509	1252.11	1252.544	1	1085.6	88.88889	K.FKFWPIIGPF.L
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	1	2.4852	0.2367	1253.62	1252.544	1	518.7	66.66667	K.FKFWPIIGPF.L
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	2.9137	0.2412	1508.45	1508.819	4	691	54.545456	K.F1K2F1W2P1I1I1G1P1F1L1E1.S
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	1	2.6734	0.1599	1263.44	1264.544	4	470.1	61.11111	K.F1K2F1W2P1I1I1G1P1F1.L
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.8377	0.2265	1262.79	1264.544	1	1048.2	88.88889	K.F1K2F1W2P1I1I1G1P1F1.L
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	3	4.5862	0.3266	2686.37	2687.84	1	551.5	32.142857	A.L1H3D1P1E1V1Y1E1N2P1D1E1F1I1P1E1R4W2V1E1G1S1.K
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	2.9245	0.3124	1254.31	1252.544	1	1200.2	88.88889	K.FKFWPIIGPF.L
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	1	2.2159	0.2293	1251.7	1252.544	1	526	66.66667	K.FKFWPIIGPF.L
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.7743	0.272	1263.69	1264.544	1	1032.6	88.88889	K.F1K2F1W2P1I1I1G1P1F1.L
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	1	2.2341	0.1628	1263.6	1264.544	4	406.4	55.555557	K.F1K2F1W2P1I1I1G1P1F1.L
gi|6323657|ref|NP_013728.1|	YMR015C	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 target of azole antifungal drugs; Erg5p	2	3.4092	0.3031	1252.47	1252.544	1	1049.3	88.88889	K.FKFWPIIGPF.L
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	3.0268	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
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	3.7311	0.3483	2480.27	2481.612	1	595.4	47.368423	Q.R4N2E1Q2T1D1D1S1I1N2P1Y1E1P1L1I1D1W2F1T1.R
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	4.2314	0.2258	2989.34	2989.23	1	835.1	30.434782	K.IQRNEQTDDSINPYEPLIDWFTRH.E
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	3.53	0.3376	2780.53	2781.94	2	352.8	33.333336	Q.R4N2E1Q2T1D1D1S1I1N2P1Y1E1P1L1I1D1W2F1T1R4H3.E
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	3.1464	0.1933	2746.43	2747.94	1	319.7	30.952381	Q.RNEQTDDSINPYEPLIDWFTRH.E
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	3.0784	0.2323	1400.51	1398.676	1	695.4	68.181816	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	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	32.03125	L.R4A1P1K2L1P1P1P1T1N2E1E1S1Y1N2P1P1E1E1Y1L1L1S1P1E1E1K2E1A1W2E 1N2T1.E
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	5.9763	0.3608	3795.56	3797.074	1	962.6	26.612906	L.R4A1P1K2L1P1P1P1T1N2E1E1S1Y1N2P1P1E1E1Y1L1L1S1P1E1E1K2E1A1W2E 1N2.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	3.0439	0.2349	1988.73	1989.245	1	284.6	46.666668	Q.WNKPSQKQLEKDICIT.I
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	6.1667	0.3813	3754.61	3756.074	1	1522.4	30.645163	L.RAPKLPPPTNEESYNPPEEYLLSPEEKEAWEN.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	3	6.6708	0.4708	3855.08	3857.179	1	1453.9	32.8125	L.RAPKLPPPTNEESYNPPEEYLLSPEEKEAWENT.E
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	6.0181	0.3689	3548	3550.854	1	1927.1	35.344826	L.R4A1P1K2L1P1P1P1T1N2E1E1S1Y1N2P1P1E1E1Y1L1L1S1P1E1E1K2E1A1W2 E
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	5.1298	0.2794	3513.32	3512.854	1	1377.8	32.75862	L.RAPKLPPPTNEESYNPPEEYLLSPEEKEAW.E
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.2484	0.201	1537.63	1535.709	1	778.4	70.83333	M.DMEDATEKVIRDL.H
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.4439	0.3927	4666.52	4668.024	1	470	19.871796	T.A1A1L1P1T1Q2N2Y1V1D1S1I1D1N2F1L1D1D1F1Y1L1Q2P1Y1E1K2E1A1I1Y1G1 E1P1D1H3V1I1T1V1D1.V
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.1289	0.2937	4594.64	4595.945	1	466.7	19.078947	A.A1L1P1T1Q2N2Y1V1D1S1I1D1N2F1L1D1D1F1Y1L1Q2P1Y1E1K2E1A1I1Y1G1E1 P1D1H3V1I1T1V1D1.V
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.1923	0.2501	2868.83	2869.978	1	234.2	40.909092	N.EVDENEERQVNEDRHSTEKHQFL.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.1927	0.1892	2018.29	2019.084	6	487.9	53.125	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1.P
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.4548	0.2044	1301.63	1301.48	8	1204.3	75	L.EKDEIVEIVLN.N
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.2495	0.2727	4083.17	4083.352	1	473.6	21.969696	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R 4R4D1T1L1.Y

gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.0668	0.2795	1210.31	1210.277	3	837	77.77778	T.G1W2D1Y1R4N2V1D1G1L1.K
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.466	0.1842	1552.73	1552.709	1	787.9	70.83333	M.D1M1E1D1A1T1E1K2V1I1R4D1L1.H
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	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 mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	4.207	0.3469	1816.05	1815.974	1	613	56.666668	Y.EKEAIYGEPDHVITVD.V
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	4.2244	0.2398	1683.65	1684.902	1	1181.8	76.92308	M.M1D1M1E1D1A1T1E1K2V1I1R4D1L1.H
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	4.2938	0.3834	1877.23	1875.146	1	1343.9	66.66667	Y.G1M1M1D1M1E1D1A1T1E1K2V1I1R4D1L1.H
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.7246	0.358	1854.61	1855.146	1	1114.9	60.000004	Y.GMMDMEDATEKVIRDL.H
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.0721	0.2241	1543.45	1542.798	4	346	58.333332	F.I1L1E1K2D1E1I1V1E1I1V1L1N2.N
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.8857	0.3864	3023.03	3024.082	1	507.5	29.347824	L.L1N2E1V1D1E1N2E1E1R4Q2V1N2E1D1R4H3S1T1E1K2H3Q2F1.L
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	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 mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.6012	0.4145	3138.41	3140.257	1	436.5	27.083334	N.E1V1D1E1N2E1E1R4Q2V1N2E1D1R4H3S1T1E1K2H3Q2F1L1T1K2.A
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	5.552	0.4187	3589.79	3590.811	1	869.4	33.62069	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4.R
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	6.1514	0.5324	2323.73	2325.499	1	1134.2	63.15789	L.E1K2D1E1I1V1E1I1V1L1N2N2Q2D1T1G1T1H3P1F1.H
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.2509	0.1521	1313.09	1314.48	1	1263.6	75	L.E1K2D1E1I1V1E1I1V1L1N2.N
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.7012	0.2034	3589.76	3590.811	1	382.4	25	D.R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.3323	0.3581	3805.73	3807.076	1	342.7	23.387096	D.R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1L1.Y
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.7485	0.309	3968.72	3969.193	5	298.9	19.53125	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1.L
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.0738	0.1806	3815.21	3818.088	1	513.1	25	Q.RDRTYDDALGEVPHSFDPDNHPAFPEYPMRRD.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.8835	0.3331	3145.88	3148.43	1	826.1	33.653847	D.A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1L1.Y
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.8896	0.3737	4297.25	4299.632	1	303.6	20.714287	R.T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1L1Y1V1R4P1Q2.S
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.0756	0.3006	4247.03	4248.632	9	185.7	17.857143	R.TYDDALGEVPHSFDPDNHPAFPEYPMRRDTLYVRPQ.S
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	4.2065	0.3518	2359.59	2358.615	1	454.8	44.736843	L.K2S1R4P1V1I1T1C1N2G1Q2F1P1W2P1D1I1T1V1N2.K
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.3181	0.1589	2934.65	2932.166	1	623.3	32.291664	D.A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	3.9023	0.2235	4097.21	4099.352	1	652.2	25	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M$R4R4D1T1L1.Y
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.5891	0.3134	3752.3	3750.999	2	453.4	26.666668	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4.D
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	3.2948	0.2736	1952.11	1949.121	1	316.2	50	D.E1I1V1E1I1V1L1N2N2Q2D1T1G1T1H3P1F1.H
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	2	2.9882	0.1787	2699.67	2698.879	2	259.5	30.434782	Y.DDALGEVPHSFDPDNHPAFPEYPM.R
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	5.2863	0.4374	3163.04	3164.343	1	1059.5	36.53846	Y.D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.6542	0.3121	3125.99	3126.343	1	661.5	31.730768	Y.DDALGEVPHSFDPDNHPAFPEYPMRRD.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.1922	0.3717	3445.01	3446.624	1	790.3	26.785713	Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M$.R

gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.1679	0.268	3389.96	3390.624	1	500.1	25.892857 R.TYDDALGEVPHSFDPDNHPAFPEYPMRRD.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in 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
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.7153	0.3653	2748.32	2745.927	4	499.9	29.545454 L.G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	5.6082	0.3808	2858.6	2860.087	1	671.7	35.869564 A.L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.6334	0.2834	2825.45	2825.087	5	376.8	32.608696 A.LGEVPHSFDPDNHPAFPEYPMRRD.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	3.8891	0.3329	2962.55	2962.192	1	378.9	25 L.G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1L1.Y
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	5.837	0.3961	4030.88	4033.351	1	337.1	21.212122 Y.D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1L1Y1V1R4P1Q2.S
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	5.4201	0.247	3984.68	3984.351	1	305.4	21.212122 Y.DDALGEVPHSFDPDNHPAFPEYPMRRDTLYVRPQ.S
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in 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
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.4657	0.3124	3032.09	3034.271	2	584.4	31 D.A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1T1.L
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in 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	25.80645 Q.R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.1188	0.2451	3111.68	3110.43	4	441.9	28.846153 D.ALGEVPHSFDPDNHPAFPEYPMRRDTL.Y
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in 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
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	4.8246	0.22	4111.88	4111.378	2	581.3	23.484848 T.I1Q2R4D1R4T1Y1D1D1A1L1G1E1V1P1H3S1F1D1P1D1N2H3P1A1F1P1E1Y1P1M1R4R4D1.T
gi|6323703|ref|NP_013774.1|	YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	3	3.9443	0.2158	4056.53	4059.378	3	458.6	21.969696 T.IQRDRTYDDALGEVPHSFDPDNHPAFPEYPMRRD.T
gi|6323712|ref|NP_013783.1|	YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	2	3.6138	0.2975	1578.45	1580.896	1	1038	79.16667 L.D1K2P1V1P1L1D1L1P1W2R4L1L1.N
gi|6323712|ref|NP_013783.1|	YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	2	3.5475	0.202	1695.73	1695.055	1	661.9	61.538464 H.L1D1K2P1V1P1L1D1L1P1W2R4L1L1.N
gi|6323712|ref|NP_013783.1|	YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	3	4.1349	0.2494	2727.32	2728.152	1	799.6	34.782608 R.F1Q2I1P1G1R4D1S1V1V1K2E1M1P1S1D1Q2P1I1A1P1I1L1R4.Q
gi|6323712|ref|NP_013783.1|	YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	2	3.0465	0.1622	2990.95	2990.476	4	180.5	26 R.F1Q2I1P1G1R4D1S1V1V1K2E1M1P1S1D1Q2P1I1A1P1I1L1R4Q2M1.S
gi|6323712|ref|NP_013783.1|	YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	3	5.4442	0.3589	2954.93	2954.476	1	832	31 R.FQIPGRDSVVKEMPSDQPIAPILRQM.S
gi|6323712|ref|NP_013783.1|	YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	3	5.4451	0.2969	2993.03	2990.475	1	611.1	29 R.F1Q2I1P1G1R4D1S1V1V1K2E1M1P1S1D1Q2P1I1A1P1I1L1R4Q2M1.S
gi|6323712|ref|NP_013783.1|	YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	3	4.3269	0.3554	1613.87	1616.861	1	803.9	45.833336 T.NREDIPFNTIKIR.F
gi|6323712|ref|NP_013783.1|	YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	3	5.2611	0.3511	2858.48	2858.283	1	1148.5	34.375 R.F1Q2I1P1G1R4D1S1V1V1K2E1M1P1S1D1Q2P1I1A1P1I1L1R4Q2.M
gi|6323722|ref|NP_013793.1|	YMR076C	Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent 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
gi|6323722|ref|NP_013793.1|	YMR076C	Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent 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
gi|6323722|ref|NP_013793.1|	YMR076C	Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent 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
gi|6323722|ref|NP_013793.1|	YMR076C	Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent manner, may function as a protein-protein interaction scaffold; Pds5p	2	2.9731	0.1903	1559.63	1559.716	1	305	61.538464 S.IAPDVPRDELAESF.T
gi|6323726|ref|NP_013797.1|	YMR080C	ATP-dependent RNA helicase of the SFI superfamily, required for nonsense 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
gi|6323726|ref|NP_013797.1|	YMR080C	ATP-dependent RNA helicase of the SFI superfamily, required for nonsense mediated mRNA decay and for efficient translation termination at nonsense codons; involved in telomere maintenance; Nam7p	2	3.1561	0.3682	1929.15	1928.195	1	1394.5	62.5 L.GHQVVDISFDVPLPKEF.S
gi|6323726|ref|NP_013797.1|	YMR080C	ATP-dependent RNA helicase of the SFI superfamily, required for nonsense 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
gi|6323726|ref|NP_013797.1|	YMR080C	ATP-dependent RNA helicase of the SFI superfamily, required for nonsense mediated mRNA decay and for efficient translation termination at nonsense codons; involved in telomere maintenance; Nam7p	2	3.5829	0.2518	2388.25	2385.557	1	547.7	47.22222 K.N2A1N2W2D1T1D1Q2W2Q2P1L1I1E1D1R4Q2L1L1.S
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	1	3.2203	0.2745	1463.71	1464.659	1	565.7	58.333332 L.GIDAGEEKEKLFK.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	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.8603	0.3771	1463.87	1464.659	1	984.1	75	L.GIDAGEEKEKLFK.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	3.5246	0.2947	1482.33	1480.659	1	490.8	62.5	L.G1I1D1A1G1E1E1K2E1K2L1F1K2.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	4.5577	0.2175	1723.77	1724.992	1	800	64.28571	L.G1I1D1A1G1E1E1K2E1K2L1F1K2K2L1.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	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 dehydrogenase isozyme III; involved in the shuttling of 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 dehydrogenase 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
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	4.0213	0.1743	1373.51	1372.653	2	903.2	77.27273	W.HGDWPLPVKLPL.V
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	3.9028	0.3171	1389.17	1388.653	1	913.2	77.27273	W.H3G1D1W2P1L1P1V1K2L1P1L1.V
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	3.3747	0.5021	1526.81	1528.838	1	977.8	61.538464	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	3.6008	0.3031	2116.01	2117.453	1	447.5	50	L.HYKDIPVPEPKPNEILIN.V
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	3.8372	0.2218	2240.43	2241.585	1	437	41.666664	L.H3Y1K2D1I1P1V1P1E1P1K2P1N2E1I1L1I1N2V1.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	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	4.0285	0.3654	1544.83	1546.838	1	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; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	1	3.1869	0.2966	1502.89	1502.782	2	347.7	50	W.P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.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	4.0856	0.2109	1911.37	1909.198	2	635.3	50	W.HGDWPLPVKLPLVGGHEG.A
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	5.3908	0.5128	1872.75	1875.146	1	2720.6	78.125	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	3.9274	0.3104	1933.63	1933.198	1	968.1	55.88235	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1.A
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	5.3715	0.1849	2164.61	2163.461	1	1184.9	57.5	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.V
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	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	3	4.5296	0.2323	2136.11	2136.461	1	1171.9	40	W.HGDWPLPVKLPLVGGHEGAGV.V
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	3.2336	0.3097	2260.61	2263.594	1	339.1	35.714287	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1V1.V

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	4.3629	0.2311	2334.91	2334.726	1	606.5	45.454548	W.HGDWPLPVKLPLVGGHEGAGVVV.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	3.1129	0.3085	1336.49	1336.485	1	404.1	63.636364	L.GIDAGEEKEKLF.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	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.6894	0.2253	1814.61	1817.136	7	295.9	50	Y.KDIPVPEPKPNEILIN.V
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	4.2176	0.189	1980.75	1980.312	1	934.9	65.625	H.YKDIPVPEPKPNEILIN.V
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	3.6992	0.4357	1534.33	1534.755	1	859.1	79.16667	L.HYKDIPVPEPKPN.E
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	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 dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH 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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH 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 alcohol dehydrogenase isozyme III; involved in the shuttling of 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	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling 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	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling 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	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling 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; Adh3p	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
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	4.1868	0.3424	2024.49	2025.349	1	802.7	53.125	K.L1H3Y1K2D1I1P1V1P1E1P1K2P1N2E1I1L1.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	4.1358	0.3584	2004.39	2003.349	1	949.9	56.25	K.LHYKDIPVPEPKPNEIL.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	3.7659	0.2226	2254.53	2255.612	1	418.8	44.444447	K.L1H3Y1K2D1I1P1V1P1E1P1K2P1N2E1I1L1I1N2.V
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	3.0099	0.2501	1788.35	1786.084	1	417.7	50	G.DWPLPVKLPLVGGHEGA.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	3.7217	0.3778	2229.05	2230.612	1	404.2	47.22222	K.LHYKDIPVPEPKPNEILIN.V
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	4.7241	0.4506	1979.05	1980.277	1	1216.4	63.88889	W.HGDWPLPVKLPLVGGHEGA.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	3	6.2768	0.1857	2005.28	2005.277	1	1495.5	47.22222	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.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	3	4.4812	0.1615	1722.65	1723.031	3	1188.6	43.333332	W.HGDWPLPVKLPLVGGH.E
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	5.0083	0.4635	1872.73	1875.146	1	2044.3	71.875	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	4.8911	0.4199	1743.59	1745.031	1	1408.3	66.66667	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E

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	5.0732	0.4569	1850.97	1852.146	1	2194.1	75	W.HGDWPLPVKLPLVGGHE.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	4.851	0.2868	1722.53	1723.031	1	2158.6	76.666664	W.HGDWPLPVKLPLVGGH.E
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	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	5.0006	0.1972	2136.17	2136.461	1	1036.8	55	W.HGDWPLPVKLPLVGGHEGAGV.V
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	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	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 alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	2	3.1536	0.2337	1560.89	1560.864	1	834.4	65.38461	D.W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	3	4.8128	0.1633	1982	1980.277	1	962.6	41.666664	W.HGDWPLPVKLPLVGGHEGA.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	4.8422	0.3295	2004.39	2005.277	1	1530.1	63.88889	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.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	3	4.9838	0.2384	2262.86	2263.594	1	939.3	38.095238	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1V1.V
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	3	4.124	0.1777	2237.69	2235.594	2	669.2	33.333336	W.HGDWPLPVKLPLVGGHEGAGVV.V
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	4.0559	0.342	1755.61	1753.048	1	1136.4	64.28571	H.YKDIPVPEPKPNEIL.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	4.2588	0.2705	1769.89	1771.048	1	1251.9	67.85714	H.Y1K2D1I1P1V1P1E1P1K2P1N2E1I1L1.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	3.9075	0.1784	2003.37	2001.312	1	874.6	65.625	H.Y1K2D1I1P1V1P1E1P1K2P1N2E1I1L1I1N2.V
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	2.9069	0.2938	1715.17	1715.005	5	354.1	50	H.GDWPLPVKLPLVGGHE.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	1	2.7936	0.2432	1387.78	1388.653	1	406.1	59.090908	W.H3G1D1W2P1L1P1V1K2L1P1L1.V
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	3.6585	0.2005	1552.65	1552.755	1	521.6	66.66667	L.H3Y1K2D1I1P1V1P1E1P1K2P1N2.E
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	1	2.5366	0.3597	1371.62	1372.653	2	457.9	59.090908	W.HGDWPLPVKLPL.V
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	4.3253	0.3016	1389.25	1388.653	1	964.5	77.27273	W.H3G1D1W2P1L1P1V1K2L1P1L1.V
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	1	4.0372	0.2692	1529.96	1528.838	1	702.8	61.538464	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	1	3.2679	0.2435	1586.92	1585.889	1	406.5	46.42857	W.HGDWPLPVKLPLVGG.H
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	3.4332	0.2331	1487.81	1488.786	1	1007.8	66.66667	W.H3G1D1W2P1L1P1V1K2L1P1L1V1.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	1	4.0023	0.3302	1547.6	1546.838	1	985.2	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	4.1249	0.3893	1584.69	1585.889	1	1560.6	71.42857	W.HGDWPLPVKLPLVGG.H
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	3.931	0.2191	1547.31	1546.838	2	1279.6	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	1	2.7133	0.168	1079.63	1080.388	7	354.4	61.11111	R.G1L1I1K2S1P1I1K2I1V1.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	3.9058	0.1778	1375.33	1372.653	4	664.6	68.181816	W.HGDWPLPVKLPL.V
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	2.9968	0.2715	1667.29	1666.915	1	413.5	61.538464	K.L1H3Y1K2D1I1P1V1P1E1P1K2P1N2.E
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	4.0178	0.1737	1528.61	1528.838	2	1290.1	69.230774	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	3.3267	0.2343	1833.73	1833.141	1	496.4	56.666668	K.GKLHYKDIPVPEPKPN.E
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	5.166	0.5049	1873.97	1875.146	1	1755.5	65.625	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	5.2552	0.4408	2002.81	2005.277	1	1189.3	61.11111	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.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	4.8338	0.4932	1721.59	1723.031	1	2181.5	76.666664	W.HGDWPLPVKLPLVGGH.E
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	3	6.6669	0.4155	1850.69	1852.146	1	1951.9	56.25	W.HGDWPLPVKLPLVGGHE.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	3	5.1465	0.1981	1981.67	1980.277	1	1548.3	50	W.HGDWPLPVKLPLVGGHEGA.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	5.0269	0.5071	1849.89	1852.146	1	3140.9	84.375	W.HGDWPLPVKLPLVGGHE.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	3	6.0883	0.3685	1743.38	1745.031	1	1820.2	56.666668	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E
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	4.5257	0.435	1978.47	1980.277	1	1250.1	61.11111	W.HGDWPLPVKLPLVGGHEGA.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	3	5.9576	0.2427	2006.42	2005.277	1	1006.6	41.666664	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.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	3	5.3805	0.2526	1723.46	1723.031	1	2156.4	60.000004	W.HGDWPLPVKLPLVGGH.E
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	5.1551	0.2685	1746.29	1745.031	1	1501.1	66.66667	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3.E
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	3	5.867	0.3839	1872.68	1875.146	1	1782.6	53.125	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	4.015	0.3807	2135.43	2136.461	1	640.2	45	W.HGDWPLPVKLPLVGGHEGAGV.V
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	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	1285.71	1286.604	7	485.5	65	Y.N2L1A1L1P1K2F1P1I1L1F1.S
gi|6323735|ref|NP_013806.1|	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	2	3.3979	0.3135	1807.73	1805.04	1	639.2	64.28571	S.S1Y1L1R4G1P1N2F1P1T1D1I1F1V1R4.I
gi|6323735|ref|NP_013806.1|	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	2	3.4507	0.3331	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	68.181816	Y.N2L1A1L1P1K2F1P1I1L1F1S1.L
gi|6323735|ref|NP_013806.1|	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	1	2.7171	0.2576	1273.42	1273.604	1	861.2	75	Y.NLALPKFPILF.S
gi|6323735|ref|NP_013806.1|	YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	2	3.2851	0.1885	1274.31	1273.604	2	507.7	65	Y.NLALPKFPILF.S
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	4.4503	0.3784	2171.55	2171.359	1	1128.7	61.764706	L.S1E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4.A
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	3.3406	0.3195	2244.63	2246.519	1	265	38.88889	S.EIPKEIYEDVVDEDVLRAI.T
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	4.8035	0.385	2355.81	2357.598	1	1320.6	55.263157	L.S1E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4A1I1.T
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	3.432	0.2508	2458.49	2459.703	1	1050.4	50	L.S1E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4A1I1T1.E
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	3.9425	0.3802	2432.43	2434.703	1	921.4	50	L.SEIPKEIYEDVVDEDVLRAIT.E
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	4.2377	0.2808	1997.53	1997.255	1	478.5	50	F.KKPVFPGIDDAEENLNPL.K
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	3.8699	0.3875	2083.97	2083.281	2	320.3	43.75	S.E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4.A
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	4.3978	0.4221	2148.71	2149.359	1	1384.3	70.588234	L.SEIPKEIYEDVVDEDVLR.A
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	3.7479	0.2719	2245.75	2243.438	1	1013.3	61.11111	L.S1E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4A1.I
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	5.3664	0.4861	2264.29	2262.519	1	1516.4	63.88889	G.LSEIPKEIYEDVVDEDVLR.A
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	3.4018	0.2578	2271.01	2269.519	1	504.8	47.22222	S.E1I1P1K2E1I1Y1E1D1V1V1D1E1D1V1L1R4A1I1.T
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	3.3013	0.2658	2332.45	2333.598	1	753	47.368423	L.SEIPKEIYEDVVDEDVLRAI.T
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	3.5125	0.2163	2444.91	2446.757	1	730.5	45	G.LSEIPKEIYEDVVDEDVLRAI.T
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	4.1986	0.3083	2165.29	2167.432	1	1005.1	61.11111	K.F1K2K2P1V1F1P1G1I1D1D1A1E1E1N2L1N2P1L1.K
gi|6323738|ref|NP_013809.1|	YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	2	4.9911	0.4066	2145.63	2144.432	1	1132	69.44444	K.FKKPVFPGIDDAEENLNPL.K
gi|6323751|ref|NP_013822.1|	YMR104C	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	4.1084	0.425	2573.53	2575.788	1	497.6	40.476192	A.NFDQEFTKEKPIDSVVDEYLSA.S
gi|6323751|ref|NP_013822.1|	YMR104C	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	4.0261	0.3963	2326.59	2327.472	1	438.1	44.444447	A.N2F1D1Q2E1F1T1K2E1K2P1I1D1S1V1V1D1E1Y1.L

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.N2V1D1T1V1F1G1Y1P1G1G1A1I1L1P1V1Y1D1A1I1H3N2.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; Ilv2p	2	5.0018	0.3511	2033.05	2033.124	1	1324.5	58.823532	A.G1G1S1G1L1D1E1F1I1N2F1D1P1E1V1E1R4Q2.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	2.5068	0.2364	1380.28	1380.467	1	342.7	54.166668	E.S1L1V1I1D1I1D1G1D1A1S1F1N2.M
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	3.1879	0.1728	1843.69	1845.1	2	558	47.058823	A.T1S1G1R4P1G1P1V1L1V1D1L1P1K2D1V1T1A1.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	4.0048	0.3264	1917.19	1917.178	1	572.2	50	A.T1S1G1R4P1G1P1V1L1V1D1L1P1K2D1V1T1A1A1.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	3.264	0.2193	1895.73	1894.178	1	748.5	52.77778	A.TSGRPGPVLVDLPKDVTAA.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	4.654	0.4007	2736.61	2738.002	1	677.7	41.666664	M.S1R4Q2N2V1D1T1V1F1G1Y1P1G1G1A1I1L1P1V1Y1D1A1I1H3N2.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; Ilv2p	2	3.4225	0.2111	1239.83	1240.433	1	671.3	77.77778	T.H3Q2L1N2P1D1F1I1K2L1.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	1	2.6559	0.2127	1224.51	1225.433	3	255.5	66.66667	T.HQLNPDFIKL.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	3.0289	0.2761	1654.45	1654.863	1	281.5	60.714287	A.SKRPEPAPSFNVDPL.E
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	4.7044	0.3428	2737.7	2738.028	1	1074.8	34.375	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	3.5896	0.2817	2736.59	2738.028	1	306.1	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	1	2.4953	0.205	1221.83	1222.385	1	537.1	70	D.P1L1E1Q2P1A1E1P1S1K2L1.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	4.5437	0.336	2635.04	2634.949	1	1585.9	44.56522	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	2	3.7851	0.2912	2637.13	2634.949	1	437.9	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	2	3.3174	0.3439	2223.53	2225.642	1	563.8	45	Q.S1I1N2K2A1A1D1L1I1N2L1A1K2K2P1V1L1Y1V1G1A1.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.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	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	28.225807 Y.S1A1S1P1L1P1A1S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1A1.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	26.666668 Y.S1A1S1P1L1P1A1S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1.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.SASPLPASKRPEPAPSFNVDPLEQPAEPSKL.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	4.2614	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; Ilv2p	3	4.9677	0.3453	3208.94	3208.577	1	601.1	27.586206 S.A1S1P1L1P1A1S1K2R4P1E1P1A1P1S1F1N2V1D1P1L1E1Q2P1A1E1P1S1K2L1.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	3.8657	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; Ilv2p	3	4.2905	0.3112	3102.11	3100.499	1	634	25.892857 A.SPLPASKRPEPAPSFNVDPLEQPAEPSKL.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	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; Ilv2p	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; Ilv2p	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; Ilv2p	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; Ilv2p	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; Ilv2p	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; Ilv2p	2	5.1302	0.3723	1829.31	1828.942	1	1547.5	71.42857 S.G1L1D1E1F1I1N2F1D1P1E1V1E1R4Q2.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; Ilv2p	2	4.5478	0.3151	1655.09	1656.731	1	1459.8	75 L.D1E1F1I1N2F1D1P1E1V1E1R4Q2.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.I1K2N2E1R4N2F1H3I1F1.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	18.75	K.Q2E1N2F1A1P1V1L1P1I1I1E1Y1E1D1L1D1E1T1I1N2K2I1I1E1E1H3D1T1P1L1V1Q2.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.N2F1A1P1V1L1P1I1I1E1Y1E1D1L1D1E1T1I1N2K2I1I1E1.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
gi|6323768|ref|NP_013839.1|	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; Ade17p	2	3.7778	0.2684	2477.71	2478.807	1	443.4	44.736843	Q.SKFEEIPKPFTPEERKEWLS.K
gi|6323768|ref|NP_013839.1|	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; Ade17p	2	3.9942	0.289	2504.81	2505.807	9	359.6	39.473686	Q.S1K2F1E1E1I1P1K2P1F1T1P1E1E1R4K2E1W2L1S1.K

gi|6323768|ref|NP_013839.1|	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; Ade17p	2	3.2658	0.2534	1928.17	1927.202	1	704.4	50	A.KVGVTIPEAVEEIDIGGVT.L
gi|6323768|ref|NP_013839.1|	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; Ade17p	2	3.1508	0.2141	2264.21	2263.555	1	604.7	52.941177	K.FEEIPKPFTPEERKEWLS.K
gi|6323768|ref|NP_013839.1|	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; Ade17p	2	3.8154	0.2937	2286.85	2287.555	1	1107.3	64.70589	K.F1E1E1I1P1K2P1F1T1P1E1E1R4K2E1W2L1S1.K
gi|6323768|ref|NP_013839.1|	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; Ade17p	3	5.0506	0.2613	2503.7	2505.807	1	834.4	39.473686	Q.S1K2F1E1E1I1P1K2P1F1T1P1E1E1R4K2E1W2L1S1.K
gi|6323768|ref|NP_013839.1|	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; Ade17p	2	2.9775	0.1827	1747.17	1745.932	1	528.8	57.14286	S.SDAFFPFPDNVYRAV.K
gi|6323768|ref|NP_013839.1|	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; Ade17p	3	4.26	0.3614	2288.27	2287.555	1	1262.9	47.058823	K.F1E1E1I1P1K2P1F1T1P1E1E1R4K2E1W2L1S1.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.N2R4T1S1I1I1N2I1P1Y1I1P1V1L1A1.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.A1I1H3N2I1I1N2F1P1F1P1T1P1P1D1R4V1A1L1S1.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	4.2034	0.2749	1831.71	1833.122	1	1016.7	63.333332	H.N2I1I1N2F1P1F1P1T1P1P1D1R4V1A1L1.S
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	3.8232	0.3281	1717.33	1717.018	1	658.3	60.714287	N.I1I1N2F1P1F1P1T1P1P1D1R4V1A1L1.S
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	3.6553	0.2991	1811.31	1812.122	1	802.3	60.000004	H.NIINFPFPTPPDRVAL.S
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	1	2.3604	0.4196	1281.56	1282.439	1	508.2	63.636364	Q.TVHPIPDVAFAD.G
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	1	3.3083	0.2415	1489.63	1490.697	1	550.9	54.166668	L.K2L1P1N2Q2I1P1G1E1Y1I1T1T1.I
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	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 glycoprotein; 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.E1R4D1S1K2D1R4Y1I1N2G1D1K2K2V1D1I1Y1.S
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	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
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	2.9645	0.2076	1243.37	1242.417	1	889.9	77.77778	A.FNFFEPIKEA.K
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	3	4.6914	0.3524	1667.9	1667.946	1	1829	53.846157	L.SKKDFKIIDNPKSF.L
gi|6323779|ref|NP_013850.1|	YMR131C	Essential nuclear protein involved in early steps of ribosome biogenesis; physically interacts with the ribosomal protein Rpl3p; Rrb1p	2	3.6957	0.3395	1988.57	1990.235	1	674	58.823532	H.MSRPLGPDEVLEADPTVY.E
gi|6323779|ref|NP_013850.1|	YMR131C	Essential nuclear protein involved in early steps of ribosome biogenesis; physically interacts with the ribosomal protein Rpl3p; Rrb1p	3	3.8727	0.1647	3739.94	3742.684	5	358.1	20.161291	L.L1K2D1D1N2E1G1E1D1D1E1E1D1D1E1D1D1V1D1P1V1I1E1N2E1N2I1P1L1R4D 1T1.T
gi|6323779|ref|NP_013850.1|	YMR131C	Essential nuclear protein involved in early steps of ribosome biogenesis; physically interacts with the ribosomal protein Rpl3p; Rrb1p	2	4.0265	0.3507	1729.41	1727.927	1	644.7	60.000004	H.MSRPLGPDEVLEADPT.V
gi|6323779|ref|NP_013850.1|	YMR131C	Essential nuclear protein involved in early steps of ribosome biogenesis; physically interacts with the ribosomal protein Rpl3p; Rrb1p	2	3.6969	0.265	1746.61	1746.927	1	920.6	66.66667	H.M1S1R4P1L1G1P1D1E1V1L1E1A1D1P1T1.V
gi|6323779|ref|NP_013850.1|	YMR131C	Essential nuclear protein involved in early steps of ribosome biogenesis; physically interacts with the ribosomal protein Rpl3p; Rrb1p	3	5.5417	0.3096	4233.77	4235.24	1	501.8	24.285715	L.L1K2D1D1N2E1G1E1D1D1E1E1D1D1E1D1D1V1D1P1V1I1E1N2E1N2I1P1L1R4D 1T1T1N2R4L1.K
gi|6323779|ref|NP_013850.1|	YMR131C	Essential nuclear protein involved in early steps of ribosome biogenesis; physically 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.Y1A1H3P1P1P1T1I1D1P1N2D1P1V1Q2I1S1F1P1T1.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	2	2.9523	0.2068	1753.67	1755.005	3	304.4	53.571426	A.S1S1T1A1K2P1K2E1N2L1F1R4E1I1L1.Q
gi|6323801|ref|NP_013872.1|	YMR152W	Protein of unknown function; proposed to be involved in responding to DNA 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	Protein of unknown function; proposed to be involved in responding to DNA damaging agents; Yim1p	3	3.9329	0.2124	3097.82	3097.476	9	229.3	19.23077	I.IKAGKDVDNRWKVGDKVNGM@YSHIYGE.R
gi|6323801|ref|NP_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
gi|6323801|ref|NP_013872.1|	YMR152W	Protein of unknown function; proposed to be involved in responding to DNA damaging agents; Yim1p	2	3.2755	0.2686	1944.13	1945.046	1	437	50	M.VEVPKDENDPYDDFVY.A
gi|6323801|ref|NP_013872.1|	YMR152W	Protein of unknown function; proposed to be involved in responding to DNA 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.E1N2V1D1V1I1D1K2N2V1E1D1A1Q2Q2D1V1E1Q2G1V1G1H3.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.S1E1F1V1A1Y1P1I1Q2L1L1.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
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	4.2186	0.3947	1896.97	1897.188	1	526.7	59.375	K.A1L1K2D1I1L1G1D1Q2V1E1K2V1V1V1S1Y1.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	32.5	L.V1D1I1T1K2D1F1E1L1E1E1T1D1E1E1K2A1E1R4E1K2E1I1K2E1Y1E1P1L1T1K2.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.R4V1F1I1T1D1E1A1E1D1L1I1P1E1W2L1S1F1V1K2.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.A1L1S1D1P1K2Q2L1E1T1E1P1D1L1F1I1R4I1T1P1K2P1E1E1K2V1L1E1I1R4.D
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	2.9259	0.1925	2181.93	2180.471	1	344.6	39.473686	S.YKLLDAPAAIRTGQFGWSAN.M
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	2.9382	0.1748	1459.56	1460.676	8	199.7	54.545456	K.RHSEFVAYPIQL.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	3.7399	0.3029	1477.59	1478.676	1	303.4	63.636364	K.R4H3S1E1F1V1A1Y1P1I1Q2L1.L
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	3.1518	0.1718	1926.47	1927.191	2	583.9	47.058823	Y.K2L1L1D1A1P1A1A1I1R4T1G1Q2F1G1W2S1A1.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	1	4.428	0.3153	1592.67	1592.835	1	330.4	62.5	K.R4H3S1E1F1V1A1Y1P1I1Q2L1L1.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	3.7613	0.269	1573.82	1573.835	1	275.8	58.333332	K.RHSEFVAYPIQLL.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	2	3.1543	0.2791	1574.45	1572.625	1	1008.4	70.83333	F.NEIAEDSEQFDKF.Y
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	3.3976	0.2138	1809.09	1808.995	1	398.6	64.28571	L.S1D1P1K2Q2L1E1T1E1P1D1L1F1I1R4.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	4.5415	0.3302	1808.63	1808.995	1	835.7	48.214287	L.S1D1P1K2Q2L1E1T1E1P1D1L1F1I1R4.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	5.5222	0.4257	2495.77	2496.687	1	1052.8	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	3	4.7356	0.2453	3125.51	3128.37	1	1096.4	37.5	T.KDFELEETDEEKAEREKEIKEYEPL.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	2.6944	0.1564	1419.28	1417.648	2	571.5	59.090908	R.HSEFVAYPIQLL.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	2.6881	0.3177	1317.74	1318.556	1	760.4	63.636364	L.KAVEKSPFLDAL.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	2.9535	0.2261	1593.83	1592.835	2	477.1	62.5	K.R4H3S1E1F1V1A1Y1P1I1Q2L1L1.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	2	3.5989	0.2981	1479.25	1479.629	1	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	44.444447 E.E1T1D1E1E1K2A1E1R4E1K2E1I1K2E1Y1E1P1L1.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.E1V1E1K2E1V1P1I1P1E1E1E1K2K2D1E1E1K2K2D1E1D1D1K2K2P1K2L1E1.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.VTKEVEKEVPIPEEEKKDEEKKDEDDKKPKLE.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 of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of 5,10-methylene-THF in the cytoplasm; Gcv2p	2	3.0982	0.2412	1545.55	1544.748	1	880.4	66.66667 N.PDLKNIDRPLDTF.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 5,10-methylene-THF in the cytoplasm; Gcv2p	3	4.9167	0.2704	2481.5	2483.76	2	942.1	35.526314 T.Q2Y1S1R4I1F1N2P1D1L1K2N2I1D1R4P1L1D1T1F1.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 5,10-methylene-THF in the cytoplasm; Gcv2p	2	3.0084	0.2254	2161.47	2162.453	1	359.8	50 Y.SRIFNPDLKNIDRPLDTF.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 5,10-methylene-THF in the cytoplasm; Gcv2p	2	3.3464	0.2365	2099.95	2101.375	2	366	46.875 S.R4I1F1N2P1D1L1K2N2I1D1R4P1L1D1T1F1.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 5,10-methylene-THF in the cytoplasm; Gcv2p	2	3.6312	0.2078	1659.33	1659.756	1	609.9	65.38461 N.A1I1E1N2D1S1C1P1H3E1L1I1N2K2.T
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 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 5,10-methylene-THF in the cytoplasm; Gcv2p	2	2.9917	0.338	1574.71	1575.774	1	708.8	62.5 F.SIPHGGGGPAGAPICVK.S
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 5,10-methylene-THF in the cytoplasm; Gcv2p	3	3.8218	0.2139	2325.23	2325.629	3	910	34.72222 Q.YSRIFNPDLKNIDRPLDTF.A
gi|6323857|ref|NP_013928.1|	YMR201C	Protein that recognizes and binds damaged DNA during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); contains zinc finger motif; homolog of human XPA protein; Rad14p	3	6.2802	0.4854	2699.78	2698.858	1	1217.4	43.75 E.C1K2E1D1Y1F1L1T1D1P1E1L1N2D1E1D1L1F1H3R4L1.E
gi|6323857|ref|NP_013928.1|	YMR201C	Protein that recognizes and binds damaged DNA during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); contains zinc finger motif; homolog of human XPA protein; Rad14p	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	1691.21	1690.875	1	1147	67.85714 H.R4Q2S1L1E1L1V1N2P1G1T1V1E1N2L1.N
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	3.7996	0.1984	1669.39	1669.875	2	924.8	64.28571 H.RQSLELVNPGTVENL.N
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

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	4.4675	0.4627	1883.15	1882.284	1	1230.7	61.764706	G.MVPITDPLMGTPIGIQPT.V
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	1	2.4142	0.2722	1281.58	1280.42	1	372.1	54.166668	V.STKPTPPPAPEAS.A
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	1	3.1714	0.3858	1564.62	1565.782	1	386.1	53.846157	N.RVTPEEADLGMIAY.Y
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.4305	0.3355	1986.29	1987.139	1	494.2	52.941177	A.EADGRFDAKPAYPGHVQQ.G
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	3	3.8762	0.2164	2192.15	2191.489	2	642	33.82353	A.DLFRSEWPSLIEELLKTN.R
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.7858	0.1843	1598.65	1600.855	1	2163.3	87.5	F.RSEWPSLIEELLK.T
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.6925	0.2352	1834.55	1837.064	1	953.7	71.42857	F.R4S1E1W2P1S1L1I1E1E1L1L1K2T1N2.R
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.8912	0.3219	1570.35	1570.891	1	449.1	58.333332	A.VNENKIVRKPLME.S
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.3213	0.2399	1858.53	1859.008	1	675.5	53.125	A.EADGRFDAKPAYPGHVQ.Q
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.8417	0.2863	1817.15	1816.064	1	1172.6	78.57143	F.RSEWPSLIEELLKTN.R
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	2.9849	0.2357	1749.47	1748.98	2	525.6	53.571426	N.SADHNEPKLPKDKRL.K
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.0285	0.3379	1590.51	1590.823	2	550.7	66.66667	A.DHNEPKLPKDKRL.K
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.0397	0.3779	2026.75	2028.316	1	590.9	52.941177	K.TTDTYPSLPKPLNRPQKA.I
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	2	3.0195	0.2442	1882.63	1883.255	4	274.1	46.666668	A.R4E1S1Y1P1A1F1R4I1P1M1V1L1I1P1A1.T
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	1	2.4812	0.2184	1084.49	1085.167	1	546	78.57143	F.HWEDVRGW.S
gi|6323861|ref|NP_013932.1|	YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and 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	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	3.229	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
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	4.6706	0.1558	1831.37	1831.122	1	1437.7	51.785713	W.QRTIEFLDENKPVKL.S
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	3.6724	0.2603	1829.81	1831.122	1	513.5	71.42857	W.QRTIEFLDENKPVKL.S
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	4.1136	0.3311	1851.89	1853.122	1	431.7	67.85714	W.Q2R4T1I1E1F1L1D1E1N2K2P1V1K2L1.S
gi|6323873|ref|NP_013944.1|	YMR217W	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 guanine but is negatively regulated by nutrient starvation; Gua1p	2	3.3023	0.1959	1922.25	1923.155	3	262.2	53.333336	F.E1R4E1A1E1K2I1K2P1K2D1G1K2E1I1Q2.F
gi|6323873|ref|NP_013944.1|	YMR217W	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 guanine but is negatively regulated by nutrient starvation; Gua1p	2	3.1001	0.2582	1898.27	1899.155	1	334.9	60.000004	F.EREAEKIKPKDGKEIQ.F
gi|6323873|ref|NP_013944.1|	YMR217W	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 guanine but is negatively regulated by nutrient starvation; Gua1p	3	5.131	0.3047	2186.21	2185.491	3	818.7	39.705883	F.E1R4E1A1E1K2I1K2P1K2D1G1K2E1I1Q2F1L1.L
gi|6323873|ref|NP_013944.1|	YMR217W	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 guanine but is negatively regulated by nutrient starvation; Gua1p	2	4.4679	0.3845	2158.17	2159.491	1	424.7	55.88235	F.EREAEKIKPKDGKEIQFL.L
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	3.4447	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 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	3.8327	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; Rrp5p	2	3.6658	0.3081	1543.51	1543.758	1	593.3	73.07692	H.EDLKQGEIVDGIVK.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	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.K2D1S1V1I1V1E1I1P1D1V1G1L1R4.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	2	4.4752	0.2541	1886.55	1885.208	1	786.7	64.28571	K.D1K2K2K2V1E1D1L1F1E1R4I1I1T1K2.K
gi|6323893|ref|NP_013964.1|	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the 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
gi|6323893|ref|NP_013964.1|	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the trans-Golgi; Bch1p	2	3.8295	0.3844	1795.63	1795.088	1	1645.1	75	K.KITDLFLDTPQIWFG.K
gi|6323893|ref|NP_013964.1|	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the trans-Golgi; Bch1p	2	3.5297	0.3158	2085.69	2086.396	1	604	52.77778	R.RIAPITSDENLHLPLPLDA.S
gi|6323893|ref|NP_013964.1|	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the trans-Golgi; Bch1p	2	3.4194	0.3132	1792.35	1790.112	1	1006.8	60.714287	F.AKKITDLFLDTPQIW.F
gi|6323893|ref|NP_013964.1|	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the 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
gi|6323893|ref|NP_013964.1|	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the trans-Golgi; Bch1p	2	4.441	0.387	1993.69	1994.341	1	812.1	56.25	F.AKKITDLFLDTPQIWFG.K
gi|6323893|ref|NP_013964.1|	YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the trans-Golgi; Bch1p	2	3.8293	0.3717	1812.43	1813.088	1	1247.6	67.85714	K.K2I1T1D1L1F1L1D1T1P1Q2I1W2F1G1.K
gi|6323894|ref|NP_013965.1|	YMR238W	Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored membrane protein required for cell wall biogenesis in bud formation, involved in filamentous growth, homologous to Dcw1p; Dfg5p	2	4.7984	0.4022	1998.15	1999.191	1	730	61.764706	L.LIHDRPAPYKEDNGGTSK.G
gi|6323894|ref|NP_013965.1|	YMR238W	Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored membrane protein required for cell wall biogenesis in bud formation, involved in filamentous growth, homologous to Dcw1p; Dfg5p	2	5.2177	0.4433	2024.77	2025.191	1	668.9	58.823532	L.L1I1H3D1R4P1A1P1Y1K2E1D1N2G1G1T1S1K2.G
gi|6323894|ref|NP_013965.1|	YMR238W	Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored membrane protein required for cell wall biogenesis in bud formation, involved in filamentous growth, homologous to Dcw1p; Dfg5p	3	4.3498	0.3539	2022.68	2025.191	5	727.6	36.764706	L.L1I1H3D1R4P1A1P1Y1K2E1D1N2G1G1T1S1K2.G
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	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
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	1	2.8028	0.1853	1367.71	1368.607	5	278.5	60.000004	K.D1L1K2F1P1L1P1H3R4V1Q2.K
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	1	2.978	0.2011	1350.7	1350.607	2	304.4	60.000004	K.DLKFPLPHRVQ.K
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	3.0778	0.2115	1366.85	1368.607	9	622.2	75	K.D1L1K2F1P1L1P1H3R4V1Q2.K
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	1	3.7127	0.3184	1531.75	1530.777	6	291	54.166668	R.R4L1P1T1E1S1V1P1E1P1K2L1F1.R
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	2	3.8937	0.3253	2177.55	2178.424	1	399.9	44.11765	A.K2D1E1V1E1L1H3F1P1K2P1E1D1P1A1C1I1M1.Y
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	2	4.2879	0.4202	2025.03	2025.349	1	937.8	52.77778	Y.A1D1E1N2K2V1K2P1V1G1I1V1V1P1N2L1G1H3L1.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	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 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	2	4.4878	0.3967	2262.75	2262.657	1	829.7	50	C.VYADENKVKPVGIVVPNLGHL.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	2	4.3788	0.3349	2288.71	2289.657	1	927.3	50	C.V1Y1A1D1E1N2K2V1K2P1V1G1I1V1V1P1N2L1G1H3L1.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	2	4.8105	0.4377	2031.13	2031.403	1	968.2	56.25	A.KDAVDKIKEVRPDIKIY.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	4.7478	0.484	2261.18	2262.657	1	1537	41.25	C.VYADENKVKPVGIVVPNLGHL.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	2	3.6289	0.3298	2227.61	2227.503	1	519.1	50	K.AKDEVELHFPKPEDPACIM.Y
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	2	4.5266	0.3629	2249.45	2250.503	1	580.7	52.77778	K.A1K2D1E1V1E1L1H3F1P1K2P1E1D1P1A1C1I1M1.Y
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	2	3.4907	0.3933	1572.35	1572.805	1	715.2	75	K.RVDGKDKPIEKTW.L
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	2	4.3264	0.2845	1825.73	1826.147	1	1027.3	66.66667	A.AKDAVDKIKEVRPDIK.I
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	2	3.9099	0.4113	2348.01	2349.735	1	1123.2	52.380955	C.VYADENKVKPVGIVVPNLGHLS.K
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	2	4.0679	0.4152	2001.01	2000.349	1	1084.4	58.333332	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	2	4.2383	0.3903	2261.89	2262.657	1	1224.5	60.000004	C.VYADENKVKPVGIVVPNLGHL.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	2	5.3345	0.4583	2102.35	2102.482	1	1301.6	55.88235	A.AKDAVDKIKEVRPDIKIY.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	2	3.5236	0.4268	2155.19	2156.424	1	401.2	44.11765	A.KDEVELHFPKPEDPACIM.Y
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	2	4.5254	0.4314	2087.55	2087.427	1	1130	57.894737	Y.ADENKVKPVGIVVPNLGHLS.K
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	2	3.7801	0.334	2112.49	2113.427	1	664.2	47.368423	Y.A1D1E1N2K2V1K2P1V1G1I1V1V1P1N2L1G1H3L1S1.K
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity 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	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.4337	0.2743	1833.21	1834.05	1	611.7	60.714287	S.AQCPELWIPRDPFGF.S
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.8453	0.3719	2475.59	2476.847	1	311.6	38.636364	L.SKVIPVDTMKPLDGVSDTPSFKN.I
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.6874	0.2893	1745.45	1746.072	1	876.2	60.714287	N.IDMDGIKELPEFPIK.K
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.1475	0.237	1761.55	1763.072	1	935.8	60.714287	N.I1D1M1D1G1I1K2E1L1P1E1F1P1I1K2.K
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	2.9383	0.1691	1815.95	1817.031	2	269.6	53.571426	Q.T1V1P1K2Q2Y1L1S1E1E1E1F1S1K2L1.F
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	3	4.6716	0.2832	1874.06	1874.246	3	1045.1	45	N.IDMDGIKELPEFPIKK.Y
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity 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	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.8016	0.2715	1875.33	1874.246	1	724.4	56.666668	N.IDMDGIKELPEFPIKK.Y
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.3721	0.2282	2057.07	2057.422	2	385.1	46.875	N.I1D1M1D1G1I1K2E1L1P1E1F1P1I1K2K2Y1.H
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.5775	0.3437	1643.39	1645.998	1	601.5	61.538464	D.MDGIKELPEFPIKK.Y
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity 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 NaCl sensitivity of sro7 mutant; Rsn1p	2	3.5786	0.2389	2549.53	2549.947	1	364.5	35.714287	Y.HAPLFM@TPVYIGIEPSDVVWFN.L
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	4.7606	0.4974	2558.53	2559.947	1	493.2	38.095238	Y.H3A1P1L1F1M1T1P1V1Y1I1G1I1E1P1S1D1V1V1W2F1N2.L
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.8824	0.3321	2533.43	2533.947	1	645.4	42.857143	Y.HAPLFMTPVYIGIEPSDVVWFN.L
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.0955	0.1501	1415.11	1414.717	4	514.9	63.636364	D.G1I1K2E1L1P1E1F1P1I1K2K2.Y
gi|6323922|ref|NP_013993.1|	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
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	3	3.8741	0.1984	3215.24	3214.684	1	726	28.57143	L.S1K2V1I1P1V1D1T1M1K2P1L1D1G1V1S1D1T1P1S1F1K2N2I1Y1K2G1I1E1.S
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity 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	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	3	4.7017	0.3083	1578.35	1578.893	1	571.4	45.833336	D.G1I1K2E1L1P1E1F1P1I1K2K2Y1.H
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.6496	0.2288	1922.27	1921.128	1	721.9	63.333332	S.AQCPELWIPRDPFGFS.K
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	2	3.6185	0.382	1764.17	1762.971	1	745.9	69.230774	A.QCPELWIPRDPFGF.S
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity 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 NaCl sensitivity of sro7 mutant; Rsn1p	2	2.9738	0.2214	1780.17	1781.971	1	360.2	46.153847	A.Q2C1P1E1L1W2I1P1R4D1P1F1G1F1.S
gi|6323922|ref|NP_013993.1|	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	1	3.1923	0.4278	1561.81	1562.893	1	446.4	54.166668	D.GIKELPEFPIKKY.H
gi|6323923|ref|NP_013994.1|	YMR267W	Mitochondrial inorganic pyrophosphatase, required for mitochondrial function and possibly involved in energy generation from inorganic pyrophosphate; Ppa2p	2	3.9114	0.3557	1924.63	1923.213	1	835.6	70	S.KIDDLEKIEEYFPGIL.D
gi|6323923|ref|NP_013994.1|	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
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-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

gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	2	3.6918	0.1744	1393.61	1392.701	2	1200.7	85	H.K2F1L1D1L1N2R4P1L1L1M$.Q
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	1	3.555	0.188	1488.87	1488.832	1	530.6	68.181816	H.KFLDLNRPLLMQ.I
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	1	2.908	0.2712	1359.59	1360.701	2	541.1	70	H.KFLDLNRPLLM.Q
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	1	3.1034	0.1588	1505.65	1506.832	2	482	63.636364	H.K2F1L1D1L1N2R4P1L1L1M1Q2.I
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	1	2.5903	0.1662	1231.49	1232.527	1	700.7	77.77778	K.FLDLNRPLLM.Q
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	2	4.0876	0.2004	1488.21	1488.832	1	1370.7	81.818184	H.KFLDLNRPLLMQ.I
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	2	4.1763	0.1537	1507.53	1506.832	1	1631.3	86.36364	H.K2F1L1D1L1N2R4P1L1L1M1Q2.I
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	2	3.6082	0.1707	1360.13	1360.701	6	1442	85	H.KFLDLNRPLLM.Q
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	2	2.9966	0.2541	1481.27	1480.808	8	432.8	59.090908	M.DKYRLVMPPTLF.V
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	2	3.4788	0.2459	1358.85	1360.701	8	1270.7	80	H.KFLDLNRPLLM.Q
gi|6323928|ref|NP_013999.1|	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	1	2.8386	0.3255	1359.83	1360.701	1	567.5	70	H.KFLDLNRPLLM.Q
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	2	3.6736	0.2727	1792.07	1792.042	1	821.3	64.28571	S.KVPLNEYEFPENKIA.N
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	2	3.5395	0.1908	1810.29	1811.042	1	642.9	53.571426	S.K2V1P1L1N2E1Y1E1F1P1E1N2K2I1A1.N
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	3	5.2575	0.2761	2449.22	2449.728	1	835.5	38.157894	I.D1E1A1D1R4I1L1E1I1G1F1E1D1E1M1R4Q2I1I1K2.I
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	3	5.1246	0.2838	2421.26	2421.728	1	760.1	35.526314	I.DEADRILEIGFEDEMRQIIK.I
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	3	6.3762	0.3554	2676.29	2678.047	1	1443.9	41.666664	L.I1I1D1E1A1D1R4I1L1E1I1G1F1E1D1E1M1R4Q2I1I1K2.I
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	3	6.4289	0.3167	2648.33	2648.047	1	1856.2	45.238094	L.IIDEADRILEIGFEDEMRQIIK.I
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	3	6.6049	0.3564	2679.2	2678.047	1	1322.8	41.666664	L.I1I1D1E1A1D1R4I1L1E1I1G1F1E1D1E1M1R4Q2I1I1K2.I
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	2	3.346	0.2194	2678.55	2678.047	1	491.9	40.476192	L.I1I1D1E1A1D1R4I1L1E1I1G1F1E1D1E1M1R4Q2I1I1K2.I
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	3	4.5175	0.2267	2330.9	2333.639	3	661.3	36.11111	D.E1A1D1R4I1L1E1I1G1F1E1D1E1M1R4Q2I1I1K2.I
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	3	4.2793	0.2389	2824.19	2826.182	4	583.4	29.545454	L.E1I1G1F1E1D1E1M1R4Q2I1I1K2I1L1P1N2E1D1R4Q2S1M1.L
gi|6323947|ref|NP_014017.1|	YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	1	2.3449	0.1595	1348.46	1348.616	2	177.4	50	L.K2F1K2P1R4N2G1T1G1I1I1V1.I
gi|6323954|ref|NP_014025.1|	YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	2	4.0573	0.3452	2170.65	2170.557	1	891.8	52.941177	N.ELTEQEKLEKLPAIPRKF.I
gi|6323954|ref|NP_014025.1|	YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	2	4.3793	0.4166	2193.69	2195.557	1	1064.1	58.823532	N.E1L1T1E1Q2E1K2L1E1K2L1P1A1I1P1R4K2F1.I
gi|6323954|ref|NP_014025.1|	YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	3	5.03	0.1568	2312.9	2311.661	7	657.3	38.88889	L.N2E1L1T1E1Q2E1K2L1E1K2L1P1A1I1P1R4K2F1.I
gi|6323954|ref|NP_014025.1|	YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	2	5.0839	0.3383	2310.37	2311.661	1	1053.8	55.555557	L.N2E1L1T1E1Q2E1K2L1E1K2L1P1A1I1P1R4K2F1.I
gi|6323954|ref|NP_014025.1|	YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	2	4.1429	0.2552	2286.15	2284.661	1	985.7	52.77778	L.NELTEQEKLEKLPAIPRKF.I
gi|6323954|ref|NP_014025.1|	YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	2	3.363	0.2722	1927.99	1928.282	1	1128	66.66667	L.TEQEKLEKLPAIPRKF.I
gi|6323954|ref|NP_014025.1|	YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	3	4.3917	0.2141	2171.06	2170.557	2	681.2	39.705883	N.ELTEQEKLEKLPAIPRKF.I
gi|6323954|ref|NP_014025.1|	YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first 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

gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.9927	0.4035	1917.37	1917.974	1	1170.8	71.42857	R.I1T1R4D1Y1E1P1N2D1E1H3L1S1F1C1.I
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	3	4.462	0.4336	2995.7	2997.227	1	502.5	27.000002	F.C1I1I1E1N2D1N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1Y1V1A1.Y
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.607	0.2695	1915.59	1917.023	1	567.2	53.571426	K.R4I1T1R4D1Y1E1P1N2D1E1H3L1S1F1.C
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.7058	0.4201	2245.31	2245.461	1	736.2	52.63158	D.N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1Y1V1A1.Y
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.026	0.2926	2331.51	2332.577	1	309.4	38.88889	N.Y1E1W2F1H3C1T1P1I1K2E1P1Q2S1G1S1V1I1K2.L
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	3	4.5126	0.2661	2535.65	2534.84	1	990.6	35	R.INYEWFHCTPIKEPQSGSVIK.L
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.7211	0.3735	2383.41	2382.637	1	341.4	42.5	D.NVPPVHYPIHEDKGEPGYVAY.V
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	3	4.3073	0.2493	2561.48	2562.84	1	1172	40	R.I1N2Y1E1W2F1H3C1T1P1I1K2E1P1Q2S1G1S1V1I1K2.L
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.6828	0.4627	2532.79	2534.84	1	1105.1	52.499996	R.INYEWFHCTPIKEPQSGSVIK.L
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	3	4.7604	0.2654	2650.25	2648	1	780.6	32.142857	R.INYEWFHCTPIKEPQSGSVIKL.W
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.8023	0.3876	2675.45	2677	1	680.6	40.476192	R.I1N2Y1E1W2F1H3C1T1P1I1K2E1P1Q2S1G1S1V1I1K2L1.W
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.0279	0.2441	2151.43	2152.445	1	623.8	52.941177	E.W2F1H3C1T1P1I1K2E1P1Q2S1G1S1V1I1K2L1.W
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	3	4.6447	0.2785	3001.88	3000.264	1	480.7	26	C.I1I1E1N2D1N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1Y1V1A1Y1.V
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.3457	0.3996	2998.57	3000.264	1	286.1	28	C.I1I1E1N2D1N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1Y1V1A1Y1.V
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.7115	0.1701	2534.17	2534.84	1	930.1	50	R.INYEWFHCTPIKEPQSGSVIK.L
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	3	3.9748	0.2248	2420.03	2420.736	1	1020.1	36.842106	N.YEWFHCTPIKEPQSGSVIKL.W
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows 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
gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	3.8685	0.4099	1907.73	1909.074	1	327.5	59.375	D.N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1.Y

gi|6323956|ref|NP_014027.1|	YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	2	4.1882	0.4697	2407.77	2409.637	1	326.3	42.5	D.N2V1P1P1V1H3Y1P1I1H3E1D1K2G1E1P1G1Y1V1A1Y1.V
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	1	2.586	0.2784	1051.64	1052.335	1	367.8	61.11111	R.G1L1V1K2S1P1I1K2V1V1.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	1	3.6608	0.2856	1531.91	1530.81	1	615.6	61.538464	W.HGDWPLPTKLPLVG.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.3583	0.3535	1532.97	1530.81	1	1662.3	73.07692	W.HGDWPLPTKLPLVG.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	1	2.2786	0.2622	1209.63	1210.546	2	391.8	54.545456	R.GLVKSPIKVVGL.S
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.3045	0.4226	1984.69	1982.249	1	1089	58.333332	W.HGDWPLPTKLPLVGGHEGA.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	3	5.7004	0.3212	1856.42	1854.119	1	2096.9	56.25	W.HGDWPLPTKLPLVGGHE.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	1	2.2794	0.2457	1039.63	1040.335	2	371.2	61.11111	R.GLVKSPIKVV.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	1	2.6647	0.1672	1223.68	1224.546	2	398.2	54.545456	R.G1L1V1K2S1P1I1K2V1V1G1L1.S
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.4865	0.4029	2141.15	2138.434	1	1097.7	57.5	W.HGDWPLPTKLPLVGGHEGAGV.V
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	5.2313	0.339	1879.79	1877.119	1	905.1	65.625	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	3	4.7776	0.3358	2167.46	2165.434	1	1391.9	40	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1G1A1G1V1.V
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	3.0002	0.2542	1855.65	1854.119	1	437.1	46.875	W.HGDWPLPTKLPLVGGHE.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	3	3.8835	0.2409	2009.9	2007.249	1	978.2	40.27778	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1G1A1.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	2.903	0.3122	1041.33	1040.335	6	576.7	77.77778	R.GLVKSPIKVV.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	3.725	0.3362	1377.55	1374.626	1	844.7	72.72727	W.HGDWPLPTKLPL.V
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.1469	0.326	1609.83	1606.862	1	1196.3	64.28571	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1.H
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.2282	0.3768	1551.37	1548.81	1	1458.3	69.230774	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.6076	0.4271	1533.63	1530.81	1	1582.2	73.07692	W.HGDWPLPTKLPLVG.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.1629	0.3169	1590.45	1587.862	1	1010.1	60.714287	W.HGDWPLPTKLPLVGG.H
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.1781	0.2032	1748.59	1747.003	1	1464.4	66.66667	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3.E
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	3	4.2899	0.2516	1983.86	1982.249	1	981.5	43.055553	W.HGDWPLPTKLPLVGGHEGA.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	3.9423	0.3421	1984.47	1982.249	1	475.4	52.77778	W.HGDWPLPTKLPLVGGHEGA.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	3	5.348	0.3145	1879.07	1877.119	1	1847.7	54.6875	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.1147	0.3858	2009.61	2007.249	1	1287.2	61.11111	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1G1A1.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	4.262	0.3376	1727.63	1725.003	1	1265.4	66.66667	W.HGDWPLPTKLPLVGGH.E
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	3.6984	0.2222	1879.47	1877.119	1	752.8	59.375	W.H3G1D1W2P1L1P1T1K2L1P1L1V1G1G1H3E1.G
gi|6323961|ref|NP_014032.1|	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	2	3.2825	0.3375	1855.15	1854.119	1	715.1	53.125	W.HGDWPLPTKLPLVGGHE.G
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	2.9165	0.3253	1592.41	1592.748	1	962.5	70.83333	S.INRDDPTWTVDLF.N
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	3.2901	0.3135	1680.27	1679.827	1	989.5	69.230774	T.SINRDDPTWTVDLF.N
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	2.9695	0.331	2090.25	2091.285	1	272.6	41.666664	L.AAPATSINRDDPTWTVDLF.N
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	2.9692	0.2277	1700.67	1698.827	1	542.9	53.846157	T.S1I1N2R4D1D1P1T1W2T1V1D1L1F1.N

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	1	2.825	0.2482	1123.56	1124.301	1	199.8	68.75	K.N2Y1R4K2I1P1V1G1Y1.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	1	2.9565	0.2058	1552.8	1553.801	1	279.5	54.166668	Y.ISDKNYRKIPVGY.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	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
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	2.9467	0.3536	1553.11	1553.801	1	698.3	70.83333	Y.ISDKNYRKIPVGY.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	1	3.7181	0.3673	1552.68	1553.801	1	321.2	58.333332	Y.ISDKNYRKIPVGY.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	1	3.3756	0.2795	1571.74	1572.801	1	286.2	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	3.2133	0.257	1575.47	1572.801	2	601.7	66.66667	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	1	2.5598	0.2631	1109.56	1110.301	1	229.9	68.75	K.NYRKIPVGY.S
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	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
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	3	4.3194	0.3745	2529.74	2529.737	1	295	30.952381	F.A1D1P1I1D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.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	3	4.4861	0.1955	2317.55	2316.57	1	1281.9	42.105263	D.PIDFIEDEPKEDSDGVKRIL.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	4.0273	0.3266	2531.49	2529.737	1	409.7	42.857143	F.A1D1P1I1D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.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	3	3.8397	0.2766	2838.29	2836.081	1	438.6	28.125	N.EFADPIDFIEDEPKEDSDGVKRILG.S
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	3	4.8449	0.3239	2341.55	2341.57	1	1826	44.736843	D.P1I1D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.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	3.7153	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
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	4.5624	0.3786	1754.47	1754.008	1	1472.7	76.92308	A.KEKLLDEMQDVYNK.I
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	3.8109	0.2863	1954.19	1954.246	1	510.6	56.666668	A.KEKLLDEMQDVYNKIS.Q
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	3	4.0037	0.2087	1956.2	1954.246	1	731.6	45	A.KEKLLDEMQDVYNKIS.Q
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	3.757	0.4018	2025.61	2025.325	1	583.3	56.25	S.AKEKLLDEMQDVYNKIS.Q
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	3	4.0111	0.3034	2027.6	2025.325	1	562.7	43.75	S.AKEKLLDEMQDVYNKIS.Q
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	3.2903	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
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	3.8833	0.3255	2530.17	2529.737	1	375	47.61905	F.A1D1P1I1D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.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	3.8595	0.241	1775.63	1773.008	1	931	73.07692	A.K2E1K2L1L1D1E1M1Q2D1V1Y1N2K2.I
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	3.687	0.2013	1175.21	1173.456	1	1191.2	83.33333	C.SLLIEIPRMT.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	4.0165	0.2089	1185.63	1186.456	1	1133.8	83.33333	C.S1L1L1I1E1I1P1R4M1T1.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	3.3871	0.2187	1527.67	1526.73	1	646	72.72727	A.K2E1K2L1L1D1E1M1Q2D1V1Y1.N
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	3.947	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
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	3	3.8921	0.1857	2129.18	2129.294	2	918.4	41.17647	I.D1F1I1E1D1E1P1K2E1D1S1D1G1V1K2R4I1L1.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	3	4.3287	0.3059	2807.12	2808.03	1	574.1	31.52174	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	3.5866	0.2621	1599.51	1598.809	2	401.2	58.333332	S.A1K2E1K2L1L1D1E1M1Q2D1V1Y1.N
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	1	2.6412	0.1543	1195.45	1196.337	3	149.9	62.5	G.N2W2R4D1S1V1K2Y1L1.R
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	1	2.9772	0.3784	1482.56	1483.618	2	227.7	42.307693	L.HSLGEELDQLTGIA.C
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	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 translation 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.-
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	3.7065	0.3353	1635.65	1635.678	1	742.4	65.38461	L.KYPLPDLDEDDGEE.-
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	4.2439	0.4089	1877.21	1878.997	1	1057.2	70	C.I1L1K2Y1P1L1P1D1L1D1E1D1D1G1E1E1.-
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	3.8488	0.4567	1861.15	1861.997	1	1193.7	70	C.ILKYPLPDLDEDDGEE.-
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	2	4.1453	0.3726	1847.33	1848.065	1	1086	63.333332	A.ALKYHPDKPTGDTEKF.K

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	2	3.6375	0.2896	1681.31	1682.827	1	850	61.538464	L.K2Y1H3P1D1K2P1T1G1D1T1E1K2F1.K
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	2	3.2703	0.3467	1956.85	1959.103	1	292.7	53.333336	Q.E1K2S1H3P1N2F1K2R4D1G1D1D1L1I1Y1.T
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	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.T1R4I1P1D1I1D1L1I1V1I1R4.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.R4I1P1D1I1D1L1I1V1I1R4E1.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.R4I1P1D1I1D1L1I1V1I1R4.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.R4I1P1D1I1D1L1I1V1I1R4.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.R4I1P1D1I1D1L1I1V1I1R4.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.R4I1P1D1I1D1L1I1V1I1R4.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.KLGDGLFRNIITEIGQK.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.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	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.R4I1P1D1I1D1L1I1V1I1R4.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	1	2.7028	0.1945	1339.71	1340.622	4	217.2	60.000004	T.R4I1P1D1I1D1L1I1V1I1R4.E
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	2	3.1629	0.1699	1578.65	1578.808	1	767.2	75	T.KDPLRYPNLSDLF.L
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	1	3.0503	0.2437	1572.64	1572.916	1	249.9	57.692307	L.K2N2L1P1D1S1V1S1P1I1K2L1I1M1.A
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	2	3.8795	0.3316	1668.59	1669.076	1	534.2	64.28571	F.LKNLPDSVSPIKLIM.A
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	2	5.427	0.3445	2166.43	2167.479	1	1921.7	71.875	L.KFDKDWENFVLNPICKL.L
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	2	6.2968	0.4694	2190.27	2190.479	1	2213.2	75	L.K2F1D1K2D1W2E1N2F1V1L1N2P1I1C1K2L1.L
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	2	3.5699	0.1519	1839.91	1841.098	5	526.7	53.571426	T.K2D1P1L1R4Y1P1N2L1S1D1L1F1L1Q2.I
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	2	3.9819	0.2838	1819.33	1820.098	1	629	60.714287	T.KDPLRYPNLSDLFLQ.I
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	2	3.5795	0.1886	1691.43	1691.968	2	690.2	69.230774	T.KDPLRYPNLSDLFL.Q
gi|6324280|ref|NP_014350.1|	YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	2	3.4872	0.173	1708.31	1710.968	1	834	73.07692	T.K2D1P1L1R4Y1P1N2L1S1D1L1F1L1.Q
gi|6324279|ref|NP_014349.1|	YNL049C	Probable component of COPII coated vesicles that binds to Sec23p; similar to and functionally redundant with Sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy; Sfb2p	2	3.7779	0.3552	1826.25	1826.021	2	539.9	53.571426	C.RFKNDVPFGFDQNLQ.G
gi|6324279|ref|NP_014349.1|	YNL049C	Probable component of COPII coated vesicles that binds to Sec23p; similar to and functionally redundant with Sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy; Sfb2p	2	3.8148	0.3461	1670.83	1671.894	1	841.1	64.28571	L.YIIRGPSINEPANLN.S
gi|6324279|ref|NP_014349.1|	YNL049C	Probable component of COPII coated vesicles that binds to Sec23p; similar to and functionally redundant with Sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy; Sfb2p	2	3.8465	0.323	1703.09	1704.833	1	1114.5	71.42857	L.H3D1M1P1D1E1V1G1L1P1D1F1E1G1K2.T
gi|6324279|ref|NP_014349.1|	YNL049C	Probable component of COPII coated vesicles that binds to Sec23p; similar to and functionally redundant with Sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy; Sfb2p	2	4.6932	0.3633	1906.27	1907.071	1	845.9	53.125	Y.S1L1H3D1M1P1D1E1V1G1L1P1D1F1E1G1K2.T
gi|6324278|ref|NP_014348.1|	YNL050C	hypothetical protein; Ynl050cp	2	2.9225	0.2159	1700.69	1700.885	2	494	62.5	Q.KEEKQEEFEFPLF.S
gi|6324278|ref|NP_014348.1|	YNL050C	hypothetical protein; Ynl050cp	2	3.0275	0.1819	1935.13	1935.14	1	629	53.571426	Q.KEEKQEEFEFPLFSF.G
gi|6324278|ref|NP_014348.1|	YNL050C	hypothetical protein; Ynl050cp	2	3.7044	0.2553	1717.49	1716.885	1	733	75	Q.K2E1E1K2Q2E1E1F1E1F1P1L1F1.S
gi|6324278|ref|NP_014348.1|	YNL050C	hypothetical protein; Ynl050cp	2	4.6555	0.3754	1954.03	1953.14	1	1105.3	71.42857	Q.K2E1E1K2Q2E1E1F1E1F1P1L1F1S1F1.G
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.3845	0.2132	1550.11	1551.706	1	812.8	75	T.M1N2C1K2L1P1N2S1N2V1N2I1E1.F
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.3971	0.4433	1709.81	1710.85	1	1154.4	67.85714	M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1.L
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.8369	0.2596	1690.53	1690.85	1	1612.1	75	M.SPPVYSDISRNINDL.L
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.3104	0.2398	1916.57	1918.114	1	388	50	M.SPPVYSDISRNINDLLN.K
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.1564	0.2945	1805.55	1804.01	1	877.9	70	M.SPPVYSDISRNINDLL.N
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.7701	0.4317	1750.79	1751.961	1	1111	64.28571	T.MNCKLPNSNVNIEFA.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.3445	0.3817	1698.63	1699.882	1	1079.4	69.230774	T.M1N2C1K2L1P1N2S1N2V1N2I1E1F1.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	1	2.3567	0.2524	1310.44	1309.563	1	457.6	54.545456	C.LKSPTFVGDLTM.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.5733	0.2193	1977.79	1977.181	4	719.8	56.25	P.PVYSDISRNINDLLNKD.F
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	5.056	0.3476	2071.07	2071.288	1	1643.2	70.588234	M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2.D
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.3633	0.3623	2160.33	2161.376	1	829	55.555557	M.SPPVYSDISRNINDLLNKD.F
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.4348	0.2236	2187.19	2187.376	1	1080.1	58.333332	M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1.F
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.3993	0.1503	1375.23	1372.534	2	399.6	70.83333	K.A1K2Q2P1V1K2D1G1P1L1S1T1N2.V
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	1	2.5018	0.211	1354.57	1355.534	1	159.1	58.333332	K.AKQPVKDGPLSTN.V

gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	1	2.7477	0.2366	1371.45	1372.534	2	203.8	62.5 K.A1K2Q2P1V1K2D1G1P1L1S1T1N2.V
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	5.5085	0.4267	2981.45	2984.249	1	639.1	31 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.9307	0.2712	2981.77	2984.249	1	479.8	36 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	5.281	0.4326	2709.41	2711.949	1	693.7	45.454548 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	5.0752	0.373	3753.02	3755.067	1	1024.3	23.4375 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1A1F1D1V1Q2T1T1.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.7774	0.2821	3552.65	3550.857	2	580.9	23.333334 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1A1F1D1V1Q2.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	2.9952	0.2438	1356.39	1355.534	2	339.6	62.5 K.AKQPVKDGPLSTN.V
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.5292	0.2675	2445.37	2445.819	1	535	45.238094 N.NLQTKLEFANLTPGLKNELITS.L
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.6201	0.3803	2384.73	2385.74	1	901.5	50 N.N2L1Q2T1K2L1E1F1A1N2L1T1P1G1L1K2N2E1L1I1T1.S
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.1492	0.316	2947.81	2949.249	1	581.3	40 M.SPPVYSDISRNINDLLNKDFYHATPA.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.7603	0.2669	2679.81	2679.949	2	691.5	45.454548 M.SPPVYSDISRNINDLLNKDFYHA.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.3529	0.33	2766.17	2765.054	2	412.9	30.434782 P.PVYSDISRNINDLLNKDFYHATPA.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	5.6272	0.4078	3204.05	3204.505	1	764.1	26.85185 M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1A1F1.D
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.5841	0.3922	1782.67	1783.035	1	487.9	59.375 K.AKQPVKDGPLSTNVEAK.L
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.7889	0.272	2358.63	2358.74	1	565	42.5 N.NLQTKLEFANLTPGLKNELIT.S
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.6176	0.3459	1758.41	1756.924	1	1117.2	76.92308 S.R4N2I1N2D1L1L1N2K2D1F1Y1H3A1.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	3.8539	0.1825	3412.55	3414.924	1	740.3	24.193548 N.TNNLQTKLEFANLTPGLKNELITSLTPGVAKS.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.2664	0.204	3528.38	3529.028	1	659.8	24.21875 W.SNTNNLQTKLEFANLTPGLKNELITSLTPGVAK.S
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	6.1724	0.4371	3731.15	3731.185	1	1468.6	27.941175 W.S1N2T1N2N2L1Q2T1K2L1E1F1A1N2L1T1P1G1L1K2N2E1L1I1T1S1L1T1P1G1V1A1K2S1A1.V
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.7526	0.3087	3485.33	3486.003	1	957	25.78125 N.TNNLQTKLEFANLTPGLKNELITSLTPGVAKSA.V
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.5379	0.3633	3146.6	3148.637	2	517.3	25 N.N2L1Q2T1K2L1E1F1A1N2L1T1P1G1L1K2N2E1L1I1T1S1L1T1P1G1V1A1K2.S
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.2618	0.2948	3271.58	3270.794	1	726	26.666668 N.NLQTKLEFANLTPGLKNELITSLTPGVAKSA.V
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.609	0.351	1620.35	1620.769	1	779.1	69.230774 M.NCKLPNSNVNIEFA.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.4685	0.2903	1638.63	1639.769	1	604.6	57.692307 M.N2C1K2L1P1N2S1N2V1N2I1E1F1A1.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.5608	0.2944	1549.63	1549.69	1	1195.5	70.83333 M.NCKLPNSNVNIEF.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.739	0.3575	1772.27	1771.961	1	758.7	60.714287 T.M1N2C1K2L1P1N2S1N2V1N2I1E1F1A1.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.5959	0.2431	1681.35	1680.882	1	931	65.38461 T.MNCKLPNSNVNIEF.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	3.199	0.2985	1524.37	1523.665	2	490.5	58.333332 N.C1K2L1P1N2S1N2V1N2I1E1F1A1.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.8243	0.4363	2679.83	2679.949	1	513.4	30.681818 M.SPPVYSDISRNINDLLNKDFYHA.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	2.9967	0.2284	1237.97	1237.405	2	716.8	70 L.CLKSPTFVGDL.T

gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	1	2.2271	0.1815	1007.49	1008.122	1	377.4	64.28571	L.LNKDFYHA.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.8902	0.4446	2710.55	2711.949	1	655.4	30.681818	M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.4431	0.2913	2948.57	2949.249	6	316.9	23	M.SPPVYSDISRNINDLLNKDFYHATPA.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	3	4.249	0.2956	2982.62	2984.249	1	545.5	27.000002	M.S1P1P1V1Y1S1D1I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1T1P1A1.A
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	2	4.3314	0.2885	1960.01	1959.162	1	724.9	60.000004	D.I1S1R4N2I1N2D1L1L1N2K2D1F1Y1H3A1.T
gi|6324273|ref|NP_014343.1|	YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein 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
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	4.3486	0.4207	2096.37	2097.166	1	1313.6	67.64706	L.SKKLDEEEAEEAEEAEME.L
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	3.2005	0.2176	1352.45	1352.533	1	631	72.72727	Y.D1A1R4E1F1P1K2V1I1G1G1F1.D
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	4.8079	0.3868	2672.57	2672.857	1	811.2	45.238094	S.RKEEEEVVEEDKDLPEVDLEEL.S
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 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
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	4.6218	0.2659	2424.35	2423.515	1	1648.5	52.499996	K.KLDEEEAEEAEEAEMELVEAE.N
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	3.1896	0.2928	1442.55	1440.645	2	700.3	66.66667	L.VNRGVNLQPIGSW.T
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	4.972	0.3529	2117.27	2117.166	1	1203.1	58.823532	L.S1K2K2L1D1E1E1E1A1E1E1A1E1E1A1E1M1E1.L
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	5.1575	0.3706	2699.83	2699.857	1	805.7	45.238094	S.R4K2E1E1E1E1V1V1E1E1D1K2D1L1P1E1V1D1L1E1E1L1.S
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 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
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	3.0877	0.2644	1811.41	1812.079	1	461.7	53.571426	K.VSRTEKDFIQIPHLQ.K
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	4.0825	0.3438	1882.27	1881.914	1	1514.4	73.333336	K.KLDEEEAEEAEEAEME.L
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 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
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	3.5922	0.3419	1458.61	1460.645	1	982.5	83.33333	L.V1N2R4G1V1N2L1Q2P1I1G1S1W2.T
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	3	4.0193	0.2778	2700.65	2699.857	1	531.1	33.333336	S.R4K2E1E1E1E1V1V1E1E1D1K2D1L1P1E1V1D1L1E1E1L1.S
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	3	3.8964	0.208	2672.78	2672.857	1	692.7	34.523808	S.RKEEEEVVEEDKDLPEVDLEEL.S
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 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
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	3	4.3294	0.2791	1625.3	1625.868	1	1391.3	54.166668	S.RTEKDFIQIPHLQ.K
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	4.8274	0.4121	2944.25	2945.969	1	581.9	39.583336	S.LFDDEEDDDEAGLVDEELKDEFDLE.Q
gi|6324268|ref|NP_014338.1|	YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	2	4.7364	0.3133	2971.13	2971.969	1	649.1	39.583336	S.L1F1D1D1E1E1D1D1D1E1A1G1L1V1D1E1E1L1K2D1E1F1D1L1E1.Q
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	1	2.3196	0.2314	1295.74	1296.571	1	351.1	62.5	V.GIVPGEVIAPGMR.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; Ydj1p	1	2.5323	0.1714	1311.56	1312.571	1	383.1	58.333332	V.G1I1V1P1G1E1V1I1A1P1G1M1R4.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; Ydj1p	1	2.2639	0.2198	1123.65	1124.409	1	442.5	60.000004	W.LKVGIVPGEVI.A
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	3.078	0.314	1583.35	1582.668	1	567.7	66.66667	T.G1D1I1I1D1P1K2D1R4C1K2S1C1.N
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	1	2.7609	0.2919	1426.57	1426.48	1	310.6	54.545456	F.K2R4D1G1D1D1L1V1Y1E1A1E1.I

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	3	3.8868	0.3479	1890.2	1891.047	1	1172.8	46.666668	L.KYHPDKNPSEEAAEKF.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; Ydj1p	2	4.9676	0.5253	2074.07	2075.285	1	1413.3	64.70589	C.ALKYHPDKNPSEEAAEKF.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; Ydj1p	3	5.2105	0.3701	2100.14	2099.285	1	1367	48.52941	C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	1	3.334	0.2869	1596.86	1597.767	1	446.7	66.66667	K.FTIKFPENHFTSE.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	4.728	0.3983	1913.97	1913.047	1	1191.3	70	L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	2	4.2543	0.4223	1892.03	1891.047	1	1470.3	73.333336	L.KYHPDKNPSEEAAEKF.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; Ydj1p	2	4.2825	0.4156	2026.53	2027.349	1	555.6	52.941177	L.EVHVEPGMKDGQRIVFKG.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	3.8696	0.2602	1994.45	1995.297	1	578.6	59.375	L.E1V1H3V1E1P1G1M1K2D1G1Q2R4I1V1F1K2.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	3.3155	0.3356	1523.59	1523.877	1	668.5	67.85714	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; Ydj1p	3	3.926	0.2219	1912.4	1913.047	1	1009	43.333332	L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	2	5.6759	0.4487	2098.35	2099.285	1	1410.5	64.70589	C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	1	4.0835	0.5011	1522.67	1523.877	1	548.8	64.28571	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; Ydj1p	2	5.3696	0.4536	2347.51	2347.742	1	1217.2	54.761906	E.H3V1S1G1D1W2L1K2V1G1I1V1P1G1E1V1I1A1P1G1M1R4.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; Ydj1p	3	4.0079	0.3794	1893.8	1891.047	1	930.7	46.666668	L.KYHPDKNPSEEAAEKF.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; Ydj1p	1	3.2142	0.2379	1465.72	1466.591	2	219.7	50	F.T1I1K2F1P1E1N2H3F1T1S1E1.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	1	3.1091	0.349	1449.61	1450.591	3	207.8	50	F.TIKFPENHFTSE.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	3.0663	0.1886	1861.57	1859.966	7	346.6	50	C.HGTGDIIDPKDRCKSC.N
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	3.9877	0.3765	1613.77	1614.767	1	1014.6	75	K.F1T1I1K2F1P1E1N2H3F1T1S1E1.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	4.3046	0.3912	1892.25	1891.047	1	1243.7	70	L.KYHPDKNPSEEAAEKF.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; Ydj1p	2	4.7249	0.3576	1911.65	1913.047	1	1059.9	66.66667	L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	2	5.8082	0.4399	2100.55	2099.285	1	1133.9	61.764706	C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	3	4.8848	0.3416	2101.64	2099.285	1	1731.8	48.52941	C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	1	3.011	0.4524	1522.71	1523.877	1	493.3	57.14286	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; Ydj1p	3	4.0344	0.3178	1912.91	1913.047	7	428.3	35	L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	2	4.3601	0.3913	1822.89	1823.25	1	1131.8	68.75	D.WLKVGIVPGEVIAPGMR.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; Ydj1p	3	4.999	0.338	1847.93	1845.25	1	1553.9	48.4375	D.W2L1K2V1G1I1V1P1G1E1V1I1A1P1G1M1R4.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; Ydj1p	3	4.1585	0.308	1823.15	1823.25	1	1275.1	45.3125	D.WLKVGIVPGEVIAPGMR.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; Ydj1p	2	3.466	0.2017	1410.45	1412.703	1	512.3	61.538464	K.V1G1I1V1P1G1E1V1I1A1P1G1M1R4.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; Ydj1p	2	4.0954	0.3683	1890.89	1891.047	1	1359	70	L.KYHPDKNPSEEAAEKF.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; Ydj1p	3	4.5157	0.3532	1890.71	1891.047	1	895.3	46.666668	L.KYHPDKNPSEEAAEKF.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; Ydj1p	3	5.0373	0.3615	1915.82	1913.047	1	1267.2	50	L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	2	5.57	0.4352	2099.85	2099.285	1	1497.8	67.64706	C.A1L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	2	4.3204	0.3337	2155.31	2156.464	1	698.6	58.333332	L.EVHVEPGMKDGQRIVFKGE.A
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	4.5759	0.328	1911.19	1913.047	1	1324.9	70	L.K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; Ydj1p	2	3.1526	0.2844	2025.11	2027.207	1	499.7	50	A.L1K2Y1H3P1D1K2N2P1S1E1E1A1A1E1K2F1.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; 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 HSP90 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	L.E1V1H3V1E1P1G1M1K2D1G1Q2R4I1V1F1K2G1.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; Ydj1p	1	3.9202	0.4939	1522.82	1523.877	1	600.1	67.85714	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; Ydj1p	1	4.1776	0.4479	1541.63	1542.877	1	647.3	67.85714	L.K2V1G1I1V1P1G1E1V1I1A1P1G1M1R4.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; Ydj1p	2	3.2776	0.1951	1791.81	1793.184	1	445.8	60.000004	L.E1E1I1L1P1P1R4I1V1P1A1I1P1K2K2A1.T
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	4.2038	0.3607	1820.91	1823.25	1	1157.4	65.625	D.WLKVGIVPGEVIAPGMR.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; Ydj1p	2	5.0701	0.5001	1843.73	1845.25	1	1220.4	71.875	D.W2L1K2V1G1I1V1P1G1E1V1I1A1P1G1M1R4.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; Ydj1p	3	4.3966	0.3542	1821.17	1823.25	1	1509.9	48.4375	D.WLKVGIVPGEVIAPGMR.K
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	5.2201	0.4046	1952.25	1951.061	1	1521.6	64.70589	K.K2E1G1D1Q2L1S1P1G1E1V1I1A1E1I1E1T1D1.K
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.577	0.3962	1914.09	1913.051	1	1883.5	67.64706	A.TVERVAVEDAAAENGFSF.D
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	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 acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.3314	0.1867	1807.39	1805.168	1	688.9	59.375	K.ILVPEGTKDIPVNKPIA.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.3795	0.2095	1769.97	1771.166	1	825.8	67.85714	M.KELKTVIENPLEMLL.-
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.5204	0.1674	1788.49	1789.166	1	784.1	67.85714	M.K2E1L1K2T1V1I1E1N2P1L1E1M1L1L1.-
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	1	2.4208	0.2395	1415.65	1416.666	2	240.6	55	Y.WLPNENVIRKF.K
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	3	5.0962	0.254	1936.28	1933.342	1	1684.6	52.941177	A.KILVPEGTKDIPVNKPIA.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.9681	0.4853	2218.47	2219.651	1	903	52.63158	A.K2I1L1V1P1E1G1T1K2D1I1P1V1N2K2P1I1A1V1Y1.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	3.1131	0.297	2052.83	2055.475	1	496.9	55.555557	A.K2I1L1V1P1E1G1T1K2D1I1P1V1N2K2P1I1A1V1.Y
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	2.93	0.2318	1760.49	1761.025	3	397.4	46.666668	V.P1E1G1T1K2D1I1P1V1N2K2P1I1A1V1Y1.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	3.1684	0.1855	1429.63	1430.717	1	983.7	77.27273	L.K2T1V1I1E1N2P1L1E1M$L1L1.-
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	1	3.7983	0.4036	1480.77	1481.645	1	1284.8	70.83333	Y.VEDKADVPAFKDF.K
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	1	3.9785	0.2711	1495.55	1496.645	1	1001	62.5	Y.V1E1D1K2A1D1V1P1A1F1K2D1F1.K
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase 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	L.K2T1V1I1E1N2P1L1E1M1L1L1.-

gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.39	0.2287	1512.79	1513.876	1	1773.1	83.33333	E.LKTVIENPLEMLL.-
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	5.0075	0.3789	2183.01	2183.34	1	1273	52.63158	W.T1K2K2E1G1D1Q2L1S1P1G1E1V1I1A1E1I1E1T1D1.K
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	3.3562	0.2877	2067.65	2067.477	5	385.1	38.88889	K.ILVPEGTKDIPVNKPIAVY.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.4414	0.3727	2091.65	2089.477	1	694.3	50	K.I1L1V1P1E1G1T1K2D1I1P1V1N2K2P1I1A1V1Y1.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.0323	0.3816	1931.95	1933.342	1	774.3	55.88235	A.KILVPEGTKDIPVNKPIA.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	3.9564	0.4711	2194.91	2195.651	1	654.8	47.368423	A.KILVPEGTKDIPVNKPIAVY.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	3.5824	0.3033	1400.45	1400.717	1	703.2	86.36364	L.KTVIENPLEMLL.-
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	1	2.5788	0.1965	1433.64	1434.666	3	186.2	50	Y.W2L1P1N2E1N2V1I1R4K2F1.K
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.7236	0.3887	1954.95	1955.342	1	1101.5	64.70589	A.K2I1L1V1P1E1G1T1K2D1I1P1V1N2K2P1I1A1.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.2533	0.296	1933.71	1933.342	1	706.3	50	A.KILVPEGTKDIPVNKPIA.V
gi|6324258|ref|NP_014328.1|	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	2	4.5034	0.387	2033.19	2032.475	1	1085.5	58.333332	A.KILVPEGTKDIPVNKPIAV.Y
gi|6324244|ref|NP_014314.1|	YNL085W	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p	1	2.3108	0.2767	1341.4	1341.593	1	445	60.000004	F.KDFNITPIFVF.N
gi|6324244|ref|NP_014314.1|	YNL085W	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p	1	2.5907	0.1822	1354.68	1354.593	1	408.3	60.000004	F.K2D1F1N2I1T1P1I1F1V1F1.N
gi|6324244|ref|NP_014314.1|	YNL085W	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p	2	3.8078	0.1547	1368.55	1366.643	1	1086.4	85	A.KLIDENVFKLF.T
gi|6324244|ref|NP_014314.1|	YNL085W	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p	1	2.816	0.1576	1365.57	1366.643	1	517.1	65	A.KLIDENVFKLF.T
gi|6324244|ref|NP_014314.1|	YNL085W	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p	2	3.7311	0.3754	2163.59	2165.375	1	452.5	52.941177	K.E1V1R4K2P1R4D1I1P1N2D1V1H3D1F1I1G1Q2.M
gi|6324244|ref|NP_014314.1|	YNL085W	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p	2	2.9455	0.2207	1355.23	1354.593	5	506.5	65	F.K2D1F1N2I1T1P1I1F1V1F1.N
gi|6324244|ref|NP_014314.1|	YNL085W	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p	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.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	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
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	4.3503	0.3154	2098.55	2098.37	1	1256.3	38.88889	L.ADNIRSIPNVLDGFKPGQR.K
gi|6324230|ref|NP_014300.1|	YNL099C	Putative protein tyrosine phosphatase, required for cell cycle arrest in response to oxidative damage of DNA; Oca1p	2	3.5036	0.2337	1855.49	1857.144	1	960.3	66.66667	Y.L1Y1R4S1G1Q2P1S1P1V1N2F1P1F1L1L1.N
gi|6324230|ref|NP_014300.1|	YNL099C	Putative protein tyrosine phosphatase, required for cell cycle arrest in response to oxidative damage of DNA; Oca1p	2	4.2032	0.3795	2211.19	2212.485	1	619.5	52.941177	H.A1P1Q2E1R4I1V1P1P1L1N2F1C1P1V1E1R4Y1.L
gi|6324230|ref|NP_014300.1|	YNL099C	Putative protein tyrosine phosphatase, required for cell cycle arrest in response to oxidative damage of DNA; Oca1p	2	3.657	0.2666	2188.53	2186.485	1	567.7	52.941177	H.APQERIVPPLNFCPVERY.L
gi|6324230|ref|NP_014300.1|	YNL099C	Putative protein tyrosine phosphatase, required for cell cycle arrest in response to oxidative damage of DNA; Oca1p	2	3.3653	0.2109	1628.89	1628.825	1	721.6	57.692307	Y.L1Y1R4S1G1Q2P1S1P1V1N2F1P1F1.L
gi|6324230|ref|NP_014300.1|	YNL099C	Putative protein tyrosine phosphatase, required for cell cycle arrest in response to oxidative damage of DNA; Oca1p	2	2.9556	0.2677	1837.41	1836.144	1	617.3	53.333336	Y.LYRSGQPSPVNFPFLL.N

gi|6324211|ref|NP_014281.1|	YNL118C	Catalytic subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes the 5' cap structure from mRNAs prior to their degradation; member of the Nudix hydrolase family; Dcp2p	3	4.0828	0.2401	2131.64	2132.223	1	785.5	39.0625	N.C1P1N2E1D1L1S1S1V1E1R4E1L1F1H3F1E1.E
gi|6324211|ref|NP_014281.1|	YNL118C	Catalytic subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes 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
gi|6324211|ref|NP_014281.1|	YNL118C	Catalytic subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes the 5' cap structure from mRNAs prior to their degradation; member of the Nudix hydrolase family; Dcp2p	2	3.9963	0.2841	1841.23	1840.089	1	1262.5	73.07692	Q.VRNEIDKIEWFDFK.K
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.5466	0.1919	1605.89	1606.816	1	1057	75	A.KELDPENIFPYIQ.L
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.2439	0.176	1719.97	1719.975	2	709.9	65.38461	A.KELDPENIFPYIQL.A
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	4.5352	0.3064	2103.41	2103.291	1	663.2	68.75	F.EEQLDKNNEDEKLKEKL.A
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.1004	0.2118	1376.01	1376.636	4	795.9	63.636364	K.ALELKPDYSKVL.L
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	1	2.8634	0.2024	1375.64	1376.636	4	632.2	63.636364	K.ALELKPDYSKVL.L
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	4.2668	0.2903	2158.49	2157.389	1	723.2	52.77778	L.STQPAKERKDKQENLPSVT.S
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	4.9035	0.3971	2398.47	2399.663	1	377.6	42.5	T.ELSTQPAKERKDKQENLPSVT.S
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	4.4711	0.301	2428.49	2429.663	2	456.5	45	T.E1L1S1T1Q2P1A1K2E1R4K2D1K2Q2E1N2L1P1S1V1T1.S
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.6042	0.1521	1538.39	1536.728	1	690	69.230774	L.KNDPLGAHEDIKKA.I
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	4.523	0.3627	1796.41	1799.005	1	597.2	57.14286	K.R4K2F1P1E1A1P1E1V1P1N2F1F1A1E1.I
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.0509	0.2674	1669.11	1670.888	1	581.2	60.714287	F.L1K2N2D1P1L1G1A1H3E1D1I1K2K2A1.I
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for 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
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for 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
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for 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
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.6424	0.3169	2130.45	2131.373	1	445.7	47.058823	S.E1A1K2R4K2F1P1E1A1P1E1V1P1N2F1F1A1E1.I
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.9457	0.4148	1581.57	1578.811	1	771.2	75	K.RKFPEAPEVPNFF.A
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	2	3.3573	0.2953	1594.65	1596.811	1	451.3	62.5	K.R4K2F1P1E1A1P1E1V1P1N2F1F1.A
gi|6324208|ref|NP_014278.1|	YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a 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	Cholinephosphotransferase, required for phosphatidylcholine biosynthesis and for inositol-dependent regulation of EPT1 transcription; Cpt1p	1	3.0487	0.2475	1303.62	1303.461	5	140.4	54.545456	R.RTGQQGPLGELF.D
gi|42742307|ref|NP_014269.2|	YNL130C	Cholinephosphotransferase, required for phosphatidylcholine biosynthesis and for inositol-dependent regulation of EPT1 transcription; Cpt1p	1	2.6802	0.2092	1320.73	1320.461	8	132.3	54.545456	R.R4T1G1Q2Q2G1P1L1G1E1L1F1.D
gi|42742307|ref|NP_014269.2|	YNL130C	Cholinephosphotransferase, required for phosphatidylcholine biosynthesis and for inositol-dependent regulation of EPT1 transcription; Cpt1p	2	3.8239	0.2507	2199.57	2199.321	1	554	56.666668	L.Y1Y1D1P1Y1F1D1Q2E1S1P1R4W2T1Y1F1.S
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency 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	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.4504	0.2934	2414.67	2413.682	1	524.3	47.368423	L.R4E1I1S1L1D1E1P1I1R4Y1A1P1G1D1P1I1E1K2W2.L
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	2.9489	0.2153	2560.17	2561.006	4	202.2	34.090908	L.FVLLPPIDPKDGGRIPDPLCVIQ.I
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.4866	0.2239	2224.79	2226.537	3	289.1	36.842106	L.L1P1P1I1D1P1K2D1G1G1R4I1P1D1P1L1C1V1I1Q2.I
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency 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
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.4077	0.1777	1936.81	1935.268	1	491.9	50	F.V1L1L1P1P1I1D1P1K2D1G1G1R4I1P1D1P1L1.C
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.4152	0.2952	2384.93	2385.682	1	634.5	50	L.REISLDEPIRYAPGDPIEKW.L
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency 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
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.7449	0.3466	2252.51	2253.494	1	419.8	44.444447	R.E1I1S1L1D1E1P1I1R4Y1A1P1G1D1P1I1E1K2W2.L

gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.4674	0.2462	1914.39	1913.268	1	503.5	50 F.VLLPPIDPKDGGRIPDPL.C
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	4.6656	0.3009	2441.63	2440.829	1	558.8	47.61905 F.V1L1L1P1P1I1D1P1K2D1G1G1R4I1P1D1P1L1C1V1I1Q2.I
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency 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
gi|6324197|ref|NP_014267.1|	YNL132W	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	47.22222 L.F1V1L1L1P1P1I1D1P1K2D1G1G1R4I1P1D1P1L1.C
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	4.1649	0.3138	2414.73	2413.829	1	854.2	57.14286 F.VLLPPIDPKDGGRIPDPLCVIQ.I
gi|6324197|ref|NP_014267.1|	YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	2	3.6611	0.278	2079.93	2081.382	2	517.3	47.058823 K.N2V1K2P1L1P1P1K2E1D1D1E1L1P1P1K2Q2L1.E
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	3.584	0.1822	1960.23	1960.194	4	507.7	47.22222 K.IDRISPGDGATFPKTGDLV.T
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	4.5249	0.3523	2337.43	2339.6	1	1040	52.380955 K.I1D1R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T1I1H3.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	3.7941	0.2527	1753.65	1752.946	2	1013.8	59.375 D.R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1.T
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	1	3.2963	0.3096	1522.55	1523.775	1	487.7	60.714287 Y.GPRGFPGLIPPNSTL.V
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	1	3.2919	0.3097	1541.57	1542.775	1	397.6	57.14286 Y.G1P1R4G1F1P1G1L1I1P1P1N2S1T1L1.V
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	3	5.2247	0.334	2084.03	2083.352	1	1454.4	43.421055 D.RISPGDGATFPKTGDLVTIH.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	5.708	0.4697	2109.43	2109.352	1	1461.9	68.42105 D.R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T1I1H3.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	3	5.6728	0.3865	2109.68	2109.352	1	1271.8	42.105263 D.R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T1I1H3.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	5.3038	0.3608	2084.79	2083.352	1	1682.3	71.05263 D.RISPGDGATFPKTGDLVTIH.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	4.5467	0.3322	2541.53	2538.907	1	756.2	50 N.VKIDRISPGDGATFPKTGDLVTIH.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	1	2.2258	0.151	916.44	917.096	2	172.3	78.57143 A.RLTIPGPY.A
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	4.9373	0.3641	2214.27	2213.501	1	947.6	57.5 N.V1K2I1D1R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1.T
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	4.0433	0.2921	2190.13	2187.501	1	665.5	50 N.VKIDRISPGDGATFPKTGDLV.T
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	5.323	0.3995	2109.21	2109.352	1	1375.3	68.42105 D.R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T1I1H3.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	4.7743	0.3816	2084.27	2083.352	1	1545.3	68.42105 D.RISPGDGATFPKTGDLVTIH.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and 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
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	3	4.3064	0.2908	2539.88	2538.907	1	775.1	35.869564 N.VKIDRISPGDGATFPKTGDLVTIH.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	3	5.229	0.2958	2572.82	2569.907	1	885.2	38.04348 N.V1K2I1D1R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T1I1H3.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	4.4168	0.3426	2568.71	2569.907	1	514.5	41.304348 N.V1K2I1D1R4I1S1P1G1D1G1A1T1F1P1K2T1G1D1L1V1T1I1H3.Y
gi|6324194|ref|NP_014264.1|	YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	2	3.123	0.2304	1734.09	1731.946	1	957	59.375 D.RISPGDGATFPKTGDLV.T
gi|6324193|ref|NP_014263.1|	YNL136W	Subunit of the NuA4 histone acetyltransferase complex, which acetylates the N-terminal tails of histones H4 and H2A; Eaf7p	2	3.4082	0.2756	1772.49	1772.921	1	604.6	53.846157 R.K2Q2D1F1T1L1P1W2E1E1Y1G1E1L1.I
gi|6324193|ref|NP_014263.1|	YNL136W	Subunit of the NuA4 histone acetyltransferase complex, which acetylates the N-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	Subunit of the NuA4 histone acetyltransferase complex, which acetylates the N-terminal tails of histones H4 and H2A; Eaf7p	2	3.1687	0.1546	1082.35	1084.29	6	827.8	87.5 W.T1I1V1D1E1I1R4L1L1.R
gi|6324180|ref|NP_014250.1|	YNL149C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum (ER) and YFP-fusion protein to the nuclear envelope-ER network; null mutants have a cell separation defect; Pga2p	3	5.1183	0.3282	3131.66	3131.424	1	846.4	28.846153 Q.VEKDKRDKEEKRSKDLIDKPDDAATAE.T
gi|6324180|ref|NP_014250.1|	YNL149C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum (ER) and YFP-fusion protein to the nuclear 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|	YNL152W	Protein required for cell viability; Ynl152wp	2	4.1736	0.3903	2392.47	2391.719	1	705.3	52.499996 S.MAMRPIPPLPTESEYDYVHGS.T
gi|6324177|ref|NP_014247.1|	YNL152W	Protein required for cell viability; Ynl152wp	3	4.3391	0.2967	2393.93	2391.719	1	962.7	36.25 S.MAMRPIPPLPTESEYDYVHGS.T
gi|6324177|ref|NP_014247.1|	YNL152W	Protein required for cell viability; Ynl152wp	2	3.4747	0.1802	2304.97	2304.641	1	409.1	44.736843 S.MAMRPIPPLPTESEYDYVHG.S
gi|6324177|ref|NP_014247.1|	YNL152W	Protein required for cell viability; Ynl152wp	2	3.7459	0.3968	2067.03	2067.317	1	620.5	56.25 A.M1R4P1I1P1P1L1P1T1E1S1E1Y1D1Y1V1H3.G

gi|6324177|ref|NP_014247.1|	YNL152W	Protein required for cell viability; Ynl152wp	3	4.5288	0.2703	2416.97	2417.719	1	910.8	33.75	S.M1A1M1R4P1I1P1P1L1P1T1E1S1E1Y1D1Y1V1H3G1S1.T
gi|6324177|ref|NP_014247.1|	YNL152W	Protein required for cell viability; Ynl152wp	2	4.0166	0.3574	2418.09	2417.719	1	770.7	50	S.M1A1M1R4P1I1P1P1L1P1T1E1S1E1Y1D1Y1V1H3G1S1.T
gi|6324177|ref|NP_014247.1|	YNL152W	Protein required for cell viability; Ynl152wp	2	3.9478	0.2936	2212.03	2213.447	1	398.4	44.444447	A.M1R4P1I1P1P1L1P1T1E1S1E1Y1D1Y1V1H3G1S1.T
gi|6324161|ref|NP_014231.1|	YNL168C	The authentic, non-tagged protein was localized to mitochondria; Fmp41p	1	3.0127	0.2271	1597.55	1598.809	1	576	53.846157	T.K2M1K2P1E1E1V1Y1D1S1I1S1G1V1.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.Q
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
gi|6324161|ref|NP_014231.1|	YNL168C	The authentic, non-tagged protein was localized to mitochondria; Fmp41p	2	4.1345	0.2818	1597.45	1598.809	1	1524.3	73.07692	T.K2M1K2P1E1E1V1Y1D1S1I1S1G1V1.A
gi|6324161|ref|NP_014231.1|	YNL168C	The authentic, non-tagged protein was localized to mitochondria; Fmp41p	2	4.2907	0.4228	2233.83	2234.483	1	566.5	45	T.GTPAGVGELKPGDRVHCELLQ.N
gi|6324161|ref|NP_014231.1|	YNL168C	The authentic, non-tagged protein was localized to mitochondria; Fmp41p	2	3.6618	0.4542	2105.25	2106.353	1	533.5	47.368423	T.GTPAGVGELKPGDRVHCELL.Q
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	3	4.0541	0.2917	2276.33	2276.632	1	1094.9	38.75	L.PDAVTIIEPKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	5.7336	0.3819	2297.63	2299.632	1	1442	65	L.P1D1A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1V1K2.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	3	5.3631	0.3381	2297.06	2299.632	1	1432.6	42.5	L.P1D1A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1V1K2.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	3.0064	0.215	1795.81	1793.111	1	409.1	50	T.IIEPKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	3.5738	0.3251	1437.45	1437.676	1	1047.5	75	E.PKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	6.2757	0.4445	2278.55	2276.632	1	2030	70	L.PDAVTIIEPKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	3	4.6041	0.3691	2845.91	2844.318	1	824.9	30.769232	R.TGPKALPDAVTIIEPKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	4.1683	0.3909	2773.29	2773.199	1	464.2	36	S.RTGPKALPDAVTIIEPKEEEPILAPS.V
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	4.2648	0.3344	2803.77	2804.199	1	711.9	44	S.R4T1G1P1K2A1L1P1D1A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1.V
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	5.3709	0.4152	2459.95	2460.871	1	1065.2	54.545456	K.ALPDAVTIIEPKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	5.7495	0.3283	2488.09	2485.871	1	1281	56.81818	K.A1L1P1D1A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1V1K2.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	3	4.0693	0.4334	2460.95	2460.871	1	649.2	38.636364	K.ALPDAVTIIEPKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	2.985	0.2532	1136.61	1136.353	1	978.4	77.77778	F.K2Y1A1P1G1T1I1V1L1Y1.A
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	3.0219	0.2461	1895.01	1894.216	1	467.7	46.875	V.TIIEPKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	5.4592	0.4198	2063.37	2064.427	1	746.5	55.555557	D.AVTIIEPKEEEPILAPSVK.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	3	4.0161	0.3728	2772.95	2773.199	1	551.8	36	S.RTGPKALPDAVTIIEPKEEEPILAPS.V
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	4.2778	0.321	1854.21	1855.12	1	719.3	62.5	D.A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1.V
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	3.7553	0.2595	1837.39	1837.12	1	618.4	59.375	D.AVTIIEPKEEEPILAPS.V
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	3.2361	0.1928	2232.41	2233.564	1	465.8	45	K.ALPDAVTIIEPKEEEPILAPS.V
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	5.4849	0.4277	2084.03	2085.427	1	761.9	55.555557	D.A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1V1K2.D
gi|6324151|ref|NP_014221.1|	YNL178W	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 S3 ribosomal proteins; Rps3p	2	3.7575	0.1569	2256.79	2255.564	8	260.6	37.5	K.A1L1P1D1A1V1T1I1I1E1P1K2E1E1E1P1I1L1A1P1S1.V
gi|6324146|ref|NP_014216.1|	YNL183C	Protein kinase that stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation; Npr1p	2	5.1904	0.4651	2324.15	2323.585	1	1143.9	58.333332	L.N2H3P1N2I1I1E1T1I1E1I1V1Y1E1N2D1R4I1L1.Q
gi|6324146|ref|NP_014216.1|	YNL183C	Protein kinase that stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation; Npr1p	2	5.5614	0.4417	2298.61	2296.585	1	1358.5	58.333332	L.NHPNIIETIEIVYENDRIL.Q
gi|6324146|ref|NP_014216.1|	YNL183C	Protein kinase that stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation; Npr1p	2	4.8446	0.4242	2436.69	2437.745	1	811.4	50	T.L1N2H3P1N2I1I1E1T1I1E1I1V1Y1E1N2D1R4I1L1.Q
gi|6324146|ref|NP_014216.1|	YNL183C	Protein kinase that stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation; Npr1p	2	3.3015	0.2579	1934.17	1935.079	1	565.4	50	L.N2H3P1N2I1I1E1T1I1E1I1V1Y1E1N2D1.R
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	5.487	0.4187	2588.84	2587.777	1	1411.1	41.25	T.Y1D1D1E1Y1I1N2I1I1S1E1R4D1V1L1K2E1P1N2A1Y1.Y
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	5.7623	0.4098	3960.86	3962.924	1	782.3	21.527777	K.E1R4D1N2A1D1K2G1D1G1E1D1I1G1E1D1I1G1E1D1I1G1E1D1I1G1E1D1I1G1E1D1I1G1E1N2L1.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	25.641027	A.S1L1K2E1R4D1N2A1D1K2G1D1G1E1D1I1G1E1D1I1G1E1D1I1G1E1D1I1G1E1D1I1G1E1D1I1G1E1N2L1.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	5.9968	0.448	4248.17	4248.336	1	1280.6	23.717949	A.SLKERDNADKGDGEDIGEDIGEDIGEDIGEDIGEDIGENL.G
gi|6324123|ref|NP_014193.1|	YNL206C	Protein with a role in regulation of Ty1 transposition; Rtt106p	1	2.3206	0.2855	1517.49	1517.808	1	376.8	54.166668	A.SFLPVPEKPNLIY.L
gi|6324123|ref|NP_014193.1|	YNL206C	Protein with a role in regulation of Ty1 transposition; Rtt106p	1	2.3117	0.2541	1531.74	1532.808	1	592.9	62.5	A.S1F1L1P1V1P1E1K2P1N2L1I1Y1.L
gi|6324123|ref|NP_014193.1|	YNL206C	Protein with a role in regulation of Ty1 transposition; Rtt106p	2	3.0255	0.2199	2156.77	2157.508	1	180.9	36.11111	S.E1T1N2T1I1F1K2L1E1G1V1S1V1L1S1P1L1R4K2.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	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.L1I1D1F1K2D1Y1P1D1V1P1K2V1P1G1N2S1.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.L1I1D1F1K2D1Y1P1D1V1P1K2V1P1G1N2S1K2I1P1P1I1G1V1.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.T1S1G1K2E1E1P1I1V1L1P1I1W2D1P1M1G1A1L1.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.TSGKEEPIVLPIWDPMGAL.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	3.5343	0.2501	1642.23	1640.935	1	755	61.538464	S.G1K2E1E1P1I1V1L1P1I1W2D1P1M1.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.T1S1G1K2E1E1P1I1V1L1P1I1W2D1P1M1G1A1.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.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	2.9355	0.2068	1474.31	1472.74	1	712.4	75	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	3.4882	0.1953	1475.69	1474.698	2	614.4	66.66667	Q.D1K2M1N2P1I1L1D1A1I1L1E1S1.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.L1V1T1I1P1K2L1P1V1D1A1P1D1V1F1L1I1N2.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.V1T1I1P1K2L1P1V1D1A1P1D1V1F1L1I1N2.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
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	5.2838	0.4067	1992.79	1995.249	1	2036.9	73.52941	M.T1Q2D1K2M1N2P1I1L1D1A1I1L1E1S1G1I1N2.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	5.1195	0.3835	1972.49	1973.249	1	1921.9	73.52941	M.TQDKMNPILDAILESGIN.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	4.1573	0.3099	2315.45	2315.644	1	674	47.5	M.TQDKMNPILDAILESGINTIQ.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	3.5656	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.V1T1I1P1K2L1P1V1D1A1P1D1V1F1.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
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	3.8071	0.3571	1641.37	1640.961	1	733.4	60.714287	T.L1V1T1I1P1K2L1P1V1D1A1P1D1V1F1.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	3.9118	0.4168	1627.61	1624.961	1	866.6	64.28571	T.LVTIPKLPVDAPDVF.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	3.4501	0.294	2303.67	2304.605	1	489.1	44.736843	N.DVDESKEIKFKKREPSVTPA.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	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

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	3.083	0.159	1433.59	1434.707	1	782.7	72.72727	S.E1H3L1R4V1D1V1P1K2P1L1L1.S
gi|6324081|ref|NP_014151.1|	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	3.9449	0.3041	2051.01	2052.419	1	829.7	56.25	S.SILKEADKEKKLELFPY.Q
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|	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	3.9316	0.3477	2315.43	2315.669	1	904.3	52.63158	D.ATDVEQIYPIESIIPKKELQ.F
gi|6324081|ref|NP_014151.1|	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	4.7509	0.3316	2165.67	2165.485	1	716.9	50	T.D1V1E1Q2I1Y1P1I1E1S1I1I1P1K2K2E1L1Q2.F
gi|6324081|ref|NP_014151.1|	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	4.3175	0.3752	2035.19	2035.354	1	899.4	56.25	T.D1V1E1Q2I1Y1P1I1E1S1I1I1P1K2K2E1L1.Q
gi|6324081|ref|NP_014151.1|	YNL248C	RNA polymerase I subunit A49; Rpa49p	2	3.2199	0.2564	2014.81	2015.354	1	727.1	50	T.DVEQIYPIESIIPKKEL.Q
gi|6324081|ref|NP_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
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	2	3.3164	0.1857	2198.45	2199.492	1	740.5	50	A.G1E1D1I1I1V1N2E1P1D1L1N2I1P1H3P1R4M1L1.E
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	2	4.1858	0.3279	2404.37	2404.712	1	441.9	47.5	L.C1E1L1I1S1P1V1H3L1H3P1V1T1A1E1P1I1V1D1H3L1.K
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	3	4.1287	0.2745	2403.29	2404.712	1	825.8	33.75	L.C1E1L1I1S1P1V1H3L1H3P1V1T1A1E1P1I1V1D1H3L1.K
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	3	4.5003	0.4191	2375.99	2377.712	1	1150	37.5	L.CELISPVHLHPVTAEPIVDHL.K
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	3	4.9015	0.2601	2332.34	2331.649	1	842.6	36.25	N.SAGEDIIVNEPDLNIPHPRML.E
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	2	3.5831	0.2659	2016.57	2017.37	2	372.9	41.17647	K.K2A1E1L1P1P1P1V1Q2S1I1I1D1N2V1V1K2F1.V
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	2	3.4666	0.2981	1993.19	1995.37	1	377.5	41.17647	K.KAELPPPVQSIIDNVVKF.V
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	2	3.2884	0.2858	2377.03	2377.712	1	242.4	37.5	L.CELISPVHLHPVTAEPIVDHL.K
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	2	3.5842	0.2531	1727.63	1726.97	1	795	73.07692	Q.HDEDTLWKLVPLPY.R
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	2	4.8573	0.4282	1948.41	1949.216	1	1409.9	70	A.HNEYFQKFPDSPLVVK.V
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	3	3.9043	0.2539	1950.02	1949.216	1	1114	46.666668	A.HNEYFQKFPDSPLVVK.V
gi|37362687|ref|NP_014143.2|	YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	3	3.9494	0.294	1970.84	1971.216	1	906.3	43.333332	A.H3N2E1Y1F1Q2K2F1P1D1S1P1L1V1V1K2.V
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	3	4.7747	0.3395	2196.71	2197.456	1	722.3	35.526314	S.S1N2R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	2	4.1001	0.3182	1990.83	1993.274	1	470.4	55.88235	N.R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	2	3.3752	0.1837	2170.85	2171.456	1	369.7	44.736843	S.SNRSSTPTSPIDLIDPIKTK.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	3	4.5819	0.1567	2173.1	2171.456	2	1129.5	39.473686	S.SNRSSTPTSPIDLIDPIKTK.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	3	5.2048	0.1701	1993.49	1993.274	3	1799.9	50	N.R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	2	3.1058	0.2319	1970.71	1970.274	1	564.1	58.823532	N.RSSTPTSPIDLIDPIKTK.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	3	4.017	0.1679	1970.57	1970.274	1	2309.5	50	N.RSSTPTSPIDLIDPIKTK.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	3	5.9931	0.2181	1994.18	1993.274	1	3418.5	52.941177	N.R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	2	4.3178	0.3251	1992.05	1993.274	1	523.3	58.823532	N.R4S1S1T1P1T1S1P1I1D1L1I1D1P1I1K2T1K2.E
gi|6324062|ref|NP_014132.1|	YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	2	3.5625	0.3075	1970.35	1970.274	2	518.8	55.88235	N.RSSTPTSPIDLIDPIKTK.E
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	3.709	0.3127	1669.81	1669.837	1	1170.8	64.28571	L.GGNSGNIIYDWFIGR.E
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	3	4.1408	0.3473	2696.99	2694.007	1	520.9	28.260868	L.G1G1N2S1G1N2I1I1Y1D1W2F1I1G1R4E1L1N2P1R4L1G1P1L1.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	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.GENWEEYERKVPYKIIPY.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	L.CDFIEDCEFNEILVR.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	3	3.8631	0.3303	2504.51	2503.72	1	702.7	35.526314	Q.D1L1D1I1I1E1R4D1L1N2R4T1F1P1D1N2I1H3F1Q2.S
gi|6324033|ref|NP_014102.1|	YNL297C	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family of proteins; Mon2p	2	5.072	0.3292	2202.61	2201.329	1	1530.3	70.588234	Q.R4I1N2P1E1L1D1N2L1T1E1I1D1D1L1N2E1Y1.S
gi|6324033|ref|NP_014102.1|	YNL297C	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family of proteins; Mon2p	2	4.2034	0.3828	2176.49	2177.329	1	1256.8	61.764706	Q.RINPELDNLTEIDDLNEY.S
gi|6324033|ref|NP_014102.1|	YNL297C	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family of proteins; Mon2p	2	4.0297	0.3281	2304.13	2305.46	1	1041.8	58.333332	L.QRINPELDNLTEIDDLNEY.S
gi|6324033|ref|NP_014102.1|	YNL297C	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family of proteins; Mon2p	2	4.5154	0.3542	2331.21	2331.46	1	770.7	50	L.Q2R4I1N2P1E1L1D1N2L1T1E1I1D1D1L1N2E1Y1.S
gi|6324033|ref|NP_014102.1|	YNL297C	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family of proteins; Mon2p	2	4.3504	0.3879	2444.41	2445.62	1	749.1	50	T.L1Q2R4I1N2P1E1L1D1N2L1T1E1I1D1D1L1N2E1Y1.S
gi|6324033|ref|NP_014102.1|	YNL297C	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family of proteins; Mon2p	2	3.867	0.3255	2417.79	2418.62	1	720.6	50	T.LQRINPELDNLTEIDDLNEY.S
gi|6324033|ref|NP_014102.1|	YNL297C	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family 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	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	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.G1P1S1P1S1P1S1P1S1P1S1P1L1N2P1Y1R4P1H3.H
gi|6324016|ref|NP_014086.1|	YNL313C	Protein required for cell viability; Ynl313cp	2	3.4591	0.2593	1843.25	1842.053	1	321	50	K.NTTPAKDPLVEEELTAL.L
gi|6324016|ref|NP_014086.1|	YNL313C	Protein required for cell viability; Ynl313cp	2	3.817	0.3607	2034.43	2033.339	1	854.1	58.823532	Q.K2S1L1F1D1V1T1P1D1Q2E1I1P1L1P1I1I1S1.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	2	3.3457	0.3672	3046.53	3046.328	1	322.5	30.000002	F.A1L1E1S1D1L1L1L1E1K2P1H3F1E1S1I1A1D1E1P1L1D1E1Q2I1Y1.S
gi|6324016|ref|NP_014086.1|	YNL313C	Protein required for cell viability; Ynl313cp	2	3.7786	0.3553	3015.79	3016.328	1	492	32	F.ALESDLLLEKPHFESIADEPLDEQIY.S
gi|6324016|ref|NP_014086.1|	YNL313C	Protein required for cell viability; Ynl313cp	3	3.8491	0.2173	1871.42	1871.141	1	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.K2E1L1P1E1S1I1H3E1D1F1K2R4E1L1.C
gi|6324016|ref|NP_014086.1|	YNL313C	Protein required for cell viability; Ynl313cp	2	3.3862	0.3482	2159.65	2160.432	1	443.1	61.764706	K.RQKVDLNEGYEEDKLLPL.A
gi|6324016|ref|NP_014086.1|	YNL313C	Protein required for cell viability; Ynl313cp	3	4.8286	0.3242	2861.36	2860.09	1	576.4	32.608696	L.E1S1D1L1L1L1E1K2P1H3F1E1S1I1A1D1E1P1L1D1E1Q2I1Y1.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|	YNL313C	Protein required for cell viability; Ynl313cp	2	3.0886	0.2004	2276.85	2274.489	2	448.5	41.666664	L.LEKPHFESIADEPLDEQIY.S
gi|6324016|ref|NP_014086.1|	YNL313C	Protein required for cell viability; Ynl313cp	2	5.0105	0.326	2184.21	2185.432	1	573.8	67.64706	K.R4Q2K2V1D1L1N2E1G1Y1E1E1D1K2L1L1P1L1.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
gi|6324009|ref|NP_014079.1|	YNL320W	hypothetical protein; Ynl320wp	2	4.1536	0.3637	1539.13	1539.836	1	871.2	70.83333	S.GLKDEIVPPFHMR.K
gi|6324009|ref|NP_014079.1|	YNL320W	hypothetical protein; Ynl320wp	2	4.0793	0.3232	1560.39	1558.836	1	797.8	70.83333	S.G1L1K2D1E1I1V1P1P1F1H3M1R4.K
gi|6324006|ref|NP_014076.1|	YNL323W	Membrane protein of the plasma membrane and ER, involved in translocation of phospholipids and alkylphosphocholine drugs across the plasma membrane; Lem3p	2	4.1426	0.24	1888.67	1889.201	1	1189.6	63.333332	Q.L1D1I1G1L1H3W2P1V1L1E1F1N2G1K2K2.G
gi|6324006|ref|NP_014076.1|	YNL323W	Membrane protein of the plasma membrane and ER, involved in translocation of 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
gi|6324006|ref|NP_014076.1|	YNL323W	Membrane protein of the plasma membrane and ER, involved in translocation of 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
gi|6324006|ref|NP_014076.1|	YNL323W	Membrane protein of the plasma membrane and ER, involved in translocation of phospholipids and alkylphosphocholine drugs across the plasma membrane; Lem3p	2	3.1414	0.2098	1568.17	1570.801	3	737.1	66.66667	Q.L1D1I1G1L1H3W2P1V1L1E1F1N2.G
gi|6324006|ref|NP_014076.1|	YNL323W	Membrane protein of the plasma membrane and ER, involved in translocation of 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
gi|6324006|ref|NP_014076.1|	YNL323W	Membrane protein of the plasma membrane and ER, involved in translocation of phospholipids and alkylphosphocholine drugs across the plasma membrane; Lem3p	3	4.077	0.2974	1889.51	1889.201	1	1503.5	51.666664	Q.L1D1I1G1L1H3W2P1V1L1E1F1N2G1K2K2.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	1	2.5449	0.1569	1195.51	1196.418	1	271.7	55	Q.K2I1I1E1E1A1P1V1T1I1A1.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	3.7457	0.1794	1337.56	1338.491	1	364.3	75	S.N2F1N2I1K2P1I1F1T1D1N2.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	1	3.4745	0.2722	1322.49	1323.491	2	328.8	75	S.NFNIKPIFTDN.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	1	2.7342	0.3668	1316.49	1317.467	1	503.5	59.090908	Q.S1A1K2V1P1C1I1P1W2S1G1T1.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	1	3.9072	0.3892	1573.53	1574.713	1	598.6	57.14286	T.G1V1D1T1V1H3V1D1E1K2T1G1L1V1S1.V
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	2.445	0.3534	1365.6	1365.572	1	628.4	68.181816	R.VHEGVTVPIVEW.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	2.3838	0.1885	1392.77	1392.51	2	405.8	55	L.YSHDDGKFYFL.E
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	3.7214	0.2292	2711.53	2713.163	1	581.4	43.75	H.ALPFEGMLPDFGSPVIEGTKPAYKF.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	2	3.2543	0.3257	2302.17	2300.747	1	632.8	44.736843	D.ALVDYKQPIIIYIPPTGELR.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	4.3396	0.3403	2140.03	2139.508	1	729.7	55.88235	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	4.2768	0.3502	2326.79	2325.747	1	711.2	50	D.A1L1V1D1Y1K2Q2P1I1I1I1Y1I1P1P1T1G1E1L1R4.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	3.2294	0.1744	2232.63	2233.565	2	296.5	34.210526	R.V1H3E1G1V1T1V1P1I1V1E1W2K2F1Q2L1P1S1A1A1.F
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	3.434	0.2637	1734.43	1732.971	1	854	73.07692	S.V1K2E1R4T1E1Q2I1E1H3I1L1K2S1.S
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	4.0933	0.3301	1805.59	1803.199	1	866.1	65.625	R.IIIKDPQTGAPVPLRAL.I
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	3.9493	0.3993	2869.71	2870.337	1	437.2	36	H.A1L1P1F1E1G1M1L1P1D1F1G1S1P1V1I1E1G1T1K2P1A1Y1K2F1K2.S
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	4.2259	0.3853	2840.13	2841.337	1	713	42	H.ALPFEGMLPDFGSPVIEGTKPAYKFK.S
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	4.0777	0.3589	2003.51	2003.287	1	481.2	50	L.P1D1F1G1S1P1V1I1E1G1T1K2P1A1Y1K2F1K2.S
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	3.1749	0.1755	1710.67	1710.971	1	855.5	69.230774	S.VKERTEQIEHILKS.S
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	3.9065	0.4098	1639.19	1639.912	1	573.1	70.83333	T.MFPVDFIHEGKRY.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	2	4.4198	0.401	1659.37	1658.912	1	615.2	75	T.M1F1P1V1D1F1I1H3E1G1K2R4Y1.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	2	3.0967	0.2457	1289.83	1290.464	8	449.7	66.66667	L.RNPKLPYSEW.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	2	4.3529	0.4336	1817.61	1819.036	1	983.5	67.85714	L.H3S1R4L1P1A1K2L1D1E1Q2M1E1E1L1.V
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	3.0183	0.1778	1707.45	1707.886	3	252.9	53.571426	Y.SERHTELPGHFIGLN.T

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	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 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	2.8577	0.3163	1592.69	1593.783	2	351.6	50 Y.SERHTELPGHFIGL.N
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	2.9851	0.2938	1871.53	1871.062	1	430.3	53.333336 T.NYSERHTELPGHFIGL.N
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	3.3624	0.3751	1896.77	1895.062	1	566.2	56.666668 T.N2Y1S1E1R4H3T1E1L1P1G1H3F1I1G1L1.N
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	3	4.3063	0.2941	1872.92	1871.062	2	948.1	41.666664 T.NYSERHTELPGHFIGL.N
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	3.7387	0.3179	1740.07	1739.111	1	882.7	67.85714 Y.KQPIIIYIPPTGELR.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	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 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	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 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	4.0473	0.2737	1557.75	1558.775	1	724.6	65.38461 A.VKNPEYNPDKLLGA.V
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	2.9122	0.2133	1694.61	1694.91	2	275.7	50 Q.L1A1D1R4E1R4E1L1L1P1I1Y1G1Q2.I
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	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 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	3.8768	0.2669	1641.19	1640.922	1	1216.9	65.38461 R.VHEGVTVPIVEWKF.Q
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	3.4846	0.3876	1658.33	1658.922	1	1169.7	76.92308 R.V1H3E1G1V1T1V1P1I1V1E1W2K2F1.Q
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	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 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	3.0503	0.3043	1292.35	1290.464	5	592.4	72.22222 L.RNPKLPYSEW.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	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 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	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 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	2.6032	0.1929	1289.58	1290.464	1	230.4	61.11111 L.RNPKLPYSEW.K
gi|6324343|ref|NP_014413.1|	YNR016C	Acetyl-CoA carboxylase, 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	3	3.9103	0.1656	2140.58	2139.508	1	806.5	42.647057 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	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-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	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-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	4.5535	0.3578	1882.93	1883.235	1	847.3	59.375 A.E1I1R4I1I1I1K2D1P1Q2T1G1A1P1V1P1L1.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
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	3.0517	0.3214	1585.57	1585.948	1	981.8	73.07692 M.SYVPAKRNMPVPIL.E
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	3.3041	0.3087	1812.81	1811.955	1	649.8	63.333332 Q.GLIPSRGWTDDLCYGT.G
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	3.7303	0.2401	1940.05	1938.095	2	358.6	46.875 A.GLDKGVEYLDLEEEQLS.S

gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	4.7912	0.4463	2008.45	2009.174	1	1398.3	64.70589	L.AGLDKGVEYLDLEEEQLS.S
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	4.5561	0.3425	2026.75	2029.174	1	1138.3	61.764706	L.A1G1L1D1K2G1V1E1Y1L1D1L1E1E1E1Q2L1S1.S
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	4.8483	0.1933	1986.93	1987.122	1	2136	71.875	L.D1K2G1V1E1Y1L1D1L1E1E1E1Q2L1S1S1L1.E
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	4.3778	0.406	1967.53	1968.122	1	1268.4	68.75	L.DKGVEYLDLEEEQLSSL.E
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the 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	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	5.0021	0.4248	2140.37	2138.333	1	1755.8	58.333332	A.GLDKGVEYLDLEEEQLSSL.E
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	3.4658	0.1939	2206.73	2209.412	1	842.9	50	L.AGLDKGVEYLDLEEEQLSSL.E
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	4.1446	0.2975	2159.73	2159.333	2	1036.8	55.555557	A.G1L1D1K2G1V1E1Y1L1D1L1E1E1E1Q2L1S1S1L1.E
gi|6324344|ref|NP_014414.1|	YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	2	4.0613	0.2119	1956.35	1957.095	3	519.9	50	A.G1L1D1K2G1V1E1Y1L1D1L1E1E1E1Q2L1S1.S
gi|6324348|ref|NP_014418.1|	YNR021W	hypothetical protein; Ynr021wp	2	4.2153	0.2716	1854.73	1855.141	1	1793.7	75	K.S1K2Q2L1E1E1F1M1E1I1V1I1R4P1N2.G
gi|6324348|ref|NP_014418.1|	YNR021W	hypothetical protein; Ynr021wp	2	3.1154	0.4371	1416.47	1416.49	1	417.6	77.27273	A.HTSENDKLPNNF.V
gi|6324348|ref|NP_014418.1|	YNR021W	hypothetical protein; Ynr021wp	2	3.2992	0.2173	2453.63	2453.668	5	178.3	35	F.TDLPVNPPRDDKEWESSIEPK.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
gi|6324350|ref|NP_014420.1|	YNR023W	73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin 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
gi|6324350|ref|NP_014420.1|	YNR023W	73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin remodeling complex; deletion mutants are temperature-sensitive; Snf12p	2	4.064	0.4378	1807.87	1808.944	1	882.6	57.14286	V.KWQYDPNNPVDFDGL.D
gi|6324350|ref|NP_014420.1|	YNR023W	73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin 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
gi|6324350|ref|NP_014420.1|	YNR023W	73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin remodeling complex; deletion mutants are temperature-sensitive; Snf12p	2	2.985	0.2372	1758.87	1758.994	1	610.9	50	N.S1T1H3L1L1P1L1Q2P1I1E1I1D1Y1T1.V
gi|6324350|ref|NP_014420.1|	YNR023W	73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin 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
gi|6324353|ref|NP_014423.1|	YNR026C	Guanine nucleotide exchange factor (GEF); glycosylated integral membrane protein of the endoplasmic reticulum, important for the initiation of transport vesicle budding 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
gi|6324353|ref|NP_014423.1|	YNR026C	Guanine nucleotide exchange factor (GEF); glycosylated integral membrane protein of the endoplasmic reticulum, important for the initiation of transport vesicle budding from the endoplasmic reticulum through activation of the GTPase Sar1p; Sec12p	2	4.4631	0.309	1979.33	1981.194	1	1107.6	66.66667	L.R4V1D1P1T1K2D1T1E1K2E1Q2F1H3I1L1.S
gi|6324353|ref|NP_014423.1|	YNR026C	Guanine nucleotide exchange factor (GEF); glycosylated integral membrane protein of the endoplasmic reticulum, important for the initiation of transport vesicle budding 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
gi|6324357|ref|NP_014427.1|	YNR030W	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 for N-glycosylation; Alg12p	2	4.3455	0.3638	2027.07	2025.277	1	566.7	62.5	F.H3L1I1Q2A1P1F1T1K2V1E1E1S1F1N2I1Q2.A
gi|6324357|ref|NP_014427.1|	YNR030W	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 for N-glycosylation; Alg12p	2	4.3906	0.3851	2003.87	2002.277	1	426.9	56.25	F.HLIQAPFTKVEESFNIQ.A
gi|6324357|ref|NP_014427.1|	YNR030W	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 for N-glycosylation; Alg12p	2	3.0518	0.2416	1531.67	1532.783	1	511.6	62.5	Y.D1H3L1K2F1P1G1V1V1P1R4T1F1.V
gi|6324366|ref|NP_014436.1|	YNR038W	Essential protein involved in ribosome biogenesis; putative ATP-dependent RNA 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
gi|6324366|ref|NP_014436.1|	YNR038W	Essential protein involved in ribosome biogenesis; putative ATP-dependent RNA helicase of the DEAD-box protein family; Dbp6p	2	4.3791	0.395	2248.41	2249.447	1	621.1	50	T.F1F1D1D1L1N2K2D1L1D1R4D1G1K2S1V1Q2P1L1.E
gi|6324570|ref|NP_014639.1|	YOL004W	DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression of meiosis-specific genes during vegetative growth and silencing; involved in telomere maintenance; Sin3p	2	3.5934	0.2602	2462.39	2463.8	2	294.2	36.842106	H.W2L1T1P1K2P1K2S1Q2L1D1F1D1F1P1D1K2N2I1F1.Y
gi|6324570|ref|NP_014639.1|	YOL004W	DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression of meiosis-specific genes during vegetative growth and silencing; involved in telomere maintenance; Sin3p	2	2.9797	0.2006	2436.67	2437.8	1	446.8	39.473686	H.WLTPKPKSQLDFDFPDKNIF.Y
gi|6324570|ref|NP_014639.1|	YOL004W	DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression of meiosis-specific genes during vegetative growth and silencing; involved in telomere maintenance; Sin3p	2	3.3102	0.316	2027.73	2028.337	1	401.3	52.941177	S.GLPSIQQPEMPAHRQIPQ.S
gi|6324570|ref|NP_014639.1|	YOL004W	DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression of meiosis-specific genes during vegetative growth and silencing; involved in telomere maintenance; Sin3p	3	4.2361	0.2528	4263.32	4265.495	1	497.8	21.527777	S.NDEDGKVPQLSEPPEEEPNTIEEEELIDEEAKNPWLT.G
gi|6324570|ref|NP_014639.1|	YOL004W	DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression of meiosis-specific genes during vegetative growth and silencing; involved in telomere maintenance; Sin3p	3	6.1884	0.4674	4309.55	4309.495	1	1086.2	25.694445	S.N2D1E1D1G1K2V1P1Q2L1S1E1P1P1E1E1E1P1N2T1I1E1E1E1E1L1I1D1E1E1A1K2N2P1W2L1T1.G
gi|6324570|ref|NP_014639.1|	YOL004W	DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression of meiosis-specific genes during vegetative growth and silencing; involved in telomere maintenance; Sin3p	2	3.1414	0.1581	1388.41	1387.57	1	1037.4	77.27273	Q.DILDLDDLVEKV.D
gi|6324570|ref|NP_014639.1|	YOL004W	DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression of meiosis-specific genes during vegetative growth and silencing; involved in telomere maintenance; Sin3p	2	3.4414	0.2036	1401.81	1400.57	1	1078.7	77.27273	Q.D1I1L1D1L1D1D1L1V1E1K2V1.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	3.3973	0.3045	1617.21	1616.817	1	692.4	64.28571	L.SKDAPVPPAPEGHKW.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.K2H3N2G1V1I1F1P1P1P1Y1Q2P1L1P1S1.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	2	3.1217	0.2751	2237.89	2239.571	2	432.2	44.11765	D.LLKKEPKYFEEIDDLTKE.D
gi|6324548|ref|NP_014617.1|	YOL025W	Protein involved in determination of longevity; LAG2 gene is preferentially expressed in young cells; overexpression extends the mean and maximum life span of cells; Lag2p	3	4.0343	0.3337	3081.02	3083.478	1	848.5	27.000002	N.R4L1L1P1V1L1F1P1P1Q2M1G1E1E1C1N2V1E1D1V1L1E1I1V1H3N2.F
gi|6324548|ref|NP_014617.1|	YOL025W	Protein involved in determination of longevity; LAG2 gene is preferentially expressed in young cells; overexpression extends the mean and maximum life span of cells; Lag2p	2	3.8918	0.3946	1804.83	1806.093	1	627	64.28571	N.R4L1L1P1V1L1F1P1P1Q2M1G1E1E1C1.N
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	4.0362	0.4433	1866.51	1868.989	1	1312.5	66.66667	F.D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	4.3959	0.3394	2607.57	2609.798	1	993.7	52.499996	V.Y1N2N2V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	5.6653	0.3028	2114.77	2117.298	1	2714.9	76.47059	W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	4.5471	0.2624	2447.25	2445.622	1	961.7	57.894737	Y.N2N2V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	3.7455	0.2662	2581.97	2583.798	1	359.2	42.5	V.YNNVRMEDLPEMIEELDIDDE.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	3	6.5468	0.3166	2115.14	2117.298	1	2338.6	50	W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	3	3.8675	0.1862	2331.32	2329.518	1	1257.6	37.5	N.N2V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	6.5187	0.3799	2329.31	2329.518	1	2103.6	69.44444	N.N2V1R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	4.5953	0.4573	2259.39	2259.486	1	493	50	A.Y1Q2L1P1K2D1Y1Q2G1D1G1K2D1V1D1H3K2I1L1.K
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	3.2551	0.2191	1940.73	1941.19	1	1079	63.333332	R.H3Q2N2V1K2Y1L1P1N2I1D1L1P1H3N2L1.V
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	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	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	5.9164	0.4473	2093.05	2093.298	1	2398.4	76.47059	W.VFDEKIGDENLTDIINTR.H
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	5.8611	0.3256	2114.81	2117.298	1	2343.8	73.52941	W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	3	6.6297	0.2753	2117.3	2117.298	1	3115.4	54.411762	W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1R4.H
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, 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.-

gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	5.4883	0.4171	2305.43	2306.518	1	1874.2	66.66667	N.NVRMEDLPEMIEELDIDDE.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	4.5299	0.2287	2193.67	2192.415	1	1646.3	64.70589	N.VRMEDLPEMIEELDIDDE.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to 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.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	3.6871	0.2605	1673.17	1670.918	1	684.6	57.692307	Q.N2V1K2Y1L1P1N2I1D1L1P1H3N2L1.V
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	1	2.7435	0.2528	1160.74	1160.418	1	288.1	66.66667	Q.R4L1G1L1G1E1I1I1K2F1.G
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	4.2488	0.3088	1956.21	1957.111	1	1551	65.625	W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2T1.R
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	1	3.1245	0.3016	1323.48	1324.508	2	549.8	70	K.Y1L1P1N2I1D1L1P1H3N2L1.V
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	1	2.6112	0.2229	1308.44	1309.508	5	324.9	60.000004	K.YLPNIDLPHNL.V
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	3.0616	0.2309	1323.43	1324.508	1	460.3	75	K.Y1L1P1N2I1D1L1P1H3N2L1.V
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to 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
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	4.9288	0.2893	2114.29	2113.282	1	1388.7	62.5	V.R4M1E1D1L1P1E1M1I1E1E1L1D1I1D1D1E1.-
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	2	3.0369	0.1943	1854.55	1855.006	1	893	56.666668	W.V1F1D1E1K2I1G1D1E1N2L1T1D1I1I1N2.T
gi|6324513|ref|NP_014582.1|	YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to 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
gi|6324512|ref|NP_014581.1|	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
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.9019	0.3294	2368.37	2365.712	1	610.2	45	F.NSGFSRIPIFLPNEPNNFIGM.L
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.7185	0.2777	1851.79	1851.109	1	818.8	63.333332	F.S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1.M
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.4015	0.1739	1960.47	1960.301	3	453	46.875	F.SRIPIFLPNEPNNFIGM.L
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.5977	0.1997	1980.53	1983.301	3	424.3	50	F.S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1M1.L
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; 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
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.8233	0.3216	2244.47	2245.637	1	541.1	44.444447	G.F1S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1M1L1.L
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.0433	0.1954	2104.51	2105.583	3	330.8	38.235294	L.V1L1M1Y1L1M1Y1P1V1A1Y1P1I1A1T1L1L1D1.Y
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	4.8996	0.4276	1830.99	1829.134	1	1058.1	67.85714	K.R4V1E1E1I1M1T1P1I1E1N2V1F1T1M1.S
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.0737	0.3552	1808.33	1810.134	1	730.2	60.714287	K.RVEEIMTPIENVFTM.S
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	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	Protein required for normal mitochondrial morphology, has similarity to hemolysins; 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
gi|6324512|ref|NP_014581.1|	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
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.9609	0.2374	2222.17	2220.637	1	811	55.555557	G.FSRIPIFLPNEPNNFIGML.L
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.3208	0.2622	2030.75	2031.386	1	599.3	46.875	K.A1K2R4V1E1E1I1M1T1P1I1E1N2V1F1T1M1.S
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	3.545	0.2403	1998.17	1999.285	1	357.9	43.75	G.F1S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1.M
gi|6324512|ref|NP_014581.1|	YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	2	4.6877	0.252	2190.39	2189.53	1	1161.5	58.333332	S.G1F1S1R4I1P1I1F1L1P1N2E1P1N2N2F1I1G1M1.L

gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	3	3.9506	0.1887	2981.33	2979.27	1	1632.7	38.541664	M.D1L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1Y1C1K2P1I1A1Q2.N
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	4.5036	0.4281	2977.61	2979.27	1	681.2	43.75	M.D1L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1Y1C1K2P1I1A1Q2.N
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	4.5994	0.3894	2948.73	2948.27	1	534.1	39.583336	M.DLHDPQFPGFFDIPVDNLYCKPIAQ.N
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	3	4.7069	0.2711	3111.77	3111.463	1	2271.7	39	T.M1D1L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1Y1C1K2P1I1A1Q2.N
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.1066	0.3388	2862.35	2863.182	1	188.4	36.95652	D.L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1Y1C1K2P1I1A1Q2.N
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.8407	0.3425	2832.61	2833.182	1	643.8	43.47826	D.LHDPQFPGFFDIPVDNLYCKPIAQ.N
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.4386	0.2283	2138.25	2137.334	1	369.8	42.105263	Q.H3R4I1P1D1Y1Q2D1A1V1I1V1S1P1D1A1G1G1A1K2.R
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, 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
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	3	4.8069	0.2658	2832.38	2833.182	1	811.7	28.260868	D.LHDPQFPGFFDIPVDNLYCKPIAQ.N
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.5342	0.2423	1584.51	1582.809	1	1007.7	69.230774	K.G1A1P1I1I1S1K2P1K2E1N2Y1T1F1.E
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	4.2977	0.3872	2380.55	2381.624	1	438.6	42.857143	Y.I1Q2H3R4I1P1D1Y1Q2D1A1V1I1V1S1P1D1A1G1G1A1K2.R
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.9372	0.3744	2353.67	2351.624	1	565.1	45.238094	Y.IQHRIPDYQDAVIVSPDAGGAK.R
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.3338	0.1957	2108.25	2109.296	3	447	47.058823	M.D1L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1.Y
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.6375	0.3198	1994.57	1993.207	1	783.9	65.625	D.L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1.Y
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.0501	0.171	1550.23	1550.857	1	535.5	61.538464	L.S1F1S1R4I1P1M1I1P1G1G1K2L1Q2.N
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, 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.D1L1H3D1P1Q2F1P1G1F1F1D1I1P1V1D1N2L1Y1.C
gi|6324511|ref|NP_014580.1|	YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	2	3.7636	0.4117	2250.63	2250.472	1	587.5	52.77778	M.DLHDPQFPGFFDIPVDNLY.C
gi|6324510|ref|NP_014579.1|	YOL062C	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.HIIEFVPPDGSMELM.K
gi|6324510|ref|NP_014579.1|	YOL062C	Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in vesicle transport; Apm4p	2	3.163	0.3143	1738.45	1737.934	7	238.2	50	N.G1H3C1K2F1V1P1E1E1N2A1M1I1W2.R
gi|6324510|ref|NP_014579.1|	YOL062C	Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in 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	Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in vesicle transport; Apm4p	2	4.2439	0.3553	2124.07	2125.415	1	489.5	55.88235	F.N2R4N2H3I1I1E1F1V1P1P1D1G1S1M1E1L1M1.K
gi|6324496|ref|NP_014565.1|	YOL077C	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; possesses a sigma(70)-like RNA-binding motif; Brx1p	3	4.4214	0.2622	2580.89	2579.723	1	902.7	35.714287	S.T1K2N2K2E1E1Y1E1D1G1E1E1D1I1S1L1V1E1I1G1P1R4.F
gi|6324496|ref|NP_014565.1|	YOL077C	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; 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
gi|6324496|ref|NP_014565.1|	YOL077C	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; 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
gi|6324496|ref|NP_014565.1|	YOL077C	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; possesses a sigma(70)-like RNA-binding motif; Brx1p	2	3.3288	0.3076	1999.65	1999.092	8	315.6	43.75	S.TKNKEEYEDGEEDISLV.E
gi|6324496|ref|NP_014565.1|	YOL077C	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; possesses a sigma(70)-like RNA-binding motif; Brx1p	2	6.1441	0.4423	2578.73	2579.723	1	1756.9	64.28571	S.T1K2N2K2E1E1Y1E1D1G1E1E1D1I1S1L1V1E1I1G1P1R4.F
gi|6324491|ref|NP_014560.1|	YOL081W	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 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
gi|6324491|ref|NP_014560.1|	YOL081W	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 nutrient limiting conditions, has similarity to Ira1p and human neurofibromin; Ira2p	2	2.9908	0.2603	2059.91	2061.252	2	337.8	46.875	H.F1H3R4S1P1E1V1Y1V1P1E1D1T1T1T1F1L1.G
gi|6324491|ref|NP_014560.1|	YOL081W	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 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
gi|6324489|ref|NP_014558.1|	YOL083W	hypothetical protein; Yol083wp	2	3.1109	0.2708	1990.43	1991.388	1	569.9	50	K.KCIILPEDKPELIKFF.S
gi|6324489|ref|NP_014558.1|	YOL083W	hypothetical protein; Yol083wp	2	2.969	0.2747	2009.61	2010.388	7	337.4	40	K.K2C1I1I1L1P1E1D1K2P1E1L1I1K2F1F1.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
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	3.3605	0.3635	1423.97	1424.523	1	563.7	58.333332	L.G1I1D1G1G1E1G1K2E1E1L1F1R4.S

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	4.0204	0.3432	1626.17	1626.761	1	1088.4	51.785713	L.G1I1D1G1G1E1G1K2E1E1L1F1R4S1I1.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	2	4.4459	0.4291	2097.51	2097.289	1	666	52.63158	L.GIDGGEGKEELFRSIGGEVF.I
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	1	3.259	0.2044	1515.77	1516.75	1	228.8	62.5	L.E1Y1K2D1I1P1V1P1K2P1K2A1N2.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	2.9051	0.1964	2101.75	2103.419	1	453.7	44.11765	L.S1T1L1P1E1I1Y1E1K2M1E1K2G1Q2I1V1G1R4.Y
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	1	2.7292	0.3167	1387.61	1388.653	2	365.1	54.545456	W.H3G1D1W2P1L1P1V1K2L1P1L1.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	1	2.5824	0.3201	1371.66	1372.653	1	428.5	59.090908	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	1	2.586	0.2784	1051.64	1052.335	1	367.8	61.11111	R.G1L1V1K2S1P1I1K2V1V1.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	2	4.0213	0.1743	1373.51	1372.653	2	903.2	77.27273	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	3.9028	0.3171	1389.17	1388.653	1	913.2	77.27273	W.H3G1D1W2P1L1P1V1K2L1P1L1.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	3.3747	0.5021	1526.81	1528.838	1	977.8	61.538464	W.HGDWPLPVKLPLVG.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	1	3.6275	0.5242	1584.61	1585.889	1	711.5	60.714287	W.HGDWPLPVKLPLVGG.H
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	1	3.9187	0.3257	1548.73	1546.838	1	763.7	65.38461	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.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	1	4.2403	0.196	1530.76	1528.838	1	669.9	61.538464	W.HGDWPLPVKLPLVG.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	2	4.0285	0.3654	1544.83	1546.838	1	1584	73.07692	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.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	1	2.2786	0.2622	1209.63	1210.546	2	391.8	54.545456	R.GLVKSPIKVVGL.S
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	4.1809	0.3378	1807.53	1807.084	1	757.9	59.375	G.D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.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	2	4.213	0.3331	2061.67	2063.329	1	950.3	52.63158	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1.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	3.393	0.1672	2035.93	2037.329	1	929.2	52.63158	W.HGDWPLPVKLPLVGGHEGAG.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	1	3.1869	0.2966	1502.89	1502.782	2	347.7	50	W.P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1.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	2	4.0856	0.2109	1911.37	1909.198	2	635.3	50	W.HGDWPLPVKLPLVGGHEG.A
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	5.3908	0.5128	1872.75	1875.146	1	2720.6	78.125	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	2	3.9274	0.3104	1933.63	1933.198	1	968.1	55.88235	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1.A
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	5.3715	0.1849	2164.61	2163.461	1	1184.9	57.5	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.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	3	6.2355	0.4098	1872.29	1875.146	1	2287.5	59.375	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	2	4.9812	0.2428	2135.53	2136.461	1	1256.1	57.5	W.HGDWPLPVKLPLVGGHEGAGV.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	3	4.4151	0.2057	2163.32	2163.461	1	925.3	36.25	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.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	3	4.5296	0.2323	2136.11	2136.461	1	1171.9	40	W.HGDWPLPVKLPLVGGHEGAGV.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	3.2336	0.3097	2260.61	2263.594	1	339.1	35.714287	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1V1.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	4.3629	0.2311	2334.91	2334.726	1	606.5	45.454548	W.HGDWPLPVKLPLVGGHEGAGVVV.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	2	3.5639	0.3331	1406.73	1407.523	1	701.2	62.5	L.GIDGGEGKEELFR.S

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	3.3694	0.3433	1607.43	1607.761	1	552.1	57.14286	L.GIDGGEGKEELFRSI.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	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, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	2	4.1478	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
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	1	2.2794	0.2457	1039.63	1040.335	2	371.2	61.11111	R.GLVKSPIKVV.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	1	2.5284	0.2438	1371.68	1372.653	1	491.7	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	1	2.8215	0.2997	1387.71	1388.653	1	473.3	63.636364	W.H3G1D1W2P1L1P1V1K2L1P1L1.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	4.1543	0.2945	1389.27	1388.653	1	794.6	72.72727	W.H3G1D1W2P1L1P1V1K2L1P1L1.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	3.2467	0.4238	1584.61	1585.889	1	754.8	53.571426	W.HGDWPLPVKLPLVGG.H
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	4.5673	0.3791	1602.57	1604.889	1	1399.2	67.85714	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1.H
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	1	3.8202	0.4412	1527.82	1528.838	1	830.4	65.38461	W.HGDWPLPVKLPLVG.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	1	4.0913	0.34	1547.81	1546.838	1	934.5	69.230774	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.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	2	3.7892	0.311	1546.45	1546.838	2	1584	73.07692	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.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	2	3.6967	0.1943	1528.03	1528.838	2	1105.1	65.38461	W.HGDWPLPVKLPLVG.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	1	2.6647	0.1672	1223.68	1224.546	2	398.2	54.545456	R.G1L1V1K2S1P1I1K2V1V1G1L1.S
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	3.69	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
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	3.5887	0.2915	1820.81	1819.136	1	635.3	60.000004	H.G1K2L1E1Y1K2D1I1P1V1P1K2P1K2A1N2.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	4.7241	0.4506	1979.05	1980.277	1	1216.4	63.88889	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	6.2768	0.1857	2005.28	2005.277	1	1495.5	47.22222	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	4.4812	0.1615	1722.65	1723.031	3	1188.6	43.333332	W.HGDWPLPVKLPLVGGH.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	5.0083	0.4635	1872.73	1875.146	1	2044.3	71.875	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	2	4.8911	0.4199	1743.59	1745.031	1	1408.3	66.66667	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	5.0732	0.4569	1850.97	1852.146	1	2194.1	75	W.HGDWPLPVKLPLVGGHE.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	2	4.851	0.2868	1722.53	1723.031	1	2158.6	76.666664	W.HGDWPLPVKLPLVGGH.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	3	6.3864	0.463	1872.47	1875.146	1	1846.9	53.125	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	2	4.8889	0.4433	2160.73	2163.461	1	1124.1	57.5	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1.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	5.0006	0.1972	2136.17	2136.461	1	1036.8	55	W.HGDWPLPVKLPLVGGHEGAGV.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	3	5.9524	0.4437	1849.85	1852.146	1	2719.1	62.5	W.HGDWPLPVKLPLVGGHE.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	5.2536	0.3403	1742.9	1745.031	1	1579.1	51.666664	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	3.1536	0.2337	1560.89	1560.864	1	834.4	65.38461	D.W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	4.8128	0.1633	1982	1980.277	1	962.6	41.666664	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	2	4.8422	0.3295	2004.39	2005.277	1	1530.1	63.88889	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	4.9838	0.2384	2262.86	2263.594	1	939.3	38.095238	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1G1A1G1V1V1.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	3	4.124	0.1777	2237.69	2235.594	2	669.2	33.333336	W.HGDWPLPVKLPLVGGHEGAGVV.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	2.9069	0.2938	1715.17	1715.005	5	354.1	50	H.GDWPLPVKLPLVGGHE.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	2	2.903	0.3122	1041.33	1040.335	6	576.7	77.77778	R.GLVKSPIKVV.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	1	2.7936	0.2432	1387.78	1388.653	1	406.1	59.090908	W.H3G1D1W2P1L1P1V1K2L1P1L1.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	1	2.5366	0.3597	1371.62	1372.653	2	457.9	59.090908	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	4.3253	0.3016	1389.25	1388.653	1	964.5	77.27273	W.H3G1D1W2P1L1P1V1K2L1P1L1.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	1	4.0372	0.2692	1529.96	1528.838	1	702.8	61.538464	W.HGDWPLPVKLPLVG.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	1	3.2679	0.2435	1586.92	1585.889	1	406.5	46.42857	W.HGDWPLPVKLPLVGG.H
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	3.4332	0.2331	1487.81	1488.786	1	1007.8	66.66667	W.H3G1D1W2P1L1P1V1K2L1P1L1V1.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	1	4.0023	0.3302	1547.6	1546.838	1	985.2	69.230774	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.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	2	4.1249	0.3893	1584.69	1585.889	1	1560.6	71.42857	W.HGDWPLPVKLPLVGG.H
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	3.931	0.2191	1547.31	1546.838	2	1279.6	69.230774	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1.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	2	3.9058	0.1778	1375.33	1372.653	4	664.6	68.181816	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	3	4.426	0.2886	1797.2	1798.136	1	1553.2	46.666668	H.GKLEYKDIPVPKPKAN.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	3.5255	0.3463	1613.25	1612.953	1	1244.1	76.92308	H.GKLEYKDIPVPKPK.A
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	4.0178	0.1737	1528.61	1528.838	2	1290.1	69.230774	W.HGDWPLPVKLPLVG.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	2	5.166	0.5049	1873.97	1875.146	1	1755.5	65.625	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	2	5.2552	0.4408	2002.81	2005.277	1	1189.3	61.11111	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	2	4.8338	0.4932	1721.59	1723.031	1	2181.5	76.666664	W.HGDWPLPVKLPLVGGH.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	3	6.6669	0.4155	1850.69	1852.146	1	1951.9	56.25	W.HGDWPLPVKLPLVGGHE.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	5.1465	0.1981	1981.67	1980.277	1	1548.3	50	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	2	5.0269	0.5071	1849.89	1852.146	1	3140.9	84.375	W.HGDWPLPVKLPLVGGHE.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	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	41.666664	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

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	5.1551	0.2685	1746.29	1745.031	1	1501.1	66.66667	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	3	5.867	0.3839	1872.68	1875.146	1	1782.6	53.125	W.H3G1D1W2P1L1P1V1K2L1P1L1V1G1G1H3E1.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	2	4.015	0.3807	2135.43	2136.461	1	640.2	45	W.HGDWPLPVKLPLVGGHEGAGV.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	3	4.3842	0.1753	2137.7	2136.461	1	916.9	35	W.HGDWPLPVKLPLVGGHEGAGV.V
gi|6324485|ref|NP_014554.1|	YOL087C	hypothetical protein; Yol087cp	2	4.0447	0.4218	2352.45	2353.692	1	414.4	47.22222	N.EKKKPEFMPDLLEQIQESY.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
gi|6324485|ref|NP_014554.1|	YOL087C	hypothetical protein; Yol087cp	2	4.5922	0.2354	1750.53	1751.033	1	558.3	73.07692	N.E1K2K2K2P1E1F1M1P1D1L1L1E1Q2.I
gi|6324485|ref|NP_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
gi|6324485|ref|NP_014554.1|	YOL087C	hypothetical protein; Yol087cp	2	5.2599	0.2973	2308.13	2307.688	1	1277.2	57.894737	Q.D1A1H3I1L1P1I1T1K2I1L1Y1P1D1I1P1G1K2N2Y1.F
gi|6324484|ref|NP_014553.1|	YOL088C	Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity; overexpression suppresses the lethality of a pdi1 deletion but does not complement all Pdi1p functions; undergoes oxidation by Ero1p; Mpd2p	2	4.6703	0.3626	1874.47	1876.866	1	762.7	73.333336	L.S1H3I1E1D1Q2L1E1D1T1S1S1H3D1E1L1.-
gi|6324484|ref|NP_014553.1|	YOL088C	Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity; overexpression suppresses the lethality of a pdi1 deletion but does not complement all Pdi1p functions; undergoes oxidation by Ero1p; Mpd2p	2	3.6437	0.3595	1625.27	1625.859	1	836	61.538464	C.KTLAPVYEELGELY.A
gi|6324484|ref|NP_014553.1|	YOL088C	Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity; overexpression suppresses the lethality of a pdi1 deletion but does not complement all Pdi1p functions; undergoes oxidation by Ero1p; Mpd2p	2	3.4656	0.287	1967.19	1969.341	1	656.6	59.375	T.LCTDLPGFPIIELVKPR.T
gi|6324484|ref|NP_014553.1|	YOL088C	Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity; overexpression suppresses the lethality of a pdi1 deletion but does not complement 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|ref|NP_014549.1|	YOL092W	hypothetical protein; Yol092wp	2	3.566	0.2837	2929.51	2930.229	1	244.6	32	N.E1E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1V1F1.N
gi|6324480|ref|NP_014549.1|	YOL092W	hypothetical protein; Yol092wp	3	5.8766	0.3883	3476.51	3474.811	1	1240.4	33.62069	L.WYDNEEKPAVDPIHLSPANPINENVLHDVF.N
gi|6324480|ref|NP_014549.1|	YOL092W	hypothetical protein; Yol092wp	3	6.3344	0.3975	3628.91	3628.97	1	1248.3	30.833334	C.L1W2Y1D1N2E1E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1V1F1.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
gi|6324480|ref|NP_014549.1|	YOL092W	hypothetical protein; Yol092wp	3	4.4316	0.3091	3587.48	3587.97	1	536.6	24.166666	C.LWYDNEEKPAVDPIHLSPANPINENVLHDVF.N
gi|6324480|ref|NP_014549.1|	YOL092W	hypothetical protein; Yol092wp	2	4.0802	0.3705	2798.53	2800.114	1	478.7	39.583336	E.E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1V1F1.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
gi|6324480|ref|NP_014549.1|	YOL092W	hypothetical protein; Yol092wp	3	5.8517	0.4743	3789.38	3790.109	1	1072.9	29.032257	Q.C1L1W2Y1D1N2E1E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1V1F1.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|	YOL092W	hypothetical protein; Yol092wp	3	7.1836	0.4867	3265.73	3266.502	1	1522.7	33.333336	L.W2Y1D1N2E1E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1.V
gi|6324480|ref|NP_014549.1|	YOL092W	hypothetical protein; Yol092wp	3	3.8262	0.387	2798.03	2800.114	1	622	30.208334	E.E1K2P1A1V1D1P1I1H3L1S1P1A1N2P1I1N2E1N2V1L1H3D1V1F1.N
gi|37362692|ref|NP_014545.2|	YOL096C	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing complex; Coq3p	2	4.7225	0.2682	1914.23	1915.224	1	992.1	66.66667	Q.V1K2I1Q2N2P1E1I1F1V1P1G1F1N2Y1K2.E
gi|37362692|ref|NP_014545.2|	YOL096C	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing complex; Coq3p	2	4.8664	0.18	1894.83	1894.224	1	1307.4	76.666664	Q.VKIQNPEIFVPGFNYK.E
gi|37362692|ref|NP_014545.2|	YOL096C	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing complex; Coq3p	1	2.933	0.3329	1459.71	1460.719	2	326	59.090908	C.WSRLNPEKGILF.L
gi|37362692|ref|NP_014545.2|	YOL096C	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing complex; Coq3p	2	3.4731	0.2702	1512.61	1511.78	1	558.6	66.66667	A.KEHAKKDPMLEGK.I
gi|37362692|ref|NP_014545.2|	YOL096C	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing complex; Coq3p	2	3.2788	0.3448	1458.45	1460.719	1	835.8	68.181816	C.WSRLNPEKGILF.L
gi|37362692|ref|NP_014545.2|	YOL096C	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing complex; Coq3p	2	3.1343	0.2589	1571.57	1573.878	1	713.2	62.5	C.WSRLNPEKGILFL.S
gi|6324472|ref|NP_014541.1|	YOL100W	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling 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
gi|6324472|ref|NP_014541.1|	YOL100W	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling 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
gi|6324472|ref|NP_014541.1|	YOL100W	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling 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
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	3.1313	0.371	1573.52	1574.718	1	497.9	66.66667	L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.926	0.411	1555.51	1556.718	1	521.6	66.66667	L.KLTDDGHLEFFPH.S

gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for 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
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.8263	0.5098	1554.25	1556.718	1	1214	83.33333	L.KLTDDGHLEFFPH.S
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.4462	0.2587	2034.59	2036.294	1	599.4	56.25	Q.NIPEPHELPLKSDYHVF.R
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.6626	0.3066	2712.83	2714.05	1	566.4	40.909092	L.WYTKPAVDKSESWSDLLRPVTSF.Q
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.638	0.3027	1425.89	1426.615	1	668.5	72.72727	S.A1H3F1D1V1K2H3P1L1N2T1K2.W
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	4.6892	0.3071	1782.79	1781.914	1	1320.2	76.666664	K.KFEENVSVDDTTATPK.T
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	3	3.8163	0.3017	1574.72	1574.718	1	862.1	50	L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	3.4852	0.3121	1391.45	1390.552	1	1209.3	77.27273	R.G1K2G1A1D1I1D1E1L1W2L1R4.T
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	4.4975	0.4601	1576.21	1574.718	1	1249.6	83.33333	L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.7892	0.3643	1573.61	1574.718	1	442.2	62.5	L.K2L1T1D1D1G1H3L1E1F1F1P1H3.S
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.6958	0.4083	1555.77	1556.718	1	506.6	62.5	L.KLTDDGHLEFFPH.S
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	4.0793	0.3062	2059.05	2059.295	1	665.8	56.25	Q.N2I1P1E1P1H3E1L1P1L1K2S1D1Y1H3V1F1.R
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	2	2.9857	0.1678	1078.59	1078.232	4	734.2	81.25	S.A1H3F1D1V1K2H3P1L1.N
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.3949	0.2696	1257.45	1257.429	6	285.5	55	K.SEDKEPLLRIG.G
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.6665	0.1577	1005.35	1006.153	9	258.7	78.57143	A.H3F1D1V1K2H3P1L1.N
gi|6324433|ref|NP_014502.1|	YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	1	2.7564	0.2369	992.39	993.153	9	263.4	78.57143	A.HFDVKHPL.N
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	3.3757	0.17	1107.57	1108.366	9	688.4	81.25	A.G1G1M1I1R4F1P1M1W2.T
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	3.9292	0.1811	1824.75	1826.898	8	771.9	67.85714	-.M1L1E1T1D1H3S1R4N2D1N2L1D1D1K2.S
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	4.1986	0.3064	2144.53	2146.16	1	596.8	52.941177	M.L1E1T1D1H3S1R4N2D1N2L1D1D1K2S1T1V1C1.Y
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	4.2443	0.3224	2278.11	2278.353	1	835.2	52.77778	-.M1L1E1T1D1H3S1R4N2D1N2L1D1D1K2S1T1V1C1.Y
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	3.4924	0.2315	2252.17	2251.353	1	689	50	-.MLETDHSRNDNLDDKSTVC.Y
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	3	3.8086	0.2974	2441.51	2442.529	1	1091.6	38.157894	-.M1L1E1T1D1H3S1R4N2D1N2L1D1D1K2S1T1V1C1Y1.S
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	4.5	0.454	2696.23	2698.009	1	1005.7	42	S.T1T1H3N2E1M1A1T1V1T1G1L1L1M1S1V1Y1Q2I1G1D1A1V1G1A1S1.I
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	5.1993	0.4917	2608.47	2609.931	1	1360.2	47.916664	S.T1T1H3N2E1M1A1T1V1T1G1L1L1M1S1V1Y1Q2I1G1D1A1V1G1A1.S
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	3.4229	0.4019	1682.65	1683.692	1	633.3	65.38461	D.H3S1R4N2D1N2L1D1D1K2S1T1V1C1.Y
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	2	3.2816	0.2377	1509.85	1510.868	1	975	66.66667	G.I1A1G1G1M1I1R4F1P1M1W2T1L1.V
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	1	2.4263	0.1592	1051.43	1052.225	1	418.5	71.42857	M.L1H3F1Y1P1H3P1K2.V
gi|6324415|ref|NP_014484.1|	YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron 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
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	4.1723	0.2697	3018.65	3020.081	3	418.6	27.173912	L.R4L1V1D1D1D1E1N2N2P1S1H3Y1P1H3P1Y1E1Y1E1I1D1H3Q2.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	3.903	0.2801	2433.57	2433.869	1	527	37.5	L.A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1E1.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	41.666664	A.N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1E1.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.D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1E1E1I1K2.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	41.666664	A.N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1E1E1I1K2T1V1D1P1A1.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.L1A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1E1E1I1K2T1V1D1P1A1.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.N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1E1.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.L1A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1A1N2L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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.L1E1D1I1I1F1E1I1E1K2P1L1V1V1P1V1K2L1.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	1	2.6738	0.1855	1265.51	1266.555	1	423.9	65	L.L1K2E1K2P1N2A1L1K2P1L1.S
gi|6324575|ref|NP_014644.1|	YOR002W	Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparagine residues of proteins during N-linked protein glycosylation; mutations in human ortholog are associated with disease; Alg6p	2	3.5816	0.3771	1814.13	1815.076	1	620.6	63.333332	R.L1L1V1N2K2P1A1E1E1S1F1Y1A1S1P1M1.Y
gi|6324575|ref|NP_014644.1|	YOR002W	Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparagine residues of proteins during N-linked protein glycosylation; mutations in human ortholog are associated with disease; Alg6p	2	3.1898	0.1878	1590.27	1593.032	6	360.9	53.846157	H.E1K2T1I1L1I1P1L1L1P1I1T1L1L1.Y
gi|6324575|ref|NP_014644.1|	YOR002W	Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparagine residues of proteins during N-linked protein glycosylation; mutations in human ortholog are associated with disease; Alg6p	2	3.9602	0.2874	1579.59	1578.032	1	577.8	65.38461	H.EKTILIPLLPITLL.Y
gi|6324575|ref|NP_014644.1|	YOR002W	Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparagine residues of proteins during N-linked protein glycosylation; mutations in human ortholog are associated with disease; Alg6p	2	3.9967	0.2892	1479.37	1478.872	1	539.4	70.83333	H.E1K2T1I1L1I1P1L1L1P1I1T1L1.L
gi|6324575|ref|NP_014644.1|	YOR002W	Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparagine residues of proteins during N-linked protein 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	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the 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
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	3.9415	0.4019	3046.73	3048.376	1	371.9	34.615387	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	5.4018	0.3439	2340.65	2341.674	1	844.3	47.368423	L.T1K2L1P1N2F1N2E1V1S1P1E1E1R4I1P1L1F1I1A1.K
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	5.7006	0.2783	2551.13	2549.886	1	1166	39.285713	F.E1R4L1P1T1P1T1K2L1N2P1D1T1D1L1E1L1I1K2T1P1Q2.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
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	4.4286	0.2448	2443.55	2443.849	1	708	47.5	L.TKLPNFNEVSPEERIPLFIAK.V
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	4.6644	0.3555	2469.05	2471.849	1	1017.7	50	L.T1K2L1P1N2F1N2E1V1S1P1E1E1R4I1P1L1F1I1A1K2.V
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	4.7494	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; Rts1p	2	3.5644	0.216	1561.95	1560.741	1	918.7	66.66667	L.NEIEDIFEVIEPL.E
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	4.5465	0.4058	3079.76	3080.376	1	499.9	24.038462	N.L1F1R4P1I1P1P1P1V1N2P1V1G1D1I1Y1D1P1D1E1D1E1P1V1N2E1L1.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	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
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	5.1078	0.2848	3540.71	3539.926	1	1094.6	29.166666	N.LFRPIPPPVNPVGDIYDPDEDEPVNELAWPH.M
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	5.2807	0.335	2549.09	2549.886	1	814.2	34.523808	F.E1R4L1P1T1P1T1K2L1N2P1D1T1D1L1E1L1I1K2T1P1Q2.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	3.9021	0.2388	2549.17	2549.886	1	285.4	38.095238	F.E1R4L1P1T1P1T1K2L1N2P1D1T1D1L1E1L1I1K2T1P1Q2.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	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
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	3.2376	0.4283	2031.95	2031.094	1	503.1	47.058823	V.NPVGDIYDPDEDEPVNEL.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	4.6969	0.4072	3047.42	3048.376	1	1213.8	31.730768	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	4.1465	0.3383	3048.67	3048.376	1	485.3	38.46154	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	4.6109	0.3382	2313.71	2315.674	1	1055.8	52.63158	L.TKLPNFNEVSPEERIPLFIA.K
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	6.1089	0.4399	3576.38	3578.926	1	858.1	24.166666	N.L1F1R4P1I1P1P1P1V1N2P1V1G1D1I1Y1D1P1D1E1D1E1P1V1N2E1L1A1W2P1H 3.M
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	3.0587	0.3202	1815.59	1815.134	2	397.3	46.666668	N.L1F1R4P1I1P1P1P1V1N2P1V1G1D1I1Y1.D
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	4.6506	0.4222	2018.35	2019.308	1	1500.1	68.75	T.KLNPDTDLELIKTPQRH.S
gi|6324595|ref|NP_014664.1|	YOR021C	hypothetical protein; Yor021cp	2	3.2264	0.1936	2320.49	2321.64	1	424.1	44.11765	D.RIAFEDIKFIDYPEFRFN.K
gi|6324595|ref|NP_014664.1|	YOR021C	hypothetical protein; Yor021cp	3	5.4351	0.2965	2346.5	2347.64	2	1627.1	42.647057	D.R4I1A1F1E1D1I1K2F1I1D1Y1P1E1F1R4F1N2.K
gi|6324595|ref|NP_014664.1|	YOR021C	hypothetical protein; Yor021cp	2	3.2389	0.1838	2346.51	2347.64	3	503.3	44.11765	D.R4I1A1F1E1D1I1K2F1I1D1Y1P1E1F1R4F1N2.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|	YOR021C	hypothetical protein; Yor021cp	2	3.5141	0.2518	2000.13	2001.215	1	583	60.714287	A.F1E1D1I1K2F1I1D1Y1P1E1F1R4F1N2.K
gi|6324595|ref|NP_014664.1|	YOR021C	hypothetical protein; Yor021cp	2	3.2893	0.2028	2164.57	2165.453	1	584.2	46.875	R.IAFEDIKFIDYPEFRFN.K
gi|6324595|ref|NP_014664.1|	YOR021C	hypothetical protein; Yor021cp	2	3.2106	0.2936	1589.23	1589.834	1	1052.8	77.27273	D.IKFIDYPEFRFN.K
gi|6324617|ref|NP_014686.1|	YOR043W	Protein required, with binding partner Psr1p, for full activation of the general stress response, possibly through Msn2p dephosphorylation; regulates growth during the diauxic shift; negative regulator of G1 cyclin expression; Whi2p	2	4.0743	0.3217	1754.39	1753.033	2	460.6	53.571426	N.N2E1Q2D1I1L1H3Q2K2P1A1I1I1V1L1.R
gi|6324617|ref|NP_014686.1|	YOR043W	Protein required, with binding partner Psr1p, for full activation of the general stress response, possibly through Msn2p dephosphorylation; regulates growth during the diauxic shift; negative regulator of G1 cyclin expression; Whi2p	2	3.6618	0.241	1731.85	1732.033	1	452.4	53.571426	N.NEQDILHQKPAIIVL.R
gi|6324617|ref|NP_014686.1|	YOR043W	Protein required, with binding partner Psr1p, for full activation of the general stress response, possibly through Msn2p dephosphorylation; regulates growth during the 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	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus; Dbp5p	2	4.3323	0.1756	1850.35	1851.048	3	891.1	64.28571	T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2.K
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	3	6.0212	0.2868	1979.96	1981.222	1	1362.8	51.666664	T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.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	4.7609	0.3397	1978.65	1981.222	1	866.2	56.666668	T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.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	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
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	3.4494	0.244	1686.31	1685.017	1	320.2	65.38461	A.EKLVPKVEEKKTKQ.E
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	3	5.4181	0.3434	1832.06	1830.048	1	1895.9	53.571426	T.RVPTDDWDEVEKIVK.K
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	3	5.2758	0.3061	1957.37	1958.222	1	2091.2	53.333336	T.RVPTDDWDEVEKIVKK.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	4.2325	0.2751	1958.13	1958.222	1	667.4	56.666668	T.RVPTDDWDEVEKIVKK.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	4.2038	0.2625	1979.95	1981.222	1	588.4	50	T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.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	3	5.4028	0.2944	1978.34	1981.222	1	1441.3	51.666664	T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.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	3.3929	0.3432	1555.91	1556.886	1	433.3	62.5	A.EKLVPKVEEKKTK.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	3.663	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
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	3	6.0309	0.3113	1978.82	1981.222	1	2001	55	T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.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	4.4144	0.3288	1979.91	1981.222	2	520.2	50	T.R4V1P1T1D1D1W2D1E1V1E1K2I1V1K2K2.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	3	5.6612	0.312	1959.44	1958.222	1	1617.2	55	T.RVPTDDWDEVEKIVKK.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	3	4.7741	0.1606	2191.46	2190.519	1	1511.2	44.11765	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	2.9429	0.2908	1493.85	1494.79	1	459.1	59.090908	K.R4F1L1P1K2D1T1Q2L1V1L1F1.S
gi|6324631|ref|NP_014700.1|	YOR057W	Probable cochaperone, regulates activity of Cyr1p (adenylyl cyclase); involved in 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
gi|6324631|ref|NP_014700.1|	YOR057W	Probable cochaperone, regulates activity of Cyr1p (adenylyl cyclase); involved in assembly of the kinetochore complex, associates with the SCF (Skp1p/Cdc53p/F box protein) ubiquitin ligase complex; Sgt1p	2	4.1915	0.3429	2050.67	2051.26	1	756.9	56.25	L.GYVDDTLPLWEDRLETK.L
gi|6324637|ref|NP_014706.1|	YOR063W	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 double stranded RNA virus; Rpl3p	2	3.4691	0.2725	1694.17	1696.841	2	469.2	58.333332	S.E1K2V1D1W2A1R4E1H3F1E1K2T1.V
gi|6324637|ref|NP_014706.1|	YOR063W	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 double stranded RNA virus; Rpl3p	1	2.6232	0.3053	1355.57	1356.527	1	321.1	63.636364	F.GKGRFQTPAEKH.A
gi|6324637|ref|NP_014706.1|	YOR063W	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 double stranded RNA virus; Rpl3p	2	3.962	0.4298	1674.67	1675.841	1	580.2	70.83333	S.EKVDWAREHFEKT.V
gi|6324637|ref|NP_014706.1|	YOR063W	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 double stranded RNA virus; Rpl3p	2	3.4041	0.3574	1671.61	1671.98	1	658.3	60.714287	R.VKAFPKDDRSKPVAL.T
gi|6324637|ref|NP_014706.1|	YOR063W	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 double stranded RNA virus; Rpl3p	2	3.0719	0.1875	1693.89	1692.98	1	472.2	60.714287	R.V1K2A1F1P1K2D1D1R4S1K2P1V1A1L1.T
gi|6324637|ref|NP_014706.1|	YOR063W	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 double stranded RNA virus; Rpl3p	1	2.2592	0.1894	1208.49	1208.365	1	353.2	61.11111	R.KYEAPRHGHL.G
gi|6324639|ref|NP_014708.1|	YOR065W	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex; Cyt1p	2	3.6112	0.2351	2692.09	2692.855	1	674.9	43.18182	M.AEEFEYDDEPDEQGNPKKRPGKL.S
gi|6324639|ref|NP_014708.1|	YOR065W	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex; Cyt1p	3	5.6883	0.4105	2724.95	2723.855	1	1481.8	42.045452	M.A1E1E1F1E1Y1D1D1E1P1D1E1Q2G1N2P1K2K2R4P1G1K2L1.S
gi|6324639|ref|NP_014708.1|	YOR065W	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex; Cyt1p	2	3.6758	0.281	2722.31	2723.855	3	298	34.090908	M.A1E1E1F1E1Y1D1D1E1P1D1E1Q2G1N2P1K2K2R4P1G1K2L1.S
gi|6324639|ref|NP_014708.1|	YOR065W	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex; Cyt1p	3	6.2668	0.4296	2724.17	2723.855	1	1594.3	42.045452	M.A1E1E1F1E1Y1D1D1E1P1D1E1Q2G1N2P1K2K2R4P1G1K2L1.S
gi|6324639|ref|NP_014708.1|	YOR065W	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex; Cyt1p	2	4.0343	0.2515	2722.63	2723.855	1	695.9	45.454548	M.A1E1E1F1E1Y1D1D1E1P1D1E1Q2G1N2P1K2K2R4P1G1K2L1.S
gi|6324639|ref|NP_014708.1|	YOR065W	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex; Cyt1p	3	4.7342	0.4688	2690.72	2692.855	1	1005.4	35.227272	M.AEEFEYDDEPDEQGNPKKRPGKL.S
gi|6324659|ref|NP_014728.1|	YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is 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
gi|6324659|ref|NP_014728.1|	YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is 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
gi|6324659|ref|NP_014728.1|	YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is important for N-glycosylation of a subset of proteins; Ost3p	2	3.8707	0.3196	2170.73	2169.376	1	515.1	50	L.K2D1S1S1F1E1N2I1L1A1P1P1H3E1N2A1Y1I1V1.A
gi|6324659|ref|NP_014728.1|	YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is important for N-glycosylation of a subset of proteins; Ost3p	2	2.9294	0.247	1460.35	1460.67	5	400.9	54.166668	V.NLEDPSKTIPKAF.Q
gi|6324659|ref|NP_014728.1|	YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is important for N-glycosylation of a subset of proteins; Ost3p	2	3.0798	0.2747	1288.45	1288.549	1	491.8	70	K.S1P1A1Y1P1F1P1L1L1R4L1.S

gi|6324659|ref|NP_014728.1|	YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which 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
gi|6324659|ref|NP_014728.1|	YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is important for N-glycosylation of a subset of proteins; Ost3p	2	3.5857	0.352	1634.31	1634.987	1	389	61.538464	F.T1I1K2S1P1A1Y1P1F1P1L1L1R4L1.S
gi|6324659|ref|NP_014728.1|	YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is 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
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	4.5754	0.3163	1871.31	1869.079	1	1081.3	67.64706	K.KLPDGSVEELPDLNTGIA.K
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.4247	0.3206	1842.17	1843.012	1	714.8	60.714287	R.T1V1R4D1T1L1N2P1V1W2D1E1T1L1Y1.V
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.3937	0.3359	1822.79	1823.012	2	663.5	57.14286	R.TVRDTLNPVWDETLY.V
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	2.9982	0.2238	1377.71	1378.612	1	996	72.72727	Q.L1L1K2V1P1D1F1D1F1V1A1T1.L
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	4.3733	0.3409	1984.19	1984.081	1	743.3	56.25	K.DENDKYEETIDEKAKVG.R
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.6923	0.2844	2006.47	2005.081	1	617.8	59.375	K.D1E1N2D1K2Y1E1E1T1I1D1E1K2A1K2V1G1.R
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	4.0632	0.4098	2069.81	2070.248	1	829.6	59.375	W.EDKDELTLDDELMDMTR.E
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	4.3817	0.3587	2495.43	2496.817	1	793.2	45.454548	T.LEEKKLPDGSVEELPDLNTGIAK.V
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	5.4207	0.4324	1996.47	1997.253	1	1563.1	66.66667	K.KLPDGSVEELPDLNTGIAK.V
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	4.6216	0.4019	2056.33	2057.304	1	559.6	59.375	R.T1V1R4D1T1L1N2P1V1W2D1E1T1L1Y1V1L1.L
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	4.3735	0.2858	2056.55	2055.251	1	791.9	68.75	T.RETFLDNIIPDSLYGDW.Y
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.5163	0.1855	1645.93	1643.835	1	902.9	63.333332	M.AKEDTGVTAPKKPETA.Q
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	3	4.6396	0.4144	3017.6	3020.392	1	656.3	29.807693	R.F1F1P1T1L1E1E1K2K2L1P1D1G1S1V1E1E1L1P1D1L1N2T1G1I1A1K2.V
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.8369	0.328	2542.51	2541.779	1	1069.2	55	T.RETFLDNIIPDSLYGDWYHSV.A
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.1454	0.217	2776.03	2776.006	3	232.2	35.714287	E.DKAKFDQEWNEVKELEDMYSNR.Q
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	2.9227	0.2368	2173.27	2171.464	1	388.8	44.11765	R.T1V1R4D1T1L1N2P1V1W2D1E1T1L1Y1V1L1L1.N
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.5144	0.2989	2370.25	2368.643	8	176.3	35.714287	T.LEEKKLPDGSVEELPDLNTGIA.K
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.1967	0.2477	2076.17	2077.251	1	291.7	43.75	T.R4E1T1F1L1D1N2I1I1P1D1S1L1Y1G1D1W2.Y
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.8546	0.3784	2150.31	2148.464	1	585.5	52.941177	R.TVRDTLNPVWDETLYVLL.N
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.3057	0.252	1366.41	1365.612	1	1115.9	77.27273	Q.LLKVPDFDFVAT.L
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	1	2.5438	0.2707	1378.78	1378.612	1	432	50	Q.L1L1K2V1P1D1F1D1F1V1A1T1.L
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.4456	0.3406	2034.59	2035.304	1	489.4	50	R.TVRDTLNPVWDETLYVL.L
gi|6324660|ref|NP_014729.1|	YOR086C	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 Tcb3p interact; Tcb1p	2	3.8098	0.3752	1620.29	1620.991	2	512	57.692307	K.K2Y1M1G1P1I1L1L1P1P1F1S1L1Q2.L
gi|6324660|ref|NP_014729.1|	YOR086C	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 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	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; 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
gi|6324673|ref|NP_014742.1|	YOR099W	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr1p	3	3.9213	0.289	1667.3	1666.843	1	1337	55.76923	Y.HVPFHSCPIDTSIR.L
gi|6324673|ref|NP_014742.1|	YOR099W	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr1p	3	4.444	0.2689	2307.62	2307.535	1	1074.4	39.0625	L.M1D1D1Y1D1W2Y1W2R4V1E1P1D1I1K2L1H3.C
gi|6324673|ref|NP_014742.1|	YOR099W	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; 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
gi|6324673|ref|NP_014742.1|	YOR099W	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr1p	3	4.2671	0.2483	2034.17	2032.234	1	939.3	46.42857	L.MDDYDWYWRVEPDIK.L

gi|6324683|ref|NP_014752.1|	YOR109W	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 endosome pathway; hyperosmotic stress causes translocation to actin patches; Inp53p	3	4.1004	0.3161	2583.02	2583.908	1	498.5	32.5 N.N2F1M1D1K2E1K2Q2Q2N2I1D1T1L1L1G1R4L1P1Y1Q2.K
gi|6324683|ref|NP_014752.1|	YOR109W	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 endosome pathway; hyperosmotic stress causes translocation to actin patches; Inp53p	2	3.4156	0.3035	1718.61	1716.117	1	772.9	71.42857 W.LFPIGEKFKPDIVVL.G
gi|6324683|ref|NP_014752.1|	YOR109W	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 endosome pathway; hyperosmotic stress causes translocation to actin patches; Inp53p	3	4.069	0.2784	2786.6	2786.161	1	826.2	32.954548 N.N2F1M1D1K2E1K2Q2Q2N2I1D1T1L1L1G1R4L1P1Y1Q2K2A1.V
gi|6324683|ref|NP_014752.1|	YOR109W	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 endosome pathway; hyperosmotic stress causes translocation to actin patches; Inp53p	2	3.0389	0.2203	1732.91	1733.117	1	532.4	64.28571 W.L1F1P1I1G1E1K2F1K2P1D1I1V1V1L1.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
gi|6324686|ref|NP_014755.1|	YOR112W	hypothetical protein; Yor112wp	2	4.4142	0.2103	1721.33	1720.792	1	1217.9	76.92308 N.KSWNDELNDDGWIQ.D
gi|6324686|ref|NP_014755.1|	YOR112W	hypothetical protein; Yor112wp	2	3.5669	0.172	1739.47	1740.792	4	714.5	61.538464 N.K2S1W2N2D1E1L1N2D1D1G1W2I1Q2.D
gi|6324686|ref|NP_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
gi|6324705|ref|NP_014774.1|	YOR131C	hypothetical protein; Yor131cp	2	3.0205	0.2367	1675.53	1675.928	1	491	57.692307 R.EFRPTKPQPDPLLH.I
gi|6324705|ref|NP_014774.1|	YOR131C	hypothetical protein; Yor131cp	3	4.5577	0.2716	2650.82	2650.007	1	880	38.095238 L.HFIDTLPTEKEKKEAHDRIELV.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.G1I1E1H3I1V1C1P1G1V1V1Q2.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
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	3.2391	0.3143	1351.45	1350.543	1	976.7	75 T.T1Y1E1N2V1D1L1V1L1I1R4.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	4.1332	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.G1L1T1P1S1A1N2I1G1H3K2I1S1I1F1.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; Idh2p	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; Idh2p	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 of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	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 of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	2	3.0941	0.2807	1235.17	1234.438	1	1288.2	83.33333 T.YENVDLVLIR.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	2.4606	0.3271	1233.69	1234.438	1	499.3	72.22222 T.YENVDLVLIR.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	3.157	0.3182	1436.7	1436.645	1	995.3	68.181816 A.KELSKEYPDLTL.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	2.4154	0.2519	993.91	994.211	1	345.1	66.66667 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; Idh2p	1	3.3565	0.3326	1191.59	1192.404	1	517.7	72.72727 L.K2G1P1L1A1T1P1I1G1K2G1H3.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; Idh2p	1	3.5449	0.3891	1176.63	1176.404	1	756	72.72727 L.KGPLATPIGKGH.R
gi|6324715|ref|NP_014784.1|	YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of 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	Nuclear actin-related protein involved in chromatin remodeling, component of 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.K2N2D1P1S1P1I1E1W2I1F1D1D1S1.K
gi|6324715|ref|NP_014784.1|	YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes; Arp8p	2	4.2047	0.3276	1864.51	1863.167	1	574.1	62.5 N.SIKIGFPKDDHPVVVPN.C

gi|6324715|ref|NP_014784.1|	YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes; Arp8p	2	2.9109	0.1541	1577.13	1576.703	1	828.8	66.66667 E.KNDPSPIEWIFDD.S
gi|6324715|ref|NP_014784.1|	YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of 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
gi|6324737|ref|NP_014806.1|	YOR163W	Diadenosine polyphosphate hydrolase, member of the MutT family of nucleotide hydrolases with high specificity for diadenosine hexa- and pentaphosphates, required for efficient hydrolysis of diphosphorylated inositol polyphosphates; Ddp1p	2	4.2429	0.2516	1941.69	1943.208	1	757	67.85714 E.D1M1R4P1P1K2D1W2N2K2D1I1K2Q2F1.E
gi|6324737|ref|NP_014806.1|	YOR163W	Diadenosine polyphosphate hydrolase, member of the MutT family of nucleotide hydrolases with high specificity for diadenosine hexa- and pentaphosphates, required for efficient hydrolysis of diphosphorylated inositol polyphosphates; Ddp1p	2	4.1038	0.2664	1920.51	1919.208	2	509.9	60.714287 E.DMRPPKDWNKDIKQF.E
gi|6324739|ref|NP_014808.1|	YOR165W	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 Defective); Sey1p	2	3.906	0.3767	1562.61	1562.822	1	747.5	75 K.K2N2L1V1P1E1L1K2D1H3V1I1H3.L
gi|6324739|ref|NP_014808.1|	YOR165W	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 Defective); Sey1p	2	3.6543	0.1623	2146.17	2146.287	1	848.6	53.125 E.NCWDQIERNKDLDLPTQ.Q
gi|6324739|ref|NP_014808.1|	YOR165W	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 Defective); Sey1p	1	2.3753	0.2459	1421.52	1422.54	1	154.6	66.66667 L.R4D1R4F1E1D1V1F1R4Y1.D
gi|6324739|ref|NP_014808.1|	YOR165W	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 Defective); Sey1p	2	3.1662	0.2219	1543.47	1542.822	1	524.6	66.66667 K.KNLVPELKDHVIH.L
gi|6324742|ref|NP_014811.1|	YOR168W	Glutamine tRNA synthetase, monomeric class I tRNA synthetase that catalyzes the specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in enzyme-tRNA interactions; Gln4p	3	4.1501	0.3181	3051.56	3053.401	1	511.3	25 E.RSDFSENVDDKEFFRLTPNQPVGLIK.V
gi|6324742|ref|NP_014811.1|	YOR168W	Glutamine tRNA synthetase, monomeric class I tRNA synthetase that catalyzes the specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in enzyme-tRNA interactions; Gln4p	2	3.1529	0.3105	1631.53	1630.866	1	337.3	61.538464 K.S1L1E1K2D1E1A1G1K2I1I1R4I1H3.V
gi|6324742|ref|NP_014811.1|	YOR168W	Glutamine tRNA synthetase, monomeric class I tRNA synthetase that catalyzes the specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in enzyme-tRNA interactions; Gln4p	1	2.8055	0.2221	1105.89	1106.357	6	269.9	68.75 E.R4Y1K2L1V1P1G1I1F1.A
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	2.4387	0.2171	1168.54	1169.277	2	552.2	65 L.HEIDLGVIGES.E
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	2.5993	0.1599	1435.57	1435.573	5	328.8	60.000004 S.KVEETYDFLYQ.L
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	3.6652	0.3316	1518.85	1519.746	1	325.6	70.83333 Q.YREIGGGSPIRKW.S
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	3.4328	0.2117	1667.67	1668.977	9	384.1	53.846157 K.LQEFPQPVRDKVVL.L
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	3.008	0.2144	1544.13	1544.67	1	459.9	62.5 L.DKTCPETAPHKPY.V
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	2.7209	0.2477	1518.7	1519.746	1	320.8	66.66667 Q.YREIGGGSPIRKW.S
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	2.9396	0.2434	1562.67	1561.67	1	418.1	66.66667 L.D1K2T1C1P1E1T1A1P1H3K2P1Y1.V
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	4.318	0.1912	1647.31	1648.869	1	931.1	61.538464 W.S1V1I1D1R4W2P1T1N2E1G1L1I1K2.A
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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
gi|6324750|ref|NP_014819.1|	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of 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	3.6043	0.2893	1538.47	1540.746	1	303.6	66.66667 Q.Y1R4E1I1G1G1G1S1P1I1R4K2W2.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine 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
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.8906	0.3456	2239.49	2241.512	1	844.5	55.555557 F.V1N2K2V1D1T1I1D1D1P1E1M1L1E1L1V1E1M1E1.M
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.705	0.3468	2009.87	2007.275	1	719.1	53.125 N.KVDTIDDPEMLELVEME.M

gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	4.347	0.2368	2142.35	2143.323	1	666.6	52.941177	L.D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1.L
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	5.2202	0.3762	3386.33	3386.78	1	567.8	25	L.D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1S1I1S1.G
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.1386	0.3128	3352.37	3352.78	1	466.8	23.214285	L.DAVDEYIPTPERDLNKPFLMPVEDIFSIS.G
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.5428	0.1917	2345.67	2346.642	1	323	39.473686	K.LLDAVDEYIPTPERDLNKPF.L
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.146	0.1604	2282.01	2283.625	1	472.8	41.666664	I.P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	2.9262	0.1774	3065.73	3065.465	1	401.6	32	L.DAVDEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	3.9634	0.3159	3063.08	3065.465	1	690.7	30.000002	L.DAVDEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.2632	0.2696	2545.79	2546.941	1	381.7	35.714287	I.PTPERDLNKPFLMPVEDIFSIS.G
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.1604	0.2774	3324.8	3324.783	1	702.8	26.85185	K.L1L1D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.6835	0.3816	3612.77	3615.099	1	661.5	23.333334	K.L1L1D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1S1I1S1.G
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.7156	0.3635	3576.14	3579.099	1	716.1	25.833332	K.LLDAVDEYIPTPERDLNKPFLMPVEDIFSIS.G
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.4145	0.3402	3453.14	3454.958	1	1136.2	28.57143	M.K2L1L1D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.2286	0.274	3466.46	3465.94	2	766.9	24.13793	L.LDAVDEYIPTPERDLNKPFLMPVEDIFSIS.G
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	3.8152	0.2617	3289.01	3291.783	1	881.5	27.777779	K.LLDAVDEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	4.4382	0.4528	2474.09	2474.816	1	772.9	47.5	M.KLLDAVDEYIPTPERDLNKPF.L
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	4.2946	0.4369	2501.85	2501.816	1	691.4	47.5	M.K2L1L1D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1.L
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.3136	0.3877	3436.64	3435.958	1	537.3	24.107143	M.KLLDAVDEYIPTPERDLNKPFLM@PVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	5.9035	0.4244	3419.36	3419.958	1	1916.9	33.035713	M.KLLDAVDEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.8481	0.2027	2119.43	2120.323	1	598.1	52.941177	L.DAVDEYIPTPERDLNKPF.L
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.8084	0.3417	2807.65	2808.165	1	588.1	38.636364	V.D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.5084	0.322	2778.49	2780.165	1	564.3	36.363636	V.DEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.3103	0.1666	2979.85	2980.376	1	401.9	33.333336	D.A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.5698	0.4366	2948.11	2950.376	1	479.6	35.416664	D.AVDEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.1874	0.3371	2978.57	2980.376	1	499.5	29.166666	D.A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	3.9599	0.2835	2949.41	2950.376	1	726.2	32.291664	D.AVDEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine 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
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	2.9991	0.3242	3063.15	3065.465	1	451	32	L.DAVDEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.1095	0.3106	3065.78	3065.465	1	652	32	L.DAVDEYIPTPERDLNKPFLMPVEDIF.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	3	4.006	0.3215	3209.15	3210.624	1	684.4	28.846153	L.L1D1A1V1D1E1Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.4766	0.2587	2561.31	2561.961	1	289.9	35	E.Y1I1P1T1P1E1R4D1L1N2K2P1F1L1M1P1V1E1D1I1F1.S

gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.0227	0.185	1926.65	1927.211	3	296	46.875	T.GRVERGNLKKGEELEIV.G
gi|6324761|ref|NP_014830.1|	YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	2	3.0932	0.1993	1952.39	1953.211	1	347.2	53.125	T.G1R4V1E1R4G1N2L1K2K2G1E1E1L1E1I1V1.G
gi|6324775|ref|NP_014844.1|	YOR201C	Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in mitochondrial 21S rRNA; Mrm1p	2	3.8509	0.4002	2660.59	2662.019	1	679	47.826088	D.F1F1V1E1I1P1F1G1G1I1E1K2G1N2R4A1P1E1P1I1V1D1S1L1.N
gi|6324775|ref|NP_014844.1|	YOR201C	Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in mitochondrial 21S rRNA; Mrm1p	2	4.0319	0.4093	2632.65	2633.019	1	684.6	45.652176	D.FFVEIPFGGIEKGNRAPEPIVDSL.N
gi|6324775|ref|NP_014844.1|	YOR201C	Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in mitochondrial 21S rRNA; Mrm1p	3	4.2546	0.3343	2662.55	2662.019	1	734.8	32.608696	D.F1F1V1E1I1P1F1G1G1I1E1K2G1N2R4A1P1E1P1I1V1D1S1L1.N
gi|6324778|ref|NP_014847.1|	YOR204W	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase, required for translation initiation of all yeast mRNAs; mutations in human DEAD-box DBY are a frequent cause of male infertility; Ded1p	2	5.5094	0.4482	2055.47	2056.267	1	1052.8	65.625	Q.IRHIVEDCDMTPVGERQ.T
gi|6324778|ref|NP_014847.1|	YOR204W	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase, required for translation initiation of all yeast mRNAs; mutations in human DEAD-box DBY are a frequent cause of male infertility; Ded1p	2	6.0152	0.518	2082.59	2082.267	1	827.5	59.375	Q.I1R4H3I1V1E1D1C1D1M1T1P1V1G1E1R4Q2.T
gi|6324778|ref|NP_014847.1|	YOR204W	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase, required for translation initiation of all yeast mRNAs; mutations in human DEAD-box DBY are a frequent cause of male infertility; Ded1p	1	2.6601	0.2187	1364.68	1365.618	5	158.4	50	A.RFTKPTPVQKY.S
gi|6324780|ref|NP_014849.1|	YOR206W	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; Noc2p	2	3.6164	0.3505	1933.35	1934.29	2	581.3	46.875	Y.C1K2N2I1A1F1P1E1L1V1T1P1V1I1I1S1L1.R
gi|6324780|ref|NP_014849.1|	YOR206W	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; Noc2p	2	3.5983	0.323	1801.67	1802.167	1	205.7	57.14286	F.FEKGIEIPKENKKLK.K
gi|6324780|ref|NP_014849.1|	YOR206W	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; Noc2p	2	5.1937	0.3192	2378.59	2379.548	4	481.4	47.22222	M.R4E1S1M1E1E1Q2D1K2E1R4E1T1E1E1A1K2L1L1.N
gi|6324780|ref|NP_014849.1|	YOR206W	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; Noc2p	2	3.4072	0.2676	1774.89	1773.151	4	680.3	50	C.K2N2I1A1F1P1E1L1V1T1P1V1I1I1S1L1.R
gi|6324780|ref|NP_014849.1|	YOR206W	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; Noc2p	2	3.3033	0.1943	1389.23	1389.656	2	516	70	Q.REVKEEKARLM.R
gi|6324780|ref|NP_014849.1|	YOR206W	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; Noc2p	2	3.7138	0.1692	1692.15	1692.993	1	797	65.38461	F.F1E1K2G1I1E1I1P1K2E1N2K2K2L1.K
gi|6324785|ref|NP_014854.1|	YOR211C	Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; 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
gi|6324785|ref|NP_014854.1|	YOR211C	Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; 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
gi|6324785|ref|NP_014854.1|	YOR211C	Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; 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
gi|6324785|ref|NP_014854.1|	YOR211C	Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; 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
gi|6324785|ref|NP_014854.1|	YOR211C	Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; 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
gi|6324787|ref|NP_014856.1|	YOR213C	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT activity; Sas5p	2	4.7748	0.3459	2354.65	2354.726	1	1360	63.88889	S.KYFDLPWKVVSPEEEMSLR.I
gi|6324787|ref|NP_014856.1|	YOR213C	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT activity; Sas5p	2	4.6018	0.3456	2379.61	2379.726	1	1338.7	63.88889	S.K2Y1F1D1L1P1W2K2V1V1S1P1E1E1E1M1S1L1R4.I
gi|6324787|ref|NP_014856.1|	YOR213C	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT activity; Sas5p	3	4.1177	0.197	2354.51	2354.726	1	1619.1	41.666664	S.KYFDLPWKVVSPEEEMSLR.I
gi|6324787|ref|NP_014856.1|	YOR213C	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT activity; Sas5p	3	4.8682	0.3334	2381.39	2379.726	1	1289.7	43.055553	S.K2Y1F1D1L1P1W2K2V1V1S1P1E1E1E1M1S1L1R4.I
gi|6324795|ref|NP_014864.1|	YOR221C	Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid synthase that produces intermediates for phospholipid remodeling; Mct1p	2	4.7353	0.3671	2236.59	2234.6	1	406.2	52.941177	S.TVLRPVQEPLYDYIWDIL.K
gi|6324795|ref|NP_014864.1|	YOR221C	Predicted malonyl-CoA:ACP transferase, putative component of a type-II 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.T1V1L1R4P1V1Q2E1P1L1Y1D1Y1I1W2D1I1L1.K
gi|6324795|ref|NP_014864.1|	YOR221C	Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid synthase that produces intermediates for phospholipid remodeling; Mct1p	2	3.021	0.2196	1892.45	1893.192	1	312.7	53.571426	S.TVLRPVQEPLYDYIW.D
gi|6324806|ref|NP_014875.1|	YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	2	4.7172	0.3406	2022.49	2023.072	1	770.9	65.625	E.ESKENNEDLTEEQSEIK.K
gi|6324806|ref|NP_014875.1|	YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	2	3.8212	0.2423	2043.21	2045.072	1	350	53.125	E.E1S1K2E1N2N2E1D1L1T1E1E1Q2S1E1I1K2.K

gi|6324806|ref|NP_014875.1|	YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	2	4.412	0.3902	2209.41	2208.433	1	547.2	50	H.GIEKLDPLGEPFDPNKHEAT.F
gi|6324806|ref|NP_014875.1|	YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	2	4.0648	0.3935	2232.37	2233.433	1	662.9	52.63158	H.G1I1E1K2L1D1P1L1G1E1P1F1D1P1N2K2H3E1A1T1.F
gi|6324806|ref|NP_014875.1|	YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	3	4.3377	0.42	3793.07	3794.209	1	562.7	24.242424	H.GIEKLDPLGEPFDPNKHEATFELPQPDKEPGTVF.H
gi|6324806|ref|NP_014875.1|	YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	3	5.1792	0.3007	3835.97	3835.209	1	1054.2	30.303032	H.G1I1E1K2L1D1P1L1G1E1P1F1D1P1N2K2H3E1A1T1F1E1L1P1Q2P1D1K2E1P1G1T1V1F1.H
gi|6324806|ref|NP_014875.1|	YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	3	3.8462	0.2927	3494.69	3494.882	1	536.2	22.5	E.KLDPLGEPFDPNKHEATFELPQPDKEPGTVF.H
gi|6324806|ref|NP_014875.1|	YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	2	3.035	0.4085	1906.51	1907.133	1	635.8	59.375	H.GIEKLDPLGEPFDPNKH.E
gi|6324808|ref|NP_014877.1|	YOR234C	Ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to Rpl33Ap and has similarity to rat L35a; rpl33b null mutant exhibits normal growth while rpl33a rpl33b double null mutant is inviable; Rpl33bp	1	2.7508	0.1985	1207.57	1208.406	1	223.3	66.66667	T.FRNNLPAKTF.G
gi|6324808|ref|NP_014877.1|	YOR234C	Ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to 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.GRFEGTEPEPRSDIPSGHIPGTQPLPYGSL.L
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
gi|6324825|ref|NP_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	27.586206	L.GRFEGTEPEPRSDIPSGHIPGTQPLPYGSL.L
gi|6324825|ref|NP_014894.1|	YOR251C	catalyzes transfer of the sulfane atom of thiosulfate to cyanide to form sulfite and thiocyanate; Yor251cp	3	4.2194	0.264	2974.25	2972.21	1	629.9	29.807693	L.G1R4F1E1G1T1E1P1E1P1R4S1D1I1P1S1G1H3I1P1G1T1Q2P1L1P1Y1.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	3.9887	0.4017	2969.99	2972.21	1	421.9	36.53846	L.G1R4F1E1G1T1E1P1E1P1R4S1D1I1P1S1G1H3I1P1G1T1Q2P1L1P1Y1.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	3.3058	0.2096	2936.13	2936.21	1	270.8	30.769232	L.GRFEGTEPEPRSDIPSGHIPGTQPLPY.G
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	3.4933	0.1718	2150.55	2151.405	1	668.5	53.125	H.E1F1K2Q2F1F1P1D1L1Q2P1T1D1F1E1K2L1.L
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	4.0881	0.3368	2129.23	2130.405	1	1120.7	62.5	H.EFKQFFPDLQPTDFEKL.L
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	3.4411	0.2783	2865.89	2866.232	1	370.1	37.5	N.D1W2E1I1G1T1I1K2I1P1L1G1Q2P1A1P1E1T1V1G1D1F1F1F1R4.V
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	3.3851	0.3392	2834.37	2835.232	1	261.7	35.416664	N.DWEIGTIKIPLGQPAPETVGDFFFR.V
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	5.226	0.4459	2361.67	2363.624	1	1670.8	63.88889	F.A1H3E1F1K2Q2F1F1P1D1L1Q2P1T1D1F1E1K2L1.L
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	3.7356	0.424	2235.61	2234.603	1	756.2	60.526318	G.TIKIPLGQPAPETVGDFFFR.V
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	4.2974	0.397	1784.51	1784.062	1	2197.9	75	G.TIKIPLGQPAPETVGDF.F
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	4.6784	0.388	1805.27	1803.062	1	2242.6	78.125	G.T1I1K2I1P1L1G1Q2P1A1P1E1T1V1G1D1F1.F
gi|6324828|ref|NP_014897.1|	YOR254C	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 the ER; Sec63p	2	3.2548	0.24	2098.89	2099.415	1	498.2	44.444447	G.T1I1K2I1P1L1G1Q2P1A1P1E1T1V1G1D1F1F1F1.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	25.833332	Q.Q2S1H3E1Q2Q2P1E1Q2P1Q2E1T1E1E1H3H3E1E1E1P1S1R4V1D1P1E1Q2E1A1H3.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	38.793106	Q.S1H3E1Q2Q2P1E1Q2P1Q2E1T1E1E1H3H3E1E1E1P1S1R4V1D1P1E1Q2E1A1H3.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	2	4.1075	0.257	1715.91	1717.015	1	1090.2	65.38461	L.R4E1V1I1E1L1P1L1K2N2P1E1I1F1.Q
gi|6324844|ref|NP_014913.1|	YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); 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	2.6526	0.256	1583.72	1584.813	1	437	53.846157	L.IAEGWIPRDELATL.Q
gi|6324844|ref|NP_014913.1|	YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V-ATPase complexes of the Golgi and endosomes; Vph1p	2	3.7008	0.2939	1402.37	1399.59	1	1316.1	86.36364	E.GWIPRDELATLQ.A
gi|6324844|ref|NP_014913.1|	YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V-ATPase complexes of the Golgi and endosomes; Vph1p	2	3.3208	0.292	1731.73	1732.943	1	643.9	60.714287	L.I1A1E1G1W2I1P1R4D1E1L1A1T1L1Q2.A
gi|6324844|ref|NP_014913.1|	YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); 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	2.4231	0.175	1416.55	1416.59	9	156.2	45.454548	E.G1W2I1P1R4D1E1L1A1T1L1Q2.A
gi|6324844|ref|NP_014913.1|	YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V-ATPase complexes of the Golgi and endosomes; Vph1p	2	3.8318	0.2213	1418.49	1416.59	1	1012	77.27273	E.G1W2I1P1R4D1E1L1A1T1L1Q2.A
gi|6324844|ref|NP_014913.1|	YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V-ATPase complexes of the Golgi and endosomes; Vph1p	2	3.7379	0.2454	1988.45	1989.275	1	690	53.125	A.Q2Y1R4E1I1N2A1G1L1P1T1I1V1T1F1P1F1.M
gi|6324844|ref|NP_014913.1|	YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V-ATPase complexes of the Golgi and endosomes; Vph1p	2	3.7574	0.274	2342.73	2341.723	1	501.9	39.473686	A.Q2Y1R4E1I1N2A1G1L1P1T1I1V1T1F1P1F1M1F1A1.I
gi|6324844|ref|NP_014913.1|	YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); 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	2.4634	0.1861	1415.62	1416.574	5	136.5	45.454548	A.E1G1W2I1P1R4D1E1L1A1T1L1.Q
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	3	4.456	0.4466	3076.1	3077.181	1	994.2	32.692307	N.NMTGGEPIDPRDLDWDGPDDPDNPHNW.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	4.1711	0.5174	3074.53	3077.181	1	1031.3	46.153847	N.NMTGGEPIDPRDLDWDGPDDPDNPHNW.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	3.0937	0.4342	2095.89	2098.447	1	437.6	50	A.RDAETGELLPVVPEKFLIA.C
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	3.6553	0.2549	2121.61	2121.447	1	377.8	47.22222	A.R4D1A1E1T1G1E1L1L1P1V1V1P1E1K2F1L1I1A1.C
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	1	3.2643	0.2964	1436.63	1436.796	2	583.6	58.333332	F.IALMPETHKGIIL.R
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	1	2.9853	0.1582	1451.64	1452.796	1	551.3	58.333332	F.I1A1L1M1P1E1T1H3K2G1I1I1L1.R
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	2.9413	0.2714	2350.83	2351.794	1	475.9	33.333336	L.GLSTVIGAPLSEVFGRKPVYLF.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	1	3.215	0.3547	1343.24	1342.64	1	674.2	54.166668	L.S1P1F1L1G1P1V1L1S1P1I1M1A1.G
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	3	5.5368	0.4399	3113.75	3114.181	1	800.3	31.730768	N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	3.0769	0.2646	3113.87	3114.181	1	365.3	28.846153	N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	3	4.3542	0.1965	1820.69	1821.05	3	1150.9	46.666668	A.R4D1A1E1T1G1E1L1L1P1V1V1P1E1K2F1.L
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	3.5363	0.3665	1799.81	1801.05	1	521.3	60.000004	A.RDAETGELLPVVPEKF.L
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	3.8949	0.2375	1822.55	1821.05	1	457.9	60.000004	A.R4D1A1E1T1G1E1L1L1P1V1V1P1E1K2F1.L
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	3	4.4479	0.3013	3533.33	3534.671	5	432.6	23.333334	N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2S1S1L1K2.K
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	3.1211	0.1754	1453.53	1452.796	8	549.7	66.66667	F.I1A1L1M1P1E1T1H3K2G1I1I1L1.R
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; 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

gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	3	5.4956	0.4147	3130.64	3130.181	1	579.7	29.807693	N.N2M$T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	3.5241	0.221	2764.23	2763.78	3	309.7	36.95652	T.G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	3	6.0002	0.3794	2762.9	2763.78	1	1438.2	40.217392	T.G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	3	5.9982	0.4331	3113.42	3114.181	1	831.7	30.769232	N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi|6324847|ref|NP_014916.1|	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	2	4.8266	0.4188	3111.67	3114.181	1	967.7	44.230766	N.N2M1T1G1G1E1P1I1D1P1R4D1L1D1W2D1G1P1D1D1P1D1N2P1H3N2W2.S
gi|6324850|ref|NP_014919.1|	YOR276W	Phosphoprotein of the mRNA cap-binding complex involved in translational control, repressor of cap-dependent translation initiation, competes with eIF4G for binding to eIF4E; Caf20p	2	4.8854	0.2551	2113.05	2113.355	1	545.4	50	S.S1N2R4P1A1D1T1R4D1I1V1A1D1K2P1I1L1G1F1.N
gi|6324850|ref|NP_014919.1|	YOR276W	Phosphoprotein of the mRNA cap-binding complex involved in translational control, repressor of cap-dependent translation initiation, competes with eIF4G for binding to eIF4E; Caf20p	2	3.8685	0.2262	2084.55	2086.355	1	515.8	47.22222	S.SNRPADTRDIVADKPILGF.N
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.T1K2E1V1P1Y1Y1C1D1N2D1D1N2N2I1I1R4L1F1.
gi|6324857|ref|NP_014926.1|	YOR283W	hypothetical protein; Yor283wp	2	5.4883	0.4689	2416.45	2416.577	1	1209.5	66.66667	M.T1K2E1V1P1Y1Y1C1D1N2D1D1N2N2I1I1R4L1F1.
gi|6324857|ref|NP_014926.1|	YOR283W	hypothetical protein; Yor283wp	3	4.8591	0.4368	2414.72	2416.577	1	1281.7	44.444447	M.T1K2E1V1P1Y1Y1C1D1N2D1D1N2N2I1I1R4L1F1.
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.
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	2.9418	0.2155	1636.25	1635.641	1	1043.8	67.85714	L.AEDRDDSGDIGLESR.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.5248	0.2913	1656.15	1656.641	1	819.8	64.28571	L.A1E1D1R4D1D1S1G1D1I1G1L1E1S1R4.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.3745	0.3666	2138.25	2139.315	1	700.5	58.823532	A.S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.5005	0.3507	2190.51	2188.394	1	913.3	63.88889	K.ASETDLSEILPEEIEERVK.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.635	0.2186	1899.99	1901.121	1	752.6	60.000004	E.TDLSEILPEEIEERVK.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.1769	0.2534	1919.53	1921.121	1	566.3	56.666668	E.T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.2179	0.1839	2130.43	2131.342	3	352.2	44.11765	S.ETDLSEILPEEIEERVKT.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.6212	0.2301	2312.29	2313.499	1	630.7	50	K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.6299	0.1895	2217.71	2218.42	1	719.4	52.77778	A.SETDLSEILPEEIEERVKT.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.2595	0.3275	2288.71	2289.499	1	769.8	57.894737	K.ASETDLSEILPEEIEERVKT.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	2.8348	0.1704	1416.47	1416.72	6	274.6	59.090908	A.I1K2E1Y1L1P1E1L1L1P1G1M1.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.2788	0.3415	2386.91	2385.577	1	996	57.5	K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.1714	0.1517	1316.75	1316.439	1	493.2	65	L.P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.1247	0.2696	2314.63	2313.499	1	798.3	60.526318	A.S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	2.3054	0.1536	1315.31	1316.439	5	306.7	55	L.P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.1603	0.2243	1656.51	1656.874	2	346	57.692307	S.EILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.8859	0.2725	2071.67	2073.305	1	569.8	55.88235	E.TDLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.6046	0.3888	2290.39	2289.499	1	549.6	52.63158	A.SETDLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.4005	0.337	1676.29	1674.874	1	788.8	73.07692	S.E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.4364	0.2358	1301.35	1301.439	1	636.4	70	L.PEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.8636	0.4402	2358.53	2360.577	1	1257.3	60.000004	K.ASETDLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.0784	0.3283	1745.61	1743.952	1	796.6	67.85714	L.SEILPEEIEERVKTA.A

gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.0498	0.1699	1416.93	1414.599	3	394.9	59.090908 I.LPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	5.151	0.3566	2358.77	2360.577	1	2148.5	47.5 K.ASETDLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.3748	0.2573	1974.51	1972.2	5	385.2	46.875 T.DLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.5512	0.3873	2225.03	2225.42	1	617.4	55.555557 S.E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	5.3501	0.3757	2402.39	2403.646	1	971.6	42.5 R.SKASETDLSEILPEEIEERVK.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.896	0.3219	2602.33	2603.83	1	1203.4	50 R.S1K2A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	6.8684	0.4589	2606.09	2603.83	1	1267	40.909092 R.S1K2A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.0472	0.2243	2211.29	2211.394	2	804.7	34.72222 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.394	0.3795	2204.47	2203.524	1	1180	66.66667 I.K2E1Y1L1P1E1L1L1P1G1M1S1D1N2D1L1S1K2M1.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.4545	0.415	2296.43	2294.683	1	1585.1	65.789474 A.IKEYLPELLPGMSDNDLSKM.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.1028	0.3196	2295.35	2294.683	1	2251.9	47.368423 A.IKEYLPELLPGMSDNDLSKM.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	2.7789	0.2514	1194.42	1195.348	2	463.9	65 L.PGMSDNDLSKM.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.7146	0.3033	2944.55	2944.374	1	648.2	30.208334 L.D1I1Y1R4A1I1K2E1Y1L1P1E1L1L1P1G1M1S1D1N2D1L1S1K2M1.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	3.0279	0.3172	1287.64	1288.489	1	396.6	70 L.KTKHDTPKYGL.L
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.8565	0.3582	2007.13	2007.392	1	881.7	58.333332 R.M1K2A1I1A1P1N2L1T1Q2L1V1G1E1L1V1G1A1R4.L
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.6711	0.312	2362.79	2360.577	1	941.3	55 K.ASETDLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.2113	0.3746	2202.25	2202.42	1	510	50 S.ETDLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.2625	0.3388	2208.73	2211.394	1	531	52.77778 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.6712	0.393	2119.69	2117.315	1	753.5	61.764706 A.SETDLSEILPEEIEERVK.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.2753	0.2519	2209.7	2211.394	2	699.2	34.72222 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.7239	0.3253	2387.54	2385.577	1	914.7	33.75 K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.4601	0.3213	2360.09	2360.577	1	1281.7	40 K.ASETDLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.0396	0.3407	2403.47	2403.646	1	1250.9	60.000004 R.SKASETDLSEILPEEIEERVK.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.756	0.4099	2574.57	2575.83	1	1353.9	52.272724 R.SKASETDLSEILPEEIEERVKTA.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.8621	0.3689	2601.91	2603.83	1	1245.8	52.272724 R.S1K2A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	6.031	0.4018	2316.53	2317.683	1	1752.4	68.42105 A.I1K2E1Y1L1P1E1L1L1P1G1M1S1D1N2D1L1S1K2M1.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.2646	0.4343	2293.57	2294.683	1	1232.8	60.526318 A.IKEYLPELLPGMSDNDLSKM.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.6075	0.3794	2519.57	2521.95	1	917.2	38.095238 Y.RAIKEYLPELLPGMSDNDLSKM.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.8505	0.4729	2521.39	2521.95	1	940.1	54.761906 Y.RAIKEYLPELLPGMSDNDLSKM.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.7727	0.4005	1915.93	1916.309	1	1626.9	70 Q.LEKLLEEIKKDKKSTL.I

gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	3.44	0.3388	1400.74	1401.649	1	682.8	72.72727	L.KTKHDTPKYGLL.Y
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.1468	0.2183	1564.19	1564.825	1	530.4	70.83333	L.KTKHDTPKYGLLY.H
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.9847	0.2957	2074.37	2073.35	1	485.2	50	K.E1Y1L1P1E1L1L1P1G1M1S1D1N2D1L1S1K2M1.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	3.297	0.208	1504.51	1504.798	1	410.7	62.5	A.I1K2E1Y1L1P1E1L1L1P1G1M1S1.D
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	3.3032	0.1853	1490.6	1490.798	1	509.2	66.66667	A.IKEYLPELLPGMS.D
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	5.0593	0.3457	2048.85	2051.237	1	951.2	71.875	S.E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.1764	0.3504	2027.73	2030.237	1	799.1	59.375	S.ETDLSEILPEEIEERVK.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.9844	0.427	2209.79	2211.394	1	832.1	63.88889	K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2.T
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	2.8408	0.2019	1415.56	1416.72	2	280.9	59.090908	A.I1K2E1Y1L1P1E1L1L1P1G1M1.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	2.6325	0.2364	1402.48	1403.72	6	272.7	54.545456	A.IKEYLPELLPGM.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.6729	0.2765	1414.69	1416.72	4	764.7	77.27273	A.I1K2E1Y1L1P1E1L1L1P1G1M1.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA 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
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA 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
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.5179	0.2535	2386.52	2385.577	1	1091.5	37.5	K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.912	0.3262	2384.43	2385.577	1	508	47.5	K.A1S1E1T1D1L1S1E1I1L1P1E1E1I1E1E1R4V1K2T1A1.A
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	3	4.5207	0.2251	2523.11	2521.95	1	1106.2	40.476192	Y.RAIKEYLPELLPGMSDNDLSKM.S
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.9212	0.3506	1935.47	1937.309	1	1359.6	66.66667	Q.L1E1K2L1L1E1E1I1K2K2D1K2K2S1T1L1.I
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.2349	0.2354	1304.23	1304.489	1	286.3	70	L.K2T1K2H3D1T1P1K2Y1G1L1.L
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	2.5434	0.2873	1305.43	1304.489	1	350.7	60.000004	L.K2T1K2H3D1T1P1K2Y1G1L1.L
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	1	3.738	0.3718	1581.46	1582.825	1	607.7	62.5	L.K2T1K2H3D1T1P1K2Y1G1L1L1Y1.H
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	4.0859	0.2365	1583.53	1582.825	1	592.7	70.83333	L.K2T1K2H3D1T1P1K2Y1G1L1L1Y1.H
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	2.9782	0.2818	1504.47	1504.798	3	452.2	58.333332	A.I1K2E1Y1L1P1E1L1L1P1G1M1S1.D
gi|6324886|ref|NP_014955.1|	YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	2	3.5721	0.3084	2053.65	2053.35	1	836.4	61.764706	K.EYLPELLPGMSDNDLSKM.S
gi|6324893|ref|NP_014962.1|	YOR317W	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 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
gi|6324893|ref|NP_014962.1|	YOR317W	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 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
gi|6324893|ref|NP_014962.1|	YOR317W	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 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
gi|6324893|ref|NP_014962.1|	YOR317W	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 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
gi|6324893|ref|NP_014962.1|	YOR317W	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 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
gi|6324893|ref|NP_014962.1|	YOR317W	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 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
gi|6324893|ref|NP_014962.1|	YOR317W	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 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

gi|6324893|ref|NP_014962.1|	YOR317W	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 nonfermentable carbon sources; essential for stationary phase; Faa1p	2	4.4386	0.2889	1870.79	1869.171	1	824.4	60.000004 L.VKIGLKPNDDDKLHLY.A
gi|6324893|ref|NP_014962.1|	YOR317W	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 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
gi|6324893|ref|NP_014962.1|	YOR317W	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 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.4468	0.2714	2122.67	2121.222	1	244.8	41.666664 L.SLLDEESRLPAGSDESWTQ.K
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.5402	0.3103	2854.37	2856.145	1	561.5	43.75 V.D1T1K2D1L1N2N2D1K2D1Q2S1L1P1L1L1R4N2P1P1I1L1E1A1T1.E
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.8013	0.3162	2175.99	2176.478	1	513	41.666664 K.DLNNDKDQSLPLLRNPPIL.E
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.8312	0.2344	2202.31	2203.478	1	535	44.444447 K.D1L1N2N2D1K2D1Q2S1L1P1L1L1R4N2P1P1I1L1.E
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	4.6922	0.372	2707.65	2707.056	1	689.6	43.47826 D.TKDLNNDKDQSLPLLRNPPILEAT.E
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	4.2487	0.2693	1747.59	1748.048	1	498.9	65.38461 K.VKENKEMTERIKEL.Q
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	4.5569	0.353	2405.55	2405.757	1	835.1	47.5 D.TKDLNNDKDQSLPLLRNPPIL.E
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	1	3.2119	0.4002	1562.42	1563.734	1	312.2	59.090908 R.C1W2Y1P1H3K2E1L1G1W2I1G1.A
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	3	4.0608	0.2734	1877.99	1876.222	2	632	42.857143 S.KVKENKEMTERIKEL.Q
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	4.1765	0.2821	1505.65	1506.679	3	456.7	62.5 K.K2E1T1T1E1E1D1I1I1S1V1V1K2.M
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	2	3.1492	0.2508	1978.31	1979.329	1	282.7	50 R.YYILIPHEQWDLIFK.K
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	3	4.0625	0.2848	2435.33	2435.757	2	1073.5	38.75 D.T1K2D1L1N2N2D1K2D1Q2S1L1P1L1L1R4N2P1P1I1L1.E
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324902|ref|NP_014971.1|	YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; 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
gi|6324905|ref|NP_014974.1|	YOR329C	Protein required for normal cortical actin organization and endocytosis; multicopy 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.S1L1P1S1E1Q2Q2E1T1E1E1E1K2K2V1L1.E
gi|6324905|ref|NP_014974.1|	YOR329C	Protein required for normal cortical actin organization and endocytosis; multicopy suppressor of clathrin deficiency; acts as a targeting subunit for protein phosphatase type 1; Scd5p	2	3.8139	0.2448	1874.65	1875.04	1	381	56.666668 S.SLPSEQQETEEEKKVL.E
gi|6324905|ref|NP_014974.1|	YOR329C	Protein required for normal cortical actin organization and endocytosis; multicopy suppressor of clathrin deficiency; acts as a targeting subunit for protein phosphatase type 1; Scd5p	3	4.3359	0.2622	4041.08	4040.099	1	823.4	23.571428 E.SSNNSEARKQDPDAEDEDQDSNNDSPLDFTLPMDQL.L
gi|6324905|ref|NP_014974.1|	YOR329C	Protein required for normal cortical actin organization and endocytosis; multicopy suppressor of clathrin deficiency; acts as a targeting subunit for protein phosphatase type 1; Scd5p	3	5.46	0.4043	4086.17	4087.099	1	639.1	26.428572 E.S1S1N2N2S1E1A1R4K2Q2D1P1D1A1E1D1E1D1Q2D1S1N2N2D1S1P1L1D1F1T1L1P1M1D1Q2L1.L
gi|6324905|ref|NP_014974.1|	YOR329C	Protein required for normal cortical actin organization and endocytosis; multicopy suppressor of clathrin deficiency; acts as a targeting subunit for protein phosphatase type 1; Scd5p	2	3.9242	0.3409	2124.15	2125.077	1	505.9	58.823532 S.ENHEEVYEEVEDDDSSAK.T

gi|6324907|ref|NP_014977.1|	YOR332W	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma4p	1	2.7989	0.1643	1407.51	1406.579	8	460.5	54.545456	K.A1L1E1R4D1V1D1L1I1E1S1M1.K
gi|6324907|ref|NP_014977.1|	YOR332W	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma4p	1	2.5528	0.2323	1392.55	1391.579	9	277.8	45.454548	K.ALERDVDLIESM.K
gi|6324907|ref|NP_014977.1|	YOR332W	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma4p	2	4.3771	0.2759	1814.17	1814.136	1	522.6	64.28571	F.IRKEAEEKAKEIQLK.A
gi|6324907|ref|NP_014977.1|	YOR332W	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma4p	2	3.2325	0.229	1573.93	1572.802	1	537.3	70.83333	F.IRKEAEEKAKEIQ.L
gi|6324907|ref|NP_014977.1|	YOR332W	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma4p	2	5.2722	0.2335	1835.77	1837.136	1	699.6	64.28571	F.I1R4K2E1A1E1E1K2A1K2E1I1Q2L1K2.A
gi|6324911|ref|NP_014980.1|	YOR335C	Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog; Ala1p	2	3.976	0.4529	1968.69	1970.1	1	1114.7	62.5	T.YFEGDEKLGLEPDTEAR.E
gi|6324911|ref|NP_014980.1|	YOR335C	Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (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	2212.91	2212.375	1	979.3	40.27778	T.YFEGDEKLGLEPDTEAREL.W
gi|6324911|ref|NP_014980.1|	YOR335C	Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog; Ala1p	2	4.6984	0.3647	2097.79	2097.196	1	898.9	52.77778	Y.S1G1N2F1G1E1N2D1K2D1G1I1D1T1A1Y1R4V1L1.A
gi|6324911|ref|NP_014980.1|	YOR335C	Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog; Ala1p	3	3.8033	0.1973	2096.57	2097.196	1	1366.5	40.27778	Y.S1G1N2F1G1E1N2D1K2D1G1I1D1T1A1Y1R4V1L1.A
gi|6324911|ref|NP_014980.1|	YOR335C	Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally 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	70	L.IKITPDTPFGF.T
gi|6324916|ref|NP_014985.1|	YOR340C	RNA polymerase I subunit A43; Rpa43p	1	2.3168	0.1841	1233.54	1234.397	1	497.5	72.22222	K.KNNIPVDWTF.V
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|	YOR356W	hypothetical protein; Yor356wp	2	3.0044	0.2903	1910.71	1912.233	1	884.3	59.375	E.LFPDEKSDIGIPLPKEL.A
gi|6324932|ref|NP_015001.1|	YOR356W	hypothetical protein; Yor356wp	2	3.8851	0.401	2574.61	2575.881	1	679.8	47.727272	E.S1I1F1E1S1I1K2G1L1P1V1L1E1E1V1E1D1E1D1A1K2M1A1.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.K2E1L1F1P1D1E1K2S1D1I1G1I1P1L1P1K2E1L1.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
gi|6324932|ref|NP_015001.1|	YOR356W	hypothetical protein; Yor356wp	2	3.1707	0.2417	2567.15	2566.881	1	287.9	34.090908	E.SIFESIKGLPVLEEVEDEDAKM@A.M
gi|6324932|ref|NP_015001.1|	YOR356W	hypothetical protein; Yor356wp	2	4.2246	0.378	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|	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	4.7037	0.3324	2239.89	2240.602	1	967.2	52.63158	W.KELFPDEKSDIGIPLPKELA.T
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
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.004	0.2452	2972.09	2970.21	1	365.6	35.416664	F.EDIKLEDIPVDDIDFSDLEEQYKVT.E
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.827	0.1825	1608.19	1607.865	1	1331.3	83.33333	W.LMDDKVRDQFVLQ.D
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.2213	0.1992	2305.85	2305.568	1	391.3	47.22222	L.T1E1R4D1I1P1V1E1K2V1E1L1K2D1S1V1F1E1F1.G
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.1711	0.2809	1864.57	1865.139	1	625.6	60.714287	F.YAPETKEKTDVIKRW.S
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	2.9096	0.2301	2577.77	2579.915	2	177.9	35	C.R4L1T1E1R4D1I1P1V1E1K2V1E1L1K2D1S1V1F1E1F1.G
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	4.0417	0.3098	1846.71	1849.147	1	416.3	57.14286	C.R4L1T1E1R4D1I1P1V1E1K2V1E1L1K2.D
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.4583	0.3466	2010.83	2012.316	1	1007.6	66.66667	R.FYAPETKEKTDVIKRW.S
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	5.0215	0.2759	1818.65	1821.001	1	1159.2	71.42857	E.E1I1V1E1E1V1L1E1E1T1K2E1K2V1E1.-
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	4.1423	0.1703	1806.91	1804.001	1	1106.2	75	E.EIVEEVLEETKEKVE.-
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	3	3.9868	0.1895	2996.27	2998.21	2	440.3	27.083334	F.E1D1I1K2L1E1D1I1P1V1D1D1I1D1F1S1D1L1E1E1Q2Y1K2V1T1.E
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	2.926	0.3609	2027.27	2028.313	1	200.6	50	C.RLTERDIPVEKVELKDS.V
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.9736	0.3658	2360.49	2361.543	1	707.9	52.63158	E.T1F1E1D1I1K2L1E1D1I1P1V1D1D1I1D1F1S1D1L1.E
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	4.6949	0.4287	2339.51	2340.543	1	700.1	52.63158	E.TFEDIKLEDIPVDDIDFSDL.E

gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.1988	0.2552	2018.23	2019.154	1	596.4	50 T.F1S1T1E1P1I1I1V1E1E1D1N2E1F1S1P1F1.T
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.356	0.3279	1724.13	1722.963	1	434	57.692307 Y.A1P1E1T1K2E1K2T1D1V1I1K2R4W2.S
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.6864	0.3036	2262.91	2263.398	1	715.9	52.77778 E.D1I1P1V1D1D1I1D1F1S1D1L1E1E1Q2Y1K2V1T1.E
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	3.4646	0.2574	1475.27	1474.698	1	938.4	77.27273 C.R4L1T1E1R4D1I1P1V1E1K2V1.E
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	5.4446	0.3823	2033.89	2035.316	1	1731.6	76.666664 R.F1Y1A1P1E1T1K2E1K2T1D1V1I1K2R4W2.S
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	4.6265	0.3688	2241.71	2242.398	1	966.8	55.555557 E.DIPVDDIDFSDLEEQYKVT.E
gi|6324937|ref|NP_015006.1|	YOR361C	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 tRNA(i)Met to ribosomes; Prt1p	2	4.2607	0.4369	2370.57	2371.471	1	712.3	52.63158 Y.N2S1D1D1F1D1T1E1F1R4E1P1D1M1P1T1F1V1P1S1.S
gi|6324937|ref|NP_015006.1|	YOR361C	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 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	Component of the spindle pole body outer plaque, required for exit from mitosis; 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 spindle 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
gi|6324949|ref|NP_015018.1|	YOR373W	Component of the spindle pole body outer plaque, required for exit from mitosis; Nud1p	2	3.2984	0.3122	1739.95	1738.037	1	562.8	57.14286 F.THLPVDLSKELPFLQ.E
gi|6324951|ref|NP_015020.1|	YOR375C	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from 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
gi|6324951|ref|NP_015020.1|	YOR375C	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh3p; expression regulated by nitrogen and carbon sources; Gdh1p	2	3.8761	0.3264	1759.89	1759.155	1	648.6	57.14286 R.K2V1L1P1I1V1S1V1P1E1R4I1I1Q2F1.R
gi|6324951|ref|NP_015020.1|	YOR375C	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh3p; expression regulated by nitrogen and carbon sources; Gdh1p	2	3.5963	0.2736	1889.69	1891.217	2	420.3	50 T.L1F1E1Q2H3P1E1Y1R4K2V1L1P1I1V1.S
gi|6325253|ref|NP_015321.1|	YPL004C	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 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
gi|6325253|ref|NP_015321.1|	YPL004C	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 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
gi|6325253|ref|NP_015321.1|	YPL004C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	3.5253	0.191	1545.55	1542.801	2	592.7	66.66667 T.K2I1P1V1L1E1Q2E1L1V1R4A1E1.A
gi|6325253|ref|NP_015321.1|	YPL004C	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 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
gi|6325253|ref|NP_015321.1|	YPL004C	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 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
gi|6325253|ref|NP_015321.1|	YPL004C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	4.3755	0.2647	2162.87	2165.416	1	703.2	55.88235 S.V1Q2P1S1R4D1R4K2E1K2I1T1D1E1I1A1H3L1.K
gi|6325253|ref|NP_015321.1|	YPL004C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	2.9979	0.2383	1802.51	1800.973	2	521.3	43.75 L.L1E1L1L1D1D1S1P1V1T1P1G1E1A1R4P1A1.Y
gi|6325253|ref|NP_015321.1|	YPL004C	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 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
gi|6325253|ref|NP_015321.1|	YPL004C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	3.6764	0.2386	1810.37	1808.809	1	320.2	60.000004 T.E1V1P1V1D1D1E1A1H3E1A1D1H3H3V1S1.Q
gi|6325253|ref|NP_015321.1|	YPL004C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	3.1537	0.3284	1789.67	1786.809	2	186.1	53.333336 T.EVPVDDEAHEADHHVS.Q
gi|6325253|ref|NP_015321.1|	YPL004C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	3	4.1671	0.2852	3653.96	3654.7	1	389	27.419355 Q.N2G1D1I1P1G1Q2V1V1E1E1E1E1V1E1W2T1T1E1V1P1V1D1D1E1A1H3E1A1D1H3H3.V
gi|6325253|ref|NP_015321.1|	YPL004C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	3	4.0906	0.2436	4517.51	4517.568	1	506.5	19.078947 E.E1E1E1P1E1I1Q2N2G1D1I1P1G1Q2V1V1E1E1E1E1V1E1W2T1T1E1V1P1V1D1D1E1A1H3E1A1D1H3H3.V
gi|6325253|ref|NP_015321.1|	YPL004C	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 Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	2	3.5713	0.236	1525.69	1524.801	1	891.3	79.16667 T.KIPVLEQELVRAE.A
gi|6325245|ref|NP_015313.1|	YPL012W	Protein required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; contains HEAT-repeats; Rrp12p	2	3.2582	0.2705	1854.39	1855.256	1	500.2	53.333336 L.G1L1P1E1E1L1M1R4P1K2V1P1E1L1L1L1.K
gi|6325245|ref|NP_015313.1|	YPL012W	Protein required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; contains HEAT-repeats; Rrp12p	2	4.0252	0.2068	1983.97	1985.43	1	618.2	50 L.G1L1P1E1E1L1M1R4P1K2V1P1E1L1L1L1K2.L
gi|6325245|ref|NP_015313.1|	YPL012W	Protein required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; contains HEAT-repeats; Rrp12p	2	3.3542	0.3869	1916.69	1915.265	1	479	50 K.T1I1V1E1L1L1P1L1D1H3L1D1F1I1V1R4.T
gi|6325245|ref|NP_015313.1|	YPL012W	Protein required for export of the ribosomal subunits; associates with the RNA 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	Protein required for export of the ribosomal subunits; associates with the RNA 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	Protein required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; contains HEAT-repeats; Rrp12p	2	2.9818	0.2073	1953.95	1955.388	1	372.7	37.5 C.V1L1G1L1P1E1E1L1M1R4P1K2V1P1E1L1L1L1.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.D1V1Y1P1P1W2K2D1S1Y1I1D1Y1E1R4L1.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.W2L1P1D1L1E1T1D1I1R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1.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.W2L1P1D1L1E1T1D1I1R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1.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.P1D1L1E1T1D1I1R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1Q2.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.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	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.W2L1P1D1L1E1T1D1I1R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1Q2.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.H3R4D1D1I1D1S1N2I1P1N2P1L1.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.I1R4K2N2P1Q2E1A1Y1E1E1E1K2K2T1L1.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.D1V1Y1P1P1W2K2D1S1Y1I1D1Y1E1R4L1K2K2L1.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	2	3.6295	0.2067	1620.45	1620.828	1	1496.2	73.07692	Q.E1K2N2L1Q2D1L1F1P1G1I1I1S1Q2.L
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	2	3.5658	0.215	1603.11	1602.828	1	1041	69.230774	Q.EKNLQDLFPGIISQ.L
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	1	2.4749	0.248	1473.46	1474.697	1	306.2	54.166668	Q.EKNLQDLFPGIIS.Q
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	2	3.1295	0.2545	1475.27	1474.697	1	850.4	66.66667	Q.EKNLQDLFPGIIS.Q
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	2	2.9366	0.3579	1868.85	1870.156	2	325.2	46.875	Y.GLPQEKNLQDLFPGIIS.Q
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	2	4.5407	0.3497	2032.55	2033.193	4	409.2	52.77778	K.A1P1A1D1A1E1K2K2D1E1A1I1P1E1L1V1E1G1Q2.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	2	3.9143	0.3407	2364.07	2365.561	2	370.1	40.476192	H.E1A1K2A1P1A1D1A1E1K2K2D1E1A1I1P1E1L1V1E1G1Q2.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	2	4.0435	0.4642	2338.69	2339.562	1	446.1	42.857143	H.EAKAPADAEKKDEAIPELVEGQ.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	2	3.3371	0.2315	1997.05	1998.287	1	463.2	52.941177	Y.GLPQEKNLQDLFPGIISQ.L
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	2.2603	0.1662	1240.35	1240.288	1	617.7	72.22222	A.F1D1V1A1P1D1W2E1S1Y1.E
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	4.1807	0.3173	1799.33	1798.87	1	758.1	64.28571	A.K2L1D1P1T1N2D1D1D1K2E1F1I1N2N2.M
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	2.5259	0.1784	1386.52	1386.594	1	570.6	66.66667	T.F1V1L1D1D1W2K2R4K2Y1.S

gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.0479	0.1706	1373.57	1370.594	1	796.6	77.77778	T.FVLDDWKRKY.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.3893	0.1854	1389.43	1386.594	1	1074.3	88.88889	T.F1V1L1D1D1W2K2R4K2Y1.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	2.9058	0.2643	1065.79	1066.236	1	451.4	81.25	W.R4A1Q2H3P1A1I1V1R4.W
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	3	4.6564	0.2105	2770.16	2770.09	1	523.6	36.904762	T.F1V1L1D1D1W2K2R4K2Y1S1N2E1D1T1R4P1V1A1L1P1W2.F
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	4.0486	0.154	1930.35	1931.063	1	769	60.000004	A.K2L1D1P1T1N2D1D1D1K2E1F1I1N2N2M1.W
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	3	4.7974	0.2861	2281.31	2281.535	1	2209	44.736843	M.W2A1W2D1K2P1V1S1V1N2G1E1P1K2E1I1V1D1G1K2.V
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.3375	0.2242	1696.79	1696.869	2	467.9	53.846157	R.K2Y1S1N2E1D1T1R4P1V1A1L1P1W2.F
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.4619	0.195	1385.95	1386.594	1	954.7	77.77778	T.F1V1L1D1D1W2K2R4K2Y1.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.6219	0.267	1489.31	1488.699	1	846.4	80	S.T1F1V1L1D1D1W2K2R4K2Y1.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.4127	0.1716	1472.35	1471.699	3	574	70	S.TFVLDDWKRKY.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	2.4315	0.1741	1385.59	1386.594	1	486.2	66.66667	T.F1V1L1D1D1W2K2R4K2Y1.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.7398	0.2308	2035.89	2035.11	1	698.6	53.125	Y.D1Y1A1K2L1D1P1T1N2D1D1D1K2E1F1I1N2.N
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.6956	0.2485	2013.59	2014.11	1	670.4	53.125	Y.DYAKLDPTNDDDKEFIN.N
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	2.9896	0.2272	1216.39	1216.355	1	1108.1	88.88889	M.W2A1W2D1K2P1V1S1V1N2.G
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	2.2461	0.1894	1265.61	1266.495	3	295.1	50	A.MDAVDKIVDIF.E
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	2.2252	0.1735	1279.58	1278.495	6	281.6	55	A.M1D1A1V1D1K2I1V1D1I1F1.E
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.9671	0.2987	1277.57	1278.495	1	1536.1	90	A.M1D1A1V1D1K2I1V1D1I1F1.E
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	2.7281	0.1813	1427.3	1428.473	1	404.5	61.11111	W.F1W2E1H3Y1N2P1E1E1Y1.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	2.6707	0.2866	1414.53	1414.473	1	572.5	72.22222	W.FWEHYNPEEY.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	4.8437	0.3339	2118.99	2119.276	1	867.5	56.25	A.K2L1D1P1T1N2D1D1D1K2E1F1I1N2N2M1W2.A
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	2.2021	0.1755	1387.79	1386.594	2	455.2	61.11111	T.F1V1L1D1D1W2K2R4K2Y1.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.3668	0.2264	1387.39	1386.594	1	770.8	77.77778	T.F1V1L1D1D1W2K2R4K2Y1.S
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	4.0728	0.2351	1560.09	1560.892	1	628.2	73.07692	R.D1F1P1L1K2K2V1P1A1F1V1G1P1K2.G
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.8056	0.349	1544.27	1543.892	8	531	69.230774	R.DFPLKKVPAFVGPK.G
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	1	4.4135	0.2466	1560.83	1560.892	1	700.7	65.38461	R.D1F1P1L1K2K2V1P1A1F1V1G1P1K2.G
gi|6325209|ref|NP_015277.1|	YPL048W	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; Cam1p	2	3.6434	0.3361	1267.85	1266.495	1	1094.1	85	A.MDAVDKIVDIF.E
gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	2	4.1457	0.3581	1981.41	1981.196	1	823.4	67.85714	Q.R4F1Y1D1E1E1K2K2Q2P1S1I1R4P1Y1.D
gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	2	3.871	0.328	1955.91	1957.196	1	786.2	60.714287	Q.RFYDEEKKQPSIRPY.D
gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	2	3.3726	0.2816	1559.21	1559.676	1	797.2	65.38461	F.NDHVEDIIPEGHIA.H

gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	2	3.2533	0.2301	1578.13	1578.676	2	649.9	61.538464	F.N2D1H3V1E1D1I1I1P1E1G1H3I1A1.H
gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	2	3.1578	0.1867	1665.23	1664.879	1	1028.5	65.38461	A.EVHRDGAMFPNFPF.Y
gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	2	3.779	0.2217	1537.69	1535.763	1	898.6	70.83333	E.VHRDGAMFPNFPF.Y
gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	1	2.7448	0.1633	1534.54	1535.763	4	299.5	54.166668	E.VHRDGAMFPNFPF.Y
gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	1	2.6389	0.2283	1553.52	1554.763	1	306.4	54.166668	E.V1H3R4D1G1A1M1F1P1N2F1P1F1.Y
gi|6325207|ref|NP_015275.1|	YPL050C	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 elongation; Mnn9p	2	3.2912	0.1943	1537.21	1535.763	2	880.6	70.83333	E.VHRDGAMFPNFPF.Y
gi|6325207|ref|NP_015275.1|	YPL050C	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 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 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	3.6597	0.3215	1898.91	1898.16	1	923.5	60.714287	Y.V1I1Y1C1P1E1L1D1F1H3F1P1K2I1T1.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	2	3.0914	0.3295	1575.79	1573.896	1	589.1	62.5	C.GILQPREKMPAFW.R
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	3.3668	0.345	2056.25	2056.301	1	396.7	58.823532	E.NAIPMEPWNGEADDKLVR.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	5.5391	0.3954	2321.49	2320.62	1	1911.3	71.05263	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	5.6064	0.369	2344.57	2345.62	1	2106.7	73.68421	F.T1L1K2D1Y1V1E1G1N2L1P1S1P1E1E1Q2M1K2I1Q2.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	3	4.1947	0.1788	2321.45	2320.62	1	1334.7	44.736843	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	1	2.7403	0.1919	1545.72	1546.822	1	363.2	59.090908	K.MIEEEKEKIRIQ.Q
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	4.4134	0.2271	1546.61	1546.822	1	1052.1	81.818184	K.MIEEEKEKIRIQ.Q
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	3	4.3983	0.2402	1603.04	1602.813	1	1184.4	53.846157	Y.S1D1K2I1A1E1K2L1D1P1I1H3A1F1.V
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	3.2237	0.2899	2525.03	2526.913	1	345.9	40.476192	E.NAIPMEPWNGEADDKLVRLIPF.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	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	2	4.3606	0.3608	1987.65	1987.183	1	1130.6	65.625	L.N2R4D1L1S1K2V1I1I1I1D1T1D1P1N2S1Y1.K
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	4.1063	0.3443	2417.67	2419.791	1	664.6	55	F.Q2E1P1P1F1P1D1L1L1P1P1P1P1P1P1P1Y1Q2R4P1L1.T
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	3	3.8701	0.349	2606.18	2608.055	2	321.2	30.681818	F.QEPPFPDLLPPPPPPPYQRPLTL.V

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	3	4.1777	0.2916	2633.3	2636.055	1	354.1	32.954548	F.Q2E1P1P1F1P1D1L1L1P1P1P1P1P1P1P1Y1Q2R4P1L1T1L1.V
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	4.6624	0.2409	1674.67	1674.996	1	1422.6	87.5	M.KMIEEEKEKIRIQ.Q
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	4.47	0.3115	1668.27	1668.89	1	852.4	73.07692	T.KFPLDLIHEEGQKN.Y
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	5.3061	0.372	2566.49	2567.967	1	725	52.380955	Y.F1Q2E1P1P1F1P1D1L1L1P1P1P1P1P1P1P1Y1Q2R4P1L1.T
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	4.4342	0.4268	1946.57	1945.225	1	644.6	56.666668	T.KFPLDLIHEEGQKNYL.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	3.1408	0.2012	2394.89	2393.791	1	500.1	50	F.QEPPFPDLLPPPPPPPYQRPL.T
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	3	4.4029	0.266	3627.56	3627.163	1	374.3	25	A.R4F1N2S1M1F1T1Y1F1Q2E1P1P1F1P1D1L1L1P1P1P1P1P1P1P1Y1Q2R4P1L1.T
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	3	4.9478	0.3306	3158.18	3158.609	1	606.1	26.923079	Y.K2L1Q2P1E1N2A1I1P1M1E1P1W2N2G1E1A1D1D1K2L1V1R4L1I1P1F1.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.K2F1P1L1D1L1I1H3E1E1G1Q2K2N2Y1L1.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.M1I1E1E1E1K2E1K2I1R4I1Q2.Q
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	3	4.6708	0.3953	2651.87	2651.997	4	625.1	30.681818	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	2	3.1085	0.2063	2247.85	2247.513	2	255.9	36.842106	L.GGSTKFPLDLIHEEGQKNYL.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	3	4.3781	0.3228	3138.17	3138.609	3	396.4	26.923079	Y.KLQPENAIPM@EPWNGEADDKLVRLIPF.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	3	4.3968	0.3125	3121.88	3122.609	1	556.1	28.846153	Y.KLQPENAIPMEPWNGEADDKLVRLIPF.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	3	4.0328	0.3337	1947.38	1945.225	1	1296.6	53.333336	T.KFPLDLIHEEGQKNYL.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	3	4.0554	0.3493	3287.27	3288.769	1	497	24.074074	Y.K2L1Q2P1E1N2A1I1P1M$E1P1W2N2G1E1A1D1D1K2L1V1R4L1I1P1F1L1.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	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	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	3	4.0578	0.1729	3271.37	3272.769	7	446.7	21.296297	Y.K2L1Q2P1E1N2A1I1P1M1E1P1W2N2G1E1A1D1D1K2L1V1R4L1I1P1F1L1.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	2.9574	0.2775	1547.79	1548.762	1	353.1	62.5	L.Q2K2E1T1K2D1D1K2P1K2S1I1L1.T
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	4.2177	0.3732	2540.05	2540.967	1	501.4	45.238094	Y.FQEPPFPDLLPPPPPPPYQRPL.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	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 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	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	2	3.0516	0.3948	1520.93	1521.803	1	776.8	70.83333	L.AKKPLEDSKHRVL.M
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	3.3667	0.2568	1593.49	1592.854	4	393.4	58.333332	S.RYKPIIEEEAGMR.Q
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	3.7581	0.3142	2317.87	2319.612	1	338.3	42.105263	S.V1A1P1P1R4Q2E1N2N2P1I1K2I1D1N2E1A1L1L1R4.R

gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	3.1392	0.2162	2286.59	2288.612	3	188.8	39.473686	S.VAPPRQENNPIKIDNEALLR.R
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	3.0517	0.2461	1614.73	1612.854	3	460.9	62.5	S.R4Y1K2P1I1I1E1E1E1A1G1M1R4.Q
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	3	5.8715	0.5142	4097.51	4099.515	1	811.4	28.846153	T.S1V1I1P1N2N2P1I1T1G1E1P1L1P1I1K2T1S1P1S1P1T1G1P1N2P1N2N2S1P1S1P1S1S1P1I1S1R4I1S1.G
gi|6325172|ref|NP_015240.1|	YPL085W	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 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	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 Sec31p; Sec16p	2	3.623	0.3933	2362.31	2363.795	1	256	33.333336	H.A1N2I1Q2P1P1T1G1I1L1P1L1A1P1L1R4P1L1D1P1L1Q2.A
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	4.1312	0.2753	2236.19	2233.665	1	814.7	52.499996	H.A1N2I1Q2P1P1T1G1I1L1P1L1A1P1L1R4P1L1D1P1L1.Q
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	4.1687	0.4461	2206.55	2207.665	1	863.3	57.5	H.ANIQPPTGILPLAPLRPLDPL.Q
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	3	3.8801	0.2899	2209.94	2207.665	1	569.8	33.75	H.ANIQPPTGILPLAPLRPLDPL.Q
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	4.0868	0.3662	2046.55	2045.482	1	265.7	52.77778	N.I1Q2P1P1T1G1I1L1P1L1A1P1L1R4P1L1D1P1L1.Q
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	3.227	0.3107	2024.45	2022.482	2	261.2	50	N.IQPPTGILPLAPLRPLDPL.Q
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	2	4.145	0.2772	2161.41	2161.586	1	783.8	57.894737	A.N2I1Q2P1P1T1G1I1L1P1L1A1P1L1R4P1L1D1P1L1.Q
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	3	3.8205	0.2279	3816.62	3818.102	1	659.7	24.21875	Q.PTIRKASTNQYRAFKPLESDADKYNDVIEDESD.D
gi|6325172|ref|NP_015240.1|	YPL085W	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 Sec31p; Sec16p	3	4.4429	0.4845	3896.63	3897.277	1	858.1	29.054054	T.S1V1I1P1N2N2P1I1T1G1E1P1L1P1I1K2T1S1P1S1P1T1G1P1N2P1N2N2S1P1S1P1S1S1P1I1S1R4.I
gi|6325172|ref|NP_015240.1|	YPL085W	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 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	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 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.S1W2K2D1I1P1T1V1A1P1A1N2D1L1L1D1I1V1L1N2.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	44.444447	S.W2K2D1I1P1T1V1A1P1A1N2D1L1L1D1I1V1L1N2.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	3	3.9688	0.2531	2952.29	2952.32	1	559.8	30.434782	N.L1K2D1K2Y1L1L1E1D1D1E1W2K2N2D1I1M1P1E1I1L1D1G1K2.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	3	3.9926	0.3191	3249.83	3249.66	1	758.2	25.961538	F.NVNLKDKYLLEDDEWKNDIMPEILDGK.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	4.1136	0.3966	2133.11	2131.439	1	811.9	58.823532	E.KFEDILKGFPNINDVHPF.H
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	2	3.6384	0.2343	2368.65	2369.67	1	354.7	44.736843	S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2.S

gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	3	4.3265	0.323	2671.07	2672.013	1	994.4	37.5	K.SARQPEIYPTIPSNKIEDQLKSR.E
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	3	6.089	0.2747	2703.71	2706.013	1	1888.9	44.31818	K.S1A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	2	4.0719	0.258	2616.43	2617.935	1	426.9	42.857143	S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	2	4.9272	0.4207	2670.89	2672.013	1	800	50	K.SARQPEIYPTIPSNKIEDQLKSR.E
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	3	6.4794	0.4431	2703.14	2706.013	1	1185.1	35.227272	K.S1A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	2	4.9013	0.4025	2704.81	2706.013	1	562.9	45.454548	K.S1A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	3	4.6882	0.2848	2616.92	2617.935	1	807.5	32.142857	S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2S1R4.E
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	3	5.0336	0.2839	2368.67	2369.67	1	994.5	42.105263	S.A1R4Q2P1E1I1Y1P1T1I1P1S1N2K2I1E1D1Q2L1K2.S
gi|41629689|ref|NP_015231.2|	YPL094C	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 the ER; Sec62p	3	5.2353	0.4366	2584.91	2584.935	1	1175.8	39.285713	S.ARQPEIYPTIPSNKIEDQLKSR.E
gi|41629689|ref|NP_015231.2|	YPL094C	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 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, 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 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	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	3.1399	0.3494	1581.77	1582.712	1	769.8	68.181816	A.VPPWYTEEQRYN.I
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	4.3547	0.3473	1847.83	1848.989	1	1314.1	78.57143	A.E1E1W2L1Y1D1E1G1F1D1S1I1K2A1K2.Y
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	3.312	0.3022	1830.19	1830.989	1	655.5	57.14286	A.EEWLYDEGFDSIKAK.Y
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	3.8248	0.3062	1591.81	1592.787	1	1412.9	84.61539	K.L1V1E1L1D1D1K2K2T1G1A1E1V1R4.F
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	3.9686	0.4494	1572.51	1573.787	1	1135.2	73.07692	K.LVELDDKKTGAEVR.F
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	3.8078	0.2209	1714.49	1714.969	1	926	66.66667	T.G1V1Q2L1P1E1G1Q2D1S1V1P1V1K2L1K2.L
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	4.8323	0.3706	1822.31	1823.081	1	944.7	64.28571	K.K2L1N2E1L1I1E1K2E1N2E1M1L1A1Q2.D
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.G1V1Q2L1P1E1G1Q2D1S1V1P1V1K2L1.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.D1I1E1V1E1E1P1I1P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1T1.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	2	3.0411	0.2414	2176.05	2175.394	3	265.9	33.333336	E.P1I1P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1.T
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	4.2447	0.4417	2894.59	2896.121	1	680.2	43.75	E.D1I1E1V1E1E1P1I1P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1.T
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	4.296	0.3685	2867.67	2868.121	1	428.8	37.5	E.DIEVEEPIPLPEDAPEDAEQEFKKV.T
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	3.1253	0.262	2998.69	2998.226	3	220.6	28	E.D1I1E1V1E1E1P1I1P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1T1.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	2	3.4903	0.3634	2967.23	2969.226	1	420.4	32	E.DIEVEEPIPLPEDAPEDAEQEFKKVT.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	2	4.0525	0.3729	1610.77	1611.836	1	1652.6	80.769226	F.KTDLPEGEEKPRIV.A

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	4.5172	0.3686	1997.01	1997.124	1	586.4	63.333332	S.W2D1K2Q2V1E1D1E1D1H3M1E1V1F1P1A1.G
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	4.4812	0.4329	1976.25	1976.124	1	814.1	66.66667	S.WDKQVEDEDHMEVFPA.G
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	4.2693	0.2606	3211.61	3211.501	2	504.1	25.925926	Y.TIEDIEVEEPIPLPEDAPEDAEQEFKKV.T
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	4.3646	0.2395	3245.15	3242.501	1	494.7	25	Y.T1I1E1D1I1E1V1E1E1P1I1P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1.T
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	5.0691	0.393	2664.33	2665.814	1	1003.9	59.090908	E.D1I1E1V1E1E1P1I1P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2.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	1	2.5417	0.1853	1174.6	1174.33	1	146.7	66.66667	A.R4N2R4G1I1D1I1V1V1N2.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	3	4.3251	0.2155	2896.79	2896.121	1	601.2	33.333336	E.D1I1E1V1E1E1P1I1P1L1P1E1D1A1P1E1D1A1E1Q2E1F1K2K2V1.T
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	4.7713	0.4459	2639.59	2640.814	1	695.3	52.272724	E.DIEVEEPIPLPEDAPEDAEQEFK.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	2	3.7438	0.2393	1583.53	1584.769	1	360.9	57.692307	F.G1P1K2N2R4Y1L1G1E1T1G1K2N2K2.Q
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	3.2358	0.2187	1565.37	1562.769	1	404.5	65.38461	F.GPKNRYLGETGKNK.Q
gi|6325147|ref|NP_015215.1|	YPL110C	Glycerophosphocholine (GroPCho) phosphodiesterase; hydrolyzes GroPCho to choline and glycerolphosphate after its uptake by Git1p permease, for use as a phosphate source and as a precursor for phosphocholine synthesis; Gde1p	1	2.8154	0.201	1179.64	1180.508	1	926.3	72.22222	L.K2Q2P1V1I1P1I1L1F1L1.T
gi|6325147|ref|NP_015215.1|	YPL110C	Glycerophosphocholine (GroPCho) phosphodiesterase; hydrolyzes GroPCho to choline and glycerolphosphate after its uptake by Git1p permease, for use as a 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.S1L1K2Q2P1V1I1P1I1L1F1L1.T
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls 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
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	5.0836	0.3731	1956.57	1955.184	1	1143.4	62.5	L.K2S1D1I1P1L1F1V1Q2P1E1D1F1G1T1I1Q2.I
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls 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
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls 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
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	4.0779	0.3137	1968.47	1969.257	1	630.2	53.125	K.S1H3V1P1D1L1P1L1P1T1L1P1D1R4Q2L1F1.Q
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls 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
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls 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.S1I1E1L1I1P1N2L1P1E1D1R4F1G1T1R4.N
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	2	3.3203	0.371	1857.69	1858.104	1	770.5	60.000004	S.SIELIPNLPEDRFGTR.N
gi|6325142|ref|NP_015210.1|	YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls 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
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	4.764	0.2361	2443.79	2445.757	1	883.8	57.894737	K.T1Q2Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	3	3.9427	0.3642	2418.14	2415.757	1	1854.2	51.315792	K.TQQHILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.8255	0.3158	1744.39	1745.072	1	673.4	60.714287	E.HVIQIPLNKPLLTEE.L
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.7669	0.3077	1763.69	1765.072	1	748.4	64.28571	E.H3V1I1Q2I1P1L1N2K2P1L1L1T1E1E1.L
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	2.941	0.2536	1385.79	1386.566	2	837.1	65	V.P1P1V1E1N2F1P1V1R4Q2W2.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	4.436	0.2254	2415.99	2415.757	1	899.1	57.894737	K.TQQHILPEVPPVENFPVRQW.S

gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.3879	0.2374	1635.61	1634.957	7	442.8	53.846157	E.H3V1I1Q2I1P1L1N2K2P1L1L1T1E1.E
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.29	0.2599	2215.83	2213.521	1	493	55.88235	Q.Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.3651	0.1819	2059.65	2058.39	1	785.5	59.375	Q.HILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.3039	0.2249	1877.61	1879.232	1	544.6	50	E.H3V1I1Q2I1P1L1N2K2P1L1L1T1E1E1L1.A
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	3	3.8441	0.2972	2415.71	2415.757	1	1219	40.789474	K.TQQHILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	4.6094	0.2084	2414.95	2415.757	1	961.3	60.526318	K.TQQHILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.3682	0.3908	1856.39	1858.232	1	897.3	63.333332	E.HVIQIPLNKPLLTEEL.A
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	3	5.9989	0.3712	2213.99	2213.521	1	1077.7	47.058823	Q.Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	1	2.7708	0.164	1457.72	1458.657	1	289.6	54.545456	A.G1E1R4K2I1P1H3D1L1N2F1L1.Q
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.1553	0.2981	1430.37	1430.598	1	1248.3	83.33333	L.TKLNEDDLVGVVQ.M
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.2033	0.1637	2103.55	2101.413	6	413.5	47.058823	K.TQQHILPEVPPVENFPVR.Q
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	3	5.0954	0.3121	2416.73	2415.757	1	1825.2	50	K.TQQHILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	4.4074	0.1961	2415.87	2415.757	1	957.6	57.894737	K.TQQHILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	4.5151	0.238	2442.79	2445.757	1	1108.1	63.15789	K.T1Q2Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	3	4.8919	0.29	2445.14	2445.757	1	1188.1	47.368423	K.T1Q2Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	3	4.889	0.2904	2060.03	2058.39	1	1922.4	51.5625	Q.HILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	4.4147	0.4193	2082.31	2083.39	1	1650	81.25	Q.H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	3	6.3139	0.4265	2184.56	2186.521	1	1698	57.352943	Q.QHILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	4.255	0.44	2057.45	2058.39	1	1227.7	71.875	Q.HILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	3	6.6271	0.4173	2213.42	2213.521	1	1574.7	54.411762	Q.Q2H3I1L1P1E1V1P1P1V1E1N2F1P1V1R4Q2W2.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.3887	0.2312	2185.47	2186.521	1	879.5	64.70589	Q.QHILPEVPPVENFPVRQW.S
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	1	2.9926	0.3306	1438.6	1439.657	3	317.4	54.545456	A.GERKIPHDLNFL.Q
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	1	2.6008	0.2367	1485.73	1486.841	1	595.2	58.333332	E.HVIQIPLNKPLLT.E
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	1	2.2904	0.2525	1503.38	1504.841	5	398.6	50	E.H3V1I1Q2I1P1L1N2K2P1L1L1T1.E
gi|6325128|ref|NP_015196.1|	YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	2	3.4091	0.3102	1486.55	1486.841	1	719.3	66.66667	E.HVIQIPLNKPLLT.E
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	2	4.259	0.4017	1614.29	1614.668	1	1621.4	79.16667	H.SENRFPGWDFETE.E
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	2	4.7879	0.4074	2449.81	2449.582	1	1133.3	63.15789	H.S1E1N2R4F1P1G1W2D1F1E1T1E1E1I1D1P1E1L1L1.R
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	2	4.1739	0.3906	2106.57	2104.25	1	1487.8	65.625	Y.MEELADDDEERFSELFK.G
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	2	3.012	0.2606	1312.57	1310.455	2	300.6	65	Y.SHELPRYGITH.G
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	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	26.470589	L.K2G1A1S1D1G1G1L1Y1V1P1H3S1E1N2R4F1P1G1W2D1F1E1T1E1E1I1D1P1E1 L1L1R4S1Y1.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	2	3.6904	0.3591	2181.25	2181.281	1	754.3	50	L.G1L1D1E1T1Y1K2G1V1E1E1V1E1G1E1Y1E1L1T1.E
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	4.7695	0.2533	2831.96	2831.024	1	1875.9	39.772728	H.SENRFPGWDFETEEIDPELLRSY.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	2	3.2876	0.1734	2861.13	2862.024	2	304.5	40.909092	H.S1E1N2R4F1P1G1W2D1F1E1T1E1E1I1D1P1E1L1L1R4S1Y1.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	2	3.3673	0.2122	1493.39	1492.631	1	824.8	72.72727	A.Y1S1H3E1L1P1R4Y1G1I1T1H3.G
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	2	3.5841	0.3938	2162.41	2161.281	1	874.1	52.77778	L.GLDETYKGVEEVEGEYELT.E
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	2	4.4928	0.3159	1630.57	1632.668	1	1407.9	79.16667	H.S1E1N2R4F1P1G1W2D1F1E1T1E1.E
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	3.854	0.3052	1789.73	1788.992	1	673.5	63.333332	T.PEEGALVPEKDDTFLK.L
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	4.6861	0.3431	1988.51	1989.23	1	683.6	58.823532	S.VTPEEGALVPEKDDTFLK.L
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	3.7968	0.3036	1841.41	1842.016	1	840	63.333332	T.LVGDKEDRKEDLSSIH.W
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	4.6467	0.3883	2125.65	2123.389	1	625.3	52.77778	S.V1T1P1E1E1G1A1L1V1P1E1K2D1D1T1F1L1K2L1.A
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	3.179	0.2302	2211.65	2211.578	1	443.2	38.88889	T.MLDIKDESYLVTPPPLHIE.G
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	4.21	0.2714	2027.79	2028.229	1	1169.1	65.625	T.LVGDKEDRKEDLSSIHW.R
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	2.9806	0.2607	1403.35	1403.707	1	730.2	72.72727	E.KKPLNPFLGELF.V
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	3.606	0.2968	1629.87	1628.786	1	678.9	65.38461	H.CLIDPEVESPELAR.M
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	4.4885	0.3656	1644.95	1645.786	1	955.3	73.07692	H.C1L1I1D1P1E1V1E1S1P1E1L1A1R4.M
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	4.3926	0.3454	2491.81	2491.732	1	429.6	42.857143	F.D1Y1S1V1T1P1E1E1G1A1L1V1P1E1K2D1D1T1F1L1K2L1.A
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	4.0394	0.4233	2465.93	2467.732	1	718.5	52.380955	F.DYSVTPEEGALVPEKDDTFLKL.A
gi|6325112|ref|NP_015180.1|	YPL145C	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; Kes1p	2	4.1505	0.3176	2104.77	2102.389	1	565	50	S.VTPEEGALVPEKDDTFLKL.A
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	3.9069	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	66.66667	-.M1L1P1E1K2R4L1L1T1P1D1D1M1K2L1W2.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	50	-.MLPEKRLLTPDDMKLW.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.L1D1C1N2T1R4D1N2L1P1D1L1I1F1.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.GYDTISVDKVVPPFYNAIQQDLLDEKRFAF.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	26.724138	F.G1K2N2F1D1N2V1P1A1E1E1E1E1I1K2E1E1T1P1A1E1K2D1H3E1D1V1T1K2F1 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	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	3.0649	0.2736	1404.78	1405.68	1	743.6	65	S.KYELPKWKEAL.G
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	2	3.8826	0.1919	1738.27	1739.009	1	1043.5	62.5	A.K2Y1F1Y1E1D1L1K2L1P1R4T1F1.S
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	2	3.2667	0.195	1404.85	1405.68	4	677.1	75	S.KYELPKWKEAL.G
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	3.0517	0.2835	1405.65	1405.68	1	714.3	65	S.KYELPKWKEAL.G
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	2	2.9474	0.2307	1720.13	1721.009	1	646.5	54.166668	A.KYFYEDLKLPRTF.S
gi|6325038|ref|NP_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; Sar1p	2	4.2375	0.1703	1630.45	1630.841	1	1329.4	83.33333	L.W2K2D1Y1F1P1E1V1N2G1I1V1F1.L
gi|6325038|ref|NP_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; Sar1p	2	4.7275	0.2747	1707.31	1706.847	1	1798.2	80	L.G1N2K2I1D1A1P1N2A1V1S1E1A1E1L1R4.S
gi|6325038|ref|NP_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; Sar1p	2	3.6814	0.3244	2266.43	2267.534	1	681.8	45.238094	L.G1N2K2I1D1A1P1N2A1V1S1E1A1E1L1R4S1A1L1G1L1L1.N
gi|6325038|ref|NP_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; Sar1p	2	4.9939	0.4088	2237.77	2239.534	1	1688.4	64.28571	L.GNKIDAPNAVSEAELRSALGLL.N
gi|6325038|ref|NP_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; Sar1p	2	3.3693	0.2063	1743.47	1745	1	1142.6	73.07692	L.W2K2D1Y1F1P1E1V1N2G1I1V1F1L1.V
gi|6325038|ref|NP_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; Sar1p	1	2.5467	0.1808	1348.59	1348.53	6	103.8	55	Q.R4I1E1G1Q2R4P1V1E1V1F1.M
gi|6325038|ref|NP_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; Sar1p	2	3.1724	0.1603	1485.27	1484.667	1	723.3	85	R.R4L1W2K2D1Y1F1P1E1V1N2.G
gi|6325038|ref|NP_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; Sar1p	1	3.0334	0.2634	1484.56	1484.667	2	135.7	60.000004	R.R4L1W2K2D1Y1F1P1E1V1N2.G
gi|6325038|ref|NP_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; Sar1p	1	2.418	0.2597	1466.69	1467.667	1	132.6	60.000004	R.RLWKDYFPEVN.G
gi|6325038|ref|NP_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; Sar1p	2	2.9647	0.2233	1469.69	1467.667	1	881.3	85	R.RLWKDYFPEVN.G
gi|6325038|ref|NP_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; Sar1p	2	3.8752	0.3952	1904.39	1905.188	1	1334.7	71.42857	R.R4L1W2K2D1Y1F1P1E1V1N2G1I1V1F1.L
gi|6325038|ref|NP_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; Sar1p	1	2.231	0.159	1466.66	1467.667	1	97.6	50	R.RLWKDYFPEVN.G
gi|6325038|ref|NP_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; Sar1p	1	2.5176	0.1803	1483.65	1484.667	1	194.3	70	R.R4L1W2K2D1Y1F1P1E1V1N2.G

gi|6325038|ref|NP_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; Sar1p	2	3.1418	0.2093	1486.01	1484.667	1	866.9	85	R.R4L1W2K2D1Y1F1P1E1V1N2.G
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	1	2.9734	0.2417	1346.55	1346.409	2	457.7	59.090908	K.H3F1E1D1V1G1L1D1S1E1I1A1.N
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	3.0031	0.1873	1420.45	1422.541	2	525.9	68.181816	A.LDCISDKENTVK.R
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	3.0666	0.2998	1881.79	1881.994	1	564.1	63.333332	L.KEDDEADKENKFSGRL.T
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	1	2.4811	0.1728	1039.54	1040.301	2	548.1	68.75	Q.M1R4F1P1P1P1G1I1L1.T
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	3.4611	0.2628	1678.55	1679.781	1	429.9	53.571426	L.DEPTNYLDRDSLGAL.A
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	3.7145	0.2942	1436.45	1437.541	1	825.3	77.27273	A.L1D1C1I1S1D1K2E1N2T1V1K2.R
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	4.0373	0.3718	1820.99	1820.932	1	775.9	68.75	S.N2L1A1K2P1S1V1D1D1D1D1S1P1A1N2I1K2.V
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	3.6697	0.2602	1904.43	1904.994	1	769.9	56.666668	L.K2E1D1D1E1A1D1K2E1N2K2F1S1G1R4L1.T
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	2.9127	0.3016	1640.65	1639.852	5	245.1	54.166668	W.RYQFGDDREVLLK.E
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	3.3976	0.1688	2071.09	2071.205	1	469.8	46.875	L.FYQEKERADEDEGIEIV.N
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	3.9317	0.2824	2092.15	2093.205	1	924.3	59.375	L.F1Y1Q2E1K2E1R4A1D1E1D1E1G1I1E1I1V1.N
gi|6325030|ref|NP_015098.1|	YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	2	3.7428	0.3282	1661.23	1660.852	1	385.3	62.5	W.R4Y1Q2F1G1D1D1R4E1V1L1L1K2.E
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	3.7031	0.3266	2133.37	2134.301	3	383.4	47.058823	L.KLEAEEIPSEDQNEFLLE.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	3	5.1229	0.4372	2647.97	2650.039	1	1092.4	35.714287	S.G1I1R4L1I1E1P1E1L1F1N2G1Y1N2P1E1K2K2E1M1I1Q2.E
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	3.3224	0.3549	1681.47	1679.868	1	262.6	57.14286	A.AIPEQGIELEHIDSK.S
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	4.918	0.4554	1770.37	1770.946	1	537.8	70	F.A1A1I1P1E1Q2G1I1E1L1E1H3I1D1S1K2.S
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	4.0215	0.3878	1750.29	1750.946	1	467.4	60.000004	F.AAIPEQGIELEHIDSK.S
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	3.9505	0.3132	2603.53	2605.805	1	521.4	38.636364	L.G1K2E1F1G1T1T1P1E1K2P1E1E1T1P1L1E1E1L1A1E1T1F1.Q
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	4.2156	0.2753	2120.29	2119.287	1	800.4	52.77778	F.GTTPEKPEETPLEELAETF.Q
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	1	3.1844	0.2795	1421.8	1422.535	1	441.3	63.636364	R.N2A1D1N2V1D1K2I1L1E1Q2F1.E
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	1	3.071	0.3066	1405.55	1406.535	1	540.4	63.636364	R.NADNVDKILEQF.E
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	3.2932	0.1983	1760.53	1760.926	1	542.4	53.571426	L.I1E1F1I1Y1D1T1E1K2N2G1G1L1G1W2.D
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	4.5273	0.3757	2242.27	2241.351	1	1029.4	61.11111	K.E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1A1.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	1	2.3394	0.1703	1066.63	1068.219	3	195.7	61.11111	E.R4V1V1E1I1G1P1S1P1T1.L
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	3.9286	0.296	2092.67	2091.235	1	1127.3	61.764706	E.HAPYTDELEEDVYLDPLA.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	3.4827	0.2516	1724.97	1726.878	1	790.8	62.5	L.A1A1K2E1E1P1A1K2E1E1A1P1A1P1T1P1A1.A
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	2.9202	0.1926	1709.87	1707.878	1	342.2	53.125	L.AAKEEPAKEEAPAPTPA.A
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	1	2.2209	0.1527	1432.54	1433.535	6	157.2	50	L.EEFEHGRTPAEM.S
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	1	2.4095	0.1882	1054.75	1055.219	7	155.6	61.11111	E.RVVEIGPSPT.L

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	3.0456	0.2975	1666.49	1666.8	1	535.4	57.692307	N.T1L1E1E1F1E1H3G1R4T1P1A1E1M1.S
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	3.4938	0.3433	1697.87	1698.868	1	325.7	64.28571	A.A1I1P1E1Q2G1I1E1L1E1H3I1D1S1K2.S
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	3.6277	0.2564	1876.23	1875.024	1	1193.1	66.66667	Y.S1K2D1A1K2E1I1Y1Y1T1P1D1P1S1E1L1.A
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	3	3.8716	0.1783	2376.65	2377.603	1	691.5	38.157894	M.D1L1D1N2G1E1R4K2F1L1K2E1K2D1T1V1A1E1L1Q2.A
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	4.9174	0.4239	2152.33	2153.329	1	1022.4	58.333332	L.G1K2E1F1G1T1T1P1E1K2P1E1E1T1P1L1E1E1L1.A
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	4.4568	0.3994	2298.27	2299.446	2	403.5	50	S.K2E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1.A
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	3.584	0.3391	2560.63	2559.736	2	139.6	35.714287	F.V1S1K2E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1A1.R
gi|6325025|ref|NP_015093.1|	YPL231W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p	2	3.7541	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
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	3.73	0.2588	1902.45	1903.14	2	518.4	53.125	W.VDSKTKEPVDDKDVKAK.Y
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	4.8753	0.3077	2377.61	2377.603	1	524.3	50	M.D1L1D1N2G1E1R4K2F1L1K2E1K2D1T1V1A1E1L1Q2.A
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	4.5978	0.2367	2346.43	2345.548	8	501.7	37.5	L.N2S1G1I1I1P1G1N2R4N2A1D1N2V1D1K2I1L1E1Q2F1.E
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	4.4219	0.2704	2315.09	2315.548	1	761.2	47.5	L.NSGIIPGNRNADNVDKILEQF.E
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	4.3235	0.3413	2139.69	2141.366	1	721.5	50	S.G1I1I1P1G1N2R4N2A1D1N2V1D1K2I1L1E1Q2F1.E
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	3.6724	0.3027	2113.55	2114.366	1	839.7	50	S.GIIPGNRNADNVDKILEQF.E
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	3.6942	0.2297	1543.13	1542.688	1	551.1	77.27273	M.F1K2D1R4F1K2D1E1P1V1Q2N2.D
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	4.4174	0.334	2146.39	2147.342	1	834.8	59.375	M.F1K2D1R4F1K2D1E1P1V1Q2N2D1I1L1Q2E1.S
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	4.2579	0.3447	2120.77	2122.342	1	1146.6	65.625	M.FKDRFKDEPVQNDILQE.S
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	3	4.9423	0.3457	2142.83	2143.44	1	1230.3	41.17647	S.G1I1R4L1I1E1P1E1L1F1N2G1Y1N2P1E1K2K2.E
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	4.5462	0.3625	2648.45	2650.039	1	500.5	47.61905	S.G1I1R4L1I1E1P1E1L1F1N2G1Y1N2P1E1K2K2E1M1I1Q2.E
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	2.9546	0.1791	1526.37	1523.688	1	462	72.72727	M.FKDRFKDEPVQN.D
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	4.2187	0.3022	1992.55	1993.227	1	941.7	63.333332	M.FKDRFKDEPVQNDILQ.E
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	4.5418	0.3141	2017.47	2017.227	1	862.8	60.000004	M.F1K2D1R4F1K2D1E1P1V1Q2N2D1I1L1Q2.E
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	3.7733	0.2143	1889.69	1887.096	1	880.7	67.85714	M.F1K2D1R4F1K2D1E1P1V1Q2N2D1I1L1.Q
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	3.345	0.298	1863.97	1865.096	1	510.5	57.14286	M.FKDRFKDEPVQNDIL.Q
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	3	4.5037	0.2209	2638.91	2639.97	1	647.2	36.904762	L.K2M1D1L1D1N2G1E1R4K2F1L1K2E1K2D1T1V1A1E1L1Q2.A
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	3.9102	0.1899	2637.61	2639.97	1	452.7	45.238094	L.K2M1D1L1D1N2G1E1R4K2F1L1K2E1K2D1T1V1A1E1L1Q2.A
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	3	4.8169	0.2911	2621.18	2620.039	1	1197	40.476192	S.GIRLIEPELFNGYNPEKKEMIQ.E
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	3.4553	0.3468	1804.27	1805.093	1	799.8	52.941177	T.A1T1D1K2I1G1R4S1V1P1A1P1G1K2G1I1L1T1.T

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	3.4906	0.3699	1907.35	1907.199	1	665.9	47.22222	A.T1A1T1D1K2I1G1R4S1V1P1A1P1G1K2G1I1L1T1.T
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	3.226	0.3547	1705.93	1702.988	1	885.2	56.25	T.A1T1D1K2I1G1R4S1V1P1A1P1G1K2G1I1L1.T
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	3.8819	0.183	2150.07	2149.272	1	655.5	50	K.EHAPYTDELEEDVYLDPL.A
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	3.8548	0.3782	2219.19	2220.351	1	682.5	52.77778	K.EHAPYTDELEEDVYLDPLA.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	3	4.1435	0.2362	1733.6	1733.015	4	1006.8	39.0625	A.T1D1K2I1G1R4S1V1P1A1P1G1K2G1I1L1T1.T
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	1	4.0258	0.4423	1507.67	1508.804	1	384.3	60.714287	T.DKIGRSVPAPGKGIL.T
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	4.6187	0.2392	2170.49	2169.272	1	918.1	58.823532	K.E1H3A1P1Y1T1D1E1L1E1E1D1V1Y1L1D1P1L1.A
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	4.556	0.3455	2139.97	2139.287	1	633.9	47.22222	F.G1T1T1P1E1K2P1E1E1T1P1L1E1E1L1A1E1T1F1.Q
gi|6325018|ref|NP_015087.1|	YPL237W	Beta subunit of the translation initiation factor eIF2, involved in the identification of 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
gi|6325018|ref|NP_015087.1|	YPL237W	Beta subunit of the translation initiation factor eIF2, involved in the identification of the start codon; proposed to be involved in mRNA binding; Sui3p	1	2.9193	0.2833	1247.41	1248.412	1	241.2	66.66667	K.L1H3R4S1P1E1H3L1I1Q2.Y
gi|6325018|ref|NP_015087.1|	YPL237W	Beta subunit of the translation initiation factor eIF2, involved in the identification of 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.K2V1I1P1D1D1F1D1A1A1.V
gi|6325018|ref|NP_015087.1|	YPL237W	Beta subunit of the translation initiation factor eIF2, involved in the identification of 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
gi|6325004|ref|NP_015071.1|	YPL252C	Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis; homologous to human adrenodoxin; Yah1p	2	3.5755	0.253	2933.63	2934.111	1	458.1	39.583336	C.HVIVDPDYYDALPEPEDDENDMLDL.A
gi|6325004|ref|NP_015071.1|	YPL252C	Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis; homologous to human adrenodoxin; Yah1p	2	4.2754	0.4651	3092.61	3094.25	1	593.2	40	T.CHVIVDPDYYDALPEPEDDENDMLDL.A
gi|6325004|ref|NP_015071.1|	YPL252C	Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis; homologous to human adrenodoxin; Yah1p	2	4.4394	0.4116	2932.35	2934.111	1	435.8	41.666664	C.HVIVDPDYYDALPEPEDDENDMLDL.A
gi|6325004|ref|NP_015071.1|	YPL252C	Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis; homologous to human adrenodoxin; Yah1p	3	4.6654	0.3008	2933.21	2934.111	1	922.5	33.333336	C.HVIVDPDYYDALPEPEDDENDMLDL.A
gi|6324993|ref|NP_015061.1|	YPL262W	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting sequence and protein conformation; Fum1p	3	3.939	0.2334	2172.2	2172.46	1	1129.6	47.058823	L.TEKEFDEWVVPEHMLGPK.-
gi|6324993|ref|NP_015061.1|	YPL262W	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting sequence and protein conformation; Fum1p	2	4.7486	0.28	2172.95	2172.46	1	1056.3	61.764706	L.TEKEFDEWVVPEHMLGPK.-
gi|6324993|ref|NP_015061.1|	YPL262W	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting sequence and protein conformation; Fum1p	3	4.7046	0.252	2193.65	2195.46	1	1361.2	48.52941	L.T1E1K2E1F1D1E1W2V1V1P1E1H3M1L1G1P1K2.-
gi|6324993|ref|NP_015061.1|	YPL262W	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting sequence and protein conformation; Fum1p	2	5.2577	0.3673	2172.69	2172.46	1	1272.4	67.64706	L.TEKEFDEWVVPEHMLGPK.-
gi|6324993|ref|NP_015061.1|	YPL262W	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting sequence and protein conformation; Fum1p	1	2.3361	0.3744	1256.43	1257.434	1	556.8	70	E.IHVPADKYWGA.Q
gi|6324993|ref|NP_015061.1|	YPL262W	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting 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.M1E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1E1T1L1.R
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	3	4.4009	0.3261	2349.44	2349.672	1	944.9	43.055553	Q.M1E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1E1T1L1.R
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	2	3.8698	0.2341	2321.99	2323.672	1	1238.6	58.333332	Q.MEIPDERSWLPHPKPFETL.R
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	3	4.7892	0.2719	2351.96	2349.672	1	1468.3	45.833336	Q.M1E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1E1T1L1.R
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	2	3.622	0.3561	2347.75	2349.672	1	505.3	41.666664	Q.M1E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1E1T1L1.R
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	2	3.6575	0.1899	1981.21	1980.292	3	343.1	50	Q.MEIPDERSWLPHPKPF.E
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	2	3.7237	0.2253	2004.03	2003.292	7	410.1	56.666668	Q.M1E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1.E
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	2	2.9777	0.2249	2216.41	2217.479	1	394.4	47.058823	M.E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1E1T1L1.R
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	2	3.1767	0.312	1848.61	1849.099	1	632.1	60.714287	M.EIPDERSWLPHPKPF.E
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	2	3.7458	0.2501	2001.77	2003.292	4	531.9	60.000004	Q.M1E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1.E
gi|6324992|ref|NP_015060.1|	YPL263C	Cytoplasmic protein of unknown function; Kel3p	3	4.2155	0.2275	2002.88	2003.292	9	609.6	41.666664	Q.M1E1I1P1D1E1R4S1W2L1P1H3P1K2P1F1.E
gi|6324992|ref|NP_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
gi|6324981|ref|NP_015049.1|	YPL274W	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-methylmethionine permease Mmp1p; Sam3p	2	4.9663	0.4299	2523.37	2523.674	1	1016	62.5	S.N2L1H3V1I1P1E1D1L1E1N2S1E1Q2T1E1Q2E1K2I1Q2.W
gi|6324981|ref|NP_015049.1|	YPL274W	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-methylmethionine permease Mmp1p; Sam3p	2	3.6794	0.321	2711.71	2711.888	1	757.4	47.61905	S.N2L1H3V1I1P1E1D1L1E1N2S1E1Q2T1E1Q2E1K2I1Q2W2.K
gi|6324981|ref|NP_015049.1|	YPL274W	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-methylmethionine permease Mmp1p; Sam3p	3	4.1424	0.3543	2841.56	2842.062	1	470.6	26.136362	S.N2L1H3V1I1P1E1D1L1E1N2S1E1Q2T1E1Q2E1K2I1Q2W2K2.L
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	1	2.7478	0.2939	1451.54	1452.665	1	736.2	68.181816	R.KWPTIDMPFSET.G
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	2.9156	0.1582	2137.79	2137.329	4	312	38.88889	A.S1P1D1Q2S1D1L1E1V1G1Q2E1V1L1D1R4I1V1L1.V
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.4057	0.2672	1682.37	1682.896	1	661.3	61.538464	N.D1V1K2D1S1F1L1T1D1R4L1E1L1L1.L
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.8344	0.2812	1669.67	1666.955	1	932.8	60.000004	W.KVEGKTPGLPIDLEIG.Y
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	4.206	0.2541	1664.71	1662.926	1	1667.9	73.07692	V.RYLPLDKEDIVGPF.E
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.5638	0.231	2889.33	2890.309	1	267.6	30.769232	E.GKTPGLPIDLEIGYVPPSTRGQYPGLY.L
gi|6325267|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.HFGFGNDEWPKEWLEKL.D
gi|6325267|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

gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.6973	0.3402	1694.73	1695.931	1	790.8	65.38461	C.SRKWPTIDMPFSET.G
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	4.9167	0.4682	2466.73	2467.868	1	1198.9	56.81818	W.KVEGKTPGLPIDLEIGYVPPSTR.G
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.3035	0.3504	1664.75	1664.896	1	1169.7	69.230774	N.DVKDSFLTDRLELL.L
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.3012	0.3243	2408.29	2405.542	1	396.6	42.5	Y.H3S1S1E1P1A1Y1I1E1E1V1N2L1I1G1D1E1S1N2K2F1.Q
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
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	5.3502	0.4855	2494.97	2495.868	1	1161.6	54.545456	W.K2V1E1G1K2T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4.G
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	5.0735	0.4411	2465.33	2467.868	1	1170.5	42.045452	W.KVEGKTPGLPIDLEIGYVPPSTR.G
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	3.829	0.306	2134.91	2133.37	1	724.5	35.9375	Q.HFGFGNDEWPKEWLEKL.D
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	4.0233	0.2251	3248.9	3246.731	1	913.6	32.75862	W.KVEGKTPGLPIDLEIGYVPPSTRGQYPGLY.L
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	4.7124	0.3796	3282.59	3282.731	1	727.7	30.172413	W.K2V1E1G1K2T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4G1Q2Y1P1G1L1Y1.L
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	3.8843	0.3349	2112.65	2113.329	7	430	41.666664	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
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	4.3578	0.3124	1684.45	1684.955	1	945.2	63.333332	W.K2V1E1G1K2T1P1G1L1P1I1D1L1E1I1G1.Y
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	2	4.8136	0.4948	2134.39	2135.446	1	1199.3	57.894737	E.G1K2T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4.G
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	4.2998	0.2171	2112.86	2111.446	1	1374.5	43.421055	E.GKTPGLPIDLEIGYVPPSTR.G
gi|6325267|ref|NP_015335.1|	YPR010C	RNA polymerase I subunit A135; Rpa135p	3	4.5809	0.2996	2495.72	2495.868	2	949.9	35.227272	W.K2V1E1G1K2T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4.G
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.K2V1E1G1K2T1P1G1L1P1I1D1L1E1I1G1Y1V1P1P1S1T1R4.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
gi|6325276|ref|NP_015344.1|	YPR019W	Essential helicase component of heterohexameric MCM2-7 complexes which bind pre-replication complexes on DNA and melt the DNA prior to replication; 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
gi|6325276|ref|NP_015344.1|	YPR019W	Essential helicase component of heterohexameric MCM2-7 complexes which bind pre-replication complexes on DNA and melt the DNA prior to replication; accumulates in the nucleus in G1; homolog of S. pombe Cdc21p; Cdc54p	2	3.9533	0.3647	1811.33	1811.005	1	897.8	71.42857	L.DKVDEKNDRELAKHL.T
gi|6325276|ref|NP_015344.1|	YPR019W	Essential helicase component of heterohexameric MCM2-7 complexes which bind pre-replication complexes on DNA and melt the DNA prior to replication; 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
gi|6325276|ref|NP_015344.1|	YPR019W	Essential helicase component of heterohexameric MCM2-7 complexes which bind pre-replication complexes on DNA and melt the DNA prior to replication; accumulates in the nucleus in G1; homolog of S. pombe Cdc21p; Cdc54p	2	4.1873	0.4115	2263.97	2263.599	1	531.3	52.63158	S.RYNPNLPVTENIDLPPPLLS.R
gi|6325276|ref|NP_015344.1|	YPR019W	Essential helicase component of heterohexameric MCM2-7 complexes which bind pre-replication complexes on DNA and melt the DNA prior to replication; 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
gi|6325291|ref|NP_015359.1|	YPR034W	Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex; Arp7p	2	3.6502	0.266	1452.41	1452.748	1	889.6	75	Q.L1K2V1S1P1E1E1L1P1L1V1I1T1.M
gi|6325291|ref|NP_015359.1|	YPR034W	Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex; Arp7p	2	3.4641	0.16	1440.63	1438.748	1	1061.5	75	Q.LKVSPEELPLVIT.M
gi|6325291|ref|NP_015359.1|	YPR034W	Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex; Arp7p	2	3.1267	0.3477	1868.87	1866.267	1	351.9	40.625	T.QLKVSPEELPLVITMPA.T
gi|6325291|ref|NP_015359.1|	YPR034W	Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex; Arp7p	2	3.1166	0.2223	1952.49	1953.345	1	676.8	50	Q.LKVSPEELPLVITMPATN.G
gi|6325291|ref|NP_015359.1|	YPR034W	Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex; Arp7p	2	3.0062	0.4158	1382.13	1382.643	1	859.6	75	C.NVTPIIDGIVVKN.A
gi|6325291|ref|NP_015359.1|	YPR034W	Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex; Arp7p	2	4.0475	0.3176	1485.33	1485.73	1	783.7	69.230774	S.GCNVTPIIDGIVVK.N
gi|6325291|ref|NP_015359.1|	YPR034W	Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex; Arp7p	2	3.6857	0.2802	1277.55	1275.401	1	1875.5	86.36364	S.DKFSPEDGLGPL.M
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.8014	0.4101	1721.51	1723.761	1	842.8	69.230774	L.C1W2S1P1P1H3V1D1N2G1F1W2S1D1.N
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.0798	0.1794	2079.79	2081.194	2	422.5	43.75	Q.S1L1S1E1R4K2Y1S1D1E1E1L1R4Q2D1I1S1.N
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.0988	0.1952	2109.55	2109.219	1	396.8	46.875	L.S1E1R4K2Y1S1D1E1E1L1R4Q2D1I1S1N2L1.K
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.0246	0.2272	1614.45	1611.884	1	731.7	66.66667	L.AVIPEYRDVIWLH.E
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.4745	0.3401	1630.79	1630.884	1	937.8	70.83333	L.A1V1I1P1E1Y1R4D1V1I1W2L1H3.E
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.3554	0.2787	1980.77	1982.29	1	410.7	46.666668	L.QELAVIPEYRDVIWLH.E
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.0656	0.2423	1853.01	1854.159	1	460.3	50	Q.ELAVIPEYRDVIWLH.E
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.0003	0.1598	1558.57	1558.805	1	494.8	63.636364	A.V1I1P1E1Y1R4D1V1I1W2L1H3.E
gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	3.2394	0.2475	2004.59	2005.29	1	373	46.666668	L.Q2E1L1A1V1I1P1E1Y1R4D1V1I1W2L1H3.E

gi|6325293|ref|NP_015361.1|	YPR036W	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-ATPase; Vma13p	2	4.1346	0.4329	1872.47	1875.159	1	917.1	67.85714	Q.E1L1A1V1I1P1E1Y1R4D1V1I1W2L1H3.E
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	1	2.2043	0.1745	1046.41	1046.185	8	412.4	68.75	A.K2L1Q2D1V1L1D1G1F1.I
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	3.7675	0.1968	1774.37	1774.807	6	443.1	61.538464	Q.H3H3D1E1D1E1D1E1L1S1R4Q2I1K2.A
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	5.35	0.2979	2193.33	2193.238	1	1133.8	58.823532	S.S1T1P1Q2H3H3D1E1D1E1D1E1L1S1R4Q2I1K2.A
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	1	3.7524	0.1711	1546.72	1546.907	1	317.3	62.5	L.E1H3K2D1L1I1P1L1L1P1K2I1L1.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.E1H3K2D1L1I1P1L1L1P1K2I1L1.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	1	3.4644	0.2538	1531.78	1529.907	3	253.3	58.333332	L.EHKDLIPLLPKIL.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	3.1073	0.3943	1528.01	1529.907	1	749.3	79.16667	L.EHKDLIPLLPKIL.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	3.8554	0.2842	1886.33	1887.114	1	956.4	64.28571	Q.LYNNDIISEEEIMRF.G
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	3.8456	0.2655	1761.81	1763.015	1	402.7	50	D.K2D1R4Y1L1V1N2G1V1H3E1P1A1K2L1.Q
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	1	2.7161	0.2036	1529.96	1529.907	2	223.5	54.166668	L.EHKDLIPLLPKIL.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	1	3.1087	0.174	1548.21	1546.907	1	222	54.166668	L.E1H3K2D1L1I1P1L1L1P1K2I1L1.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	3.027	0.3508	1529.61	1529.907	1	651.1	79.16667	L.EHKDLIPLLPKIL.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	3.1073	0.1728	1534.53	1532.64	2	425.3	65	C.R4D1N2H3D1P1F1Y1R4Y1K2.M
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	3.1097	0.2796	1546.29	1546.907	1	403.3	70.83333	L.E1H3K2D1L1I1P1L1L1P1K2I1L1.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	3.7189	0.2166	1630.11	1630.81	1	449.6	65.38461	L.V1T1P1E1Y1E1K2N2F1M1G1G1I1E1.R
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	3.8821	0.1872	1908.01	1907.114	7	309.1	53.571426	Q.L1Y1N2N2D1I1I1S1E1E1E1I1M1R4F1.G
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	3	4.5232	0.2695	2310.5	2311.605	1	1662.2	46.05263	S.I1S1V1D1K2D1R4Y1L1V1N2G1V1H3E1P1A1K2L1Q2.D
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	1	2.8667	0.1572	1317.61	1318.588	9	263.7	65	L.E1H3K2D1L1I1P1L1L1P1K2.I
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	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 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	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.K2V1K2E1G1I1E1D1F1D1D1I1Y1E1K2F1.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.L1K2K2V1K2E1G1I1E1D1F1D1D1I1Y1E1K2F1.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.V1K2E1G1I1E1D1F1D1D1I1Y1E1K2F1.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.V1K2E1G1I1E1D1F1D1D1I1Y1E1K2F1.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	2	3.7654	0.3019	2218.45	2217.524	1	632.8	47.058823	L.LKKVKEGIEDFDDIYEKF.Q
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	4.5608	0.2463	2330.49	2329.587	1	921.4	52.499996	R.K2L1S1E1T1V1L1E1D1V1Y1N2Q2L1P1E1L1I1G1G1S1.A
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	3.9938	0.2913	1933.31	1933.093	2	556.1	52.941177	L.G1S1R4T1P1G1H3P1E1F1E1L1P1G1V1E1V1T1.T
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	3.8971	0.3589	1788.43	1786.963	5	479.4	50	S.R4T1P1G1H3P1E1F1E1L1P1G1V1E1V1T1.T
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	3.6095	0.3389	1765.69	1765.963	1	588.9	56.666668	S.RTPGHPEFELPGVEVT.T
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	4.1971	0.3694	2104.03	2104.238	1	1602.8	57.894737	A.THDSIGVGEDGPTHQPIETL.A
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	3.8764	0.3786	2465.87	2463.709	1	623.7	43.47826	L.GSRTPGHPEFELPGVEVTTGPLGQ.G
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	3.1888	0.3034	2494.39	2493.709	4	197.5	30.434782	L.G1S1R4T1P1G1H3P1E1F1E1L1P1G1V1E1V1T1T1G1P1L1G1Q2.G
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	3.1348	0.2241	2306.35	2307.639	1	188.8	50	Q.M1R4M1N2P1T1N2P1D1W2I1N2R4D1R4F1V1L1.S
gi|6325331|ref|NP_015399.1|	YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	2	3.4968	0.2803	2277.93	2276.639	1	215.4	47.058823	Q.MRMNPTNPDWINRDRFVL.S
gi|6325343|ref|NP_015411.1|	YPR086W	Transcription factor TFIIB, 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|	YPR086W	Transcription factor TFIIB, a general transcription factor required for transcription initiation and start site selection by RNA polymerase II; Sua7p	2	4.3835	0.3775	2026.63	2024.3	1	832	63.333332	L.TCPECKVYPPKIVERF.S
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.9971	0.2929	1884.91	1883.121	1	903.9	70	F.R4T1E1P1I1M1D1F1E1I1E1P1I1V1S1S1.S
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.3367	0.3425	2013.43	2014.153	1	509	56.25	K.ELDHDTADEIDEKTRLL.A
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.0139	0.1736	1795.83	1795.042	1	662.3	64.28571	F.R4T1E1P1I1M1D1F1E1I1E1P1I1V1S1.S
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	2.9395	0.1598	2012.37	2011.297	1	805.6	56.25	A.FRTEPIMDFEIEPIVSS.S
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.5665	0.3351	2262.63	2263.555	1	800.2	52.77778	T.IWPRFDELGKEELPDASLF.T
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.8449	0.2277	2286.47	2287.555	1	704.3	50	T.I1W2P1R4F1D1E1L1G1K2E1E1L1P1D1A1S1L1F1.T
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	4.853	0.4174	2384.63	2385.58	1	930.2	57.894737	A.S1K2K2E1L1D1H3D1T1A1D1E1I1D1E1K2T1R4L1L1.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|	YPR091C	hypothetical protein; Ypr091cp	2	5.1014	0.4044	2359.61	2357.58	1	983.8	57.894737	A.SKKELDHDTADEIDEKTRLL.A
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.5617	0.3665	1575.15	1574.858	1	862.6	65.38461	N.KIKTPGFLDDLVVE.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	66.66667	K.L1N2K2I1K2T1P1G1F1L1D1D1L1.V
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.7664	0.2612	1917.59	1916.268	1	692.2	53.125	L.NKIKTPGFLDDLVVEKV.D
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	4.6955	0.1685	1949.81	1951.295	1	1244.2	65.625	K.L1N2K2I1K2T1P1G1F1L1D1D1L1V1V1E1K2.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|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.1111	0.216	1866.39	1864.121	1	593.7	60.000004	F.RTEPIMDFEIEPIVSS.S
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	2	3.975	0.2208	1708.31	1706.962	1	1073.5	64.28571	L.N2K2I1K2T1P1G1F1L1D1D1L1V1V1E1.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|	YPR091C	hypothetical protein; Ypr091cp	2	4.0194	0.2741	1821.57	1821.121	4	552.4	53.333336	K.L1N2K2I1K2T1P1G1F1L1D1D1L1V1V1E1.K
gi|6325349|ref|NP_015416.1|	YPR091C	hypothetical protein; Ypr091cp	3	4.5311	0.3015	2030.51	2029.428	1	1347.3	42.647057	K.LNKIKTPGFLDDLVVEKV.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.R4E1Q2E1E1I1M1K2E1E1E1Q2Q2E1E1N2A1I1V1S1.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

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	3.1491	0.1946	1603.61	1602.914	1	454.6	61.538464 A.SKVSPVKEKEKVPF.K
gi|6325423|ref|NP_015491.1|	YPR165W	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p	1	2.3708	0.166	1351.63	1352.53	1	234.9	45.454548 F.SKGQFPEVYVPT.V
gi|6325423|ref|NP_015491.1|	YPR165W	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p	2	3.2236	0.3196	1352.47	1352.53	1	568.8	72.72727 F.SKGQFPEVYVPT.V
gi|6325423|ref|NP_015491.1|	YPR165W	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p	2	3.9749	0.1576	1688.87	1690.875	1	1123.6	69.230774 C.K2V1D1L1R4N2D1P1Q2T1I1E1Q2L1.R
gi|6325423|ref|NP_015491.1|	YPR165W	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p	1	2.4295	0.2084	1365.5	1366.53	1	338.9	59.090908 F.S1K2G1Q2F1P1E1V1Y1V1P1T1.V
gi|6325423|ref|NP_015491.1|	YPR165W	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p	2	3.0304	0.2546	1354.51	1352.53	1	432.2	63.636364 F.SKGQFPEVYVPT.V
gi|6325423|ref|NP_015491.1|	YPR165W	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p	2	3.8823	0.2722	1920.51	1921.114	1	870.5	63.333332 C.FSIDLPDSLENVQEKW.I
gi|6325423|ref|NP_015491.1|	YPR165W	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p	2	3.5122	0.2404	2105.79	2105.352	3	336.2	47.058823 C.FSIDLPDSLENVQEKWIA.E
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.2678	0.2141	2384.69	2385.642	1	381.3	39.473686 L.YTPLKEYDELNVAPYNPVVC.S
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.1117	0.2913	1406.47	1406.71	2	525.2	68.181816 T.NKPVTVPPIFFF.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.7009	0.2919	1421.71	1420.711	3	510	68.181816 T.N2K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.8298	0.3435	1405.66	1406.71	3	328.3	59.090908 T.NKPVTVPPIFFF.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.7475	0.2213	1419.61	1420.71	3	278.4	54.545456 T.N2K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.2703	0.1978	1303.91	1304.607	1	888.3	80 N.K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.1632	0.3046	1291.75	1292.607	1	801.5	75 N.KPVTVPPIFFF.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.724	0.285	1303.55	1304.607	2	297.7	60.000004 N.K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.6047	0.2396	1293.61	1292.607	2	370.5	65 N.KPVTVPPIFFF.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.7505	0.3974	1518.93	1520.843	3	459.8	62.5 T.N2K2P1V1T1V1P1P1I1F1F1F1V1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.0025	0.2844	1402.49	1404.739	2	984.7	77.27273 N.K2P1V1T1V1P1P1I1F1F1F1V1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.1407	0.1802	2118.29	2119.449	1	467.6	37.5 F.S1L1N2R4F1F1L1P1L1E1Q2V1E1F1K2L1N2.Q
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	2.9997	0.2071	1389.77	1391.739	2	929.8	72.72727 N.KPVTVPPIFFFV.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.5302	0.3213	1436.23	1435.689	1	509.3	63.636364 Q.G1C1Y1K2N2I1P1A1R4I1I1L1.F
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.0038	0.1547	1783.89	1784.151	1	396.3	57.14286 E.YITNKPVTVPPIFFF.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	3	3.8359	0.4009	2359.85	2361.66	1	1008.5	42.5 A.ELLVDRFPLPRFIDTEAGGSQ.A
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	3	4.3652	0.3715	2388.89	2389.66	1	870.8	41.25 A.E1L1L1V1D1R4F1P1L1P1R4F1I1D1T1E1A1G1G1S1Q2.A
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.5551	0.3646	1405.64	1406.71	1	416.8	68.181816 T.NKPVTVPPIFFF.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.661	0.2307	1292.88	1292.607	2	429.1	70 N.KPVTVPPIFFF.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.6914	0.2176	1303.45	1304.607	4	304.7	60.000004 N.K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.4349	0.3702	1305.51	1304.607	2	891.4	80 N.K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.3703	0.2108	1363.85	1364.674	2	718.8	75 C.Y1K2N2I1P1A1R4I1I1L1F1.A

gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex 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
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; 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
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; 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
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; 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
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.5598	0.2019	1422.38	1420.711	5	223.7	50	T.N2K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; 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
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	1	2.6364	0.327	1303.46	1304.607	9	261.2	55	N.K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.3535	0.3599	1303.55	1304.607	1	1038.9	85	N.K2P1V1T1V1P1P1I1F1F1F1.V
gi|6325439|ref|NP_015507.1|	YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	2	3.3226	0.3884	1504.91	1505.843	2	433.3	58.333332	T.NKPVTVPPIFFFV.V
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	1	2.9464	0.2517	1446.47	1447.588	1	452.8	62.5	M.DADLQHPPETVPK.L
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	1	3.3175	0.2616	1463.53	1464.588	1	576.7	66.66667	M.D1A1D1L1Q2H3P1P1E1T1V1P1K2.L
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	3.3079	0.2827	1861.63	1859.116	1	686.9	60.000004	C.M1D1A1D1L1Q2H3P1P1E1T1V1P1K2L1F1.E
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	3.7178	0.4017	1762.71	1764.009	1	1335.9	66.66667	L.GTRYAPGVGIDKDWPM.Y
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	1	2.8247	0.2687	1421.53	1422.668	1	578.2	68.181816	D.L1Q2H3P1P1E1T1V1P1K2L1F1.E
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	4.8872	0.3317	1904.31	1904.034	1	891.9	75	Q.K2K2Y1L1E1N2C1N2P1R4D1I1N2S1Q2.G
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	3.2155	0.1897	1579.05	1578.78	3	576	57.692307	C.MDADLQHPPETVPK.L
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	3	4.1309	0.2317	1728.08	1726.924	2	914.3	48.214287	M.D1A1D1L1Q2H3P1P1E1T1V1P1K2L1F1.E
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	2.9149	0.3363	1838.35	1839.116	1	497.2	50	C.MDADLQHPPETVPKLF.E
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	4.2199	0.2972	1783.51	1785.009	1	726.4	53.333336	L.G1T1R4Y1A1P1G1V1G1I1D1K2D1W2P1M1.Y
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	3.8036	0.2101	1879.43	1880.034	1	415.1	57.14286	Q.KKYLENCNPRDINSQ.G
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	1	2.6572	0.3355	1405.55	1406.668	1	545.6	63.636364	D.LQHPPETVPKLF.E
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	3	4.4448	0.238	2108.66	2109.372	1	760.7	38.235294	L.G1T1R4Y1A1P1G1V1G1I1D1K2D1W2P1M1Y1R4.R
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	4.4478	0.3821	2107.39	2109.372	2	467.9	52.941177	L.G1T1R4Y1A1P1G1V1G1I1D1K2D1W2P1M1Y1R4.R
gi|6325441|ref|NP_015509.1|	YPR183W	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 glycosylation; Dpm1p	2	4.6841	0.4881	2082.55	2083.372	1	619.5	58.823532	L.GTRYAPGVGIDKDWPMYR.R