

MA6926 + Zn(II) LC-MS run 1: 6926_Zn_220709_1a2_01

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)
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	1		IAAANVPAFVSGK	70	13	24	195.23	b2b3b4b5*b5b6*b6b10y2y3y4y5y6y7°y7y8y9*y9y10*y10y11*y11y12y13	1244.69	60.221	648149	2	622.85	-4.32
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVGFGTFK	22	29	48	402.63	b2b3b4b5°b5b6°b6b7°b7b8°b8b9°b9b16b18b19b20b23b25b26b28b29y1y2y3y4°y4y6°y6y7y8y10y11y13*y13y14*y14y15y17y19y20y21y22y23y24y25y26y29	2966.57	114.932	449179	3	989.53	0.58
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	3		EGDAVQLVGFGTFK	37	14	6	32.54	b5b8*b8b12y6y14	1467.75	78.860	7111	2	734.38	0.00
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	1		AAADLQLQGV PAMFVNGK	158	18	32	267.52	b1b2b3b4b5°b5b6°b6b7b8b9b10b13b14b15y2y3*y3y4*y4y5*y5y7y8y10y11*y11y12y13*y13y14y18	1829.97	81.474	224431	2	915.49	4.00
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	2		YQINPQGMdTSSMDVFVQYYADTVK	176	25	16	92.93	b1b2*b2b3b4b11b14y3y4y5y6y7°y7*y7y12y20	2865.32	87.112	108176	3	955.78	3.66
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	3		YHVEFLGPLGK	77	11	15	118.04	b2b3b4b5°b5b6°b6b7b8°b8y2y3y5y9y11	1259.68	69.795	87852	2	630.34	0.68
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		TQTVQSAADIR	116	11	20	132.83	b2°b2b3°b3b4b8°b8*b8b9b11y2y3y5y6y7°y7*y7y8y9y11	1189.61	35.850	80603	2	595.31	-4.82
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	5		ELTQAWAVAMALGVEDK	88	17	5	16.93	b4°b4*b4b8y9	1831.95	102.267	1559	3	611.32	15.06
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	6	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	4	23.85	b6b8y7y12	1847.91	107.864	2955	2	924.46	-8.46
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	7	Oxidation+M(21)	YHVEFLGPLGKELTQAWAVAMALGVEDK	77	28	3	12.01	b5y5y12	3088.57	53.073	2362	4	772.90	-2.29
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	8	Oxidation+M(13)	AAADLQLQGV PAMFVNGK	158	18	7	44.89	b5b6°b6b8b9°b9y7	1845.97	105.092	2112	2	923.49	10.45
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	9		HVEFLGPLGK	78	10	1	8.01	b4	1096.61	69.772	9018	2	548.81	-8.57
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	10		PAMFVNGK	168	8	3	35.08	b3b4b5	863.44	81.452	3194	1	863.44	-4.31
P0A1H5 EFTU_SALTY Elongation factor Tu	1		AIDKPFLLPIDVFSISGR	205	19	29	231.41	b2b3b4°b4b6°b6b7b8b9b12b13y1y2y3y4y5y6°y6y7y8°y8y9°y9y10y11°y11y12y15y19	2117.15	104.648	377981	3	706.39	-6.92
P0A1H5 EFTU_SALTY Elongation factor Tu	2		AGENVGVLLR	270	10	12	105.38	b1b4b5°b5b6y2y3y4y5y6y7y10	1027.58	56.978	278257	2	514.30	-6.65

P0A1H5 EFTU_SALTY Elongation factor Tu	3		ELLSQYDFPGDDTPIVR	155	17	22	216.14	b2b6b7°b7b12b13b15b16y1y2y3y4y5y6y8y9y10y11y12y13y14y17	1964.97	77.466	243406	2	982.99	6.09
P0A1H5 EFTU_SALTY Elongation factor Tu	4		GITINTSHVEYDTPTR	59	16	25	184.9	b2b3°b3b9b10b12b16y3°y3y4°y4y5°y5y6y7y8y9°y9y10y12*y12y13y14°y14y16	1803.87	50.171	195031	3	601.96	-12.32
P0A1H5 EFTU_SALTY Elongation factor Tu	5		TTLTAAITTVLAK	25	13	20	150.65	b2°b2b3°b3b4°b4b6°b6b13y2y3y4y5y6y7y8y9y10y11y13	1303.78	84.987	192919	2	652.40	0.00
P0A1H5 EFTU_SALTY Elongation factor Tu	6		TTDVTGTIELPEGVEMVMPGDNI K	334	24	33	210.06	b2°b2b3°b3b4°b4b5°b5b8°b8b9b10°b10b13b17b18y2y3y5y6°y6*y6y7y8y9y10y12y14*y14y15°y15y16y24	2546.26	87.338	175572	2	1273.63	8.92
P0A1H5 EFTU_SALTY Elongation factor Tu	7		QVGVPYIIVFLNK	124	13	11	85.72	b3b4b7b13y1y4y5y6y9y11y13	1489.88	99.512	169347	2	745.44	0.25
P0A1H5 EFTU_SALTY Elongation factor Tu	8		IELAGFLDSYIPEPER	188	17	22	204.26	b2b3b4b5b7b11°b11b12b14y1y3y4y5y6y7y8y9y11°y11y12y13y17	1962.03	102.414	167915	2	981.52	3.98
P0A1H5 EFTU_SALTY Elongation factor Tu	9		ALEGDAEWEAK	177	11	7	83.46	y4y5y6y7y8y9y11	1218.56	46.757	85023	2	609.78	-2.20
P0A1H5 EFTU_SALTY Elongation factor Tu	10	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	8	59.55	b6y2y4y6y7°y7y8y10	1187.52	53.376	80215	2	594.26	-2.26
P0A1H5 EFTU_SALTY Elongation factor Tu	11		VGEEVEIVGIK	238	11	7	53.91	b1b3b5y3y5y7y11	1171.65	60.822	49849	2	586.33	-2.92
P0A1H5 EFTU_SALTY Elongation factor Tu	12	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEVR	137	18	17	117.79	b2b3b11y1y2y3°y3y5y6°y6y7y8y9y11y13y14y18	2224.01	106.536	37592	2	1112.51	12.62
P0A1H5 EFTU_SALTY Elongation factor Tu	13		NMITGAAQMDGAILVVAATDGP MPQTREHILLGR	90	34	6	18.16	b3b9b29y1y4y13	3547.80	93.809	26017	3	1183.27	-3.85
P0A1H5 EFTU_SALTY Elongation factor Tu	14		NMITGAAQMDGAILVVAATDGP MPQTR	90	27	8	26.94	b8°b8b21y7*y7y10y11y27	2729.32	106.200	24523	3	910.44	-8.14
P0A1H5 EFTU_SALTY Elongation factor Tu	15		FESEVYILSKDEGGR	304	15	4	30.42	b7b12b13y12	1728.82	86.541	9524	3	576.95	-11.72
P0A1H5 EFTU_SALTY Elongation factor Tu	16		VGEEVEIVGIKETQK	238	15	3	18.81	b3b9y12	1657.88	84.037	3146	2	829.45	-10.82
P0A1H5 EFTU_SALTY Elongation factor Tu	17		MVVTLIHPIAMDDGLR	358	16	21	203.2	b3b4°b4b5°b5b7°b7y3y4y5y6y7y8y9°y9y10°y10y11y12y13y15	1780.92	79.350	515675	3	594.31	-15.42
P0A1H5 EFTU_SALTY Elongation factor Tu	18		EHILLGR	117	7	5	57.9	b3°b3b4y3y5	837.48	40.208	135178	2	419.24	-16.98
P0A1H5 EFTU_SALTY Elongation factor Tu	19		TVGAGVVAK	382	9	9	76.69	b3°b3b4°b4b7°b7y3y7y8	801.47	29.029	111413	2	401.24	-19.50
P0A1H5 EFTU_SALTY Elongation factor Tu	20		GYRPQFYFR	325	9	9	106.77	b3b5b6y3y4y5*y5y6y7	1233.59	58.946	84139	3	411.87	-17.91
P0A1H5 EFTU_SALTY Elongation factor Tu	21		TKPHVNVGTIGHVDHGK	8	17	4	30.84	b3b14y5y6	1795.93	90.439	58060	3	599.31	-17.33
P0A1H5 EFTU_SALTY Elongation factor Tu	22	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	3	24.83	b3b4y4	1768.75	31.532	28141	4	442.94	-17.81
P0A1H5 EFTU_SALTY Elongation factor Tu	23		EEIER	284	5	1	13.53	y3	675.33	65.003	2321	1	675.33	-0.90
P0A1H5 EFTU_SALTY Elongation factor Tu	24	Carbamidomethyl+C(23)	GITINTSHVEYDTPTRHYAHVDCP GHADYVK	59	31	3	22.98	y7y8y10	3553.61	49.379	53207	5	711.53	-14.08
P0A1H5 EFTU_SALTY Elongation factor Tu	25		IIELAGFLDSYIPEPERAIDKPFLLP IEDVFSISGR	188	36	9	54.25	b3b4b6b7y5y6°y6y8y11	4060.16	123.362	53098	4	1015.80	-0.84
P0A1H5 EFTU_SALTY Elongation factor Tu	26		GTVVTGRVER	224	10	10	93.61	b3°b3b6b9y3°y3y6y7°y7y8	1073.60	26.148	46487	2	537.30	-8.53

P0A1H5 EFTU_SALTY Elongation factor Tu	27		HTPFFKGYRPQFYFR	319	15	4	32.8	b10b11y3y8	1991.01	103.368	35264	2	996.01	0.18
P0A1H5 EFTU_SALTY Elongation factor Tu	28	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLE LVEMEV	124	31	9	80.07	b4*b4b7y3y4y5y6y7y8	3694.85	128.084	18357	3	1232.29	3.30
P0A1H5 EFTU_SALTY Elongation factor Tu	29	Carbamidomethyl+C(7)	HYAHVDCPGHADYVKNMITGAA QMDGAILVVAATDGPMPQTR	75	42	6	38.17	b3b4b5y6*y6y8	4479.12	112.099	9098	5	896.63	3.05
P0A1H5 EFTU_SALTY Elongation factor Tu	30		GYRPQFYFRTTDDVTGTIELPEGVE MVMPGDNIK	325	33	6	29.75	b5b6*b6y4y7y10	3760.79	97.931	9053	3	1254.27	-12.33
P0A1H5 EFTU_SALTY Elongation factor Tu	31		AFDQIDNAPEEKAR	45	14	3	19.98	b9b13y5	1603.79	84.239	5191	2	802.40	13.85
P0A1H5 EFTU_SALTY Elongation factor Tu	32		TYGGAARAFDQIDNAPEEK	38	19	12	81.86	b4b7b8*b8b9b10b12*b12*b12y3y11y12	2052.98	92.166	3411	3	685.00	6.90
P0A1H5 EFTU_SALTY Elongation factor Tu	33	Oxidation+M(1)	MVVTLIHPIAMDDGLR	358	16	6	51.6	y3y5y8y9y10*y10	1796.92	74.182	30596	3	599.64	-11.68
P0A1H5 EFTU_SALTY Elongation factor Tu	34	Carbamidomethyl+C(3); Oxidation+M(8)	STCTGVEMFRK	253	11	4	25.08	b5y3y7*y7	1331.61	43.832	3503	2	666.31	2.84
P0A1H5 EFTU_SALTY Elongation factor Tu	35		NTSHVEYDTPTR	63	12	7	40.8	b4*b4*b4b6b7*b7b8	1419.65	50.164	2013	2	710.33	-0.95
P0A1H5 EFTU_SALTY Elongation factor Tu	36		NMITGAAQMDGAILVVAATDGP MPQTREHILGR	90	34	0	10.92		3530.74	93.867	15113	4	883.44	-13.35
P0A1H5 EFTU_SALTY Elongation factor Tu	37		GITINTSHVEYDTPTR	59	16	0	4.14		1785.86	50.182	9043	3	595.96	-6.90
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	1		DQIIEAVSAMSVM DVVELISAMEE K	5	25	27	187.07	b2*b2b3b4*b4b5b6b7*b7b8*b8b10b14y1y2*y2y3y4y5y6y7y9*y9y10y11y12y25	2737.34	137.096	29142	3	913.12	0.71
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		SITK DQIIEAVSAMSVM DVVELISAMEE K	1	29	19	123.41	b2*b2b5b9b14b16y1y2*y2y3y4y5y6y7y8y9*y9y10y12	3166.61	136.446	9478	3	1056.21	5.17
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	3		SLEEAGAEVEVK	109	12	4	23.03	b10y7y11*y11	1260.64	64.992	6096	2	630.82	6.20
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	4		FGVSAAAAVAVAAGPAEAAEEK	30	22	6	40.74	b3y6y9y10y13y16	1987.04	106.890	1902	2	994.02	12.59
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	5		AAGANKVAVIK	60	11	12	131.58	b3b7*b7b8b9b10y4y5y6y7*y7y9	1041.63	29.607	50171	2	521.32	-9.73
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	6		MSITK DQIIEAVSAMSVM DVVELISAMEE K	0	30	4	17.54	b3*b3b14b17	3297.63	99.350	7546	3	1099.88	-1.92
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	7	Phosphoryl STY(3)	GATGLGLKEAK	74	11	3	25.08	b10y8y10	1124.57	61.565	19627	2	562.79	7.92
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	8	Oxidation+M(22)	DQIIEAVSAMSVM DVVELISAMEE K	5	25	5	40.32	b9b16y12y13y14	2753.35	136.649	4626	3	918.45	6.92
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	39	260.72	b2b3b4*b4b5*b5*b5b6*b6b8*b8b14y1y3y5y6y7*y7y7y8*y8*y8y9y10*y10y11y14y15*y15y16y18*y18y19y20y21y22*y22y24*y24	2574.31	98.501	502819	3	858.78	-4.17
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	2		LVSWYDNETGYSNK	307	14	15	142.72	b8y2y3y4y5y6y7y8*y8y9y10y11y12*y12y14	1675.77	58.863	251159	2	838.39	7.65
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	3		AGIALNDNFVK	296	11	21	126.81	b3b4b10*b10*b10y1y2y3y4y5*y5y6*y6y7*y7y8*y8*y8y10y11*y11	1161.62	61.995	224435	2	581.31	-5.04

[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		GASQNIIPSSTGAAK	198	15	26	160.68	b3b4°b4*b4b5°b5*b5b6°b6*b6b7°b7*b7b13b15y2y5y6°y6y7°y7y8y9y10y11y15	1401.73	41.612	196110	2	701.37	-3.05
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		VLDLIAHISK	321	10	10	89.63	b2b3y2y3y4y5y6y7y8y10	1108.66	65.298	113166	2	554.84	-7.93
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		AATYEQIK	249	8	4	41.73	y4y5y6y8	923.47	31.377	113043	2	462.24	-13.62
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		SDIEIVAINDLLDAEYMAYMLK	24	22	27	235.35	b2b3b4°b4b5°b5b6°b6b7°b7b14b15y1y2y3y4y5y6y7y8y9y10y11y12y13y14y22	2530.24	126.223	89865	3	844.08	-3.67
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		VPTPNVSVVDLTVR	232	14	5	39.74	y3y5y11y12y14	1495.85	71.662	55170	2	748.43	1.22
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		VVLTGPSKDNTPMFVK	116	16	12	77.57	y2y9y10°y10*y10y11y12y13°y13y14y16*y16	1732.91	58.116	52248	3	578.31	-12.26
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		VLPELNGK	217	8	10	55.27	b1b2y2y3y4*y4y5y6*y6y8	869.50	45.359	36920	2	435.25	-12.64
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11		VGINGFGR	4	8	3	36.96	b3y3y7	819.45	42.446	16210	2	410.23	-0.45
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEGQDIVSNASCTTNCL APLAK	132	28	37	351.95	b3b4b5b6b7°b7b8°b8b9b10b11*b11b12°b12*b12b13b15b16b21b24°b24b26b27y4y5y6y8*y8y9y10y11y12*y12y13y14y15y16	3044.42	67.215	243020	3	1015.48	4.89
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13		LVSWYDNETGYSNKVLDLIAHISK	307	24	9	92.98	y3y4y5y7y15y19y20y21y22	2765.38	96.880	203809	4	692.10	-13.60
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14		VLPELNGKLTGMAFR	217	15	9	53.17	b7°b7b11y4y5y6y10°y10*y10	1645.89	73.356	19410	3	549.30	-10.31
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15		GGRGASQNIIPSSTGAAK	195	18	6	41.88	b5b7b8b9y8°y8	1671.88	37.081	15030	2	836.45	3.87
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		SDIEIVAINDLLDAEYMAYMLKYD STHGR	24	29	4	11.81	b10*b10b23y10	3346.64	89.192	5645	4	837.41	11.53
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		DLIAHISK	323	8	4	53.01	b3b4b5b7	896.51	65.305	34657	2	448.76	-10.48
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		LDLIAHISK	322	9	1	8.43	b3	1009.60	65.304	34043	2	505.30	-8.28
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19		LNDNFVK	300	7	0	2.26		849.44	62.036	4921	1	849.44	-9.84
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20		LIAHISK	324	7	2	21.17	b4b6	781.48	65.302	2938	2	391.24	-13.59
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	21		AATYEQIK	249	8	0	1.13		905.46	31.355	39051	2	453.24	-5.33

[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	22		VVLTGPSKDNTPMFVK	116	16	0	4.14		1715.91	58.110	37508	2	858.46	7.47
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	39	262.77	b2°b2b3°b3b4°b4b5°b5b6b7°b7b8°b8b9b11b12°b12b14b21y1y2y3y4y6°y6y7*y7y8y9y12y13y14y15y16°y16*y16y17*y17y21	2216.12	97.518	451899	2	1108.56	11.90
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	11	66.92	y2y6y7*y7y8y9*y9y10°y10*y10y11	1304.56	33.502	76235	2	652.78	-5.05
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	3		REEESAAAAEVEER	40	14	8	68.06	b2b7y3y4y5y6y7y14	1575.73	32.290	45850	2	788.37	4.03
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	4	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	5	33.35	b4y8y9y11y13	1624.76	93.202	21663	2	812.88	10.59
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	5		LQQYREMLIADGIDPNELLNSMAAAK	57	26	8	33.91	b7b9°b9b13y7y8*y8y12	2904.49	100.198	16424	4	726.88	8.99
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	6		EEESAAAAEVEER	41	13	6	64.39	b3y4y6y7y8y10	1419.62	35.582	6480	2	710.31	-0.77
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	7		TPAVIKK	114	7	5	41.35	b1y2y4y5y6	756.49	20.243	5529	2	378.75	-14.85
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	8	Carbamidomethyl+C(6)	AQARECTLETLEEMLEK	15	17	3	16.93	b7y8y12	2050.99	92.163	1694	4	513.50	6.07
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	9		MSEALK	0	6	1	13.91	b5	678.36	75.882	5237	1	678.36	11.88
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	10		YSYVDENGETKTWTGQGR	96	18	29	203.24	b3°b3b5°b5y3y4y5°y5*y5y6*y6y7°y7*y7y8°y8*y8y10°y10y11*y11y12y13y14*y14y15y16y17*y17	2090.92	47.354	179222	3	697.65	-10.04
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	11	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEVVNER	19	21	27	257.78	b3°b3b4°b4b6b7y3*y3y4*y4y5°y5y6y7y8y9y10y11y12y13y14y15y16y17°y17y19°y19	2563.26	123.982	113971	3	855.09	0.38
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	12		QLEDFLIKE	128	9	3	39.1	y3y4y7	1134.59	71.986	72164	2	567.80	-10.76
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	13		LQQYREMLIADGIDPNELLNSMAAAK	57	26	6	44.48	b10b14y7y8y12y13	2904.50	93.405	23075	3	968.84	12.69
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	14	Carbamidomethyl+C(6)	AQARECTLETLEEMLEK	15	17	3	23.92	b14b15y3	2050.96	88.289	1811	3	684.32	-10.00
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	15	Oxidation+M(7)	LQQYREMLIADGIDPNELLNSMAAAK	57	26	5	18.96	b3°b3b11b21y8	2920.42	88.275	3092	3	974.15	-10.28
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	16		AAEVEER	47	7	0	3.39		803.39	32.259	2748	2	402.20	1.44
[P64076]ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	31	257.9	b2°b2b3°b3b4°b4b5b6°b6°b6b7°b7b8b12°b12b13°b13b14y2y3y4y5y6y7y8y9y11y12y13y15*y15	1605.88	86.261	289421	2	803.45	-0.61
[P64076]ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	33	219.26	b1°b1b2°b2b3°b3b5b11b12°b12b14°b14b15b16b18b22y1y2y4y5y7y8y9y11y12*y12y13°y13y14y15y16y17y22	2118.07	76.072	165326	2	1059.54	4.26
[P64076]ENO_SALTY Enolase	3	Carbamidomethyl+C(16)	AAGYELGKDITLAMDCAASEFYKDGK	231	26	20	127.37	b2b3b4b6b9b11°b11y2y7y8°y8y9y12y13y14y16y20y21y24y26	2824.28	98.259	146788	4	706.83	-13.74

P64076 ENO_SALTY Enolase	4		AFTSEEFTHFLEELTK	266	16	16	123.65	b2b3°b3b11b12b16y3y4y5° y5y6y7y8y10y13y16	1928.91	103.358	109378	3	643.64	-11.45
P64076 ENO_SALTY Enolase	5		GMNTAVGDEGGYAPNLGSNAEA LAVIAEAVK	200	31	23	116.67	b2b4b5°b5b6°b6°b6b8b13 b30y1y2y3y5°y5y6y7y8y10 y15y18y19y31	2989.48	95.633	105224	3	997.16	6.70
P64076 ENO_SALTY Enolase	6		DAGYTAVISHR	360	11	14	118.04	b2b3b4b5y2y3y4y5y6°y6y7 y9°y9y11	1189.59	41.938	83508	2	595.30	-3.49
P64076 ENO_SALTY Enolase	7		GMPLYEHIAELNGTPGK	126	17	9	59.89	b2b10b12b15y3y4y5y11y1 7	1826.89	67.589	65072	3	609.63	-11.23
P64076 ENO_SALTY Enolase	8		YSMPVPMMNIINGGEHADNNVDI QEFMIPVGAK	143	34	18	83.21	b2°b2b3°b3b5°b5b6b10y3y 5y6°y6y7y8y13y29y31y34	3759.79	99.030	61435	3	1253.94	7.66
P64076 ENO_SALTY Enolase	9		IQLVGDDLFTVNTK	311	14	13	91.84	b2°b2b7b8y2y3y4y9y10y1 1°y11y12y14	1562.85	78.238	36952	2	781.93	4.92
P64076 ENO_SALTY Enolase	10		ILKEGIEK	325	8	8	55.27	b2y4°y4y5°y5y6y7y8	929.56	29.401	33007	2	465.28	-11.49
P64076 ENO_SALTY Enolase	11		IEEALGEK	411	8	10	50.49	b2b4b8y3°y3y6°y6y7°y7y8	888.46	31.630	18081	2	444.73	-6.87
P64076 ENO_SALTY Enolase	12		VIGREIIDSR	6	10	4	27.71	b6b8y2y3	1157.65	43.017	15522	2	579.33	-12.44
P64076 ENO_SALTY Enolase	13		MGSEVFHHLAK	184	11	5	49.14	b7b10y4y6y7	1255.61	42.416	81545	3	419.21	-16.04
P64076 ENO_SALTY Enolase	14		GIANSILJK	333	9	3	39.1	y3y6y7	928.57	60.923	77449	2	464.79	-11.50
P64076 ENO_SALTY Enolase	15		EIIDSR	10	6	1	13.91	b4	732.38	28.913	19694	1	732.38	-8.42
P64076 ENO_SALTY Enolase	16		GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	3	17.54	y4y8y12	2856.35	87.997	8946	3	952.79	-3.68
P64076 ENO_SALTY Enolase	17		AAGYELGK	231	8	3	49.51	b3b5b7	808.44	38.656	1896	1	808.44	22.12
P64076 ENO_SALTY Enolase	18		VLGDKIQLVGDDLFTVNTK	306	19	14	100.58	b7°b7b8b9y4°y4y5°y5y6y 8y10y11°y11y17	2075.12	80.050	127107	3	692.38	-6.59
P64076 ENO_SALTY Enolase	19		GMPLYEHIAELNGTPGKYSPMPV MMNIINGGEHADNNVDIQEFMIQP VGAK	126	51	16	92.03	b8b9b13°b13b14b20b22y3 y5y7y8y9y11y12y13°y13	5567.66	98.317	97567	5	1114.34	1.23
P64076 ENO_SALTY Enolase	20		DGKYVLAGEGK	254	12	6	45.53	b4b11y3y4°y4y9	1250.62	44.251	69677	2	625.81	-12.88
P64076 ENO_SALTY Enolase	21		GKGMNTAVGDEGGYAPNLGSNA EALAVIAEAVK	198	33	6	25.36	b4b5°b5b7b15y4	3174.60	90.441	29283	3	1058.87	9.31
P64076 ENO_SALTY Enolase	22		SGETEDATIADLAVGTAAGQIKTG SMSR	371	28	4	12.01	b3y4°y4y6	2737.35	74.660	9116	3	913.12	7.94
P64076 ENO_SALTY Enolase	23		EIIDSRGNPTVEAEVHLEGGFVG MAAPSASTGSR	10	36	3	10.98	b13y5y16	3569.77	93.817	5969	3	1190.59	10.33
P64076 ENO_SALTY Enolase	24		DAGYTAVISHRSGETEDATIADLA VGTAAGQIK	360	33	5	36.9	b6°b6b10b11b12	3288.63	74.653	2145	4	822.91	-0.82
P64076 ENO_SALTY Enolase	25	Oxidation+M(18)	GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	4	11.63	b10°b10b19y5	2872.35	92.700	8880	3	958.12	-0.34
P64076 ENO_SALTY Enolase	26	Oxidation+M(2)	IMIDLDGTENK	92	11	4	28.09	b7b8y8°y8	1264.61	31.063	3535	3	422.21	2.41
P64076 ENO_SALTY Enolase	27		GYTAVISHR	362	9	2	8.01	b3°b3	1003.53	41.947	30495	2	502.27	-4.74
P64076 ENO_SALTY Enolase	28		LKEGIEK	326	7	0	1.13		816.47	29.409	22988	2	408.74	-12.78
P64076 ENO_SALTY Enolase	29		AGYTAVISHR	361	10	0	2.26		1074.57	41.937	14319	2	537.79	1.36
P64076 ENO_SALTY Enolase	30		GREIIDSR	8	8	2	22.93	b3b4	945.50	43.018	4321	2	473.26	-7.10
P64076 ENO_SALTY Enolase	31		TSEEFTHFLEELTK	268	14	3	35.2	b10b11b12	1710.83	103.385	2877	2	855.92	3.57
P64076 ENO_SALTY Enolase	32		AFTSEEFTHFLEELTK	266	16	0	4.14		1910.89	103.352	3950	3	637.64	-10.67
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	1		NYDQVPANKPIVDAIK	271	16	18	137.45	b2°b2b3°b3°b3b4°b4b5y2 y3y5y7y9y10y11y12y13y1 6	1784.93	54.360	241820	3	595.65	-14.84
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	2		TQFMGPEGVANVLSNIAGESAE GLLVTKPK	240	31	24	191.62	b2b3b4b5b9b12y2y3y4y5y 6y8y13y14y17y19y20y22y 26y27°y27y28y29y31	3144.63	89.048	229426	3	1048.88	1.09

P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	3		TTGLDSDQGPTAAK	137	14	30	198.62	b2°b2b3°b3b4b5°b5b8b10* b10b11b12°b12°b12y1y2y 3y5y6y8y9°y9*y9y10°y10* y10y11y12*y12y14	1361.65	30.111	205507	2	681.33	-3.68
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	4		ENIDFVYYGGYHPMGQILR	212	20	16	101.23	b2b4°b4°b4y3y6y8y9y12°y 12*y12y13y14y16y17y20	2401.12	80.556	103418	3	801.05	-1.53
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	5	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILM ITPAATAPELTAR	92	38	24	190.92	b2b7b10b12°b12b14°b14b 23b24b25b26b27y1y4y5y6 y7y8y11y12y13y14y15y38	4078.01	89.956	99363	3	1360.01	7.18
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	6		GGVNVVFFDGITAGEKDFSTLVA R	185	24	21	190.21	b4b5°b5b6°b6b13y2y5y6y 7y8y12y13y15y16y17y18y 19y20y21y24	2499.28	102.280	96819	3	833.76	-3.42
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	7		VAVVGAMSGPVAQYGDQEFTGA EQAIADINAK	25	32	12	63.33	b1b3b6b14y3y5y6y7y10y1 2y13y32	3207.59	90.585	83249	3	1069.87	8.75
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	8		QDPSGAFVWTTYAALQSLQAGLN HSDDPAEIAK	290	33	5	11.22	b10°b10y8y10y33	3501.73	109.906	9017	3	1167.92	11.16
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	9		GATVDTVMGPLSWDEK	326	16	3	17.8	b3b11y9	1705.82	79.034	5806	2	853.41	6.94
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	10		GFEFGVFDWHANGTATDAK	346	19	4	22.45	b2y5y7y14	2069.96	84.087	2451	2	1035.48	12.50
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	11		KQDPSGAFVWTTYAALQSLQAGL NHSDPAEIAK	289	34	46	335.79	b3°b3°b3b5°b5°b5b6°b6b7 *b7b8°b8b9b10b12°b12b1 3°b13b14°b14b15b18b28y 3y6y7y9y11y12y14°y14y15 °y15°y15y16y17y18°y18y1 9y20°y20y21y22y23y24y25	3629.77	102.849	327284	4	908.20	-5.11
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	12		TQFMGPEGVANVSLNIAGESAE GLLVTKPKNYDQVPANKPIVD AIK	240	47	5	14.4	b10b25y3y10y30	4910.55	86.690	23149	5	982.92	-2.59
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	13	Carbamidomethyl+C(14)	VVNDGIKYVIGHLCSSSTQPASDI YEDEGILMITPAATAPELTAR	85	45	9	50.42	b4b5b19y3y4y6y7y11y13	4803.41	94.662	20140	4	1201.61	4.47
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	14		KGGVNVVFFDGITAGEK	184	17	5	16.93	b5°b5y3°y3y16	1737.92	33.353	17987	4	435.24	3.37
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	15		KENIDFVYYGGYHPMGQILR	211	21	3	14.38	b5b10y8	2529.25	48.230	2827	3	843.76	11.29
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	16		GDLKGFEFGVFDWHANGTATDA K	342	23	5	38.67	b7y7y9y10y11	2483.14	86.640	2323	3	828.39	-8.55
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	17	Oxidation+M(8)	GATVDTVMGPLSWDEK	326	16	3	17.8	b3b6y7	1721.83	62.922	4784	3	574.61	13.82
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	18	Carbamidomethyl+C(6); Oxidation+M(14)	TLLAGCIALSLSHMAFADDIK	4	21	5	25.52	b14°b14y7y12y13	2263.13	95.341	4452	3	755.05	-8.85
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		LADVLAANAR	57	11	15	113.27	b2b3°b3b4°b4b8y1y4y5y6* y6y7y9y10y11	1084.60	53.911	137011	2	542.80	-8.55
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGSLGDQVNVK	8	14	19	178.09	b1b2b3b4b6b12b13y3y4y6 y7y8y9y10*y10y11y12y14 *y14	1413.77	57.454	84787	2	707.39	0.69
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		MQVILLDK	0	8	7	64.03	b2b3y3y4y5y6y8	959.55	64.839	60652	2	480.28	-9.29
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		DIADAVTAAGVDVAK	97	15	5	46	b13y3y7y9y13	1415.74	66.958	54612	2	708.37	2.50

Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		INALETVTIASK	71	12	6	41.21	b3*b3b4y10y11y12	1259.72	61.720	32155	2	630.36	-3.39
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		LFGSIGTR	89	8	4	52.26	b4b7y6y7	850.47	52.387	15846	2	425.74	-9.69
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		TTGEHEVNFQVHSEVFAK	123	18	6	16.16	b1b2b9b11y16y18	2059.01	67.627	11260	2	1030.01	9.72
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		NVEYFEARR	42	9	4	31.32	b5b7y7y9	1183.57	37.778	5399	2	592.29	-12.07
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	9		AGDEGKLFSGIGTR	83	14	8	67.92	b7b10°b10b12y3y6y7y8	1407.70	55.074	79108	3	469.91	-14.13
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	10		KNVEYFEAR	41	9	3	31.32	b7b8y4	1155.58	87.052	2074	2	578.29	-2.96
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	11	Phosphoryl STY(15)	LFGSIGTRDIADAVTAAGVDVAK	89	23	5	20.88	b3b7b13°b13y9	2327.19	78.956	1586	2	1164.10	14.58
P66593 RS6_SALTY 30S ribosomal protein S6	1		AHYVLMNVEAPQEVIDELETTFR	56	23	24	181.64	b2b3b4b5b8b9b10b13°b13y2y3y4y5°y5y6y7°y7y8y9y11°y11y13y14y23	2704.33	110.516	127236	3	902.11	0.36
P66593 RS6_SALTY 30S ribosomal protein S6	2		YSAAITGAEGK	24	11	18	117.08	b2°b2b3°b3b4°b4y2y3°y3y4y5y6°y6y7°y7y9y10y11	1067.52	34.023	94714	2	534.27	-11.78
P66593 RS6_SALTY 30S ribosomal protein S6	3		FNDAVIR	79	7	11	84.97	b3°b3b5y1y2y3y4y5y6*y6y7	834.43	42.511	57138	2	417.72	-14.56
P66593 RS6_SALTY 30S ribosomal protein S6	4		HAVTEASPMVK	93	11	17	164.67	b2b3b4°b4b5°b5b6b7°b7b10y5y6y7y8y9y10y11	1169.59	30.786	39660	2	585.30	-5.43
P66593 RS6_SALTY 30S ribosomal protein S6	5		HYEIVFMVHPDQSEQVPGMIER	2	22	3	23.78	b3b7b8	2641.20	37.389	52303	3	881.07	-18.86
P66593 RS6_SALTY 30S ribosomal protein S6	6		AHYVLMNVEAPQEVIDELETTFRFNDAVIR	56	30	24	230.38	b3b4b6b7b8b9°b9b10b11b14b17y4y11y12y13y14y15y16y17y18y20*y20y21y22	3519.74	115.460	74014	4	880.69	-5.76
P66593 RS6_SALTY 30S ribosomal protein S6	7		YSAAITGAEGKIHR	24	14	4	19.98	b6°b6y3y8	1473.76	38.310	5441	3	491.93	-11.43
P66593 RS6_SALTY 30S ribosomal protein S6	8		HYEIVFMVHPDQSEQVPGMIERYSAAITGAEGK	2	33	8	36.42	b4b5°b5y4°y4y10y12y16	3689.78	120.244	2953	5	738.76	2.38
P02910 HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTQTETFGNEHWAPK	135	20	21	161.73	b1b2b4b11°b11y3y4y5y6y8y9*y9y10y11y12°y12*y12y14y15y17y20	2199.08	64.023	175905	3	733.70	-2.44
P02910 HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	23	164.18	b2b3°b3b4°b4b10y2°y2y3°y3y4y5°y5y6y7y8y9y10°y10y11y12°y12y13	1425.69	56.208	129352	2	713.35	1.37
P02910 HISJ_SALTY Histidine-binding periplasmic protein	3		NSDIQPTVASLK	120	12	21	144.52	b2°b2b3°b3°b3b4°b4b5y1y3y4y5y7y8°y8*y8y9y10*y10y11y12	1272.68	48.912	109961	2	636.84	-0.96
P02910 HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	18	134.47	b3b8b16°b16y1y2y3y4°y4y5y6y7y8y10y11y13y16y20	2273.21	104.337	96678	2	1137.11	10.53
P02910 HISJ_SALTY Histidine-binding periplasmic protein	5		NAQGELVGFDIDLAK	42	15	8	38.39	b1b3b5b7°b7y3y12y15	1589.83	79.935	31197	2	795.42	7.68
P02910 HISJ_SALTY Histidine-binding periplasmic protein	6		FGGPAVKDEK	201	10	11	83.09	b2y1y2°y2y3y4y5y6y7y9y10	1047.54	27.061	27284	2	524.27	-9.56
P02910 HISJ_SALTY Histidine-binding periplasmic protein	7	Carbamidomethyl+C(18)	NAQGELVGFDIDLAKELCK	42	19	8	34.54	b2b13y2y5y6y8y12y19	2120.06	86.797	24192	3	707.36	-5.41
P02910 HISJ_SALTY Histidine-binding periplasmic protein	8		QQEIAFTDK	99	9	4	31.32	b4°b4y3y5	1079.54	53.811	1553	2	540.28	6.22

P02910 HISJ_SALTY Histidine-binding periplasmic protein	9		LFGVGTGMGLR	211	11	3	36.84	y4y7y9	1107.60	40.535	11929	2	554.30	0.99
P02910 HISJ_SALTY Histidine-binding periplasmic protein	10		AFAEMR	234	6	2	27.44	b3y3	724.34	36.431	6333	1	724.34	-5.65
P02910 HISJ_SALTY Histidine-binding periplasmic protein	11		KYFDFDVYGG	250	10	5	55.75	b3b7b8y3y4	1210.54	75.198	47643	2	605.77	-0.50
P02910 HISJ_SALTY Histidine-binding periplasmic protein	12		IDAAFQDEVAASEGFLKQPVGK	176	22	3	13.91	b3y4y18	2320.17	78.734	33723	3	774.06	-3.05
P02910 HISJ_SALTY Histidine-binding periplasmic protein	13	Phosphoryl STY(9)	IDAIMSSLSITEKR	85	14	5	46.75	b6b8b9_HPO3 b9b10_H3PO4 b10y8	1643.82	51.338	1836	2	822.41	14.11
P02910 HISJ_SALTY Histidine-binding periplasmic protein	14	Phosphoryl STY(10)	NSDIQPTVASLK	120	12	6	51.06	b6b7b9°b9b11y6	1352.65	136.498	1689	1	1352.65	8.03
P02910 HISJ_SALTY Histidine-binding periplasmic protein	15		GGPAVKDEK	202	9	3	34.7	b3b4b8	900.47	27.062	9491	2	450.74	-9.01
P25077 MDH_SALTY Malate dehydrogenase	1		NQLPSGSELSDYDIAPVTPGVAVD LSHIPTAVK	21	33	26	91.67	b1*b1b2*b2b3*b3b6b8b9° b9b10°b10*b10b12b13b15 *b15y1y3y5y15y18y19y30° y30y33	3388.82	94.467	173094	3	1130.28	5.98
P25077 MDH_SALTY Malate dehydrogenase	2	Carbamidomethyl+C(2)	ACVGIITNPVNTTVAIAAEVLKK	111	23	20	170.23	b2b3b4b5b6b12y2y3y4y5y 6y12y13y15°y15y16y18y20 y21y23	2382.33	105.115	160044	3	794.78	-4.51
P25077 MDH_SALTY Malate dehydrogenase	3		VAVLGAAGGIGQALALLK	2	19	29	317.53	b2b3b5b6b7b8b9b10b14b1 5b16b17b18y1y2y3y4y5y6 y7y9y10y11y12y13y15y16 y19*y19	1735.08	120.245	143843	2	868.04	-0.84
P25077 MDH_SALTY Malate dehydrogenase	4		FFSQPLLLGK	262	10	10	76.1	b2b3°b3y2y3y4y5y6y8y10	1149.66	76.380	119219	2	575.33	-8.18
P25077 MDH_SALTY Malate dehydrogenase	5		IQNAGTEVVEAK	205	12	20	138.5	b2*b2b3b4b10°b10y2y3°y3 y4y5y6y7y8°y8y9y10°y10* y10y12	1258.66	35.222	109387	2	629.83	-4.75
P25077 MDH_SALTY Malate dehydrogenase	6		AGGGSATLSMGQAAAR	217	16	14	91.89	b16y6y7*y7y8y9°y9y10°y1 0*y10y11*y11y12y16	1405.68	40.657	87691	2	703.35	-1.30
P25077 MDH_SALTY Malate dehydrogenase	7		DIQLGEDFINK	301	11	7	37.82	b2b3b11y5y7y8y11	1291.65	68.558	70550	2	646.33	-2.17
P25077 MDH_SALTY Malate dehydrogenase	8		NLVQQIAK	99	8	6	36.96	b2b3y2y3y6y8	913.53	49.506	64634	2	457.27	-14.16
P25077 MDH_SALTY Malate dehydrogenase	9		SIGTLSAFEQHSLDAMLDTLKK	279	22	6	13.91	b2b3y2y17y20y22	2405.23	95.071	55194	3	802.42	-2.64
P25077 MDH_SALTY Malate dehydrogenase	10		SDLFNVNAGIVK	87	12	9	65.27	b2b3b4y2y4y6y8y9y12	1276.69	70.229	35169	2	638.85	2.29
P25077 MDH_SALTY Malate dehydrogenase	11		KDIQLGEDFINK	300	12	5	27.01	b11*b11y8y9y12	1419.74	49.638	9834	3	473.92	-2.49
P25077 MDH_SALTY Malate dehydrogenase	12		GFSGEDATPALEGADVVLISAGVA R	56	25	4	12.8	b3y4y6y25	2402.24	91.585	8109	2	1201.62	9.45
P25077 MDH_SALTY Malate dehydrogenase	13		FGLSLVR	233	7	6	54.89	y3y4°y4y5y6°y6	791.46	67.091	94441	2	396.23	-18.82
P25077 MDH_SALTY Malate dehydrogenase	14		SIGTLSAFEQHSLDAMLDTLK	279	21	3	21.02	y7y11y13	2277.12	101.148	3051	3	759.71	-10.83
P25077 MDH_SALTY Malate dehydrogenase	15		NGVEER	272	6	1	13.91	b4	703.34	100.209	2098	1	703.34	2.00
P25077 MDH_SALTY Malate dehydrogenase	16		IKGFSGEDATPALEGADVVLISAG VAR	54	27	7	54.94	b8b14y3y4y5y6y8	2643.41	87.600	38255	3	881.81	3.05
P25077 MDH_SALTY Malate dehydrogenase	17	Carbamidomethyl+C(11)	ALQGEKGVVECA YVEGDGQYAR	240	22	11	98.11	b5b12*b12b13y3y4y5y7y8 y9y10	2399.13	52.588	21379	3	800.38	0.00
P25077 MDH_SALTY Malate dehydrogenase	18		FFSQPLLLGKNGVEER	262	16	5	31.75	b5°b5b6y5y8	1833.97	80.666	15988	2	917.49	-8.32

P25077 MDH_SALTY Malate dehydrogenase	19		IQNAGTEVVEAKAGGGSATLSMG QAAAR	205	28	5	35.68	y8y12y14y17y20	2645.33	96.199	5621	3	882.45	-1.02
P25077 MDH_SALTY Malate dehydrogenase	20		AGGGSATLSMGQAAARFGLSLVR	217	23	6	30.55	b3b9b13b14*b14y3	2178.12	78.187	2297	2	1089.57	-9.30
P25077 MDH_SALTY Malate dehydrogenase	21	Oxidation+M(16)	SIGTLSAFEQHSLDAMLDTLKK	279	22	5	22.66	b13*b13y12y13*y13	2421.23	85.157	3107	4	606.06	-0.20
P25077 MDH_SALTY Malate dehydrogenase	22	Oxidation+M(10)	AGGGSATLSMGQAAAR	217	16	4	17.8	b6b8y10*y10	1421.69	40.785	2929	2	711.35	6.44
P25077 MDH_SALTY Malate dehydrogenase	23		GTLSAFEQHSLDAMLDTLKK	281	20	0	6.4		2205.10	95.046	3919	3	735.71	-8.75
P0A1D5 CH10_SALTY 10 kDa chaperonin	1		ILDNGTVQPLDVK	47	13	27	233.09	b2b3*b3b6*b6b7b8*b8b9b10b12*b12y2y3y4y5y6*y6y7y8y9y10y11*y11*y11y12y13	1411.78	58.107	197310	2	706.39	-1.04
P0A1D5 CH10_SALTY 10 kDa chaperonin	2		VGDIVIFNDGYGVK	60	14	19	195.61	b2b3b4b5*y5b6b11b13y3y4y5y6y7y8y9y10*y10y13y14	1495.78	74.103	152758	2	748.39	0.49
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	11	94.34	b7y2y3y4y6y7y8*y8y9y12y14	1188.65	44.398	124672	2	594.83	-7.29
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIVGVK	37	8	6	55.27	y2y3y4y5y6y8	786.46	42.138	23853	2	393.73	-12.34
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		STRGEIIVGVK	34	11	11	131.58	b3b4*b4b5b6b7b8b9y3y4y5	1130.64	37.893	89529	2	565.83	-8.31
P0A1D5 CH10_SALTY 10 kDa chaperonin	6		ILDNGTVQPLDVKVGDIVIFNDGY GVK	47	27	4	18.32	y3y10*y10y12	2888.53	91.525	11906	3	963.51	-3.72
P0A1D5 CH10_SALTY 10 kDa chaperonin	7		VGDIVIFNDGYGVKSEK	60	17	4	40.08	b10b11b12b14	1839.93	137.677	1519	2	920.47	-12.87
P0A1D5 CH10_SALTY 10 kDa chaperonin	8	Phosphoryl STY(8)	SAGGIVLTGSAAGK	20	14	5	28.58	b7b9y8_H3PO4 y8y12*y12	1268.61	51.354	2043	3	423.54	-1.64
P06179 FLIC_SALTY Flagellin	1		AQILQQAGTSVLAQANQVPQNVLSLLR	468	27	30	217.7	b2*b2b3b4b5b6*b6b7*b7b8*b8b11*b11b15*b15b17b18y1y2y3y4y5y6y9y10y11y12y13y14y27	2860.61	105.902	115601	3	954.21	1.88
P06179 FLIC_SALTY Flagellin	2		SQSALGTAIER	20	11	10	57.38	b2*b2b5y4y6y7*y7y9*y9y11	1132.59	42.641	52826	2	566.80	-6.57
P06179 FLIC_SALTY Flagellin	3		AQVINTNSLSLLTQNNLNK	1	19	14	50.15	b2*b2b3*b3b4y1y2y6*y6y8*y8y13y15y19	2085.14	75.502	42245	2	1043.08	6.91
P06179 FLIC_SALTY Flagellin	4		FNSAITNLGNTVNNLTSAR	432	19	21	127.51	b2b3*b3*b3b4*b4b5*b5*b5b6b11b12b13*b13b14*b14y4y7y13y14y19	2007.04	78.962	36464	2	1004.02	6.99
P06179 FLIC_SALTY Flagellin	5		VSDTAATVTGYADTTIALDNSTFK	180	24	8	20.18	b15y8*y8y13*y13y15y24*y24	2462.19	92.789	20100	3	821.40	-1.98
P06179 FLIC_SALTY Flagellin	6		SDLGAVQNR	423	9	6	55.64	b2y4y5y6y7y9	959.48	28.339	19377	2	480.25	-6.42
P06179 FLIC_SALTY Flagellin	7		IDAALAQVDTLR	411	12	7	60.83	b3b5b7y3y6y7y12	1285.71	61.886	15279	2	643.36	0.00
P06179 FLIC_SALTY Flagellin	8		QINSQTLGLDTLNVQQK	161	17	6	16.93	b11*b11b17y8y10y17	1900.03	66.077	14738	2	950.52	10.86
P06179 FLIC_SALTY Flagellin	9		TEVVSIGGK	370	9	4	39.1	b3b7b8y9	889.50	34.376	13628	2	445.25	-3.29
P06179 FLIC_SALTY Flagellin	10		ELAVQSANSTNSQSDLSIQAEITQR	93	26	7	26.25	b2b12b13*b13y3y9*y9	2805.36	71.201	11891	3	935.79	5.22
P06179 FLIC_SALTY Flagellin	11		INSAKDDAAGQAIANR	37	16	3	24.33	b6y11y12	1614.82	31.656	6179	3	538.94	-0.15
P06179 FLIC_SALTY Flagellin	12		DDAAGQAIANR	42	11	9	37.82	b4b5b8*b8*b8y2y7*y7y11	1101.53	28.738	5053	2	551.27	0.55
P06179 FLIC_SALTY Flagellin	13		MAQVINTNSLSLLTQNNLNK	0	20	4	24.32	b7b8*b8b11	2216.14	74.570	1822	2	1108.57	-13.77
P06179 FLIC_SALTY Flagellin	14		LNEIDR	119	6	2	13.91	y4*y4	759.41	97.365	16124	1	759.41	9.97
P06179 FLIC_SALTY Flagellin	15		AQPDLAEEAAATTTENPLQK	392	19	5	22.45	b4*b4b6b11*b11	1969.01	61.337	5778	2	985.01	9.92
P06179 FLIC_SALTY Flagellin	16		NVQVANADLTEAK	280	13	7	33.35	b5*b5b6*b6b8y6*y6	1372.69	14.711	2589	2	686.85	-14.58
P06179 FLIC_SALTY Flagellin	17		TYAASKAEGHNFK	379	13	4	30.7	b6b10y5y9	1423.68	41.626	38022	3	475.23	-8.75

P06179 FLIC_SALTY Flagellin	18		SDLGAVQNRFNSAITNLGNTVNN LTSAR	423	28	4	27.46	y7y11y13y14	2947.52	93.415	19453	3	983.18	5.96
P06179 FLIC_SALTY Flagellin	19		LGGADGKTEVVSIGGK	363	16	4	24.33	b7°b7b8y14	1487.79	55.751	6871	3	496.60	-12.80
P06179 FLIC_SALTY Flagellin	20		IDAALAQVDTLRSDLGAVQNR	411	21	3	14.38	b4y6y10	2226.16	75.608	5204	3	742.72	-11.84
P06179 FLIC_SALTY Flagellin	21		FNSAITNLGNTVNNLTSARSR	432	21	4	22.51	b4b6b10y14	2250.17	112.782	5008	2	1125.59	6.08
P06179 FLIC_SALTY Flagellin	22		YKVSDDTAATVTGYADTTIALDNS TFK	178	26	3	12.5	b5y8y11	2753.35	102.078	3262	3	918.45	-0.62
P06179 FLIC_SALTY Flagellin	23		VSDTAATVTGYADTTIALDNSTF KASATGLGGTDQK	180	36	3	10.98	b6b12y15	3548.71	95.867	3087	3	1183.58	-3.78
P06179 FLIC_SALTY Flagellin	24	Phosphoryl STY(6)	QINSQTLGLDITLNVQKQ	161	17	4	16.93	b4*b4b12y12	1979.98	100.313	22208	3	660.66	3.14
P06179 FLIC_SALTY Flagellin	25	Phosphoryl STY(12)	TNGEVLTAGGATSPITGGPLPATA TEDVK	252	28	9	41.62	b4b9*b9b10b11°b11b15y7 °y7	2708.29	124.731	15038	3	903.44	-0.81
P06179 FLIC_SALTY Flagellin	26	Phosphoryl STY(5)	TEVVSIGGK	370	9	3	31.32	b3b4y7	969.46	29.907	7876	2	485.23	3.65
P52616 FLJB_SALTY Phase 2 flagellin	1		AQILQQAGTSVLAQANQVPQNV SLLR	479	27	30	217.7	b2*b2b3b4b5b6*b6b7*b7b 8*b8b11°b11b15°b15b17b 18y1y2y3y4y5y6y9y10y11 y12y13y14y27	2860.61	105.902	115601	3	954.21	1.88
P52616 FLJB_SALTY Phase 2 flagellin	2		SQSALGTAIER	20	11	10	57.38	b2*b2b5y4y6y7°y7y9°y9y1 l	1132.59	42.641	52826	2	566.80	-6.57
P52616 FLJB_SALTY Phase 2 flagellin	3		AQVINTNSLSLLTQNNLNK	1	19	14	50.15	b2*b2b3*b3b4y1y2y6*y6y 8*y8y13y15y19	2085.14	75.502	42245	2	1043.08	6.91
P52616 FLJB_SALTY Phase 2 flagellin	4		TIEGGYALK	328	9	7	54.39	b5y1y2y3y6y8y9	951.51	44.195	36619	2	476.26	-8.53
P52616 FLJB_SALTY Phase 2 flagellin	5		SDLGAVQNR	434	9	6	55.64	b2y4y5y6y7y9	959.48	28.339	19377	2	480.25	-6.42
P52616 FLJB_SALTY Phase 2 flagellin	6		TAANLQGGVDGK	369	12	6	23.03	b3°b3y1y7y10y12	1130.58	35.960	16024	2	565.79	-2.81
P52616 FLJB_SALTY Phase 2 flagellin	7		ELAVQSANSTNSQSDLDLSIAEIT QR	93	26	7	26.25	b2b12b13*b13y3y9*y9	2805.36	71.201	11891	3	935.79	5.22
P52616 FLJB_SALTY Phase 2 flagellin	8		INSAKDDAAGQAIANR	37	16	3	24.33	b6y11y12	1614.82	31.656	6179	3	538.94	-0.15
P52616 FLJB_SALTY Phase 2 flagellin	9		DDAAGQAIANR	42	11	9	37.82	b4b5b8°b8°b8y2y7*y7y11	1101.53	28.738	5053	2	551.27	0.55
P52616 FLJB_SALTY Phase 2 flagellin	10		AYANNGTTLDSGLDDAAIK	189	20	4	14.9	b2b3b8y14	2009.00	75.468	4111	3	670.34	6.99
P52616 FLJB_SALTY Phase 2 flagellin	11		YFVTIGGFTGADAAK	234	15	5	26.78	b3b13y2y5y12	1517.75	83.044	3418	3	506.59	-11.34
P52616 FLJB_SALTY Phase 2 flagellin	12		MAQVINTNSLSLLTQNNLNK	0	20	4	24.32	b7b8°b8b11	2216.14	74.570	1822	2	1108.57	-13.77
P52616 FLJB_SALTY Phase 2 flagellin	13		NANDGISIAQTTEGALNEINNQL R	66	25	6	26.55	b5b6y3y14°y14*y14	2670.35	87.308	33283	2	1335.68	15.18
P52616 FLJB_SALTY Phase 2 flagellin	14		TEVVTIDGK	381	9	3	39.1	y3y5y6	961.51	52.999	31502	2	481.26	-15.68
P52616 FLJB_SALTY Phase 2 flagellin	15		FNSAITNLGNTVNNLSEAR	443	19	4	15.49	b18y3°y3y10	2035.05	90.893	10425	2	1018.03	14.10
P52616 FLJB_SALTY Phase 2 flagellin	16		VSGQTQFNGVK	125	11	6	51.62	y3y4y9*y9y10*y10	1164.59	33.875	9775	2	582.80	-6.18
P52616 FLJB_SALTY Phase 2 flagellin	17		AQPELAEAAAK	403	11	4	25.08	b3y8y10*y10	1098.56	88.151	5644	2	549.78	-16.78
P52616 FLJB_SALTY Phase 2 flagellin	18		DTPAVVSADAK	288	11	3	25.08	b3b7y4	1073.56	83.618	1979	1	1073.56	13.99
P52616 FLJB_SALTY Phase 2 flagellin	19		SRIEDSDYATEVSNMSR	462	17	7	45.39	b5b7b8y5y8*y8y13	1959.87	51.329	58697	3	653.96	-2.62
P52616 FLJB_SALTY Phase 2 flagellin	20		TIEGGYALKAGDK	328	13	3	28.84	y3y7y8	1322.69	37.958	17208	3	441.57	-4.61
P52616 FLJB_SALTY Phase 2 flagellin	21		AQPELAEAAAKTTENPLQK	403	19	6	43.7	b4b6b7°b7b10b12	2010.03	101.565	8817	2	1005.52	-11.78

P52616 FLJB_SALTY Phase 2 flagellin	22		SDLGAVQNRFSAITNLGNTVNN LSEAR	434	28	4	18.03	y4y8*y8y26	2975.48	71.527	8643	4	744.62	-5.91
P52616 FLJB_SALTY Phase 2 flagellin	23		NALIAGGVDATDANGAELVKMSY TDK	299	26	9	27.5	b3*b3b12°b12b14b16°b16 *b16y9	2624.27	74.652	8375	4	656.82	-8.19
P52616 FLJB_SALTY Phase 2 flagellin	24		TEVVTDIGKTYNASK	381	15	5	30.42	b14y6*y6y8y13	1625.84	71.218	7390	2	813.42	1.28
P52616 FLJB_SALTY Phase 2 flagellin	25		QINSQTLGLDSLNVQKAYDVK	161	21	6	40.73	b3*b3b4b8b12b16	2334.21	90.384	6914	3	778.74	-6.80
P52616 FLJB_SALTY Phase 2 flagellin	26		TYNASKAAGHDFK	390	13	5	35.11	b6°b6b9b12y9	1409.67	60.822	5882	2	705.34	-5.02
P52616 FLJB_SALTY Phase 2 flagellin	27		KDDAAGQAIANR	41	12	2	7.26	b4°b4	1229.61	31.618	5168	2	615.31	-8.24
P52616 FLJB_SALTY Phase 2 flagellin	28		NGTTLDVSGLDAAIK	193	16	4	21.69	b3b11°b11b14	1589.82	75.525	1538	2	795.41	11.98
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTASPYASYLQYGHIANIDD IAGKKPATDLGVK	125	38	34	179.03	b2b3b4b5°b5°b5b6°b6°b6 b7°b7b8°b8°b8b11°b11b1 3b14°b14y1y3y4y8y11y12y 19y22y25y27y28y31y36y3 8*y38	4001.02	83.618	265721	5	801.01	-12.33
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		AEQQLDKDSAIVPVYYYVNAR	494	21	16	127.69	b4b5b10°b10b11b12°b12y 3y4y5°y5y6y7y9y10y21	2442.23	73.695	134672	3	814.75	-0.90
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3		WSDGTPVTAHDFVYSWQR	107	18	18	149	b2°b2y1y3y4y5°y5y6y7y8y 9y10°y10y11y13y16y18*y1 8	2151.98	72.787	128257	3	718.00	-5.45
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4		SGEIDMTYNNMIELFQK	263	18	20	132.35	b1b2b3b4b5b11b14b15y1y 2*y2y3y4y7y9y10y11y12* y12y18	2130.01	87.235	116527	2	1065.51	8.14
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		LVEPEWFK	352	8	9	64.03	b2b3y3y4y5°y5y6°y6y8	1047.54	71.616	108136	2	524.28	-6.06
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		ALDDHTFEVTLSEPVYFYK	163	20	16	117.58	b6°b6b7b8b9b10°b10b11y 2y5y7y9°y9y10y11y20	2371.15	86.525	106228	3	791.06	0.51
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7	Carbamidomethyl+C(4)	AGWCADYNEPTSFLNTMLSDSSN NTAHYK	439	29	11	66.12	b4y2y4y11y12y13y15y22y 24y25y29	3294.43	90.700	90795	3	1098.82	6.60
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		TVINQVTYLPISSEVTDVNR	241	20	23	152.67	b8°b8°b8b9b10y2*y2y3y4 *y4y5y6*y6y7y8°y8*y8y11 *y11y12y14y15y20	2248.21	77.790	76266	2	1124.61	11.84
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9		NQGDLPAYSYTPPYTDGAK	333	19	10	51.85	b4b11y3y8°y8y10y11°y11y 14y19	2057.96	59.954	74340	2	1029.49	8.66
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		NLGVNVNLENQEWK	410	14	18	151.99	b1b2b3b4b6°b6b7b11b12y 6y7°y7y8y10y11y12*y12y1 4	1656.84	67.405	48263	2	828.93	5.60
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		HQGTFDVAR	430	9	8	76.69	b6y3y4y5y7y8*y8y9	1030.50	31.758	42974	2	515.75	-4.74
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		LADPNTASPYASYLQYGHIANIDD IAGK	125	29	6	11.81	b9y1y2y10y25y29	3091.56	88.946	27362	3	1031.19	6.40
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	13		LIADTLK	474	7	4	41.35	y3y5y6y7	773.47	44.033	14209	2	387.24	-13.49

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	14		KPATDLGVK	154	9	3	31.32	b5y3y4	928.53	27.292	5195	2	464.77	-13.67
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	15		DIIVNK	325	6	2	30.45	y3y5	701.42	56.014	15261	1	701.42	6.18
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	16		DLFEGLLISDVEGHPSPGVAEK	67	22	4	21.65	b6y8y10y15	2309.16	89.765	12707	3	770.39	-2.64
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	17		WENK	89	4	1	13.16	y3	576.27	33.250	3053	1	576.27	-12.60
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	18		NNGSEVQSLDPHK	43	13	6	44.45	b5b9b12y7y11°y11	1424.66	136.527	1879	1	1424.66	-11.48
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	19		TVINQVTYLPISSEVTDVNR	241	22	16	97.64	b3y5*y5y11°y11*y11y13*y13y14y16y17y18y19y20°y20*y20	2567.34	77.621	151638	3	856.45	-0.76
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	20		NNGSEVQSLDPHKIEGVPESNVSR	43	24	9	62.51	b10y3y5y7°y7y10y11y14y22	2592.24	51.859	73614	4	648.81	-11.40
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	21		FGDKWTQPANIVTNGAYK	200	18	8	62.87	b4b7°b7y6y7y9y10y11	2010.00	63.322	58588	3	670.67	-3.28
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	22	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYEINNQK	284	23	13	114.97	b3b5b7b9b15y6*y6y7y8y9y10y11y21	2920.40	76.798	32436	3	974.14	6.77
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	23		VKNQGDLPAYSYTPPYTDGAK	331	21	5	30.88	b6b12y8y9y11	2285.11	55.732	20597	3	762.38	1.28
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	24		NPQYWDNAKTVINQVTYLPISSEVTDVNR	232	29	5	22.73	b22y5y7°y7y8	3364.70	102.257	17884	3	1122.24	6.75
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	25		NQGDLPAYSYTPPYTDGAKLVEPEWFK	333	27	4	12.24	b4y5°y5y22	3086.51	85.173	17326	3	1029.51	10.99
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	26		ENAKWSDGTPVTAHDFVYSWQR	103	22	9	81.96	b11y5°y5y6y7y8y9y10y15	2594.22	69.126	16833	3	865.41	4.42
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	27		DPLDNIYVKNLYIIK	527	15	3	35.34	b4b5b6	1821.01	129.380	9538	2	911.01	-4.69
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	28		YRSGEIDMTYNNMPIELFQK	261	20	3	21.69	b4b7b9	2449.12	77.553	4659	3	817.04	-14.55
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	29		TFLDTRHQGTDFVAR	424	15	4	18.81	b8*b8y3y6	1763.86	87.645	2024	3	588.62	-14.39
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	30		KNLGVNVNLENQEWK	409	15	3	26.89	y3y4y7	1784.92	76.099	1905	3	595.64	-5.13
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	31		LSDSSNNTAHYK	456	12	0	9.04		1336.61	90.676	5848	2	668.81	0.82
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	32		PVYYYYVNAR	506	9	1	7.52	b5	1144.59	73.748	3001	2	572.80	10.56

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	33		TASPYASYLQYGHIANIDDIAGK	130	24	1	8.77	b12	2581.26	88.902	1653	4	646.07	-12.48
P0AA28 THIO_SALTY Thioredoxin-1	1		LNIDQNPGTAPK	58	12	25	175.57	b2*b2b3b4*b4*b4b5b6*b6b7b10y2y5y6y7y8*y8*y8y9*y9y10*y10*y10y11y12	1267.65	39.190	105650	2	634.33	-14.06
P0AA28 THIO_SALTY Thioredoxin-1	2		MIAPILDEIADEYQGK	37	16	16	140.2	b2b3b4b8y2y4*y4y5y6y7y9y10y11y13y14y16	1805.91	94.217	104663	2	903.46	7.64
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	11	91.47	b2b3b5y1y2y3y4y5y6y7y9	1001.63	91.054	89577	2	501.32	-11.27
P0AA28 THIO_SALTY Thioredoxin-1	4		IIHLTDDSFDTDVLK	4	15	4	18.81	b3y6y12y15	1731.89	72.098	3930	2	866.45	4.30
P0AA28 THIO_SALTY Thioredoxin-1	5		MIAPILDEIADEYQGKLTVAK	37	21	10	104.06	b3y7y11y12y15y16y17y18y19y20	2318.22	95.250	124125	3	773.41	-2.95
P0AA28 THIO_SALTY Thioredoxin-1	6		LNIDQNPGTAPKYGIR	58	16	4	17.8	b4*b4b7y13	1756.91	96.496	6160	2	878.96	-13.55
P0AA28 THIO_SALTY Thioredoxin-1	7		GIPTLLLFK	74	9	0	1.51		983.62	91.055	1772	2	492.32	-0.31
P67091 UF_SALTY Universal stress protein F	1		TILVPIDISDSELTQR	3	16	23	170.08	b2b3b4*b4y1y2*y2y3*y3y4y5y7y8*y8y9y10y11y12*y12*y12y13y14y16	1799.98	82.687	133796	2	900.50	5.22
P67091 UF_SALTY Universal stress protein F	2	Carbamidomethyl+C(4)	HAECSVLVVR	134	10	10	79.11	b1b2b7y1y3y4y6y8y9y10	1169.60	41.791	64294	2	585.31	-5.43
P67091 UF_SALTY Universal stress protein F	3		SQLEAIKK	69	9	6	46.88	b2y2y3y5y7y9	1029.62	44.995	48306	2	515.32	-7.35
P67091 UF_SALTY Universal stress protein F	4		VISHVEAEAK	19	10	12	102.37	b5b8y1y2y3*y3y4y5y6y7y8y10	1082.58	24.750	28010	2	541.79	-4.06
P67091 UF_SALTY Universal stress protein F	5		VQAHVAEGSPK	85	11	13	87	b1b2b3b4*b4y2y4*y4y5y6y7y9y11	1122.58	19.171	7282	2	561.80	-6.42
P67091 UF_SALTY Universal stress protein F	6		ILEMAK	98	6	2	27.44	b5y5	704.39	38.734	10503	1	704.39	-13.69
P67091 UF_SALTY Universal stress protein F	7		VHFLTVPISLPYYASLGLAYSaelPAMDDLK	34	31	4	22.98	y10*y10y11y13	3394.78	126.620	2300	3	1132.26	3.88
P67091 UF_SALTY Universal stress protein F	8		VQAHVAEGSPKDK	85	13	3	28.84	b4b9b10	1365.72	69.797	5379	2	683.36	7.15
P67091 UF_SALTY Universal stress protein F	9	Oxidation+M(27)	VHFLTVPISLPYYASLGLAYSaelPAMDDLK	34	31	3	11.47	b4b16y5	3410.77	94.465	115400	4	853.45	3.08
P67091 UF_SALTY Universal stress protein F	10		ISHVEAEAK	20	9	3	21.17	b3*b3b7	983.51	24.751	10715	2	492.26	-3.35
P67091 UF_SALTY Universal stress protein F	11		SHVEAEAK	21	8	4	34.7	b3b4*b4b6	870.42	24.764	7821	2	435.71	-11.15
P67091 UF_SALTY Universal stress protein F	12		QAHVAEGSPK	86	10	2	8.01	b3*b3	1023.52	19.178	1740	2	512.26	-0.78
P67091 UF_SALTY Universal stress protein F	13		SQLEAIKK	69	9	0	1.51		1012.59	45.014	2485	3	338.20	-13.56
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	1		SSIPVFGVDALPEALALVK	250	19	20	154.41	b4*b4b5b6*b6b7*b7b10y1y2y3y4y5y6y8y11y13y14y16y19	1926.10	108.382	116318	2	963.56	5.32
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	2		SGAMAGTVLNDANNQAK	269	17	21	168.22	b2b3b7b9*b9b11b17y1y4y5y6y7y8y9*y9y10y11y12*y12y13y17	1661.79	46.903	89046	2	831.40	0.81
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	3		ALAINLVDPAAGTVIEK	84	18	9	43.51	b2b3b5*b5b6y6y11y14y18	1766.02	81.205	73182	2	883.51	5.81

P23905 DGAL_SALTY D-galactose-binding periplasmic protein	4		VPYVGVDKDNLSEFTQK	315	17	12	111.55	b11y3y6y8*y8y9y11°y11y13y14y16y17	1938.98	62.176	45108	3	647.00	-1.39
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	5		YDDNFMSVVR	34	10	7	53.01	b2y2y4°y4y5y6y7	1245.57	67.078	19040	2	623.29	7.84
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	6		HWQANQGWDLNK	148	12	5	33.25	b4b7y6°y6y11	1496.72	62.687	3112	3	499.58	12.89
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	7		AYYVGTDSK	127	9	7	61.39	b5b6y4y5°y5y7°y7	1003.48	69.772	10107	2	502.24	7.91
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	8		VLTL SAVMASLLFGAHAHAADTR	4	23	3	13.49	b17y5y13	2352.29	86.469	1549	3	784.77	18.27
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	9		SAPDVQLLMNDSQNDQSKQNDQIDVLLAK	52	29	7	41.1	b3°b3y3y4y5y25y27	3227.61	78.756	40080	3	1076.54	6.73
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	10		IGVTIYKYDDNFMSVVR	27	17	3	16.93	b12y5y7	2020.02	78.238	13596	3	674.01	-1.45
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	11		AIEKD GK	45	7	3	41.35	b3b4b5	760.43	72.332	11024	1	760.43	13.24
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	12		ALDSYDKAYYVGTD SK	120	16	11	80.69	b10y3°y3y4°y4y5y6°y6y7°y7y8	1795.82	48.721	7742	3	599.28	-8.16
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	13		SSIPVFGVDALPEALALVKSGAMAGTVLNDANNQAK	250	36	5	10.98	b9y11°y11y14*y14	3568.83	74.548	7241	4	892.96	-9.51
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	14		MDAWLSGPNANKIEVVIANNDAMAMGAVEALK	214	32	4	11.34	b13y6y11°y11	3343.70	92.657	6211	3	1115.24	14.60
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	15		ELNDKGIQTEQLALDTAMWDTAQAK	187	25	8	43.65	b5b8b10b12*b12y7y8y13	2790.36	100.205	2937	4	698.35	0.87
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	16		KALDSYDK	119	8	4	33.95	b6b7y7°y7	939.46	35.891	2918	2	470.24	-14.62
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	17		IQYVLLKGEPGHPDAEAR	163	18	5	39.49	y8°y8y9y10y12	1993.03	51.337	1983	3	665.02	-7.90
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	18		ESGVIQGDLIAKHWQANQGWDLNK	136	24	3	13.12	b4b13y7	2707.33	101.631	1839	3	903.12	-9.83
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	19	Oxidation+M()	IEVVIANNDAMAMGAVEALK	226	20	7	40.35	b3y10°y10y11y12y15°y15	2075.06	67.146	24870	3	692.36	4.24
P65702 PGK_SALTY Phohoglycerate kinase	1		VLPAVAMLEER	373	11	15	102.75	b1b2b3y2°y2y3°y3y4y5y6y7y8°y8y9y11	1227.67	80.693	166594	2	614.34	-2.19
P65702 PGK_SALTY Phohoglycerate kinase	2		SVNDVKEDEQILDIGDASAQQLAEILK	272	27	25	177.61	b2b4b5°b5b8b9b11b12b13b14*b14b18b24b25b26y1y2y3y4y5y7y10y13y15y27	2941.50	100.530	152008	3	981.17	0.91
P65702 PGK_SALTY Phohoglycerate kinase	3	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	15	122.9	b2b3b8y2y3y5°y5y6y8y9y10y12y13y14y15	2002.04	99.608	127765	2	1001.52	3.35

P65702 PGK_SALTY Phohoglycerate kinase	4		TILWNGPVGVFEPNFR	302	17	16	123.85	b3b12b13*b13y4*y4y5y6*y6y7y11y12y13*y13y14y17	1993.05	106.895	111028	2	997.03	7.10
P65702 PGK_SALTY Phohoglycerate kinase	5		VATEFSETAPATLK	258	14	15	112.64	b1b2b4*b4b14y3y5*y5y6y7y9y10y11y12y14	1464.76	53.239	96387	2	732.88	-0.50
P65702 PGK_SALTY Phohoglycerate kinase	6	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	16	110.16	b2b5b6*b6b7*b7b9*b9y2y5y7y8y10y11y12y14	1599.85	69.377	87392	2	800.43	4.43
P65702 PGK_SALTY Phohoglycerate kinase	7		ADLNVPVKEGK	19	11	13	100.53	b2b4*b4b9y2y3*y3y4y5y6y7y8y11	1169.65	37.361	84644	2	585.33	-2.50
P65702 PGK_SALTY Phohoglycerate kinase	8		VMVTSHLGRPTEGEYNEEFSLLPV VNYLK	53	29	14	76.85	b1b2b5b6b14*b14b17b18b21b22y4y5y7y29	3321.66	92.647	82841	4	831.17	-6.32
P65702 PGK_SALTY Phohoglycerate kinase	9		LVKDYLDGVDV AEGEL VVLENV R	90	23	16	74.63	b1b2b7b8b10b14*b14y1y2y3y4*y4y5y6y12y23	2544.36	97.393	54481	3	848.79	1.15
P65702 PGK_SALTY Phohoglycerate kinase	10		ASLPTIELALK	38	11	6	51.62	y1y3y4y6y8y11	1155.69	77.846	51400	2	578.35	-4.33
P65702 PGK_SALTY Phohoglycerate kinase	11		MTDLDLAGKR	5	10	9	83.09	b2y1y3y4y5y6y7y9y10	1119.58	43.101	50027	2	560.29	-4.69
P65702 PGK_SALTY Phohoglycerate kinase	12		TILWNGPVGVFEPNFRK	302	18	5	33.47	y5y10y15y16y18	2121.12	97.209	41552	3	707.71	-5.06
P65702 PGK_SALTY Phohoglycerate kinase	13	Carbamidomethyl+C(5)	YAALCDVFVMDAFGTAHR	128	18	5	25.72	b2b3y4y11y13	2043.93	90.559	25744	3	681.98	-4.66
P65702 PGK_SALTY Phohoglycerate kinase	14		VMVTSHLGRPTEGEYNEEFSLLPV VNYLKDK	53	31	9	26.68	b1b6b7b12*b12b14*b14y1y31	3564.81	96.481	19960	4	891.96	0.48
P65702 PGK_SALTY Phohoglycerate kinase	15		ISYISTGGGAFLEFVEGK	355	18	3	16.16	b10y6y12	1874.96	75.990	12250	3	625.66	5.86
P65702 PGK_SALTY Phohoglycerate kinase	16		IADQLIVGGGIANTFVAAQGHSVG K	206	25	3	12.8	b5y4y14	2423.30	78.749	38933	3	808.44	-1.21
P65702 PGK_SALTY Phohoglycerate kinase	17		EPARPMVAIVGGSK	179	14	3	19.98	b5b7y9	1411.77	56.879	24250	3	471.26	-0.26
P65702 PGK_SALTY Phohoglycerate kinase	18		LSNPVR	84	6	4	40.98	b3*b3b4b5	685.40	22.984	19178	2	343.20	-4.36
P65702 PGK_SALTY Phohoglycerate kinase	19		EDEQILDIGDASAQQLAEILK	278	21	5	19.74	b10b12y12y15*y15	2299.19	62.085	7569	4	575.55	8.71
P65702 PGK_SALTY Phohoglycerate kinase	20		DYLDGVDV AEGEL VVLENVR	93	20	3	14.9	b7y7y13	2204.12	116.093	5260	3	735.38	5.21
P65702 PGK_SALTY Phohoglycerate kinase	21		GTEIVANAIDSEAFSIAGGGDTLA AIDLFGIADK	320	35	4	21.88	b3b4b14y11	3393.71	110.956	2432	3	1131.91	2.23
P65702 PGK_SALTY Phohoglycerate kinase	22		MTDLDLAGK	5	9	3	31.32	b6b8y5	963.49	25.256	1603	2	482.25	4.69
P65702 PGK_SALTY Phohoglycerate kinase	23	Carbamidomethyl+C(5)	LLTTCDIPVPTDVRVATEFSETAP ATLK	244	28	3	12.01	b9b11y9	3045.57	85.150	4691	3	1015.86	-2.89
P65702 PGK_SALTY Phohoglycerate kinase	24		TDLDLAGKR	6	9	1	8.43	b4	988.54	43.093	22106	2	494.77	-7.16
P65702 PGK_SALTY Phohoglycerate kinase	25		LNVPVKEGK	21	9	0	2.26		983.58	37.373	13519	2	492.29	-8.13
P65702 PGK_SALTY Phohoglycerate kinase	26		DLNVPVKEGK	20	10	1	8.01	b3	1098.60	37.370	12416	2	549.80	-12.00
P65702 PGK_SALTY Phohoglycerate kinase	27		PAVAMLEER	375	9	3	36.84	b3b5b7	1015.52	80.691	7242	2	508.26	-3.25
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	23	162.75	b1b2*b2b3*b3b4*b4b14b19*b19y3y4*y4y5y6y8y11y12y13y15y16y17y19	2130.16	93.031	354741	3	710.73	-5.16
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		MVAPVDGTIGK	59	11	15	117.08	b1b2b3b4y1y2y3y5*y5y6y7y8y9y10y11	1087.57	46.894	144889	2	544.29	-10.78

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		VGDPVIEFDLPLEEK	115	16	17	144.52	b4b5°b5b6b7b8°b8b10b13y3°y3y4y6y9y10y11y16	1812.97	100.241	94121	2	906.99	4.85
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		LSGSVTVGETPVIR	152	14	9	67.92	b3b7°b7b11y4y7y8y9y14	1414.79	56.286	44997	2	707.90	-2.50
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		STLTPVVISNMDEIK	133	15	3	18.81	b6b13y11	1646.88	73.831	9136	2	823.94	7.78
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		DTGTIEIVAPLSGEIVNIEDVPDVVFAEK	16	29	3	11.81	b5b12y4	3069.65	87.819	2216	3	1023.89	19.09
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		VKVGDVPVIEFDLPLEEK	113	18	15	157.35	b3b6b7b8b11y3°y3y4y5y6y7y8y9y10y13	2040.12	95.610	123061	3	680.71	-5.39
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		VGDPVIEFDLPLEEKAK	115	18	4	35.81	y3y5y12y15	2012.07	92.153	17239	3	671.36	-11.04
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9	Phosphoryl STY(9)	IFETNHAFSIESDSGIELFVHFGIDTVELK	70	30	3	17.54	b3b8b10_H3PO4 b10	3474.66	118.698	1979	4	869.42	6.68
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	1		TGEDIPITAR	66	10	16	132.45	b2b3°b3b4°b4b5y3y4y5°y5y6y7y8°y8y9y10	1072.55	43.599	56607	2	536.78	-8.31
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	2		LSGFGNFDLRDK	45	12	6	33.25	b5b7y2y5°y5y8	1368.69	51.786	24123	3	456.90	-3.75
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	3		NQRPGR	57	6	2	30.45	b3b5	727.40	50.309	4307	2	364.20	0.50
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	4		LSGFGNFDLR	45	10	7	53.01	y5°y5y6°y6y7y9*y9	1125.59	50.583	3680	3	375.87	18.33
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	5		ALENGEQVKLSGFGNFDLR	36	19	5	23.27	b7°b7y3y4*y4	2094.04	95.254	1676	3	698.69	-8.86
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	1		MITGIQITK	0	9	7	31.32	b2b6y1y2y6y7y9	1004.57	55.602	121215	2	502.79	-12.21
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	2		SGFAEDEVVAVSK	35	13	14	120.57	b3°b3b4b9y2°y2y4y5y6y8y9y10y11y13	1337.66	55.146	82265	2	669.33	-0.73
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	3		LGEIEYR	48	7	8	51.88	b2b6y2y3°y3y4y6y7	879.45	42.619	75103	2	440.23	-11.73
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	4		FNSLTPEQQRDVIAR	106	15	11	30.42	b2*b2b3°b3y1y2y4y5y10*y10y15	1773.90	48.047	55808	3	591.97	-12.94
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	5		FNSLTPEQQR	106	10	13	89.63	b2*b2b9y1y3y4°y4y5*y5y6y7y8y10	1219.60	38.560	41037	2	610.30	-6.61
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	6		EIPMEVKPEVR	55	11	7	66.92	y2y4y6y7y8y9y11	1326.71	48.986	40471	2	663.86	2.39
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	7		VEGGQHNLNVNVL	66	13	11	90.49	b4b6b7°b7y4*y4y5y6*y6y7y8	1434.76	50.550	48655	3	478.92	-18.21
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	8		AANDDLLNSFWLLDSEK	9	17	4	23.92	b7y10y11°y11	1950.94	103.349	4287	2	975.97	-4.63
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	9		AANDDLLNSFWLLDSEKGEAR	9	21	31	268.97	b3b4*b4b5°b5°b5b6°b6*b6b7°b7°b7b10b12b14y3y4y5y7y8y9y10y11°y11y13y14°y14y15y16y18y19	2364.14	93.100	195694	3	788.72	-2.69
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	10		VSGYAVRFNSLTPEQQR	99	17	5	40.08	b3°b3b4b5b14	1951.97	82.498	4592	2	976.49	-12.57
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	11		ETLEDAVKHPEK	80	12	7	48.55	b7b9b11°b11y9°y9y11	1395.72	97.353	2856	2	698.36	4.64
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	12		SGFAEDEVVAVSKLGEIEYR	35	20	3	14.9	b12b14y5	2198.10	116.976	2225	3	733.37	-0.22

Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	13	Carbamidomethyl+C(1)	CIVAKSGFAEDEVVAVSK	30	18	4	16.16	b6°b6b10y10	1908.95	65.332	1659	3	636.99	-10.30
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	14		PMEVKPEVR	57	9	2	19.33	b3b7	1084.57	48.995	37928	2	542.79	-7.20
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	15		TGIQITK	2	7	3	23.8	b4*b4b6	760.45	55.587	6306	1	760.45	-7.79
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	16		EIPMEVKPEVR	55	11	0	2.26		1308.68	48.984	10326	3	436.90	-11.29
P0A1E3 CYSK_SALTY Cysteine synthase A	1		YLSTALFADLFTEKELQQ	305	18	25	169.11	b2b4°b4b5b12b13b15b16y2*y2y5y6*y6y7°y7*y7y8y9*y9y10*y10y11y12°y12y18	2117.09	102.831	88660	2	1059.05	5.42
P0A1E3 CYSK_SALTY Cysteine synthase A	2		GVLKPGVELVEPTSGNTGIALAYVAAAR	56	28	11	88.33	y3y4y5y6y7y9y14y16y17y28*y28	2753.53	81.889	77734	3	918.51	2.93
P0A1E3 CYSK_SALTY Cysteine synthase A	3		IQGIGAGFIPGNLDLK	226	16	12	46.56	b1b2*b2b3b8y1y2y7y8y10y12y16	1612.91	84.021	68833	2	806.96	3.41
P0A1E3 CYSK_SALTY Cysteine synthase A	4		LTLTMPETMSIER	87	13	14	79.45	b2y1y2°y2y4°y4y6y8°y8y9°y9y10y11y13	1521.78	74.704	56908	2	761.39	7.70
P0A1E3 CYSK_SALTY Cysteine synthase A	5		YLLLQQFSNPANPEIHEK	137	18	19	130.36	b1b2b3b9b15y3°y3y4y6y7°y7y9*y9y10°y10y11y13y17y18	2141.09	74.669	55172	3	714.37	-3.99
P0A1E3 CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	11	99.15	b2b3b4b5y6y7y8°y8y9y10y12	1283.73	64.720	24984	2	642.37	-0.67
P0A1E3 CYSK_SALTY Cysteine synthase A	7		ALGANLVLTEGAK	105	13	9	97.75	b2y3y5y6y7y8y9y11y13	1256.72	61.889	18686	2	628.86	-3.01
P0A1E3 CYSK_SALTY Cysteine synthase A	8		VVGITNEEAISTAR	246	14	4	28.55	b1y7y9y12	1459.76	50.282	16669	2	730.38	-10.03
P0A1E3 CYSK_SALTY Cysteine synthase A	9		IGANMIWDAEK	44	11	9	28.09	b1b2b4y2y8y9°y9y11*y11	1247.62	62.606	8565	2	624.32	12.23
P0A1E3 CYSK_SALTY Cysteine synthase A	10		YLSTALFADLFTEK	305	14	4	25.42	b5y9y10y14	1618.84	103.753	7224	2	809.92	3.09
P0A1E3 CYSK_SALTY Cysteine synthase A	11		VVGITNEEAISTARR	246	15	5	24.83	b10y9y10°y10y15	1615.87	55.690	3725	3	539.29	-4.23
P0A1E3 CYSK_SALTY Cysteine synthase A	12		IGNGR	22	5	2	27.07	b4y4	516.28	37.185	49445	1	516.28	-14.54
P0A1E3 CYSK_SALTY Cysteine synthase A	13		TTGPEIWEDTDGQVDVFISGVGTGGTLTGVT	155	32	3	11.34	b7b9y16	3265.52	94.488	14418	3	1089.18	-19.89
P0A1E3 CYSK_SALTY Cysteine synthase A	14		IYEDNSLTIGHTPLVR	3	16	5	36.03	b4b8b9*b9b12	1827.95	91.858	1967	2	914.48	-7.48
P0A1E3 CYSK_SALTY Cysteine synthase A	15		GKTDLITVAVEPTDSPVIAQALAGEEIKPGPHK	193	33	7	39.05	b4b5°b5y5y10y11y22	3381.80	80.119	67605	4	846.20	-9.24
P0A1E3 CYSK_SALTY Cysteine synthase A	16		LIDKVVGITNEEAISTAR	242	18	7	47.94	b6y4y8y10y12y13*y13	1929.06	60.143	47868	3	643.69	-3.48
P0A1E3 CYSK_SALTY Cysteine synthase A	17		AEEIVASDPQKYLLLQQFSNPANPEIHEK	126	29	7	30.2	b3b13°b13y3y6y9y10	3308.66	77.706	27320	4	827.92	-5.46
P0A1E3 CYSK_SALTY Cysteine synthase A	18		LMEEEGILAGISSGAAVAALKLQEDESFTNK	261	32	5	36.11	b9b10b11b13y13	3292.66	74.697	23566	4	823.92	0.22
P0A1E3 CYSK_SALTY Cysteine synthase A	19		LQEDESFTNKNIVVILPSSGER	283	22	3	13.91	b4b10y6	2475.24	86.727	4768	3	825.75	-12.33
P0A1E3 CYSK_SALTY Cysteine synthase A	20	Phosphoryl STY(5)	VVGITNEEAISTARR	246	15	3	26.89	b3b5b10	1695.83	53.203	16894	3	565.95	0.50
P0A1E3 CYSK_SALTY Cysteine synthase A	21		LLLQQFSNPANPEIHEK	138	17	0	4.9		1978.02	74.669	9494	2	989.51	-10.43
P00924 ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	16	157.26	b2b4b5°b5b6b7b9y3y5y6y7y8y9y10*y10y12	1286.71	66.818	101489	2	643.86	-1.99
P00924 ENO1_YEAST Enolase 1	2		VNQIGTLSESIK	346	12	12	102.46	b2*b2b3y3y5y6y7y8°y8y9y10y12	1288.71	55.096	91688	2	644.86	0.00

P00924 ENO1_YEAST Enolase 1	3		SIVPSGASTGVHEALEMR	32	18	15	131.84	b2b14°b14y2y4y6°y6y7y8y9y10y11y13y15y16	1840.90	61.868	67627	3	614.31	-10.15
P00924 ENO1_YEAST Enolase 1	4		TAGIQIVADDLTVTNPK	312	17	9	81.21	b15y3y4y6y10y11y12y13y17	1755.96	73.176	39255	2	878.48	6.60
P00924 ENO1_YEAST Enolase 1	5		IEEELGDNAVFAGENFHHGDK	415	21	8	39.72	b3y1y9y10°y10y11y19y21	2328.03	58.201	32231	4	582.76	-9.23
P00924 ENO1_YEAST Enolase 1	6		AVDDFLISLDGTANK	88	15	6	44.41	b5b6y5y6y12y15	1578.81	82.842	28631	2	789.91	6.73
P00924 ENO1_YEAST Enolase 1	7		WLTGPQLADLYHSLMK	272	16	9	36.04	b6°b6b11°b11°b11y1y6y12y14	1872.95	96.489	22692	3	624.99	-10.23
P00924 ENO1_YEAST Enolase 1	8		SIVPSGASTGVHEALEMRDGDK	32	22	4	21.65	b8y6y10y14	2256.10	76.827	2154	2	1128.55	4.00
P00924 ENO1_YEAST Enolase 1	9		WLTGPQLADLYHSLMKR	272	17	3	24.33	b4b10b12	2029.07	84.979	1841	2	1015.04	-1.02
P00924 ENO1_YEAST Enolase 1	10		AADALLK	338	8	9	109.4	b4b6°b6b7y3y4y5y6y7	814.49	54.246	85121	2	407.75	-20.98
P00924 ENO1_YEAST Enolase 1	11		YDLDFK	258	6	2	30.45	y3y5	800.37	55.422	58517	2	400.69	-13.12
P00924 ENO1_YEAST Enolase 1	12		TFAEALR	178	7	6	65.41	b4°b4y3y4y5y6	807.42	46.045	57957	2	404.21	-16.63
P00924 ENO1_YEAST Enolase 1	13		HLADLSK	132	7	3	38.34	b5y4y5	783.42	26.341	47811	2	392.21	-17.22
P00924 ENO1_YEAST Enolase 1	14		NVPLYK	126	6	1	13.91	y4	733.42	37.390	19670	1	733.42	-9.57
P00924 ENO1_YEAST Enolase 1	15		IATAIEK	330	7	5	41.35	y3y5°y5y6°y6	745.43	28.983	15423	2	373.22	-16.54
P00924 ENO1_YEAST Enolase 1	16		AAQDSFAAGWGMVSHR	358	17	3	16.93	b4y6y11	1789.85	61.762	6224	2	895.43	1.71
P00924 ENO1_YEAST Enolase 1	17	Carbamidomethyl+C(5)	IGLDCASSEFFK	243	12	4	33.25	b9b11y6y11	1373.65	136.486	2756	1	1373.65	3.91
P00924 ENO1_YEAST Enolase 1	18		SVYDSR	9	6	2	13.91	y3°y3	726.35	71.991	1512	1	726.35	10.76
P00924 ENO1_YEAST Enolase 1	19		AVDDFLISLDGTANKSK	88	17	5	23.85	b5b10y10°y10y15	1793.91	65.868	147390	2	897.46	-10.00
P00924 ENO1_YEAST Enolase 1	20		IEEELGDNAVFAGENFHHGDKL	415	22	6	39.17	b3y5y10y11y12°y12	2441.11	64.508	48372	4	611.03	-12.00
P00924 ENO1_YEAST Enolase 1	21		AAQDSFAAGWGMVSHRSGETE DTFIADLVVGLR	358	34	6	22.22	b7b9b14°b14b29y14	3592.72	105.221	5492	4	898.94	-7.75
P00924 ENO1_YEAST Enolase 1	22		SVYDSRGNPTVEVELTTEK	9	19	3	22.45	b4b7b10	2124.05	69.335	5288	2	1062.53	4.14
P00924 ENO1_YEAST Enolase 1	23		VYARSVYDSR	5	10	3	37.71	y4y5y6	1215.61	70.209	5014	2	608.31	1.00
P00924 ENO1_YEAST Enolase 1	24		GVFRSIVPSGASTGVHEALEMR	28	22	3	13.91	b3y4y7	2300.19	102.255	1584	3	767.40	1.59
P00924 ENO1_YEAST Enolase 1	25	Phosphoryl STY(4)	GNPTVEVELTTEK	15	13	4	21.36	b3b5y11°y11	1496.67	50.036	15796	2	748.84	-7.10
P00924 ENO1_YEAST Enolase 1	26	Oxidation+M(17)	SIVPSGASTGVHEALEMRDGDK	32	22	5	22.66	b8b9°b9y8°y8	2272.08	47.385	85521	4	568.78	-2.15
P00924 ENO1_YEAST Enolase 1	27	Oxidation+M(15)	WLTGPQLADLYHSLMK	272	16	4	17.8	b11y10y13°y13	1888.95	87.695	6094	3	630.32	-7.56
P00924 ENO1_YEAST Enolase 1	28		GTLSESIK	350	8	0	2.64		834.46	55.080	2313	2	417.73	4.17
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	15	97.85	b1b2b3b5b7y1y2y3y4y5y7y12y14y16y18	1970.01	64.001	169494	3	657.34	-8.12
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		VVGYSQDYSNAIVEAVK	61	17	24	174.98	b1b2b3b6°b6b8b9b10°b10b11b16°b16y1y3y4y5y9y11y12°y12y13°y13y15y17	1841.94	68.493	140115	2	921.47	6.23
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		ESSVPFSYYDNQQK	47	14	11	76.67	b2°b2b3°b3b11y6y7y8y9y10y14	1691.76	56.277	135820	2	846.38	3.10
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		AVAFMMDDALLAGER	198	15	17	207.3	b3b4b5b6b11b12y3y4y5y7y8y10y11y12y13y14y15	1609.78	85.068	126559	2	805.39	5.84
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5		NGVIVVGHR	38	9	12	91.47	b2°b2b3°b3b4y2y3y4y5y6y7y9	950.54	32.807	104941	2	475.77	-13.61
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(19)	KPDNWEIVGKPSQEAYGCMLRK	217	23	12	44.16	b1b5°b5b6b8b10°b10b16y5y11°y11y23	2734.32	56.885	100336	4	684.33	-10.36
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7		LIPITSQNR	89	9	5	39.1	y5y6°y6y7y9	1041.59	43.536	43675	2	521.30	-10.31

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8		QAAFSDTIFVVGTR	122	14	6	34.02	b3b8y1y11y12y14	1511.79	77.435	38921	2	756.40	3.96
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9		NGVIVVGHRESSVPFSYYDNQQK	38	23	5	20.88	b13y3y6y10y23	2623.30	58.182	23167	3	875.11	5.40
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTTNLER	98	22	9	55.35	b3b11y1y2y9y10y11y12y22	2526.23	82.362	22035	2	1263.62	12.95
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11	Carbamidomethyl+C(19)	KPDNWEIVGKPQSQEAYGCMLR	217	22	11	56.89	b6b7*b7b10*b10y4y5y7y10y12y22	2606.26	62.135	11702	3	869.42	3.00
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12	Carbamidomethyl+C(21)	AKKPDNWEIVGKPQSQEAYGCMLR	215	24	4	24.16	b7y4y5y12	2805.40	58.163	11495	3	935.81	7.57
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	13		LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	4	17.09	b13y11y13y22	2869.44	68.055	6001	3	957.15	-0.77
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	14	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTTNLER	89	31	13	76.44	b3b10y4*y4y6y7*y7y9y10y11y14y21y29	3548.81	87.447	242850	3	1183.61	7.15
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	15		QKQAAFSDTIFVVGTR	120	16	5	45.74	b8b13y3y4y5	1767.93	69.892	40801	3	589.98	-7.32
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	16		ESSVPFSYYDNQKVVGYSDYS NAIVEAVK	47	31	3	11.47	b8y13y27	3514.70	80.714	29320	3	1172.24	10.56
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	17		ALFKAPNDK	290	9	4	46.61	b6y3y4y5	1003.55	38.826	26348	2	502.28	-11.62
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	18		DHGDSFRTLESGR	185	13	3	21.36	b10y3y12	1476.66	42.482	3159	2	738.84	-13.23
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	19		IISAKDHGDSFR	180	12	4	23.03	b9y3*y3y11	1345.68	69.791	2287	2	673.34	-5.71
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	20	Carbamidomethyl+C(13);Phosphoryl STY(16)	IPLLQNGTFDFECGSTTNLER	98	22	3	23.78	b11b14b15	2606.17	87.340	44094	3	869.40	8.34
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	21	Carbamidomethyl+C(19);Phosphoryl STY(13)	KPDNWEIVGKPQSQEAYGCMLRK	217	23	4	22.52	b9*b9y9y10	2814.34	88.065	2604	3	938.78	13.62
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	22	Oxidation+M(5)	LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	3	17.54	y3y15y23	2885.46	88.264	44358	4	722.12	6.26
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	23	Oxidation+M(2)	LMDDTIAQAQTSGEAEK	247	17	4	27.07	b3b6b8y13	1823.85	81.391	8406	3	608.62	9.17
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	24		PITSQNR	91	7	1	9.02	b6	815.43	43.537	10312	2	408.22	-14.00
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	25	Carbamidomethyl+C(12)	VGKPQSQEAYGCMLRK	224	16	0	6.78		1851.90	56.880	3909	3	617.97	-8.70
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	26	Carbamidomethyl+C(13)	IVGKPQSQEAYGCMLRK	223	17	0	6.78		1964.98	56.886	3373	3	655.66	-13.36

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	27		NGVIVVGHR	38	9	0	1.51		933.52	32.776	3066	2	467.26	-4.97
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	1		NNLAIVGFSTPNVMPYVQR	237	20	17	102.83	b2*b2b3*b3b4*b4b5*b5y3y5y12*y12y14y15y16y17y20	2276.19	78.561	132121	3	759.40	-4.18
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	2		AYPDLDAIIAPDANALPAAAQAAE NLKR	209	28	20	154.32	b2b6b7b8b9b10b15y1y3y5y6y9y10y12y13*y13y18y19y20y28	2863.50	88.258	87761	3	955.17	0.09
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	3		ISVYVANALLK	273	11	7	69.93	y2y3y6y7y8y10y11	1190.71	74.259	77918	2	595.86	-2.36
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	4		ISQEHPGWEIVTTQFGYNDATK	177	22	10	68.35	b9b10*b10b11y3y5y7y8y12y22	2521.20	73.443	77391	3	841.07	-0.10
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	5		LVGVGFFTSGGNGAQEAGK	35	19	11	49.64	b3b6b17y1y2y3y5*y5y14y15y19	1795.91	72.385	63824	2	898.46	4.35
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	6		VAFFYSSPTVTDQNQWVK	154	18	12	97.19	b5b10b12b13y8y10*y10y11y12y13y14y18	2117.05	78.340	62110	2	1059.03	9.34
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	7		SLQTAEGIIK	199	10	4	27.71	b8y4y7y10	1059.60	51.719	57708	2	530.30	-8.06
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	8		NMPMNVGDSLDPGIGK	284	17	10	54.45	b2b6b10b12y2y5y11y14y15y17	1757.87	80.330	47959	2	879.44	5.62
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	9		GTVKEFGLWDVVQQGK	257	16	11	78.1	b5*b5b8y3*y3y5y6y7y10y13y16	1790.92	76.721	47469	3	597.65	-11.93
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	10		SYIINQGTPK	124	10	8	77.07	b2b3b4y3y5y6y8y10	1170.57	38.941	45932	2	585.79	-3.75
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	11		VTVSPNSEQGYHYEAK	301	16	12	84.22	b8y1y2y4y5y7*y7y9y10y11y12y16	1808.82	37.014	43847	3	603.61	-13.83
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	12		GNGIVLLPER	317	10	8	37.71	b2*b2y2*y2y4y5y6y10	1067.62	62.120	26361	2	534.31	-3.77
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	13		EFGLWDVVQQGK	261	12	8	37.23	b3b10*b10y1y7y8*y8y12	1405.71	83.119	25731	2	703.36	0.00
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	14		QLGSMLEVMAAHQVDK	134	16	3	17.8	b5b12y4	1756.89	57.440	7152	2	878.95	9.03
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	15		VAFFYSSPTVTDQNQWVKEAK	154	21	6	32.32	b1b5b6b10b13y13	2445.20	85.287	2325	3	815.74	-2.50
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	16	Carbamidomethyl+C(12)	ILTWDSDTKPECR	111	13	15	165.94	b5b7b9*b9y3y4*y4y5y6y7y8y9y10y11y12	1620.74	50.775	94133	3	540.92	-16.87
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	17		IAFIPK	29	6	3	40.98	b3y4y5	688.43	54.506	19839	1	688.43	-14.98
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	18		VIFNK	327	5	1	13.53	b3	620.37	70.436	9983	1	620.37	-10.53
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	19		AYPDLDAIIAPDANALPAAAQAAE NLK	209	27	6	22.17	b5*b5b11y6y8y14	2707.35	95.404	1953	4	677.59	-17.13
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	20		NMPMNVGDSLDPGIGKVTVSPN SEQGYHYEAK	284	33	6	22.08	b13*b13*b13y3y6y7	3547.71	80.233	19601	4	887.68	6.19
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	21		AKISQEHPGWEIVTTQFGYNDAT K	175	24	4	13.12	b6b11y12*y12	2720.31	112.789	5496	3	907.44	-6.82
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	22		QLGSMLEVMAAHQVDKEK	134	18	10	51.37	b7*b7b8*b8b11*b11b12y4y12*y12	2014.03	105.907	1852	2	1007.52	12.30
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	23		GNGIVLLPER	317	10	0	1.88		1049.59	62.091	2219	2	525.30	-12.21
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		AYGSTNPINVVR	126	12	17	130.99	b1b2b3b4b5y1y2y3y4*y4y5y6y7y8y10*y10y12	1290.67	51.764	138399	2	645.84	-4.26
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		VFMQPASEGTHIAGGAMR	93	19	21	191.48	b2b3b4b12*b12b13b14y4y5y6y7y11y12y13*y13y14y15y16*y16y17y19	1892.95	68.737	102781	2	946.98	5.48

P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		SVEEILGK	159	8	5	41.73	y2y3y4y6y8	874.48	50.785	64090	2	437.74	-13.05
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVA AK	138	18	8	44.89	b15y3y4y11y12*y12*y12y18	1890.91	64.094	52616	2	945.96	10.59
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		ATIDGLENMNSPEMVA AKR	138	19	17	121.89	b2*b2b5y1y3y4y5y8y10*y10y11*y11y12*y12y13y16y17	2046.98	59.784	50494	3	683.00	-5.78
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		IFSFTALT TVVG DGN GR	29	16	5	26.17	y2y6y7y14*y14	1653.86	87.049	21364	2	827.44	2.36
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		AREVPAAIQK	52	10	8	91.85	b3b4b6b7b9y4y6y10	1082.63	28.989	8780	2	541.82	-6.20
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		NMINVALNNGTLQHPVK	69	17	3	25.58	b10b12b13	1862.97	83.397	1558	2	931.99	-10.75
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		AVLEVAGVHNVLAK	112	14	11	140.8	b3b4b5y4y5y6y8y9y10y11y12	1419.81	60.940	100681	3	473.94	-18.14
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		LIAVNR	14	6	1	13.91	y5	685.43	33.169	7133	1	685.43	-8.99
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		QAGELQEK	6	8	6	52.26	b3b7y6*y6y7*y7	902.45	97.429	4357	1	902.45	-5.28
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12		IFSFTALT TVVG DGN GRVGF GYGK	29	23	4	13.49	b6y3y12*y12	2362.24	73.344	268783	4	591.31	6.82
P0A7W4 RS5_SALTY 30S ribosomal protein S5	13		RNMINVALNNGTLQHPVK	68	18	3	35.08	b3b4b5	2019.08	56.716	14122	3	673.70	-3.75
P0A7W4 RS5_SALTY 30S ribosomal protein S5	14		NMINVALNNGTLQHPVKG VHTG SR	69	24	3	13.12	b3y5y15	2557.32	81.403	4087	3	853.11	-10.21
P0A7W4 RS5_SALTY 30S ribosomal protein S5	15		AYGSTNPIN VVRATIDGLENMNSPEMVA AK	126	30	6	24.46	b3b6b8b10*b10y10	3162.55	78.979	3412	3	1054.86	-1.24
P0A7W4 RS5_SALTY 30S ribosomal protein S5	16		GVHTGSRVFMQPA SEG TGIIAGGA MR	86	26	3	12.5	b10y4y8	2587.27	113.604	2047	3	863.09	-8.40
P0A7W4 RS5_SALTY 30S ribosomal protein S5	17		ATIDGLENMNSPEMVA AKR	138	19	5	15.49	b5b7*b7y12*y12	2046.99	55.739	1857	4	512.50	-3.88
P0A7W4 RS5_SALTY 30S ribosomal protein S5	18	Oxidation+M(14)	ATIDGLENMNSPEMVA AK	138	18	4	23.57	b7y8*y8y9	1906.90	83.127	3113	2	953.96	7.94
P0A7W4 RS5_SALTY 30S ribosomal protein S5	19	Oxidation+M(3)	VFMQPA SEG TGIIAGGAMR	93	19	4	26.74	b3b9b10y3	1908.91	76.084	2735	4	477.98	-12.66
P0A7W4 RS5_SALTY 30S ribosomal protein S5	20		NMINVALNNGTLQ	69	13	1	7.26	y4	1401.71	83.424	2513	2	701.36	-4.35
P41031 CY_SALTY Thiosulfate-binding protein	1		AYLNWLYSPQAQT IITHYYR	265	21	28	249.02	b2b3b4b5*b5b6*b6y2y3y4y5y6y7y8y9y10*y10y11*y11*y11y13*y13y14y15y16y17y19y21	2664.33	93.545	196129	3	888.78	1.19
P41031 CY_SALTY Thiosulfate-binding protein	2		GLGDVLISFESEVNNIRK	208	18	28	213.39	b2b3b4b5b6b13y2y3y4y5*y5y6y8*y8y9*y9*y9y10*y10y11*y11*y11y12*y12y13y14y16y18	1990.03	101.638	182579	3	664.02	-14.48
P41031 CY_SALTY Thiosulfate-binding protein	3		VNNPEIMGK	286	9	13	91.47	b2*b2b3b6b9y2y3y4y6y7y8*y8y9	1001.50	36.771	140938	2	501.25	-9.32
P41031 CY_SALTY Thiosulfate-binding protein	4		FGSWPEVMK	311	9	11	69.18	b2b3*b3b4y1y2y3y5y8*y8y9	1080.51	69.161	113100	2	540.76	-5.20
P41031 CY_SALTY Thiosulfate-binding protein	5		NIHDWSDLVR	132	10	11	89.63	b4y1y2y3y4y5y6y7y8y10*y10	1254.62	63.152	95827	2	627.81	-1.75
P41031 CY_SALTY Thiosulfate-binding protein	6		QYEAQGFEVVIPK	226	13	14	83.28	b2*b2b11*b11*b11b12b13y2y3y5y8y10y11y13	1507.78	70.549	95610	2	754.39	0.65
P41031 CY_SALTY Thiosulfate-binding protein	7		LPNNSSPFYSTMGFLVR	110	17	15	83.56	b2b3*b3b4*b4b7y1y2y3y5y6y11y12y13y17	1929.97	92.572	92030	2	965.49	7.15

P41031 CY_SALTY Thiosulfate-binding protein	8		ELFAALNPPFEQQWAK	37	16	15	73.63	b5°b5b7*b7b8y1y4y9°y9y10°y10y12y13*y13y16	1888.97	90.424	76104	2	944.99	6.27
P41031 CY_SALTY Thiosulfate-binding protein	9		TEQFMTQFLK	179	10	13	77.07	b2°b2b3b4*b4y2y3y5y7y8°y8*y8y10	1272.63	76.010	71239	2	636.82	-1.06
P41031 CY_SALTY Thiosulfate-binding protein	10		NVEVFDTGGR	189	10	10	88.84	b2b4b8y4y5y6y7y8°y8y10	1093.52	47.790	68532	2	547.26	-9.60
P41031 CY_SALTY Thiosulfate-binding protein	11		QALAILQGLK	71	10	11	76.1	b2*b2b3*b3b10y1y3y5y6y7y8	1054.65	75.571	53125	2	527.83	-9.61
P41031 CY_SALTY Thiosulfate-binding protein	12		GLGDVLISFESEVNNIR	208	17	6	16.93	b2b11y4*y4y10y17	1861.97	107.648	35998	2	931.49	4.20
P41031 CY_SALTY Thiosulfate-binding protein	13		ADVVTYNQVTDVQILHDK	81	18	4	23.57	b3y3y4y18	2058.05	64.570	9042	3	686.69	-2.14
P41031 CY_SALTY Thiosulfate-binding protein	14		TN1LAEFPVAWVDK	239	14	6	28.58	b3°b3b11y5°y5y7	1602.84	97.798	11181	2	801.93	-4.87
P41031 CY_SALTY Thiosulfate-binding protein	15		GATTTFAER	199	9	4	58.65	y3y4y6y7	953.46	31.325	5336	1	953.46	-8.07
P41031 CY_SALTY Thiosulfate-binding protein	16		YTYLAAWGAADNADGGDK	159	18	4	16.16	b6y6°y6y8	1858.84	54.098	3512	4	465.47	10.77
P41031 CY_SALTY Thiosulfate-binding protein	17		TN1LAEFPVAWVDKNVQANGTEK	239	23	19	165.74	b3b4b6*b6b14y4y5y6*y6y9y12y13y14y16y17y18°y18y19y20	2544.31	91.080	262811	3	848.77	-0.38
P41031 CY_SALTY Thiosulfate-binding protein	18		LIPADWQSRLPNNSSPFYSTMGFLVR	101	26	5	35.79	y5y8y9y11y24	2996.52	96.365	95118	3	999.51	4.56
P41031 CY_SALTY Thiosulfate-binding protein	19		YTYLAAWGAADNADGGDKAK	159	20	8	48.45	b13*b13y3y6y11y14y18*y18	2057.95	62.749	83610	3	686.65	-3.91
P41031 CY_SALTY Thiosulfate-binding protein	20		NVEVFDTGGRGATTTFAER	189	19	13	112.87	b3b4*b4b10b11b16y3y4y5y9y14y16y17	2027.97	57.248	48422	3	676.66	-6.20
P41031 CY_SALTY Thiosulfate-binding protein	21		KQYEAQGFEVVIPK	225	14	9	52.34	b4*b4b8*b8b10b11y5y12°y12	1635.86	63.869	35012	3	545.96	-11.27
P41031 CY_SALTY Thiosulfate-binding protein	22		ADVVTYNQVTDVQILHDKGK	81	20	6	54.19	b3b4y3y4y5y17	2243.13	59.288	24968	4	561.54	-14.91
P41031 CY_SALTY Thiosulfate-binding protein	23		GNPKNIHDWSDLVR	128	14	3	19.98	b3b8y9	1650.83	84.025	13712	3	550.95	-2.07
P41031 CY_SALTY Thiosulfate-binding protein	24		THFASGGELDKLLAAGR	320	17	4	16.93	b3b12°b12y4	1742.91	66.725	8328	3	581.64	-5.11
P41031 CY_SALTY Thiosulfate-binding protein	25		VEEKFGSWPEVMK	307	13	3	21.36	b12y6y9	1565.75	67.129	2432	2	783.38	-10.45
P41031 CY_SALTY Thiosulfate-binding protein	26		GSWPEVMK	312	8	0	1.51		933.45	69.203	7614	1	933.45	-2.55
P41031 CY_SALTY Thiosulfate-binding protein	27		HDWSDLVR	134	8	0	1.88		1027.51	63.109	2999	2	514.26	14.49
P41031 CY_SALTY Thiosulfate-binding protein	28		NVEVFDTG	189	8	0	1.88		880.41	47.777	2192	1	880.41	9.84
O33921 AGP_SALTY Glucose-1-phohatase	1		VTVLVGHDNSIASLLTALDFKPYQLHDQYER	304	31	36	179.39	b1b2°b2b4°b4b10b11b12°b12b13°b13b14°b14y1y2°y2y3y4°y4*y4y5°y5y6y7y9°y9y10y11°y11*y12°y12y16y17y19y20y31	3542.78	96.485	198576	5	709.36	-13.71
O33921 AGP_SALTY Glucose-1-phohatase	2		TPIGGQLVFQR	335	11	10	86.47	b1b2y3*y3y4y5y7y8y9y11	1215.68	62.075	118221	2	608.34	-2.61
O33921 AGP_SALTY Glucose-1-phohatase	3		MGTMDPFTFNPVITDDSAAFR	141	20	19	134.47	b2b3b5°b5b12y2y3y5y6y7y8y9y11°y11y12y14y15y20*y20	2186.01	79.204	105942	2	1093.51	9.27
O33921 AGP_SALTY Glucose-1-phohatase	4		NVAAPLVK	281	8	6	41.73	b2y1y4y5y6y8	811.49	40.632	74959	2	406.25	-11.81
O33921 AGP_SALTY Glucose-1-phohatase	5		IEYVYQSAR	358	9	15	76.69	b2b3°b3b9y1y2y3y5*y5y6y7y8*y8y9*y9	1128.56	43.168	59111	2	564.78	-5.19

O33921 AGP_SALTY Glucose-1-phohatase	6		NAEALTLK	370	8	11	82.33	b3b4*b4b6°b6*b6y3y4y6y8*y8	859.48	41.677	56836	2	430.24	-7.81
O33921 AGP_SALTY Glucose-1-phohatase	7	Carbamidomethyl+C(14)	EWLV AQGLIPSGECPAPDVTYAY ANSLQR	87	29	20	104.47	b3°b3b4b9b12°b12b14y2y3y4y6y7*y7y9y10°y10y11y13y15y29	3205.59	94.493	44770	3	1069.20	9.06
O33921 AGP_SALTY Glucose-1-phohatase	8		QQAVQAMEK	161	9	9	69.18	b2*b2y3y4y5*y5y6y7y9	1032.51	26.926	40432	2	516.76	-8.39
O33921 AGP_SALTY Glucose-1-phohatase	9	Carbamidomethyl+C(16)	TVATAQFFITGAFPGCDIPVHHQE K	116	25	3	19.02	y5y7y12	2771.34	79.524	34605	4	693.59	-6.25
O33921 AGP_SALTY Glucose-1-phohatase	10		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDR	226	31	5	22.98	y3°y3y6°y6y7	3486.66	105.048	30570	3	1162.89	6.44
O33921 AGP_SALTY Glucose-1-phohatase	11		APLANNGSVLAQSTPNAWPAWD VPGGQLTTK	43	31	11	45.98	b2b3b4b9°b9b14b18y8y13y14y31	3161.62	84.276	30435	3	1054.55	6.41
O33921 AGP_SALTY Glucose-1-phohatase	12		GGVLEVYMGHYTR	74	13	8	57.98	b3b5y1y3y5y6y7y13	1481.70	64.086	29569	3	494.57	-12.44
O33921 AGP_SALTY Glucose-1-phohatase	13		SQLHLDSEYK	172	10	10	53.99	b1°b1b2°b2b3b8y4y6y7y10	1219.60	40.838	24059	2	610.30	0.70
O33921 AGP_SALTY Glucose-1-phohatase	14	Carbamidomethyl+C(14)	LLEQITHYQDSPSCKEK	182	17	8	49.94	b2y2y6y7y10y11y15y17	2076.00	48.415	14373	3	692.67	-5.41
O33921 AGP_SALTY Glucose-1-phohatase	15	Carbamidomethyl+C(14)	LLEQITHYQDSPSCK	182	15	3	24.83	b8b9y3	1818.86	60.742	3465	3	606.96	-4.56
O33921 AGP_SALTY Glucose-1-phohatase	16	Carbamidomethyl+C(8); Carbamidomethyl+C(16)	VTLELKGPCVDANGFCPLDK	383	20	5	14.9	b14*b14y6°y6y9	2233.09	68.502	81463	3	745.03	-5.47
O33921 AGP_SALTY Glucose-1-phohatase	17	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	GCPVDANGFCPLDKFDNMNTA AK	389	24	8	62.51	b22y3y8y10y13y14y20y22	2641.19	79.136	78497	3	881.07	2.40
O33921 AGP_SALTY Glucose-1-phohatase	18		LKNGYQDSLFTSPTVAR	264	17	14	126.5	b7°b7b8b9b10b12b14y3y5°y5y6y7y8y11	1896.97	59.273	75131	3	632.99	-7.66
O33921 AGP_SALTY Glucose-1-phohatase	19		HNLRAPLANNGSVLAQSTPNAWP AWDVPGGQLTTK	39	35	9	32.19	b12°b12b14b15b22°b22b27y8y13	3681.87	78.273	72979	4	921.22	-4.24
O33921 AGP_SALTY Glucose-1-phohatase	20		VTVLVGHDNSNIASLLTALDFKPYQ LHDQYERTPIGGQLVFQR	304	42	6	21.64	b9b10°b10b24y3*y3	4739.43	98.476	47939	6	790.74	-14.22
O33921 AGP_SALTY Glucose-1-phohatase	21		MGTMDPTFNPVITDDSAFRQQA VQAMEK	141	29	7	26.9	b3°b3y3y4°y4y15y24	3199.52	82.501	30365	3	1067.18	9.54
O33921 AGP_SALTY Glucose-1-phohatase	22		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDRQWK	226	34	3	37.21	y6y7y8	3928.87	85.008	15437	3	1310.30	-1.18
O33921 AGP_SALTY Glucose-1-phohatase	23	Carbamidomethyl+C(24)	SQLHLDSEYKLLQITHYQDSPSCK	172	25	3	12.8	b6y3y5	3019.43	82.514	8974	5	604.69	-4.61
O33921 AGP_SALTY Glucose-1-phohatase	24		DLMKIEYVYQSAR	354	13	4	21.36	b7b9y10°y10	1615.83	66.728	6461	2	808.42	12.09
O33921 AGP_SALTY Glucose-1-phohatase	25	Phosphoryl STY(6)	NAEALTLK	370	8	3	33.95	b5y3y4	939.45	33.341	4455	2	470.23	10.20
O33921 AGP_SALTY Glucose-1-phohatase	26		LEVYMGHYTR	77	10	0	3.01		1268.61	64.084	6249	2	634.81	2.02
O33921 AGP_SALTY Glucose-1-phohatase	27		LHLDESYK	174	8	1	8.43	b6	1004.50	40.862	3374	2	502.75	-7.23
O33921 AGP_SALTY Glucose-1-phohatase	28		EVYMGHYTR	78	9	0	3.01		1155.51	64.060	2052	2	578.26	-10.04
O33921 AGP_SALTY Glucose-1-phohatase	29		NVAAPLVK	281	8	0	1.13		794.47	40.631	3529	2	397.74	-2.92
O33921 AGP_SALTY Glucose-1-phohatase	30		QQAVQAMEK	161	9	0	1.51		1015.49	26.927	3358	2	508.25	9.68
O33921 AGP_SALTY Glucose-1-phohatase	31		NAEALTLK	370	8	0	1.13		842.46	41.705	2193	2	421.73	-1.81
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	1		SDVQAAKDDAAR	52	12	12	81.81	b1°b1b2°b2b8b9y3y4y6y7°y7y8	1246.59	18.650	13018	2	623.80	-6.27

Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	2		VDQLSNDVNAMR	40	12	5	35.31	b10y8y9y11y12	1361.65	49.369	12122	2	681.33	-0.09
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	3		IDQLSSDVQTLNAK	26	14	4	27.76	b3°b3b9b10	1531.79	78.190	3462	2	766.40	-2.07
Q8ZP20 TREA_SALTY Periplasmic trehalase	1		VAAAAQAHLQLPGGLATTSVK	428	21	11	78.08	b2b3b9b10b11b12y5y8y10y19y21	2004.12	58.451	88534	3	668.71	-2.92
Q8ZP20 TREA_SALTY Periplasmic trehalase	2		TFADAIPNSDPLMILADYR	68	19	23	118.89	b1b2b4b5°b5b6°b6b13*b13b14y2y3°y3y4°y4y5°y5y7y9y13°y13y14y19	2123.07	102.130	59971	2	1062.04	9.77
Q8ZP20 TREA_SALTY Periplasmic trehalase	3		TTTIAPVDLNALLYQLEK	335	18	9	35.86	b2°b2b3°b3y1y3y5y13y14	2003.12	104.308	55414	2	1002.06	6.64
Q8ZP20 TREA_SALTY Periplasmic trehalase	4		YVPPAGQSLREHIDGLWPVLTR	113	22	7	31.76	b1b2b5y3y5y11y20	2504.30	84.364	55178	4	626.83	-14.62
Q8ZP20 TREA_SALTY Periplasmic trehalase	5		WMDNPQQLSTIR	323	12	6	30.23	y2y4y9*y9y10y12	1488.73	63.082	47005	2	744.87	5.41
Q8ZP20 TREA_SALTY Periplasmic trehalase	6		SNPNRPATEIYR	296	12	8	65.53	b2y3y4°y4y6y7y10y12	1417.71	33.137	37051	3	473.24	-7.40
Q8ZP20 TREA_SALTY Periplasmic trehalase	7		YVPPAGQSLR	113	10	9	59.55	b4b5b6b9y1y6°y6*y6y10	1087.58	20.329	31633	2	544.29	-8.19
Q8ZP20 TREA_SALTY Periplasmic trehalase	8		SAAASGWDFSSR	311	12	4	30.23	y8y9y11y12	1241.57	54.457	25956	2	621.29	12.19
Q8ZP20 TREA_SALTY Periplasmic trehalase	9		SQPPFFAFMVELLAQHEGDDALK	212	23	6	24.56	b6b7b10y2y7°y7	2590.27	91.077	12154	3	864.09	2.07
Q8ZP20 TREA_SALTY Periplasmic trehalase	10		HFVDVNFTLPK	98	11	9	32.07	b1b2b4b5b7b11*b11y11*y11	1316.70	70.210	10244	2	658.85	-2.13
Q8ZP20 TREA_SALTY Periplasmic trehalase	11		WDSLLPLPESYVVPGGR	142	17	6	33.99	b5b12°b12y4y9y12	1885.00	92.168	5888	2	943.00	6.67
Q8ZP20 TREA_SALTY Periplasmic trehalase	12		DQLTAAALFLPLYVNAAAKDR	405	20	4	23.03	b3b4y3y20	2148.11	81.360	2529	3	716.71	-14.09
Q8ZP20 TREA_SALTY Periplasmic trehalase	13		TYYLSR	206	6	1	13.91	y4	802.40	38.188	8977	2	401.71	-6.31
Q8ZP20 TREA_SALTY Periplasmic trehalase	14		ASAAAGDR	357	8	3	36.96	b3b6y3	718.36	37.081	4931	1	718.36	22.18
Q8ZP20 TREA_SALTY Periplasmic trehalase	15		VADMVANFGYEIDAWGHIPNGNR	183	23	4	13.49	b4b10*b10y6	2546.21	81.811	4275	3	849.41	7.48
Q8ZP20 TREA_SALTY Periplasmic trehalase	16	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPK	534	29	4	17.5	b13y3y14y23	3199.61	64.759	3068	3	1067.21	9.16
Q8ZP20 TREA_SALTY Periplasmic trehalase	17		DTPRPESWVEDIATAK	280	16	4	39.83	b3b5b8b12	1814.89	63.253	2640	2	907.95	1.14
Q8ZP20 TREA_SALTY Periplasmic trehalase	18		NVEKWSLLPLPESYVVPGGR	138	21	10	78.38	b6*b6b11y3y4y5y6y8y10y12	2355.24	88.425	55491	3	785.75	1.04
Q8ZP20 TREA_SALTY Periplasmic trehalase	19	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPKTPSAATQ	534	36	6	26.57	b3b4b6b26y10y21	3855.90	64.713	51814	4	964.73	1.08
Q8ZP20 TREA_SALTY Periplasmic trehalase	20		DTPRPESWVEDIATAKSNPNRPAT EIYR	280	28	3	12.01	b12b24y10	3213.58	93.659	4164	5	643.52	-4.63
Q8ZP20 TREA_SALTY Periplasmic trehalase	21		LFPDQKTFADAIPNSDPLMILADY R	62	25	3	22.34	b10b11y10	2851.42	93.342	2068	3	951.15	-4.37
Q8ZP20 TREA_SALTY Periplasmic trehalase	22	Oxidation+M(13)	TFADAIPNSDPLMILADYR	68	19	3	22.45	b5b8b13	2139.04	102.831	13751	3	713.69	-0.91
Q8ZP20 TREA_SALTY Periplasmic trehalase	23	Oxidation+M(32)	SGQQWDAPNGWAPLQWVAEGL QNYGQDDVAMEVTWR	449	37	3	10.93	b5b12y10	4189.90	76.977	2882	4	1048.23	-1.75
Q8ZP20 TREA_SALTY Periplasmic trehalase	24		PNRPATEIYR	298	10	0	2.64		1216.64	33.090	11733	2	608.82	-2.01
Q8ZP20 TREA_SALTY Periplasmic trehalase	25		HFVDVNFTLPK	98	11	1	8.01	y10	1299.67	70.218	3450	2	650.34	-2.54

Q8ZP20 TREA_SALTY Periplasmic trehalase	26		SNPNRPATEIYR	296	12	1	7.72	b9	1400.67	33.120	1845	3	467.56	-13.60
P0A1Z2 SKP_SALTY Chaperone protein skp	1		IAIVNMGNLFQQVAQK	23	16	22	147.83	b2b3b4b6*b6b8b12y1y2*y2y3y4y5*y5y6*y6y7*y7y1ly12y13y16	1773.97	90.442	119216	2	887.49	3.58
P0A1Z2 SKP_SALTY Chaperone protein skp	2		METDLQSK	59	8	9	41.73	b2b8y2y4y6°y6y7°y7y8	951.43	27.289	106590	2	476.22	-14.18
P0A1Z2 SKP_SALTY Chaperone protein skp	3		TGVSNTLENEFK	39	12	14	102.46	b2°b2b9y2y4y5y6y7y8*y8y9y10°y10y12	1338.66	58.344	105661	2	669.83	1.82
P0A1Z2 SKP_SALTY Chaperone protein skp	4		VANDQSIDL VVDANTVAYNSSDV K DITADVLK	126	32	14	53.7	b4b5°b5b6b10b14*b14b18y1y2y14y23y25y32	3392.73	90.453	63728	3	1131.58	6.84
P0A1Z2 SKP_SALTY Chaperone protein skp	5		LEKDVMSQR	82	9	4	46.1	b4b6y3y4	1105.56	49.768	3794	2	553.29	-2.76
P0A1Z2 SKP_SALTY Chaperone protein skp	6		VANDQSIDL VVDANTVAYNSSDV K	126	24	5	13.12	b3b14*b14y8*y8	2537.25	84.893	25784	3	846.42	4.81
P0A1Z2 SKP_SALTY Chaperone protein skp	7		AAELQKMETDLQSK	53	14	12	83.21	b3b8b10y3°y3*y3y7y9y10°y10*y10y12	1591.78	51.638	130366	3	531.27	-10.74
P0A1Z2 SKP_SALTY Chaperone protein skp	8		AQAFEKDR	97	8	3	41.73	y3y5y6	964.48	18.362	11706	2	482.74	-6.39
P0A1Z2 SKP_SALTY Chaperone protein skp	9		LEKDVMSQR	82	9	3	39.1	y3y6y7	1105.55	28.068	5255	2	553.28	-12.04
P0A1Z2 SKP_SALTY Chaperone protein skp	10		TGVSNTLENEFKGR	39	14	3	25.42	b8b9y13	1551.77	100.462	3395	2	776.39	-2.99
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1	Carbamidomethyl+C(13)	AAQYVA AHPGEVCPAK	153	16	13	88.25	b2b3b4b5*b5b8y2y3y4y8y11y12y16	1668.79	35.908	48834	3	556.94	-14.70
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2		YAMIGDPTGALTR	93	13	9	54.67	b1b2b3b4b9y7y10°y10y11	1365.69	63.702	47123	2	683.35	2.95
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		NFDNMREDEGLADR	106	14	8	42.75	b1*b1y4y5y6°y6y12y14	1681.70	47.654	44375	3	561.24	-12.92
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		ATFVVDPQGIIQAEIVTAEGIGR	120	23	18	114.91	b2°b2b3°b3b4b5b6b9b10y2y3y4y5y7°y7y9y10y23	2384.27	129.118	25910	3	795.43	-2.97
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		LGVDVYSVSTDTHFTHK	63	17	10	55.7	b1b3b4°b4b7y3°y3y5y6y9	1905.93	58.053	24236	3	635.98	-0.06
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTELGDVA DHYEELQK	32	31	4	11.47	b4b6y8y31	3757.75	120.029	8909	3	1253.26	9.42
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7		ATFVVDPQGIIQAEIVTAEGIGRDA SDLLR	120	30	4	11.63	b3b6y16y30	3154.69	137.222	3322	3	1052.24	5.19
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8		AWHSSSETIAK	80	11	12	103.54	b3b4b5°b5b8°b8b9°b9b10y3y8°y8	1216.57	30.038	39679	3	406.20	-18.66
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9		NGEFIEVTEK	17	10	3	34.7	y5y7y8	1165.55	89.415	2723	3	389.19	-17.28
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10		IKYAMIGDPTGALTR	91	15	6	49.2	b8b11y3y5y6y10	1606.84	63.303	23356	3	536.28	-14.74
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	11	Carbamidomethyl+C(13)	AAQYVA AHPGEVCPAKWK	153	18	4	27.48	b4b6b7y10	1982.97	47.206	6493	4	496.50	-11.45
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	12		NGEFIEVTEKDTEGR	17	15	3	18.81	b7y5y7	1723.79	86.454	4116	3	575.27	-11.26
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	13	Phosphoryl STY(17)	ATFVVDPQGIIQAEIVTAEGIGR	120	23	4	20.88	b8y3y5y8	2464.27	82.478	19911	3	822.10	13.77
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	14		STDTHFTHK	71	9	2	21.17	b4b5	1073.52	58.055	8314	2	537.26	14.67
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	15		YAMIGDPTGA	93	10	0	3.01		995.44	63.653	6215	2	498.22	-12.20
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	16	Carbamidomethyl+C(11)	QYVA AHPGEVCPAK	155	14	0	4.14		1526.73	35.940	1646	3	509.58	-7.44

P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	1		LQKENIDFVYYGGYYPEMQMLR	211	23	12	69.15	b9b15y1y2y5y6y8°y8y9y11y12y23	2814.35	85.435	53907	3	938.79	7.46
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	2		TAGLDSSQGPTAAK	139	14	19	157.75	b3°b3b4b5°b5b9b11b12y5y7°y7*y7y8y9y10y11y12y14*y14	1303.64	29.477	50523	2	652.33	-4.49
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	3		QGNANIVFFDGITAGEKDFSALIA R	186	25	11	51.6	b2b3*b3b4*b4b25y13y18y19y20y25	2654.36	105.048	44411	3	885.46	1.75
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	4		TQFMGPEGVGNASLSNIAGGAAE GMLVTMPK	242	31	13	34.22	b2°b2*b2b3b9b16y2y4y5y11y13°y13y31	3035.49	93.260	34142	3	1012.50	7.56
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	5		GYQYIMR	132	7	5	38.34	b4y1y4y5y7	930.45	47.980	33194	2	465.73	-3.21
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	6		VAIVGAMSGPVAQWGDMEFNGA R	27	23	4	13.49	b3y5y8y23	2363.15	88.063	21452	3	788.39	10.95
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	7	Carbamidomethyl+C(10)	LVGVEYDDACDPK	66	13	6	40.25	b2b3b4y2y8y9	1480.66	47.757	8410	2	740.83	-2.72
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	8		YILETVKPQR	153	10	8	83.09	y3*y3y4y5y6y7*y7y8	1246.69	45.744	58201	3	416.23	-20.56
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	9		SASHAPLDLVK	316	11	3	32.07	b4b5b10	1137.63	48.012	36179	2	569.32	3.43
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	10		IAIIHDK	163	7	3	41.35	y3y5y6	809.48	33.284	19919	2	405.24	-14.78
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	11		DPSGPYVWITYAAVQSLATAMTR	293	23	4	13.49	b5°b5y3y6	2498.23	75.237	4375	4	625.31	-5.18
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	12		QGNANIVFFDGITAGEK	186	17	4	16.93	b12*b12y6y12	1780.86	68.522	3487	2	890.93	-17.34
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	13		GDLKGFEFGVFQWHADGSSTVA K	346	23	4	13.49	b5°b5y13y16	2483.23	100.240	3715	2	1242.12	11.50
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	14		RYDQDPANK	273	9	6	46.1	b3°b3b5y3*y3y5	1106.52	16.076	1674	2	553.76	0.00
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	15	Oxidation+M()	TQFMGPEGVGNASLSNIAGGAAE GMLVTMPK	242	31	4	11.47	b3°b3b5y26	3051.50	80.766	9390	3	1017.84	12.64
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		GYLSPYFINKPETGAVELESPFILL ADKK	197	29	20	145.02	b2b3b4°b4b6°b6b7y2y3y4y5y7y9y10y11y12y13y25y26y29	3239.72	96.130	136728	4	810.68	-2.71
P0A1D3 CH60_SALTY 60 kDa chaperonin	2		EMLPVLEAVAK	231	11	9	75.68	b2b3y2y3y4y6y8y9y11	1199.66	80.646	112293	2	600.34	-5.49
P0A1D3 CH60_SALTY 60 kDa chaperonin	3		ANDAAGDGTTTATVLAQSIITEGL K	80	25	19	153.96	b2°b2b3b4b5°b5b7b15y3y4°y4y5y6y7y8y9y10y11y25	2418.23	92.786	90550	3	806.75	-1.92
P0A1D3 CH60_SALTY 60 kDa chaperonin	4		VVINKDTTTTIIDGVGEEAAIQGR	322	23	21	146.33	b2b10°b10°b10b11b12b14b20y2y3y4y5y6y7°y7y8y9°y9y12°y12y13	2399.27	68.034	86744	3	800.43	-3.46
P0A1D3 CH60_SALTY 60 kDa chaperonin	5	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDL PK	501	25	28	201.39	b2°b2b3b4b5°b5°b5b7b8b10°b10b12°b12b13y1y2y3y4y5y6y7y8°y8y9y10y11y12y25	2670.32	124.730	69542	3	890.78	1.19
P0A1D3 CH60_SALTY 60 kDa chaperonin	6		AVAAAVEELK	122	10	12	88.84	b1b2b3b4b5y1y2y5y6y7y8y10	1000.56	47.940	50992	2	500.78	-10.31
P0A1D3 CH60_SALTY 60 kDa chaperonin	7	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	11	59.55	b1b2b3°b3y1y2y4y6y7y8y10	1063.51	35.923	40180	2	532.26	-3.56
P0A1D3 CH60_SALTY 60 kDa chaperonin	8	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	11	54.41	b2°b2b9°b9b12y3y5y12y14y15y18	1957.02	62.452	39361	2	979.01	7.73
P0A1D3 CH60_SALTY 60 kDa chaperonin	9		VGAATEVEMK	380	10	7	41.25	b2b3y1y5y7y8y10	1034.52	35.943	31861	2	517.76	-2.95
P0A1D3 CH60_SALTY 60 kDa chaperonin	10		AVAAGMNPMDLK	105	12	11	102.46	b2b3y1y3y5y6y7y8y9y10°y10	1217.61	59.107	30441	2	609.31	3.21
P0A1D3 CH60_SALTY 60 kDa chaperonin	11		SFGAPTITK	42	9	9	63.16	b2b3b9y1y3y5y6y7y9	921.49	45.526	29138	2	461.25	-12.05

P0A1D3 CH60_SALTY 60 kDa chaperonin	12		VEDALHATR	395	9	9	63.16	b2b8y1y3y4y5y8°y8y9	1011.51	26.688	27359	2	506.26	-9.78
P0A1D3 CH60_SALTY 60 kDa chaperonin	13		AIAQVGTISANSDETVGK	142	18	7	33.96	b9b11y2y9y10y13y18	1760.91	49.143	22537	2	880.96	5.62
P0A1D3 CH60_SALTY 60 kDa chaperonin	14		SFGAPTITKDGVSVAR	42	16	9	36.71	b1b3°b3b7y2y6y7y9y16	1605.85	55.721	16019	3	535.95	-8.51
P0A1D3 CH60_SALTY 60 kDa chaperonin	15		ATLEDLGQAK	311	10	5	41.25	b9y3y7y8y10	1045.55	44.770	14396	2	523.28	-5.49
P0A1D3 CH60_SALTY 60 kDa chaperonin	16		AVAAGMNPMDLKR	105	13	4	21.36	b1b3b8y11	1373.72	57.594	14202	3	458.58	14.04
P0A1D3 CH60_SALTY 60 kDa chaperonin	17		VGKEGVITVEDGTGLQDELDVVE GMQFDR	168	29	6	26.03	b4b13b14y4y11°y11	3135.49	76.934	2834	4	784.63	-9.03
P0A1D3 CH60_SALTY 60 kDa chaperonin	18		LAGGVAVIK	371	9	4	46.61	b6y4y7y8	827.52	45.605	62044	2	414.26	-17.92
P0A1D3 CH60_SALTY 60 kDa chaperonin	19		DTTTHIDGVGEEAAIQGR	327	18	4	23.57	b7°b7b8y9	1845.91	100.248	40220	3	615.97	-5.29
P0A1D3 CH60_SALTY 60 kDa chaperonin	20		LIAEAMDK	160	8	4	58.28	y3y4y6y7	890.45	39.681	22938	2	445.73	-21.25
P0A1D3 CH60_SALTY 60 kDa chaperonin	21		GGDGNYGYNAAATEEYGNMIDMG ILDPTK	470	28	3	23.03	y3y4y7	2966.34	89.050	22468	2	1483.67	20.00
P0A1D3 CH60_SALTY 60 kDa chaperonin	22		GYLSPYFINKPETGAVELESPFILL ADK	197	28	4	22.22	b11b12°b12y13	3111.67	102.684	5144	3	1037.89	12.08
P0A1D3 CH60_SALTY 60 kDa chaperonin	23		AAVEEGVVAGGGVALIR	404	17	3	24.33	b3b7b11	1567.91	67.111	2384	3	523.31	20.79
P0A1D3 CH60_SALTY 60 kDa chaperonin	24		EIELEDKFENMGAMVK	58	17	10	97.75	b9y5y6°y6y7y8y10y12y14 y15	2010.94	73.979	107889	3	670.98	-5.77
P0A1D3 CH60_SALTY 60 kDa chaperonin	25		NVVLDKSFGAPTITK	36	15	5	41.22	b5y5y7y12y13	1589.87	58.648	41130	3	530.63	-13.28
P0A1D3 CH60_SALTY 60 kDa chaperonin	26		GGDGNYGYNAAATEEYGNMIDMG ILDPTKVTR	470	31	3	17.33	y3y6y23	3322.52	87.217	39284	3	1108.18	6.76
P0A1D3 CH60_SALTY 60 kDa chaperonin	27	Carbamidomethyl+C(16)	AVAAAVEELKALSVPSCDSK	122	20	7	57.62	b3y4y6y8y10y17y18	2045.04	72.687	37181	3	682.35	-8.66
P0A1D3 CH60_SALTY 60 kDa chaperonin	28		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	22	166.84	b3b4b5b6b7°b7°b7b8°b8b10y4y5y6y7°y7y10y16y21 y25y26y27y29	3675.89	122.604	33606	3	1225.97	6.51
P0A1D3 CH60_SALTY 60 kDa chaperonin	29	Carbamidomethyl+C(13)	AMEAPLRQIVLNCGEEPSVVANT VK	445	25	7	30.5	b7b12b16y5°y5y10y13	2725.41	74.738	28903	3	909.14	4.48
P0A1D3 CH60_SALTY 60 kDa chaperonin	30	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVKGGDGN YGYNAAATEEYGNMIDMGILDPTK	452	46	3	16.44	b11b14b25	4904.32	83.842	12378	5	981.67	11.05
P0A1D3 CH60_SALTY 60 kDa chaperonin	31		ANDAAGDGT°TATVLAQSIITEGL KAVAAGMNPMDLK	80	37	9	26.18	b3b11°b11y6°y6y8y9y12°y12	3616.83	132.353	7740	3	1206.28	3.17
P0A1D3 CH60_SALTY 60 kDa chaperonin	32	Carbamidomethyl+C(6)	ALSVPSCDSKAIAQVGTISANSDE TVGK	132	28	4	17.94	b12y12y14y24	2805.35	83.383	4510	4	702.09	-13.92
P0A1D3 CH60_SALTY 60 kDa chaperonin	33		DTTTHIDGVGEEAAIQGRVAQIR	327	23	4	23.58	b4b5°b5b11	2413.28	55.750	3034	3	805.10	4.35
P0A1D3 CH60_SALTY 60 kDa chaperonin	34		IADLKGQNEQNVGIK	425	16	4	29.29	b3y8y10y11	1741.91	82.318	2203	2	871.46	1.54
P0A1D3 CH60_SALTY 60 kDa chaperonin	35	Oxidation+M()	AVAAGMNPMDLKR	105	13	3	28.84	y4y5y7	1389.70	26.463	37697	3	463.90	-1.05
P0A1D3 CH60_SALTY 60 kDa chaperonin	36	Oxidation+M(9)	VGAATEVEMKEK	380	12	8	72.08	b3b5°b5b8°b8b10y8y10	1307.65	74.619	10192	3	436.55	-4.11
P0A1D3 CH60_SALTY 60 kDa chaperonin	37	Oxidation+M(22)	EGVITVEDGTGLQDELDVVEGMQ FDR	171	26	3	22.28	b7b8y10	2867.37	65.700	9090	3	956.46	13.88
P0A1D3 CH60_SALTY 60 kDa chaperonin	38	Oxidation+M(2)	EMLPVLEAVAK	231	11	3	28.09	b6b7y7	1215.65	64.556	7407	2	608.33	-12.85
P0A1D3 CH60_SALTY 60 kDa chaperonin	39	Oxidation+M(9)	VGAATEVEMK	380	10	3	27.71	b8y5y7	1050.52	95.442	1523	1	1050.52	1.39

[P0A1D3]CH60_SALTY 60 kDa chaperonin	40		EDALHATR	396	8	0	1.51		912.45	26.674	24693	2	456.73	-8.16
[P0A1D3]CH60_SALTY 60 kDa chaperonin	41		AAAVEELK	124	8	1	8.43	b6	830.45	47.947	7466	1	830.45	-11.32
[P0A1D3]CH60_SALTY 60 kDa chaperonin	42		SFGAPTITKDGV	42	12	0	4.14		1192.60	55.777	6593	2	596.81	-14.33
[P0A1D3]CH60_SALTY 60 kDa chaperonin	43	Carbamidomethyl+C(4)	SVPCSDSK	134	8	0	1.88		879.39	35.925	1509	1	879.39	6.73
[P0A1D3]CH60_SALTY 60 kDa chaperonin	44		EMLPVLEAVAK	231	11	0	2.26		1181.64	80.664	5662	2	591.33	-9.81
[P0A297]RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	11	75.99	b2b3*b3b4*b4b8y8y10y11y13	1447.78	65.910	75403	2	724.39	0.67
[P0A297]RL10_SALTY 50S ribosomal protein L10	2	Carbamidomethyl+C(9)	VVEGTQFECLKDTFVGPTLIAYSM EHPGAAAR	62	32	5	16.38	b10y13y17y30y32	3494.70	92.843	54063	4	874.43	-2.24
[P0A297]RL10_SALTY 50S ribosomal protein L10	3		AAAFEGELIPASQIDR	109	16	9	75.09	b5b9y5y7y8y9y11y12y16	1687.88	69.397	53448	2	844.44	7.23
[P0A297]RL10_SALTY 50S ribosomal protein L10	4		GALSAVVADSR	20	11	10	72.67	b3b11y4y5y6*y6y7y8*y8y11	1045.57	48.842	42907	2	523.29	7.71
[P0A297]RL10_SALTY 50S ribosomal protein L10	5		QAIVAEVSEVAK	8	12	6	23.03	b2b9*b9b12y8y10	1243.69	57.968	17033	2	622.35	-2.36
[P0A297]RL10_SALTY 50S ribosomal protein L10	6		LMATMK	138	6	1	13.91	b4	694.37	41.470	15439	1	694.37	12.66
[P0A297]RL10_SALTY 50S ribosomal protein L10	7		DTFVGPTLIAYSM EHPGAAAR	73	21	3	14.38	b10b12y11	2204.10	68.335	7348	3	735.37	8.64
[P0A297]RL10_SALTY 50S ribosomal protein L10	8		GVTVDK	31	6	1	13.91	b5	618.35	72.036	2123	1	618.35	8.69
[P0A297]RL10_SALTY 50S ribosomal protein L10	9	Carbamidomethyl+C(9)	VVEGTQFECLK	62	11	3	25.08	b9y4y7	1309.67	68.425	2018	2	655.34	16.87
[P0A297]RL10_SALTY 50S ribosomal protein L10	10		EAGVYMR	46	7	3	38.34	b5b6y6	825.39	74.649	1755	1	825.39	-4.07
[P0A297]RL10_SALTY 50S ribosomal protein L10	11		LATLPTYEEAIARLMATMK	125	19	5	21.57	b5b8y6y18*y18	2123.10	58.532	232897	3	708.37	-11.15
[P0A297]RL10_SALTY 50S ribosomal protein L10	12		AAAFEGELIPASQIDRLATLPTYEE AIAR	109	29	7	45.67	b4b5b6b10y4y9y20	3116.65	93.504	29276	3	1039.55	6.19
[P0A297]RL10_SALTY 50S ribosomal protein L10	13		ALNLQDKQAIVA EVSEVAK	1	19	5	32.46	y3y5y8*y8y9	2026.10	72.053	27306	3	676.04	-9.22
[P0A297]RL10_SALTY 50S ribosomal protein L10	14	Oxidation+M(9)	AGREAGVYMR	43	10	4	42.22	b7b8y5y7	1125.56	42.406	9372	2	563.28	13.12
[P0A297]RL10_SALTY 50S ribosomal protein L10	15	Oxidation+M(2)	LMATMK EASAGK	138	12	3	27.01	b9y9y10	1253.64	51.349	2198	3	418.55	14.51
[P0A297]RL10_SALTY 50S ribosomal protein L10	16		IAYSMEHPGAAAR	81	13	0	10.17		1373.68	92.869	2938	2	687.34	11.91
[P66038]RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	15	82.92	b3b8b9*b9b12b13b14b20y2y3y4y9y12y15y29	3110.69	98.952	87079	3	1037.57	3.69
[P66038]RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	15	133.46	b2b3b8b9y4y5y6y8y9y10y13*y13y14y15y19	2109.08	101.780	61551	2	1055.04	9.72
[P66038]RISB_SALTY 6	3		GAEAALTALEMINVLK	136	16	7	36.71	b4b5b7b16y1y4y10	1643.91	103.442	28899	2	822.46	1.49
[P66038]RISB_SALTY 6	4		ANVAAPDAR	5	9	6	39.1	b2*b2y3y5y6y9	884.45	23.575	9085	2	442.73	-9.18
[P66038]RISB_SALTY 6	5		NI IK	1	4	1	13.16	y3	487.32	37.877	11641	1	487.32	-6.45
[P66038]RISB_SALTY 6	6		VAIT IAR	14	7	3	41.35	y4y5y6	743.47	44.807	9192	2	372.24	-16.58
[P66038]RISB_SALTY 6	7		AGNKGAEAA LTALEMINVLK	132	20	9	89.72	b5b7b8b9b16y3y4y5y6	2014.08	97.577	54364	3	672.03	-9.45
[P66932]TIG_SALTY Trigger factor	1		NVALEEQA VEAVLAK	399	15	12	99.22	b2b3b7y1y3y4y5y7y11y12y13y15	1583.87	80.775	53273	2	792.44	1.39
[P66932]TIG_SALTY Trigger factor	2		ANDIDVPSALIDSEIDVLRR	296	20	8	28.73	b2*b2b3b4y1y14y16y20	2211.15	91.139	31309	3	737.72	-4.31

P66932 TIG_SALTY Trigger factor	3		SQAIEGLVK	287	9	7	31.32	b2*b2b5y1y7y8y9	944.53	47.917	30417	2	472.77	-7.69
P66932 TIG_SALTY Trigger factor	4		FGVEDGSVAGLR	255	12	7	30.23	b2y1y2y3y8y9y12	1206.61	58.000	14422	2	603.81	1.32
P66932 TIG_SALTY Trigger factor	5		ANDIDVPSALIDSEIDVLR	296	19	14	70.61	b2b4*b4b5b6*b6b7*b7b11 *b11b13y3y13y19	2055.07	95.250	9842	2	1028.04	4.99
P66932 TIG_SALTY Trigger factor	6		NKELMDNMR	390	9	6	66.17	b3y3y4y6y7y9	1150.54	35.613	7801	2	575.77	2.97
P66932 TIG_SALTY Trigger factor	7		ATSFNELMNQQA	420	12	3	33.24	b3b5b8	1353.60	50.717	6099	3	451.87	-9.11
P66932 TIG_SALTY Trigger factor	8		GLIEEMASAYEDPKEVIEFYSK	368	22	6	36.81	b5b7b10b19y6y12	2548.25	83.377	4719	4	637.82	11.88
P66932 TIG_SALTY Trigger factor	9		ATDFVLAMGQGR	181	12	5	35.31	b5b6b8y5y12	1265.65	94.463	3764	2	633.33	13.70
P66932 TIG_SALTY Trigger factor	10		AEVR	267	4	1	13.16	b3	474.26	30.774	7875	1	474.26	-8.56
P66932 TIG_SALTY Trigger factor	11		YGASVR	57	6	2	27.44	b3b4	652.34	27.468	6504	1	652.34	-7.67
P66932 TIG_SALTY Trigger factor	12		MQVSVETTQGLGR	0	13	7	56.22	b3b11y6*y6y7y9y11	1405.72	59.287	3178	2	703.36	5.21
P66932 TIG_SALTY Trigger factor	13		INPAGAPNYVPGEYK	83	15	4	26.89	b8b9*b9b12	1589.79	52.240	3065	3	530.60	-2.69
P66932 TIG_SALTY Trigger factor	14		VTITIAADSIETAVK	14	15	4	49.45	b8b9b10b11	1531.82	76.929	2272	2	766.42	-21.83
P66932 TIG_SALTY Trigger factor	15		ANDIDVPSALIDSEIDVLR	296	20	3	24.32	b10b13b14	2211.15	91.029	18938	2	1106.08	-7.51
P66932 TIG_SALTY Trigger factor	16		YGASVRQDVLGDLMSR	57	16	3	24.33	b8b9y3	1766.88	70.807	9515	3	589.63	-5.73
P66932 TIG_SALTY Trigger factor	17		AGEEFTIDVTFPEEYHAENLK GK	206	23	3	19.9	b7b9b11	2624.28	62.582	8860	3	875.43	10.98
P66932 TIG_SALTY Trigger factor	18		VKGLIEEMASAYEDPK	366	16	3	17.8	b12y6y11	1779.86	70.783	7832	3	593.96	-12.89
P66932 TIG_SALTY Trigger factor	19		RFGVEDGSVAGLR	254	13	3	21.36	b10y7y10	1362.70	49.770	5551	3	454.91	-6.27
P66932 TIG_SALTY Trigger factor	20		GHKAGEEFTIDVTFPEEYHAENLK	203	24	3	35.45	b10b11b12	2761.30	74.628	4196	3	921.11	-1.95
P66932 TIG_SALTY Trigger factor	21	Oxidation+M(6)	GLIEEMASAYEDPKEVIEFYSK	368	22	4	18.96	b3b6y11y13	2564.25	82.680	2828	2	1282.63	14.76
P66932 TIG_SALTY Trigger factor	22		SQAIEGL	287	7	0	1.51		717.38	47.865	6169	1	717.38	3.15
P66932 TIG_SALTY Trigger factor	23		ANDIDVPSALIDSEI	296	15	3	13.42	y3*y3y13	1571.78	95.274	2313	2	786.39	0.78
Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTEPTWFPDSQTLAFTSDQAG RPQVYK	287	29	12	46.31	b2b5*b5y2y9y13*y13y21y 22y24y25y29	3285.57	78.297	102913	3	1095.86	7.06
Q8ZQT5 TOLB_SALTY Protein tolB	2		VSDYDGYNQFVVHR	183	14	9	90.35	y2y4y5y6y7y9y10y12y14	1698.76	54.492	86488	3	566.93	-14.80
Q8ZQT5 TOLB_SALTY Protein tolB	3		WAGPGAAPEDIGGIVAADLR	43	20	9	63.06	b7y2y5y9y12y13y14y15y2 0	1936.00	86.119	52305	2	968.50	2.33
Q8ZQT5 TOLB_SALTY Protein tolB	4		IAYVVQTNGGQFPYELR	166	17	18	96.51	b3b9b12y1y2y3y5*y5y6*y6 y8y11*y11y12*y12y13*y13 y17	1955.02	74.077	50348	2	978.01	9.12
Q8ZQT5 TOLB_SALTY Protein tolB	5		YAGHTASDEVFEK	142	13	6	35.11	b6y4y6y9*y9y13	1453.64	37.731	49708	3	485.22	-10.83
Q8ZQT5 TOLB_SALTY Protein tolB	6		IEITQGVDSARPIGVVPPK	24	19	11	53.62	b2b8b9b11y2y3y12y16*y1 6y18y19	2026.12	71.186	47379	3	676.04	-6.63
Q8ZQT5 TOLB_SALTY Protein tolB	7		SPQPLMSPAWSPDGSK	197	16	6	42.95	b8y3y5y10y13y16	1684.81	63.370	44462	2	842.91	8.69
Q8ZQT5 TOLB_SALTY Protein tolB	8		LAYVTFESGR	213	10	5	34.7	b2y4y5y8y10	1142.58	58.284	42839	2	571.79	-3.21

Q8ZQT5 TOLB_SALTY Protein tolB	9		TGSLNLYVMDLASGQIR	264	17	5	23.85	b6b14y5y11y17	1837.96	90.096	37886	2	919.48	5.38
Q8ZQT5 TOLB_SALTY Protein tolB	10		SALVIQTLANGAVR	223	14	9	76.09	b3b4y2y5y6y8y9y10y14	1412.82	71.531	35915	2	706.91	0.35
Q8ZQT5 TOLB_SALTY Protein tolB	11		MNINGGAAQR	316	10	13	74.06	b2*b2b3*b3b4b10y1y6y7*y7y8y9y10	1031.50	28.595	35225	2	516.25	-5.80
Q8ZQT5 TOLB_SALTY Protein tolB	12		HNGAPAFSPDGTK	244	13	4	40.34	b3y4y5y6	1298.62	67.881	7884	2	649.81	4.98
Q8ZQT5 TOLB_SALTY Protein tolB	13		ITWEGSQNQDADVSSDGK	326	18	3	16.16	b5y3y11	1936.82	56.922	2958	2	968.91	-17.33
Q8ZQT5 TOLB_SALTY Protein tolB	14		IEITQGVSARPIGVVPFKWAGPG AAPEDIGGIVAADLR	24	39	9	29.92	b9°b9b16°b16y3y5y6y9y13	3943.09	95.360	65773	4	986.53	-4.58
Q8ZQT5 TOLB_SALTY Protein tolB	15		SPQPLMSPAWSPDGSKLAYVTFES GR	197	26	11	77.45	b5b24y4y5y8y9°y9y13y15y23y24	2808.39	81.699	32047	3	936.80	7.48
Q8ZQT5 TOLB_SALTY Protein tolB	16		NSGKFNPLDR	63	10	6	59.55	b9y4y5*y5y6y8	1147.58	41.743	21401	2	574.29	-3.40
Q8ZQT5 TOLB_SALTY Protein tolB	17		ARLPATDGQVK	411	11	9	119.29	b3b4b5b7b9y6y7y8y9	1155.64	29.783	13579	2	578.32	-6.34
Q8ZQT5 TOLB_SALTY Protein tolB	18		HNGAPAFSPDGTKLAFALSK	244	20	4	23.46	b5b9b16y12	2029.07	62.040	13531	3	677.03	8.36
Q8ZQT5 TOLB_SALTY Protein tolB	19		VSDYDGYNQFVVHRSPQPLMSPA WSPDGSK	183	30	4	25.34	b3b4y3y8	3364.57	70.693	4599	4	841.90	-0.94
Q8ZQT5 TOLB_SALTY Protein tolB	20		LPATDGQVKSPAWSPYL	413	17	3	16.93	b6y6y12	1829.94	91.169	3144	3	610.65	-0.07
Q8ZQT5 TOLB_SALTY Protein tolB	21		QVASFPRHNGAPAFSPDGTK	237	20	4	14.9	b13y5y8°y8	2084.06	113.098	1923	3	695.36	12.53
Q8ZQT5 TOLB_SALTY Protein tolB	22		TGSLNLYVMDLASGQIRQITDGR	264	23	6	37.69	b5b12*b12b13*b13b14	2508.29	80.598	1813	3	836.77	1.65
Q8ZQT5 TOLB_SALTY Protein tolB	23	Phosphoryl STY(9)	IEITQGVDSARPIGVVPFK	24	19	3	24.67	b7b8b12	2106.06	59.234	2470	4	527.27	-13.91
Q8ZQT5 TOLB_SALTY Protein tolB	24	Oxidation+M()	QDLVTGGVQVLSSTFLDETPLAP NGTMVIYSSSQGMGSVLNLVSTD GR	360	49	4	24.41	b7*b7b8y4	5044.41	74.744	17735	6	841.58	-12.39
Q8ZQT5 TOLB_SALTY Protein tolB	25	Oxidation+M(9)	TGSLNLYVMDLASGQIR	264	17	4	16.93	b9°b9b11y6	1853.92	55.702	1747	3	618.64	-11.98
Q8ZQT5 TOLB_SALTY Protein tolB	26		VIQTLANGAVR	226	11	1	7.38	b3	1141.65	71.524	19068	2	571.33	-12.62
Q8ZQT5 TOLB_SALTY Protein tolB	27		DYDGYNQFVVHR	185	12	0	3.39		1512.71	54.527	3014	2	756.86	14.69
Q8ZQT5 TOLB_SALTY Protein tolB	28		TGSLNLYVMDLASGQIR	264	17	0	4.52		1819.95	90.137	8105	2	910.48	7.91
Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	8	38.32	b2b3*b3b4*y12y13y14y16	1686.95	90.573	76255	2	843.98	3.47
Q7CR87 SURA_SALTY Chaperone surA	2		ITVLPQEVDALAK	149	13	9	68.78	b3°b3b4y2y8y9y10y11y13	1396.81	71.352	63595	2	698.91	1.92
Q7CR87 SURA_SALTY Chaperone surA	3		LIMDQIILQMGGK	73	13	7	69.17	b6y3y4y5y6y7y13	1530.84	88.692	52920	2	765.92	2.79
Q7CR87 SURA_SALTY Chaperone surA	4		ITDEQLDQAIANIAK	90	15	10	65.16	b7b10*b10y4y5y6y9y13y15*y15	1642.88	81.050	51253	2	821.94	6.46
Q7CR87 SURA_SALTY Chaperone surA	5		LAYDGLNYSTYR	117	12	6	51.06	b5y2y3y5y6y8	1435.69	59.204	50828	2	718.35	6.04
Q7CR87 SURA_SALTY Chaperone surA	6		GQISAPVHSSFGWHLIELLDTR	362	22	11	30.06	b2*b2b4°b4°b4b5b13y2y3y17y22	2463.25	94.095	39907	4	616.57	-12.09
Q7CR87 SURA_SALTY Chaperone surA	7		LNAGQAGQQLPDDATLR	50	17	9	72.17	b4b7y3y4y6y7y9y12y17	1767.90	51.658	37175	2	884.46	3.04
Q7CR87 SURA_SALTY Chaperone surA	8		QAESIVEEAR	197	10	4	34.7	y4y5y8y10	1131.56	38.773	29120	2	566.28	-3.56
Q7CR87 SURA_SALTY Chaperone surA	9		HILLKPSPIMNDQQAR	288	16	5	17.8	b2b3y4*y4y8	1861.00	49.730	23470	3	621.00	-7.74

Q7CR87 SURA_SALTY Chaperone surA	10		QIGTQNDASTELNLSHILALPENP TSEQVNDAGR	162	35	10	23.98	b9b12°b12y1y3*y3y5y9y1 4y35	3816.93	89.385	21527	3	1272.98	7.74
Q7CR87 SURA_SALTY Chaperone surA	11		GQSQSISVTEVHAR	274	14	6	42.75	y2y6y7y8y10y14	1498.74	37.469	16559	3	500.25	-14.09
Q7CR87 SURA_SALTY Chaperone surA	12		VAAVVNNGVVLESDVDGLMQSV K	27	23	10	55.22	b2b3b4b15y3y5y7y8y12y2 3	2343.25	91.687	8115	2	1172.13	13.23
Q7CR87 SURA_SALTY Chaperone surA	13		LAITYSADQQALK	214	13	5	21.36	b2b9y7y10y13	1421.76	55.372	5503	2	711.38	-1.46
Q7CR87 SURA_SALTY Chaperone surA	14		EMIIEVR	134	8	3	41.73	y4y5y6	976.51	53.911	34754	2	488.76	-0.31
Q7CR87 SURA_SALTY Chaperone surA	15		HQILER	67	6	3	27.44	b3*b3y4	795.44	25.729	19890	2	398.22	-8.21
Q7CR87 SURA_SALTY Chaperone surA	16		GGQMGWGR	227	8	3	33.95	b5y4y5	848.37	35.031	5681	2	424.69	-12.59
Q7CR87 SURA_SALTY Chaperone surA	17		TDAAQK	388	6	2	13.91	y4*y4	633.33	33.353	2640	1	633.33	8.96
Q7CR87 SURA_SALTY Chaperone surA	18		LAITYSADQQALKGGQMGWGR	214	21	10	73.68	b10°b10*b10y4y5y8y9y10 y11y18	2251.12	65.804	33428	3	751.05	-3.04
Q7CR87 SURA_SALTY Chaperone surA	19		QAESIVEEARNGADFGK	197	17	5	28.32	b4b5b9°b9y6	1820.90	36.616	1893	5	364.99	12.20
Q7CR87 SURA_SALTY Chaperone surA	20	Phosphoryl STY(27)	QIGTQNDASTELNLSHILALPENP TSEQVNDAGR	162	35	9	35.56	b3b4°b4*b4b6°b6y7*y7y8	3896.89	114.869	1696	4	974.98	8.40
Q7CR87 SURA_SALTY Chaperone surA	21		GQSQSISVTEVHAR	274	14	0	3.39		1481.72	37.481	1530	3	494.58	-3.95
P0A1P6 GLNA_SALTY Glutamine synthetase	1		EIPQVAGSLEEALNALDLDR	406	20	15	51.51	b4°b4b7*b7b11*b11b15y1 y6°y6y14y15°y15*y15y20	2153.10	96.454	50663	3	718.37	-2.27
P0A1P6 GLNA_SALTY Glutamine synthetase	2		SAEHVLTMLNEHEVK	1	15	11	97.58	b4b5b9b10y4y6y7y8*y8y9 y15	1736.84	55.530	26927	3	579.62	-13.71
P0A1P6 GLNA_SALTY Glutamine synthetase	3		LVPGYEAPVMLAYSAR	322	16	8	53.47	b15y4y5°y5y9y11y14°y14	1736.91	78.279	24987	2	868.96	6.04
P0A1P6 GLNA_SALTY Glutamine synthetase	4		AINALANPTTNSYKR	307	15	16	74.19	b2b3*b3b4*b4y7°y7y8°y8* y8y9*y9y10*y10y13y15	1633.85	43.355	24241	3	545.29	-10.01
P0A1P6 GLNA_SALTY Glutamine synthetase	5	Carbamidomethyl+C(1)	CDILEPGTLQGYDRDPR	89	17	9	23.85	b2b3b11y2y9°y9*y9y11°y1 1	2004.95	60.690	23142	3	668.99	0.49
P0A1P6 GLNA_SALTY Glutamine synthetase	6		GGYFPVPPVDSAQDIR	177	16	5	25.21	b3b5y2y8y12	1717.87	70.845	12328	2	859.44	10.80
P0A1P6 GLNA_SALTY Glutamine synthetase	7		GINESDMVLPMDASTAVIDPFFAD STLIIR	59	30	5	17.09	b11y6y11y13y30	3238.63	114.118	6880	3	1080.21	7.69
P0A1P6 GLNA_SALTY Glutamine synthetase	8		ATGIADTVLFGPEPEFFLFDDIR	117	23	9	42.42	b2b3y2y3y5y8y10°y10y13	2570.27	117.747	5724	3	857.43	-5.13
P0A1P6 GLNA_SALTY Glutamine synthetase	9		FGASISGSHVAIDDIEGAWNSSTK	140	24	3	13.12	b14y7y12	2449.16	76.875	2655	3	817.06	0.20
P0A1P6 GLNA_SALTY Glutamine synthetase	10		IHPGEAMDK	386	9	4	46.61	b7y5y7y8	997.47	37.295	2133	2	499.24	-7.59
P0A1P6 GLNA_SALTY Glutamine synthetase	11		AGGVFTDEAIDAYIALR	430	17	5	37.86	b5b6°b6b7y12	1781.88	77.180	69779	2	891.44	-16.58
P0A1P6 GLNA_SALTY Glutamine synthetase	12		MSAEHVLTMLNEHEVK	0	16	3	17.8	b7b12y4	1867.89	81.472	51769	3	623.30	-6.80
P0A1P6 GLNA_SALTY Glutamine synthetase	13		MTPHPVEFELYYSV	455	14	4	25.42	b7°b7y5y6	1711.83	49.879	13259	2	856.42	15.97
P0A1P6 GLNA_SALTY Glutamine synthetase	14		NLYDLPPEEAK	395	11	3	32.07	y5y6y9	1288.66	65.398	13227	2	644.84	17.52
P0A1P6 GLNA_SALTY Glutamine synthetase	15	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	6	39.67	b7b15b16y3y15y16	2565.33	136.686	6140	2	1283.17	16.75
P0A1P6 GLNA_SALTY Glutamine synthetase	16		EQHVTIPAHQVNAEFFEEGK	28	20	3	14.9	b13b19y6	2310.15	107.762	4902	2	1155.58	14.37

P0A1P6 GLNA_SALTY Glutamine synthetase	17		AINALANPTTNSYK	307	14	3	28.55	y3y7y9	1477.77	48.671	3895	2	739.39	2.07
P0A1P6 GLNA_SALTY Glutamine synthetase	18		FNTMTK	225	6	1	13.91	y4	741.36	109.830	2705	1	741.36	4.86
P0A1P6 GLNA_SALTY Glutamine synthetase	19	Carbamidomethyl+C(1)	CDILEPGTLQGYDR	89	14	5	19.98	b5y6°y6y12*y12	1636.79	61.326	1938	3	546.27	14.32
P0A1P6 GLNA_SALTY Glutamine synthetase	20		FGASISGSHVAIDIEGAWNSSTK YEGGNK	140	30	4	25.34	b9b10y5y12	3097.46	53.096	61999	3	1033.16	2.84
P0A1P6 GLNA_SALTY Glutamine synthetase	21	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK NK	360	26	5	27.5	b4b10b13b20y15	2807.41	100.229	6993	3	936.47	-6.35
P0A1P6 GLNA_SALTY Glutamine synthetase	22	Carbamidomethyl+C(22)	FGKTATFMPKPMFGDNGSGMHCHMSLAK	249	28	6	39.47	b12b18y6y7y8°y8	3085.43	133.435	5857	4	772.11	11.08
P0A1P6 GLNA_SALTY Glutamine synthetase	23		AEDYL RATGIADTVLFGPEPEFFLFD DIR	111	29	3	11.81	b6y9y11	3317.60	97.968	4466	4	830.16	-9.64
P0A1P6 GLNA_SALTY Glutamine synthetase	24	Carbamidomethyl+C(1)	CDILEPGTLQGYDRDPR	89	17	3	16.93	b9y3y8	2004.93	59.049	2279	3	668.98	-9.13
P0A1P6 GLNA_SALTY Glutamine synthetase	25	Carbamidomethyl+C(1); Phosphoryl STY(12)	CDILEPGTLQGYDRDPR	89	17	3	16.93	b3b11y5	2084.92	59.787	10766	4	521.98	7.49
P0A1P6 GLNA_SALTY Glutamine synthetase	26		NALANPTTNSYKR	309	13	0	3.77		1449.74	43.339	2438	2	725.37	-2.11
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	12	130.99	b2b3b4b5y3y5y6y7y8y9y10y12	1150.68	54.035	72276	2	575.84	-4.46
P66313 RL6_SALTY 50S ribosomal protein L6	2		INGQVITIK	18	9	6	39.1	b1y3y7y8°y8y9	985.59	49.110	50036	2	493.30	-9.29
P66313 RL6_SALTY 50S ribosomal protein L6	3		TLNDAVEVK	35	9	9	31.32	b2°b2b7y1y2y3°y3y7y9	988.52	39.071	47950	2	494.76	-10.19
P66313 RL6_SALTY 50S ribosomal protein L6	4		ALLNSMVIGVTEGFTK	69	16	11	66.12	b2b6b14y2y6y7y8y12y13°y13y16	1679.90	94.786	46537	2	840.45	-1.53
P66313 RL6_SALTY 50S ribosomal protein L6	5		YADEVVR	163	7	4	41.35	y3y4y5y7	851.42	30.928	45395	2	426.21	-11.25
P66313 RL6_SALTY 50S ribosomal protein L6	6		DGYADGWAQAGTAR	55	14	7	60.28	b3y1y4y5y7y10y11	1438.64	50.606	38770	2	719.82	5.01
P66313 RL6_SALTY 50S ribosomal protein L6	7		HADNALTFGPR	44	11	8	71.7	b2b5b6y4y5y9y10y11	1198.59	45.972	30514	2	599.80	-3.56
P66313 RL6_SALTY 50S ribosomal protein L6	8		LQLVGVG YR	86	9	7	46.88	b2*b2y2y3y5y7y9	1004.58	60.209	29394	2	502.80	-5.53
P66313 RL6_SALTY 50S ribosomal protein L6	9		QVIGQVAADLR	138	11	6	51.62	y1y2y5y6y8y9	1169.66	58.002	12137	2	585.33	-6.26
P66313 RL6_SALTY 50S ribosomal protein L6	10		GADKQVIGQVAADLR	134	15	4	32.8	b4b9y5y6	1540.83	58.996	30246	3	514.28	-6.42
P66313 RL6_SALTY 50S ribosomal protein L6	11		YADEVVRTK	163	9	3	31.32	b5b6y8	1080.58	26.250	6858	2	540.79	6.78
P64052 EFTS_SALTY Elongation factor Ts	1		VASLEGDVLGSYQHGAR	134	17	19	118.28	b2b3y4y5*y5y7*y7y8°y8*y8y9y10°y10y11*y11y12y13°y13y17	1758.86	59.594	131716	3	586.96	-10.34
P64052 EFTS_SALTY Elongation factor Ts	2		ITDVEVLK	104	8	6	58.28	y2y3y4y6y7y8	916.52	49.296	129010	2	458.77	-12.52
P64052 EFTS_SALTY Elongation factor Ts	3		AEITASLVK	1	9	6	63.16	b3y4y5y6y7y9	931.53	49.340	119284	2	466.27	-14.09
P64052 EFTS_SALTY Elongation factor Ts	4		FTGEVSLTGQPFVMEPSK	222	18	10	79.95	b4b5b6b7°b7y1y3y5y10y13	1953.97	75.479	72060	2	977.49	5.62
P64052 EFTS_SALTY Elongation factor Ts	5		IGENINIR	125	8	9	55.27	b2y2y3*y3y5y6y7*y7y8	928.51	45.095	50687	2	464.76	-11.83
P64052 EFTS_SALTY Elongation factor Ts	6		ALTEANGDIELAIENMRK	25	18	5	32.2	b7b10y5y9y16	1988.00	75.003	34040	3	663.34	-7.37
P64052 EFTS_SALTY Elongation factor Ts	7		SVGQLLKEHNADVTGFIR	240	18	8	35.86	b1b4*b4y4y6y8y9°y9	1984.05	66.237	21246	3	662.02	-7.08

P64052 EFTS_SALTY Elongation factor Ts	8		VLDAAVAGK	95	9	4	54.39	b3y3y6y8	843.48	34.212	19832	2	422.24	-13.82
P64052 EFTS_SALTY Elongation factor Ts	9	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	6	49.03	b2b4y2y3y5y7	1098.47	21.671	10886	2	549.74	-6.22
P64052 EFTS_SALTY Elongation factor Ts	10		ALTEANGDIELAIENMR	25	17	4	16.93	b7y6*y6y11	1859.91	82.666	5770	3	620.64	-4.66
P64052 EFTS_SALTY Elongation factor Ts	11		FEVGEGIEK	258	9	3	31.32	b4b8y7	1007.48	35.543	81343	2	504.24	-21.63
P64052 EFTS_SALTY Elongation factor Ts	12		IGVLVAAK	151	8	3	41.73	y3y6y7	770.50	47.719	58749	2	385.75	-20.83
P64052 EFTS_SALTY Elongation factor Ts	13		VALVAK	119	6	2	27.44	y4y5	600.41	47.714	3610	1	600.41	-0.71
P64052 EFTS_SALTY Elongation factor Ts	14		DAGFQAFADKVLDAAVAGK	85	19	4	26.74	b3y6y7y14	1893.94	98.164	96054	3	631.99	-13.47
P64052 EFTS_SALTY Elongation factor Ts	15		FEVGEGIEKVETDFAAEVAAMSK	258	23	18	153.95	b3b6b8b11b12*b12b13*b13y3y4y5y8y10y11y12y13y20y21	2457.18	106.415	87494	3	819.73	-0.99
P64052 EFTS_SALTY Elongation factor Ts	16		KAGNVAADGVIK	51	12	8	76.58	b3b5b8*b8y4y6y7y11	1142.65	31.986	51178	2	571.83	-3.74
P64052 EFTS_SALTY Elongation factor Ts	17		RVASLEGDVLGSYQHGAR	133	18	3	23.57	b8y4y5	1914.96	55.039	21374	3	638.99	-7.84
P64052 EFTS_SALTY Elongation factor Ts	18		KALTEANGDIELAIENMR	24	18	4	33.47	y4y5y12y16	1988.03	67.572	19489	2	994.52	7.74
P64052 EFTS_SALTY Elongation factor Ts	19		AQFEERVALVAK	112	13	6	28.84	b9b11*b11*b11b12*b12	1489.81	109.266	10230	2	745.41	8.44
P64052 EFTS_SALTY Elongation factor Ts	20		KFTGEVSLTGQPFVMEPSK	221	19	5	26.74	b7y7y8y12*y12	2082.07	77.863	8031	3	694.70	7.50
P64052 EFTS_SALTY Elongation factor Ts	21		EHNADVTGFIRFEVGEGIEK	247	20	4	23.03	b3b4y6*y6	2247.09	69.146	5238	3	749.70	-7.50
P64052 EFTS_SALTY Elongation factor Ts	22		FTGEVSLTGQPFVMEPSKSVGQLLK	222	25	5	28.57	b3b5b9*b9b10	2679.44	84.944	4790	3	893.82	10.84
P64052 EFTS_SALTY Elongation factor Ts	23	Oxidation+M(14)	FTGEVSLTGQPFVMEPSK	222	18	3	16.16	b3b5y5	1969.96	80.349	7429	2	985.48	1.61
P64052 EFTS_SALTY Elongation factor Ts	24		ITASLVK	3	7	0	1.51		731.46	49.337	14372	1	731.46	-4.92
P64052 EFTS_SALTY Elongation factor Ts	25		VLDAAVA	95	7	1	9.02	y5	658.38	34.219	13188	1	658.38	4.73
P64052 EFTS_SALTY Elongation factor Ts	26		TDVEVLK	105	7	3	25.19	b3*b3b4	803.44	49.304	3962	1	803.44	-12.76
P64052 EFTS_SALTY Elongation factor Ts	27	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	0	1.88		997.42	21.674	3148	2	499.22	-3.30
P26982 DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	10	83.55	b3b4b5b8b10b12y3y4y7y9	2017.09	75.520	72207	3	673.03	-9.80
P26982 DEGP_SALTY Protease do	2		GYVVTNNHVVDNASVIK	124	17	16	154.9	b2b3b6b9y2y3y6y8y9y10y11y12y13y14y15y17	1828.93	50.768	58718	3	610.31	-14.35
P26982 DEGP_SALTY Protease do	3		SDIALIQINPK	160	12	16	122.41	b3*b3b4b5b9b10*b10b12y2y3y4*y4y5y6y9y12	1339.76	64.714	51013	2	670.38	0.27
P26982 DEGP_SALTY Protease do	4		AQVGTMPVGSK	352	11	12	75.68	b2*b2b3y1y2y3y5y7y8*y8y9y11	1074.55	35.480	42426	2	537.78	-7.16
P26982 DEGP_SALTY Protease do	5		GAFVSQVMPNSSAAK	313	15	12	123.66	b3b5b7*b7b8b11b13y8y9y10y11y15	1493.75	53.963	42009	2	747.38	4.66
P26982 DEGP_SALTY Protease do	6		NLTSQMVEYGQVK	275	13	6	33.35	b5b11b12y1y5y13	1496.75	58.266	41361	2	748.88	5.63
P26982 DEGP_SALTY Protease do	7		ISLGLLR	363	7	5	54.89	y3y4y5y6y7	771.50	68.977	22561	2	386.25	-10.44
P26982 DEGP_SALTY Protease do	8		VGDYTV AIGNPFLGETVTSGIVS ALGR	186	28	18	125.63	b2b3b4b6*b6b7b11b12y2y3y4y5y6y8y10y14y20y28	2750.43	117.119	22369	3	917.48	-2.57

P26982 DEGP_SALTY Protease do	9		SGLNVENYENFIQTDAAINR	214	20	10	29.17	b2b6b13*b13y5y8*y8y12*y12y20	2268.11	78.240	18594	2	1134.56	11.09
P26982 DEGP_SALTY Protease do	10		GELGIMGTELNSELAK	289	16	3	17.8	b9y6y11	1661.85	102.098	2113	3	554.62	3.45
P26982 DEGP_SALTY Protease do	11	Carbamidomethyl+C(13) ;Carbamidomethyl+C(25))	NFQQFFGDDSPFCQDGSFPQNSPF CQGGGNGGGNGGQQQK	71	39	4	14.67	b12y8y10y13	4240.80	91.536	4818	3	1414.27	11.97
P26982 DEGP_SALTY Protease do	12		VMPSVVSVINVEGSTTVNTPR	48	20	6	31.8	b4b5b7*b7y5y13	2087.08	88.209	4555	3	696.37	1.64
P26982 DEGP_SALTY Protease do	13		NIAELR	443	6	1	13.91	b4	715.41	34.089	4337	2	358.21	-4.27
P26982 DEGP_SALTY Protease do	14		RGELGIMGTELNSELAK	288	17	13	111.6	b5b6b7b8b10b12b14y3y6y7y10*y10*y10	1817.92	69.255	47265	3	606.65	-10.34
P26982 DEGP_SALTY Protease do	15		VDAQRGAFVSQVMPNSSAAK	308	20	4	14.9	b6*b6y5y13	2063.02	48.788	11795	4	516.51	-7.46
P26982 DEGP_SALTY Protease do	16		GAFVSQVMPNSSAAKAGIK	313	19	3	22.45	b6b8b13	1862.98	63.306	8027	3	621.66	-1.77
P26982 DEGP_SALTY Protease do	17		KGDVIIGANQQPVK	429	14	5	27.76	y5*y5y7y8*y8	1466.83	39.162	7214	2	733.92	-2.16
P26982 DEGP_SALTY Protease do	18		GELGIMGTELNSELAKAMK	289	19	5	41.07	b3b4b5b10y15	1992.01	95.308	6971	2	996.51	-3.37
P26982 DEGP_SALTY Protease do	19	Phosphoryl STY(14)	GYVVTTNNHVVDNASVIK	124	17	4	16.93	b6b13y4*y4	1908.91	87.021	5760	2	954.96	-3.65
P26982 DEGP_SALTY Protease do	20	Oxidation+M(6)	AQVGTMPVGSK	352	11	3	25.08	b5b10y10	1090.56	46.043	2507	2	545.79	6.49
P26982 DEGP_SALTY Protease do	21		VTNNHVVDNASVIK	127	14	10	54.71	b4b5*b5b6*b6b11*b11b12*b12*b12	1509.80	50.763	1756	2	755.40	-4.61
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	1		TMNTPHGDAITVFDLR	23	16	15	73.63	b2b3b10b11*b11*b11y2y4y6*y6y10*y10y11y12y16	1787.86	71.822	49756	3	596.62	-9.63
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	2		MQAPAVR	13	7	6	41.35	b1b2y3y4y5y7	772.40	31.078	26800	2	386.71	-13.75
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	3		PLLDSEFAVDHTR	1	12	4	23.03	b11y5*y5y7	1370.70	56.900	21092	3	457.57	-8.19
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	4	Carbamidomethyl+C(15)	VQDQNQIPELNVYQCGTYQMHSLS SEAQDIAR	113	31	8	35.55	b10b12y3y8y11y13y24y31	3635.70	75.860	20365	3	1212.57	5.17
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	5		TGFYMSLIGTPDEQR	84	15	7	38.39	b3b13y2y7*y7y8y14	1714.82	79.151	17215	2	857.91	5.77
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	6		VADAWK	99	6	1	13.91	b5	689.37	37.307	5790	1	689.37	14.25
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	7	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCRTGFYMSLIGTPDEQR	65	34	3	22.43	b14b15y3	3792.79	107.474	7807	4	948.95	3.93
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	8		EVMPEKGIHTLEHLFAGFMR	45	20	3	23.03	b10y6y7	2342.17	87.106	4178	3	781.39	-3.96
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	9		TGFYMSLIGTPDEQRVADAWK	84	21	5	39.72	b3b9b10b11y11	2385.14	86.284	2624	3	795.72	-5.53
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	10	Oxidation+M(13)	GIHTLEHLFAGFMR	51	14	3	19.98	b7b11y8	1644.85	66.749	11738	2	822.93	11.87
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	11	Carbamidomethyl+C(18) ;Oxidation+M(16)	DHLNGNGVEIIDISPMGCR	65	19	8	44.07	b6b10*b10b11*b11y9y12y13	2112.99	108.715	2374	2	1057.00	5.20
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	1		VEIDPSLLEDDKEMLEDLVAAAFNDAAR	54	28	5	26.46	b6b7b9y7y12	3089.51	127.514	5667	3	1030.51	2.37
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	2	Carbamidomethyl+C(9)	VTINGAHNCR	43	10	9	56.02	y1y2y3*y3y4*y4y6y7y10	1141.55	21.122	4769	2	571.28	-3.53
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	3		MQEIIAQLEVTGESGAGLVK	23	20	7	46.37	b6b10b12b13*b13b14*b14	2089.04	105.298	2764	3	697.02	-4.79
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	4		EMLEDLVAAAFNDAAR	66	16	3	17.8	b9b12y4	1735.82	95.595	2295	2	868.42	-4.36
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	5		EMLEDLVAAAFNDAARR	66	17	3	16.93	b6y3y10	1891.91	87.044	2027	3	631.31	-12.13
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	6		MASVSSGMQLPPGFK	91	15	3	26.89	b5b6b9	1536.74	41.077	2885	3	512.92	-6.91
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	7		MASVSSGMQLPPGFKMPF	91	18	3	16.16	b12y5y8	1911.91	68.500	4217	2	956.46	-2.94
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	8		GGLGNLMKQAQQMQEK	4	16	3	17.8	b3b6y5	1760.88	118.428	2699	2	880.94	-1.04

[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	9		EKMASVSSGMQLPPGFK	89	17	4	23.92	b13b14y10*y10	1793.90	102.014	1847	2	897.46	6.67
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	10	Oxidation+M(1)	MQEEIAQLEVTGESGAGLVK	23	20	4	14.9	b10y14*y14y16	2105.02	85.863	7948	3	702.35	-10.67
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	11	Carbamidomethyl+C(8)	TINGAHNCR	44	9	1	8.43	b7	1042.48	21.114	3023	2	521.74	-3.98
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	1		AGLGMMEGVLENVPSAR	78	17	10	59.6	b11b13y4y7°y7y10y11°y11y12y17	1730.87	82.428	31138	2	865.94	5.92
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	2		VLVLVAAPEGIAALEK	155	16	11	108.47	b2b3b4b5b6b7y2y9y10y11y12	1592.97	86.660	23992	2	796.99	5.36
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	3		MALIVDPMLATGGSVIATIDLLKK	124	24	4	23.41	b2b3b6b7	2470.40	114.459	17709	3	824.14	-2.67
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	4		ITVVPILR	70	8	4	41.73	y4y5y6y8	910.60	70.362	12934	2	455.81	-5.63
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	5		ELASEVGSLLTYEATADLETEK	29	22	3	13.91	b7y9y15	2369.19	109.918	2161	2	1185.10	13.71
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	6		AHPDVELYTASIDQGLNEHGYYIP GLGDAGDK	171	32	3	11.34	b5b8y8	3365.68	53.907	6265	4	842.18	15.09
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	7		NEETLEPVYPYFQK	103	13	4	21.36	b6b8°b8y7	1593.76	52.991	4960	2	797.38	-10.72
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	8		VTIEGWNGPVEIDQIK	51	16	3	17.8	b6b8y4	1797.92	59.718	4176	3	599.98	-12.22
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	9		AHPDVELYTASIDQGLNEHGYYIP GLGDAGDKIFGTK	171	37	11	62.14	b5b6b7°b7b8b13°b13y11y13y14°y14	3911.94	89.296	32257	4	978.74	-1.75
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	10	Oxidation+M()	AGLGMMEGVLENVPSAR	78	17	3	25.58	b3b4b13	1746.86	64.041	16567	3	582.96	4.47
[P66170]RL29_SALTY 50S ribosomal protein L29	1		SVEELNTELLNLLR	9	14	12	105.95	b2b3b4b5y3y4y5y6y8y9y14*y14	1642.90	101.324	91518	2	821.95	-0.52
[P66170]RL29_SALTY 50S ribosomal protein L29	2		SVEELNTELLNLLREQFNLR	9	20	8	54.19	b2b3b4y13y16y17y18y20	2430.29	112.169	36655	3	810.77	-3.72
[P66170]RL29_SALTY 50S ribosomal protein L29	3		MQAASGQLQQSHLLK	29	15	7	30.42	b2*b2b4b5b11y2y5	1639.85	51.294	4525	3	547.29	-5.58
[P66170]RL29_SALTY 50S ribosomal protein L29	4		EQFNLR	23	6	4	27.44	y3*y3y4*y4	806.41	42.431	46960	2	403.71	-12.19
[P66170]RL29_SALTY 50S ribosomal protein L29	5		EKSVEELNTELLNLLR	7	16	4	29.29	b12y3y5y6	1900.02	94.984	32582	3	634.01	-10.99
[P66170]RL29_SALTY 50S ribosomal protein L29	6		EQFNLRMQAASGQLQQSHLLK	23	21	5	19.74	b6°b6b12y3y15	2427.26	85.833	11579	3	809.76	2.51
[P66170]RL29_SALTY 50S ribosomal protein L29	7	Phosphoryl.STY(7)	SVEELNTELLNLLR	9	14	3	19.98	b3b6y8	1722.85	108.192	2379	3	574.95	-5.46
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	1		TALTDHLDTMAER	70	13	6	42.38	b2y3y5y7y8y13	1473.68	52.862	48882	3	491.90	-13.83
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	2		GANFIADVHEMLDGFR	55	15	11	76.77	b7b9°b9b10°b10y3y5y6°y6y8y10	1676.80	82.661	38170	3	559.60	-14.34
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	3		AIGEAKDEDTADIFTAASR	134	19	9	51.85	b2b4b12y5y6°y6y8y10y13	1980.95	59.028	25401	3	660.99	-2.10
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	4		AVQLGGVALGTTQVINSK	83	18	7	38.2	b15y2y3°y3y9y11y15	1756.01	68.181	22309	2	878.51	5.42
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	5		ASNLLYTR	10	8	4	41.73	b3°b3b4b6	937.51	45.382	9393	2	469.26	4.23
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	6		SYPLDIHNVQDHLK	105	14	5	28.58	b6b8y3y7*y7	1678.86	58.116	9647	3	560.29	0.65
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	7		FLWFIESNIE	157	10	8	62.56	b9y3°y3y4°y4y6*y6y9	1297.67	56.249	6102	2	649.34	18.34
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	8		ASNLLYTRNDVSESDK	10	16	7	46.93	b4y11y12°y12°y12y14y15	1811.90	90.440	20151	3	604.64	11.18
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	9		GANFIADVHEMLDGFRALTDHLD TMAER	55	28	3	18.03	y4y8y16	3131.50	104.299	18905	4	783.63	-1.56

Q7CQV9 DPS_SALTY DNA protection during starvation protein	10		TALTDHLDTMAERAVQLGGVAL GTTQVINSK	70	31	3	17.33	b11b13b29	3210.64	117.951	1562	3	1070.88	-12.24
Q7CQV9 DPS_SALTY DNA protection during starvation protein	11		LTDHLDTMAER	72	11	3	28.84	b3b4b9	1301.63	52.828	6055	2	651.32	13.97
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	14	59.12	b5b6b7b23b25y2y3°y3y6y7°y7y11y13y36	3950.90	95.835	94139	4	988.48	2.29
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2		ILEVPVGR	93	8	7	55.27	b2y3y4y5y6°y6y8	882.53	53.131	46950	2	441.77	-11.34
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3		MQLNSTEISELIK	0	13	8	46.88	b2b3y2y3y8y10y11y13	1505.79	77.503	37068	2	753.40	1.22
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	7	26.74	b2b9y3y4*y4y6y19	2098.98	69.584	34293	3	700.33	-1.51
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		ASTISNVVR	201	9	6	39.1	b1y5*y5y6y7y9	946.52	37.858	31741	2	473.77	-8.06
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6		GYLADVELAK	453	10	6	59.55	b3y3y6y7y8y10	1078.57	60.974	29527	2	539.79	-7.58
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		QYAPMSVAQQSLVFAAER	434	19	7	21.57	b2*b2b3b10y4y16y19	2109.10	93.857	26966	2	1055.05	8.91
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		DSVGAVVMGPYADLAEGMK	68	19	11	60.88	b3°b3b6b8°b8b9b15y11y13y18y19	1909.93	84.274	23767	2	955.47	11.57
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9		ELAAFSQFASDLDDATR	401	17	9	71.36	b2b6b7y3y4y5y6y10y17	1856.88	89.183	21133	2	928.94	7.76
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		ELAAFSQFASDLDDATRK	401	18	3	25.08	y4y9y10	1984.95	83.886	17790	3	662.32	-6.89
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		QSVDQPVPQTGYK	139	12	12	102.46	b5°b5°b5b12y3y4y5y6y7y9y10y12	1349.67	34.736	14940	2	675.34	-1.72
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12	Carbamidomethyl+C(1)	CIIYVAIGQK	192	9	5	55.64	b3b4b5b6y9	1051.56	58.111	14646	2	526.28	-2.44
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		IAQFNVVSEAHNEGTVSVSDGVI R	15	25	5	12.8	b2b3b13*b13y15	2641.39	93.843	5370	3	881.13	10.35
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		TALAIIDAINQRDSGIK	175	17	7	37.38	b4°b4b6°b6b7b14y6	1798.98	104.628	2785	2	899.99	-12.89
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		AVDSMIPIGR	151	10	3	34.7	b4b7b8	1058.56	52.835	155439	2	529.78	-6.23
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16		GEDALIIYDDLK	252	13	4	35.48	b5b12y3y4	1451.72	68.928	40888	2	726.36	-3.03
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17		TALAIIDAINQR	175	12	3	23.03	b4y4y9	1298.74	74.802	32413	2	649.88	1.13
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18		VGGAAQTK	376	8	4	41.73	b3b4b7°b7	731.40	33.365	12578	1	731.40	-10.26
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	19		ATQSW	508	5	1	13.53	y4	592.27	76.137	9481	1	592.27	-1.24
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	20		DHAPLMQEINQSGGYNDEIEGK	477	22	3	13.91	b12y4y12	2445.10	107.404	2422	3	815.71	2.00
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	21		VNADYVEAFTK	303	11	3	28.09	b4y8y9	1256.64	40.189	2117	3	419.55	18.46
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	22		VNADYVEAFTKGEVK	303	15	4	30.42	b12y4y7y8	1669.82	63.727	58693	3	557.28	-12.06
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	23		VVNTLGAPIDKGKPGVDNDGFSAV EAIAPGVIDR	106	33	12	65.31	b4b26y3y6°y6y7y8y10y13y16y26°y26	3263.72	84.920	33155	3	1088.58	8.90
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	24		QSVDQPVPQTGYKAVDSMIPIGR	139	22	5	25.01	b5b12b13°b13y8	2389.21	98.355	32947	2	1195.11	-1.63
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	25		QKQYAPMSVAQQSLVFAAER	432	21	4	25.52	b12y4y5y13	2365.23	86.440	14119	3	789.08	-2.99
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	26		TALAQYRELAAFSQFASDLDDAT R	394	24	3	22.42	b8y5y6	2660.29	95.448	5369	3	887.44	-0.28
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	27		DRGEDALIIYDDLK	250	15	8	56.18	b3b4°b4b12b13y7y11°y11	1722.85	96.488	2604	2	861.93	-1.70

[Q7CPEI]ATPA_SALTY ATP synthase subunit alpha	28	Oxidation+M(8)	DSVGAVVMGPYADLAEGMK	68	19	6	39.63	b5b12b16y4y7y11	1925.92	67.215	3163	2	963.46	11.28
[Q7CPEI]ATPA_SALTY ATP synthase subunit alpha	29		ELAAFSQFASDLDDATRK	401	18	0	4.9		1966.95	83.884	2659	3	656.32	1.74
[P26976]PHON_SALTY Non-ecific acid phohatase	1		NGSYPSGHTAYGTLLALVLSEARPER	150	26	12	37.93	b2*b2b3*b3*b3b6b14y7y12y16y22y26	2759.38	96.799	63201	4	690.60	-10.62
[P26976]PHON_SALTY Non-ecific acid phohatase	2		LQTIPAFQK	215	9	6	46.88	b2*b2y3y5y7y9	1045.59	55.841	46800	2	523.30	-8.87
[P26976]PHON_SALTY Non-ecific acid phohatase	3		IFSPVVGAK	85	9	7	39.1	b2y1y2y3y4y7y9	917.54	51.820	41903	2	459.27	-10.64
[P26976]PHON_SALTY Non-ecific acid phohatase	4		NLLTMGGYYATASAK	108	15	11	95.08	b2b3b11b13y5y6y10y11y12y13y15	1560.78	70.472	34127	2	780.89	4.15
[P26976]PHON_SALTY Non-ecific acid phohatase	5		NLLTMGGYYATASAKK	108	16	3	24.33	b11y11y12	1688.85	64.615	19762	3	563.62	-11.64
[P26976]PHON_SALTY Non-ecific acid phohatase	6		QAAEDADVSVENIAR	70	15	15	65.16	b2*b2b4b10*b10y4*y4y9y10*y10y11*y11y13*y13y15	1587.77	51.373	7824	2	794.39	4.46
[P26976]PHON_SALTY Non-ecific acid phohatase	7		NNLSKEDHPK	236	11	3	36.84	y3y4y5	1294.66	31.042	1888	3	432.23	-11.13
[P26976]PHON_SALTY Non-ecific acid phohatase	8	Carbamidomethyl+C(12)	TRPFVLFNHSTCRPEDENTLR	128	21	4	14.38	b12*b12y9y11	2589.21	74.655	2050	3	863.74	-18.58
[P26976]PHON_SALTY Non-ecific acid phohatase	9		EELNDK	230	6	2	13.91	b3*b3	747.36	46.100	1814	1	747.36	5.88
[P26976]PHON_SALTY Non-ecific acid phohatase	10		WKQAAEDADVSVENIAR	68	17	3	23.92	b9y6y7	1901.92	54.771	16731	3	634.64	-10.21
[P26976]PHON_SALTY Non-ecific acid phohatase	11		YTSAETVQPFHSPPEESVNSQFYLP PPPGNDDPAYRYDK	16	38	5	20.54	b3b9b12b14y8	4342.99	104.134	15500	5	869.40	0.67
[P26976]PHON_SALTY Non-ecific acid phohatase	12		RGWEFGQSR	182	9	3	31.32	b7y4y7	1122.54	53.914	4684	3	374.85	-6.09
[P26976]PHON_SALTY Non-ecific acid phohatase	13		FSPVVGAK	86	8	1	9.02	b4	804.45	51.780	6943	1	804.45	-14.95
[P26976]PHON_SALTY Non-ecific acid phohatase	14		IFSPVVGAK	85	9	0	1.51		899.52	51.802	2831	2	450.27	-6.58
[P65882]PURA_SALTY Adenylosuccinate synthetase	1	Carbamidomethyl+C(7)	LLLSEACPLILDYHVALDNAR	97	21	11	51.56	b2b3b8y3y6*y6y9y11*y11y14y21	2396.26	92.232	29457	3	799.42	-3.26
[P65882]PURA_SALTY Adenylosuccinate synthetase	2		GNNVVVLGTQWGDEGK	1	16	4	25.5	y1y3y6y11	1672.83	82.502	15866	3	558.28	-2.12
[P65882]PURA_SALTY Adenylosuccinate synthetase	3		VLDDTMAVADILTSMVVDVSDLL DQAR	186	27	21	145.06	b7b8*b8b9*b9b12b17y1y3*y3y4y5y8y9y10y11*y11y12y17y18y27	2905.46	138.240	11570	3	969.16	1.76
[P65882]PURA_SALTY Adenylosuccinate synthetase	4		MGNNVVVLGTQWGDEGK	0	17	4	16.93	b2b4y9y14	1803.87	67.569	1927	2	902.44	1.08
[P65882]PURA_SALTY Adenylosuccinate synthetase	5		IEELTGVPIDIISTGPDR	402	18	5	22.64	b3b5y5*y5y10	1925.05	103.417	17751	2	963.03	15.73
[P65882]PURA_SALTY Adenylosuccinate synthetase	6		TGWLDTVAVR	307	10	4	42.49	y3y6y9*y9	1117.61	49.176	15091	2	559.31	7.86
[P65882]PURA_SALTY Adenylosuccinate synthetase	7	Carbamidomethyl+C(2)	LCVAYR	343	6	1	13.91	b3	781.39	34.961	2564	2	391.20	-14.22
[P65882]PURA_SALTY Adenylosuccinate synthetase	8		GIGPAYEDK	132	9	3	39.1	b6b7b8	949.47	77.373	1588	1	949.47	5.53
[P65882]PURA_SALTY Adenylosuccinate synthetase	9		MGNNVVVLGTQWGDEGKGK	0	19	4	29.35	b5b15y7y8	1988.98	42.482	33651	4	498.00	-2.15
[P65882]PURA_SALTY Adenylosuccinate synthetase	10		VLDDTMAVADILTSMVVDVSDLL DQARQR	186	29	3	22.22	b10b11y23	3189.62	109.917	5752	3	1063.88	1.99
[P65882]PURA_SALTY Adenylosuccinate synthetase	11	Carbamidomethyl+C(2)	LCVAYRMPDGR	343	11	3	25.08	b7y3y7	1337.66	55.962	5207	2	669.33	11.13
[P65882]PURA_SALTY Adenylosuccinate synthetase	12		YVVRYQGGHNAGHTLVINGEK	29	21	4	28.19	b11b12y12y14	2312.18	83.893	4685	3	771.40	-4.12

[P65882 PURA_SALTY Adenylosuccinate synthetase	13	Carbamidomethyl+C(11);Phosphoryl STY(8)	AVQLNSLSGFCLTK	318	14	3	19.98	b3b8y6	1617.76	40.755	127181	3	539.92	-0.83
[P65882 PURA_SALTY Adenylosuccinate synthetase	14	Phosphoryl STY(6)	TGWLDTVAVR	307	10	3	27.71	b4y5_H3PO4 y5y7	1197.57	56.181	1865	2	599.29	12.84
[P65882 PURA_SALTY Adenylosuccinate synthetase	15	Oxidation+M(9)	GVEPIYETMPGWSESTFGVKDR	367	22	4	23.78	b3b4°b4b11	2501.19	69.683	13565	4	626.05	8.10
[P65882 PURA_SALTY Adenylosuccinate synthetase	16	Oxidation+M(6)	VLDDTMAVADILTSMVVDVSDLLDQAR	186	27	4	23.09	b4°b4b8b9	2921.47	123.212	4201	3	974.49	7.02
[P65882 PURA_SALTY Adenylosuccinate synthetase	17	Oxidation+M(5)	LKEVMEYHNFQLVNYYK	161	17	4	24.33	y3y5*y5y9	2234.07	71.127	3149	2	1117.54	-13.22
[P65882 PURA_SALTY Adenylosuccinate synthetase	18	Oxidation+M(1)	MGNNVVVLGTQWGDEGK	0	17	5	27.07	b5b10*b10b12y15	1819.88	76.009	1544	4	455.73	9.79
[P02906 SUBI_SALTY Sulfate-binding protein	1		QIHWDNDLIKPGVSVITPNPK	126	21	8	46.13	b5b6b9b14y2y4y5y21	2371.25	73.259	104084	4	593.57	-11.74
[P02906 SUBI_SALTY Sulfate-binding protein	2		YLYSPEGQEIAAK	263	13	21	151.62	b2b3b4°b4b5b6b11y1y2y3y7y8°y8*y8y9*y9y10y11°y11y12y13	1468.73	51.393	73779	2	734.87	0.42
[P02906 SUBI_SALTY Sulfate-binding protein	3		NVEVLDSGAR	183	10	7	53.01	b2y5y6y7°y7y8y10	1059.54	40.633	70409	2	530.27	-7.26
[P02906 SUBI_SALTY Sulfate-binding protein	4		LFTIDEVFGGWAK	298	13	9	60.99	b2b3°b3b8y5y6y8y9y13	1482.76	102.437	59267	2	741.89	0.58
[P02906 SUBI_SALTY Sulfate-binding protein	5		WNYLAAWGYALHHNNNDQAK	153	20	4	14.9	b8b12y7y20	2386.13	93.099	30821	3	796.05	8.08
[P02906 SUBI_SALTY Sulfate-binding protein	6		QATSVINGIEADVVTALAYDVD AIAER	66	28	19	148.42	b2*b2b4b6°b6b9b11b17y3y4y5y6y7y8°y8y9y10y11y13	2917.52	128.619	15544	3	973.18	1.09
[P02906 SUBI_SALTY Sulfate-binding protein	7		LPDNSAPYTSTIVFLVR	104	17	4	25.58	b7°b7b9b10	1892.97	60.595	4711	3	631.66	-22.18
[P02906 SUBI_SALTY Sulfate-binding protein	8		AVAEAYLK	255	8	4	41.73	b3b5b6°b6	864.48	93.172	3242	2	432.74	-7.55
[P02906 SUBI_SALTY Sulfate-binding protein	9		GIGDVLIAWENEALLATNELGK	202	22	3	23.78	b4b5b12	2326.22	107.010	1604	2	1163.61	-4.51
[P02906 SUBI_SALTY Sulfate-binding protein	10		RLPDNSAPYTSTIVFLVR	103	18	6	32.2	b7b9b12°b12y4y6	2049.10	83.136	52349	3	683.70	-6.79
[P02906 SUBI_SALTY Sulfate-binding protein	11		WNYLAAWGYALHHNNNDQAKA QDFVK	153	26	4	16.47	b5b8y4y6	3074.47	66.790	3885	3	1025.50	3.02
[P02906 SUBI_SALTY Sulfate-binding protein	12		NVEVLDSGARGSTNTFVER	183	19	4	15.49	b7°b7b9y8	2051.04	65.838	2513	4	513.52	11.78
[P02906 SUBI_SALTY Sulfate-binding protein	13		QATSVINGIEADVVTALAYDVD AIAERGR	66	30	5	22.53	b7b8b12*b12y11	3130.60	117.201	2474	4	783.41	-11.07
[P02906 SUBI_SALTY Sulfate-binding protein	14		QSHGGSGKQATSVINGIEADVVTLALAYDVD AIAER	58	36	3	22.59	b10b11y10	3655.82	135.490	2421	4	914.71	-9.82
[P02906 SUBI_SALTY Sulfate-binding protein	15		DIQLNVSYSPTRELYEQYNK	20	21	9	39.33	b11°b11b12y6*y6y10°y10y11*y11	2601.30	99.470	1859	3	867.77	6.48
[P0A1H3 EFG_SALTY Elongation factor G	1		VYSGVVNSGDTVLSVK	337	17	14	105.55	b1b2b4b5b14y2y3y4y11y12y13y14y15y17	1737.91	62.805	57493	2	869.46	3.58
[P0A1H3 EFG_SALTY Elongation factor G	2		IATDPFVGNLTFFR	323	14	11	74.33	b2b4b5°b5b14y3y7y10y11y12y14	1597.84	93.852	55516	2	799.43	4.43
[P0A1H3 EFG_SALTY Elongation factor G	3		IHAEVPLSEMFYATQLR	653	18	13	77.12	b2b3b4b5b9b11y1y2y4y6y7y13y18	2062.03	89.942	50194	3	688.01	-6.75
[P0A1H3 EFG_SALTY Elongation factor G	4		SGPLAGYPVVDLGVR	562	15	14	91.56	b3°b3b5°b5b6°b6b7°b7y3y4y8y10y11y15	1499.83	77.260	40924	2	750.42	2.52
[P0A1H3 EFG_SALTY Elongation factor G	5		EFNVEANVGKPVAYR	475	16	5	25.5	y6y8*y8y12y16	1820.91	54.093	36772	3	607.64	-9.72
[P0A1H3 EFG_SALTY Elongation factor G	6		MEFPEPVISIAVEPK	408	15	6	24.83	b2b12y2y12y13y15	1685.89	86.450	35968	2	843.45	5.21
[P0A1H3 EFG_SALTY Elongation factor G	7		IGEVHDGAATMDWMEQEQR	39	20	8	36.86	b1b2b12b13y6°y6y7y20	2332.01	62.662	25389	3	778.01	3.87

[P0A1H3]EFG_SALTY Elongation factor G	8		ILFYTGVNHK	29	10	8	53.01	b10y2y5y6y7y8y10*y10	1191.65	55.323	22334	2	596.33	-3.48
[P0A1H3]EFG_SALTY Elongation factor G	9		GQYGHVVIDMYPLEPGSNPK	512	20	10	60.26	b2*b2b7*b7b8b11b12y6y9y10	2201.07	70.801	20537	3	734.36	-2.00
[P0A1H3]EFG_SALTY Elongation factor G	10	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTTGDTLCDPENPIILER	378	30	10	51.49	b3b7b9b12b17y3y4y11*y11y13	3138.63	85.761	17404	3	1046.88	8.79
[P0A1H3]EFG_SALTY Elongation factor G	11		LGANPVPLQLAIGAEEGFTGVVDLVK	161	26	6	18.65	y1y2y5y7y14y26	2607.43	120.618	16556	3	869.82	-3.00
[P0A1H3]EFG_SALTY Elongation factor G	12	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETVWR	104	24	6	13.12	b2b14y1y3y10°y10	2621.29	86.613	14755	3	874.44	3.63
[P0A1H3]EFG_SALTY Elongation factor G	13		YLGGEELTEEEIK	236	13	6	33.35	b7b9b10b13y6y13	1509.74	89.778	12043	2	755.37	4.12
[P0A1H3]EFG_SALTY Elongation factor G	14	Carbamidomethyl+C(11)	VLNNEILVTCGSAFK	255	16	6	42.57	b1b5b6y6y8y10	1777.96	79.764	11280	2	889.48	3.30
[P0A1H3]EFG_SALTY Elongation factor G	15		NIGISAHIDAGK	11	12	6	23.03	b2b4b6°b6*b6y5	1195.65	45.603	5016	3	399.22	3.47
[P0A1H3]EFG_SALTY Elongation factor G	16		GGVIPGEYIPAVDK	541	14	5	39.46	b3b4y3°y3y4	1414.77	32.682	11309	2	707.89	6.47
[P0A1H3]EFG_SALTY Elongation factor G	17		GQESEVTGVK	643	10	5	41.25	b8y4y6°y6y7	1033.51	26.166	11148	2	517.26	-9.21
[P0A1H3]EFG_SALTY Elongation factor G	18		VVGQIK	153	6	1	13.91	b5	643.41	45.602	10867	1	643.41	-7.40
[P0A1H3]EFG_SALTY Elongation factor G	19		INIIDTPGHVDFTIEVER	83	18	3	16.16	b9b13y10	2068.07	66.883	9469	4	517.77	-2.48
[P0A1H3]EFG_SALTY Elongation factor G	20		LHFGSYHDVDSSELAFK	577	17	4	23.85	b7b9y3y9	1951.92	50.568	5664	3	651.31	0.94
[P0A1H3]EFG_SALTY Elongation factor G	21	Carbamidomethyl+C(9)	DVTTGDTLCDPENPIILER	389	19	3	15.49	b4b8y10	2158.06	71.372	3701	2	1079.53	11.09
[P0A1H3]EFG_SALTY Elongation factor G	22		GVQAMLDIVIDYLPSPVDVPAINGILDDGK	273	30	6	25.64	b8°b8b14y13y15y16	3095.66	118.768	2551	3	1032.56	19.48
[P0A1H3]EFG_SALTY Elongation factor G	23		QSGGR	507	5	1	13.53	b3	504.26	47.060	2513	1	504.26	14.95
[P0A1H3]EFG_SALTY Elongation factor G	24		GITITSAATTAFWSGMAK	59	18	4	22.64	b3b14y5y9	1813.93	88.578	2189	2	907.47	5.52
[P0A1H3]EFG_SALTY Elongation factor G	25		QYEPHR	77	6	1	13.91	y5	829.40	109.161	1504	1	829.40	10.08
[P0A1H3]EFG_SALTY Elongation factor G	26		ASYTMEFLKYDDAPNNVAQAVIEAR	677	25	8	44.32	b9°b9b12b13y4y5y8y12	2816.37	84.812	63809	3	939.46	4.59
[P0A1H3]EFG_SALTY Elongation factor G	27		YLGGEELTEEEIKQALR	236	17	3	24.33	y10y12y15	1978.00	74.068	59871	3	660.00	-8.15
[P0A1H3]EFG_SALTY Elongation factor G	28		GITITSAATTAFWSGMAKQYEPHR	59	24	3	19.43	b8b10b13	2624.26	76.971	59384	4	656.82	-10.51
[P0A1H3]EFG_SALTY Elongation factor G	29		AKPVLLEPIMKVEVETPEENTGDVIGDLSR	607	30	3	22.98	y5y6y8	3278.70	84.357	30959	4	820.43	-5.14
[P0A1H3]EFG_SALTY Elongation factor G	30		DTPAERHASDDEPFSAFAFK	303	20	3	23.03	b7b8y11	2204.00	43.961	16023	3	735.34	-11.63
[P0A1H3]EFG_SALTY Elongation factor G	31		INIIDTPGHVDFTIEVERSMR	83	21	4	14.38	b3b10y7°y7	2442.28	82.492	13737	3	814.77	14.89
[P0A1H3]EFG_SALTY Elongation factor G	32		NIGISAHIDAGKTTTTER	11	18	3	23.57	b10y3y4	1884.95	85.056	6990	2	942.98	-13.08
[P0A1H3]EFG_SALTY Elongation factor G	33		TKADQEK	423	7	4	38.34	b5°b5y5y6	819.43	31.584	5988	2	410.22	7.60
[P0A1H3]EFG_SALTY Elongation factor G	34		AKVTDIEGK	495	9	3	31.32	b6y3y8	960.54	22.933	5941	2	480.77	2.92
[P0A1H3]EFG_SALTY Elongation factor G	35	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETVWRQANK	104	28	4	17.94	b5b15b19y8	3062.56	83.523	5019	3	1021.53	14.11
[P0A1H3]EFG_SALTY Elongation factor G	36		QSGGRGQYGHVVIDMYPLEPGSNPK	507	25	5	28.57	b3b5b8b9°b9	2686.34	92.275	2831	3	896.12	13.18

P0A1H3 EFG_SALTY Elongation factor G	37		VWTDEESNQTIAGMGELHLDIIV DRMK	446	28	4	12.01	b5b12*b12y4	3213.55	109.916	1898	4	804.14	-13.90
P0A1H3 EFG_SALTY Elongation factor G	38	Phosphoryl STY(11)	VYSGVVNSGDTVLSNVK	337	17	4	23.92	b9y7y8°y8	1817.87	104.541	3763	2	909.44	3.76
P0A1H3 EFG_SALTY Elongation factor G	39	Phosphoryl STY(13)	INIIDTPGHVDFTIEVER	83	18	4	16.16	b11*b11y6y10_H3PO4 y10	2148.03	118.852	2711	2	1074.52	-0.11
P0A1H3 EFG_SALTY Elongation factor G	40	Carbamidomethyl+C(10) ;Oxidation+M(7)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	3	19.43	b3b5b12	2637.28	95.322	22305	3	879.76	-1.76
P0A1H3 EFG_SALTY Elongation factor G	41	Oxidation+M(5)	GVQAMLDIVIDYLPSPVDVPAIN GILDDGK	273	30	5	14.73	b4b16y5y8°y8	3111.58	95.330	6381	3	1037.87	-2.82
P0A1H3 EFG_SALTY Elongation factor G	42		FYTGTVNHK	31	8	0	1.88		965.48	55.311	9879	2	483.24	-6.76
P0A1H3 EFG_SALTY Elongation factor G	43		LFYTGTVNHK	30	9	0	1.88		1078.55	55.283	6431	2	539.78	-12.11
P0A1H3 EFG_SALTY Elongation factor G	44		EFNVEANVGKPVAYR	475	16	1	7.26	b10	1802.90	54.078	1571	3	601.64	-5.08
P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	17	88.84	b2*b2b3*b3b6y2y3°y3y5y 6°y6y7°y7*y7y8*y8y10	1129.61	39.612	77821	2	565.31	-9.29
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	13	90.35	b1b2y4y5°y7y8°y8y9y10y1 1y12°y12y14	1452.65	58.104	61783	2	726.83	5.71
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3		GLPIPVVITVYADR	51	14	5	34.02	b3b4y1y6y10	1512.88	91.889	32171	2	756.95	2.90
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4		TPPAAVLLK	72	9	3	31.32	b4y5y7	909.57	54.955	46211	2	455.29	-12.75
P0A7K0 RL11_SALTY 50S ribosomal protein L11	5		SIEGTARSMGLVVED	127	15	5	30.42	b4y5°y5y13y14	1563.78	85.135	4009	2	782.39	6.48
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTSDAVGNAVK	84	17	18	146.13	b2b3b4b5y2y4y5y8y9y11y 12°y12y13°y13*y13y14y15 y17	1739.96	71.561	109951	2	870.49	5.12
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	2		IPVITLDR	107	8	7	55.27	y1y2y4y5y6y7y8	926.55	62.532	59876	2	463.78	-14.76
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	3		LAATIAQLPDQIGAK	253	15	14	96.21	b2b3b12y1y2y3y4y7y8y9* y9y10y12y15	1509.86	67.145	49869	2	755.43	-1.05
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	4		VIELQGIAGTSAAR	150	14	13	80.8	b1b3y1y4y6y7°y7y9y10y12 °y12*y12y14	1385.78	59.761	36544	2	693.39	2.82
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	5		GLNVMQNLLTAHPDVQAVFAQN DEMALGALR	193	31	14	55.48	b4b6*b6b15b22y2y4y9y11 y12°y12y13°y13y31	3336.69	103.338	32329	3	1112.90	2.41
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	6		IAGDYIAK	135	8	4	41.73	y3y6y7y8	850.46	36.191	24492	2	425.73	-9.90
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	7		ELANVQDLTVR	70	11	6	37.82	b10y3y5°y5y6y11	1257.68	58.434	16734	2	629.34	1.55
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	8		ADVMVVGFDGTPDGEK	231	16	5	29.29	b5°b5y10y11y14	1636.76	64.444	14491	2	818.89	6.34
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	9		GDVVSHIASDNVLGGK	119	16	5	25.21	b8b12y3y9y16	1567.80	55.372	3766	2	784.40	-3.43
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	10		GEGFQQAVALAHK	166	12	4	27.01	b3b4y2y8	1242.62	35.081	3215	2	621.82	0.39
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	11		FNVLASQPADFDR	178	13	3	26.13	b12y4y5	1479.72	84.051	1876	2	740.37	0.74
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	12		LVIK	291	4	1	13.16	y3	472.35	56.835	8510	1	472.35	-4.97
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	13		GVEVADK	268	7	4	38.34	b3y5°y5y6	717.39	26.137	2675	2	359.20	17.53
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	14		FNVLASQPADFDRTK	178	15	3	26.89	y5y7y10	1708.85	60.732	17804	3	570.29	-8.29

P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	15		GTKILLINPTDSDAVGNAVK	81	20	4	14.9	b3y3y9*y9	2026.09	58.453	16513	3	676.04	-12.41
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	16		ALQTAGKADVMVVGFDGTPDGEK	224	23	4	19.9	y7°y7y12y14	2306.11	78.979	7782	4	577.28	-10.59
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	17		GEGFQQAVAAHKFNVLASQPADFDR	166	25	6	40.33	y8y9y12*y12y13°y13	2703.36	97.869	5205	3	901.79	11.47
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	18		ADVMVVGFDGTPDGEKAVK	231	19	3	22.45	b3b6b8	1934.96	89.468	3312	2	967.98	1.32
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	19	Oxidation+M(5)	GLNVMQNLLTAHPDVQAVFAQNDEMALGALR	193	31	4	22.27	b7b8*b8y13	3352.70	90.890	2301	3	1118.24	5.39
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	20		AGDYIAK	136	7	1	9.89	b6	737.37	36.219	2272	1	737.37	-14.24
P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	17	159.02	b2b3b4b5b6°b6y3°y3y4y5y6y7°y7y8y9y10y12	1196.59	65.011	255470	2	598.80	-3.57
P0A9Y9 CC_SALTY Cold shock-like protein cC	2		GFGFITPADGSKDVFVHFSAIQGN GFK	15	27	19	146.97	b2b3b4b5b22y5*y5y6*y6y7y9y10y11y13y21y22y23y25y27	2843.38	87.772	68945	4	711.60	-11.51
P0A9Y9 CC_SALTY Cold shock-like protein cC	3		DVVFVHFSAIQNGNGFK	27	15	6	32.8	b6b11y10y11*y11y15	1665.84	74.007	17994	2	833.42	2.20
P0A9Y9 CC_SALTY Cold shock-like protein cC	4		WFNESKGFGFITPADGSK	9	18	5	35.86	b12y3y6y7y11	1987.95	76.508	25719	3	663.32	-4.42
P67093 UG_SALTY Universal stress protein G	1		HATLPVLVVR	132	10	13	90.6	b1b2b3°b3b4°b4y1y4y6y7y8y9y10	1104.68	60.788	110953	2	552.85	-5.19
P67093 UG_SALTY Universal stress protein G	2		TIIMPVDVFEMELSDK	3	16	12	73.63	b2b3b4b13y1y2y5y9y12y13y14y16	1866.93	104.968	85736	2	933.97	5.56
P67093 UG_SALTY Universal stress protein G	3		NPSITTHLLGSNASSVVR	114	18	6	27.48	b2b13y5y9y10y18	1852.97	59.202	43103	3	618.33	-7.44
P67093 UG_SALTY Universal stress protein G	4		LQTMVGHFSDPSR	69	14	9	83.39	b4*b4b11y3y4y6y7y8y12	1587.77	64.069	89291	3	529.93	-16.07
P67093 UG_SALTY Universal stress protein G	5		HAEFLAQQDGVIIHLHLVPGSASMSLHR	22	28	6	26.46	b7*b7b12b13y6y8	3063.53	69.252	5665	4	766.64	-19.44
P67093 UG_SALTY Universal stress protein G	6		TIIMPVDVFEMELSDKAIR	3	19	10	106.6	b3y3y4y9y10y11y13y15y16y17	2207.13	101.091	64318	3	736.38	-7.63
P67093 UG_SALTY Universal stress protein G	7		DVVNEMGEELDADVVGISRNPSITTHLLGSNASSVVR	94	38	6	21.7	b3°b3y9*y9y13y14	3979.95	103.376	34443	5	796.80	-14.29
P67093 UG_SALTY Universal stress protein G	8		MYKTIIMPVDVFEMELSDK	0	19	4	15.49	b10y5y9°y9	2289.10	99.357	5067	3	763.70	-11.41
P67093 UG_SALTY Universal stress protein G	9	Oxidation+M(11)	TIIMPVDVFEMELSDK	3	16	5	31.75	b4b5°b5y3y7	1882.89	63.167	1599	2	941.95	-14.20
P67093 UG_SALTY Universal stress protein G	10		IIMPVDVFEMELSDK	4	15	0	4.14		1765.85	104.970	1551	2	883.43	-12.86
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	1		LAEAGIPTQMER	60	12	15	113.65	b1b2b3b4°b4b5°b5b6y6*y6y7y8*y8y9y10	1315.66	50.731	54051	2	658.34	-2.60
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	2		QSLGGLIEAYEAVHR	215	16	6	25.5	b2°b2y1y5y7y10	1713.87	85.424	37192	3	571.96	-11.68
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	3	Carbamidomethyl+C(7)	LLSDTECLVK	72	10	6	29.47	b2b8°b8y8y9y10	1177.62	53.848	36688	2	589.31	4.15
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	4		TVYSTENPDLLVLEFR	13	16	8	53.09	b2b3b4y3y4y11y13y16	1895.99	89.156	23536	2	948.50	5.92
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	5		LGVEEGMELNPPIFDLFLK	104	19	4	15.49	b5°b5b9y14	2161.08	121.149	3817	3	721.03	-19.32

P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	6	Carbamidomethyl+C(9)	KLEMPVECVVR	82	12	7	60.83	b5b10b11y3y7*y7y11	1458.78	62.688	34727	2	729.89	0.84
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	7		FRQSLGGLIEAYEAVHR	213	18	3	16.16	b13y7y13	2017.05	79.885	23663	3	673.02	-5.51
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	8		TVYSTENPDLLVLEFRNDTSAGD GAR	13	26	5	27.5	b15y3y7y11y20	2840.39	81.380	13129	3	947.47	6.45
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	9		NDTSAGDGARIEQFDR	29	16	3	26.17	y6y12y13	1751.79	72.553	12721	3	584.60	-1.46
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	10		LEFGLYKGEVVLGDEFSPDGSR	177	22	3	22.66	b4y13y14	2414.17	96.569	5070	4	604.30	-7.89
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	11		GEVVLGDEFSPDGSRLWDK	184	19	11	84.6	b3b4*b4b7b8b9*b9b10b11 y11*y11	2106.04	76.878	3493	3	702.69	13.91
P63411 ACKA_SALTY Acetate kinase	1	Carbamidomethyl+C(14)	MLNKPVEELNIITCHLNGGGSVSA IR	195	26	5	12.5	b2b8*b8b10y14	2822.43	78.235	22980	4	706.36	-13.93
P63411 ACKA_SALTY Acetate kinase	2		EGTRPAVVPIPTNEELVIAQDASR	374	23	14	89.14	b8b9b14b15b20*b20y5y6y 7*y7y14*y14y15y23	2465.31	69.724	21037	3	822.44	2.67
P63411 ACKA_SALTY Acetate kinase	3		LGVLGFEVDHER	348	12	6	51.06	b1b7y3y8y9y10	1370.69	68.040	19004	3	457.57	-14.78
P63411 ACKA_SALTY Acetate kinase	4		SGDIDPAIIFHLHDTLGMSVDQINK	243	25	3	22.34	b13b14y17	2736.35	89.230	2903	3	912.79	-5.98
P63411 ACKA_SALTY Acetate kinase	5		DSASFAPLHNPAHLIGIAEALK	114	22	6	23.78	b5*b5b6*b6b11*b11	2272.21	83.095	10408	3	758.07	-0.97
P63411 ACKA_SALTY Acetate kinase	6	Carbamidomethyl+C(19)	FAIDAVNGDEYLSGLAECFHLPE AR	17	26	3	12.5	b3b13y11	2907.37	112.362	6997	3	969.79	-10.66
P63411 ACKA_SALTY Acetate kinase	7		YGAHGTSHFYVTQEAAK	178	17	4	24.33	y5*y5y7y13	1866.87	50.765	5669	3	622.96	-1.18
P63411 ACKA_SALTY Acetate kinase	8		LDAVVFTGGIGENAAMVR	324	18	3	16.16	b4y4y6	1819.93	83.440	4856	2	910.47	-3.29
P63411 ACKA_SALTY Acetate kinase	9	Carbamidomethyl+C(14)	ESGLLGLTEVTSDCR	272	15	3	26.89	y8y9y11	1636.76	72.709	3356	3	546.26	-16.71
P63411 ACKA_SALTY Acetate kinase	10	Carbamidomethyl+C(19)	FAIDAVNGDEYLSGLAECFHLPE ARIK	17	28	3	22.22	b15y11y12	3148.59	98.952	33571	4	787.90	5.43
P63411 ACKA_SALTY Acetate kinase	11	Carbamidomethyl+C(6)	AMDVYCHRLAK	301	11	3	25.08	b3y7y9	1363.65	47.947	5671	3	455.22	-5.55
P63411 ACKA_SALTY Acetate kinase	12		YIGSYTALMDGRLLDAVVFTGGIG ENAAMVR	312	30	3	11.63	b5b7y10	3147.57	113.652	2897	3	1049.86	2.17
P63411 ACKA_SALTY Acetate kinase	13		LDAVVFTGGIGENAAMVRELSLG K	324	24	3	23.41	b3b4b9	2447.28	75.226	2417	3	816.43	-4.69
P63411 ACKA_SALTY Acetate kinase	14	Carbamidomethyl+C(18)	MLTKESGLLGLTEVTSDCR	268	19	6	37.16	b8*b8y9*y9y10y11	2110.05	62.060	1549	3	704.02	1.04
P63411 ACKA_SALTY Acetate kinase	15	Phosphoryl STY(7)	LDAVVFTGGIGENAAMVR	324	18	3	16.16	b7y7y10	1899.88	59.958	3149	2	950.44	-8.22
Q7CPK0 UGPB_SALTY sn-glycerol-3- phohate-binding periplasmic protein ugpB	1		TGYLPITTAAYELTR	343	15	13	104.12	b3b4b7b10y1y4y5y6y7y9*y 9y11y15	1669.89	85.468	98273	2	835.45	3.58
Q7CPK0 UGPB_SALTY sn-glycerol-3- phohate-binding periplasmic protein ugpB	2		LGNMPQIR	389	8	8	68.8	b3b6y4y5y7*y7y8*y8	928.49	48.339	56655	2	464.75	-10.25
Q7CPK0 UGPB_SALTY sn-glycerol-3- phohate-binding periplasmic protein ugpB	3		TIVDEELESVWTGKK	397	15	8	41.22	b2b5y3y4y8y13*y13y15	1733.88	76.179	44660	3	578.63	-10.42

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	4		AIKPVYEVFKDAGINFDESQFVPT VAGYYTDAK	99	33	9	40.38	b1y1y5°y5y7y8y10y11y33	3682.87	94.082	37331	3	1228.29	10.08
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	5		TGNAPAILQVYEVGTATMMASK	77	22	9	49.25	b3°b3b12y5y7y9y12y14y2 2	2253.15	94.762	24191	2	1127.08	12.68
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	6		FNQANPDYK	47	9	6	31.32	b7y2y4y5°y5y9	1096.50	29.216	21445	2	548.75	-5.57
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	7		SGHLLSQPFNSSTPVLYYNK	132	20	6	28.73	b2b3b6y6y7y20	2252.13	68.870	18143	3	751.38	-1.73
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	8		SGHLLSQPFNSSTPVLYYNKDAFK	132	24	7	29.79	b3b4b7b11y7*y7y24	2713.33	107.107	18016	4	679.09	-12.51
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	9		TIVDEELESVWTGK	397	14	6	55.35	b8b13y6y10y11y12	1605.81	82.969	14514	2	803.41	7.07
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	10		FNYGVGMMPYDADIK	282	15	7	75.49	b5y7y8y10y11y12y13	1720.78	75.307	13380	2	860.89	6.31
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	11	Carbamidomethyl+C(6)	FYNGDCAMTTASSGSLANIR	258	20	4	24.32	y4y12y13y20	2135.97	61.858	9730	2	1068.49	9.60
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	12		FLDFLAKPENAAEWHQK	326	17	10	65.24	b3y3y4y5y10*y10y11°y11* y11y13	2043.99	73.872	104652	4	511.75	-19.23
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	13		QMLNKPLPFTK	374	12	3	30.23	y4y6y7	1413.77	61.874	50103	3	471.93	-15.02
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	14		HTALGLALSRAFTGQALAVTTIPF WHSMEGELGK	5	34	3	16.86	b3b8b12	3567.85	102.319	11781	4	892.72	-4.11
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	15		AIKPVYEVFK	99	10	3	37.71	y5y6y7	1193.68	60.329	7376	3	398.56	-12.17
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	16		GAPQNAIIGGASLWVMQGK	297	19	3	24.67	y11y13y14	1897.99	111.929	6348	2	949.50	-1.74
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	17		NNGFDGTDAVLEFNKPEQVK	212	20	9	86.6	b4y3y5*y5y7y10y12y16y1 8	2222.10	66.216	5587	2	1111.55	11.76
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	18		HIALLEEMNK	232	10	3	29.47	b3b4y5	1197.61	58.892	4279	2	599.31	-18.86
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	19		AGLDPEQPPKTWQELADYTAK	157	21	14	111.52	b3b4b5b6°b6b7*b7b8y4y5 °y5y11y14y17	2358.16	73.383	74935	3	786.72	-1.35
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	20		EQGYDKNPGADIATR	358	16	5	55.58	y3y4y5y8y9	1797.82	40.891	50285	3	599.95	-8.89
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	21		TPQQALDTAVDRGNQLLR	412	18	3	16.16	b4b10y15	1996.05	69.070	43745	3	666.02	-5.44
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	22		AIKPVYEVFKDAGINFDESQFVPT VAGYYTDAK	99	33	5	23.66	y6°y6y11y13y19	3682.79	87.255	38995	5	737.36	-12.00

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	23		TIVDEELESVWTGKK	397	15	3	26.89	b8b10b12	1733.88	94.521	10595	2	867.44	-11.12
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	24		EVDSLAQRFNQANPDYK	39	17	5	23.85	b6b8*b8y11y15	1994.96	93.747	4402	3	665.66	2.51
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	25		FLDFLAKPENAAEWHQKTGYLPIT TAAYELTR	326	32	3	17.15	b4b6b10	3694.90	123.804	3123	3	1232.31	3.50
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	26	Oxidation+M(16)	GAPQNAIIGGASLWVMQGK	297	19	6	32.82	b4*b4b6y3y4y11	1914.00	69.692	3898	2	957.50	4.66
P0A1P8 GLRX1_SALTY Glutaredoxin-1	1		TVGKPVETVPQIFVDQK	50	17	11	57.38	b1b3b9y2*y2y5y7y8y11y13y17	1885.03	65.606	29326	3	629.01	-7.38
P0A1P8 GLRX1_SALTY Glutaredoxin-1	2	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	MFTVIFGRPGCPYCVR	0	16	5	29.29	b3b12b13*b13y4	1959.93	68.529	6542	3	653.98	-6.10
P0A1P8 GLRX1_SALTY Glutaredoxin-1	3		ADLEK	45	5	3	27.07	b3*b3y4	575.30	29.395	4561	1	575.30	-11.14
P0A1P8 GLRX1_SALTY Glutaredoxin-1	4	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	MFTVIFGRPGCPYCVRAK	0	18	5	27.48	b6*b6b7b11y6	2159.09	74.265	2716	3	720.37	8.48
P0A1P8 GLRX1_SALTY Glutaredoxin-1	5		PQIFVDQK	59	8	0	4.52		974.54	65.601	6871	1	974.54	4.51
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1	Carbamidomethyl+C(7)	LWVNPDCGLK	719	10	12	102.37	b2b5b8b9y4y6y7*y7y8*y8y9y10	1201.60	61.220	35932	2	601.30	-1.83
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2		QAGIDLLPVGDFAWDHVLTTSL LLGNVPAR	52	31	17	105.53	b2b5°b5*b5b6°b6b7*b7y4y5y6*y6y7y8y24y25y31	3351.80	119.930	34626	3	1117.94	7.14
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	3		LAAITAQDSQRENPYEVR	395	18	9	56.39	b2b3y2y6y13y14y15y16y18	2061.02	48.142	30267	3	687.68	-7.34
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	4	Carbamidomethyl+C(1)	CVKPPVVIGDISRPAPITVEWAK	515	23	9	53.82	b2b3b4b6b7y4y15y20y23	2532.39	76.351	24628	3	844.80	-3.37
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	5		DALNSGETAALEEWSAPIQAR	360	21	3	21.02	y5y7y19	2229.11	80.980	22858	2	1115.06	13.03
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	6		LTWTQLLEEVDALALGHK	137	19	8	48.93	b2°b2y2y4y6y9y12y15	2166.13	119.397	20001	3	722.71	-6.76
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	7		QAIIEQER	466	8	9	41.73	b2*b2y4°y4y5°y5y6*y6y8	986.52	31.553	12877	2	493.76	-8.66
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8	Carbamidomethyl+C(1)	CGELALLRDALNSGETAALEEWS APIQAR	352	29	7	26.9	b6°b6y1y3y5y6y8	3141.57	104.659	12342	3	1047.86	1.94
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	9		AQESYWAGNTTR	21	12	4	45.98	y5y7y8y9	1383.62	41.566	11620	2	692.32	-3.71
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	10	Carbamidomethyl+C(1)	CGELALLR	352	8	3	36.96	b3b7y5	931.50	61.213	10881	2	466.25	-8.26
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	11		DALNSGETAALEEWSAPIQARR	360	22	3	20.43	b4b11b13	2385.16	85.886	8456	3	795.72	-9.72

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	12		LAAITAQDSQR	395	11	7	36.4	b2b8b10°b10*b10y3y6	1173.61	34.779	7552	2	587.31	-9.78
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	13	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETR	315	22	4	18.96	b7b10y4y12	2441.25	80.622	1950	6	407.71	-1.60
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	14		YAQSLTDKPVK	538	11	7	49.14	b4b7°b7b8*b8y3y10	1249.66	31.614	26562	3	417.22	-17.49
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	15	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	3	25.5	b5b12b14	1834.94	100.255	17823	2	917.98	4.92
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	16		GWPETR	731	6	1	13.91	b3	745.37	58.826	14904	1	745.37	5.49
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	17		AALANMVK	737	8	4	50.49	b4y3y5y6	817.45	44.108	12850	2	409.23	-15.31
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	18		ADLTEK	298	6	3	27.44	b3°b3y5	676.36	47.957	6361	1	676.36	13.36
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	19		GQQFR	132	5	2	13.53	y3*y3	635.32	42.388	4911	1	635.32	-2.69
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	20		SDWDAYLEWGVEAFR	611	15	3	26.89	y7y9y10	1843.86	70.394	2824	2	922.44	19.60
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	21		HWEQQK	46	6	1	13.91	y4	855.42	139.663	2447	1	855.42	12.06
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	22		WFNTNYHYIVPEFSK	117	15	4	37.69	y3y4y6y10	1944.90	53.118	1853	2	972.95	-14.62
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	23		DDVAELHQR	270	9	5	31.32	b4°b4b7y8°y8	1082.51	31.634	1647	2	541.76	-13.42
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	24		FKLPAPWPTTTIGSFPQTTEIR	420	21	5	22.51	b3y4y13*y13y15	2391.26	88.324	40187	3	797.76	-2.55
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	25		GRAPTGEPAAAAEMTK	101	16	6	51.33	b7b8b9b11y7y9	1557.75	36.359	17639	3	519.92	-10.97
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	26		VKGEPFDR	172	8	3	33.95	b7y5y6	947.50	41.670	16637	2	474.25	6.64
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	27	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETRLD TEVK	315	28	4	12.01	b12b14y5°y5	3126.63	103.527	4166	4	782.41	5.78
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	28		GNLDANHRYTGIAEHK	449	17	3	24.33	b3b8b11	1908.97	76.106	3877	2	954.99	-0.45
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	29		RGIEWVQIDEPALVLELPQAWLDA FKPAYDALAGQVK	200	37	5	15.05	b12*b12y8y13y21	4150.16	136.535	3766	3	1384.06	-9.41
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	30		KAQESYWAGNTTR	20	13	5	21.36	b4°b4y6°y6y8	1511.72	35.924	2378	2	756.36	-4.12

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	31		GWPETRAALANMVK	731	14	3	27.76	b7b8b11	1543.81	60.800	1704	2	772.41	5.46
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	32	Carbamidomethyl+C(11);Phosphoryl STY(13)	GMLTGPVTILCWSFPREDVTRETI AK	549	26	3	12.5	b4b11y12	3057.53	115.082	4721	4	765.14	14.05
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	33	Carbamidomethyl+C(11);Oxidation+M(2)	GMLTGPVTILCWSFPR	549	16	3	24.33	b13y7y8	1850.94	102.025	1805	2	925.97	6.13
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	34		YWAGNTTR	25	8	0	2.64		968.44	41.540	1712	1	968.44	-14.18
Q8ZQS2 GPMA_SALTY 2	1		AIHTLWNVLDELQAWLPVEK	62	21	14	67.48	b4°b4b12b17y1y2°y2y4°y4y5y6y7y9*y9	2490.30	117.997	52785	3	830.77	-1.37
Q8ZQS2 GPMA_SALTY 2	2		VIPYWNDTILPR	160	12	6	30.23	b2y2y5y9y10y12	1486.81	82.205	35771	2	743.91	1.15
Q8ZQS2 GPMA_SALTY 2	3		GFAVTPPELTCKDDER	117	15	7	38.39	b5b12°b12b13y5y9y15	1674.83	63.779	7846	3	558.95	-4.81
Q8ZQS2 GPMA_SALTY 2	4		EEGFSFDFAYTSVLKR	46	16	4	25.5	y2y3y10y12	1895.93	105.293	3853	2	948.47	6.95
Q8ZQS2 GPMA_SALTY 2	5		LLKEEGFSDFAYTSVLK	43	18	3	25.08	b3b7b8	2094.08	58.011	5294	4	524.28	1.17
Q8ZQS2 GPMA_SALTY 2	6		FTGWYDVDLSEKGVSEAK	21	18	6	32.2	b4b6b9y4°y4y13	2030.99	92.154	4834	2	1016.00	11.42
Q8ZQS2 GPMA_SALTY 2	7		ENRFTGWYDVDLSEK	18	15	4	26.78	b4b12y3y9	1858.88	84.348	3463	3	620.30	12.61
Q8ZQS2 GPMA_SALTY 2	8		HYGALQGLNKAETAEK	90	16	3	17.8	b6b14y11	1729.88	91.422	1711	2	865.44	-6.70
Q8ZQS2 GPMA_SALTY 2	9		GFAVTPPELTCKDD	117	13	1	7.3	y4	1389.68	63.787	7052	2	695.34	-10.19
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	1		NPQTGKEITIAAAK	61	14	9	43.74	b7°b7y1y2y3y4y6y8y14	1441.78	37.055	45037	3	481.26	-14.90
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	2		ALDAIIASVTESLKEGDDVALVGF GTFAVK	23	30	9	65.54	b4b5y1y3y4y6y7y8y19	3036.62	136.207	18933	3	1012.88	3.06
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	3		ALDAIIASVTESLK	23	14	3	21.43	b4°b4b5	1430.81	98.812	5652	2	715.91	-1.71
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	4		IAAGADISK	9	9	5	66.17	b4y3y4y7y8	845.46	28.927	230276	2	423.23	-19.92
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	5		ALDAIIASVTESLKEGDDVALVGF GTFAVK	23	30	3	22.98	y3y7y8	3036.59	123.885	2965	4	759.90	-7.24
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	1		EGGIFWMDSLAIPANAK	249	17	9	35.24	b5°b5b12°b12y5*y5y12y13y17	1819.92	94.337	46115	2	910.46	8.25
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	2		LINFLLRPDVAKEVAETIGYPTPNL AAR	273	28	6	17.94	b2b3y6y8y13*y13	3081.67	99.108	44870	4	771.17	-13.55
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	3		QAGTPLEVWVWPK	237	12	3	23.03	b10y5y8	1324.73	75.861	34493	2	662.87	-0.65
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	4		EVAETIGYPTPNLAAR	285	16	8	59.78	b6b8°b8y1y8y9y10y11	1701.89	61.812	29770	2	851.45	4.66
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	5		QAGTPLEVWVPKEGGIFWMDSLA IPANAK	237	29	8	26.03	b7b8°b8b13y2y3y5*y5	3125.64	105.188	14829	3	1042.55	9.14
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	6		LTNFHNLDPEMLNKPFDPNNDYS VPYIWGATAIGVNSDAIDPK	103	43	9	42.77	b2b8b13b24y2y7y8y10y11	4803.33	95.456	13774	4	1201.59	5.29
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	7		TITSWADLWKPEYK	146	14	6	62.04	b9y4y5y7y9y11	1737.86	82.975	62814	3	579.96	-13.63
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	8		VIYSTYESNETMYAK	53	15	3	18.81	b3b8y8	1798.83	52.320	8392	2	899.92	5.77

P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	9		EGMIQK	92	6	1	13.91	b4	705.36	41.526	4382	1	705.36	-5.54
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	10		LGYSGN'TTDPK	179	11	4	42.59	b7b8b9y9	1152.54	31.086	3498	2	576.78	-8.37
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	11		KLMPNVAAFNSDNPANPYMEGE VNLGMVWNGSAFVAR	200	37	5	10.93	b13°b13y13°y13y25	4010.90	110.797	4776	3	1337.64	0.43
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	12		DGAYDLVVPSTYYVDKMR	73	18	3	23.32	b3b8b12	2092.01	81.193	4051	2	1046.51	1.98
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	13		LGYSGN'TTDPKEIAAYEELK	179	21	3	14.38	b7y5y12	2328.12	104.290	3782	3	776.71	-1.15
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	14		QAGTPLEVVPKEGGIFWMDSLA IPANAK	237	29	4	17.5	b3b13b21y5	3125.57	113.648	3162	3	1042.53	-14.53
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	15	Phosphoryl STY(10)	EVAETIGYPTPNLAAR	285	16	6	52.37	b6b7b8°b8b9y8	1781.86	56.310	26767	3	594.63	13.56
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	16	Phosphoryl STY(10)	SLYPDAQTISK	312	11	5	28.09	b8°b8b9y6°y6	1302.60	31.154	1975	2	651.81	12.28
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	17	Phosphoryl STY(6)	EIEAAYEELK	190	10	3	37.71	b3b4b5	1274.55	28.750	1667	2	637.78	1.25
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VVGQLGQVLGPR	122	12	14	85.91	b1b2b5y1y2y3y4y5y7*y7y 8y10*y10y12	1222.72	59.795	96125	2	611.86	-5.59
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VGTVTPNVAEAVK	141	13	15	98.06	b3°b3b4°b4b13y3y7*y7y8y 9y10*y10y12*y12y13	1284.71	48.859	92647	2	642.86	-0.95
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VAVFTQGPNAEAAK	74	14	5	45.76	y7y8y10y11y14	1402.73	45.913	84288	2	701.87	-0.61
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		FNESVDVAVNLGIDAR	37	16	3	17.8	b4b14y5	1718.87	77.696	6424	3	573.63	1.56
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		AAGAELVGMEDLADQIK	88	17	5	54.71	y7y9y10y11y12	1730.87	80.413	14167	2	865.94	5.36
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		GATVLPHGTTGR	60	11	12	86.21	b3°b3b4°b4b5°b5y4°y4y5y 6°y6y7	1065.57	30.043	14083	2	533.29	-8.48
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		KGEMNFDVVIASPDAMR	105	17	7	35.24	b5°b5b10°b10y4y5y7	1879.88	41.064	44567	3	627.30	-12.34
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8	Oxidation+M(9)	AAGAELVGMEDLADQIK	88	17	4	24.33	b5°b5b7b12	1746.88	77.479	12826	2	873.94	9.92
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9	Oxidation+M(9)	AAGAELVGMEDLADQIKK	88	18	5	33.47	b5°b5b7b12b13	1874.93	77.502	8926	3	625.65	-12.70
P22107 TRAT_SALTY TraT complement resistance protein	1		NTSDKDMSDLQSLIAK	58	16	9	51.33	b9b12y2y3y4y5y9*y11y16	1765.85	66.243	73439	3	589.29	-7.12
P22107 TRAT_SALTY TraT complement resistance protein	2		ATVTTDNVAALR	177	12	9	81.81	b3°b3b4y4y5y6y8y9y12	1231.66	46.276	43015	2	616.33	-4.06
P22107 TRAT_SALTY TraT complement resistance protein	3		NTSDKDMSDLQSLIAKDIAK	58	21	7	14.38	b5y1y2y3*y3y19y21	2321.16	76.079	41845	3	774.39	-2.63
P22107 TRAT_SALTY TraT complement resistance protein	4		GYTVVTTSPDK	79	10	8	57	b2b3°b3b9y4y5y6y10	1066.54	36.767	15296	2	533.77	-3.89
P22107 TRAT_SALTY TraT complement resistance protein	5		FEEAKPVLEEQLAK	223	14	5	11.37	b2b10°b10y9y14	1630.87	53.972	11412	2	815.94	2.47
P22107 TRAT_SALTY TraT complement resistance protein	6		AYYWIQANVLK	89	11	3	25.08	b7y6y8	1368.73	78.041	25971	2	684.87	2.41

P22107 TRAT_SALTY TraT complement resistance protein	7		IQTSTETGNQHK	196	12	7	37.23	b7°b7b8y4*y4y7*y7	1343.67	95.973	1755	2	672.34	8.81
P22107 TRAT_SALTY TraT complement resistance protein	8		VNLKFEEAKPVLEEQLAK	219	18	5	25.72	b8*b8y3y7y9	2085.15	63.051	43350	3	695.72	-4.92
P22107 TRAT_SALTY TraT complement resistance protein	9		GYTVVTSPPDKAYYWIQANVLK	79	21	4	19.74	b3b12y5y9	2416.24	89.460	35499	3	806.09	-4.55
P22107 TRAT_SALTY TraT complement resistance protein	10		TKATVTTDNVAALR	175	14	3	28.55	y3y5y10	1460.79	69.682	7797	2	730.90	-10.19
P22107 TRAT_SALTY TraT complement resistance protein	11		MDLRESQGWLNR	103	12	5	45.98	b4b6b10b11°b11	1504.72	136.484	1813	1	1504.72	-6.90
P22107 TRAT_SALTY TraT complement resistance protein	12	Carbamidomethyl+C(16) ;Oxidation+M(19)	LMMVTLVSSTLALSGCGAMSTAI KK	5	25	3	22.34	b5y10y11	2586.36	76.985	267154	3	862.79	6.89
P22107 TRAT_SALTY TraT complement resistance protein	13	Carbamidomethyl+C(16) ;Oxidation+M(19)	LMMVTLVSSTLALSGCGAMSTAI K	5	24	4	13.12	b6°b6y15y17	2458.24	98.002	8186	4	615.32	0.99
O54297 RS4_SALTY 30S ribosomal protein S4	1		AALELAEQR	156	9	8	46.61	b3y1y2y4y5y6°y6y9	1000.53	43.921	42398	2	500.77	-11.96
O54297 RS4_SALTY 30S ribosomal protein S4	2		VVNIASYQVSPNDVVSIR	128	18	13	99.49	b12b15y4y8y9y10y11*y11 y13*y13y14y16y18	1960.07	72.913	33353	2	980.54	8.41
O54297 RS4_SALTY 30S ribosomal protein S4	3		VVNIASYQVSPNDVVSIREK	128	20	9	53.85	b3b14y5°y10y11y12y15y1 9y20	2217.18	66.777	22997	3	739.73	-2.97
O54297 RS4_SALTY 30S ribosomal protein S4	4	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	5	46.88	b4b6b8b9y8	1451.70	57.454	13570	3	484.57	-11.94
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	16	150.2	b3y2y3y5y7y8y9y11°y11y1 2y13°y13y14y15y17y19	2032.89	38.213	83163	3	678.30	-11.59
P02936 OMPA_SALTY Outer membrane protein A	2		GVKDVVTQPQA	339	11	9	53.91	b4°b4b6b8*b8y1y4y6y11	1141.61	37.787	59695	2	571.31	-8.13
P02936 OMPA_SALTY Outer membrane protein A	3	Carbamidomethyl+C(6)	AALIDCLAPDR	321	11	11	83.99	b2b3b6°b6y3y4°y4y5y7y8y 11	1214.62	62.682	30403	2	607.81	-3.22
P02936 OMPA_SALTY Outer membrane protein A	4		LGYPITDDLVDYTR	103	14	3	28.55	y4y7y9	1640.82	76.810	12869	2	820.91	0.37
P02936 OMPA_SALTY Outer membrane protein A	5	Carbamidomethyl+C(6)	AALIDCLAPDRR	321	12	4	27.01	b5b6y7°y7	1370.72	41.619	4569	3	457.58	-1.16
P02936 OMPA_SALTY Outer membrane protein A	6		AQSVVDYLSK	281	11	3	36.84	y7y8y9	1222.66	72.784	39890	2	611.84	-2.80
P02936 OMPA_SALTY Outer membrane protein A	7		FGQQEAAPVVAPAPAPEVQTK	194	23	3	13.49	b4y8y10	2303.25	54.835	7279	2	1152.13	19.72
P02936 OMPA_SALTY Outer membrane protein A	8		DGSVVVLGFTDR	255	12	4	23.03	b4y5°y5y10	1264.68	87.799	2680	2	632.84	21.24
P02936 OMPA_SALTY Outer membrane protein A	9		IGSDAYNQGLSEK	267	13	4	21.36	b6b8*b8y11	1381.63	110.677	1637	2	691.32	-20.76
P02936 OMPA_SALTY Outer membrane protein A	10		GIPSDKISAR	292	10	3	34.7	y3y7y8	1043.58	32.224	18703	2	522.29	-7.37
P02936 OMPA_SALTY Outer membrane protein A	11		IGSDAYNQGLSEKR	267	14	4	25.42	b3b4y11°y11	1537.78	63.158	2625	2	769.39	12.86
P67904 RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAKR	16	15	19	164.14	b3°b3b9°b9°b9y1y3y4y5y6 °y6y7y8y9y10y11y12y13y1 5	1673.88	52.755	111531	3	558.63	-14.80
P67904 RS10_SALTY 30S ribosomal protein S10	2		LIDQSTAEIVETAK	16	14	14	90.2	b2b3b4b5y2y4°y4y5y9°y9y 10°y10y11y14	1517.81	56.279	64277	2	759.41	0.88
P67904 RS10_SALTY 30S ribosomal protein S10	3		LVDIVEPTEK	72	10	8	79.11	b2b3y3y4y6y8y9y10	1142.62	52.519	34302	2	571.81	-7.37
P67904 RS10_SALTY 30S ribosomal protein S10	4		LIDQSTAEIVETAKR	16	15	3	26.89	b3b7b11	1673.91	49.791	58893	4	419.23	2.99
P67904 RS10_SALTY 30S ribosomal protein S10	5		GPIPLPTRK	37	9	4	46.61	b3y4y5y6	978.60	43.577	38394	2	489.80	-10.42

P67904 RS10_SALTY 30S ribosomal protein S10	6		RLVDIVEPTEK	71	11	7	66.65	b3b4b7y4y5°y5y6	1298.73	51.290	38049	2	649.87	-3.29
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	14	160.27	b2b3b4b9b10y3y4y5y6y8y9y10y11y12	1377.65	78.827	108518	2	689.33	-0.44
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AAVTMPSSK	22	9	3	39.1	y3y6y7	891.46	31.983	86605	2	446.23	-0.96
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3		AVVESIQR	69	8	13	64.03	b2b6°b6y1y2*y2y3y4y5°y5y6y8*y8	901.50	33.364	58533	2	451.25	-12.80
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4		VSRPGLR	77	7	4	41.35	b5°b5y4y6	784.47	22.975	21875	2	392.74	-15.87
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		QLDPLVVGQEHYDTAR	343	16	14	104.63	b2*b2y3°y3y4y5y6y8y9y10°y10y11y16*y16	1840.90	58.459	73881	3	614.31	-8.29
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		VALTGLTMAEK	219	11	8	102.75	b3y3y4y5y7y8y9y10	1133.62	59.979	52904	2	567.31	-5.71
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		TVNMMELIR	156	9	7	55.64	b2°b2y3y5y6y7y9	1106.56	76.536	42294	2	553.78	-8.49
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4		YTLAGTEVSALLGR	247	14	9	31.75	b1b2°b2b9y2y6y10y11y14	1450.79	80.606	40208	2	725.90	0.17
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		GLDVKDLLEHPIEVPVGK	65	17	7	16.93	b3b9°b9y1y2y12y17	1844.99	67.906	35700	3	615.67	-10.32
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		AAPSYEELSNSQELLETKIK	112	20	4	23.03	b12b13y4y20	2179.10	74.519	34884	2	1090.05	10.64
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	10	53.49	b2b4y5y6°y6y9y11y12y13y27	3057.41	100.298	34341	3	1019.81	7.67
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		TIAMGSSDGLRR	53	12	6	23.03	b2b11y1y4y10y12	1263.64	37.705	33957	2	632.33	-2.99
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		VGLFGGAGVGK	145	11	8	37.82	b2b9y1y2y4y7y8y11	961.54	59.640	33956	2	481.27	-5.78
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		QIASLGIYPAVDPLDSTSR	324	19	6	39	y4y11y12°y12y13y19	2003.07	81.242	32725	2	1002.04	12.19
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		FLSQPFFVAEVFTGSPGK	399	18	12	44.68	b2b3°b3b9°b9y3y7y9°y9y16°y16y18	1958.02	100.303	28213	2	979.51	7.86
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		VYDALEVQNGNEK	25	13	7	21.36	b3y2y8°y8y11°y11y13	1478.72	45.133	25856	2	739.86	2.23
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	6	40.46	b2b6b8y5y8y10	1193.61	81.344	24721	2	597.31	0.72
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		NIAIEHSGYSVFAGVGER	165	18	5	33.47	y5y10y11y13y18	1905.94	66.644	13107	3	635.98	-5.19
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15		MPSAVGYQPTLAEEMGVLQER	261	21	3	14.38	b7y4y6	2306.14	82.224	25109	2	1153.57	10.16
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16		TGSITSVQAVYVPADDLTDPSPAT TFAHLDATVVLRS	287	37	4	23.26	b6b8°b8b9	3816.00	89.678	12637	5	764.00	16.19
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17		VSLVYGMNEPPGNR	202	15	3	26.89	y6y11y12	1660.80	67.603	3048	3	554.27	-4.78
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18		YQELK	367	5	1	13.53	b4	680.37	45.808	2935	1	680.37	5.29
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19	Carbamidomethyl+C(26)	AAPSYEELSNSQELLETKIKVIDLM CPFAK	112	30	12	90.37	b5°b5b7b8y4y5y6y7y8y10y16y28	3353.68	121.228	38780	3	1118.57	5.61
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20	Oxidation+M(11)	IMNVLGEPVDMK	87	12	4	23.03	b6b9°b9y4	1361.68	34.069	24926	3	454.57	3.32
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	21	Oxidation+M(4)	TIAMGSSDGLR	53	11	4	37.82	b3b5b6y9	1123.53	88.150	6125	1	1123.53	-8.15
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	22	Carbamidomethyl+C(6); Oxidation+M(5)	VIDLMCPFAK	132	10	3	27.71	b5y5y8	1209.58	60.828	4733	3	403.87	-13.62
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	23		GYSVFAGVGER	172	11	0	4.9		1141.56	66.677	20641	2	571.28	-6.10
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	24		AMGSSDGLRR	55	10	0	2.64		1049.51	37.713	14947	2	525.26	-1.63

[Q7CPE2]ATPB_SALTY ATP synthase subunit beta	25		DVKDLEHPIEVPVGK	67	15	6	34.64	b4b7°b7b8b11°b11	1674.89	67.895	4011	3	558.97	-8.60
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta	26		QLDPLVVQGEHYDTAR	343	16	0	4.14		1822.88	58.481	2406	3	608.30	-12.32
[P0A1S4]STPA_SALTY DNA-binding protein stpA	1		MNLMLQNLNNIR	0	12	9	57.82	b2b3b4b9y4*y6y9y10y12	1473.77	76.912	19580	2	737.39	0.17
[P0A1S4]STPA_SALTY DNA-binding protein stpA	2		ADGINPEELFAMDSAMPR	66	18	12	66.72	b2b3b8b11°b11b15°b15y2y4y8y10y14	1963.91	89.615	19490	2	982.46	12.93
[P0A1S4]STPA_SALTY DNA-binding protein stpA	3		EFSIDVLEEMLEK	19	13	3	30.6	b5b8b12	1581.78	104.408	10276	2	791.39	3.32
[P0A1S4]STPA_SALTY DNA-binding protein stpA	4		TPKPIAQALAAGK	113	13	3	21.36	b4y4y10	1265.74	46.862	8066	3	422.58	-16.01
[P0A1S4]STPA_SALTY DNA-binding protein stpA	5		INAFLELMKADGINPEELFAMDSA MPR	57	27	4	27.79	y3y9y10y13	3023.49	113.023	8521	3	1008.50	6.14
[P0A1S4]STPA_SALTY DNA-binding protein stpA	6		EFSIDVLEEMLEKFR	19	15	6	38.39	b3°b3b12y3y7y8	1884.93	114.116	7015	3	628.98	-6.54
[P0A1S4]STPA_SALTY DNA-binding protein stpA	7		AMAREFSIDVLEEMLEK	15	17	5	16.93	b10y4°y4y7°y7	2011.00	65.251	5310	3	671.01	7.47
[P0A1S4]STPA_SALTY DNA-binding protein stpA	8	Oxidation+M(3)	NLMLQNLNNIR	1	11	3	25.08	b8y6y9	1358.71	47.440	4757	2	679.86	-7.10
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	1		ATAHLGNVEVVGFSDLMANFAR DR	57	24	7	39.67	b9°b9b13b14y3y10y11	2590.25	74.683	4640	4	648.32	-14.51
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	2		AVADFEYEMQLAHMNR	91	16	9	45.74	b2b3b11°b11y4*y4y5y6*y6	1924.88	76.088	4636	4	481.98	5.20
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	3		HQGDVTHFLPDNVHQALMDK	137	20	8	14.9	b2°b2b6y4y7*y7y8°y8*	2302.12	59.762	4366	4	576.29	7.00
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	4		KPMFTLDER	42	9	5	31.32	b3b9y3y7y9	1136.57	34.054	3012	2	568.79	-10.10
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	5		ATQMFDHVILAIASPSKKPMFTL DER	24	27	4	15.98	b7b9y6y21	3017.60	136.512	2828	4	755.16	13.84
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	6		ATAHLGNVEVVGFSDLMANFAR	57	22	4	22.66	b4y9y10°y10	2319.20	84.137	1557	2	1160.10	17.37
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	7	Phosphoryl.STY(7)	EWSFISSSLVK	122	11	3	32.07	b3b5b6	1362.63	33.394	1852	2	681.82	1.25
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	8		ATAHLGNVEVVGFSDLMANFA	57	21	0	7.16		2163.04	74.679	14705	3	721.69	-5.08
[Q8ZL48]COAD_SALTY Phohopantetheine adenylyltransferase	9		HVILAIASPSKKPMFTLDER	30	21	0	8.29		2324.27	136.564	2260	3	775.43	-2.73
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	1	Carbamidomethyl+C(1)	CTWVASDFDALIPSLK	66	16	8	42.57	b3°b3b5b12°b12y3y4y16	1822.91	98.801	56487	2	911.96	5.76
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	2		IGTDTTYAPFSSK	29	13	8	64.39	b12y5y6°y6y9y10y12y13	1387.68	53.846	33339	2	694.34	0.88
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	3		HVGVLQGSTQEAYANDNWR	134	19	8	57.14	b4b11y3*y6y7y8y9y19	2145.00	54.178	33170	3	715.67	-3.98
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	4		EYAFAGPSVK	198	10	6	34.7	b1b3b4°b4b6y10	1068.54	30.030	5173	2	534.78	8.00

P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	5		GVDVVAYANQDLIYSDLTAGR	155	21	3	14.38	b6b14y17	2240.13	73.378	4299	3	747.38	2.51
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	6	Carbamidomethyl+C(15)	GEFIGFDIDLGEMCK	45	16	5	42.57	b10b11y10y13y15	1844.85	79.817	34516	3	615.62	16.81
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	7		YFGDGTGVGLR	211	11	5	49.14	b3b9b10y7y9	1141.56	56.564	22005	2	571.29	-0.21
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	8		QQEIAFSDK	99	9	6	46.1	b5*b5b7y3y5°y5	1065.54	80.765	5984	2	533.28	21.08
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	9		GSPIQPTLESLK	120	12	3	23.03	b4y4y8	1269.70	62.476	1681	2	635.36	-0.77
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	10		GSPIQPTLESKKGK	120	14	3	19.98	b6y9y12	1454.82	54.473	20965	2	727.92	1.51
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	11		ALTELQDGTYDK	234	13	3	21.36	b12y5y11	1509.76	39.501	13568	2	755.38	3.56
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	12		QPAGKEYAFAGPSVK	193	15	3	18.81	b12y9y12	1549.81	75.287	2903	2	775.41	5.75
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	13		IGTDTTYAPFSSKDAK	29	16	5	36.71	b6b12y7y8y10	1701.83	113.549	1700	2	851.42	0.50
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	14	Phosphoryl STY(5)	IGTDTTYAPFSSKDAK	29	16	4	35.2	y9°y9y10y11	1781.81	89.617	2847	2	891.41	10.07
Q8ZRP4 DAPD_SALTY 2	1		EAVNQVISLLDSGALR	28	16	11	65.17	b2b4*b4b6°b6b12y4y5y9y10y16	1684.93	92.663	47496	2	842.97	3.69
Q8ZRP4 DAPD_SALTY 2	2		MQQLQNVIAFER	0	14	12	76.09	b3b4y1y7y9y10°y10y11°y11y12*y12y14	1706.86	86.533	44567	2	853.93	5.36
Q8ZRP4 DAPD_SALTY 2	3		INDNQVIDGAESR	68	13	8	79.45	y1y5y6y7y9y10y11y13	1430.69	41.887	21013	2	715.85	2.56
Q8ZRP4 DAPD_SALTY 2	4		FADYDEAR	89	8	5	50.49	b4y2y5y6y7	986.42	34.995	13513	2	493.71	-3.16
Q8ZRP4 DAPD_SALTY 2	5		YFDK	81	4	1	13.16	y3	572.28	116.036	1588	1	572.28	11.52
Q8ZRP4 DAPD_SALTY 2	6		IYDRETGEVHYGR	213	13	4	30.7	b5b12y9y11	1594.78	58.069	13877	3	532.27	12.55
Q8ZRP4 DAPD_SALTY 2	7		YFDKVPMK	81	8	4	36.96	b4°b4b7y3	1027.52	43.383	13633	2	514.26	-11.17
Q8ZRP4 DAPD_SALTY 2	8		RADITPANVDTVTR	14	14	3	19.98	b10b12y8	1528.83	99.476	10413	2	764.92	13.73
Q8ZRP4 DAPD_SALTY 2	9		VPAGSVVVSNGNLPKDGK	226	18	6	25.72	b6b9b11*b11y6°y6	1710.94	44.319	1959	2	855.97	-1.43
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	1	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	9	26.89	b2°b2b5b8y1y11°y11y12y24	2589.31	83.418	49955	3	863.78	2.07
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	2		SATPAQAQAVHK	176	12	21	112.68	b2b3°b3b5°b5b12y1y2y4y5*y5y6y7*y7y8*y8y9*y9y10°y10y12	1208.63	19.807	42529	2	604.82	-7.68
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	3	Carbamidomethyl+C(9)	KELTGVAGCDVAIAPPEMYIDLAK	27	24	4	17.6	b10b16y9y13	2561.31	103.587	3806	3	854.44	4.77
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	4		TQGAAAFEGAVIA YEPVWAIGTGK	152	24	7	31.71	b4b8b15*b15y4y9y11	2407.26	94.351	39042	2	1204.14	14.40
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	5	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	3	13.49	b7y3y10	2433.23	88.978	8209	2	1217.12	12.14
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	6		DIGAQYIIIGHSER	84	14	5	19.98	b11*b11y5°y5y9	1571.83	65.436	4922	2	786.42	7.46
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	7		AAAGSHIMLGAQNVDNLSGAFTGETSAEMLK	52	32	8	29.97	b5b8b9y7°y7y11°y11y12y1	3204.54	136.470	1641	4	801.89	-7.69

Q8ZKP7 TPIS_SALTY Triosephohate isomerase	8	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAENEAGKTEE VCAR	117	28	16	141.39	b5°b5b12y3y4y5y6y9y10y12y16y20y21y23y24y26	3090.45	73.031	105735	3	1030.82	4.82
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	9	Oxidation+M()	AAAGSHIMLGAQNVDLNLSGAFT GETSAEMLK	52	32	3	22.31	b9b10y10	3220.57	85.792	9349	4	805.90	4.02
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	10		TPAQAAVHK	178	10	6	30.23	b3°b3b7°b7b8°b8	1050.56	19.809	17055	2	525.78	-7.55
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	11		PAQAAVHK	179	9	8	62.52	b3°b3b4°b4b5b6°b6b8	949.51	19.805	14025	2	475.26	-10.28
Q7CR46 IRAP_SALTY Anti-adaptor protein iraP	1		QVEGALEGVKPDASVPDHDTELL R	50	24	10	54.33	b9°b9b24y3y7°y7y9y12y14y19	2575.28	60.392	39286	4	644.58	-7.87
Q7CR46 IRAP_SALTY Anti-adaptor protein iraP	2		NMAQNEQEMLIR	38	12	11	67.61	b2°b2b3y5y8°y8y9°y9y10y11y12	1476.70	56.683	32442	2	738.85	2.81
Q7CR46 IRAP_SALTY Anti-adaptor protein iraP	3		QVEGALEGVKPDASVPDHDTELL RQYVK	50	28	5	12.01	b5°b5b14y12°y12	3093.57	103.292	10081	4	774.15	-3.95
Q8ZLD7 UA_SALTY Universal stress protein A	1		AVSMARPYNAK	22	11	14	56.92	b2b9°b9b10y1y2y5°y5y7°y7y9°y9°y9y11	1207.62	31.625	81407	2	604.31	-4.04
Q8ZLD7 UA_SALTY Universal stress protein A	2		QLINTVHVDMLIVPLRDEEE	124	20	15	68.51	b2°b2b10°b10b11°b11y1y6y7y8y9°y9y12y20°y20	2363.22	87.073	80525	3	788.41	-2.17
Q8ZLD7 UA_SALTY Universal stress protein A	3		ISEETHHALTELSTNAGYPITETLS GSGDLGQVLVDAIK	61	39	8	12.49	b1b6°b6b12°b12y3y14y39	4067.05	98.386	79020	4	1017.52	0.00
Q8ZLD7 UA_SALTY Universal stress protein A	4		ISEETHHALTELSTNAGYPITETLS GSGDLGQVLVDAIKK	61	40	7	21.34	b9b15b17b22y2y4y22	4195.16	94.714	29756	4	1049.55	5.00
Q8ZLD7 UA_SALTY Universal stress protein A	5		ISLIHVDVNYSDLYTGLIDVNLGD MQKR	33	28	7	17.94	b13°b13y1y6y12°y12y18	3191.63	107.038	10344	4	798.66	-2.37
Q8ZLD7 UA_SALTY Universal stress protein A	6	Carbamidomethyl+C(9)	KYDMDLVVCGHHQDFWSK	100	18	3	16.16	b7b12y3	2265.05	68.450	7406	3	755.69	10.89
Q8ZLD7 UA_SALTY Universal stress protein A	7		SMARPYNAK	24	9	4	32.07	b4°b4b6b7	1037.51	31.620	90501	2	519.26	-5.29
Q8ZLD7 UA_SALTY Universal stress protein A	8		VSMARPYNAK	23	10	3	8.01	b8°b8°b8	1136.58	31.621	8520	2	568.79	-8.27
Q8ZLD7 UA_SALTY Universal stress protein A	9		LINTVHVDMLIVPLRDEEE	125	19	0	5.65		2235.14	87.037	2657	3	745.72	-11.80
Q8ZLD7 UA_SALTY Universal stress protein A	10		AVSMARPYNAK	22	11	0	2.26		1189.60	31.611	5381	3	397.21	-6.67
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	22	119.17	b5b8°b8b9°b9b11°b11b12°b12b13°b13y2y4y6°y6y7y9y10y11y12°y12y23	2379.24	65.332	98691	3	793.75	-0.62
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2		AQAFTLVAK	24	9	7	66.17	b4y2y3y4y6y7y9	948.54	53.852	61506	2	474.77	-9.65
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	7	27.48	b2b3y10y13°y13y14y18	1919.02	85.912	50534	2	960.01	7.44
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	11	68.78	b2b3b11b12°b12y4y6y12y14y15y17	1837.96	86.648	37432	2	919.49	8.90
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		DLSDVSLSQYAGK	33	13	10	56.22	b2b5b7°b7y1y5y9y11y12y13	1382.69	60.123	34106	2	691.85	5.39
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		NYGVEIVDGPLK	116	12	6	38.32	b2b3y4y8y10y12	1303.69	65.551	13306	2	652.35	-3.18
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7	Carbamidomethyl+C(15)	FNQLATEVENTVVLCSADLPFA QSR	67	26	3	12.5	b5y4y6	2908.43	110.704	2309	4	727.86	-5.54
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8		AVIVLDENDNVIFSQLVDEITHEPD YDAALNVLKA	133	35	27	230.2	b3b4b5b6b7b10b11°b11b16b18b22y3y5y6y7y8y12y13°y13y18y20y22y24y28y29y30y31	3883.00	120.693	78267	3	1295.00	7.80
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9		NNEFLKNYGVEIVDGPLK	110	18	4	33.47	b3b4b7b10	2049.05	76.889	12168	3	683.69	-6.31

Q8ZP65 TPX_SALTY Probable thiol peroxidase	10	Phosphoryl STY(13)	MSQTVHFQGNPVTVANVIPQAGS K	0	24	5	13.12	b5*b5b12*b12y12	2590.21	98.520	8394	4	648.31	-9.80
Q8ZP65 TPX_SALTY Probable thiol peroxidase	11	Oxidation+M(1)	MSQTVHFQGNPVTVANVIPQAGS K	0	24	3	19.43	y7y9y13	2526.28	76.096	5748	3	842.76	0.87
P05989 ILVC_SALTY Ketol-acid reductoisomerase	1		GFGVPTLIAVHPENDPQEGEMAIA K	167	25	11	57.23	b2b3b4y1y2y7y8y9y14y21 y25	2548.28	77.867	41539	3	850.10	-0.77
P05989 ILVC_SALTY Ketol-acid reductoisomerase	2		AYALSEQLKEIMAPLFQK	284	18	6	25.72	b2b3y3y5y16y18	2080.10	103.721	30337	3	694.04	-7.63
P05989 ILVC_SALTY Ketol-acid reductoisomerase	3		ANYFNTLNL	1	10	10	76.1	b2*b2b3y3y4y6y7y8y10*y 10	1225.63	68.528	28692	2	613.32	-2.49
P05989 ILVC_SALTY Ketol-acid reductoisomerase	4		DGAALGYSHGFNIVEVGEQIR	123	21	6	21.02	b2b3b11b14*b14y21	2232.11	92.125	14145	2	1116.56	4.05
P05989 ILVC_SALTY Ketol-acid reductoisomerase	5	Carbamidomethyl+C(6)	VVIVGCGAQGLNQLGNMR	39	18	4	16.16	b1b3y7y11	1885.99	72.691	6761	3	629.33	6.93
P05989 ILVC_SALTY Ketol-acid reductoisomerase	6		FMGRDEFADGASYLQGK	21	17	3	25.58	y3y4y15	1891.86	51.640	4911	3	631.29	-2.77
P05989 ILVC_SALTY Ketol-acid reductoisomerase	7	Carbamidomethyl+C(6)	VVIVGCGAQGLNQLGNMRDSSL DISYALR	39	29	4	25.53	b9b10y8y14	3076.54	94.972	2979	3	1026.19	-7.62
P05989 ILVC_SALTY Ketol-acid reductoisomerase	8		DGAALGYSHGFNIVEVGEQIRK	123	22	4	25.01	b4b5b13y8	2360.17	73.015	1666	4	590.80	-13.45
P05989 ILVC_SALTY Ketol-acid reductoisomerase	9	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21)	SDLMGEQTILCGMLQAGSLLCFD K	215	24	5	17.6	b4b12y12y14*y14	2687.28	93.129	26509	3	896.43	10.90
P05989 ILVC_SALTY Ketol-acid reductoisomerase	10		TAFETAPQYEGK	336	12	3	23.03	b6b10y10	1341.62	35.949	2391	3	447.88	-5.55
P05989 ILVC_SALTY Ketol-acid reductoisomerase	11		QGGITLMMDR	266	10	3	27.71	b5b9y4	1121.54	35.020	2267	2	561.27	-2.83
P05989 ILVC_SALTY Ketol-acid reductoisomerase	12		AGVLESSFVAEVK	202	13	4	30.7	b5b10y7y9	1335.69	50.519	2193	2	668.35	-18.55
P05989 ILVC_SALTY Ketol-acid reductoisomerase	13		AWAAATGGHR	192	10	4	40.46	b3b7y4y8	997.49	68.389	2173	1	997.49	-3.12
P05989 ILVC_SALTY Ketol-acid reductoisomerase	14		DEFADGASYLQGK	25	13	3	21.36	b7b10y10	1400.66	28.658	1533	2	700.84	21.88
P05989 ILVC_SALTY Ketol-acid reductoisomerase	15		VGTYEELIPQADLVVNLTDPKQHS DVVR	88	28	4	25.74	b8b14y4y5	3135.59	99.481	36252	3	1045.87	-14.17
P05989 ILVC_SALTY Ketol-acid reductoisomerase	16	Carbamidomethyl+C(9)	QQLAQLGKCR	11	10	3	34.7	y4y6y7	1201.63	39.584	14311	3	401.21	-14.02
P05989 ILVC_SALTY Ketol-acid reductoisomerase	17		LIQFGWETITEALKQGGITLMMDR	252	24	9	59.73	b3b6b7y3y4y5*y5y10y21	2751.42	119.452	7302	3	917.81	1.33
P05989 ILVC_SALTY Ketol-acid reductoisomerase	18	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21)	SDLMGEQTILCGMLQAGSLLCFD KLVAEGTDPAYAEK	215	37	6	24.27	b3y6*y6y8y9y12	4031.96	118.582	6495	3	1344.66	12.41
P05989 ILVC_SALTY Ketol-acid reductoisomerase	19		EETGKTAFETAPQYEGK	331	17	4	34.64	y6y8y9y11	1885.89	81.455	4166	3	629.30	4.92
P05989 ILVC_SALTY Ketol-acid reductoisomerase	20	Carbamidomethyl+C(11)	DITVVMVAPKCPGTEVR	145	17	4	16.93	b3*b3b9y8	1871.97	70.365	1661	3	624.66	-0.46
P05989 ILVC_SALTY Ketol-acid reductoisomerase	21	Phosphoryl STY()	SVQPLMKDGAALGYSHGFNIVEV GEQIR	116	28	3	18.03	b8b13b15	3095.53	80.255	6782	3	1032.51	10.65
P05989 ILVC_SALTY Ketol-acid reductoisomerase	22	Phosphoryl STY(6)	GFGVPTLIAVHPENDPQEGEMAIA K	167	25	9	54.61	b4b5b10*b10b11*b11y10y 11*y11	2628.25	136.429	6035	3	876.75	2.42
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	1		VQALADAAR	102	9	12	76.69	b2b3*b3y3y4*y4y5*y5y7y8 *y8y9	914.49	31.978	102114	2	457.75	-13.28
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	2		GIKDVSFDR	85	9	3	39.1	y3y4y6	1036.53	41.978	22857	2	518.77	-8.83
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	3		HIYAQVIAPNGSEVLVAASTVEK	33	23	5	29.31	b4b12b13y7y14	2396.26	63.965	163557	4	599.82	-9.88
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	14	116.63	b2b3y5*y5y6y7y9y10y11y1 2y14y17y19y21	2215.16	75.716	59677	3	739.06	-6.28

IQ56073 DNAK_SALTY Chaperone protein dnaK	2		MQELAQVSQK	587	10	7	49.03	b2b3y3°y3y6y8y10	1161.59	37.776	49446	2	581.30	-1.05
IQ56073 DNAK_SALTY Chaperone protein dnaK	3		QAVTNPQNTLFAIKR	56	15	5	53.65	y4y5y6y8y10	1700.92	59.406	33782	3	567.65	-12.56
IQ56073 DNAK_SALTY Chaperone protein dnaK	4		ASSGLNEEEIQK	502	12	6	45.98	y5y7*y7y9y10y12	1304.62	35.373	21886	2	652.82	-6.08
IQ56073 DNAK_SALTY Chaperone protein dnaK	5		SLGQFNLDGINPAPR	452	15	7	30.42	b10y4y8y10°y10*y10y15	1598.84	72.714	20647	2	799.92	7.86
IQ56073 DNAK_SALTY Chaperone protein dnaK	6		TAEDYLGEPVTEAVITVPAYFNDAQR	125	26	6	33.91	b5b7b9y5y6y9	2869.42	94.277	7569	2	1435.21	11.15
IQ56073 DNAK_SALTY Chaperone protein dnaK	7		IELSSAQQTVDNLPYITADATGPK	270	24	3	13.12	b9b11y5	2532.29	72.452	6065	3	844.77	4.34
IQ56073 DNAK_SALTY Chaperone protein dnaK	8		TFEVLATNGDTHLGGEDFDTR	214	21	4	14.38	b3b5y10y21	2295.05	65.797	5705	4	574.52	-1.60
IQ56073 DNAK_SALTY Chaperone protein dnaK	9		VAEFFGKEPR	352	10	6	34.7	b1b5°b5b7b8°b8	1179.60	44.787	2822	2	590.30	-11.28
IQ56073 DNAK_SALTY Chaperone protein dnaK	10		TIAVYDLGGGTFDISIIEIDVDGEK	188	26	6	32.44	b6b11y3y4y7y11	2769.33	119.898	32841	3	923.78	-15.43
IQ56073 DNAK_SALTY Chaperone protein dnaK	11		LMEIAQQQHAQQAGSADASANNAK	597	25	3	12.8	b8y6y9	2610.22	93.489	16960	3	870.74	-5.71
IQ56073 DNAK_SALTY Chaperone protein dnaK	12		GMPQIEVTFDIDADGILHVS AK	467	22	5	30.16	b5b7b8b13*b13	2356.14	95.247	9847	4	589.79	-19.89
IQ56073 DNAK_SALTY Chaperone protein dnaK	13		FQDEEVQR	76	8	3	36.96	b3b7y6	1050.46	74.092	2058	2	525.73	-22.08
IQ56073 DNAK_SALTY Chaperone protein dnaK	14		HSQVFSTAEDNQSAVTIHVLQGER	421	24	3	23.41	y3y4y7	2653.35	82.712	1576	2	1327.18	20.89
IQ56073 DNAK_SALTY Chaperone protein dnaK	15	Carbamidomethyl+C(15)	MGKIIGIDLGTNSCVAIMDGTQAR	0	25	5	12.8	b21y6*y6y9*y9	2622.30	85.358	277426	3	874.77	-1.77
IQ56073 DNAK_SALTY Chaperone protein dnaK	16		AKIELSSAQQTVDNLPYITADATGPK	268	26	4	18.65	y6y8y13*y13	2731.40	99.413	32026	3	911.14	-3.84
IQ56073 DNAK_SALTY Chaperone protein dnaK	17		SIEPLKVALQDAGLSVSDINDVILVGGQTR	315	30	4	22.53	b3y4y5y7	3107.70	107.344	22789	3	1036.57	2.12
IQ56073 DNAK_SALTY Chaperone protein dnaK	18		LMEIAQQQHAQQAGSADASANNAKDDDVVD AEFEEVK	597	38	6	16.62	b5°b5b9b11y4y10	4100.92	89.973	14295	5	820.99	10.48
IQ56073 DNAK_SALTY Chaperone protein dnaK	19		LPADDKTAIESALNALETALK	556	21	5	50.52	b11b12b13b14y3	2184.16	74.727	8809	3	728.72	-7.60
IQ56073 DNAK_SALTY Chaperone protein dnaK	20		ASDNKSLGQFNLDGINPAPR	447	20	6	20.6	b8b12*b12y11°y11y19	2114.06	69.743	6477	3	705.36	0.46
IQ56073 DNAK_SALTY Chaperone protein dnaK	21		DQGIDLRNDPLAMQR	246	15	5	26.89	b5b6°b6b9*b9	1741.86	48.273	3017	2	871.43	-1.61
IQ56073 DNAK_SALTY Chaperone protein dnaK	22		IIGADNGDAWLDVKGQK	92	17	4	25.58	b7b8b10*b10	1799.94	136.259	1896	2	900.47	5.09
IQ56073 DNAK_SALTY Chaperone protein dnaK	23	Phosphoryl STY(15)	IELSSAQQTVDNLPYITADATGPK	270	24	12	42.71	b9°b9*b9b11°b11*b11b12°b12b13°b13y9y14	2612.22	51.390	16488	3	871.41	-8.04
IP60446 RL3_SALTY 50S ribosomal protein L3	1		IFTEDGVSIPTVTVIEVEANR	13	20	4	9.2	b5y4°y4y20	2188.17	88.856	33508	2	1094.59	8.03
IP60446 RL3_SALTY 50S ribosomal protein L3	2		VTQVKDLANDGYR	33	13	8	80.94	b4y6y7y8y9°y9y10y12	1478.74	40.319	13234	3	493.59	-11.97
IP60446 RL3_SALTY 50S ribosomal protein L3	3		NLLLVK	184	6	4	40.98	b3*b3y3y4	699.47	56.826	17091	1	699.47	-7.85
IP60446 RL3_SALTY 50S ribosomal protein L3	4		GLWEFR	77	6	1	13.91	y4	807.42	39.249	14897	2	404.22	12.02
IP60446 RL3_SALTY 50S ribosomal protein L3	5		VGMTR	8	5	1	13.53	b4	563.30	50.550	10031	1	563.30	1.63
IP60446 RL3_SALTY 50S ribosomal protein L3	6		WNFR	124	4	1	13.16	y3	622.31	71.631	8109	1	622.31	-6.28
IP60446 RL3_SALTY 50S ribosomal protein L3	7		VDAER	179	5	2	27.07	b3b4	589.30	62.497	5236	1	589.30	3.52

[P60446]RL3_SALTY 50S ribosomal protein L3	8		VTVQSLDVVR	169	10	4	44.26	b7y3y4y5	1115.64	57.251	2420	1	1115.64	-2.30
[P60446]RL3_SALTY 50S ribosomal protein L3	9		TQDATHGNSLSHR	128	13	7	35.11	b7°b7y7*y7y9y11°y11	1423.67	112.989	1776	2	712.34	2.74
[P60446]RL3_SALTY 50S ribosomal protein L3	10		LAEGEEYTVGQSISVELFADV K	83	22	5	44.74	b3b4b5b12b14	2384.21	136.458	1744	3	795.41	7.99
[P60446]RL3_SALTY 50S ribosomal protein L3	11	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	9	79.64	b5b7b13y5y6y7y8y13y16	1809.97	56.937	83417	3	603.99	-10.66
[P60446]RL3_SALTY 50S ribosomal protein L3	12		IFTEDGV SIPVTVIEVEANRVTQVK	13	25	6	23.76	b5b7°b7y16y18y20	2743.49	95.604	42675	3	915.17	1.51
[P60446]RL3_SALTY 50S ribosomal protein L3	13		ANRVTKPEAGHFAK	56	14	3	19.98	b4b12y9	1525.82	54.730	2608	3	509.28	-3.76
[P60446]RL3_SALTY 50S ribosomal protein L3	14		WNFRTQDATHGNSLSHR	124	17	5	23.92	b5y10°y10y11°y11	2026.98	105.388	2121	4	507.50	8.13
[P0A1V4]KAD_SALTY Adenylate kinase	1		YGIPQISTGDMLR	23	13	12	59.89	b2y1y3y5y6y7°y7y10°y10*y10y13*y13	1450.74	73.354	40686	2	725.87	2.02
[P0A1V4]KAD_SALTY Adenylate kinase	2		LVEYHQMTAPLIGYYQK	167	17	13	27.07	b1b2b7°b7b9°b9b11y1y2*y2y6*y11y17	2054.04	69.808	37404	3	685.35	-1.43
[P0A1V4]KAD_SALTY Adenylate kinase	3		NGFLLDGFPR	78	10	4	44.26	b7y4y5y6	1135.59	81.161	26550	2	568.30	-2.26
[P0A1V4]KAD_SALTY Adenylate kinase	4		IILLGAPGAGK	2	11	5	36.84	b2y2y5y7y9	1009.63	61.824	18904	2	505.32	-5.56
[P0A1V4]KAD_SALTY Adenylate kinase	5		TIPQADAMKEAGIVVDYVLEFDV PDELIVDR	88	31	4	11.47	b9b14y1y8	3460.78	123.155	9693	3	1154.26	6.49
[P0A1V4]KAD_SALTY Adenylate kinase	6		VDGTQAVADV R	195	11	3	25.08	b3y8y10	1130.58	37.276	64964	2	565.79	-2.05
[P0A1V4]KAD_SALTY Adenylate kinase	7		FNPPK	136	5	3	27.07	b3y4*y4	602.32	56.516	49799	1	602.32	-9.53
[P0A1V4]KAD_SALTY Adenylate kinase	8		EAGIVVDYVLEFDV PDELIVDR	97	22	3	13.91	b14y10y12	2505.22	92.335	40214	3	835.75	-21.54
[P0A1V4]KAD_SALTY Adenylate kinase	9		GTQAQFIMEK	13	10	6	29.47	b3*b3b4°b4°b4y9	1152.58	51.307	1511	2	576.79	3.71
[P0A1V4]KAD_SALTY Adenylate kinase	10		IILLGAPGAGKGTQAQFIMEK	2	21	5	39.33	b3b4y3y4y17	2143.19	73.301	34726	3	715.07	-3.42
[P0A1V4]KAD_SALTY Adenylate kinase	11		AAVKS GSELGK	36	11	3	36.84	y5y6y7	1046.58	49.627	25203	2	523.79	-3.15
[P0A1V4]KAD_SALTY Adenylate kinase	12		VEGKDDVTGEDLTTR	141	15	5	18.81	b8b13°b13y11°y11	1634.79	79.881	16176	2	817.90	5.00
[P0A1V4]KAD_SALTY Adenylate kinase	13		DIMDAGKLVTD ELVIALVK	50	19	7	71.09	b4b8y3y4y5y6y7	2043.12	116.625	13953	3	681.71	-10.46
[P0A1V4]KAD_SALTY Adenylate kinase	14		GTQAQFIMEKYGIPQISTGDMLR	13	23	3	13.49	b8b11y12	2584.26	77.491	12775	3	862.09	-10.30
[P0A1V4]KAD_SALTY Adenylate kinase	15		LVEYHQMTAPLIGYYQKEAEAGN TK	167	25	7	28.43	b8°b8y4*y4y6y12y17	2854.37	97.963	6873	3	952.13	-11.97
[P0A1V4]KAD_SALTY Adenylate kinase	16	Oxidation+M(7)	LVEYHQMTAPLIGYYQKEAEAGN TK	167	25	5	23.8	b17y8y12°y12y13	2870.37	91.581	3211	3	957.46	-10.63
[Q56109]NRDI_SALTY Protein nrdI	1		IQVDEPYILV VPSYGGGGMAGAV PR	35	25	7	33.31	b13b21y8y13y15y16y25	2545.29	92.195	50790	3	849.10	-6.91
[Q56109]NRDI_SALTY Protein nrdI	2		FELMG TQRDIDNVR	108	14	7	28.58	b6b10°b10y4°y4y10y14	1693.84	68.410	14094	3	565.28	2.81
[Q56109]NRDI_SALTY Protein nrdI	3		SALVYFSSSSENTHR	1	15	5	52.86	b8b9y4y5y6	1684.80	60.120	4629	3	562.27	6.23
[Q56109]NRDI_SALTY Protein nrdI	4		FELMG TQRDIDNVR	108	14	3	19.98	b7y6y11	1693.84	75.591	2125	2	847.42	1.73
[Q56109]NRDI_SALTY Protein nrdI	5	Carbamidomethyl+C(16)	GVIASGNRNF GDAWGACGDVIAQ K	76	24	3	13.12	b11y12y14	2463.15	92.714	1849	4	616.54	-12.29
[P14845]CARA_SALTY Carbamoyl-phosphate synthase small chain	1	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLALASGAK	257	25	20	148.73	b2b3°b3b4b5b6b25y1y3y4y5y6y7y14°y14y19y20y21y23y25	2684.45	128.243	37977	3	895.49	-0.64

P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	2		AFPGLNGMDLAKEVTTAETYSR	148	21	4	14.38	b10b12y11°y11	2284.15	82.400	9396	3	762.05	8.23
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	3		SALLVLEDGTQFHGR	3	15	6	37.69	b1b3b8b9b11*b11	1642.85	62.010	3907	3	548.29	-0.67
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	4		TDKPAFSFQGHPEASPGPHDAAPLFDHFIELIEQYR	342	36	4	24.66	b3b5y3y4	4064.91	106.850	15760	5	813.79	-11.89
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	5		NVVMITAQNHGFAVDEDSL PANLR	302	24	5	29.79	b6b10b11b15y3	2611.25	101.605	2263	4	653.57	-16.36
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	6		SEDDLPPHFVVAYDFGAK	185	17	3	24.33	y9y11y13	1909.90	82.241	1682	3	637.30	1.53
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	7		SLFDGTLQGIHR	330	12	4	27.01	b7°b7b8y5	1343.71	59.208	1511	3	448.58	6.09
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	8	Carbamidomethyl+C(8)	EKGAQNGCIIAGDSPDAK	123	18	4	25.72	b13y3y10y16	1830.85	64.671	2077	4	458.47	-6.20
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	9	Oxidation+M(8)	AFPGLNGMDLAKEVTTAETYSR	148	21	4	25.52	b11y5y6y15	2300.14	88.669	23790	3	767.39	7.64
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	10	Oxidation+M(8)	AFPGLNGMDLAK	148	12	3	23.03	b4b7y8	1249.63	35.466	15118	3	417.22	7.52
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	11	Oxidation+M(13)	FGHHGGNHPVKMDMR	287	15	4	26.78	b5b12y3y5	1719.75	58.933	2263	2	860.38	-14.83
P66738 RRF_SALTY Ribosome-recycling factor	1		ASPSLLDGIVVEYYGTPTPLR	31	21	12	71.25	b8°b8y2y5y7y10y11°y11y12y15y19y21	2248.22	93.975	46386	2	1124.61	14.55
P66738 RRF_SALTY Ribosome-recycling factor	2		SMGPAVEK	72	8	6	52.26	b2b6b7y3y6y8	818.41	27.363	9759	2	409.71	0.82
P66738 RRF_SALTY Ribosome-recycling factor	3		AIMASDLGLNPSSAGTDIR	80	19	5	15.49	b5b11°b11y13°y13	1888.98	86.272	28023	2	945.00	21.26
P66738 RRF_SALTY Ribosome-recycling factor	4		MISDIR	0	6	1	13.91	y5	734.40	42.975	10303	2	367.70	12.22
P66738 RRF_SALTY Ribosome-recycling factor	5		AIMASDLGLNPSSAGTDIRVPLPPLTEER	80	29	7	54.82	b5b6y6y7y12y20y21	3020.59	87.054	60505	3	1007.53	4.36
P66738 RRF_SALTY Ribosome-recycling factor	6		IVRGAEQAR	115	10	5	57	b5b6b7y3y5	1128.60	16.452	9791	2	564.80	-11.36
P66738 RRF_SALTY Ribosome-recycling factor	7	Carbamidomethyl+C(1)	CVEAFKTIQISK	15	11	3	32.07	b3b7b8	1310.69	49.638	4392	3	437.57	12.20
P66738 RRF_SALTY Ribosome-recycling factor	8		INVFDRSMGPAVEK	66	14	5	25.42	b11*b11b12y8°y8	1562.81	58.977	3067	3	521.61	4.22
P66738 RRF_SALTY Ribosome-recycling factor	9	Oxidation+M(13)	VDAALADKEAELMQF	170	15	3	24.83	b12y13y14	1666.79	136.634	2249	1	1666.79	-7.91
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	1		NIIDSGEIGQPLMVHGR	137	17	8	37.38	b12°b12y7y9y11*y11y12°y12	1835.97	71.169	8187	2	918.49	14.69
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	2		TPQAIYETLIHEIDVMHWLLNEDYK	165	25	4	12.8	b8*b8b19y8	3071.52	106.653	2967	4	768.64	0.95
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	3	Carbamidomethyl+C(25)	LNAGLPPAGPTSWDGYLAAVTADACVK	289	27	5	27.9	b13y7y9y10y13	2715.31	108.013	2622	3	905.78	-12.41
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	4	Carbamidomethyl+C(4); Carbamidomethyl+C(15)	YVFCEKPLAVTAADCQR	91	17	3	25.58	b6b7b9	2027.94	53.602	2215	3	676.65	-11.26
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	5		FIDAYDIEFQDFDR	274	15	5	30.42	b4b7b8°b8y5	1940.91	67.141	18839	2	970.96	21.95
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	6		HYNASTVPEYK	154	11	6	37.82	b6b7*b7b10y7°y7	1308.60	102.775	2941	3	436.87	-16.04
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	7	Carbamidomethyl+C(14)	LANTVSGVEVVAVCDIVAGR	20	20	4	14.9	b4b14°b14y7	2029.07	73.125	2193	3	677.03	-0.42
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	8		AAKYSTDILVDWK	259	13	4	30.6	b3b8°b8b11	1509.77	114.144	3151	2	755.39	-14.39
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	9	Carbamidomethyl+C(14);Phosphoryl STY(6)	LANTVSGVEVVAVCDIVAGR	20	20	7	49.07	b8b14y7y8y14°y14y15_H3PO4 y15_HPO3 y15	2109.00	97.428	3802	3	703.67	-12.97

Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	10	Oxidation+M(8)	AGIVGIGMIGSDHLR	4	15	6	38.39	b5b14y5y6°y6y8	1511.82	99.519	10433	3	504.61	10.09
Q8ZK57 IOLG_SALTY Inositol 2-dehydrogenase	11	Oxidation+M(13)	NIIDSGEIGQPLMVHGR	137	17	3	16.93	b11y7y12	1851.91	71.325	8277	3	617.98	-14.30
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	1		ELLKEAGYPDGFSTTLWSSHNHSTAQK	335	27	7	49.74	b8°b8y7y8°y8y9y10	3004.42	66.525	36944	4	751.86	-8.61
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	2		NLTGFWIMPDTGFSDDADLK	491	21	8	27.87	b4°b4b8y2y9y11y13y21	2390.13	107.384	32636	2	1195.57	10.93
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	3		DIGFHPVGTGPYQLETWNQTDVFK	176	24	10	45.3	b9°b9b10b14b20y6y10y11°y11y24	2749.34	83.827	25578	3	917.12	5.86
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	4		FQDGADFNAAAVK	97	13	6	44.14	b2y5y9y10y11y13	1353.65	50.367	24335	2	677.33	2.16
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	5		EALNYAINR	286	9	4	39.1	y5y6y7y9	1063.55	45.736	21805	2	532.28	-6.77
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	6		AAMLQTGEAQFAFPIPYEAALLAK	229	25	4	12.8	b5b11y10y25	2679.40	97.789	20828	3	893.80	5.38
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	7		ITAMDAGQR	379	9	4	58.65	y4y5y7y8	962.47	29.779	16831	2	481.74	-6.34
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	8		YGKDIGFHPVGTGPYQLETWNQTDVFK	173	27	10	41.34	b4b8b11b19y1y2y7y8*y8y11	3097.48	76.918	14950	4	775.13	-6.62
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	9		NLELVASPSIMQR	256	13	6	54.66	b3y5y6y7y8y13	1457.78	69.319	11322	2	729.40	3.18
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	10		LDSITWRPVTDNNTR	214	15	4	42.46	y4y7y11y13	1787.93	57.508	5602	2	894.47	13.04
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	11		SFYQGLFLGLDKDMK	56	14	6	19.98	b8b11°b11*b11y8°y8	1648.80	69.859	5469	2	824.91	0.00
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	12		FAGYWQQGLPK	203	11	5	32.07	b3b9b10*b10b11	1294.68	53.054	3983	2	647.84	14.52
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	13		ASNPDNHLKR	115	10	6	37.71	y1y2y5y6y7y10	1151.58	15.006	3749	2	576.30	-6.25
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	14		TEVVDPATVK	134	10	3	42.49	y3y5y8	1058.57	39.698	25876	2	529.79	-5.65
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	15		VLQFTQQQLAQIGVK	362	15	6	26.78	b5°b5b7*b7y4y12	1700.98	72.909	16650	2	850.99	4.88
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	16		QVDSDLAAALK	442	11	4	32.07	b3b4b8°b8	1130.60	51.296	8499	2	565.80	-4.53
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	17		YISMNVTQKPFDNPK	269	15	6	30.42	b4°b4b8°b8b11y6	1781.93	69.180	4691	2	891.47	21.92
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	18		NVLAEGYTVSDDGLTYTITLR	72	21	4	14.38	b7°b7b10y11	2301.12	80.236	4084	4	576.03	-18.99
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	19		EAGYPDGFSTTLWSSHNHSTAQK	339	23	4	20.88	b12y3y6y10	2521.18	70.318	1761	3	841.07	16.85
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	20		TQFITHK	1	7	5	51.88	b3*b3b4b5y5	874.47	39.669	1720	2	437.74	-10.82
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	21		FAGYWQQGLPKLDSITWRPVTDNNTR	203	26	4	22.28	b9y5°y5y6	3063.53	83.549	73799	5	613.51	-3.51
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	22		ITLKQPFSAFINILAHPATAMISPQALEK	144	29	5	27.17	y4y6y7*y7y11	3150.70	110.345	38375	4	788.43	-10.69
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	23		SFYQGLFLGLDKDMK	56	14	4	45.76	y7y8y10y11	1648.78	80.377	37481	3	550.27	-13.77
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	24		NKNLELVASPSIMQR	254	15	5	38.82	b3°b3b4y6y7	1699.92	60.235	6114	2	850.47	5.03
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	25		VAFAGYATPATGVVPPSIAYAQSYPWPYDPAKAR	300	35	4	22.99	b4b6b11b15	3710.88	86.626	3296	3	1237.63	5.53
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	26		QGVKFDQGADFNAAAVK	93	17	5	27.07	b5b8b13*b13y11	1765.91	76.831	2506	3	589.31	12.79
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	27	Phosphoryl STY(7)	NVLAEGYTVSDDGLTYTITLR	72	21	6	22.83	b5°b5°b5b6°b6y3	2381.11	91.695	3612	4	596.03	-2.87

Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	28	Phosphoryl STY(8)	TEVVDPATVK	134	10	3	27.71	b3b7y4	1138.53	33.454	1553	2	569.77	-2.79
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	29	Oxidation+M(8)	NLTGFWIMPTDGFSDADLK	491	21	8	32.32	b4b8°b8°b8b10b11°b11y6	2406.11	136.433	4048	3	802.71	6.09
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	30		PDNHLKR	118	7	0	1.88		879.47	15.002	2061	2	440.24	-7.91
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	31		NPDNHLKR	117	8	0	1.88		993.51	15.008	1869	2	497.26	-11.55
P66764 METK_SALTY S-adenosylmethionine synthetase	1		SLQEAVMEEIHKPILSEWLNSTK	197	25	14	48.07	b2b5b9b11°b11b12b23y1y2y5°y5y10y13y25	2856.51	111.636	34044	3	952.84	2.31
P66764 METK_SALTY S-adenosylmethionine synthetase	2	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGRK	230	16	6	47.53	b8b14b15y6y8y11	1664.82	62.571	12599	3	555.61	-5.50
P66764 METK_SALTY S-adenosylmethionine synthetase	3		ADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHR	109	35	3	11.05	b5b11y5	3749.77	84.951	11282	4	938.20	4.69
P66764 METK_SALTY S-adenosylmethionine synthetase	4	Carbamidomethyl+C(1)	CEIQVSYAIGVAEPTSIMVETFGTEK	294	26	5	12.5	b4°b4b12y13y26	2859.38	94.439	7499	3	953.80	1.79
P66764 METK_SALTY S-adenosylmethionine synthetase	5		EFFDLRPYGLIQLDLLHPYKETAAAYGHFGR	331	32	6	25.04	b9b10°b10y7y9°y9	3810.91	113.817	3478	4	953.48	-8.65
P66764 METK_SALTY S-adenosylmethionine synthetase	6		QSPDINQGVDR	98	11	4	25.08	b3y5°y5y10	1228.58	43.756	7970	2	614.79	-13.41
P66764 METK_SALTY S-adenosylmethionine synthetase	7		TGMVLVGGEITTSAWVDIEEITR	47	23	3	19.9	b4b11b13	2477.28	111.703	2461	3	826.43	8.08
P66764 METK_SALTY S-adenosylmethionine synthetase	8	Carbamidomethyl+C(16)	EIGYVHSDMGFDANSCAVLSAIGK	74	24	3	22.42	b6b7y13	2541.16	62.623	1779	3	847.72	-6.24
P66764 METK_SALTY S-adenosylmethionine synthetase	9		ETAAYGHFGR	353	10	4	27.71	b4°b4b9y6	1108.53	109.788	1647	1	1108.53	11.34
P66764 METK_SALTY S-adenosylmethionine synthetase	10		MAKHLFTSESVSEGHDPK	0	18	3	16.16	b7b14y6	1999.95	102.418	51551	3	667.32	-0.31
P66764 METK_SALTY S-adenosylmethionine synthetase	11		HLFTSESVSEGHDPDKIADQISDAVLDAILQQDPK	3	34	3	11.13	b17y7y21	3703.86	78.273	29657	4	926.72	3.95
P66764 METK_SALTY S-adenosylmethionine synthetase	12		SAAYAARYVAK	273	11	5	49.14	b7b8b10y3y8	1170.64	44.204	20383	2	585.82	11.68
P66764 METK_SALTY S-adenosylmethionine synthetase	13		IIVDTYGGMARHGGGAFSGK	246	20	6	20.6	b8°b8b15°b15y7y11	1993.96	74.655	17291	3	665.33	-14.08
P66764 METK_SALTY S-adenosylmethionine synthetase	14		QSPDINQGVDRADPLEQGAGDQG LMFGYATNETDVLMPAPITYAHR	98	46	5	11.74	b4b9°b9y5y9	4959.38	88.896	16616	4	1240.60	10.14
P66764 METK_SALTY S-adenosylmethionine synthetase	15		ENFPWEKTDK	363	10	3	29.47	b9y5y6	1293.62	77.777	5844	2	647.31	4.15
P66764 METK_SALTY S-adenosylmethionine synthetase	16		SQVTFQYDDGKIVGIDAVVLSTQHAEDIDQK	166	31	3	11.47	b12y5y7	3419.65	114.806	2977	4	855.67	-14.71
P66764 METK_SALTY S-adenosylmethionine synthetase	17		AKHLFTSESVSEGHDPK	1	17	4	23.85	b9b12y7y13	1868.90	96.470	2258	2	934.95	-8.56
P66764 METK_SALTY S-adenosylmethionine synthetase	18		ETAAYGHFGRENFPWEK	353	17	4	24.33	y4y6y8°y8	2038.96	124.481	2248	3	680.32	7.06
P66764 METK_SALTY S-adenosylmethionine synthetase	19		SLQEAVMEEIHKPILPSE	197	18	0	7.53		2026.05	111.657	4847	3	676.02	-13.98
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	1		NFVDYVNSGFYNNTTFHR	54	18	14	111.31	b2b3y1y3y4y5y6*y7y8y10y11y12y16y18	2194.99	75.216	56313	3	732.33	-2.67
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	2		VIPGFMIQGGGFNEQMQQK	72	19	5	24.52	b6y5y11y13y19	2109.05	77.318	31947	2	1055.03	10.42
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	3		TADKDSATSQFFINVADNAFLDH GQR	116	26	7	36.11	b11y4y7y10y11y13y26	2868.33	86.473	31927	4	717.84	-8.85
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	4		TADKDSATSQFFINVADNAFLDH GQRDFGYAVFGK	116	35	9	23.98	b2b3b5°b5b7b12y2y3y13	3852.80	95.906	23623	5	771.36	-7.73
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	5		GMDVADKISQVPTHTDVGPYQNV PTKPVVILSAK	154	33	9	58.29	b3b4b5b22y3y4y6y11y31	3503.84	69.082	100086	4	876.72	-3.83
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	6		TADKDSATSQFFINVADNAFLDH GQR	116	26	5	22.93	b9b13y7y9y13	2868.34	107.972	1513	3	956.79	-3.57

[P20753]PIIA_SALTY Peptidyl-prolyl cis-trans isomerase A	7		TADKDSATSQFFINVADNAFLDH GQR	116	26	0	7.91		2851.32	86.477	3094	4	713.58	-2.31
[P67617]FETP_SALTY Probable Fe(2+)-trafficking protein	1		LLEQEMVSLFEGKDVHIEGYTPE DK	64	26	5	12.5	b7*b7y3y13y26	3053.49	79.843	39478	4	764.13	4.16
[P67617]FETP_SALTY Probable Fe(2+)-trafficking protein	2	Carbamidomethyl+C(4)	TIFCTYLQR	3	9	8	54.39	b7y1y3y5°y5y7y9*y9	1201.60	64.758	15090	2	601.30	-0.71
[P67617]FETP_SALTY Probable Fe(2+)-trafficking protein	3		LLEQEMVSLFEGK	64	14	6	32.54	b5°b5y3y7y12*y12	1669.87	75.319	2877	3	557.29	10.82
[P67617]FETP_SALTY Probable Fe(2+)-trafficking protein	4	Carbamidomethyl+C(6)	SRTIFCTYLQR	1	11	5	28.09	b4°b4y6y7*y7	1444.72	81.856	2565	3	482.24	-11.58
[P67617]FETP_SALTY Probable Fe(2+)-trafficking protein	5	Oxidation+M(6)	LLEQEMVSLFEGKDVHIEGYTPE DK	64	26	4	12.5	b9b25y13°y13	3069.51	136.568	2698	2	1535.26	10.66
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	1		FGSELLAK	17	8	5	41.73	b2y3y4y7y8	864.47	51.989	45417	2	432.74	-12.92
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	2		STAESIVYSALETLAQR	36	17	12	72.82	b2°b2b8b13y2y3y4y5y6*y6y7y17	1838.96	106.847	43349	2	919.98	4.45
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	3		FVNILMVDGK	25	10	6	41.25	b2b3y3y4y8y10	1135.61	76.283	18162	2	568.31	-9.03
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	4		MAEANK	143	6	2	27.44	b3y5	663.31	52.883	16821	1	663.31	-5.06
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	5		NALAMR	96	6	1	13.91	y5	675.36	36.466	5781	1	675.36	-3.98
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	6		LANELSDAADNK	119	12	5	23.03	b3*b3b7y4°y4	1260.63	45.290	2670	2	630.82	20.63
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	7		ILPDPK	11	6	1	13.91	y4	682.41	32.695	2334	1	682.41	-5.28
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	8		RVGGSTYQVPVEVRPVR	78	17	9	93.93	b4b5b6°b6b7b8b9y8y9	1899.04	49.702	39796	3	633.69	-7.71
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	1		LSIAYGIAQAMHREGAELAFITYQN DK	17	26	8	28.47	b1b11°b11y3y4y7y24y26	2897.44	107.149	106358	4	725.12	4.47
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	2		AIPNYNVMLAK	151	12	7	65.53	b1b4b5b7b9b10y12	1290.70	58.527	22834	2	645.85	7.28
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	3		FDGFVHSIGFAPGDQLDGDYVNA VTR	84	26	4	22.28	b2b10b11y5	2797.34	82.951	13813	3	933.12	6.46
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	4		TMLNPGSALLTLSYLGAER	132	19	11	40.61	b2b5b8*b8y1y2y4y7y8y15y19	2007.07	101.728	13025	2	1004.04	6.14
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	5		VNAISAGPIR	183	10	6	40.46	b2b3b5°b5y6y8	997.57	44.890	8456	2	499.29	-11.44
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	6		YMANAMGPEGVR	171	12	5	30.23	b2y6y9°y9y10	1295.59	45.501	6440	2	648.30	3.96
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	7		LSIAYGIAQAMHR	17	13	6	56.22	b10b12y4y5y9y11	1430.74	71.311	8353	3	477.58	-14.50
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	8		VAHDISSYSFVAMAK	114	15	3	24.83	b10b11y11	1625.77	77.669	7084	2	813.39	-16.67
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	9	Carbamidomethyl+C(16)	VEEFAAQLGSSIVLPCDVAEDASI DAMFAELGNVWPK	47	37	10	49.42	b4°b4b5°b5b6b7*b7b12y10°y10	3978.99	68.489	5375	5	796.60	19.08
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	10		TMLNPGSALLTLSYLGAERAIIPNY NVMLAK	132	31	4	11.47	b5°b5b11y10	3278.75	88.202	56642	5	656.56	7.30
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	11	Carbamidomethyl+C(18)	GRVEEFAAQLGSSIVLPCDVAEDA SIDAMFAELGNVWPK	45	39	3	22.91	b5b6y16	4192.03	93.911	24063	5	839.21	-0.82
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	12		EGFKVAHDISSYSFVAMAK	110	19	3	23.27	b8b9y8	2087.02	97.425	17457	3	696.35	-1.05
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	13		AIPNYNVMLAKASLEANVR	151	20	3	24.32	b6b9b10	2131.13	94.395	5498	3	711.05	-3.32
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	14	Carbamidomethyl+C(17)	VAHDISSYSFVAMAKACR	114	18	3	25.08	y3y4y6	2012.95	77.857	5067	4	503.99	-10.67
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	15	Oxidation+M(2)	TMLNPGSALLTLSYLGAER	132	19	5	26.74	b3°b3b8b9y3	2023.04	87.842	3640	2	1012.02	-8.21

P0AA07 PTHP_SALTY Phohocarrier protein HPr	1		MFQQEVTITAPNGLHTRPAAQFVK	0	24	21	122.14	b2b3*b3b5b6b7*b7b8*b8*b8y1y2y9y10y13y14y16y18y19y20y24	2684.37	63.940	410651	4	671.85	-9.91
P0AA07 PTHP_SALTY Phohocarrier protein HPr	2		GFTSEITVTSNGK	27	13	12	49.68	b2b5b11*b11*b11y10y11*y11y12*y12y13*y13	1340.67	51.413	24677	2	670.84	0.46
P0AA07 PTHP_SALTY Phohocarrier protein HPr	3		LQTLGLTQGTVVTTISAEGEDEQKA VEHLVK	49	30	25	220.59	b3*b3*b3b6*b6b11*b11y3y8y11y13*y13y14y15y16y17y18y19y20y21y22y23y24y26y28	3193.67	81.929	482463	4	799.17	-8.49
P0AA07 PTHP_SALTY Phohocarrier protein HPr	4		FQQEVTITAPNGLHTRPAAQFVKEAK	1	26	3	12.5	b9b13y3	2881.55	99.608	2092	4	721.14	4.58
P0AA07 PTHP_SALTY Phohocarrier protein HPr	5	Phosphoryl STY(9)	GFTSEITVTSNGK	27	13	4	26.13	b4y3*y3y4	1420.61	60.153	7520	3	474.21	-12.80
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	1		VLSESDFQVNQLLDILR	49	17	6	42.82	b13y3y4y5y13y17	1989.08	105.382	32982	2	995.04	6.32
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	2		SRDDLQSVMLVR	135	13	6	33.35	b4b6b7b13*b13y5	1489.78	76.169	30838	2	745.39	-0.49
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	3		GIEGASLDVPDEFVHSGK	72	18	8	44.89	b2b10*b10y5y6y11y12y18	1856.89	67.625	21152	3	619.63	-8.61
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	4		PSFDIVSEVDLQEAR	1	15	3	24.83	b5y3y4	1704.83	67.622	2627	3	568.95	-7.23
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	5		TWYVEAK	90	7	4	41.35	b5y4*y4y6	896.45	47.966	16016	2	448.73	-6.94
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	6		GGDLGQPFQFK	148	11	4	37.82	b4y3y7y8	1193.59	60.821	15153	2	597.30	-1.94
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	7		VQAQIQGEEIR	120	11	4	36.84	y4y6*y6y9	1270.67	40.132	6904	2	635.84	-0.38
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	8		MPSFDIVSEVDLQEARNGVDNAV R	0	24	8	41.32	b4b8b11b12*b12y7y13y19	2661.30	113.124	8252	3	887.77	1.10
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	9		RGIEGASLDVPDEFVHSGK	71	19	4	32.46	y6y7y11y14	2013.01	80.081	7639	3	671.68	3.46
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	10		FDFRGVEATIELNDANK	29	17	5	35.24	b4b6b7y5y10	1938.97	71.119	2766	3	647.00	7.62
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	11		NGVDNAVREVESR	16	13	3	28.84	y6y11y12	1444.72	61.275	2292	2	722.86	1.10
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	12	Oxidation+M(1)	MPSFDIVSEVDLQEAR	0	16	7	55.58	y6*y6*y6y7y8y10y11	1851.89	76.793	2236	2	926.45	4.61
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	13		IVSEVDLQEAR	5	11	0	3.77		1258.67	67.660	11879	2	629.84	1.84
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	14		EGASLDVPDEFVHSGK	74	16	0	4.9		1686.79	67.618	1916	2	843.90	-2.75
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	1		TLWFYNPFVEQATATWLK	85	18	10	57.42	b3*b3b6y2y4y9y12y13y14y18	2215.15	116.484	36307	2	1108.08	10.69
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	2		DATGNTPFMLIAR	103	13	4	21.36	b6y7y10y13	1406.71	79.115	30767	2	703.86	-0.26
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	3		TLWFYNPFVEQATATWLKDATG NTPFMLIAR	85	31	8	14.39	b2b4b6*b6y1y7y25y31	3602.84	129.942	11881	3	1201.62	7.18
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	4		FTFTPPQGVTIDDQR	187	15	5	26.89	b3*b3b9b10*b10	1721.88	57.488	2455	3	574.63	15.03
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	5		SQQNGAVDPSK	176	11	7	57.38	b9y6y7y9*y9y10*y10	1130.55	92.283	1945	1	1130.55	1.84

Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	6		NQASDWQQYNIKQDGDNFVLTPK	116	23	3	22.52	b3y20y21	2709.30	68.686	54562	3	903.77	3.42
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	7	Carbamidomethyl+C(5)	MAIACALLSSVVASSVWADAASSLKSR	3	27	5	26.94	b8b9b12y11y13	2751.41	74.901	8196	3	917.81	-2.84
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	8		SAYQLKSQQNGAVDPSK	170	17	7	44.14	b7b9*b9b12y4y7y14	1820.90	60.819	5190	2	910.96	-5.23
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	9		VTDGSGAAVQEGQGDLWVKRPNLFNWHMTQPDESILVSDGK	44	41	5	15.71	b6b9b11y5y10	4482.16	85.018	2793	4	1121.29	-5.01
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	10		VSSFHATFTQKVTDGSGAAVQEGQGDLWVK	33	30	4	11.63	b4b6y12°y12	3150.56	97.880	2378	3	1050.86	2.79
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	1		IVELEAPQLPR	178	11	6	36.84	b2y1y5y6y7y11	1264.72	67.042	66225	2	632.86	-3.67
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	2		LKDGVGLLPTSLDIVENPK	156	19	7	32.46	y2y4*y4y5y7y11y19	2008.12	79.849	33401	3	670.04	-7.11
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	3		SLDELKDGSQVAVPNDPTNLGR	122	22	7	18.96	b7°b7b13y2y6y9y22	2325.17	58.629	17522	3	775.73	2.63
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	4		FVQAYQSDEVYEAANK	245	16	8	39.15	b7y2y4y6*y6y10y11y16	1861.87	51.765	15770	2	931.44	6.82
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	5		TFVYPIAGYSK	108	11	4	48.61	y3y4y5y8	1245.66	49.611	2418	2	623.33	8.53
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	6		DGIFVEDK	215	8	3	33.95	b6y4y5	922.47	53.101	67109	2	461.74	16.08
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	7		DGSQVAVPNDPTNLGR	128	16	5	46.93	b3b4b6b7y3	1639.79	67.600	15798	3	547.27	-10.12
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	8		SLDELK	122	6	2	13.91	y4°y4	704.39	50.588	5509	1	704.39	5.98
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	9		FVQAYQSDEVYEAANKVFNGGAVK	245	24	10	84.6	b3b4*b4b5b6b7y3y6y14y22	2634.29	78.196	37936	3	878.77	3.15
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	10	Phosphoryl STY(10)	LKDGVGLLPTSLDIVENPK	156	19	4	34.22	y4y7y9y11	2088.11	85.138	330479	3	696.71	11.46
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	11	Carbamidomethyl+C(17);Phosphoryl STY(11)	TFAAVGALIGSLALAGCGQDEK	6	22	3	22.66	b12y10y11	2229.03	89.949	3479	2	1115.02	-8.87
P66541 RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAELENK	45	14	9	31.75	b7b14*b14y1y9*y9y10y12y14	1576.82	85.057	60369	2	788.91	8.13
P66541 RS2_SALTY 30S ribosomal protein S2	2		WLGGMLTNWK	95	10	6	34.7	b1y2y3y8y9y10	1205.61	85.663	49687	2	603.31	-2.63
P66541 RS2_SALTY 30S ribosomal protein S2	3	Carbamidomethyl+C(13)	AASEAVKEAANSCDQFFVNHR	74	21	7	22.51	b2b5b10b12°b12y6y21	2351.08	54.892	17010	3	784.37	-0.93
P66541 RS2_SALTY 30S ribosomal protein S2	4		EANNLGIPVFAIVDNTSDPDGVDFVIPGNDDAIR	174	34	4	11.13	b2b5y13y22	3569.77	101.776	1856	5	714.76	7.73
P66541 RS2_SALTY 30S ribosomal protein S2	5		AGVHFHGQTR	11	10	4	29.47	b6b7y4°y4	1109.56	46.890	9479	2	555.28	-4.07

[P66541]RS2_SALTY 30S ribosomal protein S2	6		ELEKLENSLGGIK	139	13	4	30.6	b3b10b12°b12	1429.78	59.606	3274	2	715.39	-7.85
[P66541]RS2_SALTY 30S ribosomal protein S2	7		EGRSQDLASQAEEFVEAE	222	19	4	21.57	b3b11y5y9	2081.94	73.862	2641	4	521.24	5.04
[P66541]RS2_SALTY 30S ribosomal protein S2	8		TVPMFNEALAELENKISAR	45	18	3	25.08	b7b11b12	2004.08	111.663	1963	3	668.70	10.23
[P66541]RS2_SALTY 30S ribosomal protein S2	9		AGVHFHGQTRYWNPK	11	15	4	44.68	b5b6b9b10	1797.89	92.627	1721	2	899.45	-0.61
[P66541]RS2_SALTY 30S ribosomal protein S2	10	Oxidation+M(11)	LENSLGGIKDMGGLPDALFVIDAD HEHIAIK	143	31	4	11.47	b11b14°b14y12	3304.68	103.462	18928	4	826.93	-1.70
[P66541]RS2_SALTY 30S ribosomal protein S2	11	Oxidation+M(6)	MATVSMRMDLK	0	11	3	25.08	b5b8y10	1298.64	79.019	1615	2	649.82	10.81
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	1		HPTIPIGLLMYANLVFNNGIDAFY AR	91	26	6	40.2	y1y4y5y10y11y26	2920.51	105.917	15598	3	974.18	-1.84
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	2		IIDLIDAGADALELGVFSDPLAD GPTIQNANLR	35	35	10	28.57	b1b4°b4b5°b5b13y1y6y14y16	3605.84	112.098	11398	4	902.21	-9.07
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	3		EGAFVPFVTLGDPGIEQSLK	15	20	6	14.9	b5°b5b7°b7y15y20	2104.11	94.815	7564	2	1052.56	8.12
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	4	Carbamidomethyl+C(9)	HNIAPIFICPPNADDDLLR	145	19	4	15.49	b5b12y12°y12	2191.12	85.602	6694	3	731.05	11.48
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	5		AGAAGAISGSAIVK	225	14	6	56.29	b6b8b9°b9b10b12	1172.67	76.040	4303	2	586.84	2.08
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	6		YENLFAQLNDRR	3	12	3	23.03	b4b11y4	1538.75	77.270	2668	3	513.59	-11.58
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	7	Carbamidomethyl+C(11)	AFAAGVTPAQCFEMLALIR	70	19	5	29.35	b3b13°b13y12y13	2066.05	102.068	15726	2	1033.53	-2.60
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	8		QMLAELR	249	7	3	38.34	b3b4y6	860.48	36.479	15413	2	430.74	12.27
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	9		YENLFAQLNDR	3	11	3	25.08	b7y4y8	1382.69	40.215	3046	2	691.85	15.45
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	10	Carbamidomethyl+C(1)	CEQVGVDSVLVADVPVEESAPFR	117	23	6	29.31	b10°b10b12b13y9y13	2502.19	81.780	2342	2	1251.60	-11.71
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	11		QVASYGRGYTYLLSR	164	15	3	26.89	b3b10b12	1733.92	51.471	3629	3	578.65	14.93
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	12	Carbamidomethyl+C(14)	QAALRHNIAPIFICPPNADDDLLR	140	24	4	19.43	y6y8y11°y11	2730.42	118.708	2922	3	910.81	2.32
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	13		SGVTGAENRGALPLHHLIEK	179	20	5	21.69	b5°b5b10°b10b13	2099.11	85.805	2215	2	1050.06	-12.79
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	14	Carbamidomethyl+C(9)	HNIAPIFICPPNADDDLLRQVASYG R	145	26	4	18.96	b3b5b10y6	2952.52	112.323	1918	3	984.84	12.65
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	15	Phosphoryl STY(10)	REGAFVPFVTLGDPGIEQSLK	14	21	3	14.38	b8b10y3	2340.13	67.407	3688	2	1170.57	-11.48
[P66643]RS9_SALTY 30S ribosomal protein S9	1		SLEQYFGR	33	8	10	49.24	b2°b2b3°b3b4°b4°b4y5y6y8	999.48	60.869	41040	2	500.25	-5.25
[P66643]RS9_SALTY 30S ribosomal protein S9	2		GGGISGQAGAIR	68	12	6	27.01	b4b5°b5y1y8y12	1043.55	34.004	15804	2	522.28	-7.95
[P66643]RS9_SALTY 30S ribosomal protein S9	3		GELR	95	4	1	13.16	y3	474.26	44.146	20156	1	474.26	-13.19
[P66643]RS9_SALTY 30S ribosomal protein S9	4		AGFVTRDAR	100	9	3	31.32	b5b7y7	992.52	86.137	9974	2	496.76	-4.86
[P66643]RS9_SALTY 30S ribosomal protein S9	5		MVVRQPLELVDMVEK	45	15	4	24.83	b12y7°y7y8	1785.97	106.532	2182	2	893.49	5.33
[P66643]RS9_SALTY 30S ribosomal protein S9	6		ALMEYDESLRGELR	85	14	4	31.75	b12y9y10y13	1681.84	83.490	1799	2	841.42	9.73
[P66643]RS9_SALTY 30S ribosomal protein S9	7		DARQVER	106	7	5	41.35	b3b5°b5b6°b6	873.46	67.917	1638	1	873.46	5.38
[P66643]RS9_SALTY 30S ribosomal protein S9	8		ISGQAGAIR	71	9	1	7.72	b8	872.50	33.964	39910	2	436.75	7.56

P55900 SERC_SALTY Phohoserine aminotransferase	1		ASIYNAMPIEGVK	335	13	5	21.36	b3°b3b5y9*y9	1392.71	59.713	52823	3	464.91	-7.36
P55900 SERC_SALTY Phohoserine aminotransferase	2	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	12	95.69	b3b4y1y3y4y6y7y9y12°y12y13y14	2567.18	74.666	28758	4	642.55	-12.27
P55900 SERC_SALTY Phohoserine aminotransferase	3		AQVFNFSSGPAMPLPAEVLK	1	19	9	53.62	b3b8b9y1y3y6y13y16y19	2006.06	92.108	23259	2	1003.53	10.34
P55900 SERC_SALTY Phohoserine aminotransferase	4		GKEFIQVAEEAEQDFR	42	16	5	24.33	b13y3y4y10°y16	1895.93	53.208	12090	3	632.65	10.24
P55900 SERC_SALTY Phohoserine aminotransferase	5		TTADYVDAGYWAASAIK	91	17	4	16.93	b4°b4b13y11	1802.88	109.181	1560	2	901.94	11.98
P55900 SERC_SALTY Phohoserine aminotransferase	6		NDVAQANR	287	8	4	55.27	b3b6y5y7	887.41	50.710	4839	1	887.41	-21.53
P55900 SERC_SALTY Phohoserine aminotransferase	7		AELLYGVIDNSDFYR	272	15	4	30.42	b6y4y5y10	1774.86	68.487	1896	2	887.93	-4.95
P55900 SERC_SALTY Phohoserine aminotransferase	8		MAQVFNFSSGPAMPLPAEVLK	0	20	3	21.69	b4b8b10	2137.13	90.902	1532	2	1069.07	20.22
P55900 SERC_SALTY Phohoserine aminotransferase	9		YGVIIYAGAQK	188	10	3	27.71	b6b8y4	1069.55	44.785	1508	2	535.28	-17.80
P55900 SERC_SALTY Phohoserine aminotransferase	10	Carbamidomethyl+C(3)	KYCAPQIIDAK	111	11	4	32.07	b7b8b10°b10	1306.67	67.480	91738	2	653.84	-8.41
P55900 SERC_SALTY Phohoserine aminotransferase	11		GQFAGVPLNLLGDKTTADYVDA GYWAASAIK	77	31	5	22.36	b6°b6b7b25y25	3212.65	97.762	19387	3	1071.55	7.07
P55900 SERC_SALTY Phohoserine aminotransferase	12		AELLYGVIDNSDFYRNDVAQANR	272	23	5	20.88	b12y10y12y14*y14	2643.30	79.852	9164	3	881.77	7.57
P55900 SERC_SALTY Phohoserine aminotransferase	13		WLKAQGGVAAMHK	254	13	3	21.36	b7y3y5	1396.75	50.604	7646	3	466.25	-4.02
P55900 SERC_SALTY Phohoserine aminotransferase	14		VVGGMRASINYAMPIEGVK	329	19	7	42.37	b6b12°b12b14b17y11y13	1992.01	64.003	3888	2	996.51	-12.99
P55900 SERC_SALTY Phohoserine aminotransferase	15		TTADYVDAGYWAASAIKEAK	91	20	3	14.9	b4b6y13	2131.03	69.783	3756	4	533.51	-2.29
P55900 SERC_SALTY Phohoserine aminotransferase	16	Carbamidomethyl+C(7); Oxidation+M(17)	LAQQELCDWHGLGTSVMEISHR	20	22	4	13.91	b7b9y12°y12	2583.21	92.200	9240	4	646.56	0.19
P55900 SERC_SALTY Phohoserine aminotransferase	17	Oxidation+M(1)	MNVPFQLADNTLDK	297	14	4	32.54	b6b9b12y12	1621.81	88.548	8820	2	811.41	11.06
P55900 SERC_SALTY Phohoserine aminotransferase	18	Oxidation+M(12)	AQVFNFSSGPAMPLPAEVLK	1	19	4	42.01	b3b4b7b8	2022.03	82.324	4141	2	1011.52	-3.44
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	1		ALFATGNFEDVR	64	12	8	70.62	b3y4y7y9y10*y10y11y12	1339.67	68.945	20931	2	670.34	1.09
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	2		VAVGAALLSMPVR	36	13	3	35.83	y4y5y6	1283.75	77.598	14381	2	642.38	-0.76
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	3		LSNMQPQIAMDR	535	12	4	30.23	y5y7y8*y8	1403.68	51.872	6118	2	702.34	2.52
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	4		AEQFQFNIGK	792	10	4	42.22	b5b8y3y4	1181.60	41.603	4359	3	394.54	2.89
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	5		SYGTDVTLGFPINEYNTLR	507	19	3	24.67	b10b11b13	2160.08	101.277	2163	2	1080.54	8.82
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	6		VSLDTATYVPIDNDHK	606	16	5	28.62	b12y4y8y10°y10	1787.86	59.212	1926	3	596.63	-9.70
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	7		TGDTVNDEDISNTIR	49	15	3	24.83	b4y10y11	1649.76	48.569	9538	2	825.39	1.78

[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	8		YLESMGQSADTSSFAADDFTFNY GWTYNK	547	29	5	22.22	b14y10*y10y11*y11	3316.38	90.713	8515	4	829.85	-7.14
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	9		AVVTPLPR	152	8	3	41.73	y4y5y6	852.52	44.780	5995	2	426.76	-16.82
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	10		VQSQPEINDADK	321	12	3	23.03	b11y8y11	1343.62	63.794	2480	3	448.54	-19.81
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	11		WVVLGR	622	6	1	13.91	b3	729.44	47.911	2010	1	729.44	-3.01
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	12		LGFFETVDTDTQR	391	13	5	42.38	y3y9°y9y11y12	1528.76	76.944	1910	3	510.26	20.52
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	13		VTIPGSDNEYK	594	12	4	27.01	b10*b10y8y9	1385.67	119.885	1844	2	693.34	5.02
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	14		FNIDSTQVSLTPDK	237	14	3	19.98	b6b9y8	1564.77	34.901	1589	2	782.89	-6.63
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	15		TGDTVNEDEISNTIRALFATGNFE DVR	49	27	3	23.09	b3b13b14	2970.38	84.423	19644	4	743.35	-8.14
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	16		LDRGYFPTDGSR	576	12	3	23.03	b10y5y9	1383.68	91.655	12883	2	692.35	12.97
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	17		FEGNDTSKDSVLR	353	13	4	21.36	b12y9°y9y11	1467.72	65.823	8866	2	734.36	8.15
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	18		QNLEASGVRVGESLDR	111	16	5	26.17	b3b4°b4b12*b12	1729.86	74.808	7227	2	865.43	-13.13
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	19		VTIPGSDNEYKVS�DTATYVPID NDHK	594	28	3	22.22	b12b13y13	3154.52	100.738	3402	4	789.39	0.39
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	20		LSGVQVSGNLAGHSAEIENLTKE PGELYNGTK	267	33	7	22.36	b15°b15*b15y4°y4y5*y5	3425.73	114.423	2823	3	1142.58	-7.84
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	21		GYARFNIDSTQVSLTPDK	233	18	6	41.36	b8*b8b9y3y5y6	2012.01	55.760	1944	3	671.34	-0.12
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	22		LAGDLETLRSYYLDR	218	15	3	24.83	b12y3y4	1784.90	82.199	1664	2	892.95	-11.69
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	23		YGYAYPRVQSQPEINDADK	314	19	3	15.49	b3b12y3	2214.05	63.163	1502	4	554.27	0.00
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	24	Phosphoryl STY(10)	FEGNDTSKDSVLR	353	13	4	30.7	b3b8y3y11	1547.65	89.783	1728	3	516.55	-12.23
[Q8ZRP0]YAET_SALTY Outer membrane protein assembly factor yaeT	25		PQIAMDR	540	7	0	2.64		830.42	51.859	4056	1	830.42	3.75
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	1		VMGFIGGTSDRPAPISDKEVDAIM NR	88	26	9	41.25	b2b3b4y5*y5y7y21y24y26	2776.35	73.678	33953	4	694.84	-8.62

P0AA02 NUSG_SALTY Transcription antitermination protein nusG	2		WYVVQAFSGFEGR	8	13	6	42.69	b2b5b7y8y10y11	1545.76	88.288	8563	2	773.39	9.79
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	3		LQQVGDKPRPK	114	11	4	32.07	b2y4y5y7	1265.71	18.200	8320	3	422.58	-14.18
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	4		VMGFIGGTSDRPAPISDK	88	18	9	82.27	b3b7b8b9b10b14y3y6y12	1847.92	102.787	3709	2	924.46	-5.48
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	5	Oxidation+M(2)	VMGFIGGTSDRPAPISDK	88	18	3	16.16	b6b8y9	1863.93	56.986	5231	3	621.98	2.29
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	6	Oxidation+M(2)	VMGFIGGTSDRPAPISDKEVDAIM NR	88	26	3	12.5	b6y7y12	2792.35	61.405	2702	4	698.84	-6.30
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	7		VVQAFSGFEGR	10	11	2	7.52	b8°b8	1196.61	88.299	4130	1	1196.61	4.18
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	1		YQAFTQADLTNLR	271	13	7	26.13	b1b2*b2b3*b3y9y10	1540.78	66.137	13289	2	770.89	3.09
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	2		QILPEANSQIVGFR	152	14	4	19.98	b10y3y12°y12	1571.87	69.852	8731	2	786.44	8.23
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	3		DFVYVGDVAAVNLWFLESGK	209	20	4	14.9	b3b6y10y20	2229.12	101.082	5563	3	743.71	-2.30
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	4		AESFQAVADATLAYHK	239	16	3	17.8	b4b13y3	1721.87	60.944	1843	3	574.63	12.19
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	5		GSIEYIPFPDK	256	11	5	42.42	b5°b5b6y3y4	1265.65	58.481	8667	3	422.55	5.02
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	6		EIPFLYASSAATYGGR	107	16	4	17.8	b6b11°b11y11	1702.86	80.095	4894	2	851.94	12.33
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	7		EYEKPLNVYGYSK	131	13	3	21.36	b7y3y5	1589.79	48.675	4129	2	795.40	5.22
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	8		GRYQAFTQADLTNLR	269	15	6	42.46	b3b8*b8b11°b11b13	1753.92	83.535	8653	2	877.46	10.37
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	9		EIPFLYASSAATYGGRTSDFIESR	107	24	5	20.18	b9y3y5y7°y7	2638.28	41.689	7427	4	660.33	2.13
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	10		DGTKFVNVLVDLNIADYMDK	34	19	3	24.67	y3y10y11	2171.09	63.693	5402	3	724.37	9.56
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	11	Oxidation+M(13)	FVNLVDLNIADYMDK	38	15	3	18.81	b3b12y10	1785.87	97.941	5442	3	595.96	-1.44
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	12	Oxidation+M(10)	TVAEGVTEYMAWLNLR	293	15	3	24.83	b6y5y6	1755.81	105.021	4481	2	878.41	-14.81
P58663 RCSB_SALTY Capsular synthesis regulator component B	1		LDHAVLITDLSPGDK	47	16	4	17.8	b5y3y14y16	1724.87	90.569	14829	3	575.63	-11.11
P58663 RCSB_SALTY Capsular synthesis regulator component B	2		LGVENDIALLNLYSSVTLSPTDKE	192	24	8	54.47	b2b4b12°b12y5y6y7y8	2591.34	109.770	10740	2	1296.17	-1.04

[P58663]RCSB_SALTY Capsular synthesis regulator component B	3		LSPK	150	4	2	13.16	b3°b3	444.28	104.336	2682	1	444.28	-12.91
[P58663]RCSB_SALTY Capsular synthesis regulator component B	4		SAMMKLGVENDIALLNYLSSVTL SPTDK	187	28	8	31.67	b9°b9b10°b10y3y9°y9y13	3010.54	114.931	21272	3	1004.19	-1.22
[P58663]RCSB_SALTY Capsular synthesis regulator component B	5		LGVENDIALLNYLSSVTLSPDKE	192	24	5	24.65	b3b8y6y10y13	2591.32	85.870	3605	2	1296.16	-11.31
[P58663]RCSB_SALTY Capsular synthesis regulator component B	6	Phosphoryl STY(17)	LGVENDIALLNYLSSVTLSPDKE	192	24	4	29.04	y6y9y11y12	2671.28	63.869	3437	4	668.58	-8.23
[P58663]RCSB_SALTY Capsular synthesis regulator component B	7	Oxidation+M(12)	LDAHVLITDLSMPGDK	47	16	3	26.17	b3b4b14	1740.86	59.700	5293	3	580.96	-12.83
[P66869]SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	1	Carbamidomethyl+C(11)	YGLPAPVGYACTTPR	14	15	3	26.89	y8y10y12	1622.81	62.280	17146	2	811.91	4.14
[P66869]SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	2		VALDPLTGPMPLYQGR	146	15	6	30.42	b13y5y11y13°y13*y13	1614.84	71.722	16972	2	807.92	6.88
[P66869]SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	3		LVTYQTDANGQPVNQILVEAATDI GKELYLGAVVDR	80	36	13	65.89	b2b7b8°b8b9y1y2y3y5y6y7y25y36	3874.05	122.028	13832	3	1292.02	5.80
[P66869]SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	4		AFAENWLGR	70	10	5	53.01	b1y3y6y7y8	1191.61	58.448	3518	3	397.88	-11.17
[P66869]SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	5		IFMGLATIFLER	179	12	3	23.03	b3y3y10	1410.78	109.269	12421	2	705.89	-3.03
[P66869]SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	6	Carbamidomethyl+C(20)	EAQAAQWELNYVALDGNIGCMV NGAGLAMGTMDIVK	241	36	4	10.98	b5y7°y7y11	3810.84	125.612	5300	5	762.97	10.38
[P66869]SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	7	Carbamidomethyl+C(6)	QGDLICLDGKLGADGNALFR	205	20	3	14.9	b6y9y13	2133.06	101.123	2006	3	711.69	-8.36
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		GHIINIGSTAGSWPYAGGNVYGAT K	126	25	4	19.02	y7y9y11°y11	2491.25	65.281	56147	4	623.57	6.86
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		AVLPGMVER	115	9	3	39.1	y4y6y7	971.53	53.634	28484	2	486.27	-7.66
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		AAIEEMMASLPAQWR	58	15	4	26.78	b5b11y5y10	1703.85	91.114	14110	2	852.43	14.62
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4		TYENTTALTPEDITEAVWWVATL PAHVNINTVEMMPVTQSFAGLSV HR	199	48	7	38.61	b2b8b9b13°b13b14y9	5340.63	136.531	7058	4	1335.91	-0.09
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		VTDIEPGLVGGTEFSSVR	171	18	6	16.16	b6°b6b14°b14y7°y7	1862.96	101.256	4093	2	931.98	6.55
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		LQALK	36	5	2	27.07	b3y4	572.37	47.620	33135	1	572.37	-14.40
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		TDLHGTAVR	162	9	3	39.1	b3b7b8	969.53	60.239	2265	2	485.27	15.93
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	8		NRGHIINIGSTAGSWPYAGGNVYG ATK	124	27	5	12.24	b4b13*b13y12*y12	2761.37	63.860	3720	4	691.10	-3.71
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	9		DELGENVLTAQLDVRNR	41	17	5	40.08	b4b9b10°b10b11	1941.98	102.734	3570	2	971.49	-10.94

[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	10	Phosphoryl STY(12)	GHIINIGSTAGSWPYAGGNVYGATK	126	25	4	12.8	b12_H3PO4 b12y11°y11y13	2571.17	102.124	5718	4	643.55	-10.63
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	11	Carbamidomethyl+C(15) ;Phosphoryl STY(6)	MIVLVTGATAGFGECIAR	0	18	3	16.16	b7b9y11	1945.90	72.572	1740	2	973.46	-7.72
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	12	Oxidation+M(9)	ASVEDWETMIDTNNK	93	15	5	32.8	b3b4°b4y4y6	1768.75	32.152	10636	4	442.94	-10.63
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	13	Carbamidomethyl+C(15) ;Oxidation+M(1)	MIVLVTGATAGFGECIAR	0	18	4	27.48	b3y6y7y14	1881.94	82.376	3351	2	941.47	-9.86
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	14		LPGMVER	117	7	0	1.51		801.42	53.631	3056	2	401.21	-13.33
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	1	Carbamidomethyl+C(25)	LLTRESFHLMVLDLMLPGEDGLSICR	42	26	4	23.17	b2y6y8y9	3015.51	108.067	5089	4	754.63	-12.39
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	2		SVANAEQMDR	32	10	8	59.55	b2b5°b5y4y5y6y8y10	1120.51	28.254	4460	2	560.76	0.76
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	3		ELLAR	110	5	3	40.6	b3b4y3	601.36	29.025	60558	1	601.36	-10.76
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	4		YIQTVWGLGYVFVPDGSK	220	18	9	64.83	b9b10°b10y5y6y7y11°y11y14	2029.01	109.889	6725	3	677.01	-14.38
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	5		EPLSR	177	5	1	13.53	y4	601.34	62.711	3297	1	601.34	13.70
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	6		LNLGTR	144	6	1	13.91	y5	673.39	44.353	2601	2	337.20	-13.32
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	7		SVANAEQMDRLLTR	32	14	4	19.98	b5y9°y9y13	1603.82	63.270	2650	2	802.41	-1.22
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	8		RQANELPGAPSQEEAVIAFGK	121	21	5	19.74	b5°b5b9y3y13	2212.11	69.763	1802	3	738.04	-11.37
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	9	Phosphoryl STY(5)	LNLGTREMFREDEPMPLTSGEFAVLK	144	26	5	23.17	b3*b3b4*b4b10_H3PO4 b10	3060.46	114.934	4745	4	765.87	4.55
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	10	Carbamidomethyl+C(25) ;Oxidation+M(10)	LLTRESFHLMVLDLMLPGEDGLSICR	42	26	6	37.23	b8b9y6°y6y11y12	3031.56	133.419	100366	3	1011.19	5.88
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	11	Carbamidomethyl+C(21) ;Oxidation+M()	ESFHLMVLDLMLPGEDGLSICR	46	22	4	13.91	b3b7y4°y4	2548.19	72.887	2703	4	637.80	-12.07
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	1	Carbamidomethyl+C(18) ;Carbamidomethyl+C(32))	ANVSQVMHHIGDVAGRDCVLVDD MIDTGGTLCK	198	33	8	27.91	b2b8b17y2y3y6y8y9	3559.70	105.971	26558	4	890.68	-1.58
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	2		LFAGNATPELAQR	5	13	7	33.35	b1b8y6y10y11*y11y13	1387.73	54.641	22287	2	694.37	0.79
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	3		ITAVIPYFGYAR	84	12	3	27.01	b4y6y7	1370.75	81.231	17457	2	685.88	0.89
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	4		LYTSLGDAAVGR	22	12	5	38.32	b6y5y7y10y12	1222.63	53.153	16726	2	611.82	-6.29
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	5		VFAYATHPIFSGNAANNLR	243	19	5	29.35	b16b17y8y12°y12	2063.03	65.876	14892	3	688.35	-8.40

P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	6		AAEALK	231	6	3	27.44	b4°b4y5	602.35	31.992	15617	1	602.35	-8.21
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	7	Carbamidomethyl+C(10)	NSVIDEVVVCDTIPLTDEIK	262	20	4	26.09	b8b9b15y7	2259.16	88.937	5624	2	1130.09	9.40
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	8		LLNDTDMAIIDK	182	12	3	27.01	b7b8y8	1361.69	34.925	2281	2	681.35	-7.80
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	9	Carbamidomethyl+C(11)	GGDIFIQSTCAPTNDNLMELVVMVDALR	49	29	3	22.22	b10b11y6	3192.60	121.794	1737	4	798.91	7.95
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	10		ASAGRITAVIPYFGYAR	79	17	3	16.93	b6y3y10	1812.95	85.081	10458	2	906.98	-14.48
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	11		LYTSLGDAAVGRFSDGEVSVQINE NVR	22	27	5	23.2	b4b7°b7b8y5	2896.41	60.809	4055	5	580.09	-12.64
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	12		MPDMKLFAGNATPELAQR	0	18	4	16.16	b5b15°b15y10	1989.99	97.890	1738	3	664.00	-0.49
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	13	Phosphoryl STY(11)	VFAYATHPIFSGNAANNLR	243	19	3	15.49	b8b10y7	2143.00	58.017	4984	4	536.50	-3.08
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	14	Carbamidomethyl+C(18) ;Carbamidomethyl+C(32) ;Oxidation+M(7)	ANVSQVMHIIGDVAGRDCVLVDD MIDTGGTLCCK	198	33	7	22.72	b6b8°b8b11*b11b13y9	3575.73	110.748	2422	4	894.69	8.40
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	15		FSGNAANNLR	252	10	0	5.27		1063.52	65.824	12597	2	532.26	-5.05
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	1		AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	8	35	17	124.53	b3b4b5b6b7b9b11b17y6y9y17y20y24y25y26y28y35	3487.82	108.158	52425	3	1163.28	5.53
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	2	Carbamidomethyl+C(3)	FICIADASK	112	9	5	39.1	y4°y4y5y7y9	1024.51	51.730	32564	2	512.76	-3.81
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	3		GADVALIGTPDGVK	201	14	6	34.02	b5b6y2y3y7y14	1312.69	58.165	26553	2	656.85	-13.02
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	4		LGGRPEYR	149	8	6	49.24	b6b7y2y3y4y8	947.50	24.372	5577	2	474.25	-8.25
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	5		GQIEGAVSSSDASTEK	43	16	5	36.04	b4b10y6y9y13	1565.73	32.361	3519	2	783.37	3.43
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	6		QVDILGKFPLPVEVIPMAR	121	19	3	24.67	y6y7y9	2122.19	100.571	34417	3	708.07	-7.36
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	7		GGRPEYR	150	7	2	28.2	b3b5	834.41	24.379	14963	2	417.71	-13.17
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	8		VGVGTGSTAAHFIDALGTMK	23	20	1	10.06	b14	1932.97	108.163	1613	2	966.99	-6.57
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1		SLTEIKDVLASR	298	12	6	45.98	y1y3y5y6y7y12	1331.74	63.678	76143	2	666.37	-9.72
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2		MQGSVTEFLKPR	0	12	5	56.77	b3b7b9b11y12	1392.75	76.998	31031	2	696.88	14.29
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3	Carbamidomethyl+C(6)	LLVDACYSPVER	170	12	10	96.14	b2b6b8y4y5y7y8y9y10y12	1421.71	60.129	27541	2	711.36	1.97
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4	Carbamidomethyl+C(9)	ILLSSMPGCAVTEVEIDGVLHEYS TK	45	26	3	12.5	b12y20y23	2848.42	91.534	20490	3	950.15	3.51
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5		EGVQEDILEILLNLK	71	15	7	45.2	b5y2y3y4y5y7y15	1725.97	122.678	12764	2	863.49	2.83
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		LVIEMETNGTIDPEEAIR	200	18	6	25.72	b13°b13y5y8y10°y10	2030.04	84.164	11008	3	677.35	12.57

P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		QPEVKEEKPEFDPILLRPVDDLELTVR	238	27	7	18.32	b2*b2b4°b4b7b9y27	3204.71	114.347	7494	3	1068.91	-0.91
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8		LVIEMETNGTIDPEEAIRR	200	19	5	26.74	b10b13b14y11°y11	2186.10	108.453	2970	3	729.37	-3.57
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9		VTLEPLER	25	8	5	41.73	y4°y4y5°y5y6	956.53	52.758	36045	2	478.77	-12.70
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	10		IHSEEDERPIGR	158	12	3	30.23	y3y4y6	1437.69	25.307	27803	3	479.90	-15.62
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	11		QPEVK	238	5	2	13.53	b3°b3	600.34	31.613	14377	1	600.34	5.59
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	12		IAYNVEAAR	182	9	3	31.32	b4b6y3	1006.53	43.340	7606	2	503.77	3.27
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	13		EEKPEFDPILLRPVDDLELTVR	243	22	4	13.91	b7b10y11°y11	2623.40	91.007	5420	4	656.61	0.93
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	14		AEAHYIGDLVQR	271	13	4	21.36	b9y4y6°y6	1484.80	43.235	2837	3	495.61	12.17
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	15	Carbamidomethyl+C(10)	RILLSSMPGCAVTEVEIDGVLHEYSTK	44	27	10	61.13	b12°b12b14b16y7y8y12°y12y13y14	3004.50	114.929	122330	4	751.88	-4.39
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	16	Carbamidomethyl+C(4)	SANCLKAEAIHYIGDLVQR	265	19	3	22.45	b5b7b14	2158.10	77.291	29888	3	720.04	-4.98
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	17		IAYNVEAARVEQR	182	13	3	21.36	b8b10y3	1518.79	43.508	21229	3	506.93	-11.41
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	18	Carbamidomethyl+C(18)	IHSEEDERPIGRLLVDACYSPPER	158	24	3	22.42	b10y12y13	2840.39	62.064	12661	4	710.85	-3.35
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	19		GYVPASTRIHSEEDERPIGR	150	20	3	14.9	b5y5y15	2269.14	69.213	8415	3	757.05	1.61
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	20		GLSLGMRLNWPPASIADE	310	19	4	15.49	b9°b9y3y5	2056.01	50.687	6725	3	686.01	-4.87
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	21		GRGYVPASTR	148	10	4	29.47	b4b5y5°y5	1063.56	24.919	4401	2	532.28	-1.72
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	22	Oxidation+M(5)	LVIEMETNGTIDPEEAIR	200	18	3	16.16	b6y7y10	2046.03	79.848	3734	4	512.26	10.62
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	23		TEIKDVLASR	300	10	1	7.72	b3	1131.63	63.730	21051	2	566.32	-3.34
O68883 CISY_SALTY Citrate synthase	1	Carbamidomethyl+C(12)	TAGSSGANPFACIAAGIASLWGPAHGGANEAAALK	240	34	5	13.51	b6b16y17y26y34	3195.58	116.909	22808	3	1065.86	4.05
O68883 CISY_SALTY Citrate synthase	2		ILILHADHEQNASTSTVR	222	18	6	16.16	b2b3y2y5y9y18	2005.03	44.490	18416	3	669.01	-9.56
O68883 CISY_SALTY Citrate synthase	3		TVGWIAHWNEMHTDGMK	388	17	10	54.45	b8°b8b10b12b13y1y2y5y7y12	2012.90	67.158	17268	3	671.64	-7.58
O68883 CISY_SALTY Citrate synthase	4	Carbamidomethyl+C(9)	DSHPMAVMCGITGALAAFYHDSL DVNNPR	127	29	7	42.6	y4y6y8y11y13y14y29	3159.45	109.015	11729	4	790.62	2.47

O68883 CISY_SALTY Citrate synthase	5		AMGIPSSMFTVIFAMAR	371	17	5	35.24	b7b12y3y4y13	1829.93	120.158	6899	2	915.47	9.14
O68883 CISY_SALTY Citrate synthase	6	Carbamidomethyl+C(18)	NDLSYAGNFLNMMFSTPCETYEYV NPVLER	189	29	6	25.53	b1b3b12y2y13y14	3411.57	112.010	6806	3	1137.86	10.09
O68883 CISY_SALTY Citrate synthase	7		ELGTKDDLLLEVAMELEHIALNDP YFIEK	328	28	6	40.01	y8°y8y9y13°y13y14	3245.62	105.352	2434	4	812.16	-2.03
O68883 CISY_SALTY Citrate synthase	8		YSIGQPFVYPR	178	11	3	25.08	b4y3y6	1326.69	69.276	17342	2	663.85	1.75
O68883 CISY_SALTY Citrate synthase	9		LMGFGHR	300	7	3	38.34	b5b6y4	817.43	28.785	2837	2	409.22	20.46
O68883 CISY_SALTY Citrate synthase	10		LYPNVDFYSGIILK	357	14	5	32.54	b4b8b12y11°y11	1641.86	63.901	1571	2	821.43	-17.99
O68883 CISY_SALTY Citrate synthase	11		TTVTRHTMIHEQITR	105	15	3	18.81	b14y9y12	1823.96	100.248	203391	2	912.48	2.01
O68883 CISY_SALTY Citrate synthase	12	Carbamidomethyl+C(10)	RDSHPMAVMCGITGALAAFYHDS LDVNNPR	126	30	4	17.54	b6b12b14°b14	3315.59	103.432	22263	4	829.65	12.59
O68883 CISY_SALTY Citrate synthase	13		TVGWIAHWNEMHTDGMKIARPR	388	22	3	13.91	b9b11y3	2606.27	136.435	11347	3	869.43	-5.81
O68883 CISY_SALTY Citrate synthase	14		ELGTKDDLLEVAMELEHIALNDP YFIEK	328	28	6	40.43	b3b9b10b11y7y10	3245.67	127.604	2354	3	1082.56	12.49
O68883 CISY_SALTY Citrate synthase	15	Carbamidomethyl+C(3)	ETCHEVLKELGTK	320	13	4	28.84	b8°b8b9b11	1543.80	102.785	2097	2	772.40	14.87
P0A1U6 YJGD_SALTY Uncharacterized protein yjgD	1		LIIEELLEDGSDPDALYTIEHHLSA DDFETLEK	15	33	10	32.75	b2b3b5b12y2y7y12y13y21 y33	3770.82	107.489	29538	4	943.46	1.04
P0A1U6 YJGD_SALTY Uncharacterized protein yjgD	2		MANPELEEQREETR	0	15	8	38.39	b6°b6b10y3°y3y4°y4y11	1844.87	83.628	10478	3	615.63	-3.24
P0A1U6 YJGD_SALTY Uncharacterized protein yjgD	3		ANPELEEQREETR	1	14	6	19.98	b9y2y6°y6y12y14	1713.82	40.327	8815	3	571.94	-14.03
P0A1U6 YJGD_SALTY Uncharacterized protein yjgD	4		MANPELEEQREETR	0	15	4	26.89	y6°y6y11y12	1844.89	98.792	10775	2	922.95	5.03
P0A1U6 YJGD_SALTY Uncharacterized protein yjgD	5		PELEEQREETR	3	12	0	3.39		1528.76	40.340	2151	2	764.88	1.12
Q7CPH8 SECB_SALTY Protein-export protein secB	1		GTFPQLNLAPVNFDAFMNYLQQ QAGEGTEEHQDA	120	35	12	42.9	b4b6°b6°*b6b9°b9b15y3y4y 8y10y13	3893.83	116.803	14341	3	1298.62	5.96
Q7CPH8 SECB_SALTY Protein-export protein secB	2		LDLDTASSQLADDVYEVVLR	41	20	7	39.93	b5b6b8y2y3y4y20	2222.15	109.853	11272	2	1111.58	12.63
Q7CPH8 SECB_SALTY Protein-export protein secB	3		IYTKDVSFEAPNAPHVFQK	15	19	6	29.35	b13°b13b17°b17y11y12	2191.12	75.968	5030	4	548.53	-0.89
Q7CPH8 SECB_SALTY Protein-export protein secB	4		DVSFEAPNAPHVFQK	19	15	3	18.81	b3y9y11	1685.82	61.237	2967	2	843.42	-2.32
Q7CPH8 SECB_SALTY Protein-export protein secB	5		DWQPEVK	34	7	3	41.35	b4b6y5	901.45	60.130	2218	2	451.23	14.63
P15888 NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase	1		TLLQYSPSSTNSQPWHFIVASTEE GK	31	26	8	37.5	b8°b8b9°*b9b10b14y3y26	2907.41	105.197	26903	3	969.81	-3.27
P15888 NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase	2		MDIVSVALQR	0	10	4	40.46	b3b6y4y6	1131.61	70.180	7417	2	566.31	-4.64
P15888 NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase	3		GYTSLVVVPVGHHSVEDFNAGLP K	181	24	8	40.97	b3b5b7b23y2y4y8y16	2522.30	71.627	4169	3	841.44	-1.65
P15888 NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase	4		FFADMHR	122	7	3	41.35	b3y3y6	923.42	66.129	24864	1	923.42	3.64
P15888 NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase	5		LPLETTLTEV	207	10	5	34.7	y3°y3y4°y4y9	1115.63	46.053	1632	3	372.55	13.68
P15888 NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase	6		SAAGNYTFNERK	62	12	6	41.33	b3°b3b4b5°*b5y11	1357.65	91.066	11742	2	679.33	-0.45
P15888 NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase	7		EKGYSLSLVVPVGHHSVEDFNAG LPK	179	26	6	16.47	b6°b6b25y10°*y10y18	2779.41	100.194	4786	4	695.61	-11.95
P15888 NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase	8		VSLKDDHQWMAK	129	12	5	48.55	b8b11y3y5y11	1457.73	86.596	2196	2	729.37	8.71

[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1	Carbamidomethyl+C(3)	FACGVIEK	169	8	12	79.32	b2b4b5y1y2°y2y3y5°y5y6y7y8	923.45	41.520	139543	2	462.23	-12.23
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2		EVPALMAGGHLDPEK	84	15	5	30.42	b14y3y8y9°y9	1563.79	58.043	19362	3	521.93	1.95
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3		GGDNYSDKPAPLGGGGAR	151	18	15	147.87	b4b7b10°b10°b10y3y5y6y7y8y9y10y11y12y14	1688.77	33.877	82958	3	563.59	-17.49
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	4		GHLGDLPLGLVVNADGTATYPLLA PR	110	25	6	37.85	b3b4b5°b5b16y14	2517.30	83.523	48444	4	630.08	-18.14
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	5		HLGPYNDKGHGLDPLGLVVNAD GTATYPLLA PR	102	33	14	85.66	b3b5b8°b8b10b14b18y3y4y5y6y8y11°y11	3441.78	81.434	133312	4	861.20	-3.12
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	6		DGKEVPALMAGGHLDPEK	81	18	4	25.72	b11b13b17y7	1863.92	68.491	16210	2	932.46	-2.29
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	7		PALMAGGHLDPEK	86	13	1	7.3	b3	1335.68	58.079	4181	2	668.35	8.87
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	8		EVPALMAGGHLDPEK	84	15	0	3.77		1545.76	58.039	2776	3	515.92	-5.53
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	1		SSDVSLPVLVLTAR	68	14	9	53.71	b1b3°b3b5b8y4y8y10y14	1456.84	87.312	19597	2	728.92	2.35
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	2		GQGYLFELR	215	9	5	31.32	b6y1y3y4y9	1082.56	72.232	15731	2	541.78	-1.92
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	3		VLVVEDNALLR	3	11	7	57.38	b3y6*y6y7°y7y8y9	1240.72	68.269	15307	2	620.86	-6.30
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	4		IQAQYPHDVITTVR	201	14	5	56.29	y6y8y9y10y12	1640.85	52.102	20866	3	547.62	-15.33
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	5		LTAFEYTIMETLIR	150	14	5	28.58	b7b12°b12y3y9	1700.91	68.414	19647	2	850.96	11.12
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	6		ELSVNEEVIK	140	10	6	27.71	b6b8°b8*b8y8*y8	1159.61	52.259	6272	2	580.31	-9.68
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	7		MQALMR	112	6	1	13.91	b3	749.39	51.344	3818	2	375.20	14.17
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	8		VEVLSSGADDYVTKPFHIEEVMAR	88	24	3	13.12	b13y7y12	2692.37	82.655	3248	4	673.85	14.33
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	9		EGWQDKVEVLSSGADDYVTKPFHIEEVMAR	82	30	6	25.64	b8b15y6°y6y7y10	3435.64	84.301	47211	4	859.67	-2.91
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	10	Oxidation+M(4)	DSLMLQLYPDaelRESHTIDVLMGR	172	25	5	23.76	b6b8b11y9y18	2918.40	107.172	4202	3	973.47	-12.88
[P14146]PHOP_SALTY Virulence transcriptional regulatory protein phoP	11	Oxidation+M(9)	LTAFEYTIMETLIR	150	14	5	31.75	b7b8b11°b11y9	1716.89	113.773	2085	2	858.95	1.56
[P58661]AAT_SALTY Aartate aminotransferase	1		ANYSNPPAHGASIVATILSNDALR	280	24	4	22.42	b2b8y6y7	2452.26	86.788	11542	3	818.09	-0.20
[P58661]AAT_SALTY Aartate aminotransferase	2		MFENITAAPADPILGLADLFR	0	21	11	39.02	b2b4b5°b5°b5b11y2y5y7y13y21	2275.20	121.188	11410	2	1138.10	8.37
[P58661]AAT_SALTY Aartate aminotransferase	3		QNGMFSFSGLTK	343	12	3	23.03	b4b6y11	1316.62	73.438	3585	3	439.54	-8.90
[P58661]AAT_SALTY Aartate aminotransferase	4		NFGLYNER	246	8	4	52.26	b6b7y5y7	1012.47	96.404	3270	1	1012.47	-10.73

P58661 AAT_SALTY Aartate aminotransferase	5		AEQYLLENETTK	51	12	3	23.03	b10y4y6	1438.67	73.361	3164	2	719.84	-22.31
P58661 AAT_SALTY Aartate aminotransferase	6	Carbamidomethyl+C(4)	VGACTLVAADAETVDR	254	16	4	28.62	b3y3y5y12	1647.81	55.646	3104	2	824.41	5.11
P58661 AAT_SALTY Aartate aminotransferase	7	Carbamidomethyl+C(15)	VNVAGMTPDNMAPLCEAIVAVL	374	22	5	18.96	b10b14y8y14°y14	2285.10	76.768	1844	3	762.37	-15.17
P58661 AAT_SALTY Aartate aminotransferase	8		AIWEQELTDMR	304	11	7	49.14	b3b4b7°b7*b7y3y10	1391.66	136.528	1550	1	1391.66	-2.02
P58661 AAT_SALTY Aartate aminotransferase	9		INLGIGVYKDETGK	28	14	3	28.55	y5y7y13	1506.81	44.806	4645	3	502.94	-7.13
P58661 AAT_SALTY Aartate aminotransferase	10		AIWEQELTDMRQR	304	13	3	21.36	b5y5y8	1675.83	37.743	1702	4	419.71	7.36
P58661 AAT_SALTY Aartate aminotransferase	11		TAQTPGGTGALRIAADFLAK	96	20	5	38.58	b10b11°b11b12b15	1959.04	62.079	1540	3	653.68	-13.65
P58661 AAT_SALTY Aartate aminotransferase	12	Oxidation+M(10)	AIWEQELTDMR	304	11	3	25.08	b4b10y8	1407.66	73.667	3878	2	704.34	5.46
P11003 METF_SALTY 5	1	Carbamidomethyl+C(11)	TGLEAAPHLTCIDATRDELRL	80	20	9	31.8	b5°b5b8b9y1y2y3y17y20	2239.11	59.769	19195	3	747.04	-3.60
P11003 METF_SALTY 5	2		EGVKDFHFYTLNR	266	13	4	33.35	b7y6y9y10	1625.79	61.748	13933	3	542.60	-8.03
P11003 METF_SALTY 5	3		LVGANIAMDMVK	250	12	4	33.24	y4°y4y7y10	1261.65	71.666	11562	2	631.33	-12.67
P11003 METF_SALTY 5	4		TIARDYWNNGIR	100	12	4	27.01	b9b10°b10y9	1478.76	72.659	4487	2	739.88	7.51
P11003 METF_SALTY 5	5		IPSWMSLMFEGLDNDNAETR	230	19	7	24.52	b6b9b12y2y10°y10y19	2212.03	111.544	4453	2	1106.52	11.81
P11003 METF_SALTY 5	6		IPSWMSLMFEGLDNDNAETRK	230	20	5	23.46	b1b6b8b11y12	2340.08	81.586	4069	2	1170.54	-10.22
P11003 METF_SALTY 5	7		FADMTNVR	222	8	4	33.95	b2b4y5y6	953.46	43.390	2711	2	477.23	4.61
P11003 METF_SALTY 5	8		EVADFDISVAAYPEVHPEAK	140	20	7	48.88	b3b5b8b11y5y11y17	2187.10	63.991	68455	4	547.53	19.87
P11003 METF_SALTY 5	9		AITQFFFDVESYLR	179	14	4	31.75	b10b11b13y10	1735.86	72.556	9967	2	868.44	-3.31
P11003 METF_SALTY 5	10		FVSVTYGANSGER	54	13	7	46.88	b3b7°b7b8b10y7°y7	1386.65	27.795	7661	2	693.83	-9.77
P11003 METF_SALTY 5	11	Carbamidomethyl+C(11)	TGLEAAPHLTCIDATR	80	16	4	25.5	b4b6°b6b9	1725.86	90.473	1887	2	863.44	2.90
P11003 METF_SALTY 5	12	Carbamidomethyl+C(8)	AEMSYAICHTLGVPRGL	279	17	3	16.93	b3b7y13	1874.95	72.607	1508	2	937.98	15.69
P11003 METF_SALTY 5	13		AITQFFFDVESYLRFR	179	16	3	17.8	b5b9y8	2039.04	58.429	11233	3	680.35	2.04
P11003 METF_SALTY 5	14	Carbamidomethyl+C(13)	ERTGLEAAPHLTCIDATR	78	18	5	23.57	b12°b12y7y8°y8	2011.03	105.381	11068	3	671.01	13.23
P11003 METF_SALTY 5	15		VDAGANRAITQFFFDVESYLR	172	21	5	14.38	b3°b3b13°b13y19	2419.17	67.505	9687	4	605.55	-14.23
P11003 METF_SALTY 5	16	Carbamidomethyl+C(1)	CVSAGIDVEIIPGILPVSNFKQAK	197	24	4	13.12	b4b11°b11y3	2555.39	63.952	6062	3	852.47	1.62
P11003 METF_SALTY 5	17	Oxidation+M(12)	GDLPPGSGKPEMYAADLVGLLKE VADFDISVAAYPEVHPEAK	118	42	4	10.86	b4°b4b7y11	4412.22	113.522	3324	4	1103.81	3.65
P11003 METF_SALTY 5	18	Carbamidomethyl+C(1)	CIDATRDELRL	90	10	0	5.65		1248.61	59.756	5843	2	624.81	4.40
P64267 GNS_SALTY Protein gns	1		TGQEVSEIEFAPR	28	13	4	35.83	y7y8y9y13	1462.73	57.902	14745	2	731.87	6.26
P64267 GNS_SALTY Protein gns	2		TGQEVSEIEFAPRETMK	28	17	8	62.9	b10b11b13b14°b14y6y9y14	1951.95	84.951	6856	3	651.32	2.13
P64267 GNS_SALTY Protein gns	3		NSEELTHK	1	8	4	36.96	b4b6y7°y7	957.48	58.951	2794	2	479.24	13.00
P64267 GNS_SALTY Protein gns	4		ETMKGLEGYHVK	41	12	3	27.01	b6b7y9	1391.71	46.740	1901	2	696.36	9.12
P64267 GNS_SALTY Protein gns	5		KTGQEVSEIEFAPR	27	14	6	41.15	b6b9y5°y5y10y12	1590.84	117.226	1871	2	795.92	14.73
P77983 KPYK1_SALTY Pyruvate kinase I	1		GDLGVEIPVEEVIFAQK	244	17	8	58.71	b3b5b7°b7b12y3y4y12	1843.00	95.429	28252	2	922.01	10.07
P77983 KPYK1_SALTY Pyruvate kinase I	2	Carbamidomethyl+C(3)	IVCTIGPK	5	8	4	36.96	b3b6y7y8	887.51	44.184	15763	2	444.26	7.50
P77983 KPYK1_SALTY Pyruvate kinase I	3		IENQEGLNNFDEILEASDGIMVAR	220	24	4	22.42	b3b4°b4y11	2677.25	113.119	7826	3	893.09	-8.66
P77983 KPYK1_SALTY Pyruvate kinase I	4		AEAGDVANAILDGTDAVMLSGESAK	292	25	4	19.54	b7b14b17y9	2405.13	75.413	5084	3	802.38	-7.82
P77983 KPYK1_SALTY Pyruvate kinase I	5		MLDAGMNVMR	22	10	4	29.47	b5°b5y6y7	1137.52	68.435	5033	2	569.26	-0.21

P77983 KPYK1_SALTY Pyruvate kinase I	6		VVITATQMLDSMIK	272	14	5	28.58	b8b10°b10y7y12	1549.81	72.268	3435	2	775.41	-12.29
P77983 KPYK1_SALTY Pyruvate kinase I	7		AHGGENIQISK	208	12	4	38.32	b4b7b11y9	1266.68	60.233	38897	2	633.84	1.25
P77983 KPYK1_SALTY Pyruvate kinase I	8		AGQTFTFITDK	86	11	4	28.09	b8*b8y5y6	1216.57	58.937	13028	3	406.19	-12.64
P77983 KPYK1_SALTY Pyruvate kinase I	9		SVVGNNEIVAVTYEGFTSDLSVG NTVLVDDGLIGMEVTAIEGNIK	97	44	12	30.48	b9°b9*b9b10°b10b14y3y7y 10°y10*y10y16	4526.28	97.419	10613	4	1132.33	7.66
P77983 KPYK1_SALTY Pyruvate kinase I	10		MMIEK	261	5	1	13.53	y3	651.31	44.474	7562	1	651.31	-10.21
P77983 KPYK1_SALTY Pyruvate kinase I	11		GAVETAEK	360	8	4	52.26	b3b6y4y5	804.42	68.459	6734	1	804.42	18.06
P77983 KPYK1_SALTY Pyruvate kinase I	12		LEGGNDVSLK	76	10	4	27.71	b4°b4b8y7	1031.55	41.658	1967	2	516.28	12.66
P77983 KPYK1_SALTY Pyruvate kinase I	13	Carbamidomethyl+C(7)	QDLIFGCEQGVDFVAASFIR	175	20	4	24.32	b3b4*b4b8	2272.10	112.797	1538	3	758.04	-1.72
P77983 KPYK1_SALTY Pyruvate kinase I	14		GAVETAEKLEAPLIVVATQGGK	360	22	4	13.91	b6b10°b10y5	2181.19	81.371	25224	3	727.74	-8.17
P77983 KPYK1_SALTY Pyruvate kinase I	15		GDLGVEIPVEEVIFAQKMMIEK	244	22	4	18.96	b6b11y5y8	2475.29	70.238	10332	3	825.77	-0.59
P77983 KPYK1_SALTY Pyruvate kinase I	16		KYFPDATILALTTNEVTAR	388	19	3	15.49	b3b6y3	2124.12	83.174	9757	3	708.71	-4.60
P77983 KPYK1_SALTY Pyruvate kinase I	17	Carbamidomethyl+C(3)	VICKVLNNGDLGENK	141	15	5	18.81	b3y3°y3*y3y12	1672.85	26.457	6980	3	558.29	-11.60
P77983 KPYK1_SALTY Pyruvate kinase I	18	Phosphoryl STY(10)	LEAPLIVVATQGGK	368	14	5	19.98	b4b11°b11*b11y3	1475.78	49.712	23102	2	738.40	4.88
P77983 KPYK1_SALTY Pyruvate kinase I	19	Phosphoryl STY(6)	DVALQSGLAQK	434	11	4	39.41	b4b10y3y4	1209.57	40.801	2364	2	605.29	-3.63
P77983 KPYK1_SALTY Pyruvate kinase I	20	Oxidation+M(8)	VVITATQMLDSMIK	272	14	3	27.76	y5y12y13	1565.83	63.816	8639	2	783.42	-1.09
P67551 YAEP_SALTY UPF0253 protein yaeP	1		VLNEVAADSALSESUREK	32	18	4	16.16	b9°b9b13y15	1916.99	79.885	2057	3	639.67	-3.06
P67551 YAEP_SALTY UPF0253 protein yaeP	2		VLNEVAADSALSESUR	32	16	5	29.29	b15°b15y9y10y14	1659.87	65.274	1833	3	553.96	6.47
P67551 YAEP_SALTY UPF0253 protein yaeP	3		AAAYAAANLLVSDYVNE	50	16	3	17.8	b4y3y8	1683.83	106.479	1573	2	842.42	1.52
P67551 YAEP_SALTY UPF0253 protein yaeP	4	Carbamidomethyl+C(18)	YAEIASGDLGYVPDALGCVLKVL NEVAADSALSESUR	11	37	3	10.93	b7b11y10	3851.97	114.845	19707	4	963.75	7.42
Q8ZP84 UE_SALTY Universal stress protein E	1		MAMYQNMLVVIDPNQDDQPALRR	0	23	6	27.28	b10b12y12°y12y13y23	2718.35	94.421	52438	3	906.79	11.86
Q8ZP84 UE_SALTY Universal stress protein E	2		ALVAVNLAASEPYHNALNEK	155	20	8	47.63	b2b3b11b16y7y9y10y16	2182.12	66.811	11830	3	728.04	0.78
Q8ZP84 UE_SALTY Universal stress protein E	3		TAWIREQAK	68	9	6	46.1	b3°b3b4y4y5y9	1102.60	49.629	11415	2	551.80	1.66
Q8ZP84 UE_SALTY Universal stress protein E	4		AMYQNMLVVIDPNQDDQPALRR	1	22	5	35.24	y10y11°y11y12*y12	2587.30	81.369	2723	4	647.58	8.02
Q8ZP84 UE_SALTY Universal stress protein E	5		VVWHNRPFETIIEQVIAGSHDLVL K	89	25	4	19.02	b3b7°b7b10	2870.51	110.669	22927	3	957.51	-20.41
Q8ZP84 UE_SALTY Universal stress protein E	6		TGLSAAFLGNTAEQVIDHLR	273	20	3	14.9	b3y10y16	2113.06	86.378	5538	3	705.02	-21.72
Q8ZP84 UE_SALTY Universal stress protein E	7		AFLPIYDFSYEMTTLLSPDER	36	21	9	56.23	b7°b7b8b10y3y6°y6y7y8	2508.23	85.365	5287	2	1254.62	13.24
Q8ZP84 UE_SALTY Universal stress protein E	8		DQPWPEGGK	146	9	4	31.32	b5b7y8*y8	1013.48	55.485	2186	2	507.25	15.78
Q8ZP84 UE_SALTY Universal stress protein E	9		VVWHNRPFETIIEQVIAGSHDLVL KMAHQHDR	89	32	9	43.87	b3b5b14y3y12y13*y13y14 *y14	3745.95	97.374	26283	5	750.00	0.20
Q8ZP84 UE_SALTY Universal stress protein E	10		MAHQHDRLEAVIFTPTDWHLLR	114	22	5	22.66	b8°b8b9°b9y7	2686.35	116.084	6834	3	896.12	-7.63

Q8ZP84 UE_SALTY Universal stress protein E	11		AFLPIYDFSYEMTTLLSPDERTAM R	36	25	3	12.8	b12y4y7	2967.40	92.291	6519	4	742.61	-7.57
Q8ZP84 UE_SALTY Universal stress protein E	12		IKAFPLPIYDFSYEMTTLLSPDER	34	23	6	40.7	y7y8*y8y10y11*y11	2749.38	74.756	2476	4	688.10	1.24
Q8ZP84 UE_SALTY Universal stress protein E	13	Carbamidomethyl+C(2)	KCPSPVWMVK	136	10	5	41.25	b4*b4b5b7y5	1231.64	60.748	1602	2	616.32	7.53
P40827 NLPD_SALTY Lipoprotein nlpD	1		VIENFGASEGGNK	265	13	5	33.35	b5b8*b8b9y6	1321.63	74.709	16013	2	661.32	-4.99
P40827 NLPD_SALTY Lipoprotein nlpD	2		IATMGSTGTSSTR	343	13	10	85.72	b8b9b11y4y6y7*y7y9y10y13	1269.61	28.726	13714	2	635.31	-2.98
P40827 NLPD_SALTY Lipoprotein nlpD	3		VVYAGNALR	297	9	6	31.32	b1b6*b6y4y7y9	962.53	40.818	10359	2	481.77	-11.03
P40827 NLPD_SALTY Lipoprotein nlpD	4		GSYTGGSSTYTVK	112	12	5	41.33	b3y6y7y8y12	1220.57	34.489	8642	2	610.79	-5.00
P40827 NLPD_SALTY Lipoprotein nlpD	5		SAQNSTVAVASQPTITYSEGSGEQ SANK	190	28	6	17.94	b9b11*b11b13y9y28	2812.34	48.626	3120	3	938.12	4.86
P40827 NLPD_SALTY Lipoprotein nlpD	6		MLPNNKPAGTVVTVAPVTAPTVST TEPNASSTSTSAPISAWR	218	41	6	35.43	b2b4y10y12y13y14	4110.13	69.240	2651	3	1370.71	11.64
P40827 NLPD_SALTY Lipoprotein nlpD	7		MGATTQQTPQQAQIQPVQRPVT QPMQTPVTEQPVQMENGR	58	42	3	23.78	y10y11y13	4684.34	58.626	5350	4	1171.84	8.34
P40827 NLPD_SALTY Lipoprotein nlpD	8		GDTLIFYAWITGNDFR	125	16	3	35.2	b8b9b10	1888.94	56.035	3861	2	944.98	11.70
P40827 NLPD_SALTY Lipoprotein nlpD	9		KGDTLIFYAWITGNDFR	124	17	3	16.93	b9y3y9	2017.02	70.706	2975	4	505.01	1.15
P40827 NLPD_SALTY Lipoprotein nlpD	10		GIDIAGSKGQAIVATADGR	278	19	3	15.49	b4b7y5	1799.95	106.500	2918	3	600.66	-5.29
P40827 NLPD_SALTY Lipoprotein nlpD	11		IATMGSTGTSSTRLHFEIR	343	19	4	24.52	b5b7b9y3	2065.04	69.675	2429	3	689.02	-5.44
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	1		LGSVFSSTGTGGGQEQTITSTWTT LAHHGMVIVPIGYAAQELFDVSQ VR	106	49	14	68.14	b7b33y1y2y3y4y5y6y7*y7y10y12y16y49	5134.57	116.792	24701	4	1284.40	3.04
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	2		TQNAPVATPQELADYDAIIFGTPT R	54	25	7	33.31	b4b11y3y4y6y12y25	2689.35	90.675	11561	3	897.12	0.18
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	3		TFLDQTGGLWASGSLYGK	88	18	4	16.16	b2b8y3y11	1900.94	115.003	2647	2	950.97	-3.98
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	4		GGTPYGATTIAGGDGSR	155	17	7	33.99	b10*b10b13y6y8y12*y12	1537.74	34.938	22145	3	513.25	8.34
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	5		FGNMSGQMR	79	9	3	31.32	b8y5y7	1027.44	38.754	12903	2	514.23	0.12
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	6		VPETMPPEIFAK	38	12	5	38.32	b3*b3b5b10y8	1358.73	84.007	3701	2	679.87	16.80
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	7		GGTPYGATTIAGGDGSRQPSQEEL SIAR	155	28	4	22.95	b14y10y23y24	2776.36	55.816	18865	3	926.13	5.19
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	8		TQNAPVATPQELADYDAIIFGTPT RFGNMSGQMR	54	34	7	15.77	b4b6*b6*b6b8*b8y5	3697.81	93.933	14675	3	1233.28	10.50
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	9		AKILVLYYSMYGHITMAHAVAE GAK	1	26	6	27.45	b13*b13b21y5y14y15	2866.44	100.244	4524	3	956.15	-9.11
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	10		VPETMPPEIFAKAGGK	38	16	4	28.62	b3b6b9y4	1671.86	40.019	2268	3	557.96	-8.10
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	11		LGSVFSSTGTGGGQEQTITSTWTT LA	106	26	0	16.57		2587.22	116.797	4407	3	863.08	-11.89
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	12		TQNAPVATPQELADYDAI	54	18	2	8.06	y12*y12	1916.92	90.698	1756	3	639.64	-3.69
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	1		TVVADGIGQGYKEVQEISPNLR	55	22	10	44.21	b2*b2b4y4*y4y6y9y11y13y22	2373.24	72.503	38767	3	791.75	0.41
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	2		SLGITNPEEIDR	6	12	3	23.03	b7b10y6	1343.70	49.933	2513	3	448.57	13.26

Q7CR64 YAEH_SALTY UPF0325 protein yaeH	3	Carbamidomethyl+C(10)	YVIDELDQICQRDR	77	14	8	49.76	b2b10y2y3y4y9°y9y10	1822.85	56.311	2398	3	608.29	-14.40
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	4		ILDDLRL	99	6	1	13.91	b5	744.42	52.531	13301	1	744.42	-9.35
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	5		ISEIEADLDK	114	10	4	34.7	y4y5°y5y9	1132.55	100.181	2231	1	1132.55	-18.86
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	6		TVVADGIGQGYKEVQEISPNLR	55	22	5	23.78	b9°b9°b9b10b20	2373.26	78.958	21417	3	791.76	8.44
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	7	Carbamidomethyl+C(10)	YVIDELDQICQRDR	77	14	5	39.74	b5b7°b7b8b12	1822.86	65.759	2789	3	608.29	-9.24
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	8	Carbamidomethyl+C(20)	EVQEISPNLRYVIDELDQICQR	67	22	4	22.66	b7°b7y5y6	2717.36	120.108	2684	3	906.46	2.34
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	9		YDNLKSLGITNPEEIDR	1	17	5	16.93	b6b13y12°y12*y12	1977.00	82.868	2147	2	989.01	6.17
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	10		SLGITNPEEIDRYSLR	6	16	6	29.29	b9b13*b13b14°b14y9	1862.94	103.425	1565	2	931.97	-13.30
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	1		IVSYAQGFSQLR	329	12	8	48.99	b2y6y7°y7y9°y9y10°y10	1368.73	63.196	10158	2	684.87	-0.80
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	2	Carbamidomethyl+C(11)	IAAVAEDGEPCVTYIGADGAGHY VK	158	25	4	12.8	b10°b10b21y10	2563.24	72.899	8487	3	855.08	9.72
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	3		NLALNIESR	16	9	4	39.1	b2y4y5y6	1029.57	72.082	4749	2	515.29	0.12
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	4		ELSAEGFNFIGTGVSGGEEGALK	113	23	8	34.66	b5b11°b11b13°b13y13°y13 y14	2269.09	68.481	3705	2	1135.05	-2.37
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	5		WTSQSALDLGEPLSLITESVFAR	264	23	9	36.7	b4b8°b8b9°b9y3y5y8y23	2520.31	117.778	2815	2	1260.66	4.65
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	6		GDIIDGGNTFFQDTIR	93	17	5	25.58	y9°y9y10*y10y13	1881.93	91.558	2295	2	941.47	-4.61
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	7		AAVLPANLIQAQR	432	13	3	21.36	b3y3y9	1364.80	65.318	6393	2	682.90	0.89
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	8		DVVVAYAVQNGIPVPTFSAAVAYY DSYR	405	27	4	23.09	y6y7y9°y9	2936.45	134.440	1963	3	979.49	0.67
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	9		AEFIEK	314	6	1	13.91	b4	736.40	84.337	1926	1	736.40	14.42
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	10		MSKQQIGVVGMAMVGR	0	16	4	31.75	b7b11y4y5	1691.85	101.729	6786	2	846.43	-12.55
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	11		ELSAEGFNFIGTGVSGGEEGALKG PSIMPGGQK	113	33	6	11.22	b7°b7b12°b12*b12y8	3221.56	84.294	6486	3	1074.53	-4.24
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	12		AQPAGDKAEFIEK	307	13	3	28.84	y3y7y8	1403.71	36.461	5618	2	702.36	-2.17
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	13		KIADEYQQALR	394	11	8	81.43	b5b6°b6b9y3y4y7y8	1334.72	44.856	3642	3	445.58	12.53
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	14	Phosphoryl STY(15)	ELSAEGFNFIGTGVSGGEEGALK	113	23	4	22.52	b13*b13b14y8	2349.04	104.335	4368	4	588.02	-6.34
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	15	Oxidation+M(8)	QQIGVVGMAMVGR	3	13	3	28.84	y3y4y9	1361.72	48.869	1935	3	454.58	11.83
P66955 TALB_SALTY Transaldolase B	1		LSYDTEASIAK	100	11	3	36.84	y8y9y10	1197.60	44.963	22145	2	599.30	-2.34
P66955 TALB_SALTY Transaldolase B	2		ISTEVDAR	92	8	6	58.28	b7y2y3y5y7y8	890.44	28.747	14770	2	445.73	-14.81
P66955 TALB_SALTY Transaldolase B	3		LYQPQDATTNPSLILNAAQIPEYR	25	24	6	13.12	b8y2y4°y4y9y24	2716.40	82.247	7846	3	906.14	3.51
P66955 TALB_SALTY Transaldolase B	4		ELAESEGAIER	250	11	4	25.08	b3y7y9y11	1203.59	37.218	5500	2	602.30	2.64
P66955 TALB_SALTY Transaldolase B	5		LYNDAGISNDR	117	11	5	39.41	b3b7y4y5y11	1237.59	63.147	3334	3	413.20	3.75
P66955 TALB_SALTY Transaldolase B	6		AAEQLEK	141	7	4	21.8	b4y4°y4*y4	788.41	35.495	2208	1	788.41	-4.80

P66955 TALB_SALTY Transaldolase B	7	Carbamidomethyl+C(11)	NVGEILELAGCDR	228	13	4	30.7	b3b7y6y11	1445.73	74.516	8221	2	723.37	17.65
P66955 TALB_SALTY Transaldolase B	8		MIGDLL	311	6	2	13.91	b5°b5	661.35	79.371	7984	1	661.35	-11.91
P66955 TALB_SALTY Transaldolase B	9		LTSLR	4	5	1	13.53	y4	589.37	64.482	6344	1	589.37	6.32
P66955 TALB_SALTY Transaldolase B	10	Carbamidomethyl+C(2)	ACAEAGVYLISPFVGR	165	16	3	17.8	b3b14y14	1709.87	95.052	3725	2	855.44	1.43
P66955 TALB_SALTY Transaldolase B	11		ITEAEFLWQH HQDPMAVDK LADG IR	275	25	3	19.02	y3y5y12	2920.43	74.820	15215	4	730.86	-4.01
P66955 TALB_SALTY Transaldolase B	12		LASTWQGIRAAEQLEK	132	16	3	17.8	b3y5y12	1800.95	78.844	2069	2	900.98	-3.73
P66955 TALB_SALTY Transaldolase B	13		LYQPQDATTN	25	10	0	7.16		1150.53	82.302	1609	2	575.77	-9.87
P0A2N2 VSDE_SALTY Virulence protein vsdE	1	Carbamidomethyl+C(12)	IIFGHELNQSYCLNSIDEVEK	110	21	4	14.38	b6°b6y5y10	2508.20	124.059	3238	3	836.74	-1.65
P0A2N2 VSDE_SALTY Virulence protein vsdE	2	Carbamidomethyl+C(6)	IKDALCIESKER	31	12	7	55.53	b8b9y2y6y7y8y12	1461.77	42.323	2480	3	487.93	-3.34
P0A2N2 VSDE_SALTY Virulence protein vsdE	3		HFSSSGEFYVR	198	11	4	25.08	b3y5y8°y8	1315.58	43.767	155814	3	439.20	-18.84
P0A2N2 VSDE_SALTY Virulence protein vsdE	4		NTASPTVGLDSAIVDK	94	16	4	25.21	b8b15y7y14	1587.81	67.947	2583	2	794.41	-10.22
P0A2N2 VSDE_SALTY Virulence protein vsdE	5	Carbamidomethyl+C(9)	HDFNAV VICEYDK	161	13	6	42.69	b4b11y4°y4y5y9	1609.77	51.380	2489	2	805.39	21.16
P0A2N2 VSDE_SALTY Virulence protein vsdE	6	Carbamidomethyl+C(19)	ESSFIISAENYIAPIIGECCR	141	20	5	14.9	b5°b5b8°b8y7	2269.12	95.404	1655	4	568.04	3.34
P0A2N2 VSDE_SALTY Virulence protein vsdE	7	Carbamidomethyl+C(4)	DALCIESKER	33	10	4	42.22	b4b7y8y9	1220.59	32.572	20393	2	610.80	-6.60
P0A2N2 VSDE_SALTY Virulence protein vsdE	8	Carbamidomethyl+C(19) ;Carbamidomethyl+C(29))	ESSFIISAENYIAPIIGECR HDFNAV VICEYDK	141	33	5	18.61	b5b9b11y7y9	3859.80	91.610	12297	3	1287.27	-9.17
P0A2N2 VSDE_SALTY Virulence protein vsdE	9	Carbamidomethyl+C(20)	RESSFIISAENYIAPIIGECCR	140	21	11	63.5	b3°b3b4b5b10°b10b14°b1 4y5y16y17	2425.21	102.810	2255	2	1213.11	-3.42
P0A2N2 VSDE_SALTY Virulence protein vsdE	10		VSGSASSQDIISRINSK	2	17	3	25.58	b4b5b7	1748.90	80.057	1795	2	874.95	-8.10
P0A2N2 VSDE_SALTY Virulence protein vsdE	11		KHFSSSGEFYVR	197	12	4	35.31	b10y5y10y11	1443.68	92.742	1526	2	722.35	-12.77
P0A2N2 VSDE_SALTY Virulence protein vsdE	12	Phosphoryl STY(8)	ILYPQNLSR	43	9	4	31.32	b6b8°b8y8	1183.56	41.711	30712	3	395.19	-12.07
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	1		ILDETFGFHEVIAQTGR	311	17	6	58.78	b3b4b5b6y5y13	1933.01	87.538	4770	3	645.01	14.52
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	2		HLNSGGELR	291	9	4	16.53	b5y3°y3y9	982.52	35.935	3892	2	491.76	13.17
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	3		QPQFSLESWWAEYNIDGLTIK	149	21	6	42.73	b5b6°b6b11b12y15	2525.29	72.894	26190	3	842.43	20.79
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	4		SAFTPASEVLLR	1	12	4	30.23	b4b10°b10b11	1290.69	67.140	12177	2	645.85	-15.32
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	5		ATLAANGLEGEVFASNVFSEVK	237	22	4	13.91	b14°b14b16y11	2253.19	95.388	5981	3	751.73	21.67
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	6		NKPEAQFQLMNILSLMPSGVDVF VVGENR	86	29	4	22.22	b7y11y12*y12	3232.59	121.783	4679	3	1078.20	-17.37

Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	7	Carbamidomethyl+C(4)	LTLCDVSAPAVEASR	222	15	3	18.81	b12y6y13	1588.80	87.794	2698	2	794.91	1.92
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	8	Carbamidomethyl+C(13)	FSLVAQASDVADCDTLIYYWPK	64	22	4	22.66	b10*b10y9y10	2562.19	81.801	2488	3	854.73	-13.24
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	9	Carbamidomethyl+C(4)	LTLCDVSAPAVEASRATLAANGL EGEVFASNVFSEVK	222	37	4	21.74	b5b9b10y13	3822.87	99.571	26170	3	1274.96	-13.28
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	10	Carbamidomethyl+C(17)	ILFAGDLQDDLPARFECAASR	22	21	3	14.38	b16y8y10	2365.15	89.100	8000	3	789.06	-2.89
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	11		QPQFSLESWWAEYNIDGLTIKTLPGVFSR	149	29	7	53.4	b4b5b8b9°b9y3y4	3382.75	103.576	4473	3	1128.26	12.63
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	12		SAEPLMADYAPLNKVD SAR	119	19	3	15.49	b7b11y5	2047.98	125.691	1526	2	1024.50	-13.17
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	13	Carbamidomethyl+C(6); Phosphoryl STY(12)	VLDVGCAGVLSAALASHSPK	199	21	6	19.74	b8°b8b11°b11y6y11	2089.03	102.770	5174	3	697.01	10.40
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	14	Oxidation+M(10)	NKPEAQFQLMNL SLMPSGVDVF VVGENR	86	29	3	11.81	b9b11y9	3248.64	95.253	2980	4	812.92	-0.23
Q8ZJW6 RSMC_SALTY Ribosomal RNA small subunit methyltransferase C	15	Oxidation+M(5)	SAEPLMADYAPLNK	119	14	3	25.42	b3b4y4	1535.75	53.761	2160	3	512.59	5.01
P06196 USHA_SALTY Silent protein ushA(0)	1		VVIQELNMNEKPDVVIATTHMGH YDNGDHGSNAPGDVEMAR	197	41	17	95.57	b1b2b3b8*b8b12y2y4°y4y 5y6y7y8y11y12*y12y13	4475.03	69.757	30860	6	746.68	-10.69
P06196 USHA_SALTY Silent protein ushA(0)	2		IAVIGLTTDDTAK	164	13	3	21.36	b3b11y5	1317.73	61.445	17014	2	659.37	-0.28
P06196 USHA_SALTY Silent protein ushA(0)	3		QNGIWIVQAHEWGK	279	14	8	84.59	y1y3y5y6y8y10y13y14	1665.85	103.443	12851	3	555.96	0.44
P06196 USHA_SALTY Silent protein ushA(0)	4		SEYGEYGLAAQK	48	12	4	30.23	y4y9y10y12	1315.61	44.632	11440	2	658.31	-6.50
P06196 USHA_SALTY Silent protein ushA(0)	5		EVAQEGGSVLLSGGDINTGVPESDLQDAEPDFR	68	34	4	13.51	b5b15y5y21	3514.64	73.292	7197	3	1172.22	-12.09
P06196 USHA_SALTY Silent protein ushA(0)	6		VQPFGNIVVYADMSGK	425	16	4	17.8	b11y5y13y16	1724.86	87.572	6305	3	575.62	-6.72
P06196 USHA_SALTY Silent protein ushA(0)	7		IGNPEYFTDIEFR	177	13	3	35.83	y7y8y9	1600.77	78.231	5232	3	534.26	5.72
P06196 USHA_SALTY Silent protein ushA(0)	8		IDNKPgyVNTGFIDAEVLK	508	19	3	15.49	b6y6y9	2093.12	69.772	33561	3	698.38	14.23
P06196 USHA_SALTY Silent protein ushA(0)	9		VLYTPEIAENPQMLSLLTPFQNK	332	23	3	22.52	b4y5y6	2646.38	101.644	12447	3	882.80	-1.38
P06196 USHA_SALTY Silent protein ushA(0)	10		GMNLIGYDAMAVGNHEFDNPLTVLR	102	25	4	28.57	b3b7b10b11	2747.39	95.517	12444	3	916.47	21.95
P06196 USHA_SALTY Silent protein ushA(0)	11	Carbamidomethyl+C(10)	QVNYVPGTPCAPDK	265	14	4	28.55	b7b10b12*b12	1545.70	70.548	9839	3	515.91	-20.93
P06196 USHA_SALTY Silent protein ushA(0)	12	Carbamidomethyl+C(20)	SLPAGSLAMIVGGHSQDPVCMAS ENK	238	26	4	12.5	b17y5y11°y11	2656.30	78.206	4629	3	886.11	18.01
P06196 USHA_SALTY Silent protein ushA(0)	13		FPFLYANIYQK	134	11	3	28.09	b7y4y5	1403.74	29.534	4478	3	468.59	6.26
P06196 USHA_SALTY Silent protein ushA(0)	14		ADFEFR	297	6	2	27.44	b5y5	784.36	51.415	4223	2	392.68	-9.34
P06196 USHA_SALTY Silent protein ushA(0)	15		MATLSFNATGGDGYPR	492	16	6	36.71	b8b13y4y5y12°y12	1657.76	81.874	3842	2	829.38	-4.71

[P06196]USHA_SALTY Silent protein ushA(0)	16		ITILHTNDHHGHFWR	33	15	3	18.81	b10b12y10	1883.94	105.721	2933	2	942.47	0.06
[P06196]USHA_SALTY Silent protein ushA(0)	17		EFIQQNSPLDAAFTPNGEVSWL	527	23	13	49.8	b8*b8b12y7*y7y9*y9*y9y 10y11y13*y13*y13	2534.26	109.651	1616	3	845.42	14.84
[P06196]USHA_SALTY Silent protein ushA(0)	18		QQEK	127	4	1	13.16	y3	532.27	64.241	1538	1	532.27	-4.70
[P06196]USHA_SALTY Silent protein ushA(0)	19		AQLEVKIGSVNGLLEGDR	357	18	4	22.64	b3b15y11y16	1898.01	60.846	22391	2	949.51	-12.61
[P06196]USHA_SALTY Silent protein ushA(0)	20		GMNLIGYDAMAVGNHEFDNPLT VLRQQEK	102	29	5	15.11	b4*b4b10y5y18	3260.56	66.279	7444	5	652.92	-5.47
[P06196]USHA_SALTY Silent protein ushA(0)	21	Carbamidomethyl+C(10)	QVNYVPGTPCAPDKQNGIWIWQA HEWGK	265	28	7	27.38	b4*b4b5*b5b7b11y23	3192.57	71.988	3887	3	1064.86	1.84
[P06196]USHA_SALTY Silent protein ushA(0)	22	Oxidation+M(10)	GMNLIGYDAMAVGNHEFDNPLT VLR	102	25	3	12.8	b7y14y17	2763.32	67.569	3860	3	921.78	-2.39
[P06196]USHA_SALTY Silent protein ushA(0)	23		VVIQELNMN	197	9	0	13.56		1059.56	69.711	21767	2	530.28	6.11
[P06196]USHA_SALTY Silent protein ushA(0)	24		GGDINTGVPESDLQDAEPDFR	81	21	4	36.93	b3b4b5b8	2232.04	73.295	8702	2	1116.52	14.88
[P06196]USHA_SALTY Silent protein ushA(0)	25		QNGIWIWQAHEWGK	279	14	0	3.39		1647.84	103.420	3280	2	824.42	4.96
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	1	Carbamidomethyl+C(13)	ISVMGHGMGIPSCSIYTKELITDFG VK	57	27	4	26.54	b5b7b9b12	2940.44	112.250	7900	4	735.86	-10.21
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	2		ATPHINAEMGDFADVVLMPGDPL R	1	24	3	22.42	b9b10y8	2566.24	76.776	6081	4	642.32	0.38
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	3		MATPHINAEMGDFADVVLMPGD PLR	0	25	4	12.8	b24y5y7*y7	2697.27	74.672	4259	4	675.07	-3.44
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	4		QTFNDMIK	218	9	4	31.32	b4b5y6y9	1097.53	51.722	3785	3	366.52	1.00
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	5	Carbamidomethyl+C(13)	ISVMGHGMGIPSCSIYTK	57	18	3	16.16	b12y10y16	1937.95	72.032	3374	4	485.24	13.48
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	6		YGVLGVEMEAAGIYGVAAEFGAK	173	23	5	36.31	b12b13y2y16y17	2302.13	81.618	1851	2	1151.57	-4.14
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	7	Carbamidomethyl+C(9)	DVVIGMGACTDSK	102	13	5	33.35	b3b7*b7b8y3	1352.65	93.545	8561	2	676.83	20.58
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	8		GMLGFTGTYK	44	10	3	34.7	b4b7b8	1074.55	27.777	3948	2	537.78	20.68
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	9	Carbamidomethyl+C(5)	ALTICTVSDHIRTHERQTTAAER	196	22	4	23.78	b3*b3b4b11	2510.22	68.662	14130	4	628.31	-7.78
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	10	Carbamidomethyl+C(14)	KISVMGHGMGIPSCSIYTK	56	19	4	15.49	b7b14y10*y10	2066.00	85.374	3565	2	1033.50	-13.59
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	11		THEQTTAAERQTFNDMIK	208	19	3	15.49	b4b8y10	2222.07	89.249	2297	2	1111.54	7.91
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	12		EVNNVRGMLGFTGTYK	38	16	5	28.62	b5*b5y7y10y12	1785.88	40.524	1897	2	893.44	-10.25
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	13	Carbamidomethyl+C(13) ;Oxidation+M(8)	ISVMGHGMGIPSCSIYTKELITDFG VK	57	27	5	35.08	b5b8b10b12b13	2956.46	134.296	7923	3	986.16	-1.49
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	14	Oxidation+M(2)	GMLGFTGTYK	44	10	5	41.25	b8y6*y6y7y9	1090.52	90.556	2556	1	1090.52	-7.28
[Q8ZJV7]DEOD_SALTY Purine nucleoside phohorylase deoD-type	15		DFADVVLMPGDPLR	11	14	3	12.27	b3b6*b6	1544.77	74.727	5604	2	772.89	-7.74
[Q8ZR01]RLPA_SALTY Rare lipoprotein A	1		LSQQFSVPGR	329	10	7	75.31	b3*b3b7y3y5y6y9	1118.59	48.445	20781	2	559.80	-2.29
[Q8ZR01]RLPA_SALTY Rare lipoprotein A	2		VIQNGAVWR	339	9	8	46.61	b2b5*b5y3y6y7*y7y9	1042.57	46.025	12109	2	521.79	-5.74
[Q8ZR01]RLPA_SALTY Rare lipoprotein A	3		FVVQVGAVSDQTR	309	13	5	26.13	b2b4y8y9y13	1405.74	57.199	7701	2	703.37	-3.47

Q8ZR01 RLPA_SALTY Rare lipoprotein A	4		LQTEAQLQSFIAAQ	366	15	3	26.89	y3y5y6	1634.85	84.021	15453	3	545.62	4.63
Q8ZR01 RLPA_SALTY Rare lipoprotein A	5		FSQAGLAAIYDAEPGSLNTASGEM FDPMQLTAAHPTLPIPSYAR	78	44	3	10.91	b4y7y10	4607.24	100.546	9399	4	1152.56	2.97
Q8ZR01 RLPA_SALTY Rare lipoprotein A	6	Carbamidomethyl+C(19)	IDPIIVAPDGSLSGPGMACTTVAK	167	24	3	13.12	b11b17y10	2370.24	70.533	3268	4	593.32	15.04
Q8ZR01 RLPA_SALTY Rare lipoprotein A	7		AAADRLNTSNNTK	152	13	3	21.36	b3y5y9	1375.70	63.040	39006	2	688.35	4.53
Q8ZR01 RLPA_SALTY Rare lipoprotein A	8	Carbamidomethyl+C(21)	VRIDPIIVAPDGSLSGPGMACTTV AK	165	26	6	36.11	b6y7y9y10y12y14	2625.38	74.295	22553	3	875.80	3.44
Q8ZR01 RLPA_SALTY Rare lipoprotein A	9		AQQYQQRLSQQFSVPGR	322	17	6	23.85	b3b5*b5y10*y10y16	2021.02	78.754	5287	2	1011.01	-4.29
Q8ZR01 RLPA_SALTY Rare lipoprotein A	10		INDRGPYGTDR	135	11	4	36.84	b5*b5b7b9	1263.60	42.430	2864	2	632.30	-5.02
Q8ZR01 RLPA_SALTY Rare lipoprotein A	11	Carbamidomethyl+C(19) ;Oxidation+M(17)	IDPIIVAPDGSLSGPGMACTTVAK	167	24	4	17.6	b14b21y9y12	2386.21	114.862	3245	3	796.07	4.19
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	1		TFDTPPTYNSLALSADGK	308	18	5	16.16	b4y2y11y14y18	1897.94	66.461	30698	2	949.47	10.23
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	2		QAGQVSVIDAK	291	11	5	28.09	b6*b6y3y4y11	1115.60	38.205	21581	2	558.30	-6.35
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	3		LLDDGKEHFFINLSLDTAGHR	223	21	3	14.38	b7y6y20	2398.22	76.703	5144	3	800.08	2.24
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	4		LYTTNADGEFITIDTASNK	198	19	3	15.49	b6b12y8	2074.00	104.047	2078	2	1037.51	2.94
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	5		ESAIWVVDGETIK	162	13	3	30.6	b7b9b12	1446.72	76.907	19696	2	723.86	-21.35
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	6		LVL DAR	126	6	1	13.91	b3	686.41	52.538	13293	1	686.41	-9.43
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	7		MSTGLALDSK	185	10	3	27.71	b4y3y9	1022.51	67.149	5116	2	511.76	-11.70
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	8		LDPVTLEITQAIHNDLKPFGATINA ATQTLWFGNTINS AVTAIDAK	73	46	4	21.74	b5y3y4y10	4894.53	128.321	4993	4	1224.39	-7.58
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	9		IAAPASLAVLFNPTR	268	15	4	24.83	b3y4y5*y5	1540.88	90.521	4963	2	770.94	-2.77
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	10		LLDDGK	223	6	2	30.45	b3b5	660.36	34.516	4545	1	660.36	7.02
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	11		GAYEMAWSQQENALWLATSQSR	41	22	5	25.01	b3y5*y5y6y9	2527.21	85.129	3736	2	1264.11	16.71
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	12		IAAPASLAVLFNPTRNEAYVTHR	268	23	9	62.53	y6y11*y11*y11y12y15y16y 18y20	2511.31	82.880	87942	4	628.58	-12.93
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	13		LLDDGKEHFFINLSLDTAGHR	223	21	3	21.02	b5b7b10	2398.18	66.118	19196	3	800.07	-12.83
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	14		NEAYVTHRQAGQVSVIDAK	283	19	3	15.49	b5b9y3	2086.08	65.206	8399	3	696.03	5.62
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	15		AQRLYTTNADGEFITIDTASNK	195	22	4	21.65	b8b11b15y11	2429.22	88.285	3790	3	810.41	12.16
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	16		STREQEATQPDDVIR	335	15	3	18.81	b7y5y10	1744.82	74.516	3353	3	582.28	-13.57
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	17	Phosphoryl STY(12)	ELVADAATNTIYISGVGKESAIWV VDGETIK	144	31	5	35.98	b9b10*b10b11y6	3329.67	68.463	56605	4	833.17	8.65
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	18		LLDDGKEHFFINLSLDTAGH	223	20	3	12.88	y8*y8y11	2242.11	76.758	35012	2	1121.56	-3.05
P65554 RPPH_SALTY RNA pyrophohydrolyase	1		VMKEFASVVMALQDNPPK	146	18	5	53.99	y5y7y8y9y10	2004.05	72.894	8287	3	668.69	10.90
P65554 RPPH_SALTY RNA pyrophohydrolyase	2	Carbamidomethyl+C(15)	IDDDGYRPNVGIVICNR	1	17	3	23.92	b11b12y13	1975.96	89.270	1579	2	988.48	-3.95

P65554 RPPH_SALTY RNA pyrophohohydrolase	3		QGQVMWAR	18	8	4	41.73	y3y4y6*y6	975.47	37.341	7885	2	488.24	-9.45
P65554 RPPH_SALTY RNA pyrophohohydrolase	4	Carbamidomethyl+C(7)	WDTKPVCIGQK	85	11	3	25.08	b4b9y8	1331.68	65.238	1941	2	666.35	4.77
P65554 RPPH_SALTY RNA pyrophohohydrolase	5	Carbamidomethyl+C(15)	IDDDGYRPNVGIVICNRQGQVMW AR	1	25	3	19.02	y4y9y20	2932.44	65.281	17628	4	733.87	4.58
P65554 RPPH_SALTY RNA pyrophohohydrolase	6	Carbamidomethyl+C(16)	MIDDDGYRPNVGIVICNRQGQVM WAR	0	26	3	12.5	b13y4y7	3063.45	133.410	9251	4	766.62	-8.21
P65554 RPPH_SALTY RNA pyrophohohydrolase	7		RFGQHSWQFPQGGINPGESAEQA MYR	26	26	4	23.48	b11y3y4y12	2978.38	129.174	1645	2	1489.69	0.49
P65554 RPPH_SALTY RNA pyrophohohydrolase	8	Oxidation+M(2)	VMKEFASVVMALQDNPPK	146	18	7	42.34	b4b14y3y12y13*y13y15	2020.04	84.976	2334	2	1010.52	6.89