

## 123 LC-MS run 3: 123\_220709\_1a2\_03

Protein name	Peptide Rank	Peptide Modification	Peptide Sequence	Peptide sequence start	Peptide sequence Length	Peptide Matched Products	Peptide Score	By Matches	Precursor MH+ (Da)	Retention time (min)	Intensity	z	Precursor m/z	MH+ Error (ppm)
P64076 ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	29	209.16	b2*b2b3*b3b4b5b7*b7b13°b13b14°b14y1y2y3y4y5y6y7y8y9y10y11°y11y12y13*y13y15*y15	1605.89	85.787	518654	2	803.45	2.28
P64076 ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	39	374.09	b2°b2b3b4b5b6b8°b8b9°b9b11b13°b13b14b15b16b18b20b22y2y3y4*y4y5y6y7y8°y8y9y10y11y12y13y14y15y16y17y18y22	2118.07	75.203	362555	2	1059.54	5.76
P64076 ENO_SALTY Enolase	3		GMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	200	31	32	220.02	b2b4b5°b5b6°b6*b6b12b13b16b25b26b30y2y3y4°y4y5y6y7y8y10y11y14y15*y15y18y19y25*y25y26y31	2989.46	94.871	182888	3	997.16	1.63
P64076 ENO_SALTY Enolase	4		DAGYTAVISHR	360	11	12	109.64	b2b3°b3b7b8y3y4y5y6y7y9y11	1189.59	41.382	133760	2	595.30	-7.49
P64076 ENO_SALTY Enolase	5		YSMPVPMMNININGEHADNNVDIQEFMIQPVGAK	143	34	18	80.34	b2°b2b5b23y2y3y5y6*y6y7y8y9y13°y13*y13y29y31y34	3759.77	98.457	127115	3	1253.93	1.17
P64076 ENO_SALTY Enolase	6		AVGAVNGPIAQAILGK	66	16	12	60.24	b1b2b3b4b5b7°b7y2y3y11y12y16	1478.87	75.088	126487	2	739.94	-0.58
P64076 ENO_SALTY Enolase	7		GIANSILIK	333	9	5	37.96	y2y3y6y7y9	928.57	60.932	115247	2	464.79	-10.85
P64076 ENO_SALTY Enolase	8		YVLAGEGNK	257	9	12	61.16	b1b2b7y5y6y7°y7*y7y8°y8y9*y9	950.50	33.155	84391	2	475.75	4.94
P64076 ENO_SALTY Enolase	9		GMPLYEHIAELNGTPGK	126	17	5	24.75	b2y2y3y4y12	1826.90	67.474	82843	3	609.64	-4.14
P64076 ENO_SALTY Enolase	10		QLVGDDLFVTNTK	311	14	15	88.75	b2*b2b3b4y1y2y4y5*y5y9y10y11°y11y12y14	1562.85	77.580	82641	2	781.93	2.58
P64076 ENO_SALTY Enolase	11		QYPIVSIEDGLDESDWDGFAYQTK	282	24	11	36.82	b2b12y1y4*y4y5°y5y6*y6y8y24	2776.27	93.599	39559	2	1388.64	3.17
P64076 ENO_SALTY Enolase	12		IEEALGEK	411	8	7	66.77	y3y4y5y6°y6y7y8	888.46	31.006	35777	2	444.73	-10.65
P64076 ENO_SALTY Enolase	13	Carbamidomethyl+C(16)	AAGYELGKIDITLAMCAASEFYKDGK	231	26	5	18.05	b7°b7b9b15y3	2824.30	101.709	13739	4	706.83	-7.69
P64076 ENO_SALTY Enolase	14		EALELRDGDK	46	10	5	26.62	b2b3y3y9y10	1145.58	54.318	9794	2	573.29	-3.41
P64076 ENO_SALTY Enolase	15		AFTSEEFTHFLEELTK	266	16	9	34.31	b2b3°b3b9b11°b11b16y10y15	1928.94	107.347	9584	2	964.97	4.05
P64076 ENO_SALTY Enolase	16		AVGAVNGPIAQAILGKDAKDQAGIDK	66	26	3	21.79	b3b4y10	2520.35	87.673	5314	3	840.79	-11.43
P64076 ENO_SALTY Enolase	17		GNPTVEAEVHLEGGFVGMAAAPSGASTGSR	16	30	4	13.97	b11b15y15y18	2856.35	102.248	4152	3	952.79	-4.53
P64076 ENO_SALTY Enolase	18		EIIDSR	10	6	1	13.52	b4	732.39	28.087	17280	1	732.39	-3.25
P64076 ENO_SALTY Enolase	19		EALELR	46	6	2	26.63	y3y4	730.40	40.861	3574	2	365.70	-14.62
P64076 ENO_SALTY Enolase	20		GKGMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	198	33	4	15.42	b5b7b15y26	3174.59	90.017	40768	3	1058.87	4.00
P64076 ENO_SALTY Enolase	21		EAIRMGSEVFHHLAK	180	15	3	25.98	b6b9b10	1724.87	90.060	4106	3	575.63	-9.27
P64076 ENO_SALTY Enolase	22	Oxidation+M(3)	YSMPVPMMNININGEHADNNVDIQEFMIQPVGAK	143	34	3	22.25	b5b6y11	3775.76	98.482	4984	3	1259.26	-0.71
P64076 ENO_SALTY Enolase	23		GYTAVISHR	362	9	0	2.49		1003.53	41.361	54448	2	502.27	-3.59
P64076 ENO_SALTY Enolase	24		ANSILIK	335	7	5	23.1	b3°b3*b3b4°b4	758.47	60.941	20630	1	758.47	-3.22
P64076 ENO_SALTY Enolase	25		DAGYTAVISHR	360	11	0	2.49		1171.57	41.301	3172	3	391.19	-11.98

P0A1D5 CH10_SALTY 10 kDa chaperonin	1		ILDNGTVQPLDVK	47	13	25	165.9	b2b3b4*b4b8*b8*b8b10b11°b11*b11b13y1y2y3y5y7y8y9y10y11°y11*y11y12y13	1411.77	57.237	323434	2	706.39	-3.63
P0A1D5 CH10_SALTY 10 kDa chaperonin	2		VGDIVIFNDGYGVK	60	14	18	189.52	b3b4b5°b5b6b11b13y2y3y4y5y6y7y8y9y10y11y14	1495.78	73.450	295070	2	748.39	-0.08
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	17	118.55	b2b3°b3b4b5°b5b14y2y3y4y6y7y8°y8y9y12y14	1188.65	43.513	244587	2	594.83	-5.13
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIVGVK	37	8	7	53.67	b2y2y3y4y5y6y8	786.46	41.494	24722	2	393.73	-12.03
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		SEKIDNEEVLIMSESDILAIVEA	74	23	6	23.53	b6b9b10*b10y12°y12	2547.26	136.258	6223	2	1274.13	-6.61
P0A1D5 CH10_SALTY 10 kDa chaperonin	6		VGDIVIFNDGYGVKSEK	60	17	4	27.06	b11y10y11y15	1839.93	111.362	3576	2	920.47	-7.90
P0A1D5 CH10_SALTY 10 kDa chaperonin	7	Phosphoryl STY(6)	ILDNGTVQPLDVK	47	13	3	29.62	y6y8y10	1491.72	37.040	1959	2	746.36	-9.00
P0A1D5 CH10_SALTY 10 kDa chaperonin	8		SAGGIVLTGSAAGK	20	14	0	3.73		1170.64	43.534	43902	2	585.82	-1.67
P0A1H5 EFTU_SALTY Elongation factor Tu	1		ELLSQYDFPGDDTPIVR	155	17	31	236.2	b2°b2b5°b5b6°b6b8°b8b12b13b15b16y1y3y4y5y6y8y9°y9y10°y10y11°y11y12°y12y13°y13y14y15y17	1964.97	76.748	331546	2	982.99	2.80
P0A1H5 EFTU_SALTY Elongation factor Tu	2		AIDKPFLLPIDVFSISGR	205	19	13	115.91	b2b5b7b8b12y3y4y5y6y7y8y11y15	2117.15	105.916	320492	3	706.39	-7.15
P0A1H5 EFTU_SALTY Elongation factor Tu	3		GITINTSHVEYDTPTR	59	16	25	196.76	b2b3°b3b10°b10b11b12b16y1y3y4y5y6°y6y7°y7y8°y8y9y10y11y12y13y14y16	1803.86	49.568	259057	3	601.96	-13.06
P0A1H5 EFTU_SALTY Elongation factor Tu	4		AGENVGVLLR	270	10	11	71.67	b4°b4b5°b5°b5y1y3y4y5y6y10	1027.58	56.361	253492	2	514.29	-9.50
P0A1H5 EFTU_SALTY Elongation factor Tu	5		TTDVTGTIELPEGVEMVMPGDNIK	334	24	45	284.17	b1b2°b2b3°b3b4b7°b7b8°b8b10°b10b13b14b15b16°b16b17°b17b18y3y5°y5y6°y6*y6y7°y7*y7y8y9*y9y10y12y13°y13y14*y14y15y16°y16y17y20y24*y24	2546.25	86.587	247851	2	1273.63	4.41
P0A1H5 EFTU_SALTY Elongation factor Tu	6		QVGVPYIIVFLNK	124	13	12	82.6	b3b4°b4b6°b6b13y4y5y6y9y11y13	1489.88	99.160	245054	2	745.44	0.41
P0A1H5 EFTU_SALTY Elongation factor Tu	7		IELAGFLDSYIPEPER	188	17	24	187.18	b2b3b7b11°b11b12b14y1y2y3°y3y4°y4y5y6y7y8°y8y9y10y11y12y13y17	1962.03	101.876	216149	2	981.52	3.98
P0A1H5 EFTU_SALTY Elongation factor Tu	8		ALEGDAEWEAK	177	11	7	35.78	b1b2y1y4°y4y6y9	1218.56	46.240	133862	2	609.78	-4.51
P0A1H5 EFTU_SALTY Elongation factor Tu	9	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	7	67.6	b2y3y4y6y7y8y10	1187.51	52.849	117169	2	594.26	-5.55
P0A1H5 EFTU_SALTY Elongation factor Tu	10	Carbamidomethyl+C(1)	CDMVDDEELLEVEMEVR	137	18	17	127.47	b2b3b9b13y2y3°y3y4y5°y5y6y7y8°y8y9y13y14	2224.00	106.003	47933	2	1112.50	6.15
P0A1H5 EFTU_SALTY Elongation factor Tu	11		TTLTAAITTVLAK	25	13	4	42.73	y7y8y9y11	1303.78	84.694	276673	2	652.39	-2.43
P0A1H5 EFTU_SALTY Elongation factor Tu	12		TVGAGVVAK	382	9	4	54.08	y3y6y7y8	801.47	28.243	163753	2	401.24	-17.52

P0A1H5 EFTU_SALTY Elongation factor Tu	13		MVVTLIHPIAMDDGLR	358	16	3	25.31	y7y8y10	1780.96	55.979	36056	3	594.32	7.81
P0A1H5 EFTU_SALTY Elongation factor Tu	14	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	4	29.09	b8y3y8y10	1768.76	39.788	35425	4	442.94	-17.53
P0A1H5 EFTU_SALTY Elongation factor Tu	15		LLDEGR	264	6	4	39.73	y3°y3y4y5	702.37	26.487	13453	1	702.37	-9.04
P0A1H5 EFTU_SALTY Elongation factor Tu	16		GYRPQFYFR	325	9	3	30.18	b7y5y7	1233.60	122.929	2256	1	1233.60	-12.67
P0A1H5 EFTU_SALTY Elongation factor Tu	17	Oxidation+M(23)	NMITGAAQMDGAILVVAATDGP MPQTREHILLGR	90	34	3	16.68	b4b8b13	3563.80	90.216	8507	3	1188.61	-3.43
P0A1H5 EFTU_SALTY Elongation factor Tu	18	Oxidation+M()	TTDVTGTIELPEGVEMVMPGDNI K	334	24	5	39.26	b3b15y8y9y10	2562.24	79.268	2646	2	1281.63	4.38
P0A1H5 EFTU_SALTY Elongation factor Tu	19		TGTIELPEGVEMVMPGDNIK	338	20	5	28.05	b5°b5b10b11b15	2130.03	86.535	16431	2	1065.52	-5.62
P0A1H5 EFTU_SALTY Elongation factor Tu	20		TINTSHVEYDTPTR	61	14	2	14.24	b4b7	1633.79	49.553	10905	2	817.40	3.14
P0A1H5 EFTU_SALTY Elongation factor Tu	21		TTDVTGTIELPEGVEMVMPGD	334	21	0	7.88		2191.01	86.546	5796	2	1096.01	-2.45
P0A1H5 EFTU_SALTY Elongation factor Tu	22		IELAGFLDSYIPEPER	189	16	0	4.98		1848.94	101.790	2844	2	924.98	3.24
P0A1H5 EFTU_SALTY Elongation factor Tu	23		VDDEELLELVEMEVR	140	15	0	5.39		1817.89	106.043	1963	2	909.45	4.83
P0A1H5 EFTU_SALTY Elongation factor Tu	24		GITINTSHVEYDTPTR	59	16	0	4.56		1785.86	49.577	17010	3	595.96	-4.58
P0A1S2 HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	53	375.9	b2°b2b3°b3b4°b4b5°b5b6°b6b7°b7b8°b8b9b10b12°b12b13°b13b14°b14b15b16b18b21y1y2y3y4y5y6°y6y7*y7y8*y8y9y10y12°y12*y12y13°y13y14y15y16°y16y17°y17*y17y18y21	2216.10	96.762	623111	2	1108.56	4.52
P0A1S2 HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	10	86.44	b3°b3y2y4y6y7y8y9y10y11	1304.56	32.652	100186	2	652.78	-5.15
P0A1S2 HNS_SALTY DNA-binding protein H-NS	3	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	9	29.3	b2b3°b3b7y1y5y9°y9y13	1624.75	92.933	88087	2	812.88	6.09
P0A1S2 HNS_SALTY DNA-binding protein H-NS	4		EEESAAAAEVEER	41	13	4	27.86	y3°y3y8y9	1419.63	34.507	15973	2	710.32	5.25
P0A1S2 HNS_SALTY DNA-binding protein H-NS	5		MSEALK	0	6	1	13.52	y5	678.35	29.268	5704	1	678.35	5.85
P0A1S2 HNS_SALTY DNA-binding protein H-NS	6		YSYVDENGETKKTWTGQGR	96	18	10	77.63	b3°b3y4y6y8y14y15y16y17*y17	2090.92	46.860	228021	3	697.65	-8.52
P0A1S2 HNS_SALTY DNA-binding protein H-NS	7	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEVVNER	19	21	7	38.19	b11y3y4*y4y5y7°y7	2563.27	128.028	4056	3	855.09	1.71
P0A1S2 HNS_SALTY DNA-binding protein H-NS	8	Carbamidomethyl+C(6); Phosphoryl.STY(7)	AQARECTLETLEEMLEK	15	17	6	25.82	b5°b5y3y5y11°y11	2130.95	69.667	2058	4	533.49	6.07
P0A1S2 HNS_SALTY DNA-binding protein H-NS	9	Oxidation+M(2)	EMLIADGIDPNELLNSMAAAK	62	21	4	13.7	b12°b12y5y12	2232.10	91.283	32611	2	1116.55	5.47
P0A1S2 HNS_SALTY DNA-binding protein H-NS	10	Carbamidomethyl+C(6); Oxidation+M(14)	AQARECTLETLEEMLEK	15	17	6	44.52	b10b12b13y7y9y10	2066.98	84.427	32123	3	689.67	3.90
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	1		DQHIEAVSAMSVMDEVVELISAMEE K	5	25	29	201.85	b2°b2*b2b3b4b5°b5b6b7b8b9°b9°b9b10b11b13y2°y2y4y5°y5y6°y6y7y8y9y10y12y25	2737.32	137.136	81491	3	913.11	-4.55
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		EAKDLVESAPAALKEGVSK	82	19	6	23.92	b5b8°b8b9°b9y19	1942.05	54.981	55876	3	648.02	1.01

[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	3		DLVESAPAALKEGVSKDDAEALK	85	23	3	21.93	b3b4y7	2356.21	68.293	6001	3	786.07	-6.11
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	4		VAVIK	66	5	2	26.21	b3y4	529.37	26.075	3509	1	529.37	-4.73
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	5		FGVSAAAVAVAAAGPAEAAEEK	30	22	7	35.88	b10b14b15y7y10y16°y16	1987.01	70.499	1511	2	994.01	-1.11
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	6	Phosphoryl STY(5)	DLVESAPAALKEGVSK	85	16	3	16.93	b4b13y13	1693.83	101.880	1874	2	847.42	1.66
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	7	Oxidation+M(26)	SITKQIIEAVSAMSVM DVVELISA MEEK	1	29	4	21.93	b11y11y13y14	3182.60	102.110	30185	3	1061.54	2.38
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	46	312.29	b2b3b4*b4b5°b5*b5b6°b6*b6b8*b8y1y3y4y5y6y7°y7*y7y8°y8y9*y9y10*y10y11y12*y12y13y14°y14y15*y15y16°y16*y16y17y18y19y20y21y22*y22y24*y24	2574.32	97.990	666722	3	858.78	-2.94
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	2		AGIALNDNFVK	296	11	15	114.42	b1b3b4b5y1y2y3y4y5y6y7*y7y8y11*y11	1161.62	61.351	417390	2	581.31	-4.41
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	3		GASQNIIPSSTGAAK	198	15	25	171.39	b5°b5*b5b6°b6*b6b7°b7*b7b14b15y1y2y3y4y5y6y7y8y9y10y11y13°y13y15	1401.73	40.618	298435	2	701.37	-5.66
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		LVSWYDNETGYSNK	307	14	14	145.56	b5b8b11y2y3y4y5y6y8y9y10y11y12y14	1675.77	58.184	251404	2	838.39	3.35
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		VPTPNVSVVDLTVR	232	14	12	99.43	b3°b3b8y2y4y5y6y7y8y11y12y14	1495.85	70.924	127670	2	748.43	-0.73
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		VVLTGPSKDNTPMFVK	116	16	6	56.87	y3y5y8y11y14y16	1732.90	57.654	77433	3	578.31	-14.79
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		VLPELNGK	217	8	12	66.77	b2y2y3*y3y4*y4y5°y5y6*y6y7y8	869.50	44.616	53718	2	435.25	-11.86
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		AATYEQIK	249	8	4	47.64	b3b4y5y6	923.47	30.816	164291	2	462.24	-15.27
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		LTGMAFR	225	7	3	37.13	b6y5y6	795.41	49.306	73868	2	398.21	-16.27
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10	Carbamidomethyl+C(20)	GVLGYTEDDVVSTDFNGEVCTSV FDAK	269	27	4	21.8	b12y12*y12y13	2924.37	136.513	9768	2	1462.69	17.95
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11		SDIEIVAINDLLAEY MAYMLK	24	22	8	53.43	b5b6b7b8°b8y6y9°y9	2530.25	136.308	5298	3	844.09	0.10
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12	Carbamidomethyl+C(18);Carbamidomethyl+C(22)	GANFDKYEGQDIVSNASCTTNCL APLAK	132	28	41	314.28	b3b4b5*b5b7b8*b8b10b11°b11*b11b12°b12b13°b13b16b20b23°b23b24°b24b26b27y3y4y5y6y8y9*y9y10y11y12*y12y13°y13y14*y14y15*y15y16	3044.40	66.762	393569	3	1015.47	-1.76
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13		GGRGASQNIIPSSTGAAK	195	18	3	22.78	b8b9y8	1671.85	36.627	11393	3	557.96	-13.95

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14		AGIALNDNFVKLVSWYDNETGYS NK	296	25	3	22.76	y4y5y12	2818.37	103.429	4566	3	940.13	2.25
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15		VINDNFGIIEGLMTTVHATTATQK TVDGPSHK	160	32	5	11.08	b5y3°y3y10*y10	3395.68	78.790	4524	4	849.68	-13.01
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		TVDGPSHKDWR	184	11	4	50.14	b4b5b7b9	1297.62	76.353	1895	2	649.31	-8.00
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	1		SGFAEDEVVAVSK	35	13	14	116.59	b2b3b4b12y1y2y3y4y7y8y 9y10y11y13	1337.66	54.248	229659	2	669.33	-2.01
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	2		MITGIQITK	0	9	9	57.09	b1b2y2y3y4*y4y6y7y9	1004.57	54.952	196977	2	502.79	-9.11
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	3		LGEIEYR	48	7	10	63.35	b3y1y2y3y4y5°y5y6°y6y7	879.45	42.083	186998	2	440.23	-11.87
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	4		EIPMEVKPEVR	55	11	10	70.33	b4°b4y2y4°y4y5y6y8y9y11	1326.70	48.768	107134	2	663.86	-2.85
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	5		FNSLTPEQQR	106	10	23	99.93	b2*b2b3°b3*b3b10°b10y2 y3*y3y4y5*y5y6°y6y7y8°y 8*y8y9°y9*y9y10	1219.60	37.845	106708	2	610.30	-8.01
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	6		FNSLTPEQQRDVIAR	106	15	13	62.54	b2*b2b3°b3b5y1y3y4y6y1 0*y10y13y15	1773.90	47.444	87718	3	591.97	-11.63
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	7		VEGGQHLNVNVLR	66	13	4	31.94	b5y4y6y7	1434.76	50.418	112927	3	478.92	-15.91
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	8		TFTESL	121	6	7	65.94	b3b4°b4b5°b5y3y4	697.34	55.164	82026	1	697.34	-1.23
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	9		AANDDLLNSFWLLDSEKGEAR	9	21	29	254.94	b3b4b5°b5*b5b6°b6*b6b7° b7*b7y4y5y7y8y9°y9y10°y 10y11°y11y12y13y14y15y1 6y17y18y19	2364.14	92.745	512624	3	788.72	-3.30
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	10		SGFAEDEVVAVSKLGEIEYR	35	20	5	14.19	b14y5°y5y7°y7	2198.11	115.616	27385	3	733.38	6.22
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	11		PMEVKPEVR	57	9	4	50.14	b3b4b7b8	1084.58	48.768	105219	2	542.79	-5.52
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	12		EIPMEVKPEVR	55	11	0	2.49		1308.68	48.782	42436	3	436.90	-11.29
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	13		MITGIQITK	0	9	0	1.66		986.55	54.911	2540	2	493.78	-14.60
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	13	119.6	b2b3b4b6y1y3y5y7y8y9y1 0y11y13	1365.68	63.010	87392	2	683.35	0.98
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2	Carbamidomethyl+C(13)	AAQYVAAHPEGVCPAK	153	16	10	84.22	b4y2y3y4y5y8y9y11y12y1 6	1668.79	35.169	79648	3	556.94	-14.34
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		ATFVVDPPQGIQAEIVTAEGIGR	120	23	13	117.61	b2b3°b3b4b5b8y4y5y6y7y 8y9y10	2384.28	129.008	55269	3	795.43	-0.82
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		ATFVVDPPQGIQAEIVTAEGIGRDA SDLLR	120	30	5	21.77	b8b9°b9b13y7	3154.67	137.206	3473	3	1052.23	-1.78
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		LGVDVYSVSTDTHFTHK	63	17	4	29.58	b13b14y11y13	1905.95	66.594	2132	2	953.48	6.02
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTELGDVA DHYEELQK	32	31	3	22.68	b3b8b9	3757.74	120.054	12021	3	1253.25	4.22
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7	Carbamidomethyl+C(13)	AAQYVAAHPEGVCPAKWK	153	18	3	22.78	b11b12y11	1982.98	72.081	4227	4	496.50	-6.46
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8	Phosphoryl STY()	LGVDVYSVSTDTHFTHK	63	17	3	23.09	b7b8y7	1985.86	88.982	14932	3	662.63	-13.89
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9	Carbamidomethyl+C(11)	QYVAAHPEGVCPAK	155	14	1	7.25	b6	1526.72	35.215	2519	3	509.58	-12.71

P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10	Carbamidomethyl+C(10)	YVAAHPGEVCPAK	156	13	2	14.24	b3b5	1398.69	35.188	2085	2	699.85	3.05
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	1		IAAANVPAFVSGK	70	13	24	189.1	b2b3b4b5*b5b6*b6b11y1y2y3y4y5y6y7*y7y8y9y10*y10y11*y11y12y13	1244.69	59.386	1068927	2	622.85	-6.67
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVGFGTFK	22	29	4	11.44	b4°b4b6y13	2966.55	116.034	38477	4	742.39	-8.39
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	3		TQLIDVIADK	3	10	4	26.62	b2b3b5y6	1115.62	65.957	10061	2	558.31	-11.93
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	4		EGDAVQLVGFGTfK	37	14	7	39.35	b6b9b13y6°y6y13*y13	1467.72	64.678	28787	2	734.36	-19.21
P0AA28 THIO_SALTY Thioredoxin-1	1		LNIDQNPGTAPK	58	12	29	181.61	b2*b2b3*b3b4°b4*b4b6°b6*b6b7b10y2y3y4y5y6y7y8°y8*y8y9°y9*y9y10°y10y11*y11y12	1267.66	38.289	233799	2	634.33	-4.53
P0AA28 THIO_SALTY Thioredoxin-1	2		MIAPILDEIADEYQGK	37	16	23	169.46	b2b3b4b12°b12y1y2y3*y3y4*y4y5°y5y6y7y8*y8y10y11y13y14y15y16	1805.91	93.608	155158	2	903.46	5.20
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	10	74.27	b2b3y1y2y3y4y5y6y7y9	1001.63	91.160	98656	2	501.32	-8.77
P0AA28 THIO_SALTY Thioredoxin-1	4		GQLKEFLDANLA	97	12	4	31.8	b6b8y4y10	1318.70	77.037	19939	2	659.85	0.19
P0AA28 THIO_SALTY Thioredoxin-1	5		EFLDANLA	101	8	5	35.79	b6y3*y3y6y8	892.43	113.131	1512	1	892.43	-10.53
P0AA28 THIO_SALTY Thioredoxin-1	6		MIAPILDEIADEYQGKLTVAK	37	21	11	111.55	b3b4y4y5y7y11y12y14y16y18y19	2318.22	94.780	169879	3	773.41	-2.84
P0AA28 THIO_SALTY Thioredoxin-1	7		PTLLLFK	76	7	2	23.1	b3b4	831.52	91.158	99935	2	416.26	-14.39
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		VFMQPASEGTGIIAGGAMR	93	19	28	286.44	b2b3b4b6b10b11b12b13b14°b14*b14b15b17y4y5y6y7y9y10y11y12y13y14y15°y15y16y17y19	1892.94	68.031	352243	2	946.97	3.42
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		AVLEVAGVHNVLAK	112	14	12	107.88	b2b3b4y2y3y6y8y9y10y11y12y14	1419.83	60.985	232086	2	710.42	-1.29
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		AYGSTNPINVVR	126	12	16	112.4	b1b2b3y2y3y4*y4y6y7y8y9y10*y10y11y12*y12	1290.67	51.102	200381	2	645.84	-8.13
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVAAK	138	18	27	201.16	b2b5°b5b8b11°b11b15°b15°b15b16y2y3y4y5y6°y6y7y8y10y11y12*y12y13y14y15y18*y18	1890.90	63.150	125656	2	945.95	2.97
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		ATIDGLENMNSPEMVAAKR	138	19	17	156.93	b2b4y1y3y4y5y6y8y9°y9y10y11°y11y12y13y16y17	2046.98	58.945	104021	3	683.00	-5.49
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		EVPAAIQK	54	8	4	40.56	y3y4y6y8	855.48	29.654	39831	2	428.25	-10.84
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		VGFGYGK	45	7	6	40.15	b1b2b6y4y6y7	727.37	39.806	31839	2	364.19	-13.76
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		IFSFTALTTVGDGNR	29	16	5	37.42	b4b6b13b14y14	1653.83	100.657	3184	2	827.42	-15.87
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		NMINVALNNGTLQHPPKGVHTGSR	69	24	5	39.83	b5b6b8b9y15	2557.36	109.013	2651	3	853.12	5.82
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		EVPAAIQKAMEK	54	12	3	22.01	b5y3y5	1314.71	81.546	1755	2	657.86	-0.84

P0A7W4 RS5_SALTY 30S ribosomal protein S5	11	Oxidation+M()	ATIDGLENMNSPEMVAAK	138	18	3	15.37	b4y4y12	1906.91	53.981	1644	2	953.96	9.92
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12		LEVAGVHNVLAK	114	12	2	20.91	b8b9	1249.72	60.949	41581	2	625.36	-6.74
P0A7W4 RS5_SALTY 30S ribosomal protein S5	13		EVPAAIQK	54	8	0	1.24		837.47	29.689	15438	2	419.24	-11.73
P0A1Z2 SKP_SALTY Chaperone protein skp	1		IAIVNMGNLFQQVAQK	23	16	18	111.7	b2b3b4b8b15y1y2y3y4y5*y5y7y10*y10y11y12*y12y16	1773.97	90.024	73664	2	887.49	1.65
P0A1Z2 SKP_SALTY Chaperone protein skp	2		TGVSNTLENEFK	39	12	8	86.86	b9b10y3y5y7y8y11y12	1338.66	57.993	62046	2	669.83	2.83
P0A1Z2 SKP_SALTY Chaperone protein skp	3		VANDQSIDLVDANTVAYNSSDV KDITADV LK	126	32	11	39.73	b3b7*b7b8b10*b10*b10b13b15y12y16	3392.71	89.864	42331	3	1131.58	1.51
P0A1Z2 SKP_SALTY Chaperone protein skp	4		AQAFEKDR	97	8	9	53.67	b2*b2y2y3y4*y4y5y6y8	964.48	17.067	6791	2	482.74	-9.94
P0A1Z2 SKP_SALTY Chaperone protein skp	5		TGVSNTLENEFKGR	39	14	6	41.94	b6y6y8y9y11*y11	1551.75	54.139	142103	3	517.92	-14.16
P0A1Z2 SKP_SALTY Chaperone protein skp	6		KWLLAAGLGLAMV TSAQAADK	2	21	4	23.35	y4y9*y9y10	2115.14	80.638	2595	3	705.72	-12.81
P0A1Z2 SKP_SALTY Chaperone protein skp	7	Oxidation+M(11)	WLLAAGLGLAMV TSAQAADK	3	20	5	37.44	y3*y3y7y8y9	2003.07	81.628	3505	2	1002.04	2.80
P0A1Z2 SKP_SALTY Chaperone protein skp	8		AYNSSDVKDITADV LK	142	16	1	9.99	b3	1738.87	89.922	2058	2	869.94	-7.58
O54296 RS11_SALTY 30S ribosomal protein S11	1		STPFAAQVAAER	57	12	9	63.66	b1y1y4y6y7y8y10*y10y12	1247.64	49.489	65064	2	624.32	1.37
O54296 RS11_SALTY 30S ribosomal protein S11	2		QGNALGWATAGGSGFR	37	16	14	138.31	b7b16y1y3y5y6y7y8y9y10y11y12y14y16	1549.75	66.032	59890	2	775.38	1.34
O54296 RS11_SALTY 30S ribosomal protein S11	3		ALNAAGFR	98	8	5	40.56	y2y4y5y6y8	819.44	41.991	42150	2	410.22	-9.83
O54296 RS11_SALTY 30S ribosomal protein S11	4		QVSDGVAHIHASFNNTIVTITDR	14	23	5	39.68	y3y4y10y11*y11	2495.26	83.779	8123	3	832.43	0.49
O54296 RS11_SALTY 30S ribosomal protein S11	5	Carbamidomethyl+C(1)	CADAVK	69	6	2	29.64	y3y5	663.32	66.143	3336	1	663.32	10.77
O54296 RS11_SALTY 30S ribosomal protein S11	6	Carbamidomethyl+C(13)	STPFAAQVAAERCADAVK	57	18	5	30.55	b3b7b15y3y10	1891.91	86.290	6628	3	631.31	-10.19
O54296 RS11_SALTY 30S ribosomal protein S11	7		QGNALGWATAGGSGFRGSR	37	19	3	22.52	b5y8y9	1849.91	48.582	1583	2	925.46	3.76
O54296 RS11_SALTY 30S ribosomal protein S11	8	Phosphoryl STY(9)	QGNALGWATAGGSGFR	37	16	4	16.93	b7y5*y5y8	1629.72	43.332	41582	3	543.91	9.06
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		LADVLAANAR	57	11	15	113.45	b2b3b4y1y4*y4y5y6*y6y7*y7y8y9y10y11	1084.60	53.269	203304	2	542.81	-6.42
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGSLGDQVNVK	8	14	20	156.32	b2b3b4b10*b10b13*b13y3y4y6y7*y7y8y9y10*y10y11y12*y12y14	1413.77	56.436	164478	2	707.39	-1.55
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		VIINVVAE	141	8	6	40.56	b1b4b5b6*b6y8	856.51	63.286	135160	1	856.51	-5.77
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		DIADAVTAAGVDVAK	97	15	13	120.52	b2b3b4b5b6b10y4y6y7y8y9y10y15	1415.74	66.007	112653	2	708.37	0.95
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		NVEYFEAR	42	8	4	40.56	y2y4y5y6	1027.48	46.777	97669	2	514.24	-4.99
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		INALETVTIASK	71	12	5	39.88	b4y9y10y11y12	1259.72	61.029	68385	2	630.36	-2.91
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		MQVILLDK	0	8	3	40.56	y3y4y5	959.55	64.352	114903	2	480.28	-10.94
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		TTGEHEVNFQVHSEVFAK	123	18	4	24.5	b8b10b12y9	2059.02	66.762	2697	3	687.01	14.94
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	9		AGDEGKLFGSIGTR	83	14	3	26.82	y3y7y8	1407.70	55.040	106626	3	469.91	-13.09

Q8ZK80 RL9_SALTY 50S ribosomal protein L9	10		RAELEAK	50	7	5	50.24	b3b4b5y5°y5	816.45	15.794	8455	2	408.73	-12.86
O54297 RS4_SALTY 30S ribosomal protein S4	1		LSDYGVQLR	47	9	7	59.4	b3b7y2y5y6y8y9	1050.55	51.060	105178	2	525.78	-5.81
O54297 RS4_SALTY 30S ribosomal protein S4	2		VVNIASYQVSPNDVVSIR	128	18	26	171.06	b1b3*b3b4b7*b7b8b9°b9*b9b14b17*b17y1y3y4°y4y5y8y9y11*y11y12y13y14y18	1960.06	72.080	96744	2	980.53	3.43
O54297 RS4_SALTY 30S ribosomal protein S4	3		LDNVVYR	97	7	7	40.15	y2y3y5y6°y6y7*y7	878.46	37.885	60637	2	439.74	-10.49
O54297 RS4_SALTY 30S ribosomal protein S4	4		VVNIASYQVSPNDVVSIREK	128	20	6	24.95	b1b7°b7y5y10y11	2217.18	66.040	39151	3	739.73	-2.64
O54297 RS4_SALTY 30S ribosomal protein S4	5		MGFGATR	104	7	3	40.15	y3y4y5	739.35	36.121	18578	2	370.18	-11.06
O54297 RS4_SALTY 30S ribosomal protein S4	6		AALELAEQREKPTWLEVDAGK	156	21	3	13.7	b8b10y4	2354.25	95.492	12853	3	785.42	4.56
O54297 RS4_SALTY 30S ribosomal protein S4	7		LSDYGVQLREK	47	11	4	27.03	b7b8y4y11	1307.69	64.159	4413	2	654.35	-4.57
O54297 RS4_SALTY 30S ribosomal protein S4	8		IYGVLER	63	7	3	37.13	b3y5y6	849.47	49.824	46883	2	425.24	-10.49
O54297 RS4_SALTY 30S ribosomal protein S4	9		KPER	184	4	1	12.69	y3	529.31	45.061	28987	1	529.31	-7.15
O54297 RS4_SALTY 30S ribosomal protein S4	10		MEGTYK	177	6	1	13.52	y5	728.33	42.920	10018	1	728.33	-2.68
O54297 RS4_SALTY 30S ribosomal protein S4	11		AALELAEQR	156	9	9	74.27	b3y3y4*y4y6*y6y7*y7y8	1000.54	43.198	7951	1	1000.54	-1.65
O54297 RS4_SALTY 30S ribosomal protein S4	12		IEQAPGQHGAR	33	11	4	36.34	b7y4y6y7	1163.57	15.540	5020	3	388.53	-21.40
O54297 RS4_SALTY 30S ribosomal protein S4	13	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	4	38.93	b9y3y4y5	1451.70	56.440	21726	3	484.57	-11.52
O54297 RS4_SALTY 30S ribosomal protein S4	14		IEQAPGQHGARKPR	33	14	3	26.82	b3b7b8	1544.82	54.317	1692	3	515.61	-12.25
O54297 RS4_SALTY 30S ribosomal protein S4	15		VVNIASYQVSPN	128	12	0	6.22		1290.65	65.952	2165	3	430.89	-14.19
O54297 RS4_SALTY 30S ribosomal protein S4	16		LSDYGVQLR	47	9	0	1.66		1032.55	51.157	2344	3	344.86	10.40
P0A1E3 CYSK_SALTY Cysteine synthase A	1		IQGIGAGFIPGNLDLK	226	16	20	123.83	b2*b2b3b4b8b9b14y1y2y3y6*y6y7*y7y10y11y12y14°y14y16	1612.91	83.520	113039	2	806.96	4.09
P0A1E3 CYSK_SALTY Cysteine synthase A	2		LTLTMPETMSIER	87	13	14	82.6	b2°b2b5°b5b8b9°b9y6y8y9y10y11°y11y13	1521.77	73.879	102924	2	761.39	0.00
P0A1E3 CYSK_SALTY Cysteine synthase A	3		YLLLQQFSNPANPEIHEK	137	18	10	51.88	b2b3y3y6y9y11°y11*y11y14y18	2141.10	74.173	99461	3	714.37	-2.85
P0A1E3 CYSK_SALTY Cysteine synthase A	4		NIVVILPSSGER	293	12	10	82.09	b2b3b4y6y7°y7y8y9y10y12	1283.73	63.974	42960	2	642.37	-2.66
P0A1E3 CYSK_SALTY Cysteine synthase A	5		ALGANLVLTEGAK	105	13	4	20.38	b12y3y5y13	1256.72	61.147	41936	2	628.86	-2.33
P0A1E3 CYSK_SALTY Cysteine synthase A	6		LQEDSFNTK	283	10	4	36.62	y6y7y8y10	1210.56	34.919	41253	2	605.78	3.33
P0A1E3 CYSK_SALTY Cysteine synthase A	7		AEEIVASDPQK	126	11	12	87.24	b3b4°b4y1y3y5°y5y6y7y9y11*y11	1186.59	31.220	26417	2	593.80	-1.95
P0A1E3 CYSK_SALTY Cysteine synthase A	8		VVGITNEEAISTAR	246	14	4	27.21	b3b10y4y10	1459.77	49.313	24330	2	730.39	-2.26
P0A1E3 CYSK_SALTY Cysteine synthase A	9		YLSTALFADLFTEK	305	14	4	19.04	b9°b9y5y7	1618.84	103.561	15582	2	809.92	2.94
P0A1E3 CYSK_SALTY Cysteine synthase A	10		LTLTMPETMSIERR	87	14	8	19.04	b2°b2b7°b7b13°b13y11y14	1677.89	96.464	10262	2	839.45	12.15
P0A1E3 CYSK_SALTY Cysteine synthase A	11		YLSTALFADLFTEKELQQ	305	18	5	24.5	b5°b5b14b16y6	2117.09	102.602	118287	2	1059.05	4.15



P0A1E3 CYSK_SALTY Cysteine synthase A	12		AEEIVASDPQKYLLQQFSNPANP EIHEK	126	29	8	33.81	b3b6b12y3y9y11y12°y12	3308.65	77.302	60609	4	827.92	-10.26
P0A1E3 CYSK_SALTY Cysteine synthase A	13		GYKLTLTMPETMSIER	84	16	3	23.46	b11b12y6	1869.93	77.298	40594	2	935.47	-8.55
P0A1E3 CYSK_SALTY Cysteine synthase A	14		LTLTMPETMSIERR	87	14	3	19.04	b8b11y11	1677.85	92.680	1731	2	839.43	-8.15
P0A1E3 CYSK_SALTY Cysteine synthase A	15	Carbamidomethyl+C(8)	NPSFSVKCR	35	9	5	30.18	b7*b7y4y6°y6	1094.53	136.343	1518	1	1094.53	-7.47
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	1		AAADLQLQGVPMFVNGK	158	18	21	136.4	b2b5b7b8b9b10y1y3*y3y4 *y4y5*y5y6y8*y8y10y11* y11y12y18	1829.96	80.643	65888	2	915.48	2.33
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	2		YQINPQGMDTSSMDVFFVQQYAD TVK	176	25	14	53.44	b2*b2b4b6y1y4y7*y7y8y9 y12y14*y14y25	2865.31	86.370	24105	2	1433.16	2.64
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	3		TQTVQSAADIR	116	11	7	41.11	b2b9y2y4y7y9y11	1189.61	35.014	22065	2	595.31	-2.98
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		ELTQAWAVAMALGVEDK	88	17	5	25.82	b5*b5y3y6y11	1831.91	53.273	1790	4	458.73	-11.39
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	5	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	4	29.58	b10b12y6y7	1847.93	83.504	7481	2	924.47	4.76
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	6	Oxidation+M(21)	YHVEFLGPLGKELTQAWAVAMA LGVEDK	77	28	4	17.11	b12y4y9y14	3088.56	78.707	7318	4	772.90	-6.24
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	7		NPQGMDTSSMDVFFVQQYADTVK	179	22	0	8.3		2461.13	86.311	3990	3	821.05	10.91
P66593 RS6_SALTY 30S ribosomal protein S6	1		YSAAITGAEGK	24	11	14	113.45	b1b3°b3b4y2y3y4y5y6y7y9 °y9y10y11	1067.52	33.202	164571	2	534.27	-12.12
P66593 RS6_SALTY 30S ribosomal protein S6	2		FNDAVIR	79	7	6	53.25	y2y3y4y5y6y7	834.44	42.336	107845	2	417.72	-12.14
P66593 RS6_SALTY 30S ribosomal protein S6	3		HAVTEASPMVK	93	11	6	36.34	b2b3b4°b4b10y8	1169.59	31.405	80406	2	585.30	-6.68
P66593 RS6_SALTY 30S ribosomal protein S6	4		AHYVLMNVEAPQEVIDELETTFR	56	23	15	97.31	b3b5b6b8°b8b10b14y1y4y 6y7y8y9°y9y13	2704.34	113.211	72708	3	902.12	3.07
P66593 RS6_SALTY 30S ribosomal protein S6	5		HYEIVFMVHPDQSEQVPGMIER	2	22	4	13.27	b4°b4b12y8	2641.25	78.589	10249	3	881.09	-2.03
P66593 RS6_SALTY 30S ribosomal protein S6	6		LEDWGR	38	6	2	29.64	y3y5	775.37	38.757	25768	2	388.19	-9.60
P66593 RS6_SALTY 30S ribosomal protein S6	7		MRHYEIVFMVHPDQSEQVPGMIE R	0	24	8	27.22	b7b10°b10b11°b11y8y10°y 10	2928.41	136.454	3799	3	976.81	5.75
P66593 RS6_SALTY 30S ribosomal protein S6	8	Oxidation+M(6)	AHYVLMNVEAPQEVIDELETTFR	56	23	4	12.89	b11b14y12*y12	2720.33	111.996	4284	2	1360.67	2.06
P66593 RS6_SALTY 30S ribosomal protein S6	9	Oxidation+M(19)	HYEIVFMVHPDQSEQVPGMIER	2	22	8	20.59	b5y9°y9*y9y11°y11y13°y1 3	2657.26	128.592	3617	3	886.43	4.50
P0A2B1 RS20_SALTY 30S ribosomal protein S20	1		AFNEMQPIVDR	49	11	17	114.42	b2b3b4b5b11y2y3y5y6°y6 *y6y7y8°y8y9y11*y11	1319.64	57.010	169945	2	660.32	-2.50
P0A2B1 RS20_SALTY 30S ribosomal protein S20	2		ANLTAQINK	76	9	5	37.96	b2y5y6y7y9	972.54	35.256	38736	2	486.77	-10.54
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		MVAPVDGTIGK	59	11	11	99.55	b2b3y2y3y5y6y7y8y9y10y 11	1087.57	45.979	196673	2	544.29	-8.64
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		VGDPVIEFDLPLLEEK	115	16	15	113.74	b1b3b4b5b6b7b10y2y4y6y 9y10°y10y11y16	1812.97	99.530	110032	2	906.99	3.84

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		STLTPVVISNMDEIK	133	15	6	25.98	y5°y5y8°y8*y8y11	1646.87	73.178	9569	2	823.94	3.93
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		DTGTIEIVAPLSGEIVNIEDVPDVV FAEK	16	29	7	24.8	b6b7b10°b10y8°y8y10	3069.60	111.328	4635	3	1023.87	5.41
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		IFETNHAFSIESDSGIELFVHFGIDT VELK	70	30	8	39.16	b2b4b5b11°b11b12°b12y1	3394.73	125.911	3276	3	1132.25	13.74
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		IVGDGIAIKPTGNK	45	14	13	136.43	b3b4b5y3y4y5°y5*y5y6y7y8y10y11	1382.77	43.529	244213	3	461.60	-19.51
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		STLTPVVISNMDEIKELIK	133	19	4	23.34	b13y3y15y17	2130.15	93.114	328481	3	710.72	-9.17
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		VKVGDPVIEFDLPLEEK	113	18	6	42.31	b5°b5b6b7y3y6	2040.11	96.032	129632	3	680.71	-6.10
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9		IVGDGIAIKPTGNKMVAPVDGTIG K	45	25	3	12.27	b3b5y3	2451.35	84.888	2088	3	817.79	-5.18
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	10		APVDGTIGK	61	9	0	2.49		857.46	45.999	6349	1	857.46	-9.32
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	11		PVDGTIGK	62	8	4	35.78	b3b4b5°b5	786.43	45.998	3408	1	786.43	-9.00
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		ANDAAGDGTTTATVLAQSIITEGL K	80	25	24	177.35	b2°b2b3°b3b4°b4b5b13b14b15°b15b25y2y3y4y5y6y7y8y9y10y11y21y25	2418.23	91.970	192078	3	806.75	-2.12
P0A1D3 CH60_SALTY 60 kDa chaperonin	2		EMLPVLEAVAK	231	11	11	86.44	b2°b2b3y2y3y4y5y6y7y8y11	1199.66	80.215	190169	2	600.33	-6.61
P0A1D3 CH60_SALTY 60 kDa chaperonin	3		AVAAAVEELK	122	10	8	60.61	b1b2b3y3y5y6y8y10	1000.56	47.377	124115	2	500.78	-6.71
P0A1D3 CH60_SALTY 60 kDa chaperonin	4		QQIEEATSDYDREK	350	14	18	109.13	b6°b6b14y2°y2y3y4°y4y5y6y7°y7y8y9°y9y12y14*y14	1711.75	33.424	108893	3	571.26	-14.83
P0A1D3 CH60_SALTY 60 kDa chaperonin	5	Carbamidomethyl+C(6)	QIVLNCGEPSVVANTVK	452	18	17	124.61	b12°b12°b12y3y5y6°y6y9y10y11y12y13*y13y14y15y18*y18	1957.01	61.525	96715	2	979.01	4.30
P0A1D3 CH60_SALTY 60 kDa chaperonin	6	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDL PK	501	25	8	43.26	b3b7y2y4y5y10y11°y11	2670.32	125.831	88650	3	890.78	0.64
P0A1D3 CH60_SALTY 60 kDa chaperonin	7		GVNVLADAVK	18	10	11	73.72	b1b2b9y1y3y5y6y7y8*y8y10	985.56	56.266	87174	2	493.28	-9.60
P0A1D3 CH60_SALTY 60 kDa chaperonin	8	Carbamidomethyl+C(6)	ALSVPCCDSK	132	10	12	86.82	b1b2b3°b3y2y4y5y6y7y8y9y10	1063.50	35.018	74015	2	532.26	-4.48
P0A1D3 CH60_SALTY 60 kDa chaperonin	9		SFGAPTITK	42	9	7	52.83	b2b3°b3y2y3y5y7	921.49	44.890	58052	2	461.25	-13.38
P0A1D3 CH60_SALTY 60 kDa chaperonin	10		AVAAGMNPMDLK	105	12	9	65.3	b1b3y2y5y7y8y9y10y12	1217.60	58.450	56893	2	609.30	-0.20
P0A1D3 CH60_SALTY 60 kDa chaperonin	11		AIAQVGTISANSDETVGK	142	18	7	69.55	y8y9y10y12y13y14y18	1760.91	48.189	53291	2	880.96	2.22
P0A1D3 CH60_SALTY 60 kDa chaperonin	12		VEDALHATR	395	9	9	64.18	b2b5y1y2y3y4y6y7y9	1011.52	26.525	53067	2	506.26	-6.40
P0A1D3 CH60_SALTY 60 kDa chaperonin	13		GGDGNYGYNAAATEEYGNMIDMG ILDPTK	470	28	8	26.62	b2y2y3y4y9y14*y14y28	2966.29	88.218	45846	3	989.44	3.21
P0A1D3 CH60_SALTY 60 kDa chaperonin	14		AGKPLLIIAEDVEGEALATLVVNT MR	242	26	15	115.22	b5b6b7y1y2y3y4*y4y5*y5y6*y6y7y8y9	2723.50	136.288	41504	3	908.50	-2.15

[P0A1D3]CH60_SALTY 60 kDa chaperonin	15		AVAAGMNPMDLKR	105	13	7	40.97	b1b2y3y6y7y9y13	1373.70	51.182	34533	2	687.35	-3.73
[P0A1D3]CH60_SALTY 60 kDa chaperonin	16		GQNEQNVGIIK	430	11	8	68.02	b2y3y4y6y8y9*y9y11	1201.58	26.775	25222	2	601.30	3.25
[P0A1D3]CH60_SALTY 60 kDa chaperonin	17		ATLEDLGQAK	311	10	5	40.69	b7b8y2y4y7	1045.55	19.513	5813	2	523.28	0.93
[P0A1D3]CH60_SALTY 60 kDa chaperonin	18		LAGGVAVIK	371	9	6	74.27	b4b5b6y4y7y8	827.52	45.086	113917	2	414.26	-18.96
[P0A1D3]CH60_SALTY 60 kDa chaperonin	19		DTTTIIDGVGEEAAIQGR	327	18	4	21.42	b3b7y8y10	1845.91	99.618	47713	3	615.98	-2.84
[P0A1D3]CH60_SALTY 60 kDa chaperonin	20		LIAEAMDK	160	8	4	40.56	y4y6y7*y7	890.45	39.209	33217	2	445.73	-14.74
[P0A1D3]CH60_SALTY 60 kDa chaperonin	21		VAAVK	272	5	1	13.11	b3	487.32	44.829	16892	1	487.32	-0.50
[P0A1D3]CH60_SALTY 60 kDa chaperonin	22		FGNDAR	7	6	1	13.52	y5	679.31	41.308	4075	1	679.31	-3.95
[P0A1D3]CH60_SALTY 60 kDa chaperonin	23		GYLSPYFINKPETGAVELESPFILLADKK	197	29	3	11.44	b4b9y5	3239.70	96.522	239140	4	810.68	-5.88
[P0A1D3]CH60_SALTY 60 kDa chaperonin	24		EIELEDKFENMGAMQMVK	58	17	8	51.91	b3*b3b8b12y6y7y10y13	2010.94	73.721	183902	3	670.98	-7.10
[P0A1D3]CH60_SALTY 60 kDa chaperonin	25		IADLKGQNEQNVGIIK	425	16	10	92.97	b3b11y3y4y8y9y11*y11y12y14	1741.89	40.083	165710	3	581.30	-11.49
[P0A1D3]CH60_SALTY 60 kDa chaperonin	26	Carbamidomethyl+C(16)	AVAAAVEELKALSVPSCDSK	122	20	8	41.89	b8y4*y4y6y7y10*y10y18	2045.04	72.135	74321	3	682.35	-8.12
[P0A1D3]CH60_SALTY 60 kDa chaperonin	27		GGDGNYGYNAAATEEYGNMIDMGILDPTKVTR	470	31	3	11.18	b25y6y25	3322.53	86.630	64072	3	1108.18	8.23
[P0A1D3]CH60_SALTY 60 kDa chaperonin	28		NVVLKDSFGAPTITK	36	15	4	29.09	b10y5y7y9	1589.87	58.342	63285	3	530.63	-12.59
[P0A1D3]CH60_SALTY 60 kDa chaperonin	29	Carbamidomethyl+C(13)	AMEAPLRQIVLNCGEEPSVVANTVK	445	25	5	22.38	b3b10y9y11y13	2725.40	74.208	48654	3	909.14	1.34
[P0A1D3]CH60_SALTY 60 kDa chaperonin	30		VVINKDTTTTIIDGVGEEAAIQGR	322	23	5	28.54	y3y4y6y12*y12	2399.29	67.906	11559	2	1200.15	3.77
[P0A1D3]CH60_SALTY 60 kDa chaperonin	31		EVASKANDAAGDGTTTATVLAQSIIIEGLK	75	30	5	26.15	b3b8*b8b9b12	2932.52	136.277	7214	3	978.18	3.16
[P0A1D3]CH60_SALTY 60 kDa chaperonin	32	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVKGGDGNYGYNAAATEEYGNMIDMGILDPTK	452	46	3	11.28	b6y3y14	4904.27	89.411	6603	4	1226.82	0.00
[P0A1D3]CH60_SALTY 60 kDa chaperonin	33		VGAATEVEMKEK	380	12	4	33.86	b4b6b7y6	1291.67	80.604	2835	2	646.34	13.51
[P0A1D3]CH60_SALTY 60 kDa chaperonin	34	Phosphoryl STY(6)	GYLSPYFINKPETGAVELESPFILLADK	197	28	3	21.82	b4b5y3	3191.62	110.315	4559	4	798.66	10.40
[P0A1D3]CH60_SALTY 60 kDa chaperonin	35		AAGMNPMDLKR	107	11	1	7.39	b4	1203.60	51.163	57696	2	602.30	-1.83
[P0A1D3]CH60_SALTY 60 kDa chaperonin	36		EDALHATR	396	8	0	1.66		912.45	26.555	37880	2	456.73	-8.16
[P0A1D3]CH60_SALTY 60 kDa chaperonin	37		AAAVEELK	124	8	1	8.19	b6	830.46	47.378	13379	1	830.46	-6.98
[P0A1D3]CH60_SALTY 60 kDa chaperonin	38		AGMNPMDLKR	108	10	0	3.32		1132.55	51.173	7559	2	566.78	-9.05
[P0A1D3]CH60_SALTY 60 kDa chaperonin	39		GMNPMDLKR	109	9	0	3.32		1061.52	51.214	6860	2	531.27	1.38
[P0A1D3]CH60_SALTY 60 kDa chaperonin	40		AAVEELK	125	7	1	8.19	b5	759.42	47.327	6081	1	759.42	-6.99
[P0A1D3]CH60_SALTY 60 kDa chaperonin	41		EMLPVLEAVAK	231	11	0	2.49		1181.64	80.185	12984	2	591.32	-12.50
[P0A1D3]CH60_SALTY 60 kDa chaperonin	42		QQIEEATSDYDREK	350	14	0	3.73		1694.73	33.365	3122	3	565.58	-8.28
[P66038]RISB_SALTY 6	1		IGQVKDDNITVVVWVPGAYELPLATEALAK	40	29	13	64.33	b9b10*b10b12b13b14*b14y2y4y9y12y15y29	3110.68	98.511	144825	3	1037.56	-0.24

P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	20	146.82	b2b4b5b8°b8b9b14*b14b15y2y4y6y8y9y10y13y14y15*y15y19	2109.08	101.685	83660	2	1055.04	6.95
P66038 RISB_SALTY 6	3		GAEAALEMINVLK	136	16	16	117.42	b2b3°b3b4b5b6°b6b7°b7b8°b8b10b11b12y1y4	1643.90	103.423	25814	2	822.46	-0.37
P66038 RISB_SALTY 6	4		ANVAAPDAR	5	9	8	59.4	b2b3b4y2y4y6y7y9	884.45	22.165	16650	2	442.73	-12.15
P66038 RISB_SALTY 6	5		VAITAR	14	7	3	40.15	y4y5y6	743.46	44.161	18008	2	372.24	-18.31
P65702 PGK_SALTY Phohoglycerate kinase	1		VLPVAMLEER	373	11	11	99.55	b2b3y2y4y5y6y7y8y9y10y11	1227.67	80.205	219967	2	614.34	-5.47
P65702 PGK_SALTY Phohoglycerate kinase	2	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	23	173.4	b2b5°b5b6b7°b7b9b12°b12b13y1y2y3°y3y5y7y8y9y10y11°y11y12y14	1599.85	68.512	210914	2	800.43	2.98
P65702 PGK_SALTY Phohoglycerate kinase	3	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	17	147.98	b2b3b5b8b17y1y2y3y4y5y6y7y8y9y13y14y15	2002.04	99.075	164324	2	1001.53	6.52
P65702 PGK_SALTY Phohoglycerate kinase	4		VATEFSETAPATLK	258	14	26	188.55	b1b2b3°b3b4°b4b6°b6b7b9y1y2y3y4y5°y5y6y7y9y10y11°y11y12°y12y13y14	1464.76	52.422	134618	2	732.88	-1.67
P65702 PGK_SALTY Phohoglycerate kinase	5		SLYEADLVDEAKR	231	13	8	78.24	b5y3y4y5y6y10y11y13	1508.74	54.317	115317	3	503.58	-12.86
P65702 PGK_SALTY Phohoglycerate kinase	6		ADLNPVKEGK	19	11	11	93.53	b5°b5b9b10y2y4y6y7y8*y8y9	1169.65	36.821	109495	2	585.33	-3.86
P65702 PGK_SALTY Phohoglycerate kinase	7		TILWNGPVGVFEFPNFR	302	17	18	137.06	b2b4b13*b13y3*y3y4y5y6°y6y7y8y11*y11y12y13y14y17	1993.04	106.576	96424	2	997.03	5.08
P65702 PGK_SALTY Phohoglycerate kinase	8		LTVLDSLSK	197	9	6	37.96	y2°y2y5y6y7y9	975.56	61.980	75106	2	488.29	-8.26
P65702 PGK_SALTY Phohoglycerate kinase	9		MTDLDLAGK	5	9	5	30.18	b6y2y5y8y9	963.48	48.305	56959	2	482.24	-6.71
P65702 PGK_SALTY Phohoglycerate kinase	10		SVNDVKEDEQILDIGDASAQQLAELK	272	27	7	22.33	b9y2y3y4y15*y15y27	2941.50	101.079	55011	3	981.17	0.08
P65702 PGK_SALTY Phohoglycerate kinase	11		IADQLIVGGGIANTFVAAQGHSVGK	206	25	4	16.06	b3b5y9y19	2423.30	78.229	47151	3	808.44	-3.63
P65702 PGK_SALTY Phohoglycerate kinase	12		AQASTHGIGK	146	10	13	86.82	b2°b2b4°b4y1y2y3y4y5y6y7y8y10	969.50	15.675	33163	2	485.25	-9.19
P65702 PGK_SALTY Phohoglycerate kinase	13		MTDLDLAGKR	5	10	6	39.72	b4y5y8°y8y9y10	1119.58	42.901	31714	2	560.29	-4.47
P65702 PGK_SALTY Phohoglycerate kinase	14		DYLDGVDVAEGELVVLENVR	93	20	3	14.19	b8b15y7	2204.11	115.625	11645	3	735.37	-0.44
P65702 PGK_SALTY Phohoglycerate kinase	15	Carbamidomethyl+C(5)	YAALCDVFVMDAFGTAHR	128	18	3	15.37	b8y9y13	2043.96	90.235	10100	3	681.99	6.81
P65702 PGK_SALTY Phohoglycerate kinase	16		ISYISTGGGAFLEFVEGK	355	18	7	34.22	b5°b5b7°b7b8b11y11	1874.98	61.815	7995	2	937.99	14.45
P65702 PGK_SALTY Phohoglycerate kinase	17		KDDEALSK	119	8	4	32.78	b3°b3y6y7	905.47	49.853	8954	2	453.24	13.21
P65702 PGK_SALTY Phohoglycerate kinase	18		SLYEADLVDEAKR	231	13	4	27.86	b4b5b12°b12	1508.74	107.221	3212	2	754.88	-10.68
P65702 PGK_SALTY Phohoglycerate kinase	19		TDLDLAGK	6	8	0	1.66		832.45	48.326	67791	2	416.73	13.78
P65702 PGK_SALTY Phohoglycerate kinase	20		YEADLVDEAKR	233	11	0	3.32		1308.64	54.368	34116	2	654.83	-0.28
P65702 PGK_SALTY Phohoglycerate kinase	21		PAVAMLEER	375	9	2	18.7	b3b5	1015.52	80.257	26395	2	508.26	-8.35
P65702 PGK_SALTY Phohoglycerate kinase	22		DLNPVKEGK	20	10	1	7.81	b3	1098.60	36.762	18617	2	549.80	-13.56
P65702 PGK_SALTY Phohoglycerate kinase	23		VLDSLSK	199	7	2	8.74	b4°b4	761.43	61.973	17885	1	761.43	-11.22

P65702 PGK_SALTY Phohoglycerate kinase	24		LNVPVKEGK	21	9	0	2.49		983.58	36.743	11281	2	492.30	-3.66
P65702 PGK_SALTY Phohoglycerate kinase	25		TDLDLAGKR	6	9	0	2.07		988.54	42.873	10597	2	494.77	-1.98
P65702 PGK_SALTY Phohoglycerate kinase	26		ASTHGIGK	148	8	3	36.62	b4b5b6	770.41	15.680	5050	2	385.71	-11.09
P65702 PGK_SALTY Phohoglycerate kinase	27		QASTHGIGK	147	9	3	20.5	b6*b6b8	898.47	15.705	2962	2	449.74	-9.71
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	1		YTTEINVPIGGVMQMLGGR	97	20	18	92.43	b2*b2b3*b3b4*b4b7*b7b9b12b15*b15y4y5y9y10y13y20	2164.11	96.553	30533	2	1082.56	8.91
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	2		VILVGNLQDPEVR	8	14	9	58.05	b3y2y4*y4y5y7y8y10y14	1508.84	65.794	28172	2	754.93	0.97
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	3		GSQVYIEGQLR	74	11	3	35.78	b8b9b10	1249.66	31.398	26646	3	417.23	6.64
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	4		YMPSGGAVANLTLATSESWR	22	20	3	14.19	b15y13y17	2111.01	72.160	5605	3	704.34	-4.74
P00499 HIS1_SALTY ATP phohoribosyltransferase	1		LIAMAENMPIDILR	38	14	15	163.31	b3b6b8b10b11b12y2y3y6y8y9y10y11y12y14	1599.86	90.672	104977	2	800.43	1.68
P00499 HIS1_SALTY ATP phohoribosyltransferase	2		LSLATPVDEAWDGPAALDGKR	105	21	11	58.42	b13b14y2y3y11*y11y12*y12y16y17y21	2182.11	76.288	92810	3	728.04	-3.24
P00499 HIS1_SALTY ATP phohoribosyltransferase	3	Carbamidomethyl+C(8)	AGLADAICDLVSTGATLEANGLREVEVIYR	160	30	17	131.44	b3b4b5*b5b6b7b8b9b12y3y4y14y15y17y19y23y30	3176.63	136.565	71187	3	1059.55	2.54
P00499 HIS1_SALTY ATP phohoribosyltransferase	4		ALGASSILVLPIEK	282	14	14	86.14	b1b2b3b5*b5b7*b7y1y4y5y6y7y8y14	1410.86	84.576	69538	2	705.93	1.47
P00499 HIS1_SALTY ATP phohoribosyltransferase	5		LEEVIALLPGAERPTILPLAGEQQR	237	25	9	32.95	b2*b2b3b4b6y3y6y17y25	2713.51	90.046	33077	3	905.17	-6.48
P00499 HIS1_SALTY ATP phohoribosyltransferase	6	Carbamidomethyl+C(8)	AGLADAICDLVSTGATLEANGLR	160	23	5	29.09	b8b10b16b17y15	2288.14	114.523	6505	3	763.39	-4.59
P00499 HIS1_SALTY ATP phohoribosyltransferase	7		VAMHMOVSETLFWETMEK	262	18	4	21.42	b4b8y3y7	2156.02	75.241	108017	3	719.35	15.97
P00499 HIS1_SALTY ATP phohoribosyltransferase	8		ELLAR	22	5	2	26.21	b3b4	601.36	28.239	90909	1	601.36	-5.28
P00499 HIS1_SALTY ATP phohoribosyltransferase	9	Carbamidomethyl+C(2)	ACLIQR	192	6	1	13.52	y4	760.41	32.340	14399	2	380.71	-2.57
P00499 HIS1_SALTY ATP phohoribosyltransferase	10	Carbamidomethyl+C(2)	SCLLNGSVEVAPR	147	13	5	38.93	b10*b10y7y8y9	1401.69	36.550	4245	2	701.35	-19.77
P00499 HIS1_SALTY ATP phohoribosyltransferase	11		LSLATPVDEAWDGPAALDGK	105	20	4	14.19	b4*b4y8y14	2026.03	85.411	3226	3	676.02	10.18
P00499 HIS1_SALTY ATP phohoribosyltransferase	12		LSDDSR	16	6	1	13.52	y3	692.32	29.097	1529	1	692.32	-0.26
P00499 HIS1_SALTY ATP phohoribosyltransferase	13	Carbamidomethyl+C(6)	LDFGGCRLSLATPVDEAWDGPAALDGK	98	27	4	11.8	b3b12*b12y14	2831.39	76.242	48825	3	944.47	7.33
P00499 HIS1_SALTY ATP phohoribosyltransferase	14	Carbamidomethyl+C(1)	CDLVSTGATLEANGLREVEVIYR	167	23	4	22.65	b3b4b15*b15	2565.29	136.618	26210	3	855.77	-4.09
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	11	96.95	b2b3b4y2y3y4y6y8y9y10y12	1377.65	78.426	203354	2	689.33	0.27
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AVVESIQR	69	8	14	92.98	b2b3b4b5y1y2*y2y4*y4y5*y5y6y7y8	901.50	32.651	100463	2	451.25	-13.81
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3		AAVTMPSSK	22	9	15	74.27	b2b4y1y2*y2y3*y3y4*y4y5y6*y6y7*y7y9	891.45	31.144	100159	2	446.23	-11.30
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4	Carbamidomethyl+C(10)	QAGLGGEIICYVA	117	13	10	55.93	b3b7b10*b10*b10y3y6y9y13*y13	1350.66	80.968	13685	1	1350.66	-8.59
P0A7X0 RS8_SALTY 30S ribosomal protein S8	5		VEGDTKPELELTLYFQGK	50	19	9	47.41	b3b7*b7b8b9*b9b11*b11y5	2195.15	103.429	23959	3	732.39	-5.67
P0A7X0 RS8_SALTY 30S ribosomal protein S8	6		NGQAANKAAVTMPSSK	15	16	3	16.93	b9b11y12	1574.80	53.689	15306	3	525.60	-0.31

P0A7X0 RS8_SALTY 30S ribosomal protein S8	7	Oxidation+M(2)	SMQDPIADMLTR	1	12	3	32.22	y3y6y9	1393.66	70.522	8314	2	697.33	7.62
Q7CR46 IRAP_SALTY Anti-adapter protein iraP	1		NMAQNEQEMLIR	38	12	7	39.88	b2b3y8y9*y9y10y12	1476.70	55.972	60455	2	738.85	5.04
Q7CR46 IRAP_SALTY Anti-adapter protein iraP	2		QVEGALEGVKPDASVPDHDTELLR	50	24	10	77.57	b8b9y3y7y8*y8y9y10y11y24	2575.27	59.907	57510	4	644.57	-10.33
Q7CR46 IRAP_SALTY Anti-adapter protein iraP	3		LAQKEESKELVAQVEALEIIVTAMLR	11	27	6	36.21	b2b8b9b10b13y27	3040.66	105.978	22634	3	1014.22	-0.40
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VGTVTPNVAEAVK	141	13	19	139.03	b2b3*b3b4*b4y3y4*y4y5y7y8y9*y9y10y11*y11y12*y12y13	1284.71	47.882	230075	2	642.86	-1.52
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VAVFTQGPNAEAAK	74	14	29	207.4	b2b3b6b9*b9*b9b11*b11*b11b12b13y1y3y4*y4y5y7y8y9*y9y10*y10*y10y11*y11*y11y12y13y14	1402.73	45.031	223631	2	701.87	-4.87
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VVGQLGQVLGPR	122	12	9	68.31	b2b4y3y6y7y8y10*y10y12	1222.72	59.084	160618	2	611.86	-4.19
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		GATVLPHTGTR	60	11	9	70.33	b3*b3y3y4y5y6*y6y7y11	1065.57	29.957	35397	2	533.29	-4.81
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		QYDINEAIALLK	19	12	6	39.88	b4b12y3y4y5y12	1390.76	85.408	31681	2	695.89	3.77
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		AAGAELVGMEDLADQIK	88	17	6	27.06	b7y9*y9y10y12y17	1730.87	79.704	30834	2	865.94	4.09
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		AAGAELVGMEDLADQIKK	88	18	4	21.42	b4b8y9y11	1858.97	81.539	4912	3	620.33	4.14
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		ELATAK	31	6	2	13.52	b5*b5	632.36	28.150	16566	1	632.36	-4.44
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9		FNESVDVAVNLGIDAR	37	16	6	56.55	b10y3y4y5y11y12	1718.86	59.352	3320	3	573.62	-7.74
P0A2A3 RL1_SALTY 50S ribosomal protein L1	10		NGIIHTTIGKVDFDADK	167	17	3	23.5	y3y5y8	1843.97	79.047	20190	2	922.49	9.67
P0A2A3 RL1_SALTY 50S ribosomal protein L1	11		KGEMNFDVVIASPDAMR	105	17	8	22.59	b10*b10*b10b12*b12*b12y3y11	1879.90	108.296	3401	2	940.45	-2.08
P0A2A3 RL1_SALTY 50S ribosomal protein L1	12	Oxidation+M(9)	AAGAELVGMEDLADQIK	88	17	4	27.06	b6y4y7y8	1746.85	63.876	6345	3	582.96	-1.96
P0A2A3 RL1_SALTY 50S ribosomal protein L1	13		TVLPHGTGR	62	9	0	2.49		937.51	29.937	27203	2	469.26	-9.24
P0A2A3 RL1_SALTY 50S ribosomal protein L1	14		LPHGTGR	64	7	0	2.49		737.40	29.919	3229	2	369.20	-12.42
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	1		ISELSEEQIDTLRDEVAK	44	18	15	134.76	b3*b3b7b11b15y6y8y9y10y13y14y15y16y17y18	2075.03	66.376	156752	3	692.35	-9.53
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	2		IAGINIPDQK	3	10	8	33.61	y1y2*y2y4*y4y8y9y10	1068.60	54.380	96861	2	534.80	-6.17
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	3		ISELSEEQIDTLR	44	13	4	20.38	b6*b6b8y11	1532.79	82.826	20394	2	766.90	3.58
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	4		AILAAAGIAENVK	31	13	3	20.38	b3y7y9	1240.71	61.221	10368	2	620.86	-9.05
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		AGLGMMEGVLENVPSAR	78	17	10	61.83	b12b13*b13y4y6y7y12*y12y14y17	1730.87	81.999	58023	2	865.94	5.99
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		VLVLVAAPEGIAALEK	155	16	9	71.32	b1b2b3b4b5b6b7y9y11	1592.97	86.013	42835	2	796.99	5.21
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		NEETLEPVYPYFK	103	13	4	27.86	y5y7y8y13	1593.78	65.371	18653	2	797.40	1.99
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		ISVVGMYR	95	8	3	40.56	y4y5y7	924.49	54.998	14682	2	462.75	-5.88
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		ITVVPILR	70	8	4	40.56	y2y4y5y6	910.60	70.145	14155	2	455.81	-5.70

[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	6		LGLMRENDISTK	14	12	5	22.01	b6y2y6y8*y8	1376.73	66.289	7527	2	688.87	7.98
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	7		AHPDVELYTASIDQGLNEHGYYIP GLGDAGDK	171	32	4	11.08	b4b8*b8y5	3365.65	102.078	3037	4	842.17	5.08
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	8		ELASEVGSLLTYEATADLETEK	29	22	5	25.21	b4b7b13y3y7	2369.16	108.905	1505	2	1185.08	-0.41
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	9		ISVVGMYRNEETLEVPYFQK	95	21	4	22.15	b12*b12b13y17	2499.23	73.023	6935	3	833.75	-11.82
[P64052]EFTS_SALTY Elongation factor Ts	1		VASLEGDVLGSYQHGAR	134	17	14	114.82	b2b8b9*b9b14y3y4y6y7y8 y11y12y13y17	1758.86	59.104	161257	3	586.96	-9.86
[P64052]EFTS_SALTY Elongation factor Ts	2		ITDVEVLK	104	8	8	62	b3y1y2y3y5y6y7y8	916.52	48.611	134439	2	458.77	-12.19
[P64052]EFTS_SALTY Elongation factor Ts	3		AEITASLVK	1	9	9	59.4	b4*b4b5*b5y2y5y6y7y9	931.54	48.718	112606	2	466.27	-9.96
[P64052]EFTS_SALTY Elongation factor Ts	4		IGENINIR	125	8	6	53.67	y3y4y5y7*y7y8	928.51	44.490	105548	2	464.76	-10.91
[P64052]EFTS_SALTY Elongation factor Ts	5		FTGEVSLTGQPFVMEPSK	222	18	7	34.22	b15y3y10*y10y12y13y18	1953.97	74.688	99852	2	977.49	4.81
[P64052]EFTS_SALTY Elongation factor Ts	6		IGVLVAAK	151	8	7	66.77	b2y3y4y5y6y7y8	770.50	47.344	70436	2	385.75	-14.18
[P64052]EFTS_SALTY Elongation factor Ts	7	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	5	41.39	y1y3y5y7y10	1098.47	20.951	54510	2	549.74	-4.11
[P64052]EFTS_SALTY Elongation factor Ts	8		AGNVAADGVIK	52	11	5	27.03	b9y1y6y7y11	1014.55	36.606	21777	2	507.78	-6.08
[P64052]EFTS_SALTY Elongation factor Ts	9		DAGFQAFADK	85	10	6	26.62	b2b3b5y8*y8y10	1069.51	28.175	16547	2	535.26	9.93
[P64052]EFTS_SALTY Elongation factor Ts	10	Carbamidomethyl+C(13)	IDGNVAFILEVNCQTDFVAK	65	20	5	20.97	b6*b6b8b13y20	2253.14	83.410	2000	2	1127.07	7.15
[P64052]EFTS_SALTY Elongation factor Ts	11		ALTEANGDIELAIENMR	25	17	6	33.56	b6*b6b12y3y7y8	1859.92	58.825	3517	3	620.65	2.76
[P64052]EFTS_SALTY Elongation factor Ts	12		EYQVQLDIAMQSGKPK	193	16	4	16.93	b7b14y5*y5	1834.90	99.578	1806	4	459.48	-21.22
[P64052]EFTS_SALTY Elongation factor Ts	13	Carbamidomethyl+C(13)	IDGNVAFILEVNCQTDFVAKDAGF QAFADK	65	30	6	35.05	b5b6*b6b10y5y6	3303.64	107.325	2992	3	1101.89	13.15
[P64052]EFTS_SALTY Elongation factor Ts	14	Phosphoryl STY(12)	EYQVQLDIAMQSGKPK	193	16	3	16.93	b10y5y10	1914.91	67.964	209044	3	638.97	7.08
[P64052]EFTS_SALTY Elongation factor Ts	15	Oxidation+M(4)	QLAMHVAASKPEFVKPEDVSADV VEK	167	26	7	39.7	b4*b4b6y7y8y9y11	2840.45	136.340	7284	3	947.49	-0.95
[P64052]EFTS_SALTY Elongation factor Ts	16		GVLVAAK	152	7	0	1.24		657.43	47.394	17896	1	657.43	-2.60
[P64052]EFTS_SALTY Elongation factor Ts	17		ITASLVK	3	7	0	1.66		731.46	48.724	15490	1	731.46	-4.09
[P64052]EFTS_SALTY Elongation factor Ts	18	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	0	2.07		997.42	20.901	12711	2	499.22	-3.18
[P64052]EFTS_SALTY Elongation factor Ts	19		VASLEGDVLGS	134	11	1	7.29	y3	1046.54	59.003	5205	2	523.77	4.67
[P64052]EFTS_SALTY Elongation factor Ts	20		TDVEVLK	105	7	3	24.44	b3b4*b4	803.45	48.629	4748	1	803.45	-5.62
[P66541]RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAE LNK	45	14	8	82.36	y1y3y5y7y9y11y12y14	1576.81	84.563	221832	2	788.91	1.55
[P66541]RS2_SALTY 30S ribosomal protein S2	2		WLGGM LTNWK	95	10	11	52.04	b7b9*b9y3*y3y4*y4*y4y8 *y8y10	1205.61	86.565	149533	2	603.31	-2.43
[P66541]RS2_SALTY 30S ribosomal protein S2	3		MATVSMR DMLK	0	11	6	24.02	b4y1y2y4y10y11	1282.62	59.373	64144	3	428.21	-5.71
[P66541]RS2_SALTY 30S ribosomal protein S2	4	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	4	44.39	y3y4y7y8	1694.71	47.371	59662	3	565.58	-12.61
[P66541]RS2_SALTY 30S ribosomal protein S2	5		EANNLGIPVFAIVDTNSDPDGVDF VIPGNDDAIR	174	34	17	63.32	b5*b5*b5b7*b7*b7b8b25y3y4y6y7y8*y8y10*y10y34	3569.75	104.345	30106	3	1190.59	2.94

P66541 RS2_SALTY 30S ribosomal protein S2	6		DLETQSQDGTFEK	115	13	5	27.86	b2y6y9y10°y10	1497.68	40.126	10442	2	749.34	4.16
P66541 RS2_SALTY 30S ribosomal protein S2	7		ILFVGTK	66	7	4	53.25	y3y4y5y6	777.48	57.270	40755	2	389.24	-15.15
P66541 RS2_SALTY 30S ribosomal protein S2	8		YWNPK	21	5	1	13.11	b3	707.35	33.030	16226	1	707.35	-7.42
P66541 RS2_SALTY 30S ribosomal protein S2	9		AGVHFGHQTR	11	10	6	53.8	b7b8y6y8y9°y9	1109.54	87.779	2845	1	1109.54	-15.51
P66541 RS2_SALTY 30S ribosomal protein S2	10		MATVSMRDMLK	0	11	4	24.02	b10°b10y3y6	1282.62	127.000	1611	2	641.81	-11.99
P66541 RS2_SALTY 30S ribosomal protein S2	11	Oxidation+M(5)	ATVSMRDMLK	1	10	4	51.48	y4y6y7y8	1167.57	38.771	9506	2	584.29	-13.28
P66541 RS2_SALTY 30S ribosomal protein S2	12	Oxidation+M(5)	WLGGMLTNWK	95	10	6	39.72	b4b7b8°b8*b8y7	1221.61	136.421	2147	1	1221.61	2.40
P66643 RS9_SALTY 30S ribosomal protein S9	1		GGGISQAGAIR	68	12	9	53.96	b2b3y5y6y7*y7y8*y8y12	1043.55	33.305	110457	2	522.28	-10.76
P66643 RS9_SALTY 30S ribosomal protein S9	2		SLEQYFGR	33	8	8	62	b3y2y3y4y5y6°y6y8	999.48	60.636	101771	2	500.25	-4.76
P66643 RS9_SALTY 30S ribosomal protein S9	3		AENQYYGTGR	1	10	5	26.62	b2°b2b4y6y8	1158.51	26.758	72596	2	579.76	-3.06
P66643 RS9_SALTY 30S ribosomal protein S9	4		ALMEYDESLRGELR	85	14	4	19.04	b4°b4b10y8	1681.84	72.102	41752	3	561.29	12.85
P66643 RS9_SALTY 30S ribosomal protein S9	5		SGQAGAIR	72	8	0	2.9		759.41	33.369	2644	1	759.41	-7.07
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	1		YLSLLPYTDR	63	10	9	86.03	b2b3b9y4y5y6y7y8y10	1240.65	75.236	164651	2	620.83	-3.44
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	2		NYITESGK	30	8	7	40.56	b1y3y4°y4y6°y6y8	911.44	29.180	67760	2	456.23	-2.28
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	3		FTAEGVQEIDYK	12	12	3	35.23	b5b6b7	1399.64	91.034	13169	3	467.22	-22.15
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	4		YLSLLPYTDRHQ	63	12	3	32.22	y3y7y10	1505.76	67.866	76866	3	502.59	-13.05
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	1	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	8	32.07	b3°b3b6y4y10y12y18y24	2589.31	82.839	99674	3	863.78	1.98
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	2		DIGAQYIIHGSERR	84	15	5	25.44	b5b11y4y8y15	1727.93	59.142	66148	2	864.47	7.21
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	3		SATPAQAQAVHK	176	12	19	109.09	b2b3b9b12y1y2y4y5*y5y6y7*y7y8*y8y9*y9y10*y10y12	1208.63	18.180	65956	2	604.82	-6.97
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	4		TQGAAAFEGAVIAYEPVWAI GTG K	152	24	14	74.65	b2b3b4b5b10b11b13b14*b14y1y2y4y16y24	2407.24	93.647	30041	2	1204.12	3.96
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	5		DIGAQYIIHGSER	84	14	6	32.65	b5b12°b12y4y5y14	1571.83	64.552	10411	2	786.42	7.46
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	6	Carbamidomethyl+C(9)	EQGLTPVLCIGETEAENEAGK	117	21	3	13.7	b5y5y8	2245.10	56.997	9749	4	562.03	16.86
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	7		AAAGSHIMLGAQNVDNLSGAFTGETSAEMLK	52	32	4	15.69	b4b9b11y12	3204.62	106.536	1985	3	1068.88	16.61
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	8	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAENEAGKTEEVCAR	117	28	17	123.98	b5°b5b7°b7y4y6y7y9y10y16y18y20y21y23°y23y24y26	3090.43	72.181	188735	3	1030.82	-0.87
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	9		TPAQAQAVHK	178	10	10	60.65	b3°b3b4°b4*b4b5°b5b7b8°b8	1050.56	18.179	24841	2	525.78	-9.18
P0A2A1 RL19_SALTY 50S ribosomal protein L19	1		VFQTHSPVVDLSIAVK	72	15	11	101.98	b1b4b6b7b8b11b13y5y6y9y11	1626.87	56.024	150849	3	542.96	-11.10
P0A2A1 RL19_SALTY 50S ribosomal protein L19	2		VWVVEGTK	29	8	5	32.78	b2b5y2y4y5	917.50	25.823	4812	2	459.25	-10.38
P0A2A1 RL19_SALTY 50S ribosomal protein L19	3		QNVPSFRPGDTVEVK	14	15	5	17.9	b7°b7b9y12°y12	1672.84	73.019	4184	2	836.92	-16.49



P0A2A1 RL19_SALTY 50S ribosomal protein L19	4		QLEQEQMKNVPSFRPGDTVEVK	6	23	4	26.25	b10b11y9y12	2687.32	54.603	59360	4	672.59	-9.54
P0A2A1 RL19_SALTY 50S ribosomal protein L19	5		MSNIIKQLEQEOMK	0	14	5	30.38	b4y5*y5y6y8	1719.90	72.098	12520	2	860.45	10.65
P0A1P6 GLNA_SALTY Glutamine synthetase	1		LVPGYEAPVMLAYSAR	322	16	17	152.68	b2b9°b9b10b14b15y3y4y5°y5y7y8°y8y9y10y13y14	1736.92	77.591	50028	2	868.96	6.54
P0A1P6 GLNA_SALTY Glutamine synthetase	2		AINALANPTTNSYK	307	14	9	75.14	b3y5y7y8y9°y9y10y12y14	1477.77	47.739	35504	2	739.39	0.74
P0A1P6 GLNA_SALTY Glutamine synthetase	3		AINALANPTTNSYKR	307	15	5	34.43	b2y8y9y10y15	1633.87	42.791	28402	3	545.29	0.30
P0A1P6 GLNA_SALTY Glutamine synthetase	4		ATGIADTVLFGPEPEFFLFDDIR	117	23	7	24.18	b2b10b13y2y3y11y13	2570.27	117.345	19457	3	857.43	-3.61
P0A1P6 GLNA_SALTY Glutamine synthetase	5		GINESDMVLMPDASTAVIDPFFADSTLIIR	59	30	8	48.42	b8b9b11y3y11y12°y12y13	3238.61	113.500	17925	3	1080.21	2.56
P0A1P6 GLNA_SALTY Glutamine synthetase	6		AGGVFTDEAIDAYIALR	430	17	7	62.7	b3b9b10b14b15b16y13	1781.90	76.315	17776	3	594.64	-4.38
P0A1P6 GLNA_SALTY Glutamine synthetase	7		EQHVTIPAHQVNAEFFEEGK	28	20	4	23.61	y4y5°y5y11	2310.10	68.656	7956	3	770.71	-4.65
P0A1P6 GLNA_SALTY Glutamine synthetase	8		SAEHLVTMLNEHEVK	1	15	4	25.44	b3b5y4y7	1736.89	36.452	9462	4	434.98	13.35
P0A1P6 GLNA_SALTY Glutamine synthetase	9		GGYFPVPPVDSAQDIR	177	16	6	44.41	b3b4b6b13y6y10	1717.83	92.573	3286	2	859.42	-12.01
P0A1P6 GLNA_SALTY Glutamine synthetase	10		NLYDLPPEEAK	395	11	6	55.46	b8y5°y5y6y8y10	1288.62	80.608	2836	2	644.82	-13.83
P0A1P6 GLNA_SALTY Glutamine synthetase	11	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	5	28.37	b6b7b12b14y8	2565.28	105.448	2619	3	855.77	-2.38
P0A1P6 GLNA_SALTY Glutamine synthetase	12		EIPQVAGSLEEALNALDLDR	406	20	4	27.59	b5b9y4y5	2153.06	81.530	1759	2	1077.03	-22.11
P0A1P6 GLNA_SALTY Glutamine synthetase	13	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK NK	360	26	6	26.28	b3b6b10*b10b13*b13	2807.42	129.071	29476	3	936.48	-1.04
P0A1P6 GLNA_SALTY Glutamine synthetase	14		NGTNLFSGDKYAGLSEQUALYYIG GVIK	277	27	6	38.65	b4b8b13b15y3y4	2878.46	100.704	25088	3	960.16	-1.95
P0A1P6 GLNA_SALTY Glutamine synthetase	15		GHRPGVKGGYFPVPPVDSAQDIR	170	23	4	12.89	b15b17y16°y16	2449.27	136.728	1624	3	817.10	0.40
P0A1P6 GLNA_SALTY Glutamine synthetase	16	Phosphoryl STY(13)	AGGVFTDEAIDAYIALR	430	17	6	22.59	b6°b6b12y6y8°y8	1861.88	50.770	10398	2	931.44	7.15
P0A1P6 GLNA_SALTY Glutamine synthetase	17	Phosphoryl STY(8)	EIPQVAGSLEEALNALDLDR	406	20	6	31.79	b6y5y7°y7y11y12	2233.07	103.317	2699	3	745.03	2.08
P0A1P6 GLNA_SALTY Glutamine synthetase	18		FTDEAIDAYIALR	434	13	4	24.75	b3b11°b11b12	1497.76	76.290	5446	2	749.38	-0.33
P0A1P6 GLNA_SALTY Glutamine synthetase	19		NALANPTTNSYKR	309	13	0	4.15		1449.74	42.803	2601	2	725.37	-3.87
P0A1P6 GLNA_SALTY Glutamine synthetase	20		ANPTTNSYKR	312	10	0	4.15		1151.59	42.804	1661	2	576.30	9.54
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		QLDPLVVGQEHYDTAR	343	16	9	83.29	y3°y3y4y5y6y9y10y11°y11	1840.90	57.990	44312	3	614.31	-8.62
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		MPSAVGYQPTLAEEMGVLQER	261	21	9	45.2	b6°b6b8y3y4y6y9y13y21	2306.13	81.531	39195	2	1153.57	6.78
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		TVNMMELIR	156	9	6	45.05	b3y3y6°y6y7y9	1106.57	76.359	37026	2	553.79	-4.08
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	4	28.38	b9y6y7y8°	1193.59	81.028	36177	2	597.30	-9.10
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		FLSQPFFVAEVFTGSPGK	399	18	8	30.55	b8b11*b11y3y14°y14y16y18	1958.02	99.926	31446	2	979.51	4.80
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		QIASLGIYPAVDPLDSTSR	324	19	7	47.41	b12y4y7y11y12y13y19	2003.05	80.418	30076	2	1002.03	4.21
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		VGLFGGAGVGK	145	11	3	31.01	y4y7y8	961.54	59.091	28139	2	481.27	-10.47

Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		AAPSYEELSNSQELLETGIK	112	20	5	14.19	b3b14y1y18y20	2179.09	73.566	26620	2	1090.05	5.15
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		VALTGLTMAEK	219	11	12	110.44	b2b3b5y3y4y5y7y8°y8y9y10y11	1133.62	59.186	19834	2	567.31	-5.17
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	6	17.87	y1y2y5y7°y7y25	3057.38	101.698	8594	3	1019.80	-2.79
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		NIAIEHSGYSVFAGVGER	165	18	4	24.29	y8y11°y11y12	1905.94	67.678	4357	3	635.99	-1.41
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		TIAMGSSDGLRR	53	12	3	22.01	b4b9y9	1263.63	33.331	3640	2	632.32	-13.91
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		YQELK	367	5	2	26.21	b3b4	680.36	30.850	7570	1	680.36	-5.74
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		GEIGEERWAIHR	99	13	3	25.15	b3b4y12	1581.78	104.500	22210	2	791.40	4.24
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15		ATLGRIMNVLGEPVDMK	82	17	3	16.1	b5y4y10	1843.96	86.877	4878	2	922.48	-10.86
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16	Phosphoryl STY(8)	QIASLGIYPAVDPLDSTSR	324	19	4	20.39	b6b9y5y13_H3PO4 y13	2082.98	117.017	6754	3	695.00	-11.72
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17	Phosphoryl STY(4)	VALTGLTMAEK	219	11	5	51.99	b4b10y4y6y9	1213.58	73.258	3607	2	607.29	-1.81
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18	Oxidation+M(2)	IMNVLGEPVDMK	87	12	3	25.99	b4y6y7	1361.70	90.976	12291	2	681.35	13.63
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19		MPSAVGYQPTLAEEMGVLQ	261	19	1	7.7	y13	2021.00	81.434	8514	2	1011.00	13.89
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20		QIASLGIYPAVDPLDS	324	16	0	5.81		1658.85	80.354	3713	3	553.62	-9.79
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	18	140.07	b2b3b4b5y1y2y3y4y5°y5y6°y6y7°y7y8y9y10y12	1150.67	53.245	152451	2	575.84	-8.81
P66313 RL6_SALTY 50S ribosomal protein L6	2		YADEVVR	163	7	5	50.24	b6y3y4y5y7	851.42	30.641	108357	2	426.21	-10.32
P66313 RL6_SALTY 50S ribosomal protein L6	3		ALLNSMVIGVTEGFTK	69	16	6	25.31	y1y6y8y9°y9y16	1679.91	94.760	89044	2	840.46	1.53
P66313 RL6_SALTY 50S ribosomal protein L6	4		DGYADGWAQAGTAR	55	14	13	72.13	b3y1y4y6y7°y7°y7y9y10*y10y11°y11y14	1438.64	49.506	87822	2	719.82	0.76
P66313 RL6_SALTY 50S ribosomal protein L6	5		INGQVITIK	18	9	10	45.05	b2*b2b3y1y2y3y7y8*y8y9	985.60	48.453	84522	2	493.30	-7.99
P66313 RL6_SALTY 50S ribosomal protein L6	6	Carbamidomethyl+C(26)	GNVVNLSLGFSHPDHQLPAGIT AECTPTQEIVLK	99	35	4	22.37	b3b4y10*y10	3741.86	95.685	2953	3	1247.96	-17.16
P67904 RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAK	16	14	20	158.66	b2b3b7°b7b10y3y4y5y7y8y9y10°y10y11*y11y12°y12*y12y13y14	1517.81	55.311	152115	2	759.41	2.65
P67904 RS10_SALTY 30S ribosomal protein S10	2		LVDIVPETEK	72	10	8	76.73	b2b3y3y4y6y8y9y10	1142.62	51.703	61137	2	571.81	-8.76
P67904 RS10_SALTY 30S ribosomal protein S10	3		RTGAQVR	30	7	4	37.13	b4b5y6*y6	787.45	36.384	163759	2	394.23	-7.36
P67904 RS10_SALTY 30S ribosomal protein S10	4		RLVDIVPETEK	71	11	5	65	b3b4b5b6b10	1298.72	52.053	70905	2	649.87	-6.02
P67904 RS10_SALTY 30S ribosomal protein S10	5		AFDHRLIDQSTAEIVETAK	11	19	5	20.39	b6b9y9y14*y14	2144.07	97.859	2615	3	715.36	-14.57
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	1		SVDGIQVGEGR	266	11	6	36.34	b3y4y5y9°y9y11	1116.56	41.151	28295	2	558.79	-0.44
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	2		AAPNTIPTAAK	149	11	9	84.13	b1y2y3y4y5y7y8y9y11	1054.58	31.909	25827	2	527.79	-7.41
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	3		AGGNYLSSLLVGSEAR	160	16	7	41.52	b3b5b6y2y3y4y16	1593.82	79.409	19766	2	797.42	-0.15
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	4		IQQAFFGLTGETEDK	284	16	12	59.28	b2b3b5°b5b7°b7b14*b14y8y10°y10y11	1830.90	93.667	13404	2	915.95	2.80

[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	5		VHVMShALHYGTSVFEGIR	22	19	4	23.34	b14y7y9y11	2140.08	78.743	1689	3	714.03	0.46
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	6		ESLYLADeVFMSTAAEITPVR	244	22	6	29.09	b4b7°b7b8b15°b15	2399.18	82.569	29808	3	800.40	1.93
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	7	Carbamidomethyl+C(14)	FPVSQSIDELMEACR	69	15	5	25.44	b5*b5b12y4y9	1781.85	101.758	3423	2	891.43	16.17
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	8		ADYIWfNGEMVR	5	12	6	43.66	b3b5b6°b6y4y10	1500.71	68.511	3176	3	500.91	11.63
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	9		DGVLFTPPFTSSALPGITR	204	19	5	28.99	b4b11b13y3y12	1976.01	99.243	2907	2	988.51	-17.91
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	10	Carbamidomethyl+C(12)	SVDGIQVGEGRCPVTK	266	17	4	16.1	b3y3y10°y10	1758.86	77.580	10656	3	586.96	-9.72
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	11		IQQAFFGLFTGETEDKWGWLDPVNS	284	25	6	22.85	b3y3y4y7°y7*y7	2885.38	112.303	6330	3	962.46	-0.34
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	12	Carbamidomethyl+C(14)	FPVSQSIDELMEACRDVIR	69	19	4	14.74	b8*b8b13y10	2265.09	103.172	2244	3	755.70	-3.66
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	13		WEDAKVHVMShALHYGTSVFEGIR	17	24	3	22.85	b10b12b13	2769.35	74.178	1939	3	923.79	-1.15
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	14	Phosphoryl STY(12)	DGVLFTPPFTSSALPGITR	204	19	3	23.92	b3b10b11	2056.04	75.218	1520	2	1028.52	14.49
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	15	Carbamidomethyl+C(14);Oxidation+M(11)	FPVSQSIDELMEACRDVIR	69	19	3	14.74	b5b8y9	2281.10	106.854	135288	2	1141.05	0.00
[P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	16		PNTIPTAAK	151	9	1	7.81	b3	912.50	31.934	5461	2	456.75	-14.65
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	1		VITDVHEASQAQPVADVVDVIQLPAFLAR	91	29	6	25.67	b7b8b12b21y2y6	3101.67	104.697	42937	3	1034.56	1.50
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	2		VANDLPFVLFGGMNVLERS	12	19	18	105.08	b2b3b4b5°b5b8y2y3°y3y4y7y8*y8y10°y10y13y14y19	2078.09	110.308	21217	2	1039.55	6.46
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	3		LGIPYVFK	47	8	3	35.79	b3y3y5	936.54	76.851	12792	2	468.77	-14.01
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	4		AGMAVGLAGLFLESHPDPANAK	226	22	6	28.56	b3b6y4y12°y12y13	2166.13	121.458	2854	3	722.72	14.77
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	5	Carbamidomethyl+C(17)	VSGNSPVIFDVTHALQCR	189	18	5	26.26	b4b7b8°b8y3	2000.03	109.425	4182	2	1000.52	14.16
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	6		GANFGYDNLVVDMLGFSSVMK	168	20	4	27.59	b10b15y10y11	2177.03	102.525	1959	3	726.35	-4.71
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	7		ANRSSIHSYR	60	10	3	26.62	b4y3y5	1190.60	18.174	23940	3	397.54	-0.41
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	8	Carbamidomethyl+C(18)	KVSGNSPVIFDVTHALQCR	188	19	3	14.74	b7y9y11	2128.08	84.422	5939	2	1064.54	-8.26
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	9		KPQFVSPGQMGNIVDKFHEGGNDK	138	24	5	25.9	b10b11*b11y10y13	2629.29	109.174	3370	3	877.10	2.32
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	10	Oxidation+M(13)	VANDLPFVLFGGMNVLERS	12	19	7	41.62	b3b7*b7y7y8y9*y9	2094.05	66.643	1989	3	698.69	-7.11
[P0A1V4 KAD_SALTY Adenylate kinase	1		YGIPQISTGDMLR	23	13	6	40.97	y5y7y8y10*y10y13	1450.74	72.828	66394	2	725.87	0.76
[P0A1V4 KAD_SALTY Adenylate kinase	2		LVEYHQMTAPLIGYYQK	167	17	10	76.18	b8b9y3y4*y4y5y8y11y12*y12	2054.03	69.560	53646	3	685.35	-6.54
[P0A1V4 KAD_SALTY Adenylate kinase	3		VDGTQAVADVR	195	11	8	70.33	b4y2y4y5y8y9y10y11	1130.57	36.366	52256	2	565.79	-6.80
[P0A1V4 KAD_SALTY Adenylate kinase	4		NGFLLDGFPR	78	10	4	28.38	b2b3y4y5	1135.58	81.152	35178	2	568.29	-8.06
[P0A1V4 KAD_SALTY Adenylate kinase	5		GTQAQFIMEK	13	10	6	51.48	y2y3y4y5y7y10	1152.58	48.506	25350	2	576.79	4.24
[P0A1V4 KAD_SALTY Adenylate kinase	6		IILLGAPGAGK	2	11	5	41.11	b2b3y5y6y7	1009.63	61.095	25029	2	505.32	-7.74

P0A1V4 KAD_SALTY Adenylate kinase	7		DDVTGEDLTTR	145	11	3	24.02	b5y6y9	1221.59	78.849	1675	2	611.30	21.29
P0A1V4 KAD_SALTY Adenylate kinase	8		IILLGAPGAGKGTQAQFIMEK	2	21	7	44.24	b3y3y7°y7y13y15y17	2143.18	72.929	35317	3	715.06	-7.86
P0A1V4 KAD_SALTY Adenylate kinase	9		VDGTQAVADVRAALEK	195	16	4	24.64	b7°b7b9b13	1642.86	80.385	18438	2	821.93	-8.77
P0A1V4 KAD_SALTY Adenylate kinase	10		GTQAQFIMEKYGIPQISTGDMLR	13	23	4	26.25	b7b8y6y8	2584.30	91.017	4055	3	862.10	3.87
P0A1V4 KAD_SALTY Adenylate kinase	11		NGFLLDGFPRTIPQADAMK	78	19	3	21.7	b6b10b13	2091.06	81.346	1989	3	697.69	-2.45
P0A1V4 KAD_SALTY Adenylate kinase	12		EAEAGNTKYAK	184	11	4	24.02	b4b10y10*y10	1181.58	96.763	1884	1	1181.58	4.13
P0A1V4 KAD_SALTY Adenylate kinase	13	Oxidation+M(7)	LVEYHQMTAPLIGYYQKEAEAGN TK	167	25	4	18.59	b13y8y10y13	2870.43	97.265	14517	4	718.36	9.95
P0A1V4 KAD_SALTY Adenylate kinase	14	Oxidation+M(8)	GTQAQFIMEK	13	10	3	28.38	b7b8y9	1168.57	38.795	10201	3	390.20	3.55
P0A1V4 KAD_SALTY Adenylate kinase	15		LVEYHQMTAPLIGY	167	14	0	4.98		1634.82	69.629	2866	2	817.91	-4.18
P02910 HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTQTETFGNEHWAPK	135	20	13	68.72	b2b3b4b11*b11y2y9y10°y 10y11y12y17y20	2199.07	63.666	84601	3	733.70	-4.44
P02910 HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	18	158.92	b4b5°b5b10y3°y3y4y5y6y7 y8y9°y9y10°y10y11y12y13	1425.69	55.175	64333	2	713.35	2.83
P02910 HISJ_SALTY Histidine-binding periplasmic protein	3		NSDIQPTVASLK	120	12	17	104.83	b2°b2*b2b3°b3b4*b4b9y3 y4y7°y7y8*y8y9y10y12	1272.67	47.963	52178	2	636.84	-4.32
P02910 HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALPSLK	62	20	4	14.19	b16y4y7y20	2273.20	103.813	42357	2	1137.10	6.98
P02910 HISJ_SALTY Histidine-binding periplasmic protein	5		GIEIVSYQGQDNIYSDLTAGR	155	21	3	20.34	y3y12y17	2299.16	74.606	10657	3	767.06	17.63
P02910 HISJ_SALTY Histidine-binding periplasmic protein	6		AFAEMR	234	6	2	26.63	b3y5	724.34	36.445	4612	1	724.34	-3.29
P02910 HISJ_SALTY Histidine-binding periplasmic protein	7		QQEIAFTDKLYAADSR	99	16	6	23.92	b3b8°b8y7°y7y10	1855.94	99.628	33633	2	928.47	9.54
P02910 HISJ_SALTY Histidine-binding periplasmic protein	8		IGTDPTYAPFESKNAQGELVGFDI DLAK	29	28	4	21.82	b13b14y13*y13	2996.51	96.091	25365	3	999.51	5.95
P41031 CY_SALTY Thiosulfate-binding protein	1		VNNPEIMGK	286	9	7	54.08	b2y2y3y6y7y8y9	1001.50	35.964	48487	2	501.25	-6.09
P41031 CY_SALTY Thiosulfate-binding protein	2		ELFAALNPPFEQQWAK	37	16	8	34.31	b7°b7b11y1y6y8y12°y12	1888.97	89.970	36752	2	944.99	6.27
P41031 CY_SALTY Thiosulfate-binding protein	3		NVEVFDTGGR	189	10	8	90.8	b3b5b9y4y6y7y8y10	1093.53	47.098	32789	2	547.27	3.46
P41031 CY_SALTY Thiosulfate-binding protein	4		FPQTELFR	299	8	7	53.67	b2b3b6b8*b8y4y6	1037.56	52.386	16673	2	519.28	13.53
P41031 CY_SALTY Thiosulfate-binding protein	5		LPNNSSPFYSTMGFLVRK	110	18	4	24.29	b5°b5b10b11	2058.08	70.512	4815	3	686.70	14.47
P41031 CY_SALTY Thiosulfate-binding protein	6		LPNNSSPFYSTMGFLVR	110	17	7	50.56	b8y2y5y9y11y12y13	1929.94	92.077	4724	3	643.98	-6.77
P41031 CY_SALTY Thiosulfate-binding protein	7		ADVVTYNQVTDVQILHDK	81	18	5	26.26	b1b5b10b11y3	2058.02	63.769	4527	3	686.68	-14.00
P41031 CY_SALTY Thiosulfate-binding protein	8		AYLNWLYSPQAQTIITHYYR	265	21	7	35.72	b4b13y5y6y9°y9y12	2664.33	93.855	75585	3	888.78	1.83
P41031 CY_SALTY Thiosulfate-binding protein	9		FGSWPEVMK	311	9	4	37.96	y3y4y5°y5	1080.52	68.954	36450	2	540.76	1.13
P41031 CY_SALTY Thiosulfate-binding protein	10		GATTTFAER	199	9	5	54.08	y4y5y6°y6y8	953.46	30.752	13212	2	477.24	-4.80
P41031 CY_SALTY Thiosulfate-binding protein	11		TNILAEFPVAVVDKNVQANGTEK	239	23	7	34.81	b3b4b7y4y6°y6y14	2544.31	91.022	86556	3	848.78	1.63

P41031 CY_SALTY Thiosulfate-binding protein	12		GLGDVLISFESEVNNIRK	208	18	4	24.5	b4b10b13y8	1990.05	103.334	13976	3	664.02	-7.12
P41031 CY_SALTY Thiosulfate-binding protein	13		TSGNARYTYLAAWGAADNADGG DK	153	24	3	22.85	b4b14b15	2445.11	100.119	8023	3	815.71	1.00
P41031 CY_SALTY Thiosulfate-binding protein	14		ELFAALNPPFEQQWA	37	15	2	14.24	y6y14	1760.85	89.898	2686	3	587.62	-7.97
P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	18	86.03	b2*b2b3*b3b6y1y2y3*y3*y3y4*y4y5*y5y6y8*y8y10	1129.62	38.786	256934	2	565.31	-3.78
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		TPPAAVLLK	72	9	8	54.08	b1b2y1y3y5y6y7y9	909.57	54.420	129953	2	455.29	-12.82
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3		AADMTGADIEAMTR	113	14	3	19.04	b4y8y12	1452.64	57.263	2346	1	1452.64	-5.88
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4		AQLQEIAQTKAADMTGADIEAMT R	103	24	3	12.56	b3y5y8	2563.26	74.232	3722	3	855.09	2.95
P0A7K0 RL11_SALTY 50S ribosomal protein L11	5		QLQEIAQTK	104	9	2	8.19	b8*b8	1058.58	38.800	5195	2	529.79	-6.00
P0A7K0 RL11_SALTY 50S ribosomal protein L11	6		AQLQEIAQTK	103	10	0	2.07		1112.59	38.826	1928	3	371.54	3.95
P66032 RIBB_SALTY 3	1		MNQTLSSFGTPFER	0	15	10	88.2	b4y3y4y6y7y8y9y10*y10y15	1727.86	84.795	60639	2	864.43	8.55
P66032 RIBB_SALTY 3	2		AQAGGVLTR	141	9	4	30.18	b3b7y7y9	872.49	29.265	34938	2	436.75	-7.83
P66032 RIBB_SALTY 3	3		VELALDALR	15	9	3	30.18	b3y4y7	999.57	69.271	37433	2	500.29	-8.43
P66032 RIBB_SALTY 3	4		DGAKPSDLNRPGHVFPLR	123	18	4	32.25	b7b8b11b14	1976.04	92.813	5778	2	988.52	-3.58
P66032 RIBB_SALTY 3	5		NQTLSSFGTPFER	1	14	3	19.04	b11b13y13	1596.83	65.159	4611	2	798.92	20.18
P66032 RIBB_SALTY 3	6	Carbamidomethyl+C(4)	APECIAFAGQHNMNAVVTIEDLVA YR	184	25	3	21.81	b10b11y8	2775.42	101.728	3206	3	925.81	20.76
P66032 RIBB_SALTY 3	7		KQLDLPMMVENNTSAYGTGFTV TIEAAEGVTTGVSAADR	75	39	3	10.88	b12b15y6	4044.98	106.935	7556	4	1012.00	6.28
P66032 RIBB_SALTY 3	8	Oxidation+M(7)	QLDLPMMVENNTSAYGTGFTVTI EAAEGVTTGVSAADR	76	38	5	14.4	b6y3*y3y12y15	3932.91	108.207	1976	3	1311.64	14.15
P68684 RS21_SALTY 30S ribosomal protein S21	1		ENEPFDVALR	7	10	7	51.48	b2y2y4y5y6y7y10	1189.58	63.460	79551	2	595.30	-1.03
P68684 RS21_SALTY 30S ribosomal protein S21	2		AGVLAEVR	25	8	6	48.89	b6y2y4y5y7y8	814.47	44.134	41928	2	407.74	-13.34
P68684 RS21_SALTY 30S ribosomal protein S21	3		VRENEPFDVALR	5	12	5	33.86	b3b5b6y9y12	1444.74	47.562	36049	2	722.87	-11.91
P68684 RS21_SALTY 30S ribosomal protein S21	4		EFYEKPTTER	35	10	4	28.38	b5*b5b6y3	1299.62	73.086	5404	3	433.88	-3.95
P0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	14	96.12	b2b3*b3b13y1y4y5y7y8y9° y9y10y11y13	1447.77	65.028	136965	2	724.39	-5.56
P0A297 RL10_SALTY 50S ribosomal protein L10	2		AAAFEGELIPASQIDR	109	16	20	128.78	b1b5b8*b8b9b13°b13y2y3° y3y5*y5y7y8*y8y9y10y11y12y16	1687.87	68.622	90702	2	844.44	4.48
P0A297 RL10_SALTY 50S ribosomal protein L10	3	Carbamidomethyl+C(9)	VVEGTQFECLKDFTVGP TLIAYSM EHPGAAAR	62	32	6	24.58	b8y6y7y10y16y32	3494.69	92.371	47741	4	874.43	-5.24
P0A297 RL10_SALTY 50S ribosomal protein L10	4		DFTVGP TLIAYSMEHPGAAAR	73	21	7	29.35	b3°b3b5b6°b6y6y10	2204.10	82.631	10792	3	735.37	10.63
P0A297 RL10_SALTY 50S ribosomal protein L10	5	Carbamidomethyl+C(9)	VVEGTQFECLK	62	11	3	27.03	b3b4y4	1309.66	66.133	8053	2	655.33	10.07
P0A297 RL10_SALTY 50S ribosomal protein L10	6		LMATMK	138	6	1	13.52	y5	694.35	38.800	3482	1	694.35	-14.42
P0A297 RL10_SALTY 50S ribosomal protein L10	7		AAAFEGELIPASQIDRLATLPTYEE AIAR	109	29	5	25.67	b10y4y8y9y21	3116.63	92.949	44267	3	1039.55	1.02
P0A297 RL10_SALTY 50S ribosomal protein L10	8	Carbamidomethyl+C(9)	VVEGTQFECLKDFTVGP TLIAYSM EHPGAAAR	62	32	4	22.05	b7y8y9°y9	3494.69	63.678	13307	4	874.43	-6.01
P0A297 RL10_SALTY 50S ribosomal protein L10	9	Carbamidomethyl+C(10)	RVVEGTQFECLK	61	12	3	22.01	b9y6y11	1465.76	70.505	2556	2	733.38	9.08

[P0A297]RL10_SALTY 50S ribosomal protein L10	10		AGREAGVYMR	43	10	4	40.69	b4b9y5y6	1109.54	62.841	1872	2	555.28	-6.93
[P0A297]RL10_SALTY 50S ribosomal protein L10	11	Oxidation+M(13)	DTFVGPTLIAYSMEHPGAAAR	73	21	4	13.7	b7°b7b12y10	2220.09	115.610	5495	3	740.70	6.27
[P0A297]RL10_SALTY 50S ribosomal protein L10	12	Oxidation+M(2)	LMATMKEASAGK	138	12	4	35.78	b6b7y8y10	1253.62	80.894	1688	2	627.31	-2.43
[P02936]OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(6)	AALIDCLAPDR	321	11	11	75.65	b2b3b4b6y1y3y6y7y8°y8y11	1214.63	61.910	47101	2	607.82	4.92
[P02936]OMPA_SALTY Outer membrane protein A	2	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	9	32.93	b3y1y2y10y11y13°y13y17y19	2032.90	37.569	44070	3	678.31	-8.29
[P02936]OMPA_SALTY Outer membrane protein A	3		LEYQWTNNIGDANTIGTRPDNGL LSVGVSYR	163	31	5	18.48	b6b11y3y5y12	3423.64	111.530	2183	4	856.67	-14.48
[P02936]OMPA_SALTY Outer membrane protein A	4		DGSVVVLGFTDR	255	12	4	22.01	b4b6y3°y3	1264.65	97.945	33412	2	632.83	-0.39
[P0A1H3]EFG_SALTY Elongation factor G	1		IATDPFVGNLTFFR	323	14	15	86.32	b2b4°b4b11y2y3y4y7*y7y10y11*y11y13*y13y14	1597.84	93.410	88063	2	799.42	3.13
[P0A1H3]EFG_SALTY Elongation factor G	2		VYSGVVNSGDTVLSNVK	337	17	12	83.17	b2b4b5b7y4y9y10y11*y11y12y15y17	1737.91	62.105	74352	2	869.46	4.00
[P0A1H3]EFG_SALTY Elongation factor G	3		SGPLAGYPVVDLGVR	562	15	10	36.63	b2b5°b5b7y1y2y4y8y10y15	1499.82	76.626	69912	2	750.42	1.30
[P0A1H3]EFG_SALTY Elongation factor G	4		EFNVEANVGKPVAYR	475	16	4	16.93	b11y6*y6y8	1820.91	53.554	35195	3	607.64	-9.99
[P0A1H3]EFG_SALTY Elongation factor G	5	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTGDTLCDPEN PIILER	378	30	4	11.3	b26y2y3y11	3138.61	85.242	25140	3	1046.88	3.97
[P0A1H3]EFG_SALTY Elongation factor G	6		GQYGHVVIDMYPLEPGSNPK	512	20	4	30.45	y6y8y9y13	2201.06	70.661	22504	3	734.36	-2.44
[P0A1H3]EFG_SALTY Elongation factor G	7	Carbamidomethyl+C(11)	VLNNEILVTCGSAFK	255	16	6	23.46	b5*b5y1y8y9°y9	1777.98	108.259	16850	3	593.33	13.46
[P0A1H3]EFG_SALTY Elongation factor G	8		YDDAPNNVAQVIEAR	686	16	4	16.93	b5b12y8y16	1745.82	73.177	14954	2	873.41	-13.15
[P0A1H3]EFG_SALTY Elongation factor G	9		VEVETPEENTGDVIGDLR	618	19	9	32.93	b2°b2b3b7b14b15°b15y9y19	2058.96	94.802	9507	3	686.99	-12.45
[P0A1H3]EFG_SALTY Elongation factor G	10		MEFPEPVISIAVEPK	408	15	3	25.98	b7b8b11	1685.88	83.012	8327	2	843.44	-2.61
[P0A1H3]EFG_SALTY Elongation factor G	11		YLGGEELTEEEIK	236	13	4	20.38	b4b9b13y5	1509.75	89.770	5185	2	755.38	14.63
[P0A1H3]EFG_SALTY Elongation factor G	12	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	6	12.56	b2b7y2y6y13y24	2621.26	111.331	1643	3	874.43	-9.31
[P0A1H3]EFG_SALTY Elongation factor G	13		VVGQIK	153	6	1	13.52	b4	643.41	45.091	18699	1	643.41	-6.17
[P0A1H3]EFG_SALTY Elongation factor G	14		IHAEVPLSEMFYATQLR	653	18	3	15.37	b9b12y6	2062.04	65.040	15344	3	688.02	-1.54
[P0A1H3]EFG_SALTY Elongation factor G	15		IGEVHDGAATMDWMEQEQR	39	20	4	14.19	b11y3*y3y10	2332.02	73.137	11555	3	778.01	10.57
[P0A1H3]EFG_SALTY Elongation factor G	16		GGVIPGEYIPAVDK	541	14	3	19.04	b4b6y8	1414.78	71.995	6224	2	707.89	16.14
[P0A1H3]EFG_SALTY Elongation factor G	17		LHFGSYHDVDSSELAFK	577	17	3	16.1	b3y6y9	1951.94	44.991	4468	2	976.47	11.69
[P0A1H3]EFG_SALTY Elongation factor G	18		GGVIPGEYIPAVDKIGIEQLK	541	21	3	20.34	b3b8b10	2211.18	74.508	13993	3	737.73	-9.94
[P0A1H3]EFG_SALTY Elongation factor G	19	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTGDTLCDPEN PIILER	378	30	4	11.3	b6b22y11°y11	3138.58	92.898	13142	4	785.40	-6.30
[P0A1H3]EFG_SALTY Elongation factor G	20		GITITSAAATAFWSGMAKQYEPHR	59	24	4	22.85	y4y6y7*y7	2624.29	76.295	9925	3	875.43	-1.86
[P0A1H3]EFG_SALTY Elongation factor G	21	Carbamidomethyl+C(13)	SMRVLDGAVMVYCAVGGVQPQS ETVWR	101	27	3	11.8	b8y3y12	2995.50	85.785	9069	3	999.17	14.67
[P0A1H3]EFG_SALTY Elongation factor G	22		IHAEVPLSEMFYATQLRSLTK	653	22	3	23.15	b9b10b12	2491.30	125.996	2485	3	831.10	-0.69

P0A1H3 EFG_SALTY Elongation factor G	23	Carbamidomethyl+C(10) ;Oxidation+M(7)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	9	57.03	b12b13b16y6y9y10°y10y1 ly22	2637.27	94.866	135666	3	879.76	-2.50
P0A1H3 EFG_SALTY Elongation factor G	24		EANVGKPKQVAYR	479	12	0	4.56		1331.69	53.523	1739	2	666.35	-14.48
P00924 ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	14	76.86	b2b4b5°b5°b5b6°b6y2y5y 7y9y10°y10y12	1286.71	66.115	108839	2	643.86	-3.61
P00924 ENO1_YEAST Enolase 1	2		VNQIGTLESIK	346	12	15	107.84	b1b2°b2b3b5b9y1y2y3y5y 6y8y9y10y12	1288.71	54.334	67172	2	644.86	-1.04
P00924 ENO1_YEAST Enolase 1	3		TAGIQIVADDLTVTNPK	312	17	4	23.5	y4y10y12y17	1755.96	72.397	29479	2	878.48	3.55
P00924 ENO1_YEAST Enolase 1	4		IEEELGDNAVFAGENFHHGDK	415	21	3	22.15	b4b5y7	2328.04	58.035	12277	4	582.77	-6.08
P00924 ENO1_YEAST Enolase 1	5		TFAEALR	178	7	3	40.15	b3b5y3	807.43	38.783	121060	2	404.22	-4.23
P00924 ENO1_YEAST Enolase 1	6		AADALLK	338	8	3	40.56	y4y5y6	814.49	53.920	65912	2	407.75	-16.41
P00924 ENO1_YEAST Enolase 1	7		GNPTVEVELTTEK	15	13	3	20.38	b12y7y12	1416.71	62.811	50591	2	708.86	-6.89
P00924 ENO1_YEAST Enolase 1	8		SGETEDTFIADLVVGLR	375	17	4	23.09	b14°b14b15y12	1821.90	77.638	10909	2	911.45	-15.21
P00924 ENO1_YEAST Enolase 1	9		NVPLYK	126	6	1	13.52	y4	733.41	37.038	7545	1	733.41	-13.40
P00924 ENO1_YEAST Enolase 1	10		AVDDFLISLDGTANK	88	15	3	17.9	b4b13y9	1578.77	57.219	7394	2	789.89	-19.56
P00924 ENO1_YEAST Enolase 1	11		WLTGPQLADLYHSLMK	272	16	5	30.45	b5b7°b7y6y7	1872.96	82.587	5695	2	936.98	-6.00
P00924 ENO1_YEAST Enolase 1	12		YPIVSIEDPFAEDDWEAWSHFFK	289	23	6	24.18	b11b13y6y8y11°y11	2828.34	129.002	4264	3	943.45	17.44
P00924 ENO1_YEAST Enolase 1	13	Oxidation+M(17)	SIVPSGASTGVHEALEMRDGDK	32	22	4	17.89	b9b11y4y9	2272.10	63.032	32925	3	758.04	5.59
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	14	100.09	b4b7y1y6y7°y7y9y10y11y 12y14y17y19y21	2215.16	74.946	56014	3	739.06	-4.63
Q56073 DNAK_SALTY Chaperone protein dnaK	2		MAPPQISAEVLKK	109	13	5	20.38	b8°b8y3y11y13	1411.78	56.039	44678	3	471.26	-12.45
Q56073 DNAK_SALTY Chaperone protein dnaK	3		ASSGLNEEEIQK	502	12	8	68.43	y1y3y5y7y9y10°y10y12	1304.63	34.424	27978	2	652.82	-5.80
Q56073 DNAK_SALTY Chaperone protein dnaK	4		SLGQFNLDGINPAPR	452	15	14	89.84	b2°b2b4°b4b11b12°b12y1 y4y5y7y8y10y13	1598.83	71.966	27219	2	799.92	3.28
Q56073 DNAK_SALTY Chaperone protein dnaK	5		MQELAQVSQK	587	10	7	47.51	b2b3y3y6y8°y8y10	1161.59	36.970	27166	2	581.30	-5.36
Q56073 DNAK_SALTY Chaperone protein dnaK	6		QAVTNPQNTLFAIK	56	14	4	34.6	y9y10y11y14	1544.85	67.323	24747	2	772.93	2.37
Q56073 DNAK_SALTY Chaperone protein dnaK	7		MAPPQISAEVLK	109	12	6	44.53	b5b9b10°b10b11y12	1283.70	91.177	16186	2	642.35	-1.14
Q56073 DNAK_SALTY Chaperone protein dnaK	8		TAEDYLGEVPVTEAVITVPAYFNDA QR	125	26	11	29.7	b2b13b16y5°y5y8y12°y12 y14°y14y26	2869.39	93.462	12290	2	1435.20	0.43
Q56073 DNAK_SALTY Chaperone protein dnaK	9		GMPQIEVTFDIDADGILHVS AK	467	22	3	19.79	b5b8b14	2356.13	94.762	12950	4	589.79	-21.66
Q56073 DNAK_SALTY Chaperone protein dnaK	10		TIAVYDLGGGTFDISIIEIDEVDGE K	188	26	5	22.57	b6y4°y4y11y12	2769.41	76.427	4529	3	923.81	14.81
Q56073 DNAK_SALTY Chaperone protein dnaK	11		VLENAEGDR	25	9	4	45.05	b3y4y5y6	1002.50	116.993	3353	1	1002.50	11.51
Q56073 DNAK_SALTY Chaperone protein dnaK	12		MPMVQK	345	6	1	13.52	b4	733.38	26.516	3229	2	367.19	5.58
Q56073 DNAK_SALTY Chaperone protein dnaK	13		LMEIAQQQHAQQAGSADASAN NAK	597	25	3	12.27	b10y8y11	2610.21	38.118	1568	3	870.74	-9.07
Q56073 DNAK_SALTY Chaperone protein dnaK	14		TAEDYLGEVPVTEAVITVPAYFNDA QRQATK	125	30	4	22.65	y9y10°y10y13	3297.58	99.185	14060	3	1099.87	-13.18
Q56073 DNAK_SALTY Chaperone protein dnaK	15		VLENAEGDRTPSIIAYTQDGETL VGQPAK	25	30	7	29.48	b6b8b10°b10y10y12y13	3173.59	70.537	4713	3	1058.53	-2.85
Q56073 DNAK_SALTY Chaperone protein dnaK	16		DDDVDAEFEEVKDK	622	15	4	25.98	y8y9y12°y12	1752.77	78.635	3613	3	584.93	-5.99
Q56073 DNAK_SALTY Chaperone protein dnaK	17	Phosphoryl.STY(7)	MAPPQISAEVLK	109	12	3	22.01	b4b6y6	1363.65	113.193	2080	2	682.33	-10.56
Q56073 DNAK_SALTY Chaperone protein dnaK	18	Oxidation+M(13)	FQDEEVQRDVSIMPYK	76	16	6	44.01	b8b9b10y8y13°y13	1999.96	101.888	62725	3	667.32	7.20

[P60446]RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	12	73.72	b2°b2b5y1y2y3y5y6°y6y7y8y10	1115.63	56.429	133349	2	558.32	-8.43
[P60446]RL3_SALTY 50S ribosomal protein L3	2		IFTEDGVSIPTVIEVEANR	13	20	6	51.33	y3y4y5y6y13y20	2188.16	88.195	129006	2	1094.58	5.69
[P60446]RL3_SALTY 50S ribosomal protein L3	3	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	5	22.53	b2y4y7y15y18	1738.93	54.093	39180	3	580.32	-11.72
[P60446]RL3_SALTY 50S ribosomal protein L3	4		AVQVTTGAK	46	9	7	54.08	b2y3y4y5y7*y7y9	874.49	21.557	14165	2	437.75	-11.52
[P60446]RL3_SALTY 50S ribosomal protein L3	5		NLLLVK	184	6	3	39.73	y3y4y5	699.48	56.989	48279	1	699.48	1.13
[P60446]RL3_SALTY 50S ribosomal protein L3	6		GLWEFR	77	6	1	13.52	y5	807.41	61.438	12871	1	807.41	-11.26
[P60446]RL3_SALTY 50S ribosomal protein L3	7		VPGSIGQNQTPGK	141	13	3	25.15	b11y7y8	1282.65	64.243	4076	3	428.22	-21.22
[P60446]RL3_SALTY 50S ribosomal protein L3	8	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	7	59.06	b6y5y6y7y9y12y16	1809.97	56.212	142538	3	603.99	-11.87
[P60446]RL3_SALTY 50S ribosomal protein L3	9		IFTEDGVSIPTVIEVEANRVTVQVK	13	25	4	26.95	y14y16y18y21	2743.49	95.116	103841	3	915.17	0.18
[P60446]RL3_SALTY 50S ribosomal protein L3	10		KMAGQMGNER	159	10	4	39.72	b5y5y8y9	1121.53	18.238	15268	2	561.27	12.41
[P60446]RL3_SALTY 50S ribosomal protein L3	11		QVTTGAK	48	7	0	1.66		704.39	21.577	4556	1	704.39	-1.04
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	1		EGGIFWMDSLAIPANAK	249	17	14	51.91	b3°b3b6°b6b14b17y1y2y5*y5y12y13y15y17	1819.91	93.704	48589	2	910.46	3.22
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	2		EVAETIGYPTPNLAAR	285	16	7	54.41	b3b7b12y1y8y9y10	1701.89	60.784	42738	2	851.45	3.66
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	3		EVFQMALR	170	8	4	32.78	b7y2y3y4	993.51	63.499	18318	2	497.26	-8.17
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	4		LGYSGNTTDPK	179	11	5	36.34	b4°b4b8b9y9	1152.53	76.167	2250	3	384.85	-21.39
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	5		TITSWADLWKPEYK	146	14	5	39.35	b5b9b12y3y12	1737.90	101.793	1775	2	869.45	6.25
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	6		DGAYDLVVPSTYYVDK	73	16	4	34.34	b12°b12b13b14	1804.90	91.151	1728	3	602.30	17.86
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	7		KLGYSGNTTDPK	178	12	4	31.8	b6b11y6y8	1280.66	69.943	8119	2	640.83	5.91
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	8		EVAETIGYPTPNLAARK	285	17	4	23.5	b7b9°b9b15	1829.95	90.225	6661	2	915.48	-12.07
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	9	Oxidation+M(5)	EVFQMALR	170	8	3	35.79	b3b6y6	1009.52	68.690	19633	1	1009.52	3.39
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	1		AYLAGQGVEIR	245	11	6	36.34	b2b3y5y7y8y11	1176.63	51.191	53435	2	588.82	-9.34
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	2	Carbamidomethyl+C(10)	VAEVIDIPFCVAGGIR	68	16	8	68.7	b3b4b5b6y1y7y9y10	1715.92	90.841	49212	2	858.46	2.99
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	3		VTQWETLDWVQEVQQR	153	16	9	63.54	b3*b3b13y3y4y5y8y9y16	2045.03	84.426	42415	2	1023.02	8.24



P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	4		QIINIGELK	236	9	3	37.96	y4y6y7	1027.61	65.570	32074	2	514.31	-9.03
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	5	Carbamidomethyl+C(5)	FGVQCIVVGIDTWFDATGK	119	20	4	19.46	b11b13y7y13	2228.11	91.514	12505	3	743.38	20.27
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	6		DADVDGALAASVFHK	221	15	4	29.09	b3y7y10y13	1515.73	81.396	4966	2	758.37	-11.44
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	7	Carbamidomethyl+C(10)	VAEVIDIPFCVAGGIRSIDDAAK	68	23	5	33.21	b3b4y4y6y14	2416.26	89.682	34901	3	806.09	3.33
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	8		YHVNQYTGDENRTR	139	14	3	27.61	y3y8y13	1752.80	71.834	10604	2	876.90	-2.44
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	9		DGQVVKGVQFR	13	11	4	27.03	b10y3y4*y4	1232.69	47.582	6157	3	411.57	13.57
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	10		ILSFGADKISINSPALADPTLITR	91	24	3	22.85	b8b17b18	2513.41	136.865	5875	3	838.47	4.66
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	11	Carbamidomethyl+C(9)	LADRFGVQCIVVGIDTWFDATG K	115	24	5	16.61	b6*b6b10y7y14	2683.35	88.844	2240	3	895.12	9.92
P0A1S4 STPA_SALTY DNA-binding protein stpA	1		ADGINPEELFAMDSAMPR	66	18	11	73.76	b2b3b4b9b11y2y3y5y6y7y 13	1963.91	88.992	25492	2	982.46	8.70
P0A1S4 STPA_SALTY DNA-binding protein stpA	2		MNLMLQNLNNIR	0	12	6	36.87	b2b5b7b11y7y12	1473.77	76.447	21750	2	737.39	0.25
P0A1S4 STPA_SALTY DNA-binding protein stpA	3		AMAREFSIDVLEEMLEK	15	17	4	16.1	b4y2y6y10	2010.98	96.246	2434	2	1005.99	-4.49
P0A1S4 STPA_SALTY DNA-binding protein stpA	4		INAFLELMK	57	9	4	30.18	b5*b5y5y7	1078.59	85.125	20967	2	539.80	-6.22
P0A1S4 STPA_SALTY DNA-binding protein stpA	5	Oxidation+M(1)	MNLMLQNLNNIR	0	12	3	22.01	b5b11y3	1489.75	54.681	22977	2	745.38	-4.59
P0A1S4 STPA_SALTY DNA-binding protein stpA	6	Oxidation+M(14)	AMAREFSIDVLEEMLEK	15	17	7	33.56	b9°b9b12b13y5y8°y8	2027.00	104.889	12486	3	676.34	6.93
P26976 PHON_SALTY Non-ecific acid phohatase	1		LQTIPAFQK	215	9	9	45.75	b2*b2b9y3y5*y5y7*y7y9	1045.60	55.071	116090	2	523.30	-4.67
P26976 PHON_SALTY Non-ecific acid phohatase	2		NLLTMGGYYATASAK	108	15	7	71.57	b3b4y8y10y11y12y13	1560.78	70.149	101853	2	780.89	3.28
P26976 PHON_SALTY Non-ecific acid phohatase	3		YVGAVEFAR	206	9	6	30.18	b2b3b9y7y8y9	1011.52	51.436	75163	2	506.26	-8.69
P26976 PHON_SALTY Non-ecific acid phohatase	4		NLLTMGGYYATASAKK	108	16	6	16.93	b1*b1b6y8y12°y12	1688.85	64.653	23959	3	563.62	-10.99
P26976 PHON_SALTY Non-ecific acid phohatase	5	Carbamidomethyl+C(3)	VICGAHWQSDVDAGR	191	15	5	43.35	y3y4y9y10y15	1670.77	45.932	21042	2	835.89	-2.48
P26976 PHON_SALTY Non-ecific acid phohatase	6	Carbamidomethyl+C(12)	TRPFVLFNHSTCRPEDENTLR	128	21	5	23.35	b1y7°y7y11y12	2589.26	92.588	12773	2	1295.13	-2.36
P26976 PHON_SALTY Non-ecific acid phohatase	7		IFSPVVGAK	85	9	6	67.19	y3y4y6y7y8°y8	917.53	51.196	105182	2	459.27	-15.57
P26976 PHON_SALTY Non-ecific acid phohatase	8		QAAEDADVSVENIAR	70	15	5	29.09	b12y10y11°y11y13	1587.76	50.362	23884	2	794.39	1.23
P26976 PHON_SALTY Non-ecific acid phohatase	9		YTSAETVQPFFHSPEESVNSQFYLP PPPGNDDPAYR	16	35	4	12.7	b5b8y9y13	3936.79	122.167	2209	3	1312.94	-0.99
P26976 PHON_SALTY Non-ecific acid phohatase	10		YLVFFLPLIVAKYTSAETVQPPFHSP EESVNSQFYLP PPPGNDDPAYR	4	47	4	13.66	b4b10b12y14	5340.61	136.538	17488	4	1335.91	-9.33
P26976 PHON_SALTY Non-ecific acid phohatase	11		DTPETWNMLKNLLTMGGYYATA SAK	98	25	6	36.18	b11b12b23y14°y14y15	2776.37	136.524	2110	3	926.13	14.25

[P26976]PHON_SALTY Non-ecific acid phohatase	12	Phosphoryl STY(4)	NLLTMGGYYATASAKK	108	16	3	25.31	y11y12y14	1768.83	94.666	12317	2	884.92	0.90
[P26976]PHON_SALTY Non-ecific acid phohatase	13		GAVEFAR	208	7	1	8.74	b3	749.39	51.488	4400	1	749.39	-9.28
[P26976]PHON_SALTY Non-ecific acid phohatase	14		YVGAVEFAR	206	9	0	1.66		993.50	51.464	3128	1	993.50	-14.19
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	1		TLFEPGEMVR	125	10	7	42.73	b1°b1b9y6y7y8y10	1178.59	65.207	41370	2	589.80	-2.07
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	2		VNDGPFADFNQVVEVDYEK	135	20	6	22.32	b3y3y5°y5y8y20	2243.04	86.271	28023	2	1122.02	12.73
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	3		VMGFIGGTSDRPAPISDKEVDAIM NR	88	26	6	18.05	b2b3b9b14y11°y11	2776.38	103.571	3111	3	926.13	-0.09
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	4		VMGFIGGTSDRPAPISDK	88	18	7	40.27	b3b6y4y7y9°y9y10	1847.92	104.305	17232	2	924.46	-6.34
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	5		LHNMEELFGEVMVPTEEVVEIR	31	22	3	13.27	b7b12y7	2600.27	68.461	5957	3	867.43	-3.10
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	6		ATPVELDFSQVEKA	167	14	11	94.26	b12y3y6y8*y8y9*y9y10°y10y11y12	1533.78	69.706	20237	2	767.40	3.26
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	7		WYVVQAFSGFEGRVATSLR	8	19	3	14.74	b10b13y14	2173.11	82.719	9583	2	1087.06	-2.70
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	8	Oxidation+M(8)	TLFEPGEMVR	125	10	3	28.38	b5b6y8	1194.59	82.190	2962	2	597.80	4.50
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTASPYASYLQYGHIANIDD IAGKKPATDLGVK	125	38	5	24.1	b10b21y1y3y4	4001.01	83.542	46276	5	801.01	-13.06
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	2		AEQQLDKDSAIVPVYYYVNAR	494	21	8	51.21	b10b11b12°b12y3y9y10y21	2442.23	73.102	27317	3	814.75	-1.40
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	3	Carbamidomethyl+C(4)	AGWCADYNEPTSFLNTMLSDSSN NTAHYK	439	29	4	17.4	y4y7y11y29	3294.43	90.193	20909	3	1098.82	6.82
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	4		TVINQVTYLPISSEVTDVNR	241	20	6	31.79	b1b4y5y10y11y14	2248.19	77.098	17430	2	1124.60	3.04
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	5		NQGDLPAYSYTPPYTDGAK	333	19	6	36.77	b7b8y5y11y14y19	2057.96	58.834	14607	2	1029.49	9.37
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	6		NLGVNVNLENQEWK	410	14	5	19.04	b6b11°b11*b11y12	1656.84	66.800	10458	2	828.92	3.90
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	7		LADPNTASPYASYLQYGHIANIDD IAGK	125	29	9	25.67	b3°b3b7*b7b8*b8b15*b15y3	3091.51	132.868	10278	3	1031.18	-7.19
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	8		ALDDHTFEVTLSEPVPYFYK	163	20	6	45.2	b10b11y4y9y10y12	2371.13	58.881	10214	3	791.05	-7.41
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	9		HQGTFDVAR	430	9	6	45.05	b4*b4b5b8y8*y8	1030.49	94.790	4221	1	1030.49	-13.50

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		WSDGTPVTAHDFVYSWQR	107	18	8	30.55	b4b7y4°y4y6y9°y9*y9	2152.00	86.492	3059	2	1076.50	3.52
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		SGEIDMTYNNMPIELFQK	263	18	4	15.37	b4y3*y3y10	2130.01	136.237	2201	2	1065.51	10.89
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		NNGSEVQSLDPHKIEGVESNVSR	43	24	5	25.9	b13b14°b14y6y10	2592.26	117.327	23761	3	864.76	-1.04
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	13		NPQYWDNAKTVINQVTYLPISSEV TDVNR	232	29	3	11.44	b11y5y10	3364.68	102.076	20786	3	1122.23	-1.02
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	14		FGDKWTQPANIVTNGAYK	200	18	3	22.78	b7y4y5	2010.00	64.565	7723	3	670.67	-1.58
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	15		SELYAKAEQQLDK	488	13	3	29.62	b6b9b11	1522.76	68.364	4621	2	761.88	-10.74
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	1		LFNELGPR	78	8	7	65.01	b7y3y4y6*y6y7y8	945.51	55.415	156622	2	473.26	-8.33
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	2		AGDNAPMAYIELVDR	103	15	8	36.63	b5*b5b13b14y2y5y10y15	1634.79	79.247	57912	2	817.90	3.58
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	3		VVEPLITLAK	46	10	4	33.61	y3y4y7y10	1082.67	69.229	53635	2	541.84	-6.88
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	4		RVVEPLITLAK	45	11	7	84.23	b4b6b8b9b10y3y7	1238.78	63.141	140700	2	619.89	-3.55
P66932 TIG_SALTY Trigger factor	1		NVALEEQAWEAVLAK	399	15	8	29.09	b1b2b3b5b7y2y11y15	1583.85	80.282	91733	2	792.43	-6.09
P66932 TIG_SALTY Trigger factor	2		INPAGAPNYVPGEYK	83	15	8	55	b4y2y5y8y9y11y13y15	1589.79	50.769	22060	2	795.40	-2.84
P66932 TIG_SALTY Trigger factor	3		ANDIDVPSALIDSEIDVLR	296	19	9	48.11	b6°b6b7°b7b10b11y3y13y19	2055.07	94.671	17448	2	1028.04	6.18
P66932 TIG_SALTY Trigger factor	4		GLIEEMASAYEDPKEVIEFYK	368	22	3	23.15	y4y11y12	2548.18	81.643	5300	3	850.06	-14.66
P66932 TIG_SALTY Trigger factor	5		NFVDAIK	73	8	3	32.78	b6y4y5	919.51	45.544	20299	2	460.26	-12.61
P66932 TIG_SALTY Trigger factor	6		GLIEEMASAYEDPK	368	14	3	24.48	b13y12y13	1552.73	136.620	9626	1	1552.73	6.45
P66932 TIG_SALTY Trigger factor	7		AGEEFTIDVTFPEEYHAENLK	206	21	4	20.34	y6*y6y9y12	2439.18	64.521	7063	3	813.73	19.32
P66932 TIG_SALTY Trigger factor	8		IDGFR	40	5	1	13.11	y4	607.32	28.361	4022	1	607.32	6.23
P66932 TIG_SALTY Trigger factor	9		VTIDFTGSVDGEFEFGGKATDFVL AMGQGR	163	30	7	23.28	b10y5y10°y10y12y15*y15	3133.50	102.651	7831	4	784.13	6.54
P66932 TIG_SALTY Trigger factor	10		GLIEEMASAYEDPKEVIEFYK	368	22	3	13.27	b9y4y12	2548.25	75.204	6657	3	850.09	11.69
P66932 TIG_SALTY Trigger factor	11		YGASVRQDVLGDLMSR	57	16	3	24.64	y5y8y10	1766.88	71.698	2766	3	589.63	-1.31
P66932 TIG_SALTY Trigger factor	12		VKGLIEEMASAYEDPK	366	16	4	30.45	b11b12y7y13	1779.86	117.267	2658	2	890.43	-11.66
P66932 TIG_SALTY Trigger factor	13	Phosphoryl STY(10)	VEERELPELTEEFIK	239	15	4	17.9	b4°b4b8y5	1940.89	43.411	3072	3	647.64	-11.57
P66932 TIG_SALTY Trigger factor	14	Phosphoryl STY(4)	VTITIAADSJETAVK	14	15	3	25.98	y9y11y12	1611.82	78.123	2620	2	806.41	2.95
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	1		TMNTPHGDITVFDLR	23	16	6	27.33	b12y2y4y6y10°y10	1787.85	71.691	47172	3	596.62	-11.95
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	2	Carbamidomethyl+C(15)	VQDQNQIPELNVYQCGTYQMHSLSAQDIAR	113	31	9	31.06	b2b6y1y4y7y10y17y24y31	3635.69	75.009	26545	3	1212.57	1.07

[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	3		TGFYMSLIGTPDEQR	84	15	6	29.09	b3y2y3°y3y10y12	1714.82	78.706	25936	2	857.92	7.40
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	4		MQAPAVR	13	7	5	40.15	y2y4y5y6y7	772.40	30.387	16029	2	386.71	-13.43
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	5		GIHTLEHLFAGFMR	51	14	3	19.04	b7y3y6	1628.87	76.219	4489	2	814.94	20.83
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	6		PLLDSTFAVDHTR	1	12	4	22.01	b5b10y4°y4	1370.72	56.431	2598	3	457.58	11.93
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	7	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCR	65	19	8	31.21	b4*b4b9y8y10°y10y11°y11	2097.02	136.351	1652	2	1049.02	18.86
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	8		EVMPEKGIHTLEHLFAGFMR	45	20	4	22.32	b18y6y8y12	2342.17	86.416	1811	2	1171.59	-2.29
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	9	Carbamidomethyl+C(15) ;Oxidation+M(20)	VQDQNQIPELNVYQCGTYQMHSLS SEAQDIAR	113	31	4	25.95	b3b4b7b26	3651.68	104.377	6482	4	913.67	-1.14
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	1		GFGVPTLIAVHPENDPQGEGMAIA K	167	25	8	32.95	b2b3b4b6y10y14y21y25	2548.29	77.444	43762	3	850.10	-0.10
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	2		ANYFNTLNL	1	10	7	52.04	b2b3b7y3y6y7y10	1225.64	68.160	21443	2	613.32	2.49
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	3		LIQFGWETITEALK	252	14	4	27.21	b8b12y3y11	1648.89	101.779	9105	2	824.95	-4.66
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	4		DGAALGYSHGFNIVEVGEQIR	123	21	5	22.15	b13*b13y2y6y7	2232.09	88.208	7961	3	744.70	-6.67
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	5	Carbamidomethyl+C(6)	VVIVGCGAQGLNQGLNMR	39	18	6	21.42	b8b14*b14y5y11*y11	1885.95	88.851	6543	2	943.48	-14.56
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	6		LVAEGTDPAYAEK	239	13	3	25.15	b11y5y6	1363.66	37.579	5767	2	682.33	-11.55
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	7		EIMAPLFQK	293	9	4	54.08	b3b5b6b7	1076.57	26.316	8847	2	538.79	-11.34
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	8		AWAAATGGHR	192	10	6	56.81	b6b7b8y6°y6y7	997.50	76.433	2551	1	997.50	0.67
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	9		DEFADGASYLQGK	25	13	3	27.86	y8y9y11	1400.63	93.613	2418	2	700.82	-1.22
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	10		VGTYEELIPQADLVVNLTDPKQHS DVVR	88	28	4	26.62	y11y13y14y20	3135.62	81.971	19816	4	784.66	-3.35
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	11	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21) )	SDLMGEQTILCGMLQAGSLLCFD KLVAEGTDPAYAEK	215	37	9	49.55	b3b11y6y7y8y10°y10y11°y11	4031.91	118.071	10025	3	1344.64	-0.06
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	12		LIQFGWETITEALKQGGITLMMDR	252	24	5	19.19	b7y6y10°y10y14	2751.39	129.154	1871	3	917.80	-11.62
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	13		QGGITLMMDRLSNPAK	266	16	4	23.46	b13y12*y12y13	1731.86	86.811	1605	2	866.44	-13.67
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	14	Oxidation+M(6)	SVQPLMKDGAALGYSHGFNIVEV GEQIR	116	28	9	30.4	b3°b3b7b11°b11y4°y4y5°y5	3031.56	132.878	143649	3	1011.19	10.95
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	15	Carbamidomethyl+C(6); Oxidation+M(17)	VVIVGCGAQGLNQGLNMR	39	18	4	15.37	b14y6y8*y8	1901.98	86.434	13871	2	951.49	3.47
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	16		LGYSHGFNIVEVGEQIR	127	17	0	6.64		1917.95	88.191	12554	2	959.48	-14.13
[P0A2A7]RL30_SALTY 50S ribosomal protein L30	1		ATLLGLGLR	21	9	8	54.08	b2°b2y1y3y5y6y7y9	913.57	74.187	130022	2	457.29	-10.56
[P0A2A7]RL30_SALTY 50S ribosomal protein L30	2		GMVNAVSMVK	45	11	8	24.02	b2b7°b7y2y4y8°y8y11	1182.60	73.365	89217	2	591.80	-4.85
[P0A2A7]RL30_SALTY 50S ribosomal protein L30	3		ATLLGLGLR	21	9	0	1.66		895.56	74.194	4826	2	448.28	-6.95
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	1		SSDVSLPVLVLTAR	68	14	10	59.81	b1b3°b3y3°y3y4y8y9y10y14	1456.84	86.778	69263	2	728.92	1.09

P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	2		VLVVEDNALLR	3	11	7	55.46	b1b2b3y6y7y8y9	1240.72	67.562	65445	2	620.86	-2.85
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	3		GQGYLFELR	215	9	3	30.18	b4y4y7	1082.56	72.195	31487	2	541.78	-6.20
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	4		VQLQDSGHQVDAEDAR	18	17	7	16.1	b6*b6y2y9*y9y15y17	1838.85	36.020	18393	3	613.62	-9.56
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	5		IQAQYPHDVITTVR	201	14	6	71.57	y4y7y8y9y10y12	1640.85	51.667	63205	3	547.62	-16.66
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	6		MQALMR	112	6	3	26.63	b3b4*b4	749.38	31.126	21831	1	749.38	3.10
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	7		DSLMLQLYPDaelR	172	14	4	32.65	b3b10y5y6	1663.83	80.557	2401	2	832.42	-4.48
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	8		VEVLSSGADDYVTKPFHIEEVMA R	88	24	5	16.61	b3b13y5°y5y9	2692.28	62.070	2091	3	898.10	-16.23
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	9	Phosphoryl STY(11)	LTAFEYTIMETLIR	150	14	5	31.17	b10y4°y4y7y9	1780.83	66.554	1716	3	594.28	-10.83
Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTIPTWFPDSQTLAFTSDQAG RPQVYK	287	29	6	16.7	b5y1y13y16y24y29	3285.55	77.665	51345	3	1095.85	0.89
Q8ZQT5 TOLB_SALTY Protein tolB	2		WAGPGAAPEDIGGIVAADLR	43	20	9	46.45	b7b11b14y2y6y9y13y15y2 0	1936.01	85.506	23109	2	968.51	7.76
Q8ZQT5 TOLB_SALTY Protein tolB	3		IEITQGVDSARPIGVVPFK	24	19	12	55.1	b2°b2b8*b8b9b10b11*b11 y2y3y16y19	2026.12	70.617	22085	3	676.05	-5.72
Q8ZQT5 TOLB_SALTY Protein tolB	4		LPATDGQVK	413	9	4	37.96	y4y6y7y9	928.51	27.674	20750	2	464.76	-2.50
Q8ZQT5 TOLB_SALTY Protein tolB	5		SALVIQTLANGAVR	223	14	5	32.65	b3b4y2y3y9	1412.82	70.959	19821	2	706.91	-4.67
Q8ZQT5 TOLB_SALTY Protein tolB	6		MNINGGAAQR	316	10	6	51.48	b2y4y6y7y8y10	1031.50	27.780	17155	2	516.26	-1.89
Q8ZQT5 TOLB_SALTY Protein tolB	7		QWLRYAGHTASDEVFEK	138	17	6	32.31	b5b7b10y7°y7y9	2037.00	94.786	27447	2	1019.00	7.19
Q8ZQT5 TOLB_SALTY Protein tolB	8		VIQTLANGAVR	226	11	0	3.73		1141.66	71.046	32301	2	571.33	-11.55
Q8ZQT5 TOLB_SALTY Protein tolB	9		AAPEDIGGIVAADLR	48	15	0	6.22		1467.76	85.430	27922	2	734.38	-12.23
P25077 MDH_SALTY Malate dehydrogenase	1		NQLPSGSELSLYDIAPVTPGVAVD LSHIPTAVK	21	33	17	50.1	b2*b2b3*b3b10b12°b12*b 12b13b15y1y3y5y15y18y3 0y33	3388.80	93.788	66729	3	1130.27	1.30
P25077 MDH_SALTY Malate dehydrogenase	2		VAVLGAAGGIGQALALLK	2	19	8	32.93	b3y1y2y3y4y9y13y19	1735.09	120.093	55284	2	868.05	1.69
P25077 MDH_SALTY Malate dehydrogenase	3		IQNAGTEVVEAK	205	12	12	68.31	b2b6*b6y1y3°y3y4y5y8°y8 y10*y10	1258.66	34.376	32834	2	629.83	-2.23
P25077 MDH_SALTY Malate dehydrogenase	4		SDLFVNAGIVK	87	12	5	49.3	b3b4b5b6y1	1276.68	69.860	12760	2	638.85	-4.11
P25077 MDH_SALTY Malate dehydrogenase	5		AGGGSATLSMGQAAAR	217	16	7	41.52	b9b13b14°b14*b14y6y7	1405.69	77.117	6355	2	703.35	3.04
P25077 MDH_SALTY Malate dehydrogenase	6		FFSQPLLLGK	262	10	4	28.38	b5°b5b6y6	1149.66	76.091	45693	2	575.33	-6.90
P25077 MDH_SALTY Malate dehydrogenase	7		DIQLGEDFINK	301	11	5	27.03	b4°b4b5*b5y6	1291.64	97.950	2600	2	646.32	-12.76
P25077 MDH_SALTY Malate dehydrogenase	8		IQNAGTEVVEAKAGGGSATLSMG QAAAR	205	28	5	17.11	b3b7*b7b15y11	2645.36	119.894	4943	4	662.10	12.64

P25077 MDH_SALTY Malate dehydrogenase	9	Oxidation+M(16)	SIGTLSAFEQHSLDAMLDTLK	279	21	5	21.41	b3°b3b5b19y7	2293.14	103.405	2804	3	765.05	-0.32
P25077 MDH_SALTY Malate dehydrogenase	10		AGGGSATLSMGQAA	217	14	1	7.25	y12	1178.55	77.181	2859	1	1178.55	1.66
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	31	175.83	b2°b2*b2b3b4°b4b5b7b9°b9*b9b11b12°b12b13*b13b16*b16y4y5°y5*y5y6°y6y7y8y9y10*y10y12y23	2379.23	64.492	216768	3	793.75	-4.41
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	13	84.93	b2b3b5°b5y6y7y9y10y13°y13y14y15y18	1919.02	85.280	151954	2	960.01	6.49
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	9	54.92	b2b3b7b12y4y6y13y15y17	1837.96	86.204	131309	2	919.48	7.11
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4		DLSDVLSQYAGK	33	13	7	45.62	b4b5y6*y6y7y11y13	1382.68	58.987	73607	2	691.85	2.65
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		NYGVEIVDGPLK	116	12	7	36.87	b2°b2b3y4y8y10y12	1303.68	64.865	32146	2	652.35	-3.28
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		DLSDVLSQYAGKR	33	14	6	27.21	b7b12°b12y7*y7y9	1538.76	54.746	15959	3	513.59	-11.66
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		AQAFTLVAK	24	9	6	78.53	b4b5y3y4y6y7	948.54	53.270	114007	2	474.77	-15.25
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8		NNEFLK	110	6	1	13.52	b3	764.40	37.440	9886	2	382.70	2.08
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9	Carbamidomethyl+C(15)	FNQLATEVENTVVLCSADLPFAQSR	67	26	3	12.02	b5y8y12	2908.39	112.419	6628	3	970.14	-19.47
Q8ZP65 TPX_SALTY Probable thiol peroxidase	10		AVIVLDENDNVIFSQLVDEITHEPDYDAALNVLKA	133	35	26	202.13	b3b4b5b9°b9b10b11°b11b32y3y4y5y6y7y12y13°y13y14*y14y16y22y24y26y29y30y31	3882.95	120.464	147455	3	1294.99	-2.70
Q8ZP65 TPX_SALTY Probable thiol peroxidase	11		DLSDVLSQYAGKR	33	14	5	38.56	b10b13y6y7y9	1538.78	63.696	9107	3	513.60	-0.48
Q8ZP65 TPX_SALTY Probable thiol peroxidase	12	Phosphoryl STY(13)	MSQTVHFQGNPVTVANVIPQAGSK	0	24	5	35.21	b11_H3PO4 b10b11b12_H3PO4 b12y6°y6	2590.21	86.594	56028	3	864.08	-9.80
Q8ZP65 TPX_SALTY Probable thiol peroxidase	13	Carbamidomethyl+C(2); Phosphoryl STY(14)	FCGAEGLSNVITLSTLR	93	17	4	16.1	b12°b12y5y10	1917.92	88.693	8365	3	639.98	9.87
Q8ZP65 TPX_SALTY Probable thiol peroxidase	14	Phosphoryl STY(8)	DLSDVLSQYAGKR	33	14	4	19.04	b3b7°b7y6	1618.75	82.445	4460	3	540.25	6.41
Q8ZRP4 DAPD_SALTY 2	1		EAVNQVISLLDSGALR	28	16	6	41.52	b6b7y5y6y10y16	1684.94	92.434	86387	2	842.97	7.68
Q8ZRP4 DAPD_SALTY 2	2		INDNQVIDGAESR	68	13	8	77.18	y5y6y7y8y9°y9y10y13	1430.68	40.955	39514	2	715.85	-1.79
Q8ZRP4 DAPD_SALTY 2	3		MQQLQNVIETAFER	0	14	4	19.04	b3y4y6°y6	1706.87	92.427	24208	3	569.63	12.80
Q8ZRP4 DAPD_SALTY 2	4		VPAGSVVVSGNLPKSKDGK	226	18	4	15.37	b4b6y11y18	1710.92	43.321	23684	3	570.98	-13.70
Q8ZRP4 DAPD_SALTY 2	5		VGINELLR	263	8	3	48.34	y3y5y7	913.53	66.050	49665	2	457.27	-18.24
Q8ZRP4 DAPD_SALTY 2	6		SEVVEGVIVEEGSVISMGVYLGQSTK	187	26	5	15.56	b4°b4b15y10y15	2696.35	106.521	13907	3	899.45	-8.15
Q8ZRP4 DAPD_SALTY 2	7		QQLQNVIETAFER	1	13	9	55.93	b4b8°b8b11y3°y3y5°y5y12	1575.79	66.098	3956	2	788.40	-16.19
Q8ZRP4 DAPD_SALTY 2	8		SEVVEGVIVEEGSVISMGVYLGQSTKIYDR	187	30	11	32.98	b3°b3b5°b5b10°b10b11y4y8*y8y17	3243.62	136.338	3186	3	1081.88	-7.23
Q8ZRP4 DAPD_SALTY 2	9	Oxidation+M(17)	SEVVEGVIVEEGSVISMGVYLGQSTK	187	26	5	26.16	b14y5y10y13y22	2712.37	120.582	1572	2	1356.69	2.07
Q8ZQS2 GPMA_SALTY 2	1		VIPYWNDILPR	160	12	10	81.54	y1y2y3y5y7y8°y8y9y10y12	1486.81	81.719	64599	2	743.91	0.33
Q8ZQS2 GPMA_SALTY 2	2		VIIAAHGNSLR	178	11	5	50.14	b2y5y6y8y9	1150.66	37.941	31721	2	575.83	-7.74
Q8ZQS2 GPMA_SALTY 2	3		LSEKELPLTESLALTIDR	142	18	4	15.37	b5b11y2y6	2028.12	83.362	7443	2	1014.57	0.48
Q8ZQS2 GPMA_SALTY 2	4		LNER	86	4	1	12.69	b3	531.29	46.871	15453	1	531.29	0.34
Q8ZQS2 GPMA_SALTY 2	5		GVSEAK	33	6	3	26.63	b5°b5y5	590.32	28.101	13772	1	590.32	4.24

Q8ZQS2 GPMA_SALTY 2	6		GFAVTPPELTKDDER	117	15	4	17.9	b5y10°y10y12	1674.81	54.215	34473	2	837.91	-13.19
Q8ZQS2 GPMA_SALTY 2	7		IAAHGNSLR	180	9	1	7.81	b6	938.51	37.979	30880	2	469.76	-6.57
P10372 HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1		MIIPALDLIDGTVVR	0	15	5	36.36	b2y5y6y9y12	1625.93	103.002	81957	2	813.47	-0.23
P10372 HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	2		QVAVSGWQENSGVSLEQLVETYL PVGLK	138	28	9	35.74	b3b4*b4b7b13b16y3y5y28	3030.60	118.084	12162	3	1010.87	6.20
P10372 HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	3		YPQIAFQSSGGIGDIDDIAALR	193	22	4	20.59	b11b13b18y13	2307.16	118.268	5312	2	1154.08	-2.22
P10372 HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	4		QIPLIK	60	6	2	26.63	b4b5	711.48	54.445	4003	1	711.48	3.35
P10372 HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	5	Carbamidomethyl+C(5)	EAIQCWQNV	236	9	3	30.18	b3y4y7	1147.52	82.716	3082	1	1147.52	-0.43
P10372 HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	6		LQDYAAQGAGVLHLVDLTGAK	34	21	3	13.7	b10y3y6	2140.10	81.100	2817	3	714.04	-19.51
P10372 HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	7	Carbamidomethyl+C(9)	FTVKEAQCWQNV	232	13	4	25.15	b9*b9y3y4	1622.81	53.235	6093	3	541.61	5.42
P10372 HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	8	Carbamidomethyl+C(4); Carbamidomethyl+C(25)	HVLCTDISRDGTLAGSNVSLYEEV CAR	166	27	5	25.66	b4b7°b7b11b13	3022.43	121.478	1522	3	1008.15	-1.70
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	1		QTMLINEK	45	8	9	48.89	b7y2°y2y3*y3y4y5y8*y8	976.51	41.179	24658	2	488.76	-2.75
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	2		DAEQQDFQLYPGELGK	12	16	3	16.93	b11b14y13	1766.83	68.466	15893	2	883.92	6.01
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	3		LLEQEMVSFLFEGK	64	14	7	27.21	b5°b5b13y7°y7y12*y12	1669.87	101.741	17814	2	835.44	10.45
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	4	Phosphoryl STY(6)	IYNEISKDAWAQWQHK	29	16	8	71.11	b4y4y5y6y7y8y10°y10	2096.96	65.280	3057	3	699.66	3.03
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	5	Oxidation+M(6)	LLEQEMVSFLFEGKDVHIEGYTPE DK	64	26	3	18.16	y5y11y20	3069.51	132.869	23906	3	1023.84	10.66
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	6		GQDFQLYPGELGK	15	13	0	4.56		1451.70	68.388	2699	3	484.57	-12.11
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		AVLPGMVER	115	9	4	37.96	b1y4y6y7	971.52	53.102	33549	2	486.27	-11.87

[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		VTDIEPGLVGGTEFSSVR	171	18	10	48.87	b2b3°b3y5y9y12y13y14°y14y18	1862.96	69.125	28394	2	931.98	6.95
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		AAIEEMMASLPAQWR	58	15	4	41.13	y4y8y10y14	1703.84	90.955	15155	2	852.42	8.38
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4		GHIINIGSTAGSWPYAGGNVYGATK	126	25	3	21.81	b4y12y13	2491.26	99.185	2460	3	831.09	9.70
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		DIDVLVNNAGLALGLEPAHK	73	20	5	14.19	b3b7°b7°b7y7	2059.16	109.967	12625	2	1030.08	18.02
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6	Carbamidomethyl+C(15)	MIVLVTGATAGFGECIAR	0	18	5	21.42	b9b15y8y12°y12	1865.99	79.010	3249	3	622.67	15.57
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		IINIGSTAGSWPYAGGNVYGATK	128	23	1	8.39	b13	2297.17	99.269	3411	2	1149.09	4.25
[P66193]RL31B_SALTY 50S ribosomal protein L31 type B	1		TFDSESSAAR	62	10	8	67.6	y1y4°y4y5y6y7y8y10	1070.47	24.555	77256	2	535.74	-7.41
[P66193]RL31B_SALTY 50S ribosomal protein L31 type B	2		TEREIELDGVTPYPVTIDVSSK	30	22	4	13.27	b8b10y11°y11	2514.24	113.733	2062	3	838.75	-9.52
[P66193]RL31B_SALTY 50S ribosomal protein L31 type B	3		TVVFHDTSANEEYVK	10	14	12	104.87	b10b11y3y4°y4y8y9°y9y10°y10y11y12	1609.76	47.127	356267	3	537.26	-17.52
[P66193]RL31B_SALTY 50S ribosomal protein L31 type B	4		VGSTIKTER	24	9	3	37.96	y3y4y5	990.54	18.237	28863	2	495.78	-13.68
[P66193]RL31B_SALTY 50S ribosomal protein L31 type B	5		EIELDGVTPYPVTIDVSSKSHPFYTG	33	27	6	20.86	b5b8y7y12°y12y25	3073.47	76.356	5572	3	1025.16	-13.50
[P66193]RL31B_SALTY 50S ribosomal protein L31 type B	6		TEREIELDGVTPYPVTIDVSSK	30	22	3	13.27	b3b9y10	2514.24	102.037	4368	3	838.75	-10.10
[Q8ZL56]GPMI_SALTY 2	1	Carbamidomethyl+C(8)	AVEALDNCIEQVTK	416	14	6	30.38	b1b12y2y7y10y11	1589.79	61.213	21381	2	795.40	3.30
[Q8ZL56]GPMI_SALTY 2	2		LSDIAPTMLSLMGMEIPQEMTGKPLFIVE	485	29	7	36.14	b3b4b5b7y1y2y29	3191.60	121.279	19730	3	1064.54	-2.68
[Q8ZL56]GPMI_SALTY 2	3		VATYDLQPEMSSAELTEK	364	18	8	30.55	b1b7b9y2y9y11y17y18	2011.97	63.150	12528	2	1006.49	8.55
[Q8ZL56]GPMI_SALTY 2	4		TAVAYPPASLANTFGEWMAK	303	20	6	27.59	b9b15y14*y14y15°y15	2125.05	95.757	12374	2	1063.03	3.68
[Q8ZL56]GPMI_SALTY 2	5		AFVNADFDGFARK	272	13	3	20.38	b3y10y12	1457.72	74.900	3289	2	729.36	2.09
[Q8ZL56]GPMI_SALTY 2	6		YAHVTFFFNGGVVEEPFAGEER	336	21	3	13.7	b5b12y6	2403.12	94.927	1877	3	801.71	5.99
[Q8ZL56]GPMI_SALTY 2	7	Carbamidomethyl+C(6)	YDTIICNYPNGDMVGHTGVMEAAIK	391	25	8	37.15	b4b7b9b11y4y8°y8y11	2769.31	119.483	49066	3	923.78	16.93
[Q8ZL56]GPMI_SALTY 2	8		TPVMDALWAK	31	10	3	28.38	b4b5y3	1131.59	72.001	20479	2	566.30	-0.22
[Q8ZL56]GPMI_SALTY 2	9		DPATGQAHTAHTNLPVPLIYVGEK	452	24	5	19.19	b9b11b15y5°y5	2529.27	84.729	6081	3	843.76	-15.83
[Q8ZL56]GPMI_SALTY 2	10		KPMVLVILDGYGYR	5	14	3	24.48	b3b4y12	1623.91	101.826	5341	2	812.46	13.46
[Q8ZL56]GPMI_SALTY 2	11		TFFANPVLTNVAVDQAK	91	16	3	16.93	b7y5y9	1735.87	82.778	4906	2	868.44	-16.46
[Q8ZL56]GPMI_SALTY 2	12		GAEK	141	4	1	12.69	y3	404.21	29.961	3911	1	404.21	0.98
[Q8ZL56]GPMI_SALTY 2	13		ERTFFANPVLTNVAVDQAK	89	18	8	26.26	b12°b12°b12y4°y4y7y8°y8	2021.03	104.397	2840	2	1011.02	-7.13
[Q8ZL56]GPMI_SALTY 2	14	Oxidation+M(5)	AVHIMGLLSAGGVHSHEDHIMAMVELAAER	111	30	5	11.3	b5y8°y8y11°y11	3197.53	115.623	4625	3	1066.51	-12.22
[Q8ZL56]GPMI_SALTY 2	15	Oxidation+M(5)	AYDLMTLAQGEFQADTAVAGLQAAYARDENDEFVK	202	35	6	16.73	b4b7b9y10*y10y12	3837.84	131.438	2890	4	960.21	11.77
[Q8ZL56]GPMI_SALTY 2	16	Carbamidomethyl+C(1)	CIEQVTK	423	7	1	7.3	b5	877.45	61.144	6054	1	877.45	4.17
[P02906]SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQEIAAK	263	13	7	46.8	b10°b10y7y9y10y11y13	1468.73	50.532	38633	2	734.87	-0.58



[P02906]SUBI_SALTY Sulfate-binding protein	2		NVEVLDSGAR	183	10	5	51.48	b2y4y5y6y8	1059.54	39.990	23744	2	530.27	-6.34
[P02906]SUBI_SALTY Sulfate-binding protein	3		DIQLLNVSYPDTRELYEQYNK	20	21	5	21.41	b4b9b12*b12y11	2601.31	77.530	1931	2	1301.16	10.04
[P02906]SUBI_SALTY Sulfate-binding protein	4		GSTNTFVER	193	9	4	30.18	b5°b5b7y3	1010.50	38.337	9693	2	505.76	12.81
[P02906]SUBI_SALTY Sulfate-binding protein	5		QSHGGSGKQATSVINGIEADVVTL ALAYDVIDAIAER	58	36	4	23.08	b11°b11b12b19	3655.82	87.672	5741	5	731.97	-8.61
[P02906]SUBI_SALTY Sulfate-binding protein	6		NVEVLDSGARGSTNTFVER	183	19	3	14.74	b12b14y16	2051.03	91.500	3566	3	684.35	7.14
[P02906]SUBI_SALTY Sulfate-binding protein	7		DIQLLNVSYPDTRELYEQYNK	20	21	4	18.63	b3b12y4y8	2601.27	118.073	1504	3	867.76	-5.54
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	1		LNSAVFPSAQGGPLMHVIAGK	251	21	9	29.35	b2b4°b4*b4b11y3y4y15y2 1	2094.11	78.635	79024	3	698.71	-5.48
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	2		SPFVTSGIR	354	9	3	30.18	b3y5y6	963.52	49.301	46198	2	482.26	-6.97
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	3		VMQAQGSQLTNK	42	12	13	107.84	b3b5b10y2y3y4y7y8*y8y9 y10*y10y12	1304.66	29.551	43606	2	652.83	-2.81
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	4		EMNIADYDAELWQAMEQEK	4	19	6	21.7	y2y6y11°y11y13y19	2314.02	92.598	21741	2	1157.51	6.65
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	5		VYQQQVAK	285	8	7	40.56	b2y2y5y6*y6y7y8	963.52	19.506	20716	2	482.26	-7.28
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	6		MIIGGFSAYSGVVDWAK	168	17	8	49.18	b9°b9b10y8°y8y11y12y16	1800.89	103.432	15597	3	600.97	-3.46
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	7		AVALKEAMEPEFK	272	13	4	20.38	b1b11y5y11	1462.76	59.422	10449	2	731.88	-2.75
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	8	Carbamidomethyl+C(7)	ELAGWMCDVLDNINDEATIER	380	21	11	30.79	b2°b2b4y2y6°y6y7°y7y10* y10y13	2464.13	101.841	9887	2	1232.57	7.33
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	9		QEEHIELIASENYTSR	25	17	3	24.75	b9b11b12	2015.99	80.158	5150	2	1008.50	13.02
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	10	Carbamidomethyl+C(5)	VLDICAR	405	7	3	40.15	y4y5y6	846.44	44.649	42028	2	423.72	-15.86
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	11		NSVPNDPK	346	8	5	48.89	b5y5y6y7°y7	870.43	104.514	3625	1	870.43	-3.51
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	12		LYNIVPYGIDESGKIDYDEMAK	138	22	3	22.02	b3y17y18	2533.23	76.699	82680	3	845.08	6.46
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	13		NSVPNDPKSPFVTSGIR	346	17	6	33.56	b5b9y8y9°y9y14	1814.92	52.356	40314	3	605.64	-12.58
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	14		VMQAQGSQLTNKYAEGYPGK	42	20	4	30.45	y6y10y11y13	2170.09	108.968	1777	3	724.03	13.50
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	15	Oxidation+M(1)	MIIGGFSAYSGVVDWAK	168	17	6	29.58	b7°b7b10y12y13°y13	1816.91	66.681	12778	3	606.31	7.46
[P0A9Y9]CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	24	154.15	b2b3b4b5b6°b6b12y1y2°y2 y3°y3y4°y4y5y6°y6y7°y7y8 °y8y9y10y12	1196.59	64.325	594583	2	598.80	-4.18
[P0A9Y9]CC_SALTY Cold shock-like protein cC	2		DVVFHFSAIQNGGFK	27	15	4	31.46	b8b13y5y6	1665.82	74.349	72888	3	555.94	-11.07
[P0A9Y9]CC_SALTY Cold shock-like protein cC	3		GPAAVNVTAI	59	10	5	41.39	b2b3b7b9y10	912.51	59.556	27180	1	912.51	-4.15
[P0A9Y9]CC_SALTY Cold shock-like protein cC	4		TLAEGQNVEFEIQDGQK	42	17	4	22.59	b9b13y4y12	1905.92	74.037	1816	2	953.46	1.73
[P0A9Y9]CC_SALTY Cold shock-like protein cC	5		WFNESK	9	6	1	13.52	b3	810.39	106.580	4976	1	810.39	13.48
[P0A9Y9]CC_SALTY Cold shock-like protein cC	6		TLAEGQNVEFEIQDGQKGPAAVN VTAI	42	27	4	17.87	b3b11b22°b22	2799.42	75.968	80446	3	933.81	1.48
[P0A9Y9]CC_SALTY Cold shock-like protein cC	7		GFGFITPADGSKDVVFVHFSAIQGN GFK	15	27	4	25.1	b4b7y10y11	2843.39	88.933	32561	4	711.60	-9.02

[P0A9Y9]CC_SALTY Cold shock-like protein cC	8		DVFBVHFSAIQNGFGKTLAEGQNV EFEIQDQGQK	27	32	5	13.38	b5b8y3*y3y10	3552.78	116.449	9122	3	1184.93	11.00
[P0A9Y9]CC_SALTY Cold shock-like protein cC	9		GFITPADGSK	17	10	0	2.9		992.50	64.305	2486	1	992.50	-7.63
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	1		ELLTQMGQLYGHVADELATPSSAI LDIERK	174	30	4	11.3	b9y5y27y30	3298.66	129.241	29405	3	1100.23	-10.95
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	2	Carbamidomethyl+C(14)	ILNTASVIPVDGLCVR	252	16	8	51.32	b3y2y3y5y8°y8y9y11	1726.95	77.830	29355	2	863.98	-0.42
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	3		MKDDAIIILDVPNQDVITDGLNNG VK	103	26	4	21.79	b6b7y1y13	2810.46	86.338	27417	3	937.49	-1.56
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	4		GMVGSVLMQR	10	10	7	38.93	b5b7y2*y2y3y7y10	1077.55	59.026	17362	2	539.28	-0.11
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	5		ELLTQMGQLYGHVADELATPSSAI LDIER	174	29	6	21.93	b2b13y4y10y11°y11	3170.61	106.526	8355	3	1057.54	2.85
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	6		SGELPVDNFGVPLAGSLIPWIDK	210	23	4	12.89	b2b9b15y5	2424.27	111.569	5108	3	808.76	-4.53
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	7		ELTPAAVTGTLTTPVGR	315	17	3	16.1	b12y4y14	1683.94	68.588	23445	2	842.47	4.93
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	8	Carbamidomethyl+C(8)	ALDIIVTCQGGDYTNEIYPK	65	20	10	68.6	b3b4b9*b9b12*b12b13b15 y6y7	2270.06	96.808	22477	3	757.36	-19.79
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	9		LNMGPPEFLSAFTVGDQLWGAAE PLR	335	26	5	12.02	b9*b9b11°b11y4	2832.39	103.461	2916	3	944.80	-16.64
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	10	Carbamidomethyl+C(8)	ALDIIVTCQGGDYTNEIYPKLR	65	22	5	36.87	b11°b11b13b14b15	2539.28	99.371	4259	3	847.10	-2.02
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	11		GMVGSVLMQRMVEER	10	15	6	29.09	b6y3y4°y4y11°y11	1721.87	75.189	2482	2	861.44	11.49
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	12		VVPNDRDITMR	304	11	4	35.78	b6*b6b7b8	1315.67	119.897	1595	2	658.34	-6.59
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	13	Oxidation+M(2)	GMVGSVLMQR	10	10	4	26.62	b7y7*y7y9	1093.55	68.494	11860	2	547.28	-2.68
[P10370]HISX_SALTY Histidinol dehydrogenase	1		AGFSALASTIETLAAER	397	18	14	88.91	b2b8b14y1y4°y4y5y6y7°y7 y8°y8y11y12	1778.93	103.424	77838	2	889.97	2.74
[P10370]HISX_SALTY Histidinol dehydrogenase	2		NIETFHSAQTLPPVDVETQPGVR	93	23	6	33.21	b6b9b11°b11y11y12	2535.28	62.332	62481	3	845.77	0.00
[P10370]HISX_SALTY Histidinol dehydrogenase	3		VTPEEIAAAGAR	67	12	5	44.53	y6y8y9y10y12	1184.62	49.163	57449	2	592.81	-5.46
[P10370]HISX_SALTY Histidinol dehydrogenase	4	Carbamidomethyl+C(5)	DLAQCAISNQYGPEHLIQTR	311	22	6	20.59	b11*b11y10y14y16y22	2526.28	75.386	47829	3	842.77	3.19
[P10370]HISX_SALTY Histidinol dehydrogenase	5	Carbamidomethyl+C(11)	SFNTLIDWNSCSPEQQR	1	17	5	22.59	b3b12y3y5y17	2081.95	74.591	32463	2	1041.48	7.51
[P10370]HISX_SALTY Histidinol dehydrogenase	6	Carbamidomethyl+C(1)	CQQVTRPVSSVGLYPGGSAPLFS TVLMLATPAR	116	34	5	12.9	b2b3b9y14y19	3573.91	112.829	23446	3	1191.97	4.03
[P10370]HISX_SALTY Histidinol dehydrogenase	7		MTVQELSK	389	8	5	40.56	b4b5b7b8°b8	935.49	56.160	5467	2	468.25	4.05
[P10370]HISX_SALTY Histidinol dehydrogenase	8		TVSDILDNVK	34	10	4	38.93	b4b8y5y8	1103.59	60.646	26156	2	552.30	-6.75
[P10370]HISX_SALTY Histidinol dehydrogenase	9		LDGAAIDMPAGPSEVLVIADSGAT PDFVASDLLSQAHEGPDQSVILLT PDADIAR	224	55	26	195.73	b3b4b5b6b7b8b10b11b13° b13b14b15b16°b16b17y3y 5°y5y7y8y9°y9y10y11y14y 31	5541.73	113.168	13553	4	1386.19	-5.20
[P10370]HISX_SALTY Histidinol dehydrogenase	10		QVSQR	219	5	1	13.11	y3	617.33	70.232	8551	1	617.33	-3.46
[P10370]HISX_SALTY Histidinol dehydrogenase	11	Carbamidomethyl+C(42)	DLVDAITSAGSVFLGDWSPESAG DYASGTNHVLPPTYGTATCSSLG LADFQKR	336	53	3	12.08	b5b9y6	5568.61	99.148	44732	5	1114.53	-1.49
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTDSDAVGNAVK	84	17	9	53.16	b2b3b4b10b12y11y12y14y 17	1739.96	70.781	22721	2	870.48	2.03
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	2		DTIALVISTLNNPFFVSLKDGAQK EADK	26	28	6	33.16	y1y5y8y12y13y25	3034.58	114.523	15365	4	759.40	-11.18

[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	3		LVIK	291	4	1	12.69	y3	472.35	56.989	24701	1	472.35	-5.81
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	4		DGAQK	45	5	1	13.11	y4	518.26	35.507	20756	1	518.26	8.83
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	5		YPVDLK	285	6	2	26.63	b4b5	734.41	73.028	11653	1	734.41	8.14
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	6		GDVVSHIASDNVLGGK	119	16	4	27.33	b5y7y9y14	1567.84	68.602	8455	2	784.42	19.93
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	7		IAGDYIAK	135	8	3	40.56	y4y6y7	850.45	35.781	4123	2	425.73	-22.10
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	8		FNVLASQPADFDRTK	178	15	3	17.9	b7y8y12	1708.86	92.523	6142	2	854.93	-1.64
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	9		ERGEGFQQAFAAHK	164	14	4	30.38	b10y3y12y13	1527.76	90.773	2897	2	764.38	-2.64
[P55900]SERC_SALTY Phohoserine aminotransferase	1		AQVFNFSSGPAMLPAEVLK	1	19	11	71.25	b2b3b12b13b17y3y6y13y14y15y19	2006.05	91.467	43991	2	1003.53	5.42
[P55900]SERC_SALTY Phohoserine aminotransferase	2		AELLYGVIDNSDFYR	272	15	5	29.09	b3b5b11*b11y12	1774.85	77.572	3869	3	592.29	-8.18
[P55900]SERC_SALTY Phohoserine aminotransferase	3		ALTFDMIDFERR	348	12	5	35.23	b5b6b7*b7b12	1513.75	116.040	2071	2	757.38	2.66
[P55900]SERC_SALTY Phohoserine aminotransferase	4		ASIYNAMPIEGVK	335	13	5	25.15	b6*b6y7y8*y8	1392.74	76.368	6459	2	696.87	15.78
[P55900]SERC_SALTY Phohoserine aminotransferase	5	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	3	23.15	b9b11b12	2567.18	118.976	6394	3	856.40	-11.03
[P55900]SERC_SALTY Phohoserine aminotransferase	6		MAQVFNFSSGPAMLPAEVLK	0	20	4	22.32	b4b8b16y14	2137.12	90.156	6374	2	1069.06	16.11
[P55900]SERC_SALTY Phohoserine aminotransferase	7		MNVPFQLADNTLDK	297	14	3	19.04	b6b11y3	1605.79	75.421	2894	2	803.40	-4.71
[P55900]SERC_SALTY Phohoserine aminotransferase	8		EFIQVAEEAEQDFR	44	14	7	56.13	b6b8*b8b10b13y6y11	1710.83	125.987	1757	3	570.95	16.63
[P55900]SERC_SALTY Phohoserine aminotransferase	9	Carbamidomethyl+C(4)	VLFCGGGGR	68	9	3	37.96	y5y7y8	1002.48	120.417	1573	1	1002.48	-15.10
[P55900]SERC_SALTY Phohoserine aminotransferase	10	Carbamidomethyl+C(3)	KYCAPQIIDAK	111	11	4	24.02	b5b10y10*y10	1306.69	47.885	12039	2	653.85	8.97
[P55900]SERC_SALTY Phohoserine aminotransferase	11	Carbamidomethyl+C(4)	VLFCGGGGRQFAGVPLNLLGDK	68	23	5	36.97	b4b5b7b10b15	2412.24	92.609	10675	2	1206.63	-7.19
[P55900]SERC_SALTY Phohoserine aminotransferase	12	Carbamidomethyl+C(14)	DLNIPSNYKVLFCGGGGR	58	19	3	14.74	b4y5y11	2160.11	84.995	2687	2	1080.56	1.92
[P55900]SERC_SALTY Phohoserine aminotransferase	13		AELLYGVIDNSDFYRNDVAQANR	272	23	6	21.93	b13*b13*b13y13y14*y14	2643.27	79.462	2050	2	1322.14	-2.31
[P55900]SERC_SALTY Phohoserine aminotransferase	14		ASIYNAMPIEGVKALTFDMIDFER	335	24	5	16.61	b8*b8b12y5y7	2731.37	118.172	1544	3	911.13	10.19
[Q7CPL5]RL14_SALTY 50S ribosomal protein L14	1		MIQEQTMLNVADNSGAR	0	17	18	108.43	b2b3b5b7b12b13*b13b17y1y5y6y7y8y9*y9*y9y12y17	1877.89	58.922	101865	2	939.45	4.94
[Q7CPL5]RL14_SALTY 50S ribosomal protein L14	2		IISLAPEVL	114	9	4	30.18	b5y4y5y9	954.58	85.460	67128	1	954.58	-5.18
[Q7CPL5]RL14_SALTY 50S ribosomal protein L14	3		IQEQTMLNVADNSGAR	1	16	12	59.28	b3*b3*b3b5*b5b7*b7b9y1y7y8y11	1746.85	94.652	14982	2	873.93	1.75
[Q7CPL5]RL14_SALTY 50S ribosomal protein L14	4		IFGPVTR	98	7	3	40.15	y3y5y6	789.45	45.063	91775	2	395.23	-18.25
[Q7CPL5]RL14_SALTY 50S ribosomal protein L14	5	Carbamidomethyl+C(6)	FDGNACVILNNSEQPIGTR	78	20	4	24.95	b7y3y11y12	2219.07	59.083	15437	2	1110.04	6.71
[Q7CPL5]RL14_SALTY 50S ribosomal protein L14	6	Carbamidomethyl+C(3)	VMCIK	18	5	3	39.32	b3y3y4	650.33	40.149	12763	1	650.33	-11.92
[Q7CPL5]RL14_SALTY 50S ribosomal protein L14	7	Oxidation+M(1)	MIQEQTMLNVADNSGAR	0	17	9	42.19	b8b10*b10y6y9*y9y10*y10y13	1893.90	121.317	5509	2	947.46	13.34
[Q7CPL5]RL14_SALTY 50S ribosomal protein L14	8	Oxidation+M(7)	MIQEQTMLNVADNSGARR	0	18	4	21.42	b4b10y7y13	2049.98	68.439	4402	2	1025.49	0.95

Q7CPP7 RL21_SALTY 50S ribosomal protein L21	1		MYAVFQSGGK	0	10	7	39.72	b2b3y1y3y4y7y10	1087.52	52.437	78089	2	544.26	-6.96
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	2		VSEGTQTVR	13	8	5	40.56	b2y5y6y7y8	875.45	16.161	4669	2	438.23	-3.83
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	3		IGVPFVDGGVIK	48	12	3	29.21	y5y6y8	1200.69	77.010	35715	2	600.85	-6.91
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	4		QQGHRQWFTDVK	85	12	3	29.21	y6y7y11	1529.75	70.688	21482	2	765.38	-6.78
P26982 DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	8	33.04	b1b3°b3y1y3y7y9y15	2017.09	75.014	25865	3	673.03	-11.01
P26982 DEGP_SALTY Protease do	2		NLTSQMVEYGVVK	275	13	7	40.85	b5b6b11y9y11°y11y13	1496.74	57.959	24870	2	748.88	1.14
P26982 DEGP_SALTY Protease do	3		GAFVSQVMPNSSAAK	313	15	9	43.44	b3y1y2y7y8y9y11°y11y15	1493.74	53.243	17199	2	747.38	0.82
P26982 DEGP_SALTY Protease do	4		SDIALIQINPK	160	12	4	35.23	b2b3b4b5	1339.76	63.998	16417	2	670.38	-0.73
P26982 DEGP_SALTY Protease do	5		VGDYTVAIGNPFLGETVTSGIVS ALGR	186	28	8	35.71	b3b7b8y3y5°y5y6y28	2750.41	116.497	11315	3	917.48	-7.99
P26982 DEGP_SALTY Protease do	6		SGLNVENYENFIQTDAAINR	214	20	5	22.32	b3b5°b5b13y5	2268.11	77.592	7246	2	1134.56	8.18
P26982 DEGP_SALTY Protease do	7		VMPSVVSINVEGSTTVNTPR	48	20	3	14.19	b3b9y12	2087.08	64.688	6816	3	696.37	1.99
P26982 DEGP_SALTY Protease do	8		AQVGTMPVGSK	352	11	9	81.12	y3°y3y5y6y8°y8y9y10*y10	1074.55	34.532	13790	2	537.78	-5.79
P26982 DEGP_SALTY Protease do	9		GELGIMGTELNSELAK	289	16	4	28	b3b4b7y8	1661.81	46.015	2577	2	831.41	-21.67
P26982 DEGP_SALTY Protease do	10	Oxidation+M(39)	GNSGGALVNLNGELIGINTAILAP DGGNIGIGFAIPSNMVK	234	41	5	11.86	b8°b8b14y4y8	3965.06	103.567	6316	3	1322.36	-5.73
P26982 DEGP_SALTY Protease do	11		GAFVSQVMPNSSAAK	313	15	0	4.15		1476.73	53.229	4772	2	738.87	12.73
P67093 UG_SALTY Universal stress protein G	1		TIIMPVDVFEMELSDK	3	16	7	34.98	b2b3b12y6y12y13y16	1866.93	104.659	55664	2	933.97	5.56
P67093 UG_SALTY Universal stress protein G	2		NPSITHTLLGSNASSVVR	114	18	5	34.29	b5°b5b6b7°b7	1852.97	59.150	29118	3	618.33	-10.28
P67093 UG_SALTY Universal stress protein G	3		LQTMVGHFSDPSR	69	14	3	19.04	b12y8y12	1587.77	64.811	50905	3	529.93	-13.99
P67093 UG_SALTY Universal stress protein G	4		DVVNEMGEELDADVVVIGSR	94	20	5	14.19	b3b5°b5°b5y14	2146.06	91.958	4285	2	1073.54	14.68
P67093 UG_SALTY Universal stress protein G	5	Oxidation+M(11)	TIIMPVDVFEMELSDK	3	16	5	40.85	b11b12y3y5y10	1882.94	77.492	2231	3	628.32	12.77
Q08016 OTC_SALTY Ornithine carbamoyltransferase	1	Carbamidomethyl+C(2); Carbamidomethyl+C(12)	ACWPQAALVAECSAMAKK	190	18	6	15.37	b1b13y7y10°y10y18	1991.93	74.692	24426	3	664.65	-9.25
Q08016 OTC_SALTY Ornithine carbamoyltransferase	2	Carbamidomethyl+C(4)	FLHCLPAFHDDETTLGKK	270	18	4	9.32	b3b10°y9°y9	2129.06	117.003	16977	3	710.36	4.01
Q08016 OTC_SALTY Ornithine carbamoyltransferase	3		DYQVNSQMMALTGNPQVK	252	18	9	67.06	b5b12b14y4y8y11y13y16y18	2023.97	64.937	15639	2	1012.49	5.25
Q08016 OTC_SALTY Ornithine carbamoyltransferase	4		AFNEMTLVYAGDAR	152	14	9	53.12	b9b13y2y3°y3y5y6y7y14	1557.76	69.640	14159	2	779.38	12.85
Q08016 OTC_SALTY Ornithine carbamoyltransferase	5		GADFIYTDVWVSMGEPKEK	224	19	3	22.52	b12b13y8	2172.04	102.360	2773	3	724.69	5.17
Q08016 OTC_SALTY Ornithine carbamoyltransferase	6		GADFIYTDVWVSMGEPK	224	17	3	16.1	b4y4y9	1914.90	97.195	2188	3	638.97	4.97
Q08016 OTC_SALTY Ornithine carbamoyltransferase	7	Carbamidomethyl+C(2); Carbamidomethyl+C(12)	ACWPQAALVAECSAMAK	190	17	4	16.1	b12°b12y6y14	1863.87	73.307	17663	2	932.44	5.89
Q08016 OTC_SALTY Ornithine carbamoyltransferase	8	Carbamidomethyl+C(4)	FLHCLPAFHDDETTLGK	270	17	3	16.1	b4b9y10	2001.00	79.692	4453	3	667.67	21.47
Q08016 OTC_SALTY Ornithine carbamoyltransferase	9		VTYLGSSGSQIGHK	73	14	5	31.17	b3y4y9°y9y11	1433.72	45.609	1828	2	717.36	-12.60
Q08016 OTC_SALTY Ornithine carbamoyltransferase	10	Oxidation+M(13)	GADFIYTDVWVSMGEPK	224	17	4	25.82	b5y7y10y12	1930.90	105.076	3293	2	965.96	7.40
Q08016 OTC_SALTY Ornithine carbamoyltransferase	11		QVNSQMMALTGNPQVK	254	16	0	5.39		1745.85	64.991	27025	2	873.43	-11.12

P63411 ACKA_SALTY Acetate kinase	1	Carbamidomethyl+C(7)	LVLVLNCGSSSLK	4	13	5	38.84	b3b4y2y8y9	1389.76	67.086	49930	2	695.39	-9.31
P63411 ACKA_SALTY Acetate kinase	2		EGTRPAVVIPTNEELVIAQDASR	374	23	11	78.07	b8b9y4y5°y5*y5y6y7y8y14y23	2465.29	69.036	42153	3	822.44	-1.98
P63411 ACKA_SALTY Acetate kinase	3	Carbamidomethyl+C(19)	FAIDAVNGDEYLSGLAECFHLPEAR	17	26	6	12.02	b2b3y2y4y9y26	2907.39	104.806	40068	3	969.80	-1.60
P63411 ACKA_SALTY Acetate kinase	4		LDAVVFTGGIGENAAMVR	324	18	4	24.5	b4b8b12y6	1819.94	89.704	4731	2	910.47	0.07
P63411 ACKA_SALTY Acetate kinase	5		ELSLGKLGVLGFVDHER	342	18	3	22.78	b3y4y5	1998.06	68.494	4457	3	666.69	-5.19
P63411 ACKA_SALTY Acetate kinase	6	Oxidation+M(16)	LDAVVFTGGIGENAAMVR	324	18	4	15.37	b4y11y14°y14	1835.93	99.481	6878	3	612.65	-3.32
P63411 ACKA_SALTY Acetate kinase	7	Oxidation+M(9)	YIGSYTALMDGR	312	12	3	29.21	b3b4b6	1362.63	72.979	1676	1	1362.63	-2.06
P0A7V6 RS3_SALTY 30S ribosomal protein S3	1		VVADIAGVPAQINIAEVRKPELDAK	89	25	4	26.95	y3y5y11y17	2616.43	70.900	39653	4	654.86	-14.46
P0A7V6 RS3_SALTY 30S ribosomal protein S3	2		LVADSITSQLER	114	12	11	78.52	b2y5y6y8y9°y9y10°y10y11y12*y12	1331.71	60.492	38538	2	666.36	-1.83
P0A7V6 RS3_SALTY 30S ribosomal protein S3	3		ADIDYNTSEAHTTYGVIGVK	179	20	5	22.32	b2b3b4y11y20	2154.03	56.281	27345	3	718.68	-4.19
P0A7V6 RS3_SALTY 30S ribosomal protein S3	4		GEILGGMAAVEQPEKPAAQPK	204	21	6	39.2	b3°b3b4b6b8b12	2121.11	97.857	36072	3	707.71	5.76
P0A7V6 RS3_SALTY 30S ribosomal protein S3	5		LGIVKPWNSTWFANTK	11	16	5	30.45	b12b13y10y13°y13	1862.01	113.197	1991	3	621.34	5.90
P0A7V6 RS3_SALTY 30S ribosomal protein S3	6		LGGAEIARTEWYR	156	13	3	25.15	b11y3y4	1521.76	69.588	3635	2	761.38	-14.12
P0A7V6 RS3_SALTY 30S ribosomal protein S3	7		LVADSITSQLER	114	12	0	2.9		1314.68	60.465	24808	2	657.85	-2.04
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	1		TDGLMPAIVQHAVSGEVLM LGY MNPQALDK	14	30	5	11.3	b12y11y27°y27y30	3198.59	136.544	16770	4	800.40	-2.44
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	2		TADPTSSYTAK	126	11	8	51.99	b1b3b8y7y8y9°y9y11	1141.54	26.487	15392	2	571.27	-1.28
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	3		TIESGHVTFFSR	44	12	3	22.01	b7y9y11	1380.69	97.522	23089	2	690.85	1.59
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	4		VGEEGVETALAATVNDR	149	17	4	16.1	b4b7y5*y5	1730.86	124.071	2383	2	865.93	2.12
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	5		ELDWEK	8	6	2	13.52	y3°y3	819.39	84.339	2297	1	819.39	6.85
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	6		IAQKVGEEGVETALAATVNDR	145	21	4	13.7	b11y4y7*y7	2171.13	67.609	77834	3	724.38	1.12
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	7		KTADPTSSYTAK	125	12	3	22.01	b7b9y10	1269.62	79.656	21389	2	635.31	-12.98
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	8	Oxidation+M(23)	TDGLMPAIVQHAVSGEVLM LGY MNPQALDK	14	30	7	24.45	b11b14°b14y7y10*y10y11	3214.60	115.602	2513	3	1072.20	0.76
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	1		TFDTPPTYNSLALSADGK	308	18	4	15.37	b4y11y14y18	1897.92	65.434	28931	2	949.47	2.89
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	2		EQEATQPDDVIR	338	12	6	68.43	y3y4y6y8y10°y10	1400.67	39.192	23712	2	700.84	1.74
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	3		LLDDGKEHFFINLSLDTAGHR	223	21	6	13.7	b7y1y7°y7y13y21	2398.19	82.583	23132	2	1199.60	-8.96

Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	4		LYTTNADGEFTIDTASNK	198	19	6	25.56	b11°b11y6y13y14y19	2074.00	65.320	13281	2	1037.50	1.65
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	5		ELVADAATNTIYISGVGK	144	18	4	24.29	b6b13°b13b14	1821.95	73.181	30053	3	607.99	-7.64
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	6		AQRLYTTNADGEFTIDTASNK	195	22	9	39.24	b5b14°*b14b15°b15y5y7y8° y8	2429.21	93.593	6765	2	1215.11	8.24
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	7		DDGKEHFFINLSLDTAGHR	225	19	2	7.7	b15°b15	2172.08	82.531	1882	3	724.70	13.60
P67179 YEBC_SALTY UPF0082 protein yebC	1		LGGGDPDANPR	37	11	7	81.12	b2y4y5y6y7y9y10	1068.50	22.634	20240	2	534.75	-8.23
P67179 YEBC_SALTY UPF0082 protein yebC	2		ADMDAETAPK	205	10	4	33.61	y2y4y6y7	1048.46	25.038	12082	2	524.73	-0.47
P67179 YEBC_SALTY UPF0082 protein yebC	3	Carbamidomethyl+C(1)	CGGNLGTGDSVAYLFSK	119	17	5	23.09	b14°*b14y11y12°y12	1745.82	86.700	3652	2	873.41	0.35
P67179 YEBC_SALTY UPF0082 protein yebC	4		ELVTAAKLGGGDPDANPR	30	18	4	26.26	b16y8y9y12	1780.92	79.449	724801	3	594.31	-1.44
P67179 YEBC_SALTY UPF0082 protein yebC	5		DALEAAGLKADSAEVSMPSTK	183	22	5	20.59	b3b6b12°b12y4	2204.10	67.724	18281	3	735.37	-4.98
Q8ZRP3 DXR_SALTY 1-deoxy-D-xylulose 5-phohate reductoisomerase	1	Carbamidomethyl+C(11)	VTSGAQPLDFCK	289	12	7	60.65	b2y5y6y7°y7y10y11	1322.63	54.621	33096	3	441.55	-8.31
Q8ZRP3 DXR_SALTY 1-deoxy-D-xylulose 5-phohate reductoisomerase	2		ISVDSATMMNK	217	11	4	27.03	b5y3y4y11	1196.57	70.498	2839	3	399.53	8.16
Q8ZRP3 DXR_SALTY 1-deoxy-D-xylulose 5-phohate reductoisomerase	3		HPNWSMGR	208	8	3	40.56	y3y4y7	984.47	59.022	10790	2	492.74	21.58
Q8ZRP3 DXR_SALTY 1-deoxy-D-xylulose 5-phohate reductoisomerase	4		QMEVLIHPQSVIHSMVR	244	17	5	35.7	b3b5b9b10y4	2004.02	72.061	5034	2	1002.52	-13.64
Q8ZRP3 DXR_SALTY 1-deoxy-D-xylulose 5-phohate reductoisomerase	5		IMLQQHGSR	66	9	4	30.18	b5°*b5y4y5	1069.54	14.366	3554	2	535.27	-19.74
Q8ZRP3 DXR_SALTY 1-deoxy-D-xylulose 5-phohate reductoisomerase	6		YQDGSVLAQLGEPDMRTPIAHTM AWPNR	261	28	6	14.69	b10b13°*b13y3°*y3y6	3154.49	102.596	16919	4	789.38	-7.97
Q8ZRP3 DXR_SALTY 1-deoxy-D-xylulose 5-phohate reductoisomerase	7		YAVMDDTSSAEQLKIMLQQHGSR	52	23	4	19.85	b3y5y7y20	2608.29	76.282	8588	4	652.83	14.23
Q8ZRP3 DXR_SALTY 1-deoxy-D-xylulose 5-phohate reductoisomerase	8	Oxidation+M(2)	QMEVLIHPQSVIHSMVR	244	17	3	23.09	b10b11y11	2020.06	80.895	6499	3	674.02	4.89
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	1		SPDIPSILVETGFISNHGEER	366	21	8	21.41	b1b2b4b7b13y1y6°*y6	2297.14	120.593	10497	3	766.38	-2.34
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	2		VESAPRPTEPAR	140	12	8	25.99	b2b5°b5y1y3y4°y4y12	1309.69	12.490	5815	3	437.23	0.56
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	3		QSELLGGAGDVLANSQSDPYLSQ AVLDLQFGHSQR	298	35	6	36.4	b9b14°*b14b15b16°*b16	3700.77	116.139	3257	3	1234.26	-14.58
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	4		DAQSLR	91	6	2	13.52	y4°y4	689.36	36.682	6113	1	689.36	5.67
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	5	Carbamidomethyl+C(11)	NAVIAALILLCAQAGAASLSDIQVS NGEQAR	6	32	5	21.53	b3y4°*y4y5y8	3252.64	107.401	5489	3	1084.89	-17.41

P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	6		QNaNFLVSIHADAAPNR	253	17	5	25.82	b5y6*y6y12y14	1837.90	79.285	3683	2	919.45	-18.20
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	7		VGYDVATNVLSQLDGVGSLHK	333	21	4	35.54	b13b14y11y12	2172.08	105.926	2237	3	724.70	-21.69
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	8		YQQQIADAIYRGLR	393	14	4	27.61	b6b8°b8b12	1694.88	126.011	9352	2	847.94	-9.29
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	9		SSDDRLTGVTSSNTVTRPAAR	156	21	4	30.52	b7b9b11b15	2191.09	82.697	4150	3	731.04	-5.57
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	10		RANSEMANWLEQHEK	283	15	8	36.63	b5b11y4°y4y8°y8y9°y9	1842.88	127.142	1821	2	921.94	10.93
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	11	Phosphoryl STY(20)	YFAAHPIQSAPQGGPGQTASTNQP GAITAA	408	31	6	24.12	b6b12°b12y10y11y13_H3P O4 y13	3103.41	118.267	11926	2	1552.21	-3.07
P26366 AMIB_SALTY N-acetylmuramoyl-L-alanine amidase amiB	12	Oxidation+M(14)	GVLTRDGDYFISVMGR	231	16	4	27.33	b13y3y5y8	1801.91	90.030	3291	2	901.46	11.72
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	1		TVVADGIGQGYK	55	12	9	47.54	b1b2y5y6y8*y8y9°y9y12	1207.61	31.641	73995	2	604.31	-14.25
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	2	Carbamidomethyl+C(10)	YVIDELDQICQRDR	77	14	6	46.34	b6b8y2y5y6y7	1822.89	81.958	40016	3	608.30	6.16
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	3	Carbamidomethyl+C(10)	YVIDELDQICQR	77	12	8	49.68	b9b11y8°y8°y8y9y10y12	1551.77	68.164	13357	2	776.39	11.72
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	4		HLESVVANKISEIADLDK	105	19	3	22.52	b3y9y10	2110.10	85.375	21668	3	704.04	-3.59
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	5	Carbamidomethyl+C(10)	YVIDELDQICQRDR	77	14	4	19.04	b10y9°y9y11	1822.87	55.183	10420	2	911.94	-4.42
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	6		TVVADGIGQGYK	55	12	0	2.9		1189.60	31.667	2126	3	397.21	-12.31
P66955 TALB_SALTY Transaldolase B	1		LYQPQDATTNPSLILNAAQIPEYR	25	24	9	32.07	b4b7b9b13*b13y2y4y7y24	2716.39	81.463	11894	3	906.13	-2.88
P66955 TALB_SALTY Transaldolase B	2		LYNDAGISNDR	117	11	5	36.34	b7y4y9*y9y10	1237.59	35.846	10596	2	619.30	3.65
P66955 TALB_SALTY Transaldolase B	3	Carbamidomethyl+C(2)	ACAEAGVYLISPFVGR	165	16	3	16.93	b10b15y6	1709.88	86.765	10054	2	855.44	7.85
P66955 TALB_SALTY Transaldolase B	4		DYAPAEDPGVVSVTEIYEYYK	193	21	5	40.49	b11b12b13y4y6	2408.13	92.680	6944	3	803.38	6.79
P66955 TALB_SALTY Transaldolase B	5		KDYAPAEDPGVVSVTEIYEYYK	192	22	4	13.27	b4b15°b15y5	2536.22	91.510	1933	4	634.81	4.43
P66955 TALB_SALTY Transaldolase B	6		LSYDTEASIAK	100	11	3	35.78	y7y8y9	1197.60	44.194	12708	2	599.30	-0.82
P66955 TALB_SALTY Transaldolase B	7		ILDWYK	181	6	1	13.52	b5	837.45	57.476	3271	2	419.23	-5.76
P66955 TALB_SALTY Transaldolase B	8		LIDDAVAWAK	50	10	4	26.62	b4°b4b8y3	1101.59	71.871	3032	2	551.30	-1.33
P66955 TALB_SALTY Transaldolase B	9		LIDDAVAWAKQSSDR	50	16	3	16.93	b5b8y5	1802.90	79.426	56179	3	601.64	0.74
P66955 TALB_SALTY Transaldolase B	10		QQSSDRAQQVVDATDK	60	16	3	24.64	y8y11y15	1775.88	74.907	7410	2	888.44	14.64
P66955 TALB_SALTY Transaldolase B	11		AEAGVYLISPFVGR	167	14	2	14.24	b9b12	1478.79	86.790	6278	3	493.60	-7.84
P0A2B3 RS7_SALTY 30S ribosomal protein S7	1		FVNILMVDGKK	25	11	9	64.31	b3b5b9°b9y3y4y7y11*y11	1263.69	67.346	110486	3	421.90	-14.30
P0A2B3 RS7_SALTY 30S ribosomal protein S7	2		STAESIVYSALETLAQR	36	17	14	57.35	b3°b3b7b15°b15y1y2*y2y3 y5y6°y6y7y17	1838.93	107.333	32977	3	613.65	-11.15

P0A2B3 RS7_SALTY 30S ribosomal protein S7	3		FGSELLAK	17	8	4	56.68	y3y4y6y7	864.47	51.637	129078	2	432.74	-18.00
P0A2B3 RS7_SALTY 30S ribosomal protein S7	4		WIVEAAR	102	7	4	53.25	y3y4y5y6	844.45	50.505	91397	2	422.73	-15.18
P0A2B3 RS7_SALTY 30S ribosomal protein S7	5		NALAMR	96	6	3	39.73	y3y4y5	675.35	35.945	5484	1	675.35	-9.31
P0A2B3 RS7_SALTY 30S ribosomal protein S7	6		ILPDPK	11	6	1	13.52	y4	682.41	32.378	2097	1	682.41	-1.88
P0A2B3 RS7_SALTY 30S ribosomal protein S7	7		RVGGSTYQVPVEVRPVR	78	17	3	24.75	b6b7b9	1899.04	50.519	88775	3	633.68	-9.26
P0A2B3 RS7_SALTY 30S ribosomal protein S7	8		SGKSELEAFEVALENVRPTVEVK	53	23	3	22.98	b7b9b10	2531.31	91.191	5763	4	633.58	-11.48
P0A2B3 RS7_SALTY 30S ribosomal protein S7	9		MAEANKAFAHYR	143	12	3	22.01	b4b9y3	1408.68	57.460	1615	2	704.84	1.65
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	1		LAEAGIPTQMER	60	12	12	86.95	b2b3b4b6°b6y6y8y9y10°y10y11y12	1315.66	49.802	72717	2	658.34	-1.95
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	2		TVYSTENPDLLVLEFR	13	16	11	45.38	b1b4°b4b7b12*b12y1y3°y3y4y9	1895.98	88.668	58577	2	948.49	3.61
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	3	Carbamidomethyl+C(7)	LLSDTECLVK	72	10	5	51.48	y3y4y5y8°y8	1177.61	53.359	42368	2	589.31	-5.91
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	4		LWDK	199	4	2	12.69	y3°y3	561.31	31.172	15151	1	561.31	9.13
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	5		ETLDK	203	5	1	13.11	y4	605.32	48.325	14040	1	605.32	14.22
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	6		GMVNNKFNFHIMTK	46	14	3	19.04	b7b10y3	1680.82	101.661	33650	3	560.95	-6.61
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	7		TVYSTENPDLLVLEFRNDTSAGD GAR	13	26	7	39.48	b3b4y3y5°y5y7y23	2840.37	80.613	13477	3	947.46	-1.03
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	8		GEVVLGDEFSPDGSRWLWDK	184	19	4	14.74	b5b9°b9y8	2106.04	77.221	6049	3	702.68	12.17
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	9		FNHFIMTKLAEAGIPTQMER	52	20	5	19.46	b4b15y5°y5y7	2334.21	41.595	2802	3	778.74	14.64
P25924 CYSG_SALTY Siroheme synthase	1	Carbamidomethyl+C(4)	DRDCLIVGGGDVAER	11	15	4	25.98	b6°b6b7b9	1631.78	47.098	17447	2	816.39	-2.99
P25924 CYSG_SALTY Siroheme synthase	2		GLQQIQQADIVVYDR	234	15	3	25.98	b6b9b14	1745.93	87.854	8602	2	873.47	4.33
P25924 CYSG_SALTY Siroheme synthase	3		AVNATTER	198	8	3	32.78	b4y6y7	861.44	24.732	6928	2	431.22	-2.27
P25924 CYSG_SALTY Siroheme synthase	4		LIAFGMQADMPVALVENGTSVK	393	22	4	23.15	b1b11b12b14	2291.19	101.617	4119	2	1146.10	5.22
P25924 CYSG_SALTY Siroheme synthase	5		QTLVFYMGLENQAATIQEK	375	18	4	24.29	b7b8°b8b12	2055.05	115.358	1700	3	685.69	-5.35
P25924 CYSG_SALTY Siroheme synthase	6		LFSEPLDHR	206	9	3	30.18	b5b8y8	1113.56	111.433	1702	1	1113.56	-12.17
P25924 CYSG_SALTY Siroheme synthase	7		LAQSLANADEKAVNATTER	187	19	4	20.39	b6b11y4y13	2002.03	53.402	16247	2	1001.52	3.66
P25924 CYSG_SALTY Siroheme synthase	8		FWEKFFVNDR	177	10	5	28.38	b8°b8b9y6*y6	1387.66	62.993	7671	2	694.33	-12.58
P25924 CYSG_SALTY Siroheme synthase	9	Carbamidomethyl+C(3)	IFCNVVDAPKAASFIMPSIIDR	97	22	7	30.27	b5b7b10°b10*b10b13y3	2464.26	136.321	7660	3	822.09	-4.06



P25924 CYSG_SALTY Siroheme synthase	10	Carbamidomethyl+C(8); Carbamidomethyl+C(15) ;Oxidation+M(1)	MDHLPIFCQLRDRDCLIVGGGDV AER	0	26	4	18.16	y5y7°y7y9	3058.43	118.364	2406	2	1529.72	-11.34
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1		VTLEPLER	25	8	6	53.67	y1y3y4y5y6y8	956.53	52.170	60922	2	478.77	-13.02
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2	Carbamidomethyl+C(6)	LLVDACYPVER	170	12	11	94.64	b2y5y6°y6y7y8y9y10y11°y 11y12	1421.71	59.245	57607	2	711.36	0.00
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3		IHSEEDERPIGR	158	12	6	49.19	b3°b3b4b5b9y7	1437.72	66.022	32273	2	719.36	5.01
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4		AEAIHYIGDLVQR	271	13	3	25.15	b7b8y3	1484.81	77.673	18263	2	742.91	14.96
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5		QPEVK	238	5	1	13.11	b4	600.33	70.759	6355	1	600.33	-5.69
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6	Carbamidomethyl+C(4)	SANCLK	265	6	1	13.52	b3	692.34	97.997	3742	1	692.34	6.61
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		GRGYVPASTR	148	10	3	28.38	b6y5y6	1063.55	74.502	10894	2	532.28	-12.85
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8		GYVPASTRIHSEEDERPIGR	150	20	4	19.46	b11b17y6y11	2269.13	69.250	8612	3	757.05	-0.22
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	1		DLPLIASNFR	83	10	4	36.62	b2y4y5y6	1145.62	76.032	21469	2	573.32	-6.93
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	2		AFPGLNGMDLAK	148	12	7	33.86	b6*b6y6y9y10*y10y12	1233.62	72.030	19718	2	617.32	-4.55
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	3		NVVMITAQNHGFAVDEDSL PANL R	302	24	6	12.56	b1b11b14*b14y10°y10	2611.29	82.819	9113	3	871.10	-0.93
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	4	Carbamidomethyl+C(6)	GAQNGCIIAGDSPDAK	125	16	4	16.93	b13y11y13y16	1573.73	37.844	8564	2	787.37	1.16
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	5	Carbamidomethyl+C(18)	MNPDGIFLSNGPGDPAPCDYAITA IQK	230	27	11	36.76	b2b8b9b12b14°b14b16y11 y13*y13y27	2862.35	82.915	6167	2	1431.68	1.36
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	6		SEDDLPHFVVAYDFGAKR	185	18	4	22.78	b11°b11y7y8	2066.01	69.655	3625	3	689.34	4.02
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	7	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLALASGAK	257	25	9	54.53	b3b5b6b13y4y5y7y14y19	2684.44	128.509	121287	3	895.49	-2.73
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	8		SALLVLEDGTQFHGR	3	15	5	31.46	b7b14*b14y8y9	1642.87	125.108	30174	2	821.94	10.48
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	9		WTQGSWTLK	169	9	4	30.18	b3b4y8*y8	1106.58	34.549	7439	2	553.79	12.58
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	10		AIGATGSAVGEVVFNTSMTGYQEI LTDPSYSR	18	32	8	30.03	b4b8°b8b13b15°b15b16y2 6	3321.59	109.972	1728	3	1107.87	-0.59
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	11		EVTTAETRYRWTQGSWTLK	160	18	5	40.24	b4b6b7b8y13	2157.07	82.569	20657	2	1079.04	4.19
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	12	Carbamidomethyl+C(8)	EKGAQNGCIIAGDSPDAK	123	18	3	22.78	b13b14y10	1830.89	78.641	8558	2	915.95	13.60
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	13	Oxidation+M(18)	AIGATGSAVGEVVFNTSMTGYQEI LTDPSYSR	18	32	3	11.08	b8y3y8	3337.59	129.207	2430	3	1113.20	0.37
P14845 CARA_SALTY Carbamoyl- phohate synthase small chain	14		NVVMITAQNHGFAVDEDSL PANL R	302	24	0	7.88		2594.24	82.800	5731	2	1297.62	-9.69
Q8ZRM7 DKGB_SALTY 2	1		ENLASSLLAQDLHLDAEDK	225	19	6	31.21	b5°b5b14y7y8y12	2082.06	78.676	6267	2	1041.53	11.02
Q8ZRM7 DKGB_SALTY 2	2		AIAAVGADNIATNQIELSPYLQNR	138	24	4	16.61	b12b14y5y8	2542.34	99.770	5161	3	848.12	6.05

Q8ZRM7 DKGB_SALTY 2	3		AVDTAQIYDNEAAVGQAIAESGV PR	31	25	4	12.27	b4y11°y11y14	2545.24	74.504	7837	3	849.08	-6.71
Q8ZRM7 DKGB_SALTY 2	4		AHGIHITSYMTLAYGK	169	16	4	16.93	b8b12°b12y12	1762.90	81.568	4056	3	588.31	5.47
Q8ZRM7 DKGB_SALTY 2	5	Oxidation+M(14)	HNATPAQVILAWAMGEGYSVIPSS TRR	198	27	3	11.8	b3b6y14	2928.51	94.915	3167	4	732.88	10.75
Q8ZRM7 DKGB_SALTY 2	6	Oxidation+M(10)	AHGIHITSYMTLAYGK	169	16	3	16.93	b3y4y8	1778.88	99.017	1993	3	593.63	-6.24
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	1		VQALADAAR	102	9	9	59.4	b2°b2b3b7y5y6y7°y7y9	914.49	31.442	149287	2	457.75	-13.01
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	2		AIAEQLK	56	7	6	59.27	b4b6y2y3y5y7	772.45	32.207	29943	2	386.73	-13.91
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	3		VQALADAAREAGLQF	102	15	5	17.9	b2b3y4y6y15	1559.80	88.691	6773	3	520.61	-10.57
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	4		EAGLQF	111	6	5	52.84	b3b4b5y5*y5	664.33	61.950	75342	1	664.33	-4.78
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	5		HIYAQVIAPNGSEVLVAASTVEK	33	23	4	22.98	b5b6b11*b11	2396.25	83.986	9817	3	799.42	-11.92
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	6		DAAAAVGKAVAER	68	13	3	20.38	b4b10y6	1228.65	51.742	19055	2	614.83	-7.85
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	1		GDVLQVSGDAR	351	11	5	55.46	b10y3y5y6y9	1116.56	27.317	19211	2	558.78	-5.69
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	2		VGPELVAWTDGK	219	12	8	55.51	b1b2b8b10b11y6y7y10	1271.68	58.950	7881	2	636.34	11.62
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	3		LQHQDLQ TSAQQIAR	183	15	5	17.9	b6b12°b12y9*y9	1736.90	68.485	6968	3	579.64	-0.28
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	4		NGKEVFRDLLDMR	287	14	3	19.04	b10y6y8	1707.83	76.547	4200	2	854.42	-8.15
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	5		YLPK	179	4	1	12.69	b3	520.31	37.055	29504	1	520.31	-6.69
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	6		SQIEMPIDDNVVLNK	336	15	4	17.9	b7b10°b10y3	1714.88	82.635	14988	2	857.94	6.62
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	7		LFGWDIGLTAGMLAGSMTSTPVL VGAGDTLR	112	31	4	15.99	b3b8b15y24	3107.56	96.330	7886	4	777.65	-8.56
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	8	Carbamidomethyl+C(2)	TCAPAMEIISDTAR	513	14	3	19.04	b4b12y11	1535.71	79.143	2464	2	768.36	-4.61
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	9		IVTEEIVVKNHNAVGR	301	16	3	16.93	b5y3y7	1777.98	109.043	3637	3	593.33	-9.20
Q8ZQK4 YBJL_SALTY Putative tranort protein ybjL	10	Oxidation+M()	LFGWDIGLTAGMLAGSMTSTPVL VGAGDTLR	112	31	4	36.17	y5y7y8y9	3123.61	137.440	2109	3	1041.87	7.11
P60726 RL4_SALTY 50S ribosomal protein L4	1		DATGIDPVSLIAFDK	170	15	5	17.9	b2b5y3y10y15	1561.81	88.116	50012	2	781.41	2.03
P60726 RL4_SALTY 50S ribosomal protein L4	2		QVEEMLA	194	7	6	50.24	b3b4°b4b6y6y7	819.39	51.331	22906	1	819.39	-5.59
P60726 RL4_SALTY 50S ribosomal protein L4	3		DAQSALTVSETTFGR	6	15	5	17.9	b2°b2b13y4y12	1582.79	60.874	15615	2	791.90	11.41
P60726 RL4_SALTY 50S ribosomal protein L4	4		LKDMALEDVLIITGELDENLFLAA R	137	25	8	40.25	b5b20y2y3y4y5y9*y9	2802.51	136.416	8793	3	934.84	3.57
P60726 RL4_SALTY 50S ribosomal protein L4	5		DAQSALTVSETTFGRDFNEALVH QVVVAYAAGAR	6	34	6	37.81	b9°b9b10b12b13y7	3593.75	103.360	6303	4	899.19	-14.40
P60726 RL4_SALTY 50S ribosomal protein L4	6		FSVEAPK	123	7	3	40.15	y3y5y6	777.40	41.258	69456	2	389.20	-16.09
P60726 RL4_SALTY 50S ribosomal protein L4	7		DFNEALVHQVVVAYAAGAR	21	19	3	23.92	y6y7y12	2030.06	83.926	41911	3	677.36	7.94
P60726 RL4_SALTY 50S ribosomal protein L4	8		DATGIDPVSLIAFDKVVMTADAV K	170	24	7	28.37	b3b4°b4b7b9°b9y3	2476.30	101.989	37505	3	826.10	-0.79
P60726 RL4_SALTY 50S ribosomal protein L4	9		SGGVTFFAARPQDHSQKVNK	79	19	3	23.92	b7b8b10	2027.05	77.677	7949	3	676.35	2.95
P60726 RL4_SALTY 50S ribosomal protein L4	10	Phosphoryl STY(9)	ELVLKDAQSALTVSETTFGR	1	20	4	22.32	b9y11°y11y12	2245.13	78.914	1571	3	749.05	14.03

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	8	30.55	b6b11y1y4y12*y12y16y18	1970.00	63.326	62144	3	657.34	-9.17
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		AVAFMMDDALLAGER	198	15	5	25.98	b1y8y11y13y15	1609.78	84.516	53491	2	805.39	6.90
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		ESSVPFSYYDNQKK	47	14	4	19.04	b11y6y10y14	1691.76	55.194	52615	2	846.39	5.92
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		VVGYSQDYSNAIVEAVK	61	17	9	48.25	b2b17y3y4y10*y10y11y15y17	1841.94	67.735	42647	2	921.47	4.84
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5		AVVVTSGTTSEILLHK	154	16	3	23.46	b3b4y12	1654.92	57.884	5369	3	552.31	-13.35
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(19)	KPDNWEIVGKPKQSQEAYGCMLR	217	22	10	45.18	b4*b4b10*b10b11y3y7y8y10*y10	2606.26	136.334	19395	3	869.42	3.47
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTNNLER	98	22	4	13.27	b10*b10y9y12	2526.15	62.894	1974	2	1263.58	-18.36
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTNNLER	89	31	5	24.91	b3y6y9y10y12	3548.79	86.900	125761	3	1183.60	3.03
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9		AVVVTSGTTSEILLHKLNEEQK	154	22	6	38.82	b3y4y8y17y18y20	2396.28	63.732	25475	3	799.43	-9.17
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		TLESGRAVAFMMDDALLAGER	192	21	8	43.13	b4*b4b7*b7y3y8y9y10	2253.13	136.302	2947	2	1127.07	14.19
P66431 RS15_SALTY 30S ribosomal protein S15	1		YTALIER	77	7	8	53.25	b7y2°y2y3y4y5y6y7	865.47	43.077	128304	2	433.24	-10.93
P66431 RS15_SALTY 30S ribosomal protein S15	2		SLSTEATAK	1	9	5	37.96	b2y3y6y7y9	907.46	22.020	68765	2	454.24	-10.36
P66431 RS15_SALTY 30S ribosomal protein S15	3		DVAR	73	4	1	12.69	b3	460.25	30.333	9596	1	460.25	2.12
P66431 RS15_SALTY 30S ribosomal protein S15	4		STEATAK	3	7	1	8.74	b4	707.36	21.985	21224	1	707.36	0.17
P66431 RS15_SALTY 30S ribosomal protein S15	5		SLSTEATAK	1	9	0	1.66		889.46	22.017	5203	2	445.23	0.55
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1	Carbamidomethyl+C(7)	LWVNPDCGLK	719	10	6	42.73	b2b4y6y7y8y10	1201.61	60.773	40358	2	601.31	2.84
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2		LAAITAQDSQRENPYEV	395	18	4	22.78	b11y13y14y18	2061.02	47.391	28278	3	687.68	-5.57
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	3		SDWDAYLEWGVEAFR	611	15	6	25.98	b1y8°y8y10°y10y11	1843.83	93.624	27240	3	615.28	2.98
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	4		QAGIDLLPVGDFAWYDHVLTTSLLGNV	52	31	6	39.18	y2y3y4y6y7y31	3351.78	119.585	25442	3	1117.93	1.09
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	5	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	5	16.93	b6b13y2y8y16	1834.95	99.524	18817	2	917.98	6.05
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	6	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETR	315	22	4	13.27	b2b9b12y5	2441.24	104.343	13105	4	611.07	-2.20

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	7		AQESYWAGNTTR	21	12	4	35.23	y5y6y7*y7	1383.63	40.734	11515	2	692.32	1.85
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8		LPAPWTTTIGSFPQTTEIR	422	19	3	14.74	b4y9y11	2116.08	78.647	6995	3	706.03	-12.34
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	9		DALNSGETAALEEWSAPIQAR	360	21	3	22.15	b12b13y11	2229.10	80.237	2765	3	743.71	11.94
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	10		LAAITAQDSQR	395	11	4	24.02	b3y4°y4y8	1173.61	48.446	4852	2	587.31	-13.31
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	11		ETIAK	570	5	1	13.11	y3	561.32	24.595	2671	1	561.32	-10.33
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	12		APTGEPA AAAEMTK	103	14	3	19.04	b9y6y9	1344.65	91.656	2106	3	448.89	-0.45
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	13	Phosphoryl STY(6)	YAQSLTDKPVK	538	11	4	24.02	b4y7y9*y9	1329.65	79.598	7665	2	665.33	8.54
Q7CPZ4 GRPE_SALTY Protein grpE	1		FVNELLPVIDSLDR	90	14	5	19.04	b2b5y1y4y8	1629.89	97.149	52997	2	815.45	3.89
Q7CPZ4 GRPE_SALTY Protein grpE	2		IANLEVQLAEAQTR	43	14	4	32.65	b3b4y4y11	1555.82	63.286	18549	2	778.42	-12.87
Q7CPZ4 GRPE_SALTY Protein grpE	3		TPEGQAPEEIIIMDQHEEVEAVEPN DSAEQVDPRDEK	7	36	5	10.88	b6y2y5y7y36	4060.80	63.240	6311	4	1015.95	-5.53
Q7CPZ4 GRPE_SALTY Protein grpE	4		AEMENLR	66	7	3	40.15	b3y4y6	862.43	80.774	3820	1	862.43	19.89
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	1	Carbamidomethyl+C(10)	MNVVILDTGCANLSSVK	0	17	4	23.09	b2b14y10y11	1820.93	72.328	14127	2	910.97	3.02
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	2		MTDFGLPLPHMGWNR	105	15	5	29.09	b2b10y5y7y8	1771.82	87.780	12966	3	591.28	-11.99
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	3		LFLPGVGTAQAAMDQLRER	41	19	4	23.34	b15y5y7y11	2073.09	84.949	10808	3	691.70	-1.30
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	4	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	ACTQPVLGICLGMQLLGR	67	18	4	15.37	b12b14*b14y3	1987.05	120.989	4980	2	994.03	11.43
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	5		GVDLLNIIEQDVPK	91	14	4	19.04	b3b12*b12y3	1552.85	101.622	35739	2	776.93	-2.52
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	6		NFLEM	191	5	2	26.21	b3b4	653.30	73.834	16332	1	653.30	10.84
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	7	Carbamidomethyl+C(9)	NVVILDTGCANLSSVK	1	16	4	25.31	b4*b4b14b15	1689.92	91.174	12973	2	845.46	22.18
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	8		SGAAGAQLLKNFLEM	181	15	3	23.92	b3y6y7	1549.79	102.549	2831	2	775.40	-7.40
P0A1R4 HIS5_SALTY Imidazole glycerol phohate synthase subunit hisH	9	Oxidation+M(11)	MTDFGLPLPHMGWNR	105	15	3	17.9	b6y3y14	1787.84	79.273	7286	3	596.62	4.85
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	1		ITAVIPYFGYAR	84	12	3	29.21	y3y7y8	1370.74	80.759	23638	2	685.87	-5.88

[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	2		LFAGNATPELAQR	5	13	5	31.94	b7y6y10y11y13	1387.73	53.889	23230	2	694.37	-0.97
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	3	Carbamidomethyl+C(10)	NSVIDEVVVCDTIPLTDEIK	262	20	3	14.19	b11y4y11	2259.16	88.375	11641	2	1130.08	7.67
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	4		ANVSQVMHIIGDVAGR	198	16	3	16.93	b6b8y3	1666.86	92.499	3932	3	556.29	-4.91
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	5		AAEALK	231	6	1	13.52	y5	602.36	40.927	14539	1	602.36	9.93
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	6		FSDGEVSVQINENVR	34	15	6	36.63	b8b9b11*b11y12y14	1692.84	103.407	1702	3	564.95	11.11
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	7		ITAVIPYFGYARQDR	84	15	3	17.9	b4y3y8	1769.95	67.604	9692	3	590.65	7.52
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	1		LPMVDDLRL	278	8	3	32.78	b5y6y7	958.50	56.869	35010	2	479.76	0.70
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	2		SPLREREEAK	477	10	5	51.48	b3b5b6b7y1	1214.67	12.447	4075	3	405.56	13.87
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	3		YAEALLSELGQGTADWVPNFDGT MQEPK	127	28	6	14.69	b2b5b22y6y11*y11	3109.50	132.908	1588	3	1037.17	4.48
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	4		LALHEFTENAYLNYSMYVIMDR	7	22	3	13.27	b8y4y6	2693.32	94.527	22667	3	898.44	15.86
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	5		GQGEPLTGK	564	9	5	30.18	b7*b7y5y7*y7	886.48	79.016	18443	1	886.48	20.31
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	6		LEEMK	427	5	1	13.11	b3	649.33	41.412	14859	1	649.33	8.18
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	7		EDGAVVISALPHQVSGAK	247	18	4	32.25	b6b9b13b14	1777.98	107.413	14713	3	593.33	19.98
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	8		SNQPVVFIIDTTGR	538	13	5	34.07	b5*b5b11y3y4	1433.74	94.903	2590	2	717.37	1.79
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	9	Carbamidomethyl+C(13)	LLMASDAGYGFVCTFNDLVAR	593	21	7	45.2	b6b7b9b12b14y7y10	2320.15	91.120	2035	2	1160.58	17.15
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	10		EEAKAMSEHDMLPSEPVTVLSQ MGWVR	483	28	4	17.11	b14y7y12y26	3170.54	136.650	18418	2	1585.77	1.93
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	11		GEQDELEKER	434	10	6	54.5	y4*y4y6y8y9*y9	1232.58	136.337	2037	1	1232.58	5.35
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	12	Phosphoryl STY(8)	MLMFVPVDSLPLSK	651	14	3	19.04	b4b6y7	1685.79	93.566	9188	2	843.40	-3.69
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	13	Oxidation+M()	LALHEFTENAYLNYSMYVIMDR	7	22	3	13.27	b9y8y18	2709.29	68.009	32855	3	903.77	9.01
[P26973]PARC_SALTY DNA topoisomerase 4 subunit A	14		SPLREREEAK	477	10	0	2.07		1196.65	12.446	1770	3	399.55	11.83
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	1	Carbamidomethyl+C(16) ;Carbamidomethyl+C(25) )	ALSYNNIADTDAALECVKEFNEPA CVIVK	258	29	10	26.79	b7*b7b9*b9b11b13y11*y11y22y29	3254.57	82.905	17182	3	1085.53	0.38
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	2		VNGGLLVQDR	381	10	5	22.26	b1y3y4*y4y10	1070.59	68.461	5957	1	1070.59	-1.82
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	3	Carbamidomethyl+C(3)	EGCSLEDAVENIDIGGPTMVR	114	21	4	20.34	y7y9*y9y15	2262.06	81.409	5585	2	1131.53	8.53
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	4		VNGGLLVQDRDLGMVSEAE LR	381	21	4	13.7	b1b4y8y14	2271.19	86.752	3829	2	1136.10	7.20
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	5	Carbamidomethyl+C(13)	DGIDAAAAGVSCVIQPGGSIR	482	22	4	23.15	b2b12b15b16	2113.05	69.525	3201	3	705.02	-7.97
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	6		GLPVTESDYTGFPMMMDGR	47	20	5	23.61	b3b9*b9b10y2	2201.01	115.647	3163	4	551.01	10.20

[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	7		EMDANEGSLTLDTR	158	14	4	26.82	y3°y3y10y11	1551.69	73.500	2618	3	517.90	-1.34
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	8	Carbamidomethyl+C(13)	QPTEQELRDALFCWK	407	15	3	17.9	b5y5y10	1920.91	65.490	2342	3	640.97	-10.36
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	9		GSAMASDAFFPFR	469	13	3	27.86	y4y6y7	1403.67	50.193	31506	2	702.34	22.18
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	10		AFEHTAAYDSMIANYFGSMVPAY HGESK	178	28	5	17.62	y3°y3y6y11°y11	3094.43	61.351	5736	4	774.36	18.78
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	11	Carbamidomethyl+C(16)	ALSYNNIADTDAALECVK	258	18	4	24.29	b9b10b12°b12	1967.90	84.284	5262	4	492.73	-19.54
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	12	Carbamidomethyl+C(8)	QNVRLVTCGQWAQR	359	14	10	64.47	b9b11°b11b12°b12*b12b13y4y9y10	1715.87	103.467	17705	2	858.44	-5.34
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	13	Carbamidomethyl+C(7); Carbamidomethyl+C(16)	EFNEPACVIVKHANPCGVAVSTTI LDAYDR	276	30	3	22.65	y10y12y13	3346.65	86.426	12309	5	670.14	9.56
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	14		AADEGLEVKGSAMASDAFFPFR	460	22	3	13.27	b11y9y12	2316.10	106.885	8228	3	772.71	2.64
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	15		DDEVIAAADEHGIAMIFTDMRHFR	504	24	7	29.86	b6b8°b8b22y3y5y7	2760.30	136.336	3622	2	1380.66	5.93
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	16	Carbamidomethyl+C(5)	HANPCGVAVSTTILDAYDRAYK	287	22	5	40.68	b3b4b12b13y3	2422.16	72.083	2033	3	808.06	-7.66
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	17	Oxidation+M(20)	SNAIVYAKENMTIGIGAGQMSR	428	22	3	13.27	b12y5y7	2327.14	88.227	12412	3	776.38	-4.62
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	18	Carbamidomethyl+C(13); Oxidation+M()	DGIDAAAAGVSCVIQPGGSIRDD EVIAAADEHGIAMIFTDMR	482	43	8	25.91	b3b9°b9b12°b12b13b15y8	4430.16	136.316	5961	5	886.84	12.45
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	19	Oxidation+M(11)	AFEHTAAYDSMIANYFGSMVPAY HGESK	178	28	3	11.6	b3b16y8	3110.38	118.402	3774	2	1555.70	6.04
[P26978]PUR9_SALTY Bifunctional purine biosynthesis protein purH	20	Carbamidomethyl+C(16)	ALSYNNIADTDAALECVKEFNE	258	22	2	9.26	y13°y13	2487.15	82.819	4862	3	829.72	4.71
[P14846]CARB_SALTY Carbamoyl-phosphate synthase large chain	1		AQLGSNSTMK	930	10	4	26.62	b2b3b5y7	1036.52	28.088	17379	2	518.77	13.31
[P14846]CARB_SALTY Carbamoyl-phosphate synthase large chain	2		VHYDTTLNGGFATTMALNADAT EK	1037	24	9	32.41	b5b10b11b13°b13y1y9y11y24	2541.18	87.791	15227	3	847.73	-3.27
[P14846]CARB_SALTY Carbamoyl-phosphate synthase large chain	3		NASMAVLREIGVETGGSNVQFAV NPK	265	26	5	12.02	b2b10b14y14*y14	2688.36	98.353	5161	2	1344.68	-5.72
[P14846]CARB_SALTY Carbamoyl-phosphate synthase large chain	4		GLDLSPTNELLIDESLIGWKEYEM EVVR	194	28	4	8.52	b2b14y11°y11	3248.62	106.413	4403	3	1083.55	-4.96
[P14846]CARB_SALTY Carbamoyl-phosphate synthase large chain	5		QGVLEEFGVTMIGATADAIDK	104	21	8	29.35	b12b14°b14*b14y3y4y9°y9	2165.07	107.498	3938	2	1083.04	-4.17
[P14846]CARB_SALTY Carbamoyl-phosphate synthase large chain	6		SLTEQGVQTQEIPPPYSVK	872	19	3	14.74	b12y5y7	2152.11	74.712	3716	2	1076.56	-2.16
[P14846]CARB_SALTY Carbamoyl-phosphate synthase large chain	7		IGLDTAR	138	7	4	56.26	b5b6y4y6	745.43	28.139	35634	2	373.22	15.48
[P14846]CARB_SALTY Carbamoyl-phosphate synthase large chain	8		LAGVR	504	5	1	13.11	b3	515.33	74.203	13440	1	515.33	-0.95

[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	9		GLMNVQFAVK	823	10	3	26.62	b3b8y3	1106.58	53.287	7857	2	553.80	-17.54
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	10		VAEVGITGLNADFLR	475	15	7	36.63	b5°b5b7y3y4y8°y8	1574.86	81.842	7187	2	787.93	0.93
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	11		ALEAAGVPVIGTSPDAIDR	652	19	4	22.52	b17y5°y5y6	1851.94	80.655	7079	2	926.47	-21.16
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	12	Carbamidomethyl+C(10) ;Carbamidomethyl+C(11) )	IGQGIEFDYCCVHASLALR	571	19	6	45.77	b3b7b8°b8b12b13	2209.08	107.424	3336	3	737.03	11.94
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	13		LAVGYTLDELMNDITGGR	325	18	4	15.37	b3y6°y6y14	1937.93	111.541	2299	2	969.47	-19.97
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	14		YFQTAVSVSNDAPVLLDR	736	18	11	54.92	b7b9°b9°b9b10b11b13y10°y10y15°y15	1995.00	104.254	2198	2	998.00	-10.77
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	15		FPGVDPLLGPEMRSTGEVMGVGR	899	23	5	17.22	b3b6°b6y3y11	2401.22	64.508	39943	3	801.08	7.63
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	16		DNEVYLIEVNPRAAR	833	15	4	17.9	b7b9°b9y3	1758.90	82.531	26886	2	879.95	-9.79
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	17		EIGVETGGSNVQFAVNPKNGR	273	21	5	30.79	b3b4b10b13y10	2173.10	92.652	7182	2	1087.06	1.69
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	18		QGVLEEFGVTMIGATADAIDKAE DR	104	25	5	25.6	b12°b12b13y5y16	2636.31	85.070	5473	3	879.44	8.98
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	19		DAGADRIWYIADAFR	429	15	5	41.13	b4b8b10b13°b13	1739.84	39.010	4423	3	580.62	-5.89
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	20		FAGANDRLTTQMK	366	13	4	25.15	b10b11y5*y5	1452.73	76.181	3335	2	726.87	0.76
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	21		ELKDAGADR	426	9	3	30.18	b4y7y8	974.48	83.512	2871	1	974.48	-8.89
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	22		STGEVMGVGRTFAEAFK	912	18	5	36.23	b8b9y6°y6y7	1857.91	136.191	2111	2	929.46	-1.58
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	23		SVGEVMAIGRTQQESLQK	379	18	3	15.37	b6b9y7	1960.99	67.645	1899	2	981.00	-10.08
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	24	Phosphoryl STY(22)	GLDLSPTNELLIDESLIGWKEYEM EVVR	194	28	3	21.82	b13y5y6	3328.57	82.081	2234	3	1110.20	-6.67
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	25	Oxidation+M(11)	QGVLEEFGVTMIGATADAIDK	104	21	3	13.7	b12b14y6	2181.10	77.333	2147	2	1091.05	12.09
[P14846]CARB_SALTY Carbamoyl-phohate synthase large chain	26		QGVLEEF	104	7	2	21.09	y4y5	821.41	107.448	4748	1	821.41	7.06
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	1		TVLDSGWITGPK	21	13	4	25.15	b9b10y9y13	1374.73	81.280	36281	2	687.87	2.04
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	2		APQAEVLAPGYK	223	12	6	35.23	b1b4b5b6°b6°b6	1243.68	57.163	12876	2	622.35	13.15
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	3		SDFLPFSRPAMGAEEAIAVK	1	20	5	22.32	b4b8b12y11y20	2136.10	122.212	7160	2	1068.56	11.32
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	4		FPTLTLPDTEWNSER	336	15	7	25.44	b2b5b13°b13y9y11y15	1805.88	82.663	3734	2	903.44	6.42
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	5		AHPVHYAGAPADLDAIYALGER	123	23	3	12.89	b4y4y16	2396.26	85.411	3166	3	799.42	-2.14
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	6		YGIPVIEDAAHATGTSYK	146	18	6	21.42	b4b8°b8y6°y6y13	1892.91	64.641	30347	3	631.64	-15.93
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	7	Carbamidomethyl+C(2)	ICSLPLFPDMTESDFDR	351	17	3	24.75	b4b5b7	2042.96	135.555	25753	3	681.66	19.78

[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	8		FHGLGVDAWDR	207	11	4	36.34	b5b6b9y8	1272.60	33.202	1874	2	636.80	-11.22
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	9		FHGLGVDAWDRQSGGR	207	16	3	16.93	b11y3y13	1757.87	79.614	6729	2	879.44	11.53
[Q8ZNF3]ARNB_SALTY UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	10		AIPVHYAGAPADLDAIYALG	123	21	3	19.3	y7y10y14	2111.11	85.346	7375	2	1056.06	-5.20
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	1		QGNANIVFFDGITAGEK	186	17	6	32.31	b9b11°b11y3y11y14	1780.91	114.087	10670	2	890.96	10.76
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	2		TQFMGPEGVGNASLSNIAGGAAE GMLVTMPK	242	31	3	11.18	b5b15y3	3035.47	92.538	7274	3	1012.50	3.54
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	3		TAGLDSQSGPTAAK	139	14	4	31.17	b10y8y10y12	1303.65	28.451	5722	2	652.33	-2.62
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	4		VAIVGAMSGPVAQWGDMEFNGA R	27	23	9	54.44	b8b14°b14b18y3y4y7y8y1 0	2363.13	136.301	2237	2	1182.07	2.38
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	5		SVQDGLKQGNANIVFFDGITAGE K	179	24	4	16.61	b4b12y3y14	2508.31	73.999	3794	2	1254.66	14.41
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	6	Oxidation+M(21)	DPSGPYVWITYAAVQSLATAMTR	293	23	4	21.93	b13y5°y5y6	2514.20	108.990	1563	3	838.74	-12.24
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	1		AVDSMIPIGR	151	10	8	38.93	b7b9°b9b10y1y3y6y10	1058.55	52.223	129786	2	529.78	-13.26
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	2		IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	4	22.49	b5y2y6y7	3950.88	96.399	39503	4	988.47	-2.60
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	3		DSVGAVVMGPYADLAEGMK	68	19	4	14.74	b6b8y1y12	1909.92	83.608	34342	2	955.46	8.69
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	4		QYAPMSVAQQSLVLFAAER	434	19	5	14.74	b3y2y5y16°y16	2109.09	93.191	28057	2	1055.05	2.66
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	5		ELAASFQFASDLDDATR	401	17	9	42.19	b3°b3b6y1y3y4°y4y9y13	1856.88	88.776	20409	2	928.95	9.40
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	6		QSVDQPQVTGYK	139	12	7	33.86	b9°b9b12y7y9y10°y10	1349.67	33.827	19363	2	675.34	-2.35
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	7		YAIALNLERDSVGAVVMGPYADL AEGMK	59	28	4	17.62	y2y7y11y13	2953.50	115.216	2725	3	985.17	7.27
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	8		GEDALIYDDLK	252	13	5	25.15	b10b11b13°b13y5	1451.71	90.009	2249	2	726.36	-9.25
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	9		IAQFNVVSEAHNEGTVSVSDGVI R	15	25	3	18.5	b9b13b15	2641.35	102.788	1705	3	881.12	-3.97
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	10		GYLADVELAK	453	10	4	42.73	b3y6y7y8	1078.57	60.765	39612	2	539.79	-3.28
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	11		VVNTLGAPIDGKGVPVDNDGFSAV EAIAPGVIDR	106	33	12	49.17	b4°b4b5°b5b27y6°y6y7y10 y13y15y28	3263.70	84.197	50530	3	1088.57	2.77
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	12		AARVNADYVEAFTK	300	14	4	27.21	b8b13y5y11	1554.77	78.627	5176	2	777.89	-13.27
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	13		VNADYVEAFTKGEVK	303	15	3	25.98	b3b7b14	1669.84	78.702	2672	2	835.42	-1.68
[Q7CPE1]ATPA_SALTY ATP synthase subunit alpha	14		DHAPLMQEINQSGGYNDEIEGKL K	477	24	3	12.56	b22y10y16	2686.26	92.605	1530	2	1343.64	-5.63
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	1		SQGETLWHTSNVFTNEPALR	68	20	8	41.79	b13°b13y6y7y12y13°y13y 20	2287.11	71.998	34783	3	763.04	-0.85
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	2	Carbamidomethyl+C(8)	AVMDDHTCAVVVEPIQEGGVQ AATPEFLK	180	30	6	24.58	b12b13y1y12y14y30	3168.55	75.340	24563	3	1056.85	4.31
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	3		FAPSLVVEADIHEGMQR	377	18	9	71.52	b13y5°y5y6°y6y7y10y11y1 2	2027.97	68.468	70990	3	676.66	-5.24



[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	4		TGDLFAYMHYGVTPDILTSAK	234	21	5	24.42	b3*b3b4b7y14	2300.12	88.582	58878	3	767.38	-0.96
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	5		VLFMNSGTEANETAFK	101	16	6	34.31	b7b12y4y9y12*y12	1758.85	67.826	41164	2	879.93	6.18
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	6	Carbamidomethyl+C(3); Carbamidomethyl+C(17)	DLCDEHQALLVFDEVQCGMGR	213	21	3	13.7	b10b13y4	2492.12	85.355	13000	3	831.38	7.84
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	7	Carbamidomethyl+C(4)	HYACVR	120	6	1	13.52	y3	805.38	55.057	2011	2	403.19	-1.36
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	8		QQFVQHLQAIDEQFDIFSDIR	315	21	5	13.7	b13*b13y10y12*y12	2577.24	79.584	1824	3	859.75	-14.21
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	9		ATFDEVILPVYAPADFIPVKGK	10	22	9	54.22	b4*b4b7b14b16b20y5y14y 21	2390.30	94.770	30217	3	797.44	-2.25
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	10		ARDFLYAGAEAGVMVLNAGADV MR	353	24	5	28.37	b7y7y8y10y15	2497.26	69.498	7144	3	833.09	9.78
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	11	Carbamidomethyl+C(6); Carbamidomethyl+C(20)	GLRDLCEHQALLVFDEVQCGM GR	210	24	4	12.56	b6*b6y7y12	2818.33	138.149	3606	3	940.11	7.36
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	12		RQQFVQHLQAIDEQFDIFSDIR	314	22	6	25.21	b4b7y7y11y13*y13	2733.40	75.198	2052	3	911.81	11.16
[Q8ZNK6]END4_SALTY Probable endonuclease 4	1		YIGAHVSAAGGLANAPAR	2	18	5	26.26	b6b7b12y8y18	1695.87	52.392	6223	2	848.44	-10.44
[Q8ZNK6]END4_SALTY Probable endonuclease 4	2	Carbamidomethyl+C(1); Carbamidomethyl+C(25)	CEQLGLTLLNFHPGSHLMQIAQED CLAR	97	28	9	38.74	b6*b6b12y4y8y9*y9y10*y 10	3251.54	124.765	5812	4	813.64	-12.09
[Q8ZNK6]END4_SALTY Probable endonuclease 4	3		TFAEFGK	198	7	3	40.15	b3b5y4	799.40	111.392	2556	1	799.40	4.50
[Q8ZNK6]END4_SALTY Probable endonuclease 4	4		SAFGSRVDR	221	9	3	30.18	b4y6y7	994.52	88.806	5700	2	497.76	14.24
[Q8ZNK6]END4_SALTY Probable endonuclease 4	5		GMHLNDAKSAFGSR	213	14	4	32.65	b5b9y4y5	1490.72	114.797	2135	2	745.87	5.00
[P67537]YBED_SALTY UPF0250 protein ybeD	1		VMGQALPELVDQVVEVVQR	18	19	7	28.99	b4b6*b6b12y1y3y5	2109.14	108.926	13819	3	703.72	-0.81
[P67537]YBED_SALTY UPF0250 protein ybeD	2		GNYHSVSITINATHIEQVETLYEEL GNIDIVR	52	32	4	13.38	b7b12y12y19	3627.85	112.057	6951	3	1209.95	5.52
[P67537]YBED_SALTY UPF0250 protein ybeD	3		LNELLEFPPTPTYK	4	14	5	27.21	b6b13y3*y3y8	1711.89	94.733	14470	2	856.45	-1.28
[Q8ZRT5]GUAC_SALTY GMP reductase	1	Carbamidomethyl+C(3)	SACTYVGASR	313	10	3	26.62	b6y5y7	1071.48	27.235	12499	2	536.24	-6.38
[Q8ZRT5]GUAC_SALTY GMP reductase	2	Carbamidomethyl+C(9)	VGIGPGSVCTTR	177	12	5	49.19	b3y4y7y8y9	1203.62	42.575	11347	2	602.31	0.00
[Q8ZRT5]GUAC_SALTY GMP reductase	3		ELTK	325	4	2	12.69	b3*b3	490.28	33.318	25975	1	490.28	-9.03
[Q8ZRT5]GUAC_SALTY GMP reductase	4		IEEDLK	2	6	1	13.52	b3	746.39	28.299	10723	1	746.39	-3.43
[Q8ZRT5]GUAC_SALTY GMP reductase	5		EAWPTK	146	6	1	13.52	b5	731.37	91.916	3950	1	731.37	0.17
[Q8ZRT5]GUAC_SALTY GMP reductase	6	Carbamidomethyl+C(14) ;Carbamidomethyl+C(31 )	TGVGYPQLSAVIECADA AHGLGG MIVSDGGCTMPGDVAK	191	39	6	22.44	b5b10*b10b11y5y7	3861.81	105.051	1644	3	1287.94	5.06
[Q8ZRT5]GUAC_SALTY GMP reductase	7	Carbamidomethyl+C(10)	DILGGLRSACTYVGASR	306	17	4	27.06	b3y10y11y15	1795.93	90.008	42204	3	599.31	8.77

P40861 PROA_SALTY Gamma-glutamyl phohate reductase	1	Carbamidomethyl+C(3)	QVCNLADPVGQVIDGGLDLSGLR	81	23	5	12.34	b12*b12b21y6°y23	2396.25	91.889	21741	3	799.42	11.11
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	2		IADELEAQMESILSANVQDVEQAR	30	24	12	47.03	b2b4b9b12y8°y8y10y11°y11*y11y15y22	2659.27	94.880	14537	3	887.10	-5.60
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	3		FVNEVDSAAVYVNASTR	353	17	10	42.03	b5b10b13*b13y5°y5*y5y10y13°y13	1841.88	93.681	8019	2	921.44	-12.26
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	4		WIGFGDGTIR	405	10	6	39.72	b6b10y6y8y9y10	1121.59	115.448	3403	2	561.30	13.28
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	5		GPMGLEALTTYK	393	12	6	53.96	b4b5b6°b6b7y9	1280.63	97.926	12355	2	640.82	-20.87
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	6	Carbamidomethyl+C(2)	ACGLPEAAVQAIDNPDR	164	17	5	22.59	b9°b9b14y9y12	1796.83	59.086	4679	3	599.61	-18.68
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	7		AIADDVR	74	7	3	37.13	b4b5y4	759.41	40.479	2032	1	759.41	11.41
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	8		FTDGGQFGLGAEVAVSTQK	370	19	13	45.1	b9°b9*b9b11b12b13°b13*b13y6*y6y10°y10*y10	1911.96	136.302	2004	2	956.49	10.15
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	9		ANGLSEAMLDLDR	54	11	5	24.02	b4b10°b10y6°y6	1176.55	136.357	1608	1	1176.55	-12.45
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	10		LHARGPMGLEALTTYK	389	16	3	16.93	b8y7y13	1757.92	103.270	8900	2	879.46	-10.49
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	11		SLVNEMLRMDK	181	11	3	24.02	b10y3y8	1335.69	38.864	6777	2	668.35	13.62
P40861 PROA_SALTY Gamma-glutamyl phohate reductase	12	Phosphoryl STY(5)	LALLSSGEK	15	9	4	30.18	b5b7y3°y3	997.49	136.211	2268	1	997.49	-1.41
P0A7S6 RS12_SALTY 30S ribosomal protein S12	1	Carbamidomethyl+C(9)	SNVPALEACPQKR	18	13	8	58.05	b2y4y6y7y8y9°y9*y9	1469.73	37.052	46454	3	490.58	-14.45
P0A7S6 RS12_SALTY 30S ribosomal protein S12	2	Carbamidomethyl+C(9)	SNVPALEACPQK	18	12	5	29.21	b2y6y7y9y12	1313.65	41.069	11744	2	657.33	-1.67
P0A7S6 RS12_SALTY 30S ribosomal protein S12	3	Carbamidomethyl+C(5)	GALDCSGVK	99	9	5	44.54	b3b4y5y7°y7	906.43	76.296	5181	1	906.43	-0.20
P0A7S6 RS12_SALTY 30S ribosomal protein S12	4		DLPGVR	88	6	1	13.52	y4	656.37	52.522	4629	1	656.37	-10.04
Q9L9I8 THIE_SALTY Thiamine-phohate pyrophohorylase	1		QMPSAPQGLAQLASHIER	137	18	6	36.56	b2b5y6y9y13y16	1933.98	75.415	27674	3	645.33	-8.21
Q9L9I8 THIE_SALTY Thiamine-phohate pyrophohorylase	2		MYQPDPFTVPFR	0	12	4	22.01	b3y3y9°y9	1497.73	78.080	24224	2	749.37	9.70
Q9L9I8 THIE_SALTY Thiamine-phohate pyrophohorylase	3		EATAELLAIAAGVGDE	196	15	3	17.9	b8y10y12	1458.73	69.522	3815	2	729.87	-3.93
Q9L9I8 THIE_SALTY Thiamine-phohate pyrophohorylase	4		AYGVHLGQEDLETTDLK	79	17	3	16.1	b10b13y6	1888.92	110.329	2609	3	630.31	-5.17
Q9L9I8 THIE_SALTY Thiamine-phohate pyrophohorylase	5		APAVLATGVGSIAVVSQAADWR	171	25	7	27.62	y4°y4y5°y5y7°y7y9	2424.32	108.083	1762	3	808.78	-0.30
Q8ZMB5 PTRA_SALTY Protease 3	1		TAFYLEVENDALPGAVDR	126	18	5	28.83	b2b9b10y6y14	1979.95	90.916	3527	2	990.48	-8.14
Q8ZMB5 PTRA_SALTY Protease 3	2		LADFFHQAVVEPQGMAILSQIAGSQNGK	904	28	4	24.9	b5b6y7y11	2956.51	136.440	1942	3	986.18	4.71
Q8ZMB5 PTRA_SALTY Protease 3	3		NAVNAELTMAR	163	11	3	24.02	b7y3y8	1189.59	46.324	28757	2	595.30	-6.98
Q8ZMB5 PTRA_SALTY Protease 3	4		QGLVEGISADSDPIVNGNSGVFAISATLTDK	329	31	5	35.25	b14b15b16y14*y14	3075.58	136.623	23685	2	1538.29	8.89
Q8ZMB5 PTRA_SALTY Protease 3	5		YFDELAHVLDLDFR	387	14	3	26.82	b8b9b11	1752.82	79.681	15644	3	584.95	-19.71
Q8ZMB5 PTRA_SALTY Protease 3	6		DVVVEK	735	6	2	26.63	b5y3	688.39	40.187	9475	1	688.39	7.18
Q8ZMB5 PTRA_SALTY Protease 3	7		IDNNSAQFR	295	9	5	30.18	b6°b6°b6y3y4	1064.53	88.793	2497	1	1064.53	17.20
Q8ZMB5 PTRA_SALTY Protease 3	8		LAMMTPQNAR	445	10	3	26.62	b4y5y7	1132.55	27.764	2331	2	566.78	-5.82

Q8ZMB5 PTRA_SALTY Protease 3	9		AEYVHPTGWK	932	10	4	47.51	b3b5b8y9	1187.58	136.439	2099	1	1187.58	-6.06
Q8ZMB5 PTRA_SALTY Protease 3	10		AYEQAIMPVQMISQVPYFSR	652	20	5	14.19	b10°b10y3y12°y12	2358.14	110.436	1820	3	786.72	-8.39
Q8ZMB5 PTRA_SALTY Protease 3	11		TEEQLGYAVFAFPM SVGR	792	18	4	26.26	b9y5y11y12	2002.00	113.330	1595	2	1001.50	10.55
Q8ZMB5 PTRA_SALTY Protease 3	12		DFDR	878	4	1	12.69	y3	552.24	23.690	1549	1	552.24	-3.76
Q8ZMB5 PTRA_SALTY Protease 3	13		AYEQAIMPVQMISQVPYFSRDER	652	23	6	33.21	b10°b10b11y4y9y11	2758.31	66.790	14955	4	690.33	-7.79
Q8ZMB5 PTRA_SALTY Protease 3	14		HGGSHNASTAPYRTAFYLEVEND ALPGA VDR	113	31	4	11.18	b3b14°b14y9	3315.60	103.423	9789	4	829.65	5.23
Q8ZMB5 PTRA_SALTY Protease 3	15		TAFYLEVENDALPGA VDR LADAI AAPLLNK	126	30	5	17.2	b8°b8b11b13°b13	3170.65	91.959	8793	4	793.42	-8.55
Q8ZMB5 PTRA_SALTY Protease 3	16		QAPQTLGEEASRLSK	863	15	3	25.98	b3b4b9	1614.85	38.702	8533	3	538.95	1.51
Q8ZMB5 PTRA_SALTY Protease 3	17		ADVSVL RNPQAMDSAR	547	17	3	16.1	b5y3y10	1828.91	73.053	5175	2	914.96	-11.48
Q8ZMB5 PTRA_SALTY Protease 3	18		RYFDELAHVLDLDFR	386	15	4	25.44	b4b11y3y13	1908.93	61.498	4440	2	954.97	-13.49
Q8ZMB5 PTRA_SALTY Protease 3	19		NWQQKAQGIALSLPELNPYPDDF TLVK	487	28	3	22.62	b5b6b12	3198.67	106.228	3412	3	1066.90	-3.13
Q8ZMB5 PTRA_SALTY Protease 3	20		ISEQTFKNWQKQ	480	12	3	22.01	b8b10y5	1536.78	70.752	2643	3	512.93	-3.50
Q8ZMB5 PTRA_SALTY Protease 3	21	Phosphoryl STY(11)	VWDNV SALQQTLP LMSEK	942	18	4	15.37	b11_H3PO4 b11y6y11°y11	2139.02	71.679	1501	3	713.68	2.63
Q8ZMB5 PTRA_SALTY Protease 3	22	Oxidation+M(15)	VWDNV SALQQTLP LMSEK	942	18	3	15.37	b10b16y6	2075.03	91.073	16661	3	692.35	-7.29
Q8ZMB5 PTRA_SALTY Protease 3	23	Oxidation+M(18)	GLANRDEVVA AIFS YL NMLREK	360	22	4	23.95	b3b4b6y8	2525.31	71.990	7427	2	1263.16	-4.16
Q8ZMB5 PTRA_SALTY Protease 3	24	Oxidation+M(15)	LADFFHQAVVEPQGMAILSQIAGS QNGK	904	28	3	17.62	y5y7y9	2972.45	98.141	5891	3	991.49	-13.96
Q8ZMB5 PTRA_SALTY Protease 3	25	Oxidation+M()	AYEQAIMPVQMISQVPYFSRDER	652	23	6	29.09	b6y7y9°y9y10y12	2774.34	99.289	5652	4	694.34	6.07
Q8ZMB5 PTRA_SALTY Protease 3	26		LADFFHQAVVEPQGMAILSQ	904	20	6	35.63	y8y9*y9y10°y10*y10	2201.11	136.380	1884	3	734.38	3.99
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	1		AVGWAA LQYVQPGTIVGVGTGST AAHFIDALGTMK	8	35	8	22.55	b2b4b11y7y10y14y19y35	3487.80	107.712	51988	3	1163.27	-1.33
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	2	Carbamidomethyl+C(3)	FICIADASK	112	9	7	61.16	b2b5y3y5y6y7y9	1024.51	51.026	29444	2	512.76	-6.08
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	3		GADVALIGTPDGVK	201	14	8	39.35	b4b6b11y1y2y5y7y14	1312.71	57.221	23588	2	656.86	-3.53
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	4		GQIEGAVSSSDASTEK	43	16	4	27.33	b4y3y5y9	1565.74	33.224	3264	2	783.37	7.02
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	5		LGGRPEYR	149	8	4	48.89	b7y3y4y6	947.51	56.135	1657	1	947.51	2.06
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	6		GQIEGAVSSSDASTEKLK	43	18	7	34.22	b3*b3b4*b4b8b13y10	1806.91	38.922	2339	2	903.96	1.55
P21267 GSA_SALTY Glutamate-1- semialdehyde 2	1		IIGGGMPVGA FGGRR	265	15	4	31.46	b12b13y7y10	1444.79	103.279	15010	2	722.90	7.01
P21267 GSA_SALTY Glutamate-1- semialdehyde 2	2		GLSFGAPTEMEVK	81	13	9	42.61	b5°b5b7y2y6°y6y8y12y13	1365.68	66.093	11291	2	683.34	2.50
P21267 GSA_SALTY Glutamate-1- semialdehyde 2	3	Carbamidomethyl+C(18)	VALAGA QDY YGVV PDLTCLGK	244	21	9	52.02	b2b10b11b12b13°b13b15y 2y12	2210.14	103.383	5679	2	1105.57	9.61
P21267 GSA_SALTY Glutamate-1- semialdehyde 2	4		AFTGVGGTPLFIEK	24	14	3	19.04	b7b11y3	1436.77	71.445	2635	2	718.89	-5.86
P21267 GSA_SALTY Glutamate-1- semialdehyde 2	5		GLSFGAPTEMEVKMAELVTNLVP TMDMVR	81	29	4	16.7	b7b13b16y11	3166.61	88.507	3672	3	1056.21	13.42

P21267 GSA_SALTY Glutamate-1-semialdehyde 2	6	Phosphoryl STY(11)	MAELVTNLVPTMDMVR	94	16	3	23.46	b8b9y4	1899.88	58.929	15387	2	950.44	4.37
P21267 GSA_SALTY Glutamate-1-semialdehyde 2	7	Carbamidomethyl+C(3); Oxidation+M(16)	ALCDEFGALLIIDEVMTGFR	224	20	6	30.23	b3b4b13y4°y4y9	2286.15	118.290	2998	2	1143.58	13.67
P37168 MVIM_SALTY Virulence factor mviM	1		ESVQAVTDGGLYDVTDMR	221	18	5	36.23	b7b8y3y4y18	1955.91	71.928	9100	2	978.46	2.43
P37168 MVIM_SALTY Virulence factor mviM	2		AGSQRESVQAVTDGGLYDVTDMR	216	23	5	35.29	b6y14y15*y15y16	2455.17	98.016	3219	2	1228.09	8.45
P37168 MVIM_SALTY Virulence factor mviM	3		FTLLDDYLHVVDTALWLAGGEAR	158	23	3	12.89	b7y8y14	2575.31	99.710	5930	3	859.11	-1.90
P37168 MVIM_SALTY Virulence factor mviM	4		AWLPVLTNTAGWTLQGAWSPSR	17	22	4	20.59	b4b11b13y21	2412.24	94.777	3322	4	603.81	-4.05
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	1		TMLNPGSALLTLSYLGAER	132	19	4	23.34	b11y4y7y14	2007.07	101.425	24703	2	1004.04	3.77
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	2		YMANAMGPEGVR	171	12	6	33.86	b2b5y6°y6y10y11	1295.59	44.979	18104	2	648.30	-1.22
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	3		VAHDISSYSFVAMAK	114	15	3	17.9	b7y8y11	1625.83	70.540	2493	2	813.42	19.82
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	4	Oxidation+M(13)	VAHDISSYSFVAMAK	114	15	3	17.9	b6y12y14	1641.79	113.470	1762	2	821.40	-1.86
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	1		AWDYLYEPDPK	202	11	4	27.03	b1b5y7y8	1396.63	48.106	4661	2	698.82	-5.16
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	2		YVESQVYQGIVENLASEQAAR	222	21	4	24.42	b4b5b9y3	2340.15	73.085	4579	2	1170.58	2.19
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	3		GVSFFNSVGGNVVAQVTGMGDNPSLSELIGPVK	121	33	4	16.78	b5°b5b13b23	3276.68	129.219	67496	3	1092.90	8.20
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	4		FINTMSQVPTITQLLPLASEDDDLK	174	26	7	21.59	b3*b3b9°b9y3y9y16	2886.42	94.771	36415	3	962.81	-20.64
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	5		IASVQNTQK	10	9	5	52.83	b4y3y5y7°y7	988.53	18.202	2426	2	494.77	-15.68
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	6		MAASRPYAETMR	38	12	4	36.87	b4y3y6y10	1383.68	113.271	1968	2	692.34	20.20
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	7		QASITQELTEIVSGAAAV	269	18	3	15.37	b4b6y5	1787.93	112.936	1769	2	894.47	-4.78
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	8	Phosphoryl STY(9)	QASITQELTEIVSGAAAV	269	18	7	39.71	b12b13°b13y9y10°y10y12_H3PO4 y12	1867.91	108.354	1647	2	934.46	8.50
Q8ZKW8 ATPG_SALTY ATP synthase gamma chain	9	Oxidation+M(5)	FINTMSQVPTITQLLPLASEDDDLKR	174	27	6	35.63	b7b8b10*b10y7y8	3058.56	136.236	15874	4	765.40	-4.79
P62405 RL5_SALTY 50S ribosomal protein L5	1		LLDNAAADLTAISGQKPLITK	48	21	9	48.2	b3b4b5*b5y2y5y9y14y21	2153.21	75.458	92254	3	718.41	-4.42
P62405 RL5_SALTY 50S ribosomal protein L5	2		LMTEFNYSVMQVPR	15	15	6	17.9	b13y2y10°y10y13*y13	1828.86	76.222	6891	3	610.29	-6.67
P62405 RL5_SALTY 50S ribosomal protein L5	3		EQIIFPEIDYDK	133	12	4	22.01	b9°b9b11y3	1509.73	67.743	5985	3	503.92	-9.06
P62405 RL5_SALTY 50S ribosomal protein L5	4		LHDYYK	3	6	3	39.73	b4y3y4	838.41	73.154	10692	1	838.41	4.73
P62405 RL5_SALTY 50S ribosomal protein L5	5		DEVVNK	9	6	1	13.52	b3	703.35	43.321	9645	1	703.35	-12.15
P62405 RL5_SALTY 50S ribosomal protein L5	6		EQIIFPEIDYDKVDR	133	15	6	55	b12y3y6y7y10y11	1879.93	73.214	54716	3	627.31	-7.27
P62405 RL5_SALTY 50S ribosomal protein L5	7		SFDGRGNYSMGVR	120	13	5	29.3	b6b12y7y11°y11	1445.66	55.097	10146	3	482.56	-2.20
Q7CPH8 SECB_SALTY Protein-export protein secB	1		GTFPQLNLAPVNFDAFMNYLQQQAGEGTEEHQDA	120	35	4	12.7	b6b9y3y26	3893.81	116.102	10263	3	1298.61	1.63
Q7CPH8 SECB_SALTY Protein-export protein secB	2		IYTKDVSFEAPNAPHVFQK	15	19	3	21.7	b3b7b17	2191.12	75.479	8610	4	548.54	2.34
Q7CPH8 SECB_SALTY Protein-export protein secB	3		LDLDTASSQLADDVYEVVLR	41	20	5	22.32	b8b10*b10b13y11	2222.11	109.712	5568	3	741.37	-5.16

Q7CPH8 SECB_SALTY Protein-export protein secB	4		DVSFEAPNAPHVFQKDWQPEVK	19	22	4	19.79	b3°b3b8b10	2568.22	86.572	330677	3	856.74	-12.36
Q7CPH8 SECB_SALTY Protein-export protein secB	5		IYTKDVSFEAPNAPHVFQK	15	19	3	23.92	y12y13y15	2191.15	88.639	20917	3	731.05	13.71
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1		GGDNYSDKPAPLGGGGAR	151	18	10	82.86	b2b12y6y7y8y9y10y11y13y18	1688.78	33.167	80168	3	563.60	-13.95
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2	Carbamidomethyl+C(3)	FACGVIEK	169	8	8	66.77	y2°y2y3y4y5y6y7y8	923.46	41.171	16765	1	923.46	-4.10
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3		EVPALMAGGHLDPEK	84	15	6	36.63	b7°b7b10b14y5y13	1563.80	84.049	7490	2	782.40	11.79