

SA123 + Zn(II) LC-MS run 3: 123_Zn_220709_1a2_03

Protein name	Peptide Rank	Peptide Modification	Peptide Sequence	Peptide sequence start	Peptide sequence Length	Peptide Matched Products	Peptide Score	By Matches	Precursor MH+ (Da)	Retention time (min)	Intensity	z	Precursor m/z	MH+ Error (ppm)
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	50	373.87	b2°b2b3°b3b4°b4b5°b5b6°b6b7°b7b8°b8b9b10b12b13°b13b14°b14b15b17b21y1y2y3y4y6y7°y7°y7y8y9y10y11y12°y12*y12y13°y13y14y15y16°y16y17*y17y18y19y21	2216.10	97.000	488246	2	1108.55	1.54
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	11	86.67	b3°b3y2y5y6y7y8y9y10°y10y11	1304.56	32.693	108295	2	652.78	-2.99
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	3	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	4	20.46	b7y5y11y13	1624.75	93.187	49430	2	812.88	6.09
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	4		TPAVIKK	114	7	4	50.38	b4y3y4y6	756.49	19.220	13174	2	378.75	-13.72
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	5		TPAVIK	114	6	1	13.55	y5	628.40	27.031	4296	2	314.70	-4.37
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	6		YSYVDENGETKTWTGQGR	96	18	13	124.96	b3°b3y4y5y8y11y12*y12y13y14y15y16y17	2090.93	46.878	213528	3	697.65	-6.54
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	7		TPAVIKK	114	7	3	37.24	b4y5y6	756.50	20.054	3120	1	756.50	6.21
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	8	Oxidation+M()	EMLIADGIDPNELLNSMAAAK	62	21	4	22.21	b7°b7y14y15	2232.11	91.388	21181	2	1116.56	8.31
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	9	Oxidation+M(22)	LQQYREMLIADGIDPNELLNSMAAAK	57	26	7	30.81	b3°b3b13y6y11y12y14	2920.49	105.797	6144	3	974.17	11.37
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	10	Carbamidomethyl+C(6); Oxidation+M(14)	AQARECTLETLEEMLEK	15	17	10	54.8	b3b4°b4b5°b5°b5b8y7°y7y8	2067.00	136.283	2467	2	1034.00	12.28
[P0A1D5]CH10_SALTY 10 kDa chaperonin	1		VGDIVIFNDGYGVK	60	14	22	213.96	b3b4b5°b5b6b8b11b13°b13y1y2y3y4y5y6y7°y7y8y9y10y11y14	1495.78	73.397	264675	2	748.39	0.82
[P0A1D5]CH10_SALTY 10 kDa chaperonin	2		ILDNGTVQPLDVK	47	13	30	200.41	b2b3b4°b4b6°b6°b6b7°b7b8°b8°b8b9b11°b11b13y1y2y3y5°y5y7y8y9y10y11°y11*y11y12y13	1411.78	57.075	258523	2	706.39	-0.69
[P0A1D5]CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	21	139.8	b2°b2b4°b4b5°b5b6°b6b14y1y2y3y4y6y7y8°y8y9y11y12y14	1188.65	43.544	186754	2	594.83	-3.08
[P0A1D5]CH10_SALTY 10 kDa chaperonin	4		GEIIVGK	37	8	7	53.8	b2y2y3y4y5y6y8	786.46	41.530	20400	2	393.74	-9.00
[P0A1D5]CH10_SALTY 10 kDa chaperonin	5		IDNEEVLIMSESDILAIVEA	77	20	5	25.04	b12°b12y3y12y13	2203.13	83.847	2130	3	735.05	11.64
[P0A1D5]CH10_SALTY 10 kDa chaperonin	6		VGDIVIFNDGYGVKSEK	60	17	3	23.57	y10y12y14	1839.95	92.244	12156	2	920.48	1.53
[P0A1D5]CH10_SALTY 10 kDa chaperonin	7		SAGGIVLTGSAAGK	20	14	0	3.7		1170.64	43.576	46853	2	585.82	-2.09
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	1		IAAANVPAFVSGK	70	13	27	189.62	b2b3b4b5°b5b6°b6b8y1y2y3y4°y4y5y6y7°y7y8y9y10*y10y11°y11*y11y12y13*y13	1244.70	59.264	702918	2	622.85	-0.29
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVGFGTFK	22	29	7	24.79	b4b5°b5y1y3y7°y7	2966.55	136.167	6949	3	989.52	-7.74
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	3		NPQTGKEIK	61	9	6	30.28	b3y2y3°y3y5y9	1014.55	14.821	6202	2	507.78	-8.24

P0A1H5 EFTU_SALTY Elongation factor Tu	1		ELLSQYDFPGDDTPIVR	155	17	29	231.4	b2°b2b3°b3b5b6°b6°b6b7b15b16y1y3y4y5y6y7y8y9°y9y10°y10y11°y11y12y13y14y15y17	1964.97	76.672	479097	2	982.99	7.58
P0A1H5 EFTU_SALTY Elongation factor Tu	2		AIDKPFLLPIDVFSISGR	205	19	8	53.05	b7b8y1y3y5y6y7y19	2117.15	106.678	382737	3	706.39	-7.96
P0A1H5 EFTU_SALTY Elongation factor Tu	3		IIELAGFLDSYIPEPER	188	17	26	221.26	b1b2b3b4b6b7b12°b12b14y1y2y3y4y5°y5y6y7y8°y8y10y11y12y13y14y15y17	1962.02	102.328	330949	2	981.52	1.12
P0A1H5 EFTU_SALTY Elongation factor Tu	4		TTLTAAITTVLAK	25	13	9	74.36	b1b2y2y4y6y7y8y9y10	1303.78	84.931	317728	2	652.39	-1.12
P0A1H5 EFTU_SALTY Elongation factor Tu	5		AGENVGVLLR	270	10	13	88.02	b2b4b5°b5°b5y1y2y3y4y5y6y7y10	1027.58	56.219	309457	2	514.29	-8.91
P0A1H5 EFTU_SALTY Elongation factor Tu	6		GITINTSHVEYDTPTR	59	16	27	192.53	b2b3°b3b8b9b12y1y3y4°y4y5y6y7°y7y8°y8y9y10°y10y11°y11y12°y12°y12y13y14y16	1803.87	49.460	285681	3	601.96	-11.71
P0A1H5 EFTU_SALTY Elongation factor Tu	7		TTDVTGTIELPEGVEMVMPGDNI K	334	24	45	267.01	b2°b2b3°b3b4b7°b7b9°b9b10°b10b12b14°b14b16°b16b18°b18y3y4°y4°y4y5°y5y6°y6°y6y7°y7°y7y8y9°y9°y9y10y12y13°y13y14°y14y15y16y17y20y24	2546.25	86.631	237265	2	1273.63	3.45
P0A1H5 EFTU_SALTY Elongation factor Tu	8		QVGVPYIIVFLNK	124	13	9	66.7	b3b4°b4b13y4y6y9y11y13	1489.88	99.505	231582	2	745.44	-0.90
P0A1H5 EFTU_SALTY Elongation factor Tu	9		ALEGDAEWEAK	177	11	7	52.61	b2b4y4y7y8y9°y9	1218.56	46.160	175693	2	609.78	-1.20
P0A1H5 EFTU_SALTY Elongation factor Tu	10		TVGAGVVAK	382	9	9	45.18	b2°b2b7y1y2y3y7y8y9	801.47	28.318	161576	2	401.24	-14.09
P0A1H5 EFTU_SALTY Elongation factor Tu	11	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	10	67.76	b2°b2y2y3y4y6y7y8°y8y10	1187.52	52.747	116578	2	594.26	0.51
P0A1H5 EFTU_SALTY Elongation factor Tu	12	Carbamidomethyl+C(1)	CDMVDDEELLELEVEMEVR	137	18	13	89.19	b2b3b13y1y2y3y4y5°y5y6y7y8y14	2224.00	106.565	52532	2	1112.50	8.34
P0A1H5 EFTU_SALTY Elongation factor Tu	13		VGEEVEIVGIK	238	11	5	50.26	b4b7b8b10y11	1171.67	44.926	8611	2	586.34	7.50
P0A1H5 EFTU_SALTY Elongation factor Tu	14		MVVTLIHPIAMDDGLR	358	16	24	216.16	b3b4°b4b5°b5b6b14b15y3y4°y4y5°y5y6y7y8y9°y9y10°y10y11y13y15°y15	1780.92	79.501	820769	3	594.31	-15.42
P0A1H5 EFTU_SALTY Elongation factor Tu	15		TKPHVNVGTIGHVDHGK	8	17	5	16.17	b3y6°y6y9°y9	1795.93	90.125	85488	3	599.31	-16.11
P0A1H5 EFTU_SALTY Elongation factor Tu	16		LLDEGR	264	6	1	13.55	y4	702.38	23.063	5835	1	702.38	5.04
P0A1H5 EFTU_SALTY Elongation factor Tu	17		HTPFFK	319	6	1	13.55	y4	776.41	53.206	3965	2	388.71	-2.59
P0A1H5 EFTU_SALTY Elongation factor Tu	18	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLE LVEMEVR	124	31	13	106.29	b3b4°b4b5b6y4y5y6y7y8°y8y14y27	3694.85	128.025	46738	3	1232.29	2.38
P0A1H5 EFTU_SALTY Elongation factor Tu	19		TYGGAARAFDQIDNAPEEK	38	19	5	28.26	b10°b10b11y4y15	2052.99	74.499	6122	2	1027.00	13.68
P0A1H5 EFTU_SALTY Elongation factor Tu	20	Oxidation+M(23)	NMITGAAQMDGAILVVAATDGP MPQTR	90	27	4	21.83	b14b15y15°y15	2745.33	136.659	15026	2	1373.17	-0.98
P0A1H5 EFTU_SALTY Elongation factor Tu	21	Oxidation+M()	TTDVTGTIELPEGVEMVMPGDNI K	334	24	5	23.25	b6b8°b8b9y4	2562.26	105.958	1825	3	854.76	12.48
P0A1H5 EFTU_SALTY Elongation factor Tu	22		GAGVVAK	384	7	4	54.21	b3b4b5b6	601.37	28.323	83818	1	601.37	-2.74

P0A1H5 EFTU_SALTY Elongation factor Tu	23		TINTSHVEYDTPTR	61	14	3	14.28	b4°b4b10	1633.79	49.454	13834	2	817.40	5.16
P0A1H5 EFTU_SALTY Elongation factor Tu	24		TTDVTGTIELPEGVEM	334	16	2	12.25	y4y13	1691.78	86.661	3532	3	564.60	-12.70
P0A1H5 EFTU_SALTY Elongation factor Tu	25		LEGDAEWEAK	178	10	0	2.47		1147.53	46.043	2389	2	574.27	-0.74
P0A1H5 EFTU_SALTY Elongation factor Tu	26		GITINTSHVEYDTPT	59	15	0	4.53		1647.79	49.450	1676	2	824.40	3.85
P0A1H5 EFTU_SALTY Elongation factor Tu	27		GITINTSHVEYDTPTR	59	16	0	4.53		1785.87	49.471	21792	3	595.96	-2.32
P64076 ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	20	171.86	b2°b2b3°b3b4b5b14y2y3y4y6y7y8y9y10y11°y11y12y13y15	1605.88	85.871	341815	2	803.45	-0.68
P64076 ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	30	251.29	b2b3b9°b9b10b11b12b13°b13b14b16b18b22y2y3y4*y4y5y6y7*y7y8y9y10y12y13y14y15y17y22	2118.06	75.106	235375	2	1059.54	3.11
P64076 ENO_SALTY Enolase	3		YSMPVPMMNINGGEHADNNVDI QEFMIQPVGAK	143	34	19	104.19	b2b4b5°b5b23y3y5y6*y6y8y10y11y12y13y16y29*y29y31y34	3759.77	98.792	171484	3	1253.93	1.30
P64076 ENO_SALTY Enolase	4		GMNTAVGDEGGYAPNLGSNAEA LAVIAEAVK	200	31	30	215.04	b2b3b4b5°b5b6°b6°b6b12b13b16°b16b27y1y2y3y4y5y6y7y8y10y11y14y15y18y19y25y26y31	2989.46	95.028	140212	3	997.16	2.12
P64076 ENO_SALTY Enolase	5		AVGAVNGPIAQAILGK	66	16	10	75.34	b2b3b5y3y5y10y11y12y14y16	1478.87	75.011	138654	2	739.94	1.16
P64076 ENO_SALTY Enolase	6		DAGYTAVISHR	360	11	13	97.6	b2b4°b4b7y2y3y4y5y6y7y9°y9y11	1189.59	41.417	122840	2	595.30	-3.59
P64076 ENO_SALTY Enolase	7		GMPLYEHIAELNGTPGK	126	17	3	23.57	y3y11y13	1826.90	67.508	105473	3	609.64	-5.28
P64076 ENO_SALTY Enolase	8		IQLVGDDLFTNTNK	311	14	20	117.63	b2°b2b3b10y1y2y4*y4y5°y5y6*y6y8y9y10y11°y11y12y14*y14	1562.85	77.530	72986	2	781.93	3.98
P64076 ENO_SALTY Enolase	9		IEEALGEK	411	8	8	24.51	b2y2°y2y6°y6y7°y7y8	888.46	31.071	40755	2	444.73	-11.47
P64076 ENO_SALTY Enolase	10		QYPIVSIEDGLDESDWDGFAYQTK	282	24	7	12.61	b2b3b24y2y6y8y24	2776.28	93.762	36621	2	1388.64	4.66
P64076 ENO_SALTY Enolase	11	Carbamidomethyl+C(16)	AAGYELGKDITLAMDCAASEFYK DGK	231	26	7	34.56	b3b6°b6b7b11b16b26	2824.33	103.773	18172	3	942.11	3.89
P64076 ENO_SALTY Enolase	12		YVLAGEGNK	257	9	5	30.28	b3y3y7°y7*y7	950.51	33.293	122270	2	475.76	19.59
P64076 ENO_SALTY Enolase	13		GIANSILIK	333	9	3	38.06	y3y6y7	928.57	60.893	111108	2	464.79	-11.96
P64076 ENO_SALTY Enolase	14		EIIDSR	10	6	2	26.69	y4y5	732.40	26.247	32206	1	732.40	14.50
P64076 ENO_SALTY Enolase	15		GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	3	17.23	y4y8y18	2856.37	92.099	25265	3	952.80	5.56
P64076 ENO_SALTY Enolase	16		DGKYVLAGEGNK	254	12	4	22.09	b11y4°y4y9	1250.63	43.349	62002	2	625.82	-5.08
P64076 ENO_SALTY Enolase	17		VLGDKIQLVGDDLFTVNTNK	306	19	3	14.8	b4y10y14	2075.15	80.370	25644	2	1038.08	6.94
P64076 ENO_SALTY Enolase	18		EAIRMGSEVFHHLAK	180	15	7	52.04	b3b5°b5b8b10b11°b11	1724.87	90.135	10344	3	575.63	-8.92
P64076 ENO_SALTY Enolase	19		DQAGIDKIMIDLDGTENK	85	18	3	15.44	b8b15y16	1975.96	84.181	6254	3	659.32	-3.58
P64076 ENO_SALTY Enolase	20		IEEALGEKAPYNGR	411	14	3	27.69	y5y9y12	1546.77	88.306	3022	2	773.89	-12.86
P64076 ENO_SALTY Enolase	21		GYTAVISHR	362	9	2	7.83	b3°b3	1003.53	41.447	41333	2	502.27	-0.06
P64076 ENO_SALTY Enolase	22		AGYTAVISHR	361	10	0	2.47		1074.57	41.339	5483	2	537.79	-1.70
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	1		AAADLQLQGVPAMFVNGK	158	18	23	176.23	b2b4b5b6b7b8b9b10y1y2y3*y3y4*y4y5y7y8*y8y10y11*y11y12y18	1829.96	80.571	133407	2	915.49	3.27
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	2		YQINPQGMDTSSMDVFVQYAD TVK	176	25	18	72.18	b2°b2b4°b4b6b7b14y1y4y5y7°y7y8y9*y9y14°y14y25	2865.30	86.427	77475	3	955.77	-1.70

P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	3		TQTVQSAADIRK	116	12	9	68.5	b8*b8y2y3y6y7y8y10y12	1317.69	29.069	71248	3	439.90	-13.90
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		TQTVQSAADIR	116	11	9	36.46	b2*b2b6y2y7*y7y9y10y11	1189.61	35.021	36166	2	595.31	-5.34
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	5		ELTQAWAVAMALGVEDK	88	17	4	25.92	b13y6y8y11	1831.93	60.157	5956	2	916.47	0.07
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	6		VFVDAGVKGEDYDAAWNSFVVK	128	22	4	34.66	b10b11*b11b12	2416.20	117.074	3771	3	806.07	9.30
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	7	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	3	16.17	b3b6y5	1847.93	102.645	2938	2	924.47	6.80
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	37	271.9	b2b3b4*b4b5°b5*b5b6*b6b12b14y3y5y6y7*y7y8°y8y9y10*y10y11y13y14°y14y15*y15y16*y16y18°y18y19y20y21y22y24*y24	2574.32	98.323	575244	3	858.78	-0.76
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	2		AGIALNDNFVK	296	11	16	130.87	b3b4b7b8b10*b10y1y2y3y5*y5y6y7*y7y8y11	1161.62	61.254	286842	2	581.31	-6.31
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	3		GASQNIIPSSTGAAK	198	15	22	155.71	b5°b5*b5b6°b6*b6b7°b7*b7b13b15y2y3y4y5y6y7y8y9y10y11y15	1401.73	40.606	281915	2	701.37	-2.87
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		LVSWYDNETGYSNK	307	14	16	156.76	b3b9b11b12y2y3y4y5y6y8y9y10y11y12°y12y14	1675.77	58.040	244222	2	838.39	3.57
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		AATYEQIK	249	8	13	53.8	y2y4°y4*y4y5*y5y6*y6y7°y7*y7y8*y8	923.47	30.918	148889	2	462.24	-11.70
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		VPTPNVSVVDLTVR	232	14	17	138.71	b2b3°b3y1y2y3y4y5y6y7y8y9y11y12°y12y13y14	1495.85	70.790	132750	2	748.43	0.49
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		LTGMAFR	225	7	5	40.25	y1y4y5y6y7	795.41	49.311	82990	2	398.21	-11.13
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		VVLTGPSKDNTPMFVK	116	16	4	24.71	b2y5y8y13	1732.91	57.560	61609	3	578.31	-12.75
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		VLPELNGK	217	8	11	66.94	b2y2y3y4y5°y5y6°y6*y6y7y8	869.50	44.613	52529	2	435.25	-8.28
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		SDIEIVAINDLLDAEYMAYMLK	24	22	10	42.4	b4b6°b6b10°b10*b10b13y4y6y13	2530.21	87.842	13791	2	1265.61	-15.73
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11	Carbamidomethyl+C(12) ;Carbamidomethyl+C(16))	YEQDIVSNASCTTNCLAPLAK	138	22	5	17.98	b3b9y11y15*y15	2412.12	119.417	2040	3	804.71	-0.61
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEGQDIVSNASCTTNCLAPLAK	132	28	34	282.31	b3b4b5b7b8b11°b11*b11b12°b12b13°b13*b13b15b16b18b24*b24b27y3y4y5y6y8y9y10*y10y11y12y13y14y15*y15y16	3044.41	66.771	346053	3	1015.48	1.04

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13		RSDIEIVAINDLLDAEYMayMLK	23	23	6	33.57	b4b6b7b14y6y9	2686.35	136.185	21812	3	896.12	0.00
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14		GGRGASQNIIPSSTGAAK	195	18	6	26.36	b8°b8*b8y3y8y9	1671.86	36.698	6302	3	557.96	-11.46
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15	Oxidation+M(20)	SDIEIVAINDLLDAEYMayMLK	24	22	3	13.32	b5y5y11	2546.24	131.500	1738	2	1273.62	-0.10
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		NTPMFVK	125	7	0	4.53		836.43	57.548	1659	1	836.43	-7.37
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		AATYEQIK	249	8	0	1.23		905.46	30.906	57467	2	453.23	-7.01
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		LTGMAFR	225	7	0	0.82		777.40	49.263	5757	2	389.20	-3.61
P41031 CY_SALTY Thiosulfate-binding protein	1		ELFAALNPPFEQQWAK	37	16	32	187.18	b2°b2b3°b3b4°b4b5°b5b6b7*b7b12°b12*b12b14b15y1y2y4*y4y6y7y8y9*y9y11°y11*y11y12*y12y13°y13	1888.97	90.078	89005	2	944.99	4.72
P41031 CY_SALTY Thiosulfate-binding protein	2		QYEAQGFVVIPK	226	13	9	45.86	b3*b3b4b10°b10b11°b11y2y13	1507.78	69.768	75731	2	754.39	0.97
P41031 CY_SALTY Thiosulfate-binding protein	3		VNNPEIMGK	286	9	8	67.35	b2y3y4y6y7*y7y8y9	1001.50	35.979	73677	2	501.26	-4.33
P41031 CY_SALTY Thiosulfate-binding protein	4		LPNNSSPFYSTMGFLVR	110	17	9	74.37	y2y3y5y7y8y9y11y12y17	1929.97	92.212	73103	2	965.49	6.70
P41031 CY_SALTY Thiosulfate-binding protein	5		TEQFMTQFLK	179	10	6	51.61	b2y3y5y6y7y10	1272.63	75.676	71361	2	636.82	3.65
P41031 CY_SALTY Thiosulfate-binding protein	6		QALAILQGLK	71	10	6	26.71	b3*b3y1y2y5y7	1054.66	75.194	51375	2	527.83	-6.13
P41031 CY_SALTY Thiosulfate-binding protein	7		LIFPNPK	146	7	8	40.25	b2y2y4y5*y5y6*y6y7	828.49	55.965	50687	2	414.75	-11.35
P41031 CY_SALTY Thiosulfate-binding protein	8		NVEVFDTGGR	189	10	8	73.91	b6y4y5°y5y6y7y8y10	1093.53	47.050	49657	2	547.27	1.90
P41031 CY_SALTY Thiosulfate-binding protein	9		GATTTFAER	199	9	5	45.18	b8y4y5y6y9	953.47	30.853	23927	2	477.24	-3.33
P41031 CY_SALTY Thiosulfate-binding protein	10		AYLNWLYSPQAQTIIHYYR	265	21	6	13.75	b2b5b8°b8y2y9	2664.33	94.054	7728	2	1332.67	2.38
P41031 CY_SALTY Thiosulfate-binding protein	11		GLGDVLISFESEVNNIRK	208	18	4	24.6	b3b10b12y3	1990.05	105.340	6297	3	664.02	-6.13
P41031 CY_SALTY Thiosulfate-binding protein	12		ADVVTYNQVTDVQILHDK	81	18	7	26.36	b8°b8b12b13°b13y13*y13	2058.01	91.585	6859	3	686.67	-20.64
P41031 CY_SALTY Thiosulfate-binding protein	13		TSGNAR	153	6	1	13.55	b5	605.30	87.109	1831	1	605.30	-4.03
P41031 CY_SALTY Thiosulfate-binding protein	14		TNILAEFPVAVDKNVQANGTEK	239	23	5	37.01	b3b4y6y19y20	2544.31	91.225	153486	3	848.78	0.86
P41031 CY_SALTY Thiosulfate-binding protein	15		YTYLAAWGAADNADGGDKAK	159	20	3	21.03	y6y9y13	2057.94	61.988	50707	3	686.65	-5.58
P41031 CY_SALTY Thiosulfate-binding protein	16		TSGNARYTYLAAWGAADNADGGDK	153	24	5	23.25	b9b14b15y15°y15	2445.13	93.922	8687	4	612.04	8.99
P41031 CY_SALTY Thiosulfate-binding protein	17		FGSWPEVMKTHFASGGELDK	311	20	10	51.62	b7b9°b9y5y6°y6y8y9y11°y11	2223.08	136.386	5662	2	1112.04	12.41
P41031 CY_SALTY Thiosulfate-binding protein	18		QADKFPQTELFR	295	12	3	32.3	b3b5b10	1479.76	68.616	3525	2	740.38	-2.72
P41031 CY_SALTY Thiosulfate-binding protein	19		THFASGGELDKLLAAGR	320	17	3	16.17	b4b9y14	1742.93	76.053	3517	3	581.65	5.74

P41031 CY_SALTY Thiosulfate-binding protein	20		NVEVFDTGGRGATTTFaER	189	19	6	40.5	b5b9b12b15y10y14	2027.99	72.935	2517	3	676.67	6.68
P41031 CY_SALTY Thiosulfate-binding protein	21	Phosphoryl STY(11)	GLGDVLISFESEVNNIRK	208	18	3	24.36	b4b9b10	2070.02	136.259	7079	2	1035.51	0.59
P41031 CY_SALTY Thiosulfate-binding protein	22	Oxidation+M(8)	FGSWPEVMK	311	9	6	78.73	b4b5y4y5y7y8	1096.51	112.656	1656	1	1096.51	-2.56
P41031 CY_SALTY Thiosulfate-binding protein	23		AYLNWLYSPQAQTII	265	15	0	6.58		1780.92	94.121	1697	2	890.96	-5.35
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	1		SGFAEDEVVAVSK	35	13	17	131.82	b2b3b4°b4b5b10y1y2°y2y3y4y6y7y8y9y10y13	1337.66	54.140	226772	2	669.33	0.73
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	2		LGEIEYR	48	7	10	82.68	b3b5y2y3y4y5°y5y6°y6y7	879.45	42.134	184742	2	440.23	-10.62
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	3		MITGIQITK	0	9	9	59.57	b1b2b3b6y2y3y6y7y9	1004.57	54.814	174793	2	502.79	-9.72
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	4		EIPMEVKPEVR	55	11	8	65.16	y1y2y4y5y6y8y9y11	1326.71	48.771	131483	2	663.86	-1.01
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	5		VEGGQHNLNVNVLr	66	13	7	52.6	b3b4b8y4y6y7y13	1434.76	50.424	108467	3	478.92	-14.55
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	6		FNSLTPEQQR	106	10	23	112.55	b2°b2b3°b3°b3b9b10y1y2y3°y3y4y5°y5y6°y6y7y8°y8y9°y9y10°y10	1219.60	37.841	104997	2	610.31	-2.00
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	7		FNSLTPEQQRDVIAr	106	15	9	36.78	b3°b3b11y1y6y10°y10y13y15	1773.91	47.437	51369	3	591.98	-7.16
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	8		AANDDLLNSFWLLDSEK	9	17	3	16.17	b3b15y9	1950.96	101.429	6032	2	975.98	8.76
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	9		TFTESL	121	6	10	79.26	b3°b3b4°b4b5°b5y3y4y5°y5	697.34	55.033	89932	1	697.34	-2.10
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	10		AANDDLLNSFWLLDSEKGear	9	21	24	199.6	b3b5°b5b6°b6y4y5y7°y7y8y9°y9y10y11y12y13y14°y14y15y16y17°y17y19°y19	2364.14	92.999	563921	3	788.72	-4.23
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	11	Carbamidomethyl+C(1)	CIVAKSGFAEDEVVAVSK	30	18	3	15.44	b4b8y10	1908.95	121.869	19235	2	954.98	-11.57
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	12		ITGIQITKAANDDLLNSFWLLDSEK	1	25	7	50.13	y5y6y7°y7y9°y9y10	2805.47	136.352	4523	3	935.83	0.96
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	13		VSGYAVRFNSLTPEQQR	99	17	4	25.92	b12y5y11y13	1951.98	103.667	2124	3	651.33	-10.26
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	14		PMEVKPEVR	57	9	3	31.1	b3b4b7	1084.58	48.794	134579	2	542.79	-6.08
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	15		EIPMEVKPEVR	55	11	0	2.47		1308.68	48.789	47524	3	436.90	-10.82
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	28	187.38	b2°b2b3b5°b5b7°b7b9b11b12°b12°b12b13b14b16y2y4°y4y6°y6y7y8y9y10y11y12y17y23	2379.24	64.418	162086	3	793.75	-1.03
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	7	38.85	b2b3y4y6y13y15y17	1837.95	86.290	130563	2	919.48	3.85
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	10	46.46	b2b3b5°b5y9y13°y13y14y15y18	1919.02	85.327	119137	2	960.01	5.47
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4		AQAFTLVAK	24	9	6	57.22	y2y3y4y6y7y9	948.54	53.183	95043	2	474.78	-8.17
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		NYGVEIVDGPLK	116	12	10	71.07	b1b2b3b4b9y4y8y9y10y12	1303.69	64.815	33770	2	652.35	-1.59
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		DLSDVSLSQYAGKR	33	14	5	27.32	b7b12y7y9°y9	1538.76	54.618	13671	3	513.59	-11.66

Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		AVIVLDENDNVIFSQLVDEITHEPDYDAALNVLK	133	34	4	10.96	b2b10y12y14	3811.92	119.489	6444	3	1271.31	-2.56
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8	Carbamidomethyl+C(15)	FNQLATEVENTVVLCSADLPFAQSR	67	26	4	21.83	b6b7y8°y8	2908.44	87.623	4827	3	970.15	-2.10
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9		DLSDVLSQYAGK	33	13	12	123.91	b4°b4b5b6y4y5y6*y6y7y9y10y11	1382.67	58.858	6661	1	1382.67	-5.30
Q8ZP65 TPX_SALTY Probable thiol peroxidase	10		AVIVLDENDNVIFSQLVDEITHEPDYDAALNVLKA	133	35	15	123.47	b3b4b5b6b11y3y4y5y8y12y13y14y24y29y30	3882.97	121.450	108171	3	1294.99	1.32
Q8ZP65 TPX_SALTY Probable thiol peroxidase	11	Phosphoryl STY(12)	SQTVHFQGNPVTVANVIPQAGSK	1	23	8	29.21	b4b6b10*b10b11*b11y6°y6	2459.23	136.369	2120	2	1230.12	13.40
Q8ZP65 TPX_SALTY Probable thiol peroxidase	12		AQAFTLVAK	24	9	0	1.65		931.51	53.299	5530	2	466.26	-11.53
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		LADVLAANAR	57	11	16	126.89	b2b3b4y1y3*y3y4*y4y5y6*y6y7y8y9y10y11	1084.60	53.127	230109	2	542.80	-8.44
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGSLGDQVNVK	8	14	16	122.69	b2b3b9*b9b10*b10b13y3y7y8y9y10°y10y11y12y14	1413.77	56.251	141651	2	707.39	2.50
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		DIADAVTAAGVDVAK	97	15	16	152.4	b2b3b5b6b9°b9b12y3y6y7y8y9y10y11y13y15	1415.74	65.905	96474	2	708.37	3.45
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		INALETVTIASK	71	12	4	22.09	b4y9y11y12	1259.71	60.956	60738	2	630.36	-4.94
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		MQVILLDK	0	8	3	40.66	y3y4y5	959.55	64.363	96400	2	480.28	-6.23
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		NVEYFEAR	42	8	3	40.66	y3y5y6	1027.48	46.767	86462	2	514.25	-0.95
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		AGDEGKLFGSIGTR	83	14	5	45.1	b7y3y6y7y8	1407.70	55.000	83223	3	469.91	-12.92
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		LPNGVLRTTGEHEVNFQVHSEVFAK	116	25	4	12.31	b23°b23y7y10	2808.48	112.600	7957	3	936.83	11.47
P0A1E3 CYSK_SALTY Cysteine synthase A	1		LTLTMPETMSIER	87	13	14	112.53	b2°b2b5°b5y1y4y5y6y8y9y10y11y12y13	1521.77	73.820	132711	2	761.39	2.97
P0A1E3 CYSK_SALTY Cysteine synthase A	2		IQGIGAGFIPGNLDLK	226	16	14	76.73	b1b2°b2b3b4b8b9y1y2y7y10y12y14y16	1612.91	83.544	120975	2	806.96	3.33
P0A1E3 CYSK_SALTY Cysteine synthase A	3		YLLLQQFSNPANPEIHEK	137	18	15	94.7	b2b3y2°y2y3°y3y4y6°y6y7y9y11*y11y12y16	2141.10	74.136	106656	3	714.37	0.57
P0A1E3 CYSK_SALTY Cysteine synthase A	4		IYEDNSLTIGHTPLVR	3	16	5	24.71	y2y4y7°y7y14	1827.94	61.786	58172	3	609.98	-12.09
P0A1E3 CYSK_SALTY Cysteine synthase A	5		LQEDESFTNK	283	10	4	36.71	y6y7y8y10	1210.56	34.912	47742	2	605.78	2.82
P0A1E3 CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	9	82.32	b2b3b4y6y7y8y9y10y12	1283.73	63.870	47604	2	642.37	-2.00
P0A1E3 CYSK_SALTY Cysteine synthase A	7		ALGANLVLTEGAK	105	13	4	29.7	b2y5y7y9	1256.71	61.051	42387	2	628.86	-4.76
P0A1E3 CYSK_SALTY Cysteine synthase A	8		AEEIVASDPQK	126	11	12	112.96	b3b4°b4b5°b5b6y3y6y7y8y9y11	1186.59	31.254	31954	2	593.80	-4.32
P0A1E3 CYSK_SALTY Cysteine synthase A	9		VVGITNEEAISTAR	246	14	4	38.49	y4y9y10y12	1459.78	49.191	26794	2	730.39	2.17
P0A1E3 CYSK_SALTY Cysteine synthase A	10		GYKLTLTMPETMSIER	84	16	3	25.38	y7y12y13	1869.96	86.390	22168	2	935.49	10.71
P0A1E3 CYSK_SALTY Cysteine synthase A	11		MSKIYEDNSLTIGHTPLVR	0	19	5	37.91	b10°b10b11b12b14	2174.12	84.911	1539	2	1087.57	-1.35
P0A1E3 CYSK_SALTY Cysteine synthase A	12	Oxidation+M(5)	IGANMIWDAEK	44	11	3	24.11	b3y3y6	1263.61	43.349	53557	2	632.31	6.09
P0A1E3 CYSK_SALTY Cysteine synthase A	13		LTMPETMSIER	89	11	0	3.29		1307.63	73.871	4585	2	654.32	-0.84

[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	1		DQIIEAVSAMSVM DVVELISAMEE K	5	25	26	196.21	b2°b2*b2b3b4b5b6b7b8b9°b9b10y2°y2y3°y3y4y5°y5y6y7y8°y8y9y10y25	2737.34	137.221	66727	3	913.12	0.45
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	2		DLVESAPAALK	85	11	7	59.73	b3b4b8y5y7y8y11	1113.61	53.225	36269	2	557.31	-7.78
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	3		DLVESAPAALKEGVSK	85	16	3	17	b5b7y10	1613.86	56.454	6135	3	538.63	-8.02
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	4		SLEEAGAEVEVK	109	12	4	32.3	b3°b3b5b11	1260.65	58.983	9128	3	420.89	17.53
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	5		FGVSAAA AVAVAAGPAEAAEEK	30	22	8	54.21	b9b10°b10y4y5°y5y9y10	1987.00	105.895	2755	2	994.01	-4.61
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	6		FGVSAAA AVAVAAGPAEAAEEKT EFDVILK	30	30	9	32.2	b3b4°b4b7°b7b10°b10b23°b23	2932.51	136.256	14733	3	978.18	-5.41
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	7		SITKDQIIEAVSAMSVM DVVELISAMEEK	1	29	4	26.43	y7y8y10y13	3166.62	90.122	5340	3	1056.21	7.79
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	8		EAKDLVESAPAALK	82	14	3	19.11	b4b9y8	1441.79	61.072	2325	2	721.40	2.62
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	9	Phosphoryl STY()	EAKDLVESAPAALK	82	14	4	26.89	b6b7°b7b9	1521.74	43.427	2697	2	761.38	-2.25
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	1	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	8	42.53	b13y10y11y12°y12y14y19y24	2589.31	82.887	88722	3	863.77	1.79
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	2		SATPAQAQAVHK	176	12	19	108.14	b2b3°b3b5°b5b7°b7y1y2y4y5°y5y6y7°y7y8°y8y9y12	1208.63	18.395	59198	2	604.82	-6.06
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	3		TQGAAAFEGAVIAYEPVWAIGTG K	152	24	13	47.25	b3°b3b5°b7b11b13b14y1y2y7y10y12y24	2407.25	93.886	25589	2	1204.13	6.90
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	4	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	5	23.03	y1y3y4y10y23	2433.20	88.212	18934	2	1217.11	0.10
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	5	Carbamidomethyl+C(9)	EQGLTPVLCIGETEAEENEAGK	117	21	3	12.65	b4b9b13°	2245.10	72.114	3049	2	1123.05	13.59
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	6	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAEENEAGKTEE VCAR	117	28	15	124.41	b5°b5b7y3y4y7y10y12y13y18y20y21y23y24y26	3090.44	72.057	175231	3	1030.82	2.05
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	7	Carbamidomethyl+C(9); Phosphoryl STY(13)	EQGLTPVLCIGETEAEENEAGK	117	21	4	18.72	b5b12y4y7	2325.05	68.572	5513	3	775.69	13.97
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	8		TPAQAQAVHK	178	10	10	78.72	b3°b3b4°b4b5°b5b6°b6b7b8	1050.56	18.401	23630	2	525.78	-6.86
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	9		PAQAQAVHK	179	9	9	78.72	b3°b3b4b5b6°b6b7°b7b8	949.51	18.388	22972	2	475.26	-8.29
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	10		VAIAPPEMYIDLAK	37	14	0	7.41		1530.81	88.235	1534	3	510.94	-7.42
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	11		SATPAQAQAVHK	176	12	0	2.88		1190.61	18.399	19025	3	397.54	-14.35
[P66593]RS6_SALTY 30S ribosomal protein S6	1		YSAAITGAEGK	24	11	18	142.25	b3b4b6b9b11°b11y2y3y4°y4y5y6°y6y7y9y10°y10y11	1067.53	33.240	136177	2	534.27	-5.49
[P66593]RS6_SALTY 30S ribosomal protein S6	2		FNDAVIR	79	7	6	53.39	y2y3y4y5y6y7	834.44	42.456	85401	2	417.72	-13.09
[P66593]RS6_SALTY 30S ribosomal protein S6	3		HAVTEASPMVK	93	11	14	98.57	b2b4°b4b7°b7b10°b10y1y4y7y8y9y10y11	1169.59	31.693	68179	2	585.30	-4.80
[P66593]RS6_SALTY 30S ribosomal protein S6	4		AHYVLMNVEAPQVEIDELETTFR	56	23	7	27.97	b3b6b7°b7y8y11°y11	2704.33	114.679	63454	3	902.12	1.44
[P66593]RS6_SALTY 30S ribosomal protein S6	5		LEDWGR	38	6	2	29.7	y3y5	775.37	38.894	17361	2	388.19	-8.82
[P66593]RS6_SALTY 30S ribosomal protein S6	6		YSAAITGAEGKIHR	24	14	4	34.68	b6b7°b7b8	1473.78	76.399	16455	2	737.39	-3.48

P66593 RS6_SALTY 30S ribosomal protein S6	7	Oxidation+M(9)	HAVTEASPMVK	93	11	4	38.04	b7b8y3y10	1185.58	90.077	10451	2	593.29	-11.63
P66593 RS6_SALTY 30S ribosomal protein S6	8	Oxidation+M(19)	HYEIVFMVHPDQSEQVPGMIER	2	22	4	13.32	b8y6y9*y9	2657.25	129.550	3639	3	886.42	1.84
P65702 PGK_SALTY Phohoglycerate kinase	1		VLPVAMLEER	373	11	10	70.52	b2b3y1y2y4y6y7y8y9y11	1227.67	80.211	221897	2	614.34	-6.07
P65702 PGK_SALTY Phohoglycerate kinase	2	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	21	191.83	b2b3b4b5b8b11y1y2y3y4y5y6y7y8y9y12y13y14y15y16y20	2002.04	99.335	177008	2	1001.52	4.27
P65702 PGK_SALTY Phohoglycerate kinase	3	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	17	119.68	b2b5b6*b6b7*b7b9b12y1y2y5y7y8y10y11y12y14	1599.84	68.400	167268	2	800.43	1.37
P65702 PGK_SALTY Phohoglycerate kinase	4		VATEFSETAPATLK	258	14	20	129.01	b1b2b3*b3b4*b4b9y2y5*y5y6y7y9*y9y10y11*y11y12y13y14	1464.76	52.242	143283	2	732.88	-0.17
P65702 PGK_SALTY Phohoglycerate kinase	5		SLYEADLVDEAKR	231	13	9	81.48	b5y2y4y5y6y8y9y10y13	1508.74	54.238	124468	3	503.59	-12.22
P65702 PGK_SALTY Phohoglycerate kinase	6		TILWNGPVGVFEPNFR	302	17	16	128.57	y3*y3y4*y4y5y6y7y8*y8y11*y11y12y13*y13y14y17	1993.04	107.113	105774	2	997.03	5.94
P65702 PGK_SALTY Phohoglycerate kinase	7		ADLNPVKEGK	19	11	12	81.45	b1b3b5*b5y2y4*y4y6y7y8y9y11	1169.65	36.840	105765	2	585.33	-1.46
P65702 PGK_SALTY Phohoglycerate kinase	8		MTDLDLAGKR	5	10	6	70.77	y3y4y5y7y9y10	1119.58	43.041	56615	2	560.29	-4.03
P65702 PGK_SALTY Phohoglycerate kinase	9		VMVTSHLGRPTEGEYNEEFSLPVVNYLK	53	29	6	14.38	b2b6b22y7y25y29	3321.70	93.568	36928	3	1107.90	4.41
P65702 PGK_SALTY Phohoglycerate kinase	10		AQASTHGIGK	146	10	14	87.06	b2*b2b4*b4y1y2y3y4y5y6y7y8*y8y10	969.51	15.841	31039	2	485.26	-4.66
P65702 PGK_SALTY Phohoglycerate kinase	11	Carbamidomethyl+C(5)	YAALCDVFVMDAFGTAHR	128	18	3	15.44	b14y5y13	2043.95	91.597	1505	4	511.74	5.49
P65702 PGK_SALTY Phohoglycerate kinase	12		MTDLDLAGK	5	9	3	30.28	b6y4y5	963.48	48.214	20370	2	482.24	-3.48
P65702 PGK_SALTY Phohoglycerate kinase	13		LSNPVR	84	6	1	13.55	y4	685.40	27.997	9028	2	343.20	-2.40
P65702 PGK_SALTY Phohoglycerate kinase	14		ISYISTGGGAFLEFVEGK	355	18	4	24.6	b6b10b12y15	1874.92	80.551	2856	3	625.65	-16.21
P65702 PGK_SALTY Phohoglycerate kinase	15		DYLDGVDVAEGELVVLENVR	93	20	7	47.23	b10b11b14b15*b15y4y6	2204.11	100.675	2342	2	1102.56	0.55
P65702 PGK_SALTY Phohoglycerate kinase	16		ISYISTGGGAFLEFVEGKVLPVAMLEER	355	29	9	35.43	b6b8*b8b9y3*y3y7y8*y8	3083.62	136.402	3327	4	771.66	1.43
P65702 PGK_SALTY Phohoglycerate kinase	17	Carbamidomethyl+C(6)	KYAALCDVFVMDAFGTAHR	127	19	5	33.06	b6b10b11b14y14	2172.05	86.365	2612	3	724.69	7.31
P65702 PGK_SALTY Phohoglycerate kinase	18		YEADLVDEAKR	233	11	1	7.4	b3	1308.65	54.267	28723	2	654.83	2.61
P65702 PGK_SALTY Phohoglycerate kinase	19		LNVPVKEGK	21	9	0	2.47		983.59	36.848	24333	2	492.30	-1.49
P65702 PGK_SALTY Phohoglycerate kinase	20		DLNPVPKEGK	20	10	1	7.83	b3	1098.60	36.806	23726	2	549.81	-9.67
P65702 PGK_SALTY Phohoglycerate kinase	21		TDLDLAGKR	6	9	1	8.21	b3	988.54	42.991	12585	2	494.77	-2.41
P65702 PGK_SALTY Phohoglycerate kinase	22		PAVAMLEER	375	9	2	18.75	b3b5	1015.52	80.238	10642	2	508.26	-7.57
P65702 PGK_SALTY Phohoglycerate kinase	23		ASTHGIGK	148	8	5	51.61	b4b5b6b7*b7	770.41	15.846	4697	2	385.71	-8.87
P65702 PGK_SALTY Phohoglycerate kinase	24		QASTHGIGK	147	9	2	8.21	b4*b4	898.46	15.862	1819	2	449.73	-13.59

P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VAVFTQGPNAEAAK	74	14	25	187.81	b4b8b9°b9b11°b11°b11b13y1y3y4y5y7y8y9°y9y10y11°y11°y11y12°y12y13y14°y14	1402.73	44.990	174748	2	701.87	0.70
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VVGQLGQVLGPR	122	12	10	68.5	b2b4y6y7y8°y8y9y10°y10y12	1222.72	58.978	124644	2	611.86	-5.79
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VGTVTPNVAEAVK	141	13	15	126.25	b2b3°b3b4°b4y3y4y5y6y8y9y10y12°y12y13	1284.71	47.780	124497	2	642.86	-1.14
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		AAGAELVGMEDLADQIK	88	17	9	53.37	b7b10b14°b14b15y4y10y11y17	1730.87	79.648	28097	2	865.94	4.23
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		GATVLPHTGTR	60	11	5	50.26	y4y5y6y7y11	1065.58	30.185	24682	2	533.29	-4.70
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		GEMNFDVVIASPDAMR	106	16	3	17	b14y3y5	1751.83	62.347	15094	3	584.62	13.52
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		SDQNVRGATVLPHTGTR	54	17	4	24.82	b4b11b12°b12	1764.91	59.292	7757	2	882.96	-2.42
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		KGEMNFDVVIASPDAMR	105	17	5	16.17	b10°b10y9°y9y13	1879.90	108.888	4002	2	940.45	-1.04
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9	Oxidation+M(3)	GEMNFDVVIASPDAMR	106	16	3	23.54	b12y9y10	1767.79	53.272	3318	2	884.40	-5.73
P0A2A3 RL1_SALTY 50S ribosomal protein L1	10		TVLPHTGTR	62	9	0	2.47		937.51	30.184	17184	2	469.26	-10.42
P0AA28 THIO_SALTY Thioredoxin-1	1		LNIDQNPGTAPK	58	12	25	155.8	b2°b2b3b4°b4b6°b6°b6b7b10y2y3y6y7y8°y8°y8y9°y9°y9y10°y10y11°y11y12	1267.66	38.298	219078	2	634.33	-5.20
P0AA28 THIO_SALTY Thioredoxin-1	2		MIAPILDEIADEYQGK	37	16	25	185.41	b2b3b12b14°b14y1y2y3y4°y4y5°y5y6y7y8°y8y10y11°y11y12y13y14°y14y15y16	1805.91	93.811	157478	2	903.46	4.73
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	8	67.35	b2y2y3y4y5y6y7y9	1001.63	91.393	87864	2	501.32	-7.68
P0AA28 THIO_SALTY Thioredoxin-1	4		IIHLTDDSFDTDLK	4	15	3	26.06	b8b9b14	1731.86	86.743	2770	2	866.43	-13.25
P0AA28 THIO_SALTY Thioredoxin-1	5		EFLDANLA	101	8	3	32.88	b4b5y4	892.44	136.270	2120	1	892.44	0.68
P0AA28 THIO_SALTY Thioredoxin-1	6		MIAPILDEIADEYQGKLTVAK	37	21	8	46.64	b3b4b8b14y12°y12y18y19	2318.22	95.037	120604	3	773.41	-3.79
P0AA28 THIO_SALTY Thioredoxin-1	7		SDKIIHLTDDSFDTDLK	1	18	3	15.44	b3b12y6	2062.01	56.137	1843	3	688.01	-12.20
P0AA28 THIO_SALTY Thioredoxin-1	8		PTLLLFK	76	7	2	23.16	b3b4	831.52	91.403	85417	2	416.27	-12.70
P0AA28 THIO_SALTY Thioredoxin-1	9		GIPTLLLFK	74	9	0	1.65		983.62	91.406	2421	2	492.31	-2.85
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	12	57.37	b2b3°b3b4°b4b19y3y5y12y13y15y19	2130.15	93.453	300478	3	710.72	-9.86
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		MVAPVDGTIGK	59	11	14	123.09	b2b3b4b10y2y3y5y6y7y8°y8y9y10y11	1087.58	45.876	159596	2	544.29	-3.03
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		VGDPVIEFDLPLEEK	115	16	17	99.49	b2b4b5°b5b6b7°b7b10y2y4y6y9y10°y10y11°y11y16	1812.97	99.818	140839	2	906.99	1.75
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		STLTPVVISNMDEIK	133	15	5	17.98	b1b13y5°y5y11	1646.89	73.028	13161	2	823.95	12.45

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		DTGTIEIVAPLSGEIVNIEDVPDVV FAEK	16	29	4	11.47	b3b7y2y11	3069.59	111.982	3662	3	1023.87	-0.40
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		IVGDGIAIKPTGNK	45	14	12	109.42	b5y3y4°y4y5°y5*y5y6y7y9 y10y13	1382.78	43.558	257111	3	461.60	-17.30
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		IFETNHAFSIESDSGIELFVHFGIDT VELK	70	30	3	17.23	b10b12b15	3394.76	126.829	2919	3	1132.26	21.58
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		VKVGDPVIEFDLPLEEK	113	18	6	30.68	b5b11y3°y3y6y10	2040.11	96.367	151992	3	680.71	-9.99
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTASPYASYLQYGHIANIDD IIAGKKPATDLGVK	125	38	11	38.28	b3b6°b6b8b10b21y1y3y4y 8y38	4001.02	83.717	170679	5	801.01	-11.35
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		AEQQLDKDSAIVPVYYYVNAR	494	21	19	127.92	b1b3b4b6b10b11°b11b12° b12y1y3y4*y4y5y6y7y9y1 0y21	2442.23	73.071	102368	3	814.75	0.70
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3		WSDGTPVTAHDFVYSWQR	107	18	10	34.35	b2b11y1y4y6y7°y7*y7y13y 18	2151.99	72.963	80648	3	718.00	2.84
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4	Carbamidomethyl+C(4)	AGWCADYNEPTSFLNTMLSDSSN NTAHYK	439	29	7	51.08	y6y7y13y14y15y20y29	3294.42	90.326	79196	3	1098.81	3.63
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		LVEPEWFK	352	8	4	32.88	b6y5y6y8	1047.54	71.239	68315	2	524.28	-6.76
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		SGEIDMTYNNMPIELFQK	263	18	12	28.93	b1b2b3°b3b13y2y10y11°y1 1*y11y13°y18	2130.02	86.588	51857	2	1065.51	13.75
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7		TVINQVTYLPISSEVTDVNR	241	20	10	98.21	y3y5y6y9y11y12y13y14y1 5y20	2248.20	76.975	51354	2	1124.60	7.49
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		NQGDLPAYSYTPPYTDGAK	333	19	9	49.6	b7b8b11y2y8y9y11y14y19	2057.96	58.650	49487	2	1029.48	7.47
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9		NLGVNVNLENQEWK	410	14	13	79.29	b2*b2b4b7b11b12y1y6y8y 10*y10y12y14	1656.84	66.712	40350	2	828.92	4.35
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	6	11.47	b2b3b9°b9y1y15	3091.54	88.411	22003	3	1031.18	0.71
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		WTQPANIVTNGAYK	204	14	4	27.69	b3b6b13*b13	1562.80	73.992	4907	3	521.61	5.55
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		WENKDFK	89	7	3	40.25	y3y4y6	966.45	44.502	1548	3	322.82	-13.64
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	13		TFLDTR	424	6	1	13.55	y4	752.39	44.015	14875	1	752.39	-4.30
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	14		DLFEGLLISDVEGHPSPGVAEK	67	22	4	19.84	b3b10°b10b14	2309.13	82.891	5744	3	770.38	-17.55
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	15		DSAIVPVYYYVNAR	501	14	4	31.28	b4b6b8y8	1629.81	104.543	4768	2	815.41	-8.46

[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	16	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYEINNQK	284	23	8	29.21	b4°b4b6°b6b11b13y7*y7	2920.39	76.267	31041	3	974.14	4.10
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	17		NPQYWDNAKTVINQVTYLPISSSEV TDVNR	232	29	3	11.47	b4b12y7	3364.69	102.671	26617	3	1122.24	3.77
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	18		FGDKWTQPANIVTNGAYK	200	18	4	38.37	b5b6b7b10	2010.01	64.751	19757	3	670.67	0.61
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	19		VADDTQRSELYAK	481	13	4	29.41	b3b10y4y8	1495.73	30.694	19253	3	499.25	-7.92
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	20		VKNQGDLPAYSYTPPYTDGAK	331	21	4	48.01	y5y6y7y8	2285.13	54.799	13541	3	762.38	8.23
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	21	Carbamidomethyl+C(6)	VDPYLCTYYYEINNQKAPFNDVR	291	23	7	26.33	b5°b5b9y6*y6y7°y7	2882.35	76.356	12707	3	961.45	1.44
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	22		IVLERNPQYWDNAK	227	14	5	30.49	b12*b12y8y10y11	1745.92	87.848	7348	2	873.46	11.40
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	23		SELYAKAEQQLDK	488	13	4	20.46	b9°b9b11y10	1522.77	68.226	5596	2	761.89	-5.53
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTQTETFGNEHWAPK	135	20	11	59.75	b2b3b4y2y10y11y13y16*y16y17y20	2199.08	63.638	144987	3	733.70	-2.78
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	13	137.84	b4b8b10y4y5y6y7y9°y9y10y11y12y13	1425.69	55.016	126954	2	713.35	0.60
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	3		NSDIQPTVASLK	120	12	17	136.64	b2°b2*b2b3°b3b4b6b10y3y4y7y8°*y8y9y10y11y12	1272.68	47.886	105379	2	636.84	-0.86
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	10	44.22	b2*b2b5b9y2y4y5y6y14y20	2273.20	104.195	62924	2	1137.10	7.73
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	5		FGGPAVKDEK	201	10	6	52.2	b2b6b9y4y5y8	1047.54	27.164	22475	2	524.27	-6.06
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	6		AFAEMR	234	6	1	13.55	b3	724.35	36.441	6261	1	724.35	0.84
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	7	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLKAK	62	22	5	20.68	b3b11b14y20*y20	2472.32	98.986	147773	3	824.78	1.38
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	8		DEKLFGVGTGMGLR	208	14	7	42.08	b5b8°b8b10°b10b11y8	1479.74	58.903	6132	2	740.37	-14.35
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	9	Phosphoryl STY(14)	GIEIVSYQGQDNIYSDLTAGR	155	21	3	13.75	b10y7y9	2379.11	94.077	41488	3	793.71	14.78
[P64052]EFTS_SALTY Elongation factor Ts	1		VASLEGDVLGSYQHGAR	134	17	14	113.93	b2b6°b6b8b10y4y5y7y8y10y11y12y13y17	1758.86	59.110	151188	3	586.96	-11.04
[P64052]EFTS_SALTY Elongation factor Ts	2		ITDVEVLK	104	8	7	32.88	b3°b3y1y2y6y7y8	916.53	48.583	136362	2	458.77	-9.92
[P64052]EFTS_SALTY Elongation factor Ts	3		AEITASLVK	1	9	6	45.18	b4y1y3y5y6y9	931.54	48.692	98418	2	466.27	-7.53
[P64052]EFTS_SALTY Elongation factor Ts	4		IGENINIR	125	8	6	53.8	y3y4y5y7*y7y8	928.51	44.483	96748	2	464.76	-8.02
[P64052]EFTS_SALTY Elongation factor Ts	5		FTGEVSLTGQPFVMEPSK	222	18	7	52.05	b5y3y5y8y10y13y18	1953.98	74.605	77420	2	977.49	8.12
[P64052]EFTS_SALTY Elongation factor Ts	6		IGVLVAAK	151	8	9	62.17	b2b3y1y2y3y5y6y7y8	770.50	47.317	57590	2	385.76	-12.75
[P64052]EFTS_SALTY Elongation factor Ts	7	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	7	73.91	b3y1y4y5y6y7y8	1098.47	21.177	38209	2	549.74	-1.33
[P64052]EFTS_SALTY Elongation factor Ts	8		ALTEANGDIELAIENMRK	25	18	9	49.6	b7b11b14y4*y4y5*y5y7y14	1988.01	74.332	36017	3	663.34	-2.58

P64052 EFTS_SALTY Elongation factor Ts	9		AGNVAADGVIK	52	11	10	73.53	b1b6y2y4y6y7y8y10*y10y11	1014.55	36.602	21876	2	507.78	-7.16
P64052 EFTS_SALTY Elongation factor Ts	10		VALVAK	119	6	1	13.55	b3	600.41	41.512	9620	1	600.41	-4.68
P64052 EFTS_SALTY Elongation factor Ts	11		QLAMHVAASKPEFVKPEDVSADVVEK	167	26	8	40.59	b4b5*b5y3y4y8y11°y11	2824.45	110.768	3030	3	942.16	-0.52
P64052 EFTS_SALTY Elongation factor Ts	12	Carbamidomethyl+C(13)	IDGNVAFILEVNCQTDVFAK	65	20	3	14.24	b3y5y10	2253.11	107.407	2277	3	751.71	-5.53
P64052 EFTS_SALTY Elongation factor Ts	13		DAGFQAFADKVLDAAVAGK	85	19	4	23.44	b3y3y6y8	1893.96	100.077	96574	3	631.99	-6.12
P64052 EFTS_SALTY Elongation factor Ts	14		FEVGEGIEKVETDFAAEVAAMSK	258	23	4	12.94	b8y3y14°y14	2457.18	109.880	3372	3	819.73	-2.98
P64052 EFTS_SALTY Elongation factor Ts	15		EIAEKMVEGR	209	10	3	28.47	b4b5y4	1161.58	21.431	1614	2	581.29	-10.82
P64052 EFTS_SALTY Elongation factor Ts	16	Oxidation+M(16)	ALTEANGDIELAIENMRK	25	18	3	15.44	b5b9y12	2004.01	71.988	5408	2	1002.51	4.08
P64052 EFTS_SALTY Elongation factor Ts	17		GVLVAAK	152	7	0	1.23		657.43	47.358	21183	1	657.43	-3.81
P64052 EFTS_SALTY Elongation factor Ts	18	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	0	2.06		997.43	21.135	10986	2	499.22	-0.37
P0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	13	105.33	b2b3°b3b9y5y6y7y8y9°y9y11y12y13	1447.78	64.939	116187	2	724.39	1.26
P0A297 RL10_SALTY 50S ribosomal protein L10	2		AAAFEGELIPASQIDR	109	16	18	146.12	b5b8b9b13°b13b15y2y3°y3y5y7y8y9y11y12y13*y13y16	1687.87	68.546	80003	2	844.44	4.48
P0A297 RL10_SALTY 50S ribosomal protein L10	3	Carbamidomethyl+C(9)	VVEGTQFECLKDTFVGPTLIAYSM EHPGAAAR	62	32	12	58.26	b2b3b4b12b24y6y7y10y12y13y16y32	3494.68	92.576	61150	4	874.43	-7.61
P0A297 RL10_SALTY 50S ribosomal protein L10	4		GALSAVVADSR	20	11	9	100.61	b5b6y2y3y4y5y6y7y8	1045.56	48.635	41232	2	523.28	-2.22
P0A297 RL10_SALTY 50S ribosomal protein L10	5		DTFVGPTLIAYSM EHPGAAAR	73	21	8	34.92	b6b7°b7y1y8y12y14y21	2204.11	116.358	10738	3	735.38	14.62
P0A297 RL10_SALTY 50S ribosomal protein L10	6		LATLPTYEEAIARL MATMK	125	19	3	14.8	b12y3y6	2123.10	57.688	114583	3	708.37	-12.65
P0A297 RL10_SALTY 50S ribosomal protein L10	7		AAAFEGELIPASQIDRLATLPTYEEAIAR	109	29	4	14.38	b4b15y7y11	3116.62	93.154	13245	3	1039.54	-3.60
P0A297 RL10_SALTY 50S ribosomal protein L10	8		AGREAGVYMR	43	10	5	59.98	b5b9y3y6y8	1109.54	87.825	2899	1	1109.54	-7.70
P0A297 RL10_SALTY 50S ribosomal protein L10	9	Phosphoryl STY(4)	GALSAVVADSR	20	11	3	24.11	b3b8y6	1125.51	40.217	14258	2	563.26	-6.40
P0A297 RL10_SALTY 50S ribosomal protein L10	10		DTFVGPTLIAYSM EHPGAAAR	73	21	0	6.58		2186.08	116.339	2731	2	1093.55	8.71
P0A1Z2 SKP_SALTY Chaperone protein skp	1		IAIVNMGNLFQQVAQK	23	16	15	92.89	b2b3b4b8b15y1y2y3y6y7y11y12y13*y13y16	1773.97	90.122	168190	2	887.49	1.58
P0A1Z2 SKP_SALTY Chaperone protein skp	2		TGVSNTLENEFK	39	12	10	81.73	y2y4y5y6y7y9°y9y11*y11y12	1338.65	57.897	147762	2	669.83	-1.46
P0A1Z2 SKP_SALTY Chaperone protein skp	3		METDLQSK	59	8	6	40.66	b8y2y4y5y6y8	951.44	26.505	145527	2	476.22	-7.95
P0A1Z2 SKP_SALTY Chaperone protein skp	4		VANDQSIDLVDANTVAYNSSDV K DITADV LK	126	32	12	62.14	b1b4b5b6b7°b7b9b10b13°y1y2y3	3392.71	90.056	55339	3	1131.58	1.44
P0A1Z2 SKP_SALTY Chaperone protein skp	5		VANDQSIDLVDANTVAYNSSDV K	126	24	4	12.61	b4b12y5°y5	2537.25	84.969	44700	3	846.42	5.10
P0A1Z2 SKP_SALTY Chaperone protein skp	6		AQAFEKDR	97	8	8	53.8	y2°y2y3y4y5y6°y6y8	964.48	17.307	9525	2	482.74	-4.75
P0A1Z2 SKP_SALTY Chaperone protein skp	7		WLLAAGLGLAMVTSAQAADK	3	20	3	21.03	y5y10y16	1987.04	121.948	3241	2	994.03	-12.41
P0A1Z2 SKP_SALTY Chaperone protein skp	8		TGVSNTLENEFKGR	39	14	6	31.28	b6°b6b8b13y10°y10	1551.76	68.076	34373	2	776.38	-11.25

P0A1Z2 SKP_SALTY Chaperone protein skp	9		AQAFEKDR	97	8	4	49.03	b3y4y5y6	964.48	18.322	14808	2	482.74	-3.29
P0A1Z2 SKP_SALTY Chaperone protein skp	10		KVANDQSIDLVDANTVAYNSSD VK	125	25	6	12.31	b5°b5*b5b9°b9y7	2665.33	136.146	3426	3	889.12	1.19
P0A1Z2 SKP_SALTY Chaperone protein skp	11	Oxidation+M(11)	WLLAAGLGLAMVTSQAADK	3	20	4	21.03	y3y6*y6y8	2003.07	81.586	16369	2	1002.04	5.42
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		QLDPLVVGQEHYDTAR	343	16	10	118.02	b2y3y4y5y6y8y9y11y12y14	1840.90	57.893	57683	3	614.31	-8.02
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	6	42.86	b9y5y6y7y8°y10	1193.60	80.978	46517	2	597.30	-7.16
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		VALTGLTMAEK	219	11	11	112.96	b2b5y3y4y5y6y7y8y9y10y11	1133.62	59.041	46471	2	567.31	-3.23
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4		MPSAVGYQPTLAEEMGVLQER	261	21	9	29.48	b8b14b21y3°y3*y3y4y6y21	2306.13	81.478	35932	2	1153.57	8.26
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		TVNMMELIR	156	9	9	45.18	b3b9*b9y3y6°y6y7*y7y9	1106.57	76.354	35006	2	553.79	-1.32
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		FLSQPFFVAEFTGSPGK	399	18	6	44.03	y3y6y7y9y11y18	1958.01	100.266	34574	2	979.51	1.25
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		AAPSYEELSNSQELLETGK	112	20	7	37.53	b2y1y12y13y14y18y20	2179.09	73.440	29730	2	1090.05	6.95
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		QIASLGIYPAVDPLDSTSR	324	19	13	74.16	b2*b2b3y1y4y5y6°y6y7y11y12y14y19	2003.05	80.304	27954	2	1002.03	4.57
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		VGLFGGAGVGK	145	11	3	24.11	b3y4y7	961.54	58.986	27550	2	481.27	-9.01
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		NIAIEHSGYSVFAGVGER	165	18	4	26.36	b12b13b16y3	1905.96	66.654	1909	2	953.48	8.20
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	3	11.83	b4b10y5	3057.44	92.676	32061	3	1019.82	18.45
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		YQELK	367	5	2	13.14	b3*b3	680.36	30.925	6726	1	680.36	-5.74
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		TIAMGSSDGLR	53	11	4	24.11	b5°b5b10y10	1107.55	80.910	2111	1	1107.55	0.00
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		DEGRDVLLFVDNIYR	232	15	5	29.2	b8°b8b13b14y7	1823.95	99.876	290037	2	912.48	11.91
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15		WAIHRAAPSYEELSNSQELLETK	107	25	3	12.31	b3b11y4	2842.42	83.614	6499	3	948.15	-5.67
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16		VSLVYQGMNEPPGNRLR	202	17	5	27.17	b10y11°y11y12y14	1929.99	103.572	4615	3	644.00	-5.63
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17		IMNVLGEPVDMKGEIGEEER	87	20	5	19.56	b3b14*b14y8y10	2245.08	93.091	2482	3	749.03	-2.50
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18	Phosphoryl STY(8)	QIASLGIYPAVDPLDSTSR	324	19	5	23.44	b9y4y6y11°y11	2083.03	47.387	1916	2	1042.02	14.30
O54297 RS4_SALTY 30S ribosomal protein S4	1		VVNIASYQVSPNDVVSIR	128	18	20	145.89	b3b9°b9*b9b10b12b14*b14b15°b15b17y3y4y5y9y12y13y14*y14y18	1960.06	71.990	71590	2	980.53	4.61
O54297 RS4_SALTY 30S ribosomal protein S4	2		AALELAEQR	156	9	14	87.61	b3y1y2*y2y3y4y5y6°y6*y6y7y8°y8y9	1000.54	43.221	70045	2	500.77	-2.75
O54297 RS4_SALTY 30S ribosomal protein S4	3		KPER	184	4	1	12.73	y3	529.31	45.110	20752	1	529.31	-5.42
O54297 RS4_SALTY 30S ribosomal protein S4	4		GNTGENLLALLEGR	83	14	4	31.28	b5b7b10y11	1456.77	95.048	6259	2	728.89	-6.87
O54297 RS4_SALTY 30S ribosomal protein S4	5		IEQAPGQHGAR	33	11	5	50.26	y5*y5y6y7y8	1163.57	15.762	3309	3	388.53	-16.47
O54297 RS4_SALTY 30S ribosomal protein S4	6	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	3	27.94	y6y11y12	1451.72	68.811	20305	2	726.36	-0.50
O54297 RS4_SALTY 30S ribosomal protein S4	7	Phosphoryl STY(4)	SDLSADINEHLIVELYSK	188	18	5	15.44	b3_H3PO4 b3°b3y3°y3y14	2126.01	136.285	2062	2	1063.51	6.66

P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		VFMQPASEGTGIIAGGAMR	93	19	24	185.14	b1b2b3b4b6b10b11b12b13°b13b14y2y4y5y6y7y11y12y13y15°y15y16*y16y19	1892.94	67.945	176279	2	946.98	3.93
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		AVLEVAGVHNVLAK	112	14	6	27.69	b2y1y3y6y12y14	1419.83	61.084	158511	2	710.42	-2.32
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		AYGSTNPINVVRR	126	12	15	105.13	b1b2b3b6°b6b7y2y4*y4y6y7y8y9y10y12	1290.68	50.990	134206	2	645.84	-1.04
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVA AK	138	18	24	144.52	b2b5°b5b8°b8°b8b11b14°b14b15°b15°b15y2y3y4y5y6y7y10*y10y11y12y14y18	1890.90	63.007	88977	2	945.96	5.23
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		ATIDGLENMNSPEMVA AKR	138	19	12	107.93	b4y1y3y4y8y9°y9y10y11y12y16y17	2046.99	58.840	78609	3	683.00	-3.46
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		IFSFTALTTVVGDN GR	29	16	6	34.84	b2y1y6y8y9y12	1653.86	86.597	35536	2	827.43	-0.44
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		NMINVALNNGTLQHPVK	69	17	3	24.82	b3b4b6	1862.97	63.267	8388	3	621.66	-11.86
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		SVEEILGK	159	8	4	35.89	b5°b5y3y6	874.48	50.350	61054	2	437.74	-10.33
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		VGFGYGK	45	7	3	40.25	b6y4y6	727.37	39.880	22342	2	364.19	-11.50
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		LIAVNR	14	6	3	26.69	y4y5*y5	685.43	32.969	15987	1	685.43	-1.25
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		MAHIEKQAGELQEK	0	14	6	39.5	b4b6°b6b10y6y8	1611.79	54.701	11892	2	806.40	-13.63
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12		AYGSTNPINVV RATIDGLENMNSPEMVA AK	126	30	4	11.32	b5y10y14°y14	3162.54	77.938	3425	3	1054.85	-5.71
P0A7W4 RS5_SALTY 30S ribosomal protein S5	13		GVHTGSRVFMQPASEGTGIIAGGA MR	86	26	3	12.06	b5b14y5	2587.31	103.736	3302	3	863.11	7.93
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		ANDAAGDGTTTATVLAQSIITEGLK	80	25	18	143.93	b2*b2b3b4b5b15°b15y2y3y4y5y6y7y8y9y10y11y25	2418.24	92.080	191315	3	806.75	-0.20
P0A1D3 CH60_SALTY 60 kDa chaperonin	2		GYLSPYFINKPETGA VELESPFILLADKK	197	29	10	39.1	b2b4b6b7b11°b11y2y25y26y29	3239.70	97.168	179998	4	810.68	-6.48
P0A1D3 CH60_SALTY 60 kDa chaperonin	3		EMPLVLEAVAK	231	11	11	86.67	b2°b2b3y2y3y4y5y6y7y8y11	1199.66	80.198	148798	2	600.34	-5.09
P0A1D3 CH60_SALTY 60 kDa chaperonin	4		QQIEEATSDYDREK	350	14	14	91.51	b3*b3b14y2°y2y3y4y5y7y8y9y10y14*y14	1711.76	33.493	91361	3	571.26	-11.48
P0A1D3 CH60_SALTY 60 kDa chaperonin	5		LAGGVAVIK	371	9	9	75.72	b3b4b5b6y1y2y7y8y9	827.52	45.108	81898	2	414.27	-12.24
P0A1D3 CH60_SALTY 60 kDa chaperonin	6	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	11	77.43	b2b12°b12b13y3y5y12y13y14y15y18	1957.01	61.373	77695	2	979.01	2.74
P0A1D3 CH60_SALTY 60 kDa chaperonin	7		GVNVLADAVK	18	10	11	73.91	b2b4°b4y1y3y4y5y6y8*y8y10	985.56	56.175	65800	2	493.28	-8.92
P0A1D3 CH60_SALTY 60 kDa chaperonin	8	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	6	33.7	b2y2y4y6y7y10	1063.50	35.000	59983	2	532.26	-3.79
P0A1D3 CH60_SALTY 60 kDa chaperonin	9		VEDALHATR	395	9	7	93.63	b4b5b7b8y4y5y6	1011.52	26.815	47710	2	506.26	-1.87
P0A1D3 CH60_SALTY 60 kDa chaperonin	10		AIAQVGTISANSDET VGK	142	18	8	49.04	b3y2y4y9y10y13y14y18	1760.91	48.058	46491	2	880.96	4.02
P0A1D3 CH60_SALTY 60 kDa chaperonin	11		SFGAPTITK	42	9	8	59.57	b2b3°b3b6y2y3y4y7	921.50	44.884	46355	2	461.25	-8.15
P0A1D3 CH60_SALTY 60 kDa chaperonin	12	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDLPK	501	25	10	39.27	b1b3°b3b10y9y10y12y14y20y25	2670.32	86.623	36323	2	1335.66	0.09
P0A1D3 CH60_SALTY 60 kDa chaperonin	13		AVAAGMNPMDLK	105	12	6	44.65	y2y5y8y9y10y12	1217.60	58.311	35532	2	609.30	-1.60
P0A1D3 CH60_SALTY 60 kDa chaperonin	14		AGKPLLIIAEDVEGEALATLVVNTMR	242	26	13	75.31	b6b7y1y2y3y4°y4y5°y5*y5y6°y6y7	2723.50	136.374	26611	3	908.51	-0.09

P0A1D3 CH60_SALTY 60 kDa chaperonin	15		ATLEDLGQAKR	311	11	4	50.26	y5y6y7y8	1201.65	39.400	23299	2	601.33	-0.61
P0A1D3 CH60_SALTY 60 kDa chaperonin	16		AVAAGMNPMDLKR	105	13	12	80.38	b2y2y3y4y6y7y9*y9y11*y11*y11y13	1373.70	51.161	19863	2	687.35	-2.49
P0A1D3 CH60_SALTY 60 kDa chaperonin	17		GQNEQNVGK	430	11	5	31.1	b2y3y8y9y11	1201.58	26.830	19365	2	601.30	2.24
P0A1D3 CH60_SALTY 60 kDa chaperonin	18		DTTIIIDGVGEEAAIQGR	327	18	4	15.44	b9b16y14*y14	1845.91	99.876	70379	3	615.97	-6.61
P0A1D3 CH60_SALTY 60 kDa chaperonin	19		GGDGNYGYNAAATEEYGNMIDMGILDPTK	470	28	3	35.67	y3y4y5	2966.29	88.310	39879	3	989.43	2.06
P0A1D3 CH60_SALTY 60 kDa chaperonin	20		VTLGPK	28	6	4	42.84	b4*b4y3y5	614.38	28.146	7916	1	614.38	-3.87
P0A1D3 CH60_SALTY 60 kDa chaperonin	21		AVAAAVEELK	122	10	5	52.2	b3b9y3y5y6	1000.57	47.349	6751	1	1000.57	0.18
P0A1D3 CH60_SALTY 60 kDa chaperonin	22		VGAATEVEMK	380	10	3	33.7	y6y7y9	1034.52	35.304	1898	1	1034.52	0.35
P0A1D3 CH60_SALTY 60 kDa chaperonin	23		EIELEDKFENMGAQMVK	58	17	7	42.37	b5b10*b10y5y6y8y10	2010.94	73.808	193101	3	670.99	-3.04
P0A1D3 CH60_SALTY 60 kDa chaperonin	24		IADLKGQNEQNVGK	425	16	10	80.11	b3b4y3y4y8*y8y11*y11y12y14	1741.89	40.200	144947	3	581.30	-9.95
P0A1D3 CH60_SALTY 60 kDa chaperonin	25	Carbamidomethyl+C(16)	AVAAAVEELKALSVPSCDSK	122	20	6	33.17	b8y6y8y11*y11y18	2045.04	72.125	43902	3	682.35	-6.63
P0A1D3 CH60_SALTY 60 kDa chaperonin	26	Carbamidomethyl+C(13)	AMEAPLRQIVLNCGEPSVVANTVK	445	25	5	27.83	b3b7b8b10y13	2725.40	74.174	21705	3	909.14	0.27
P0A1D3 CH60_SALTY 60 kDa chaperonin	27		GIDKAVAAAVEELK	118	14	3	26.89	b3b11b12	1413.80	65.712	13502	2	707.40	1.30
P0A1D3 CH60_SALTY 60 kDa chaperonin	28		VGAATEVEMKEK	380	12	6	47.79	b6*b6b7y5y8y9	1291.67	76.375	2589	2	646.34	8.41
P0A1D3 CH60_SALTY 60 kDa chaperonin	29	Oxidation+M(22)	EGVITVEDGTGLQDELDVVEGMQFDR	171	26	4	26.35	b7b10b14b16	2867.32	114.678	70755	3	956.45	-0.43
P0A1D3 CH60_SALTY 60 kDa chaperonin	30	Oxidation+M(21)	AMLQDIATLTGGTVISEIGMELEK	286	25	3	21.86	b8y11y12	2665.29	92.683	6820	2	1333.15	-14.66
P0A1D3 CH60_SALTY 60 kDa chaperonin	31		EDALHATR	396	8	0	1.65		912.45	26.753	38857	2	456.73	-3.68
P0A1D3 CH60_SALTY 60 kDa chaperonin	32		LEDLGQAKR	313	9	0	2.47		1029.56	39.370	12260	2	515.28	-13.04
P0A1D3 CH60_SALTY 60 kDa chaperonin	33		NVLADAVK	20	8	2	8.21	b6*b6	829.48	56.108	8975	1	829.48	0.74
P0A1D3 CH60_SALTY 60 kDa chaperonin	34	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDLP	501	24	1	8.36	y12	2542.25	86.714	5542	3	848.09	11.52
P0A1D3 CH60_SALTY 60 kDa chaperonin	35		GMNPMDLKR	109	9	1	7.4	b3	1061.54	51.104	4689	2	531.27	14.26
P0A1D3 CH60_SALTY 60 kDa chaperonin	36		AGMNPMDLKR	108	10	1	7.4	b4	1132.56	51.125	4106	2	566.78	-4.31
P0A1D3 CH60_SALTY 60 kDa chaperonin	37		SALQYAASVAGLMIT	501	15	0	8.23		1495.78	86.732	1704	2	748.40	0.33
P0A1D3 CH60_SALTY 60 kDa chaperonin	38		QQIEEATSDYDREK	350	14	0	3.7		1693.77	33.430	4857	3	565.26	2.67
P25077 MDH_SALTY Malate dehydrogenase	1		NQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVK	21	33	26	106.37	b1b2*b2b3*b3b4b6b9*b9b10*b10b12b13*b13b15*b15b18y1y3y5y12y15y18y19y30y33	3388.80	93.956	221372	3	1130.27	0.79
P25077 MDH_SALTY Malate dehydrogenase	2	Carbamidomethyl+C(2)	ACVGITNPVNTTVAIAAEVLKK	111	23	12	49.83	b2b4b5b8*b8b13*b13y3y13y15y20y23	2382.34	105.760	147653	3	794.78	-3.07
P25077 MDH_SALTY Malate dehydrogenase	3		VAVLGAAGGIGQALALLK	2	19	16	124.8	b3b6b7b9b10y1y2y3y4y5y7y9y12y13y15y19	1735.09	120.983	136916	2	868.05	4.22
P25077 MDH_SALTY Malate dehydrogenase	4		FFSQPLLLGK	262	10	8	47.63	b2b3y1y2y4y6y8y10	1149.66	76.035	120995	2	575.34	-2.87

P25077 MDH_SALTY Malate dehydrogenase	5		IQNAGTEVVEAK	205	12	16	96.25	b2b3b10*b10y1y3°y3y4°y4y5y8°y8y9y10°y10*y10	1258.66	34.384	96199	2	629.83	-2.23
P25077 MDH_SALTY Malate dehydrogenase	6		AGGGSATLSMGQAAAR	217	16	8	78.32	b6y7y8y9y10y11y12y16	1405.69	39.744	84678	2	703.35	1.04
P25077 MDH_SALTY Malate dehydrogenase	7		DIQLGEDFINK	301	11	9	47.38	b3b6y2y5y8°y8y9°y9y11	1291.65	67.643	77356	2	646.33	-0.66
P25077 MDH_SALTY Malate dehydrogenase	8		KDIQLGEDFINK	300	12	3	22.09	b6b9y8	1419.74	74.235	19122	2	710.37	-4.73
P25077 MDH_SALTY Malate dehydrogenase	9	Carbamidomethyl+C(2)	ACVGITNPVNTTVAIAAEVLK	111	22	3	19.84	b3b5b11	2254.24	114.037	8168	3	752.09	-2.06
P25077 MDH_SALTY Malate dehydrogenase	10		SNTFVAELK	153	9	3	30.28	b3y4y7	1008.54	54.553	55325	2	504.77	-0.18
P25077 MDH_SALTY Malate dehydrogenase	11		SDLFVNAGIVK	87	12	4	36.99	b3y3y6y8	1276.69	69.768	38501	2	638.85	-3.44
P25077 MDH_SALTY Malate dehydrogenase	12	Carbamidomethyl+C(11)	ALQGEKGVVECAYPEGDGQYAR	240	22	5	20.68	b5b7b13*b13y12	2399.11	99.250	134024	3	800.37	-9.16
P25077 MDH_SALTY Malate dehydrogenase	13		IQNAGTEVVEAKAGGGSATLSMGQAAAR	205	28	5	38.31	b5b6b7y4y7	2645.36	120.713	5974	3	882.46	9.32
P25077 MDH_SALTY Malate dehydrogenase	14		FFSQPLLLGKNGVEER	262	16	4	23.54	b5b6*b6y6	1833.99	108.755	3401	3	612.00	1.66
P25077 MDH_SALTY Malate dehydrogenase	15	Oxidation+M(10)	AGGGSATLSMGQAAAR	217	16	4	17	b6°b6b9y9	1421.70	68.539	11747	2	711.35	12.88
P67093 UG_SALTY Universal stress protein G	1		TIIMPVDVFEMELSDK	3	16	11	64.72	b2°b2b3b4°b4b9b14y12y13y14y16	1866.93	105.053	79321	2	933.97	6.28
P67093 UG_SALTY Universal stress protein G	2		HAEFLAQQDGVHLLHVLPGSASMSLHR	22	28	3	11.63	b9b11y13	3063.57	115.177	1645	4	766.65	-8.13
P67093 UG_SALTY Universal stress protein G	3		DVVNEMGEELDADVVVIGSR	94	20	6	30.36	b6*b6b7b12y12y14	2146.07	119.398	4002	2	1073.54	19.11
P67093 UG_SALTY Universal stress protein G	4		RFEHLQHEAETR	56	13	6	56.12	b4b7b11y3y6y8	1681.81	82.742	5984	3	561.27	1.23
P67093 UG_SALTY Universal stress protein G	5		FEEHLQHEAETRLQTMVGHFSIDPSR	57	26	3	22.72	y5y6y12	3094.46	61.383	3629	4	774.37	-6.94
P0A1P6 GLNA_SALTY Glutamine synthetase	1		LVPGYEAPVMLAYSAR	322	16	12	124.76	b2b7b15y3y4y5y7y8y9y10y11y14	1736.92	77.459	48122	2	868.96	6.68
P0A1P6 GLNA_SALTY Glutamine synthetase	2		GGYFPVPPVDSAQDIR	177	16	6	27.43	b12y2y7y10y12y16	1717.86	69.997	31521	2	859.43	3.48
P0A1P6 GLNA_SALTY Glutamine synthetase	3		EIPQVAGSLEEALNALDLDR	406	20	7	19.56	b10b15y1y4°y4y12y20	2153.09	96.153	31209	3	718.37	-8.73
P0A1P6 GLNA_SALTY Glutamine synthetase	4		AINALANPTTNSYKR	307	15	6	55.05	y5y7y8y9y10y15	1633.86	42.870	28280	3	545.29	-3.36
P0A1P6 GLNA_SALTY Glutamine synthetase	5		ATGIADTVLFGPEPEFFLFDDIR	117	23	6	28.62	y2y3°y3y5y8y13	2570.27	118.167	18370	3	857.43	-5.70
P0A1P6 GLNA_SALTY Glutamine synthetase	6	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	7	36.63	b14°b14b15y7y15y16y24	2565.29	136.704	17596	2	1283.15	0.19
P0A1P6 GLNA_SALTY Glutamine synthetase	7		AINALANPTTNSYK	307	14	5	41.5	y2y4y9y10y11	1477.76	47.662	10445	2	739.39	-0.17
P0A1P6 GLNA_SALTY Glutamine synthetase	8		EIPQVAGSLEEALNALDLREFLK	406	24	6	18.92	b1b2b4°b4b8b15	2670.39	103.690	9232	3	890.80	-1.92
P0A1P6 GLNA_SALTY Glutamine synthetase	9		MSAEHVLTMLNEHEVK	0	16	5	17	b11b13*b13y10y16	1867.92	105.108	5525	3	623.31	6.21
P0A1P6 GLNA_SALTY Glutamine synthetase	10		AGGVFTDEAIDAYIALR	430	17	3	16.17	b5b10y12	1781.89	76.355	102810	2	891.45	-10.76
P0A1P6 GLNA_SALTY Glutamine synthetase	11		GINESDMVLPDASTAVIDPFFADSTLIIR	59	30	10	69.68	b3b8b9b10b16y3y6y11y12y13	3238.62	114.270	14236	3	1080.21	6.03
P0A1P6 GLNA_SALTY Glutamine synthetase	12		SAEHVLTMLNEHEVK	1	15	3	17.98	b10b14y10	1736.85	82.781	13133	3	579.62	-9.21
P0A1P6 GLNA_SALTY Glutamine synthetase	13		FVDLR	16	5	2	13.14	y4°y4	649.36	43.566	5284	1	649.36	-11.84

[P0A1P6]GLNA_SALTY Glutamine synthetase	14		EQHVTIPAHQVNAEFFEEGK	28	20	5	25.04	b13y3y4°y4y7	2310.12	106.991	3030	2	1155.56	1.27
[P0A1P6]GLNA_SALTY Glutamine synthetase	15		MSAEHVLTMLNEHEVKFVDLR	0	21	6	29.48	b10b11b13y10y13°y13	2498.29	91.749	14769	3	833.43	14.76
[P0A1P6]GLNA_SALTY Glutamine synthetase	16		VRMTPHPVEFELYYSV	453	16	4	27.43	b11y6y8y13	1966.97	110.814	1728	3	656.33	-0.99
[P0A1P6]GLNA_SALTY Glutamine synthetase	17	Carbamidomethyl+C(4); Oxidation+M(3)	SEMCLVMEQMGLVVEAHHHEVA TAGQNEVATR	193	32	3	11.1	b6y8y11	3579.65	118.087	15847	3	1193.89	2.39
[P0A1P6]GLNA_SALTY Glutamine synthetase	18		EIPQVAGSLE	406	10	1	8.17	y6	1042.55	103.625	4973	1	1042.55	6.91
[P0A1P6]GLNA_SALTY Glutamine synthetase	19	Carbamidomethyl+C(11)	FPDPAANPYLCFAA	360	14	0	7.82		1553.72	136.687	4832	1	1553.72	8.88
[P0A1P6]GLNA_SALTY Glutamine synthetase	20		NALANPTTNSYKR	309	13	0	4.12		1449.75	42.865	2756	2	725.38	0.93
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	8	42.76	b2b3b6y1y5y7y10y13	1365.68	62.912	84628	2	683.34	-0.72
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2	Carbamidomethyl+C(13)	AAQYVAAHPGVECPAK	153	16	9	66.3	b3b4y3y8y9°y9y11y12y16	1668.80	35.208	71567	3	556.94	-12.73
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		ATFVVDPQGHIAIEVT AEGIGR	120	23	12	63.94	b2°b2b4b8b9b14y2y3y4y6y7y10	2384.27	130.121	40819	3	795.43	-6.45
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		LGVDVYSVSTDTHFTHK	63	17	3	16.17	b10y9y11	1905.96	70.075	1647	2	953.48	12.68
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTELGDVA DHYEELQK	32	31	6	27.52	b5b6b8b11y7y12	3757.71	79.993	7744	4	940.18	-2.08
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6		YAMIGDPTGALTRNFDNMR	93	19	3	22.58	b4b5y12	2142.98	100.309	3022	4	536.50	-13.10
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7	Carbamidomethyl+C(10)	YVAAHPGEVCPAK	156	13	1	7.25	b3	1398.70	35.235	2009	2	699.85	11.00
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	1	Carbamidomethyl+C(15)	VQDQNQIPELNVYQCGTYQMHSLSAQDIAR	113	31	13	62.79	b2b6b7b11y2y8y10y12y13y17y24y25y31	3635.70	74.886	27225	3	1212.57	3.63
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	2		TGFYMSLIGTPDEQR	84	15	4	17.98	b3y2y7y11	1714.83	78.706	25835	2	857.92	9.04
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	3	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCR	65	19	5	20.48	b5b10y5y8y19	2096.97	66.470	8326	3	699.66	-8.50
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	4		PLLDSEFVDHTR	1	12	4	35.9	b3b10y6y7	1370.69	62.686	95823	3	457.57	-15.32
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	5		VADAWK	99	6	2	26.69	b5y5	689.37	47.408	6494	1	689.37	8.68
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	6		GIHTLEHLFAGFMR	51	14	3	34.68	y7y8y9	1628.81	58.323	4047	3	543.61	-17.01
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	7	Carbamidomethyl+C(2)	FCIPNK	39	6	1	13.55	y5	778.39	129.024	1834	1	778.39	0.55
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	8		EVMPEK	45	6	1	13.55	y5	732.36	60.968	1502	1	732.36	4.67
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	9	Carbamidomethyl+C(18)	TMNTPHGDAITVFDLRF CIPNK	23	22	6	20.68	b12y6*y6y9*y9y18	2547.27	136.347	7729	2	1274.14	9.68
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	10	Carbamidomethyl+C(15);Oxidation+M(20)	VQDQNQIPELNVYQCGTYQMHSLSAQDIAR	113	31	3	11.2	b6y5y13	3651.72	104.670	10882	3	1217.91	9.89
[P00924]ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	11	77.09	b2b4b5°b5b6y5y6y7y10*y10y12	1286.71	66.055	77723	2	643.86	2.28
[P00924]ENO1_YEAST Enolase 1	2		VNQIGTLSSEIK	346	12	12	93.24	b2b3b9y1y2y3y5y6y8y9y10y12	1288.71	54.184	64197	2	644.86	-0.95
[P00924]ENO1_YEAST Enolase 1	3		TAGIQIVADDLTVTNPK	312	17	4	16.17	b5y6y10y17	1755.96	72.320	37921	2	878.48	4.17
[P00924]ENO1_YEAST Enolase 1	4		IATAIEK	330	7	6	37.24	b4°b4y1y5y6y7	745.44	28.271	28668	2	373.22	-9.01
[P00924]ENO1_YEAST Enolase 1	5		LGANAILGVSLAASR	105	15	4	10.4	b5°b5y1y3	1412.82	70.851	27698	2	706.91	0.09
[P00924]ENO1_YEAST Enolase 1	6		SIVPSGASTGVHEALEMR	32	18	6	24.6	b1b9y3y4°y8y12	1840.93	74.279	14585	3	614.31	2.45
[P00924]ENO1_YEAST Enolase 1	7		AVDDFLISLDGTANK	88	15	5	48.23	y5y6y7y8y15	1578.81	82.233	14192	2	789.91	3.87
[P00924]ENO1_YEAST Enolase 1	8		AAQDSFAAGWGV MVSHR	358	17	5	23.57	b1y3y5y11°y11	1789.85	60.874	6566	2	895.43	3.96

P00924 ENO1_YEAST Enolase 1	9		WLTGPQLADLYHSLMK	272	16	3	17	b11b13y12	1872.96	89.740	5561	2	936.98	-5.28
P00924 ENO1_YEAST Enolase 1	10		AADALLLK	338	8	3	40.66	y5y6y7	814.49	53.860	65563	2	407.75	-10.64
P00924 ENO1_YEAST Enolase 1	11		IEEELGDNAVFAGENFHHGDK	415	21	7	38.32	b11y4y12*y12y13*y13y14	2328.09	81.464	42198	3	776.70	15.84
P00924 ENO1_YEAST Enolase 1	12		NVPLYK	126	6	1	13.55	y4	733.41	37.137	11818	1	733.41	-14.48
P00924 ENO1_YEAST Enolase 1	13		IGSEVYHNLK	185	10	4	39.06	b3b7y5y8	1159.60	93.345	5343	2	580.30	-11.05
P00924 ENO1_YEAST Enolase 1	14		GNPTVEVELTTEK	15	13	5	33.82	b3b6b8y12*y12	1416.74	97.278	4250	2	708.87	9.82
P00924 ENO1_YEAST Enolase 1	15		TFAEALR	178	7	3	37.24	b4b5y6	807.44	43.467	3976	2	404.22	3.48
P00924 ENO1_YEAST Enolase 1	16		YGASAGNVGDEGGVAPNIQTAAEE ALDLIVDAIK	201	33	3	16.8	b3b5b16	3257.58	125.719	2230	3	1086.53	-10.49
P00924 ENO1_YEAST Enolase 1	17	Phosphoryl STY(11)	WLTGPQLADLYHSLMKR	272	17	4	27.17	b9y7y8y15	2109.05	76.415	22586	2	1055.03	9.72
P00924 ENO1_YEAST Enolase 1	18	Oxidation+M(17)	SIVPSGASTGVHEALEMRDGDGK	32	22	4	20.68	b7b9b11y4	2272.12	62.931	2444	2	1136.56	13.65
P00924 ENO1_YEAST Enolase 1	19		IATAIEK	330	7	0	0.82		727.43	28.163	5032	2	364.22	-4.95
Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTTEPTWFPDSQTLAFTSDQAG RPQVYK	287	29	11	35.32	b2*b2b4b5°b5y1y2y12y13 y24y29	3285.56	77.563	70810	3	1095.86	3.94
Q8ZQT5 TOLB_SALTY Protein tolB	2		SPQPLMSPAWSPDGSK	197	16	6	44.89	b3b9b12y9y11y13	1684.81	62.401	56256	2	842.91	7.61
Q8ZQT5 TOLB_SALTY Protein tolB	3		IEITQGVSARPIGVVPPFK	24	19	8	33.06	b2b4y1y3y14y16y17y19	2026.11	70.589	40734	3	676.04	-10.18
Q8ZQT5 TOLB_SALTY Protein tolB	4		LPATDGQVK	413	9	6	45.18	b5b9y6y7y8y9	928.51	27.726	37672	2	464.76	0.26
Q8ZQT5 TOLB_SALTY Protein tolB	5		WAGPGAAPEDIGGIVAADLR	43	20	12	90.22	b3b5b6b7b8y2y5y6y9y13y 14y20	1936.00	85.590	37657	2	968.51	6.43
Q8ZQT5 TOLB_SALTY Protein tolB	6		MNINGGAAQR	316	10	7	53.96	b2b3b4y3y6y7y10	1031.51	27.846	28406	2	516.26	4.26
Q8ZQT5 TOLB_SALTY Protein tolB	7		TGSLNLYVMDLASGQIR	264	17	4	29.68	b9b14y9y10	1837.93	89.776	13060	2	919.47	-8.97
Q8ZQT5 TOLB_SALTY Protein tolB	8		YAGHTASDEVFEK	142	13	3	25.23	b6y7y8	1453.69	97.276	5386	3	485.23	19.48
Q8ZQT5 TOLB_SALTY Protein tolB	9		FNPLDR	67	6	1	13.55	y4	761.39	46.250	1714	2	381.20	-9.14
Q8ZQT5 TOLB_SALTY Protein tolB	10		QVASFPRHNGAPAFSPDGTK	237	20	4	14.24	b6b9*b9y14	2084.01	82.894	4895	2	1042.51	-8.43
Q8ZQT5 TOLB_SALTY Protein tolB	11		QWLRYAGHTASDEVFEK	138	17	3	16.17	b14y8y12	2037.00	107.201	3595	2	1019.00	9.89
Q8ZQT5 TOLB_SALTY Protein tolB	12		AAPEDIGGIVAADLR	48	15	0	6.17		1467.76	85.586	17959	2	734.38	-12.39
P67091 UF_SALTY Universal stress protein F	1		TILVPIDISDSELTQR	3	16	17	139.08	b2b3°b3b4y2y3y5y6°y6y7* y7y8y9y10y12y14y16	1799.98	81.960	109165	2	900.49	2.71
P67091 UF_SALTY Universal stress protein F	2		VQAHVAEGSPK	85	11	6	35.87	b1y5°y5y6y7°y7	1122.57	18.337	11284	2	561.79	-14.14
P67091 UF_SALTY Universal stress protein F	3		VQAHVAEGSPKDK	85	13	5	32.05	b4y2y4y7y8	1365.70	16.018	4389	3	455.90	-9.92
P67091 UF_SALTY Universal stress protein F	4		VISHVEAEAK	19	10	3	28.47	b8y5y6	1082.58	106.371	12918	2	541.79	-3.50
P67091 UF_SALTY Universal stress protein F	5	Oxidation+M(27)	VHFLTVPISLPYYASLGLAYSALP AMDDLK	34	31	3	21.99	b3b4y5	3410.76	93.956	151555	4	853.45	0.86
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	14	112.7	b2b3y1y2°y2y3y4y5y6y7y8 y9y10y12	1377.65	78.405	151651	2	689.33	-0.80
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AAVTMPSSK	22	9	10	74.47	b1b3y2y3y4°y4y5y6y7y9	891.46	31.188	80573	2	446.23	-6.09
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3		AVVESIQR	69	8	11	66.94	b2b3b5y1y4*y4y5y6*y6y8 *y8	901.50	32.707	77606	2	451.25	-11.37
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4	Carbamidomethyl+C(10)	QAGLGGEIICYVA	117	13	7	39.04	b2b10°b10y2y7y8y9	1350.67	80.988	21198	2	675.84	1.27

P0A7X0 RS8_SALTY 30S ribosomal protein S8	5		MSMQDPIADMLTR	0	13	5	42.76	b4b8y3y5y10	1508.71	47.374	1827	3	503.57	11.73
P0A7X0 RS8_SALTY 30S ribosomal protein S8	6		VEGDTKPELELTLYFQGK	50	19	9	52.61	b3b7°b7b8°b8y4y5y6*y6	2195.13	136.248	3079	2	1098.07	-12.46
P0A7X0 RS8_SALTY 30S ribosomal protein S8	7		VTMPSSK	24	7	0	1.65		749.38	31.141	16051	1	749.38	-4.81
P0A7X0 RS8_SALTY 30S ribosomal protein S8	8		AVTMPSSK	23	8	0	1.65		820.42	31.227	4180	2	410.71	-1.26
P0A7X0 RS8_SALTY 30S ribosomal protein S8	9		VVESIQR	70	7	0	1.23		830.48	32.776	2321	1	830.48	10.66
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	9	44.03	b2y1y2y4y6y7y12y16y18	1970.01	63.255	183828	3	657.34	-8.18
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		ESSVPFSYYDNQQK	47	14	15	109.55	b3°b3b4°b4b5b11y4*y4y5y6y7y8y10*y10y14	1691.76	55.047	157008	2	846.38	3.90
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		VVGYSQDYSNAIVEAVK	61	17	17	101.16	b2b3b6b17y1y2y3y4y5y10*y10y11*y11y12y13y15y17	1841.94	67.647	95887	2	921.47	6.49
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		AVAFMMDDALLAGER	198	15	8	58.41	b3b5b14y4y10y11y13y15	1609.78	84.567	86109	2	805.39	5.84
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5		GGDIKDFPDLK	141	11	5	24.11	b2b3y6y10y11	1204.63	69.650	33104	2	602.82	7.19
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTTNNLER	98	22	9	13.32	b2b14*b14y1y6y9°y9*y9y22	2526.19	81.619	25060	3	842.74	-0.77
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTTNNLER	89	31	6	43.99	y4y6y7y9y10y21	3548.79	86.969	216325	3	1183.60	3.03
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8		AVVVTSGTTSEILLHKLNEEQK	154	22	4	24.03	b3y8y18y19	2396.29	63.713	54476	3	799.44	-4.79
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9		KLMDDTIAQAQTSGEAEK	246	18	4	15.44	b11y9y12*y12	1935.95	84.124	4711	2	968.48	10.91
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		NPIPPKNLNMNFELSDEMK	271	19	4	28.26	b11b12y6y12	2231.11	107.132	1680	2	1116.06	10.72
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11	Phosphoryl STY(5)	QAAFSDTIFVVGTR	122	14	5	24.55	b4*b4y11°y11y12	1591.75	57.503	2548	3	531.25	3.68
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12	Oxidation+M(8)	LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	4	36.21	b7b8b9b18	2885.46	87.651	9630	3	962.49	8.21
Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	13	35.13	b2*b2b3*b3b4*b4b15y1y2y3°y3y12y16	1686.95	90.137	54000	2	843.98	2.53
Q7CR87 SURA_SALTY Chaperone surA	2		LAYDGLNYSTYR	117	12	7	49.34	b5y4y7*y7y8y10y12	1435.69	58.441	37481	2	718.35	6.04
Q7CR87 SURA_SALTY Chaperone surA	3		LNAGQAGQQLPDDATLR	50	17	13	97.64	b1b3y3y4°y4y5y7°y7y8y9y11y12y17	1767.90	50.468	29654	2	884.45	2.07
Q7CR87 SURA_SALTY Chaperone surA	4		ITVLPQEV DALAK	149	13	11	25.23	b2°b2b3°b3y1y2y9°y9*y9y10y13	1396.81	70.594	28339	2	698.91	2.18
Q7CR87 SURA_SALTY Chaperone surA	5		TTFAAAAKEYSQDPGSANQGDDL GWATPDIFDPAFR	318	36	7	21.31	b1b7b9°b9b10y1y4	3772.80	136.263	15825	4	943.96	12.68
Q7CR87 SURA_SALTY Chaperone surA	6		GQSQSISVTEVHAR	274	14	4	32.77	b8b9y3y10	1498.76	36.918	15028	3	500.26	-1.87

Q7CR87 SURA_SALTY Chaperone surA	7		QIGTQNDASTELNLSHILALPENP TSEQVNDAGR	162	35	5	10.91	b13y1y3y9y35	3816.90	88.724	14932	3	1272.97	0.13
Q7CR87 SURA_SALTY Chaperone surA	8		ITDEQLDQAIANIAK	90	15	3	24	b8y8y9	1642.87	80.289	33528	2	821.94	1.34
Q7CR87 SURA_SALTY Chaperone surA	9		QAESIVEEAR	197	10	3	26.71	b4y6y9	1131.59	71.949	19158	2	566.30	19.85
Q7CR87 SURA_SALTY Chaperone surA	10		VAAVVNNGVVLESVDGLMQSV K	27	23	4	12.94	b16y5y9°y9	2343.21	91.095	16876	2	1172.11	-3.44
Q7CR87 SURA_SALTY Chaperone surA	11		NNEVR	142	5	1	13.14	y3	631.31	21.024	1966	1	631.31	-7.93
Q7CR87 SURA_SALTY Chaperone surA	12		LAITYSADQQALKGGQMGWGR	214	21	3	13.75	b12b15y18	2251.13	65.232	23603	3	751.05	2.17
Q7CR87 SURA_SALTY Chaperone surA	13		KFSEEAATWMQEQR	404	14	4	27.32	b4b11y5y9	1740.79	84.289	16689	2	870.90	-8.70
Q7CR87 SURA_SALTY Chaperone surA	14		NGADFGKLAITYSADQQALK	207	20	3	22.37	b11b12y6	2111.06	85.553	7479	4	528.52	-7.98
Q7CR87 SURA_SALTY Chaperone surA	15		LNAGQAGQQLPDDATLRHQILER	50	23	4	23.03	b3b7*b7b8	2544.29	109.750	3569	3	848.77	-13.91
P61179 RL22_SALTY 50S ribosomal protein L22	1		IFVDEGPSMK	73	10	8	73.91	b2b6y5y6y7y8y9y10	1122.55	50.921	59253	2	561.78	-3.91
P61179 RL22_SALTY 50S ribosomal protein L22	2		IFVDEGPSMKR	73	11	5	36.46	b6y5°y5y7y8	1278.63	45.627	28971	3	426.88	-13.65
P61179 RL22_SALTY 50S ribosomal protein L22	3		VSQALDILTYTNK	28	13	7	52.76	b3b4*b4y4*y4y5y6	1465.78	70.479	5524	3	489.27	-5.33
P61179 RL22_SALTY 50S ribosomal protein L22	4		METIAK	0	6	1	13.55	y5	692.36	24.713	3582	2	346.68	-3.09
O33921 AGP_SALTY Glucose-1- phohatase	1		MGTMDFTFNPVITDDSAAFR	141	20	11	73.85	b3b5y1y3y5y8y9y11y12y1 5y20	2186.00	78.321	41467	2	1093.51	6.92
O33921 AGP_SALTY Glucose-1- phohatase	2	Carbamidomethyl+C(14)	EWLV AQGLIPSGECPADPTVYAY ANSLQR	87	29	18	98.05	b3°b3b4b7b12b16y2y3y4y 5y6y7°y7y9y13°y13y20y29	3205.58	94.023	26416	3	1069.20	4.80
O33921 AGP_SALTY Glucose-1- phohatase	3		IEYVYQSAR	358	9	6	45.18	b8y6*y6y7y8y9	1128.57	42.569	25370	2	564.79	-2.81
O33921 AGP_SALTY Glucose-1- phohatase	4		APLANNGSVLAQSTPNAWPAWD VPGGQLTTK	43	31	10	32.37	b1b2b4b8b14y8y10y13y14 y31	3161.61	83.407	19714	3	1054.54	1.54
O33921 AGP_SALTY Glucose-1- phohatase	5		DTFSANYQQEPGVQGPLK	208	18	5	22.6	y4y8y12*y12y18	1978.97	56.108	15699	2	989.99	8.51
O33921 AGP_SALTY Glucose-1- phohatase	6	Carbamidomethyl+C(14)	LLEQITHYQDSPCK	182	15	3	17.98	b11y11y13	1818.86	79.466	14786	4	455.47	-4.77
O33921 AGP_SALTY Glucose-1- phohatase	7		TPIGGQLVFQR	335	11	5	36.46	b6°b6y3y8y9	1215.67	61.451	66278	2	608.34	-11.25
O33921 AGP_SALTY Glucose-1- phohatase	8		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDR	226	31	3	21.99	b12y9y10	3486.65	105.334	15778	3	1162.89	1.75
O33921 AGP_SALTY Glucose-1- phohatase	9		SQLHLDESYK	172	10	3	26.71	b3b8y8	1219.58	40.335	1994	2	610.30	-10.21
O33921 AGP_SALTY Glucose-1- phohatase	10	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	GCPVDANGFCPLDKFDNMNTA AK	389	24	4	27.78	y7y12y20y22	2641.20	78.537	60896	3	881.07	5.92
O33921 AGP_SALTY Glucose-1- phohatase	11		NAEALTLSKSPAQR	370	13	4	25.23	b4y5*y5y6	1398.77	41.475	5282	2	699.89	-2.18
O33921 AGP_SALTY Glucose-1- phohatase	12	Carbamidomethyl+C(27) ;Oxidation+M(8)	GGVLEVYMGHYTREWLVAQGLIP SGECPADPTVYAYANSLQR	74	42	10	33.92	b3b4b9y5y7°y7y8°y8y10*y 10	4684.28	136.412	6013	4	1171.83	4.90
O33921 AGP_SALTY Glucose-1- phohatase	13		NYQQEPGVQGPLK	213	13	0	5.35		1457.74	56.161	2659	2	729.37	0.59
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	1		TQFMGPEGVANVSLSNIAGESAE GLLVTKPK	240	31	15	97.13	b2°b2b3b4b5y4y5y6y13y1 9y22y26y27y29y31	3144.63	88.565	121179	3	1048.88	1.01

P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	2		NYDQVPANKPIVDAIK	271	16	7	24.03	b2*b2b3b10y3y11y16	1784.94	53.829	117550	3	595.65	-10.53
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	3		TTGLDSQDGPTAAK	137	14	13	83.57	b2°b2b3°b3b5y3y5y9y10y11y12*y12y14	1361.66	29.146	96320	2	681.33	1.26
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	4		VAVVGAMSGPVAQYGDQEFTGA EQAIADINAK	25	32	15	73.15	b2b3b7b17y4y5°y5y6*y6y7y10y13y15y25y32	3207.57	89.922	53001	3	1069.86	1.45
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	5		QQYGEGLAR	168	9	6	38.06	b9y2y4y6y7y9	1021.50	32.915	35730	2	511.25	-5.44
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	6		QDPSGAFVWTTYAALQSLQAGLN HSDDPAEIAK	290	33	5	13.18	b6b11y10y15y33	3501.69	109.803	4847	3	1167.90	0.42
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	7	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILM ITPAATAPELTAR	92	38	9	72.85	b5b12b25b27y8y9y10y11y12	4077.97	89.675	64810	3	1360.00	-0.96
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	8		YILEK	151	5	1	13.14	y4	665.38	36.718	12070	1	665.38	-3.49
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	9		GFEFGVFDWHANGTATDAK	346	19	3	21.76	b3b7b9	2069.98	89.679	6600	2	1035.49	20.76
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	10	Carbamidomethyl+C(6)	TLLAGCIALSLSHMAFADDIK	4	21	6	35.63	b9°b9b10y13°y13y14	2247.20	95.094	4439	3	749.74	21.40
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	11		ENIDFVYYGGYHPMGQILR	212	20	4	14.24	b5b13*b13y8	2401.12	94.098	3403	2	1201.06	-4.07
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	12		QAVAVANKVVNDGIK	77	15	3	24	b7y5y6	1525.86	45.594	19086	2	763.44	-4.56
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	13		KQDPSGAFVWTTYAALQSLQAGL NHSDDPAEIAK	289	34	4	12.95	b5b10y9y18	3629.75	99.841	5121	3	1210.59	-10.56
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	14		GDLKGFEFGVFDWHANGTATDA K	342	23	4	19.94	b10b12b20y15	2483.17	92.082	5079	2	1242.09	3.93
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	15		QQYGEGLARAVQDGLK	168	16	3	25.38	b9b10b14	1732.88	90.338	3853	2	866.95	-8.10
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	16		KENIDFVYYGGYHPMGQILR	211	21	4	20.4	b3°b3b9b11	2529.25	138.262	1509	3	843.75	10.43
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	17	Oxidation+M(16)	KENIDFVYYGGYHPMGQILR	211	21	6	29.48	b11b12°b12b15y7y10	2545.22	92.110	2009	4	637.06	-0.10
P0A1V4 KAD_SALTY Adenylate kinase	1		VDGTQAVADVR	195	11	6	47.25	y2y6y8y9y10y11	1130.58	36.382	56935	2	565.79	-1.40
P0A1V4 KAD_SALTY Adenylate kinase	2		LVEYHQMTAPLIGYYQK	167	17	11	66.05	b2b4b6b8°b8b13b14y3y5y6y17	2054.03	69.528	52579	3	685.35	-5.23
P0A1V4 KAD_SALTY Adenylate kinase	3		YGIPQISTGDMLR	23	13	9	42.76	b4b12°b12y2y3y7y10°y10y13	1450.74	72.766	45831	2	725.87	3.03
P0A1V4 KAD_SALTY Adenylate kinase	4		NGFLLDGFPR	78	10	5	47.63	b2b3b7b9y4	1135.59	81.198	27626	2	568.30	-3.44
P0A1V4 KAD_SALTY Adenylate kinase	5		GTQAQFIMEK	13	10	5	36.71	b10y2y3y4y5	1152.58	48.443	27562	2	576.79	7.10
P0A1V4 KAD_SALTY Adenylate kinase	6		IILLGAPGAGK	2	11	6	55.62	b2b3y4y5y7y9	1009.63	60.973	26434	2	505.32	-8.46
P0A1V4 KAD_SALTY Adenylate kinase	7		DDQEETVR	157	8	4	40.66	y4y5°y5y7	991.45	36.784	7151	2	496.23	16.38
P0A1V4 KAD_SALTY Adenylate kinase	8		IILLGAPGAGKGTQAQFIMEK	2	21	6	31.71	b3y5y7y17°y17y19	2143.19	72.893	25783	3	715.07	-1.71
P0A1V4 KAD_SALTY Adenylate kinase	9	Oxidation+M(11)	YGIPQISTGDMLR	23	13	4	29.41	b10b12y4y7	1466.74	63.124	7009	3	489.59	9.49
P0A1V4 KAD_SALTY Adenylate kinase	10	Oxidation+M(7)	LVEYHQMTAPLIGYYQK	167	17	4	27.17	b6b7b9y11	2070.01	110.014	2006	3	690.68	-11.32
P66038 RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	12	53.02	b3b4b9°b9b13b14°b14y2y4y15y16y29	3110.68	98.828	101552	3	1037.56	0.39
P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	16	127.02	b2b3b11b15y2y4y5y6y8y9y10y13y14y15°y15y19	2109.07	102.170	64398	2	1055.04	4.75
P66038 RISB_SALTY 6	3		ANVAAPDAR	5	9	9	74.47	b2b3b4b8y2y5y6y7y9	884.45	22.313	22578	2	442.73	-13.53

[P66038]RISB_SALTY 6	4		DDNITVVVWPGAYELPLATEALAK	45	24	4	12.61	b7b12°b12y3	2585.34	104.936	3027	2	1293.17	-2.83
[P66038]RISB_SALTY 6	5		VAAPDAR	7	7	0	1.65		699.38	22.300	2312	1	699.38	7.94
[P67904]RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAKR	16	15	12	107.61	b2b3y1y3y4y5y6y8y9y11y13y15	1673.89	52.144	191452	3	558.63	-11.23
[P67904]RS10_SALTY 30S ribosomal protein S10	2		LIDQSTAEIVETAK	16	14	15	117.63	b2b3b9°b9y4y5y8y9y10y11°y11y12°y12y13y14	1517.81	55.162	105411	2	759.41	2.33
[P67904]RS10_SALTY 30S ribosomal protein S10	3		LVDIVEPTEK	72	10	7	57.76	b2b3y4y6y7y8y10	1142.63	51.571	49425	2	571.82	-2.78
[P67904]RS10_SALTY 30S ribosomal protein S10	4		FTVLISPHVNK	48	11	5	35.87	y5y6°y6°y6y7	1254.70	58.929	23033	3	418.91	-14.59
[P67904]RS10_SALTY 30S ribosomal protein S10	5		LDLAAGVDVQISLG	89	14	3	24.55	b5b6y11	1370.73	41.709	1867	3	457.58	-18.17
[P67904]RS10_SALTY 30S ribosomal protein S10	6		IVEPTEK	75	7	0	2.06		815.46	51.692	22380	1	815.46	11.98
[P67904]RS10_SALTY 30S ribosomal protein S10	7		DQSTAEIVETAKR	18	13	0	4.12		1447.73	52.124	6936	2	724.37	-5.57
[P02906]SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQEIAAK	263	13	11	82.86	b2b4b10b11°b11y3y4y9y10y11y13	1468.74	50.370	66716	2	734.87	2.74
[P02906]SUBI_SALTY Sulfate-binding protein	2		NVEVLDSGAR	183	10	5	33.7	b1b2y4y5y8	1059.54	39.982	41985	2	530.27	-4.26
[P02906]SUBI_SALTY Sulfate-binding protein	3		AQKDHFANGGTFDQISK	311	17	8	22.7	b1b4°b4°b4b11y10y12°y12	1863.88	73.239	5963	2	932.44	-10.02
[P02906]SUBI_SALTY Sulfate-binding protein	4		FEIVTPSESILAEPTVSVVDK	226	21	3	13.75	b10y7y11	2260.23	77.505	56075	3	754.08	14.37
[P02906]SUBI_SALTY Sulfate-binding protein	5		AVAEAYLK	255	8	3	32.88	b5y5y6	864.48	92.526	13321	2	432.74	-6.21
[P02906]SUBI_SALTY Sulfate-binding protein	6		GIGDVLIAWENEALLATNELGK	202	22	3	13.32	b11b13y14	2326.23	99.081	2727	3	776.08	-1.05
[P02906]SUBI_SALTY Sulfate-binding protein	7		WNYLAAWGYALHHNNNDQAKAQDFVK	153	26	3	12.06	b5b9y4	3074.51	136.224	6230	4	769.38	14.69
[P02906]SUBI_SALTY Sulfate-binding protein	8		ELYEQYNKAFAHWK	33	15	5	31.57	b5b6y5°y5y7	1913.94	118.031	1845	2	957.47	8.99
[P0A1H3]EFG_SALTY Elongation factor G	1		VYSGVVNSGDTVLSNVK	337	17	13	89.99	b2b4°b4b5°b5b6y4y5y10y11y12y15y17	1737.90	61.972	81031	2	869.45	-0.91
[P0A1H3]EFG_SALTY Elongation factor G	2		IATDPFVGNLTFFR	323	14	12	58.24	b1b2b4y2y4y7°y7°y7y8y10y11y14	1597.84	93.579	64478	2	799.42	2.06
[P0A1H3]EFG_SALTY Elongation factor G	3		SGPLAGYPVVDLGVR	562	15	10	36.78	b2b3b5°b5y1y2y4y8y10y15	1499.83	76.554	60692	2	750.42	3.50
[P0A1H3]EFG_SALTY Elongation factor G	4	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTTGDTLCDPENPIILER	378	30	4	11.32	b26y3y10y30	3138.60	85.369	28926	3	1046.87	-0.62
[P0A1H3]EFG_SALTY Elongation factor G	5		GQYGHVVIDMYPLEPGSNPK	512	20	9	41.92	b4y1y6°y6°y6y7y9y10°y10	2201.06	70.661	28293	3	734.36	-3.55
[P0A1H3]EFG_SALTY Elongation factor G	6		EFNVEANVGKPVAYR	475	16	6	24.03	b7b11y6°y6y8y16	1820.91	53.479	27039	3	607.64	-7.91
[P0A1H3]EFG_SALTY Elongation factor G	7		VEVETPEENTGDVIGDLR	618	19	11	39.98	b2°b2b5b10°b10°b10b11y3y5y14°y14	2058.99	66.598	25497	2	1030.00	5.22
[P0A1H3]EFG_SALTY Elongation factor G	8		IGEVHDAATMDWMEQEQR	39	20	6	21.03	b4b10°b10b13°b13y2	2332.03	73.033	8757	3	778.01	13.51
[P0A1H3]EFG_SALTY Elongation factor G	9		AINWNDADQGVTFEYEDIPADMQLANEWHQNLIESAASEELMEK	189	47	11	41.39	b2b3b9b11y3y5y6y7°y7y9y29	5380.37	127.019	7212	4	1345.85	-1.91
[P0A1H3]EFG_SALTY Elongation factor G	10		LGANPVPLQLAIGAEEGFTGVVDLVK	161	26	4	18.2	b3b6°b6b19	2607.42	120.780	26854	3	869.81	-8.15
[P0A1H3]EFG_SALTY Elongation factor G	11		VWTDDEESNQTHIAGMGELHLDIIVDR	446	26	5	35.2	b12b13b14°b14y15	2954.41	136.700	24084	2	1477.71	-15.70
[P0A1H3]EFG_SALTY Elongation factor G	12		VVGQIK	153	6	2	13.55	b4°b4	643.41	45.116	17104	1	643.41	-1.80

P0A1H3 EFG_SALTY Elongation factor G	13		IHAEVPLSEMGYATQLR	653	18	3	15.44	b9y3y8	2062.06	96.311	10200	3	688.03	9.35
P0A1H3 EFG_SALTY Elongation factor G	14	Carbamidomethyl+C(9)	DVTTGDTLCDPENPIILER	389	19	3	14.8	b5b8y11	2158.05	70.101	8458	2	1079.53	6.45
P0A1H3 EFG_SALTY Elongation factor G	15		GITITSAAATFAWSGMAK	59	18	8	41.61	b6b8b14°b14y4y8°y8y9	1813.90	90.093	3131	2	907.45	-7.27
P0A1H3 EFG_SALTY Elongation factor G	16		TTTTERILFYTGVDNHK	23	16	3	17	b4b11y5	1880.99	48.724	20090	3	627.67	0.13
P0A1H3 EFG_SALTY Elongation factor G	17		AKVTDIEGK	495	9	4	45.18	b7y3y6y7	960.53	26.287	8773	2	480.77	-9.79
P0A1H3 EFG_SALTY Elongation factor G	18		QSGGRGQYGHVVIDMYPLEPGSN PK	507	25	3	22.8	b12b14b15	2686.31	136.624	8324	2	1343.66	2.73
P0A1H3 EFG_SALTY Elongation factor G	19	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETV WRQANK	104	28	8	34.87	b3b11b14b15y4*y4y11y27	3062.48	123.891	5791	3	1021.50	-12.12
P0A1H3 EFG_SALTY Elongation factor G	20		EDPSFRVWTDDESNQTIAGMGEL HLDIIVDR	440	32	3	22.07	b11y23y24	3685.79	81.883	4727	3	1229.27	3.05
P0A1H3 EFG_SALTY Elongation factor G	21		NIGISAHIDAGKTTTTER	11	18	3	15.44	b11y4y6	1884.99	91.646	2955	2	943.00	4.53
P0A1H3 EFG_SALTY Elongation factor G	22	Carbamidomethyl+C(10) ;Oxidation+M(7)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	8	38.88	b3°b3b6b10b14y6y9y11	2637.27	95.126	21294	3	879.76	-4.44
P0A1H3 EFG_SALTY Elongation factor G	23	Oxidation+M(10)	GQYGHVVIDMYPLEPGSNPK	512	20	4	25.04	b7b8b13y10	2217.04	73.401	3468	3	739.69	-10.02
P0A1H3 EFG_SALTY Elongation factor G	24		GQYGHVVIDMYPLEPGSN	512	18	0	6.17		1975.92	70.783	14598	3	659.31	0.56
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	14	114.16	b2b3b4b5y1y2y3y5y7°y7y8 y9y10y12	1150.68	53.058	121761	2	575.84	-5.73
P66313 RL6_SALTY 50S ribosomal protein L6	2		TLNDAVEVK	35	9	7	38.06	b2°b2y2y6y7y8y9	988.52	38.326	107546	2	494.77	-6.92
P66313 RL6_SALTY 50S ribosomal protein L6	3		DGYADGWAQAGTAR	55	14	9	42.08	b3y1y4y6°y6y7y11*y11y14	1438.64	49.346	71996	2	719.82	3.14
P66313 RL6_SALTY 50S ribosomal protein L6	4		INGQVITIK	18	9	6	45.18	b2b3y3y7y8y9	985.60	48.406	62820	2	493.30	-5.33
P66313 RL6_SALTY 50S ribosomal protein L6	5		ALLNSMVIGVTEGFTK	69	16	8	65.59	b2y3y5y6y7y9y11y16	1679.90	95.140	39072	2	840.45	-0.80
P66313 RL6_SALTY 50S ribosomal protein L6	6		GADKQVIGQVAADLR	134	15	3	17.98	b3y4y7	1540.82	60.478	18032	3	514.28	-12.68
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	1		VQALADAAR	102	9	9	74.47	b2b3*b3y3y4y5y6y7y9	914.50	31.535	145948	2	457.75	-11.08
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	2		SGFQYHGR	94	8	4	40.66	y3y4y6y8	951.45	28.503	6626	2	476.23	4.43
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	3		EAGLQF	111	6	3	26.69	b4°b4b5	664.33	61.788	61704	1	664.33	-2.94
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	8	55.32	b2b4y6y10y11y12y17y19	2215.16	74.885	48536	3	739.06	-4.30
Q56073 DNAK_SALTY Chaperone protein dnaK	2		SLGQFNLDGINPAPR	452	15	19	127.21	b2°b2b5°b5b8b12b14y1y4 y5y7*y7y8y10*y10y11*y1 1y13y15	1598.83	71.900	42021	2	799.92	1.60
Q56073 DNAK_SALTY Chaperone protein dnaK	3		MQELAQVSQK	587	10	7	39.85	b2b7y5*y5y6y8y10	1161.59	36.990	26156	2	581.30	-3.57
Q56073 DNAK_SALTY Chaperone protein dnaK	4		ASSGLNEEEIQK	502	12	10	78.72	b1y4y5y7°y7y8y9y10°y10y 12	1304.63	34.421	25353	2	652.82	0.09
Q56073 DNAK_SALTY Chaperone protein dnaK	5		TAEDYLGEVPVTEAVITVPAYFNDA QR	125	26	8	41.17	b2b7y6y8y9y12y13y26	2869.40	93.600	19066	3	957.14	3.74
Q56073 DNAK_SALTY Chaperone protein dnaK	6		NDPLAMQR	253	8	3	40.66	y4y6y7	944.46	39.316	11163	2	472.74	2.07
Q56073 DNAK_SALTY Chaperone protein dnaK	7		QAVTNPQNTLFAIK	56	14	4	26.89	b3b4*b4b7	1544.85	67.229	10576	2	772.93	1.34

Q56073 DNAK_SALTY Chaperone protein dnaK	8		LMEIAQQQHAQQAGSADASAN NAKDDDVVDAEFEEVK	597	38	3	10.86	b6b8y3	4100.88	89.683	8664	5	820.98	0.83
Q56073 DNAK_SALTY Chaperone protein dnaK	9	Carbamidomethyl+C(12)	IIGIDLGTNSCVAIMDGTQAR	3	22	4	19.84	y5y11y14*y14	2306.17	79.151	6400	2	1153.59	11.12
Q56073 DNAK_SALTY Chaperone protein dnaK	10		DVNPDEAVAIGAAGVQGGVLTGD VK	363	24	4	16.69	b4b16y4y10	2295.16	104.217	62157	3	765.72	-11.06
Q56073 DNAK_SALTY Chaperone protein dnaK	11		TIAVYDLGGGTFDISIIEIDEVDGE K	188	26	5	18.12	b5y3y8°y8y11	2769.32	120.436	35092	3	923.78	-18.42
Q56073 DNAK_SALTY Chaperone protein dnaK	12		GMPQIEVTFDIDADGILHVS AK	467	22	4	13.32	b8°b8b13y13	2356.14	95.033	7896	4	589.79	-17.82
Q56073 DNAK_SALTY Chaperone protein dnaK	13		VLENAEGDR	25	9	4	30.28	b5b7°b7y6	1002.47	126.495	1540	1	1002.47	-13.52
Q56073 DNAK_SALTY Chaperone protein dnaK	14	Carbamidomethyl+C(15)	MGKIIIGIDLGTNSCVAIMDGTQA R	0	25	3	21.86	b16y18y19	2622.30	86.193	13132	2	1311.65	-1.77
Q56073 DNAK_SALTY Chaperone protein dnaK	15		FEELVQTRNQGDHLLHSTR	528	19	3	22.58	b9y11y12	2280.18	90.369	6351	3	760.73	12.63
Q56073 DNAK_SALTY Chaperone protein dnaK	16		DVSIMPYKIIADNGDAWL DVK	84	22	5	17.98	b6°b6b16y12y14	2420.24	105.713	5801	4	605.81	8.07
Q56073 DNAK_SALTY Chaperone protein dnaK	17		VALQDAGLSVSDINDVILVGGQT RMPMVQK	321	30	4	16.39	b5b12b16y8	3154.62	98.820	5666	3	1052.21	-12.77
Q56073 DNAK_SALTY Chaperone protein dnaK	18		ASDNKSLGQFNL DGINPAPR	447	20	3	14.24	b10b12y8	2114.06	65.159	4404	3	705.36	-2.19
Q7CPZ4 GRPE_SALTY Protein grpE	1		FVNELLPVIDSLDR	90	14	7	61.76	b2b4b5y5y6y8y9	1629.89	97.421	45881	2	815.45	1.05
Q7CPZ4 GRPE_SALTY Protein grpE	2		IANLEVQLAE AQTR	43	14	4	32.77	b3b10y4y5	1555.83	63.229	24417	2	778.42	-10.36
Q7CPZ4 GRPE_SALTY Protein grpE	3		TPEGQAPEEII MDQH EEEV AEPN DSAEQV DPRDEK	7	36	3	10.88	b10b13y5	4060.84	63.093	4249	4	1015.96	3.91
Q7CPZ4 GRPE_SALTY Protein grpE	4		ANPDMAAMVEGIELTLK	111	17	5	16.17	b15°b15y14°y14y16	1802.91	79.488	52891	3	601.64	3.79
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		AGLGMMEGVLENVPSAR	78	17	8	42.37	b3b13y4y6°y6y7y12y17	1730.86	81.998	51825	2	865.94	4.58
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		VLVLVA APEGIAALEK	155	16	6	44.16	b2b3b4b5y9y11	1592.96	86.075	44562	2	796.99	1.61
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		NEETLEPVVPYFQK	103	13	5	27.94	b2y5y7y8y13	1593.78	65.268	18590	2	797.40	2.14
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		ITVVPILR	70	8	4	40.66	y2y4y5y6	910.60	70.136	13932	2	455.81	-4.29
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		ELASEVGSLLTYEATADLETEK	29	22	4	17.98	b7b9y7y10	2369.18	109.361	2428	2	1185.09	9.17
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	6		ELASEVGSLLTYEATADLETEKVT IEGWNGPVEIDQIK	29	38	4	16.48	b12°b12b15b20	4148.02	112.679	8728	4	1037.76	-13.65
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	7	Oxidation+M(4)	LGLMRENDISTK	14	12	3	22.09	b6b8y5	1392.71	60.072	30922	3	464.91	-3.59
P60446 RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	9	67.76	y1y2y3y5y6y7*y7y8y10	1115.64	56.280	106677	2	558.32	-2.52
P60446 RL3_SALTY 50S ribosomal protein L3	2		IFTEDGV SIPVTVIEVEANR	13	20	8	51.46	b2y3y4y5*y5y6y15y20	2188.16	88.328	90418	2	1094.58	4.69
P60446 RL3_SALTY 50S ribosomal protein L3	3	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	4	15.44	b7y4y15y18	1738.93	53.961	24358	3	580.32	-10.39
P60446 RL3_SALTY 50S ribosomal protein L3	4		MAGQMGNER	160	9	6	38.06	b2y4y7*y7y8y9	993.42	20.252	22028	2	497.22	-0.55
P60446 RL3_SALTY 50S ribosomal protein L3	5		AVQVTTGAK	46	9	7	38.06	b2y5y6y7°y7*y7y9	874.49	21.672	12415	2	437.75	-8.17
P60446 RL3_SALTY 50S ribosomal protein L3	6		VPGSIGQNQTPGK	141	13	4	29.7	b4b6b12°b12	1282.66	65.264	2460	3	428.23	-8.66
P60446 RL3_SALTY 50S ribosomal protein L3	7	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	6	46.52	b3b4y5y7y8y12	1809.97	56.114	104804	3	604.00	-9.10

P60446 RL3_SALTY 50S ribosomal protein L3	8		QVTTGAK	48	7	0	1.65		704.39	21.688	3562	1	704.39	1.39
P26982 DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	8	49.28	b3b4b9y1y4y7y9y15	2017.09	75.028	47066	3	673.04	-8.35
P26982 DEGP_SALTY Protease do	2		GAFVSQVMPNSSAAK	313	15	11	70.17	b3b4b7*b7y1y8y9y10y11*y1y15	1493.75	53.077	33357	2	747.38	2.94
P26982 DEGP_SALTY Protease do	3		SDIALIQIQNPK	160	12	5	26.07	b3b4y6*y6y12	1339.76	63.900	30498	2	670.38	-0.18
P26982 DEGP_SALTY Protease do	4		AQVGTMPVGSK	352	11	9	50.26	b1b2*b2y3y5y8*y8y9y11	1074.56	34.521	26710	2	537.78	-2.73
P26982 DEGP_SALTY Protease do	5		VGDYTV AIGNPFGLGETVTSIGIVS ALGR	186	28	14	81.06	b3b6*b6b8b11y2y3y4y5y6y8y9y14y28	2750.41	117.284	22774	3	917.47	-9.50
P26982 DEGP_SALTY Protease do	6		ANSPAAQIGLK	418	11	6	41.05	b1b7b8y9y10y11	1069.60	45.665	16772	2	535.30	-1.83
P26982 DEGP_SALTY Protease do	7		SGLNVENYENFIQTDAAINR	214	20	5	19.56	b3b5*b5y3y7	2268.11	77.482	7677	2	1134.56	7.53
P26982 DEGP_SALTY Protease do	8		GELGIMGTELNSELAK	289	16	4	27.43	b4b8b13y12	1661.83	64.826	3374	3	554.61	-8.89
P26982 DEGP_SALTY Protease do	9		RGELGIMGTELNSELAK	288	17	4	16.17	b9b12*b12y13	1817.96	86.475	2744	2	909.48	9.94
P26982 DEGP_SALTY Protease do	10	Oxidation+M(6)	NLTSMQMV EYGQVK	275	13	3	25.23	b9y6y7	1512.75	38.922	27716	3	504.92	7.34
P26982 DEGP_SALTY Protease do	11	Oxidation+M(6)	GELGIMGTELNSELAK	289	16	4	17	b11y10y12*y12	1677.84	68.032	8884	3	559.95	0.22
P26982 DEGP_SALTY Protease do	12	Oxidation+M(8)	GAFVSQVMPNSSAAK	313	15	4	37.59	b9b10y7y8	1509.75	94.963	4507	2	755.38	6.79
P26982 DEGP_SALTY Protease do	13		ANSPAAQIGL	418	10	0	2.47		941.49	45.554	2209	2	471.25	-12.25
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	1	Carbamidomethyl+C(3)	FICIADASK	112	9	6	54.21	b2y3y4y5y7y9	1024.51	50.916	27888	2	512.76	-3.57
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	2		GADVALIGTPDGVK	201	14	8	44.94	b5b6y1y2y3y5y7y14	1312.71	57.088	26343	2	656.86	-1.58
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	3		GQIEGAVSSSDASTEK	43	16	5	25.38	b2*b2y9y12y13	1565.73	31.461	8433	2	783.37	2.11
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	4		AVGWAA LQYVQPGTIVGVGTGST AAHFIDALGTMK	8	35	5	22.98	b17*b17b18b20*b20	3487.75	136.830	7899	2	1744.38	-15.82
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	5		MTQDELK	0	7	7	50.38	b6y4*y4y5*y5*y5y6	864.42	136.293	2085	1	864.42	6.43
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	6		GQIEGAVSSSDASTEKLK	43	18	7	28.93	b4*b4*b4b11*b11y10y11	1806.92	38.946	2402	2	903.97	8.99
P63411 ACKA_SALTY Acetate kinase	1	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPE AR	17	26	5	27.32	y2y4y7y8y19	2907.42	105.416	39478	3	969.81	6.05
P63411 ACKA_SALTY Acetate kinase	2		EGTRPAVVIPTNEELVIAQDASR	374	23	13	82.05	b2b8b9b15y3*y3y6y7y8y9y12y14y23	2465.29	68.926	29431	3	822.44	-3.66
P63411 ACKA_SALTY Acetate kinase	3		LDVAVFTGGIGENAAMVR	324	18	8	41.61	b5b8b15*b15y10y11y13y18	1819.92	93.883	23022	2	910.46	-9.79
P63411 ACKA_SALTY Acetate kinase	4	Carbamidomethyl+C(1)	CVDTSMGLTPLEGLVMGTR	224	19	9	47.58	b15*b15y1y3y4y7*y7y8y10	2037.00	94.972	22616	2	1019.00	9.95
P63411 ACKA_SALTY Acetate kinase	5		YIGSYTALMDGR	312	12	6	44.65	b1y2y5y8y9y10	1346.65	64.741	8544	2	673.83	9.88
P63411 ACKA_SALTY Acetate kinase	6		SGFINKEGTRPAVVIPTNEELVIAQ DASR	368	29	3	11.47	b11y7y26	3111.63	103.366	4427	3	1037.88	-5.88
P63411 ACKA_SALTY Acetate kinase	7	Carbamidomethyl+C(14)	ESGLLGLTEVTSDCR	272	15	6	62.04	y7y8y9*y9y10y11	1636.79	71.765	21427	2	818.90	4.10
P63411 ACKA_SALTY Acetate kinase	8		NVAVFDTA FHQTMPEESYLYALP YSLYK	144	28	5	22.18	b14*b14y5y6y8	3297.60	99.643	10622	3	1099.87	4.22
P63411 ACKA_SALTY Acetate kinase	9		YTSSVVIDESVIOGIK	98	16	3	25.38	b4b5b11	1737.89	113.103	1784	2	869.45	-18.61
P63411 ACKA_SALTY Acetate kinase	10		YGAHGTSHFYVTQEAAK	178	17	3	16.17	b14y5y13	1866.85	93.643	1765	3	622.96	-14.25
P63411 ACKA_SALTY Acetate kinase	11		NEELVIAQDASR	385	12	0	7.41		1344.66	68.902	25126	2	672.84	-8.26
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	1		AYPDLDAIIAPDANALPAAAQAAE NLKR	209	28	6	20.3	b2b8b14y4y12y19	2863.49	87.656	63080	3	955.17	-1.53
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	2		VAFFYSSPTVTDQNQWVK	154	18	7	36.36	b2b12y2y11y12y13y18	2117.05	77.666	41147	2	1059.03	6.69
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	3		LVGVGFFTSGGNGAQEAGK	35	19	10	61.05	b2b15b16y2y5y14y15y17*y17y18	1795.90	71.511	33641	2	898.45	2.92

Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	4		NMPMNVGDSLDPGIGK	284	17	7	16.17	b2b12°b12y5y15*y15y17	1757.87	79.551	32801	2	879.44	6.04
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	5		VTVSPNSEQGYHYEAK	301	16	8	34.46	b6b9°b9y2y4y7y13y16	1808.83	36.385	32594	3	603.61	-10.87
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	6		NNLAIVGFSTPNVMRPYVQR	237	20	6	19.56	b1b11b13y4*y4y7	2276.17	77.580	23309	4	569.80	-12.01
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	7		VTVSPNSEQGYHYEAKGNGIVLLPER	301	26	3	35.28	b7b8b9	2857.48	59.943	28701	4	715.13	10.94
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	8		SYIINQGTQPKQLGSMLVEMAAHQVDK	124	26	3	18.2	b4b11b14	2908.42	110.548	3882	4	727.86	-3.27
P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	22	165.93	b2b3b4b5b6°b6b8y1y2y3°y3y4°y4y5y6°y6y7°y7y8y9y10y12	1196.59	64.262	526750	2	598.80	-1.84
P0A9Y9 CC_SALTY Cold shock-like protein cC	2		DVVFVHFSAIQGNGFK	27	15	6	36.78	b8b12b13y6y9°y9	1665.83	74.266	39353	3	555.95	-7.91
P0A9Y9 CC_SALTY Cold shock-like protein cC	3		GPAAVNVTAI	59	10	6	47.63	b2b3b7b9y6y10	912.51	59.410	32846	1	912.51	-4.35
P0A9Y9 CC_SALTY Cold shock-like protein cC	4		TLAEGQNVEFEIQDGQK	42	17	4	36.71	b8b9b10y10	1905.93	54.957	4666	2	953.47	5.96
P0A9Y9 CC_SALTY Cold shock-like protein cC	5		TLAEGQNVEFEIQDGQKGPAAVNVTAI	42	27	4	21.83	b13*b13y15y16	2799.38	136.662	11549	2	1400.19	-13.69
P0A9Y9 CC_SALTY Cold shock-like protein cC	6		TPADGSK	20	7	2	21.38	b4b5	675.33	64.334	4640	1	675.33	4.16
P0A9Y9 CC_SALTY Cold shock-like protein cC	7		GFITPADGSK	17	10	1	7.57	b3	992.50	64.243	2735	1	992.50	-1.05
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	1		DGIFVEDKDSPLYVNLIVTREDNK	215	23	3	12.94	b6y5y7	2666.35	63.865	22045	4	667.34	7.42
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	2		DGIFVEDKDSPLYVNLIVTREDNKDAENVK	215	29	4	17.42	y2y6y8y11	3322.62	70.457	21072	4	831.41	-7.27
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	3		SLDELKDGSQVAVPNDPTNLGR	122	22	4	24.03	b13y6y7y9	2325.17	57.885	16215	3	775.73	1.16
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	4		IVELEAPQLPR	178	11	3	27.12	b3y5y6	1264.73	65.985	11037	2	632.87	5.69
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	5		YGLDVELVTFNDYVLPNEALSK	56	22	5	30.01	b5y6y10y13y14	2499.29	103.880	21967	3	833.77	8.50
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	6		FVQAYQSDEVYEAANK	245	16	3	17	b6b8y11	1861.88	81.870	5344	3	621.30	8.06
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	7		VGLIK	151	5	2	26.28	b3y4	529.37	26.148	3429	1	529.37	-0.58
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	8	Carbamidomethyl+C(17)	TFAAVGALIGSLALAGCGQDEK	6	22	4	24.03	b5y4y12y13	2149.06	96.109	2757	3	717.03	-16.36
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	9		DGSQVAVPNDPTNLGR	128	16	3	23.54	b9y10y11	1639.80	72.953	2734	2	820.40	-4.47
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	10		KFVQAYQSDEVYEAANK	244	17	4	16.17	b12*b12y3y7	1989.97	76.445	49302	2	995.49	6.56
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	11		FVQAYQSDEVYEAANKVFNGGAVK	245	24	4	25.98	b6b7y5y22	2634.30	77.530	41101	3	878.77	6.86

Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	12	Phosphoryl STY(18)	DGIFVEDKDSPYVNLIVTREDNKD AENVK	215	29	6	21.88	b15_HPO3 b15°b15b16*b16y13*y13	3402.58	136.764	7263	2	1701.79	-5.81
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	1		LAEAGIPTQMER	60	12	6	47.79	b4b5y6y9y10y12	1315.67	49.659	41709	2	658.34	2.23
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	2	Carbamidomethyl+C(7)	LLSDTECLVK	72	10	6	33.7	b2y5y7y8°y8y10	1177.61	53.223	37180	2	589.31	-1.24
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	3		TVYSTENPDLLVLEFR	13	16	10	41.66	b4°b4b5°b5b12*b12y1y3y4y16	1895.98	88.759	27352	2	948.49	2.12
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	4		IEQFDRK	39	7	3	37.24	b3b4y6	935.49	26.418	12174	2	468.25	-7.83
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	5		NDTSAGDGAR	29	10	5	52.2	b3b9y3y7y8	963.42	80.653	3597	2	482.21	7.60
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	6		QSLGGLIEAYEAVHR	215	16	4	30.56	b7b8y3y6	1713.89	137.475	2538	2	857.45	1.50
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	7	Carbamidomethyl+C(8)	LEMVPVECVVR	83	11	3	24.11	b3b5y4	1330.70	82.013	1669	2	665.85	9.08
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	8		GMVNNKFNFHIMTK	46	14	3	19.11	b8b12y13	1680.83	102.208	28053	3	560.95	-1.60
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	9		TVYSTENPDLLVLEFRNDTSAGD GAR	13	26	4	12.06	b12°b12b24y13	2840.34	136.666	14925	2	1420.67	-10.49
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	10		LEFGLYKGEVVLGDEFSPDGSR	177	22	3	22.07	b6y6y7	2414.16	93.801	2477	2	1207.58	-12.24
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	11		ETLDKMDK	203	8	4	32.88	b4°b4y4y5	979.48	119.291	2020	1	979.48	1.43
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	1		TFDTPTYPNSLALSADGK	308	18	6	32.45	b4b7y11y13y14y18	1897.94	65.320	20471	2	949.47	9.07
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	2		LYTTNADGEFITIDTASNK	198	19	3	22.58	b12y12y13	2074.01	65.225	16166	2	1037.51	7.06
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	3		LLDDGKEHFFINLSLDTAGHR	223	21	10	57.15	b3°b3b4b5b6°b6b8y7y9y21	2398.19	82.573	15823	2	1199.60	-11.81
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	4		MSTGLALDSK	185	10	4	39.06	b5b9y3y6	1022.51	45.931	16211	2	511.76	-4.18
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	5		EQEATQPDDVIR	338	12	3	22.09	b7b11y6	1400.69	36.363	2121	3	467.57	14.21
Q8ZL56 GPMI_SALTY 2	1		TFFANPVLTVNAVDQAK	91	16	6	17	b1b7°b7y4y7y16	1735.91	76.704	40106	2	868.46	3.16
Q8ZL56 GPMI_SALTY 2	2		LSDIAPTMLSLMGMEIPQEMTGKPLFIVE	485	29	9	32.71	b2b3b5b7°b7b8b14y1y2	3191.62	122.198	19016	3	1064.54	1.30
Q8ZL56 GPMI_SALTY 2	3		VATYDLQPEMSSAELTEK	364	18	11	55.13	b1b3°b3b7b8b9b11y2y11y17y18	2011.97	62.995	16498	2	1006.49	9.95
Q8ZL56 GPMI_SALTY 2	4		TAVAYPPASLANTFGEWMAK	303	20	5	22.41	b7y5y7y15y20	2125.06	96.041	15881	2	1063.03	6.43
Q8ZL56 GPMI_SALTY 2	5	Carbamidomethyl+C(8)	AVEALDNCIEQVTK	416	14	10	42.08	b7°b7b9°b9b11°b11°b11b12y5y14	1589.80	50.617	14893	2	795.40	9.21
Q8ZL56 GPMI_SALTY 2	6		IVYQDLTR	75	8	6	53.8	b4b7y4°y4y6y8	1007.55	46.479	8638	2	504.28	-4.24
Q8ZL56 GPMI_SALTY 2	7		KPMVLVILDGYGYR	5	14	3	19.11	b3y4y7	1623.91	102.296	8521	2	812.46	12.85
Q8ZL56 GPMI_SALTY 2	8		AVESVGGQLLITADHGNAEQMR	430	22	3	13.32	b4b15y6	2296.12	82.710	4716	3	766.05	-5.95

Q8ZL56 GPMI_SALTY 2	9		TPVMDALWAKRPHTLIDASGLEV GLPDR	31	28	4	11.63	b3y1y4y7	3058.59	137.677	4381	4	765.40	-7.90
Q8ZL56 GPMI_SALTY 2	10		VVNLNFVMLTEYAADIK	286	17	3	23.16	b12y11y12	1940.04	118.202	3334	3	647.35	11.77
Q8ZL56 GPMI_SALTY 2	11		AVHIMGLLSAGGVHSHEDHIMAM VELAAER	111	30	3	17.23	y4y12y14	3181.59	97.075	5875	3	1061.20	5.29
Q8ZL56 GPMI_SALTY 2	12		DPATGQAHTAHTNLPVPLIYVGE K	452	24	3	12.61	b5b11y4	2529.27	47.290	4055	3	843.76	-15.35
Q8ZL56 GPMI_SALTY 2	13		YAHVTFFNGGVVEEPFAGEER	336	21	10	60.45	b3b4b5°b5b10y5y7y13y14 *y14	2403.13	95.024	4039	3	801.72	12.39
Q8ZL56 GPMI_SALTY 2	14		AFVNADFDGFARK	272	13	3	25.23	b5b6y6	1457.71	50.454	2558	3	486.57	-6.11
Q8ZL56 GPMI_SALTY 2	15	Oxidation+M(8)	VVNLNFVMLTEYAADIK	286	17	3	16.17	b13y7y10	1956.03	73.602	110274	2	978.52	7.99
Q8ZL56 GPMI_SALTY 2	16	Oxidation+M(21)	AVESVGGQLLITADHGNAEQMR	430	22	3	13.32	b4b8y13	2312.13	81.050	19727	3	771.38	-1.80
Q8ZL56 GPMI_SALTY 2	17	Oxidation+M(20)	LSDIAPTMLSLMGMEIPQEMTGKP LFIVE	485	29	3	17.42	b3b9b15	3207.58	73.007	4001	5	642.32	-7.69
Q8ZL56 GPMI_SALTY 2	18		ATYDLQPEMSSAELTEK	365	17	0	5.35		1912.86	63.003	21940	3	638.29	-14.42
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		VTDIEPGLVGGTEFSSVR	171	18	11	49.04	b2b7°b7y6°y6y7y9y13y14° y14y18	1862.96	69.004	27792	2	931.99	7.08
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		AVLPGMVER	115	9	4	38.06	y4y5y6y9	971.53	52.983	21435	2	486.27	-3.77
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		AAIEEMMASLPAQWR	58	15	7	29.2	b11y4*y4y5y11*y11y15	1703.83	91.182	11180	2	852.42	5.87
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4	Carbamidomethyl+C(15)	MIVLVTGATAGFGECIAR	0	18	4	22.6	y4y8°y8y10	1865.94	101.081	3812	2	933.47	-11.25
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		TYENTTALTPEдитеAVWWVATL PAHVNINTVEMMPVTQSFAGLSV HR	199	48	5	25.54	b11b13*b13b23b24	5340.60	136.636	31332	4	1335.91	-6.22
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		DELGENVLTAQLDVR	41	15	4	26.06	b3°b3b4b9	1671.84	33.008	18348	3	557.95	-7.30
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7	Carbamidomethyl+C(15) ;Oxidation+M(1)	MIVLVTGATAGFGECIAR	0	18	4	22.84	b14°b14y10y11	1881.96	120.880	13625	2	941.49	4.61
O68883 CISY_SALTY Citrate synthase	1	Carbamidomethyl+C(12)	TAGSSGANPFACIAAGIASLWGPA HGGANEAAALK	240	34	7	12.95	b2b7b18y2y7y9y34	3195.57	117.071	22656	3	1065.86	0.46
O68883 CISY_SALTY Citrate synthase	2	Carbamidomethyl+C(18)	NDLSYAGNFLNMMFSTPCETYEYV NPVLER	189	29	6	19.68	b2b3b5b10y5y10	3411.55	112.865	5382	3	1137.86	6.23
O68883 CISY_SALTY Citrate synthase	3		AMGIPSSMFTVIFAMAR	371	17	7	47.81	b3b4b5b13y5y13°y13	1829.92	121.052	3333	2	915.46	2.13
O68883 CISY_SALTY Citrate synthase	4		ILILHADHEQNASTSTVR	222	18	12	68.72	b10y6y7y8°y8y9°y9y10°y1 0*y10y17°y17	2005.04	136.288	48014	2	1003.02	-2.37
O68883 CISY_SALTY Citrate synthase	5		HTMIHEQITRLFHAFR	110	16	6	51.5	b4b5b9b11b13y6	2037.05	72.026	20145	3	679.69	-3.96
O68883 CISY_SALTY Citrate synthase	6		LMGFGRHVYK	300	10	3	33.7	b4b7b8	1207.63	77.669	6673	2	604.32	-12.64
O68883 CISY_SALTY Citrate synthase	7		AMDRILILHADHEQNASTSTVR	218	22	4	23.2	y6y11°y11y12	2478.24	109.097	5052	2	1239.62	-4.83
O68883 CISY_SALTY Citrate synthase	8		KLYPNVDIFYSGIILK	356	15	4	26.06	b7b9°b9b11	1769.96	67.608	3881	3	590.66	-14.55
P06179 FLIC_SALTY Flagellin	1		AQILQQAGTSVLAQANQVPQNVL SLLR	468	27	12	34.59	b2*b2b3*b3b5b7b9y1y4y9 y13y27	2860.60	105.857	81419	3	954.21	0.17
P06179 FLIC_SALTY Flagellin	2		FNSAITNLGNTVNNLTSAR	432	19	9	55.82	b2y4y6y7y11y13y14*y14y 19	2007.03	78.596	46273	2	1004.02	2.92
P06179 FLIC_SALTY Flagellin	3		SQSALGTAIER	20	11	5	31.1	b2y6y8y9y11	1132.59	41.869	42239	2	566.80	-5.17
P06179 FLIC_SALTY Flagellin	4		INSAKDDAAGQAIANR	37	16	5	48.06	y3y4y5y6y16	1614.80	30.442	42229	3	538.94	-11.64

P06179 FLIC_SALTY Flagellin	5		VSGQTQFNGVK	125	11	7	36.46	b2b4y5y9y10*y10y11	1164.60	33.043	40663	2	582.80	-3.46
P06179 FLIC_SALTY Flagellin	6		AQVINTNSLSLLTQNNLNK	1	19	8	21.76	b1b2*b2y2y7y15y17y19	2085.14	74.502	38558	2	1043.07	2.69
P06179 FLIC_SALTY Flagellin	7		VSDTAATVTGYADTTIALDNSTF K	180	24	9	50.3	b1y6y7°y7y8y9*y9y13y24	2462.19	92.053	35241	3	821.40	0.59
P06179 FLIC_SALTY Flagellin	8		IDAALAQVDTLR	411	12	6	50.8	b4b5y4y7y10y12	1285.71	60.942	28865	2	643.36	-3.23
P06179 FLIC_SALTY Flagellin	9		ELAVQSANSTNSQSDLDLSIQAEIT QR	93	26	4	12.06	b9y3*y3y6	2805.36	70.091	2920	2	1403.18	3.31
P06179 FLIC_SALTY Flagellin	10		FTANIK	53	6	1	13.55	y5	693.38	34.202	10271	2	347.20	-14.00
P06179 FLIC_SALTY Flagellin	11		TYAASK	379	6	1	13.55	b5	640.33	85.323	4832	1	640.33	-5.43
P06179 FLIC_SALTY Flagellin	12		AQPDLAEEAAATTTENPLQK	392	19	3	14.8	b8b12y9	1968.99	60.039	4779	2	985.00	3.60
P06179 FLIC_SALTY Flagellin	13		YTADDGTSKTALNK	349	14	4	19.11	b3b12y11*y11	1484.73	77.740	13232	2	742.87	4.03
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	1		LFNELGPR	78	8	8	66.94	y3y4y5y6*y6y7*y7y8	945.51	55.354	96999	2	473.26	-8.20
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	2		AGDNAPMAYIELVDR	103	15	10	53.21	b4*b4b5y4y5y7°y7y10y13 *y15	1634.79	79.183	46283	2	817.90	4.41
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	3		NMAGSLVR	22	8	4	32.88	b3y6y7y8	847.44	41.225	43777	2	424.22	-6.19
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	4		AGGYTR	90	6	2	26.69	b3b4	624.32	30.184	3749	1	624.32	12.22
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	5		FASRAGGYTR	86	10	3	33.7	b3b4b7	1085.55	26.474	4190	3	362.52	5.17
P35891 DNAA_SALTY Chromosomal replication initiator protein dnaA	1	Carbamidomethyl+C(9)	MSLSLWQQCLAR	0	12	9	59.17	b7b11°b11*b11b12y4y5y6 y11	1492.72	76.395	10140	2	746.86	-11.94
P35891 DNAA_SALTY Chromosomal replication initiator protein dnaA	2	Carbamidomethyl+C(13)	YLNNINGLLNTFCGADAPQLR	54	21	3	20.4	b4b7b13	2364.18	91.218	2356	2	1182.60	2.89
P35891 DNAA_SALTY Chromosomal replication initiator protein dnaA	3		SNVNVK	128	6	1	13.55	b4	660.36	34.104	6265	1	660.36	-6.19
P35891 DNAA_SALTY Chromosomal replication initiator protein dnaA	4		HTFDNFVEGK	134	10	4	39.85	b3b7b8y3	1193.54	45.074	3995	2	597.27	-15.03
P35891 DNAA_SALTY Chromosomal replication initiator protein dnaA	5		SGWDNVPAPAEPTYR	113	15	3	17.98	b10y4y10	1659.80	64.877	3829	2	830.41	17.36
P35891 DNAA_SALTY Chromosomal replication initiator protein dnaA	6		QMAMALAKELTNHSLPEIGDAFG GR	406	25	7	32.03	b12b14b16°b16y14y15*y1 5	2657.32	136.713	4996	2	1329.16	0.64
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1	Carbamidomethyl+C(3)	FACGVIEK	169	8	9	66.94	y1y2°y2y3y4y5y6y7y8	923.46	41.276	95319	2	462.23	-7.87
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2		GGDNYSDKPAPLGGGGGAR	151	18	8	66.71	b2y5y6y7y8y11y12y18	1688.78	33.228	70795	3	563.60	-10.84
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3		EVPALMAGGHLDPEK	84	15	7	29.2	b3b7b9y2y4°y4y15	1563.80	63.000	5701	2	782.41	13.27
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	4		DGKEVPALMAGGHLDPEK	81	18	5	21.52	b5b12y7y11°y11	1863.95	61.109	2573	3	621.99	11.26
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	5		DGKEVPALMAGGHLDPEK	81	18	4	41.38	b4b5b12b13	1863.91	67.645	15571	2	932.46	-6.88
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	6	Carbamidomethyl+C(21)	GGDNYSDKPAPLGGGGGARFACG VIEK	151	26	3	12.06	b16y6y12	2593.25	102.270	1500	3	865.09	1.04
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	7	Oxidation+M(9)	DGKEVPALMAGGHLDPEK	81	18	4	21.52	b9b14y4y7	1879.95	73.245	74578	3	627.32	12.40
O54296 RS11_SALTY 30S ribosomal protein S11	1		ALNAAGFR	98	8	4	40.66	y4y5y6y8	819.44	42.120	29918	2	410.22	-6.78
O54296 RS11_SALTY 30S ribosomal protein S11	2		QGNALGWATAGGSGFR	37	16	5	34.84	y5y10y11y14y16	1549.76	65.990	20428	2	775.38	6.93

O54296 RS11_SALTY 30S ribosomal protein S11	3		STPFAAQVAAER	57	12	5	29.29	b1y2y7y8y10	1247.64	49.419	14072	2	624.33	5.67
O54296 RS11_SALTY 30S ribosomal protein S11	4	Carbamidomethyl+C(15)	ITNITDVTPIPHNGCRPPK	106	19	6	23.44	b3*b3b8b13y8*y8	2130.08	78.505	26339	3	710.70	-15.13
O54296 RS11_SALTY 30S ribosomal protein S11	5		QVSDGVAHIHASFNNTIVTITDR	14	23	4	12.94	b4*b4b9y20	2495.26	89.204	16821	3	832.42	-3.33
O54296 RS11_SALTY 30S ribosomal protein S11	6	Carbamidomethyl+C(13)	STPFAAQVAAERCADAVK	57	18	4	22.84	b8y4*y4y5	1891.95	59.145	3942	2	946.48	7.48
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	1		SFELPALPYAK	1	11	9	35.03	b2b3*b3b9y1y2y4y7y11	1235.66	79.239	42812	2	618.34	-2.27
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	2	Carbamidomethyl+C(22)	TSEGGIFNNAQVWNHTFYWNCL APNAGGEPTGK	58	34	12	50.21	b1b2b3b11b14b15b16y7y9 y10*y10y34	3708.70	97.058	20923	3	1236.90	0.72
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	3		DALAPHISAETLEYHYGK	12	18	6	34.35	b3y6y7y11y13*y13	2015.00	107.101	40822	3	672.34	4.60
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	4	Phosphoryl STY(7)	HHQTYVTNLNLIK	30	14	4	27.32	b6b12_HPO3 b12y8y10	1774.85	77.418	3153	3	592.29	-4.95
P77983 KPYK1_SALTY Pyruvate kinase I	1		GDLGVEIPVEEVIFAQK	244	17	9	32.45	b5*b5b7*b7y1y4*y4y10y12	1842.99	95.013	28055	2	922.00	2.72
P77983 KPYK1_SALTY Pyruvate kinase I	2		MLDAGMNVMR	22	10	4	36.71	y7y8y9y10	1137.54	57.399	16106	2	569.27	12.66
P77983 KPYK1_SALTY Pyruvate kinase I	3	Carbamidomethyl+C(3)	IVCTIGPK	5	8	3	35.89	b5y3y6	887.49	35.957	9739	2	444.25	-12.79
P77983 KPYK1_SALTY Pyruvate kinase I	4		IENQEGLNNFDEILEASDGIMVAR	220	24	3	12.61	b4b7y7	2677.26	112.928	7740	3	893.09	-4.65
P77983 KPYK1_SALTY Pyruvate kinase I	5		AGQTFTFTTDDK	86	11	3	31.1	y6y7y9	1216.60	75.375	1848	2	608.80	9.33
P77983 KPYK1_SALTY Pyruvate kinase I	6		AEAGDVANAILDGTDAVMLSGES AK	292	25	3	22.8	y5y13y14	2405.14	95.562	27087	2	1203.07	-4.36
P77983 KPYK1_SALTY Pyruvate kinase I	7	Carbamidomethyl+C(6)	ITEAVCR	353	7	4	37.24	b4*b4y5y6	848.42	24.857	10372	2	424.71	-8.99
P77983 KPYK1_SALTY Pyruvate kinase I	8	Carbamidomethyl+C(13)	YPLEAVSIMATICER	319	15	3	17.98	b10y4y13	1752.86	79.413	8783	2	876.94	-1.60
P77983 KPYK1_SALTY Pyruvate kinase I	9	Carbamidomethyl+C(7)	QDLIFGCEQGVDFAASFIR	175	20	4	14.24	b5*b5y9y14	2272.10	112.693	3825	3	758.04	-2.47
P77983 KPYK1_SALTY Pyruvate kinase I	10	Carbamidomethyl+C(9)	DKQDLIFGCEQGVDFAASFIR	173	22	4	13.32	b7*b7b9y13	2515.26	74.319	5201	3	839.09	10.58
P77983 KPYK1_SALTY Pyruvate kinase I	11	Carbamidomethyl+C(6)	ITEAVCRGAVETAEK	353	15	8	36.78	b6b7*b7b10*b10y5y7*y7	1633.80	136.194	1625	2	817.41	-10.39
P77983 KPYK1_SALTY Pyruvate kinase I	12	Phosphoryl STY(12)	YFPDATILALTNEVTAR	389	18	4	26.36	b7y5y6y11	2075.97	54.876	2447	4	519.75	-11.41
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	1		IFGPVTR	98	7	4	40.25	y3*y3y5y6	789.45	45.120	56129	2	395.23	-14.38
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	2		MIQEQTMLNVADNSGAR	0	17	14	83.25	b2b3b9y1y5*y5y6y7y9*y9 y11y12y14y17	1877.89	58.792	50477	2	939.45	2.41
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	3	Carbamidomethyl+C(6)	FDGNACVILNNSEQPIGTR	78	20	5	30.54	y3y4y7y12y20	2219.07	59.003	6980	2	1110.04	7.59
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	4		IQEQTMLNVADNSGAR	1	16	12	68.95	b3b6b12y8y10*y10*y10y1 1*y11y13y15*y15	1746.86	94.953	6960	2	873.94	10.76
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	5	Carbamidomethyl+C(14)	RPDGSVIRFDGNACVILNNSEQPI GTR	70	28	5	38.31	b3b14y10y11y12	3099.57	121.206	2545	3	1033.86	11.11
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	6	Phosphoryl STY(6)	IFGPVTRELR	98	10	4	33.7	y3y6y7*y7	1267.64	114.646	2000	2	634.32	-7.99
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	7	Oxidation+M(7)	MIQEQTMLNVADNSGAR	0	17	6	50.74	b4b5b6b9b12y3	1893.89	95.963	6630	2	947.45	4.45
P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	1		EIPFLYASSAATYGGR	107	16	8	68.91	b10b13*b13b14y6y7y8y9	1702.84	73.033	28054	2	851.92	-4.30

[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	2		QILPEANSQIVGFR	152	14	3	26.89	b3b8b9	1571.84	64.364	8835	2	786.42	-11.88
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	3		YQAFTQADLTNLR	271	13	5	20.46	b2b12y2y6y10	1540.78	65.238	8631	2	770.90	6.02
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	4		SGIFNLGTGR	229	10	4	26.71	b6b10y3y7	1021.53	57.634	4804	2	511.27	-12.37
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	5		TVAEGVTEYMAWLN RDA	293	17	5	22.7	b9b14*b14y9y11	1925.91	98.764	2641	2	963.46	4.12
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	6	Carbamidomethyl+C(6)	ELLHYCLEREIPFLYASSAATYGG R	98	25	5	27.7	b2y5y6y11y13	2916.46	110.429	2263	3	972.82	8.29
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	7		GSIEYIPFPDK	256	11	4	35.03	b7b9y4y8	1265.63	53.185	8067	2	633.32	-6.56
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	8		GSMASVAFHLNTQLNNGESPK	178	21	6	29.48	b9b10b14°b14y10y20	2202.02	74.805	3881	2	1101.51	-19.62
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	9		FVNLVDLNIADYMDK	38	15	3	17.98	b4b6y10	1769.89	79.940	3760	3	590.63	6.90
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	10		DFVYVGDVAAVNLWFLESGK	209	20	10	65.81	b8b9°b9b10°b10y4y6y7°y7 y8	2229.16	136.316	3333	2	1115.08	16.43
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	11	Carbamidomethyl+C(6)	ELLHYCLER	98	9	6	61.33	b3b4b5°b5b6y7	1232.59	136.341	3328	1	1232.59	-14.06
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	12		TVAEGVTEYMAWLN R	293	15	5	42.8	b5b7b11y8y9	1739.85	91.298	2245	2	870.43	7.23
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	13		TVAEGVTEYMAWLN RDA	293	17	4	16.17	b8b10y6*y6	1925.91	66.210	3223	2	963.46	1.46
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	14	Oxidation+M(3)	GSMASVAFHLNTQLNNGESPK	178	21	7	34.21	b8b11b13y10°y10y12y17	2218.09	127.064	2034	2	1109.55	14.75
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	15		EIPFLYASSAATYGG R	107	16	1	7.25	b7	1684.84	72.958	4141	2	842.92	5.80
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	1	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLALASGAK	257	25	7	26.75	b3b5b6y2y3y19y25	2684.45	129.709	46939	3	895.49	1.18
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	2		AFPGLNGMDLAK	148	12	7	43.81	b6b11b12y6y9y10y12	1233.62	71.967	16539	2	617.32	-3.96
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	3		EVTTAETYR	160	9	5	54.21	y4y5y6y7y9	1069.51	28.238	9441	2	535.26	-9.02
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	4		SALLVLEDGTQFHGR	3	15	6	24	b1b3°b3y2y10y11	1642.84	67.838	9370	3	548.28	-11.67
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	5		NVVMITAQNHGFAVDEDSL PANL R	302	24	5	12.61	b1b11y2y10y15	2611.31	82.870	7317	3	871.11	4.58
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	6	Carbamidomethyl+C(6)	GAQNGCIIAGDSPDAK	125	16	6	46.23	b9b10b13y9y10y12	1573.73	37.810	5806	2	787.37	2.40
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	7	Carbamidomethyl+C(18)	MNPDGIFLSNGPGDPAPCDYAITA IQK	230	27	3	17.91	y11y13y20	2862.36	82.913	6139	2	1431.68	5.97
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	8		AIGATGSAGVEVVFN TSM TGYQE I LTDPSSYSR	18	32	5	11.1	b15y9°y9y11°y11	3321.63	103.478	5428	5	665.13	10.80

[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	9		AFPGLNGMDLAKEVTTAETYR	148	21	5	18.72	b4b7*b7y3y7	2284.14	110.358	8156	3	762.05	5.02
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	10	Carbamidomethyl+C(7)	MLVDRGCR	207	8	4	53.8	b4b6y3y7	1006.48	67.962	3337	1	1006.48	-8.55
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	11	Oxidation+M(8)	AFPGLNGMDLAKEVTTAETYR	148	21	4	13.75	b12b17y11°y11	2300.13	88.719	28962	3	767.38	2.65
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	1		LNSAVFPSAQGGPLMHVIAGK	251	21	9	37.22	b4°b4b14b16b21y3y4y15y21	2094.10	78.609	88354	3	698.71	-5.71
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	2		VMQAQGSQLTNK	42	12	10	59.17	b2b3b9y2y3y7y9y10*y10y12	1304.67	29.590	56673	2	652.84	2.15
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	3		SPFVTSGIR	354	9	10	90.62	b3°b3b7b8y1y4y5y6y7y9	963.52	49.271	48988	2	482.27	-1.96
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	4	Carbamidomethyl+C(5)	VLDICAR	405	7	5	40.25	b2y4y5y6y7	846.44	44.700	44255	2	423.72	-11.61
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	5		VYQQQVAK	285	8	7	56.81	b2b3y3y5*y5y7y8	963.51	19.660	24637	2	482.26	-14.13
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	6		AMVEVFLNR	296	9	5	38.06	b4b7°b7b8°b8	1078.59	85.398	18271	2	539.80	14.03
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	7		MIIGFSAYSQGVVDWAK	168	17	3	16.17	b8b11y4	1800.94	74.053	16178	3	600.98	20.33
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	8		EAMEPEFK	277	8	3	40.66	y4y5y6	980.44	43.406	13610	2	490.72	1.37
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	9		LYNIVPYGIDESGKIDYDEMAK	138	22	3	22.07	b3y17y18	2533.24	76.669	95489	3	845.08	9.25
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	10		EMNIADYDAELWQAMEQEKVR	4	21	3	13.75	b5y17y19	2569.14	74.500	45489	3	857.05	-10.26
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	11		QEEHIELIASENYTSPRVMAQGSQLTNK	25	29	6	22.65	b10*b10b11°b11b13*b13	3301.65	84.226	5550	3	1101.22	11.17
[P0A1R8]DBHB_SALTY DNA-binding protein HU-beta	1		IAAGADISK	9	9	15	87.61	b2b6°b6y1y2°y2y3y4y5y6°y6y7°y7y8y9	845.46	28.162	348099	2	423.23	-14.22
[P0A1R8]DBHB_SALTY DNA-binding protein HU-beta	2		ALKDAVN	83	7	6	37.24	b1b2b5b6y5y7	730.41	22.657	4115	1	730.41	2.01
[P0A1R8]DBHB_SALTY DNA-binding protein HU-beta	3		EITIAAAK	67	8	7	80.08	b3°b3b7y3y4y5y6	816.46	38.330	64133	2	408.74	-21.60
[P0A1R8]DBHB_SALTY DNA-binding protein HU-beta	4		SQLEIK	3	6	3	39.83	b3y3y4	717.41	25.913	37563	2	359.21	-12.68
[P0A1R8]DBHB_SALTY DNA-binding protein HU-beta	5		ALDAIIASVTESLKEGDDVALVGFGTFAVK	23	30	8	50.02	b3b4b5°b5y4y6y8y23	3036.62	136.294	25700	3	1012.88	2.25
[P0A1R8]DBHB_SALTY DNA-binding protein HU-beta	6		EGDDVALVGFGTFAVKER	37	18	3	24.36	b10b12b13	1909.95	117.825	5930	2	955.48	-9.78
[P0A1R8]DBHB_SALTY DNA-binding protein HU-beta	7		AGADISK	11	7	3	38.06	b3b4b5	661.35	28.162	57132	1	661.35	3.05
[P0A1R8]DBHB_SALTY DNA-binding protein HU-beta	8		AAGADISK	10	8	4	38.06	b3b4b5°b5	732.39	28.159	22019	1	732.39	1.67
[P58661]AAT_SALTY Aartate aminotransferase	1		MFENITAAPADPILGLADLFR	0	21	9	44.42	b2b4b6b13y3y5y7y13y21	2275.19	121.449	13050	2	1138.10	5.58
[P58661]AAT_SALTY Aartate aminotransferase	2		TAQTPGGTGALR	96	12	5	33.98	b4*b4y3y7y8	1129.60	29.376	11501	2	565.30	2.70
[P58661]AAT_SALTY Aartate aminotransferase	3	Carbamidomethyl+C(4)	VGACTLVAADAETVDR	254	16	4	25.38	b3b11°b11b12	1647.80	54.409	5346	2	824.41	2.30
[P58661]AAT_SALTY Aartate aminotransferase	4		GWLPLFD FayQGFAR	204	15	3	17.98	b11b13y12	1787.88	117.374	5146	2	894.44	-4.98
[P58661]AAT_SALTY Aartate aminotransferase	5		ANYSNPPAHGASIVATILSNDALR	280	24	6	25.98	b8°b8b14y6*y6y7	2452.28	98.298	16283	3	818.10	9.96
[P58661]AAT_SALTY Aartate aminotransferase	6		AIWEQELTDMR	304	11	3	35.87	b4b5b6	1391.68	70.588	3597	2	696.34	9.12
[P58661]AAT_SALTY Aartate aminotransferase	7		QLFVNTLQEK	322	10	6	39.85	b3y3°y3y6*y6y7	1219.67	59.162	2612	2	610.34	4.50

P58661 AAT_SALTY Aartate aminotransferase	8	Carbamidomethyl+C(4)	VGACTLVAADAETVDRAFSQMK	254	22	3	22.07	b9b10y7	2340.15	72.958	7832	2	1170.58	7.30
P58661 AAT_SALTY Aartate aminotransferase	9		LREEFGVYAVASGR	360	14	4	19.11	b6°b6b8y10	1553.80	96.983	5571	2	777.40	-4.16
P58661 AAT_SALTY Aartate aminotransferase	10		AIWEQELTDMRQR	304	13	5	29.7	y6°y6y9y12*y12	1675.81	84.962	3623	3	559.27	-9.47
P58661 AAT_SALTY Aartate aminotransferase	11		GWLPLFD FayQG	204	12	1	7.26	y10	1413.68	117.288	2183	2	707.35	0.09
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	1		MLQSNEYFSGK	0	11	4	24.11	b10y4y10y11	1303.60	49.267	31378	2	652.30	0.00
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	2		VLLPGTVEWK	53	10	4	33.7	y5y7y8y10	1141.65	70.960	30476	2	571.33	-7.16
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	3	Carbamidomethyl+C(28)	VYTAGEVFNVPGHSEFHLQVAEP ASYLCR	63	29	3	11.47	b7b14y7	3277.61	104.291	6033	3	1093.21	11.32
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	4		LQSNEYFSGK	1	10	3	26.71	b4y3y9	1172.56	97.034	1691	1	1172.56	-1.67
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	1		SSIPVFGVDALPEALALVK	250	19	9	47.38	b4°b4b8b9b14y4y14y16y19	1926.10	108.347	46864	2	963.55	3.68
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	2		SGAMAGTVLNDANNQAK	269	17	10	42.37	b3b9°b9y4y9y10y12*y12y17*y17	1661.80	45.937	38262	2	831.40	4.92
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	3		ALAINLVDPAAGTVIEK	84	18	8	24.6	b3y1y2°y2y7y11y14y18	1766.01	80.364	27232	2	883.51	4.98
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	4		IEVVIANN DAMAMGAVEALK	226	20	7	19.56	b2°b2b10b12y2y10y12	2059.07	90.053	9589	3	687.03	5.57
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	5		ELNDK	187	5	1	13.14	y3	618.31	80.586	14702	1	618.31	-0.20
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	6		GQNVPVVFFNK	104	11	6	50.39	b5°b5b6b8y4y5	1248.65	58.991	13469	2	624.83	-15.93
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	7		MDAWLSGPNANK	214	12	3	22.09	b3b6y4	1303.64	57.438	1762	2	652.32	21.07
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	8		GIQTEQLALDTAMWDTAQAK	192	20	4	14.24	b8b10°b10y9	2191.05	68.186	1598	3	731.02	-7.13
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	9		SAPDVQLLMNDSQNDQSKQNDQI DVLLAK	52	29	4	21.88	b9b10y15*y15	3227.57	94.012	54359	3	1076.53	-4.24
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	10		DGKSAPDVQLLMNDSQNDQSK	49	21	3	13.75	b6b12y4	2290.05	59.011	6942	3	764.02	-3.41
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	11		ALDSYDKAYYVGTD SK	120	16	5	34.84	y5y6y8y12°y12	1795.86	93.833	4710	2	898.43	12.03
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	12	Phosphoryl STY(12)	VPYVGVDKDNLSEFTQK	315	17	4	27.17	b3y4y5y10	2018.95	67.975	9375	3	673.65	5.38
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	13	Oxidation+M(4)	SGAMAGTVLNDANNQAK	269	17	3	16.17	b4b10y3	1677.80	45.040	8868	4	420.21	8.37
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	1		AAPNTIPTAAK	149	11	7	55.62	b2b5y2y3y5y7y8	1054.58	31.928	22036	2	527.79	-8.22
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	2		IQQAF FGLTGETEDK	284	16	3	25.38	y4y12y13	1830.90	78.552	8352	2	915.95	4.07

[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	3		AGGNYLSSLLVGSEAR	160	16	4	17	b7°b7b11y4	1593.81	91.708	5031	2	797.41	-8.12
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	4		DGVLFTPPFTSSALPGITR	204	19	3	14.8	b6y13y15	1976.05	92.979	9933	2	988.53	0.43
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	5		SVDGIQVGEGR	266	11	3	24.11	b10y4y7	1116.56	27.380	7111	2	558.79	-0.22
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	6		ADYIWFNGEMVR	5	12	4	22.09	b6b8y5°y5	1500.71	68.412	5009	3	500.91	13.75
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	7	Carbamidomethyl+C(14)	FPVQSIDELMEACR	69	15	3	26.06	b3b7b9	1781.84	69.836	3189	2	891.42	12.19
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	8		AAPNTIPTAAKAGGNYLSSLLVGS EAR	149	27	3	22.68	b3b4b7	2629.37	81.799	9157	2	1315.19	-8.26
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	9	Carbamidomethyl+C(14) ;Oxidation+M(11)	FPVQSIDELMEACRDVIR	69	19	5	42.6	b7b8b10b11y9	2281.09	107.261	104934	2	1141.05	-1.61
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	1		QANELPGAPSQEEAVIAFGK	122	20	5	22.41	b5b8°b8b10y15	2056.07	68.476	6365	2	1028.54	14.84
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	2		YIQTVWGLGYVFVPDGSK	220	18	6	26.36	b4°b4b6b7°b7y4	2029.07	117.686	3180	3	677.03	14.02
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	3		SVANAEQMDR	32	10	3	36.71	b4b5b6	1120.53	117.504	1746	1	1120.53	20.37
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	4	Carbamidomethyl+C(21)	ESFHLMVLDLMLPGEDGLSICR	46	22	4	19.84	y3y6y12°y12	2532.26	71.790	1648	3	844.76	13.59
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	5		MQENYKILVDDDMR	0	15	4	24	b8b9y12*y12	1868.91	88.905	5143	2	934.96	12.67
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	6		SQSNPMPIIMVTAKGEEVDR	71	20	10	37.23	b8*b8b11*b11y3°y3y5y8°y 8y9	2202.09	136.299	5045	2	1101.55	-1.66
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	7		YLTEQGFQVRSVANAEQMDR	22	20	3	14.24	b8b13y4	2342.14	97.221	1646	2	1171.57	9.28
[P0AA19]OMPR_SALTY Transcriptional regulatory protein ompR	8	Carbamidomethyl+C(25) ;Oxidation+M()	LLTRESFHLMVLDLMLPGEDGLSI CR	42	26	5	22.64	b8y3y4y8°y8	3031.56	136.310	9295	3	1011.19	4.83
[P55900]SERC_SALTY Phohoserine aminotransferase	1		AQVFNFSSGPAMLPAEVLK	1	19	7	31.34	b7*b7b8b12y3y6y19	2006.05	91.585	30927	2	1003.53	5.84
[P55900]SERC_SALTY Phohoserine aminotransferase	2	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	8	45.38	b3b5b6b10y6y7y13y22	2567.24	128.373	12031	3	856.42	8.84
[P55900]SERC_SALTY Phohoserine aminotransferase	3		ALTDFMIDFER	348	11	4	24.11	b5y2y3y9	1357.65	90.909	9756	2	679.33	0.18
[P55900]SERC_SALTY Phohoserine aminotransferase	4		GKEFIQVAEEAEQDFR	42	16	5	17	b10b13y6*y6y16	1895.93	52.299	5325	3	632.65	7.92
[P55900]SERC_SALTY Phohoserine aminotransferase	5		AELLYGVIDNSDFYR	272	15	4	25.55	b6b12y5y11	1774.87	108.493	2145	2	887.94	0.41
[P55900]SERC_SALTY Phohoserine aminotransferase	6		ITVDGK	122	6	1	13.55	b4	632.36	28.285	12670	1	632.36	-8.49
[P55900]SERC_SALTY Phohoserine aminotransferase	7		MNVPFQLADNTLDK	297	14	3	24.55	b6y8y9	1605.82	68.909	12099	3	535.95	16.95
[P55900]SERC_SALTY Phohoserine aminotransferase	8		MAQVFNFSSGPAMLPAEVLK	0	20	6	56.45	b4b5b6b8b10b11	2137.06	90.164	4417	3	713.02	-11.77
[P55900]SERC_SALTY Phohoserine aminotransferase	9		EFIQVAEEAEQDFR	44	14	3	19.11	b12y4y7	1710.83	72.909	3819	3	570.95	17.41
[P55900]SERC_SALTY Phohoserine aminotransferase	10	Carbamidomethyl+C(4)	VLFCHGGGR	68	9	4	44.67	b5b7y4y5	1002.48	114.753	1721	1	1002.48	-9.01

P55900 SERC_SALTY Phohoserine aminotransferase	11		AQGGVAAMHK	257	10	5	52.2	b7b9y4y5y8	969.50	70.548	1704	2	485.25	5.92
P55900 SERC_SALTY Phohoserine aminotransferase	12		AELLYGVIDNSDFYRNDVAQANR	272	23	3	12.94	b4b14y5	2643.26	79.524	19976	3	881.76	-6.56
P55900 SERC_SALTY Phohoserine aminotransferase	13		ASIYNAMPIEGVKALTDFMIDFER	335	24	5	19.27	b6y5y7°y7y17	2731.34	121.423	3819	2	1366.17	-4.11
P55900 SERC_SALTY Phohoserine aminotransferase	14		SRMNVPFQLADNTLDDK	295	16	3	17	b14y6y8	1848.93	107.428	3189	2	924.97	-1.12
P55900 SERC_SALTY Phohoserine aminotransferase	15	Phosphoryl STY(8)	AQVFNFSSGPAMPLPAEVLK	1	19	3	14.8	b4b7y12	2086.03	136.448	1693	2	1043.52	13.46
P55900 SERC_SALTY Phohoserine aminotransferase	16	Oxidation+M(12)	AQVFNFSSGPAMPLPAEVLK	1	19	3	21.76	b8b10b12	2022.06	66.689	1527	3	674.69	12.01
P52616 FLJB_SALTY Phase 2 flagellin	1		AQILQQAGTSVLAQANQPQNVLSLLR	479	27	12	34.59	b2*b2b3*b3b5b7b9y1y4y9y13y27	2860.60	105.857	81419	3	954.21	0.17
P52616 FLJB_SALTY Phase 2 flagellin	2		SQSALGTAIER	20	11	5	31.1	b2y6y8y9y11	1132.59	41.869	42239	2	566.80	-5.17
P52616 FLJB_SALTY Phase 2 flagellin	3		INSAKDDAAGQAIANR	37	16	5	48.06	y3y4y5y6y16	1614.80	30.442	42229	3	538.94	-11.64
P52616 FLJB_SALTY Phase 2 flagellin	4		VSGQTQFNGVK	125	11	7	36.46	b2b4y5y9y10*y10y11	1164.60	33.043	40663	2	582.80	-3.46
P52616 FLJB_SALTY Phase 2 flagellin	5		AQVINTNSLSLLTQNNLNK	1	19	8	21.76	b1b2*b2y2y7y15y17y19	2085.14	74.502	38558	2	1043.07	2.69
P52616 FLJB_SALTY Phase 2 flagellin	6		TEVVTIDGK	381	9	4	30.28	b3°b3b6y5	961.51	52.250	11831	2	481.26	-13.90
P52616 FLJB_SALTY Phase 2 flagellin	7		TAANQLGGVDGK	369	12	6	50.8	b4b7b9y4y5y12	1130.58	35.103	11368	2	565.79	-3.89
P52616 FLJB_SALTY Phase 2 flagellin	8		ELAVQSANSTNSQSDLDSIQAEITQR	93	26	4	12.06	b9y3*y3y6	2805.36	70.091	2920	2	1403.18	3.31
P52616 FLJB_SALTY Phase 2 flagellin	9		NANDGISIAQTTEGALNEINNNLQ R	66	25	6	30.98	b6b9b12b14y5y9	2670.31	127.140	63916	3	890.78	2.29
P52616 FLJB_SALTY Phase 2 flagellin	10		TIEGGYALK	328	9	3	38.06	b3b4b6	951.51	43.622	33707	2	476.26	-3.98
P52616 FLJB_SALTY Phase 2 flagellin	11		AYANNGTTLDSVGLDDAAIK	189	20	6	45.36	b13b14y6y11y15y16	2008.95	73.934	23041	3	670.32	-17.14
P52616 FLJB_SALTY Phase 2 flagellin	12		YFVTIGGFTGADAAK	234	15	4	29.2	b7y8y9y14	1517.78	59.481	16133	3	506.60	13.75
P52616 FLJB_SALTY Phase 2 flagellin	13		AQPELAEAAAK	403	11	3	35.87	b3b5b9	1098.57	86.560	9956	2	549.79	-11.00
P52616 FLJB_SALTY Phase 2 flagellin	14		DTPAVVSADAK	288	11	4	31.1	b7°b7b9b10	1073.55	71.938	5413	2	537.28	5.23
P52616 FLJB_SALTY Phase 2 flagellin	15		NGDYEENVATDGTVTLAAGATK	249	22	3	13.32	b10y5y15	2167.09	66.237	2739	3	723.03	17.80
P52616 FLJB_SALTY Phase 2 flagellin	16		NALIAGGVDATDANGAELVKMSYTDK	299	26	10	30.81	b3*b3b10°b10b14*b14b15*b15y3y14	2624.29	76.219	83205	4	656.83	1.21
P52616 FLJB_SALTY Phase 2 flagellin	17		QINSQTLGLDSLNVQKAYDVK	161	21	5	29.81	b3b7b8*b8b10	2334.22	90.014	9221	3	778.74	-4.71
P52616 FLJB_SALTY Phase 2 flagellin	18		AAGHDFKAQPELAEAAAK	396	18	5	32.35	b10b11°b11b13b15	1824.92	82.986	5534	2	912.97	0.07
P52616 FLJB_SALTY Phase 2 flagellin	19		AKTTSYTAADGTTK	355	14	3	26.89	b3b4b7	1415.71	38.751	3592	3	472.57	2.85
P52616 FLJB_SALTY Phase 2 flagellin	20		TEVVTIDGKTYNASK	381	15	4	26.06	b3°b3b5b6	1625.85	84.959	1562	3	542.62	4.50
P0A2B3 RS7_SALTY 30S ribosomal protein S7	1		WIVEAAR	102	7	6	40.25	b1y4°y4y5y6y7	844.46	50.462	50636	2	422.73	-10.91
P0A2B3 RS7_SALTY 30S ribosomal protein S7	2		FVNILMVDGKK	25	11	3	31.1	y3y4y7	1263.70	67.425	43254	3	421.91	-9.27
P0A2B3 RS7_SALTY 30S ribosomal protein S7	3		STAESIVYSALETLAQR	36	17	8	22.7	b7b14y2*y2y3y6*y6y17	1838.93	108.088	23741	3	613.65	-13.21

P0A2B3 RS7_SALTY 30S ribosomal protein S7	4		FGSELLAK	17	8	4	40.66	y3y6°y6y7	864.47	51.616	76661	2	432.74	-11.37
P0A2B3 RS7_SALTY 30S ribosomal protein S7	5		NALAMR	96	6	1	13.55	y5	675.36	36.004	6319	1	675.36	-0.81
P0A2B3 RS7_SALTY 30S ribosomal protein S7	6		LANELSDAADNK	119	12	4	26.07	b3y7y8*y8	1260.59	91.707	1681	1	1260.59	-10.46
P0A2B3 RS7_SALTY 30S ribosomal protein S7	7		LANELSDAADNKGTAVK	119	17	13	103.8	b3b4*b4b5y5°y5y8y9y10*y10y12y13y16	1716.86	39.063	148432	3	572.96	-12.16
P60726 RL4_SALTY 50S ribosomal protein L4	1		DATGIDPVSLIAFDK	170	15	9	45.23	b2b3°b3b4b5y2y3y10y15	1561.81	88.181	44224	2	781.41	0.16
P60726 RL4_SALTY 50S ribosomal protein L4	2		VVMTADAVK	185	9	5	57.22	b2y3y4y6y7	933.50	36.546	26235	2	467.25	-6.54
P60726 RL4_SALTY 50S ribosomal protein L4	3		MELVLKDAQSALTVSETTFGR	0	21	3	13.75	b4y5y12	2296.15	92.546	1559	2	1148.58	-14.25
P60726 RL4_SALTY 50S ribosomal protein L4	4		DFNEALVHQVVVAYAAGAR	21	19	3	21.76	b6b8b10	2030.03	54.771	2662	3	677.35	-8.18
P60726 RL4_SALTY 50S ribosomal protein L4	5		SGGVTFARPQDHSQK	79	16	3	23.54	b10b11y13	1685.80	93.654	2264	2	843.40	-22.16
P60726 RL4_SALTY 50S ribosomal protein L4	6		SGGVTFARPQDHSQKVNK	79	19	14	74.53	b4°b4b8°b8b9°b9b10b12y7*y7y8*y8y9°y9	2027.02	136.266	81275	2	1014.01	-11.32
P60726 RL4_SALTY 50S ribosomal protein L4	7		DATGIDPVSLIAFDKVVMTADAVK	170	24	4	19.27	b3b5b8y8	2476.29	102.422	44875	3	826.10	-2.76
P60726 RL4_SALTY 50S ribosomal protein L4	8		VVMTADAVKQVEMLA	185	16	7	51.12	b5b7b8b12y5y6°y6	1733.88	95.035	5050	2	867.44	-0.49
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1		LVDIEQVSSTHAK	12	13	4	33.82	b7y3y5y11	1426.74	45.445	59981	3	476.25	-11.89
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2	Carbamidomethyl+C(6)	LLVDACYSPVER	170	12	8	65.49	b2b9y2y5y6y8y9y10	1421.71	59.123	48754	2	711.36	0.26
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3	Carbamidomethyl+C(9)	ILLSSMPGCAVTEVEIDGVLHEYS TK	45	26	3	12.06	b10y12y19	2848.41	91.637	12256	3	950.14	-1.20
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4		EGVQEDILEILLNLK	71	15	5	26.06	b2b3b7°b7b8	1725.96	124.005	10116	2	863.48	-1.77
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5		LVIEMETNGTIDPEEAIK	200	18	4	26.36	b8b14b15y11	2030.05	83.985	28481	3	677.36	20.45
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		AEAIHYIGDLVQR	271	13	4	27.94	b3b4°b4b11	1484.82	43.364	11058	2	742.91	19.98
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		GYVPASTR	150	8	3	35.89	b7y3y5	850.43	28.240	5600	2	425.72	-12.56
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8		GYVPASTRIHSEEDERPIGR	150	20	4	22.41	b9b11b13y10	2269.13	69.175	43651	3	757.05	1.18
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9	Carbamidomethyl+C(4)	SANCLKAEAIHYIGDLVQR	265	19	5	23.44	b3b10*b10b14y12	2158.09	98.412	4116	3	720.03	-8.48
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTSDAVGNAVK	84	17	15	91.04	b2b3b4b5y1y2y10y11y12*y12y13*y13y14*y14y17	1739.96	70.639	58502	2	870.48	1.75
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	2		LAATIAQLPDQIGAK	253	15	4	17.98	b3y7y9y15	1509.85	66.023	52884	2	755.43	-6.55
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	3		IAGDYIAK	135	8	4	35.89	b7y4y7y8	850.46	35.830	11227	2	425.73	-7.46

P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	4		ADVMVVGFDGTPDGEK	231	16	6	28.1	b12y11y13°y13y14°y14	1636.77	63.388	7657	2	818.89	10.22
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	5		ELANVQDLTVR	70	11	3	24.11	b4b10y8	1257.67	57.538	6698	2	629.34	-6.70
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	6		VIELQGIAGTSAAR	150	14	4	44.51	y5y6y9y10	1385.77	58.696	21767	2	693.39	-4.93
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	7		AGEGAK	144	6	1	13.55	y5	532.28	28.337	7796	1	532.28	12.61
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	8		FNVLASQPADFDR	178	13	4	27.94	y3y11y12°y12	1479.74	105.954	2054	2	740.37	12.13
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	9		FNVLASQPADFDRTK	178	15	3	17.98	b13y7y11	1708.87	86.696	35709	2	854.94	5.50
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	10	Phosphoryl STY(7)	ILLINPTDSDAVGNAVK	84	17	4	16.17	b8°b8b13y9	1819.93	82.774	2557	2	910.47	8.59
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	11		AGDYIAK	136	7	1	9.6	b5	737.38	35.881	2114	1	737.38	-2.32
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	1		MASVSSGMQLPPGFK	91	15	5	17.98	b13y1y5y11y15	1536.76	66.566	30525	2	768.88	4.77
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	2		MQEIIAQLEVTGESGAGLVK	23	20	3	21.03	b10b14b16	2089.04	104.996	6498	2	1045.02	-6.19
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	3		VEIDPSLLEDDKEMLEDLVAAAFN DAAR	54	28	3	11.63	b10y6y12	3089.46	126.806	2160	4	773.12	-11.14
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	4		EMLEDLVAAAFNDAAR	66	16	5	30.56	b13b14y5°y5y8	1735.86	96.931	1666	2	868.43	14.49
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	5		EKMASVSSGMQLPPGFK	89	17	7	49.36	b4b5b7b13°b13y9y10	1793.92	64.810	124382	2	897.46	13.13
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	6		GGLGNLMKQAQQMQEK	4	16	6	27.43	b5y5y7°y7y9*y9	1760.89	124.683	2275	2	880.95	5.06
Q8ZP20 TREA_SALTY Periplasmic trehalase	1		VAAAAQAHL LQPGGLATTSVK	428	21	4	24.51	b4b5b9y10	2004.11	57.641	19379	3	668.71	-7.49
Q8ZP20 TREA_SALTY Periplasmic trehalase	2		TFADAIPNSDPLMILADYR	68	19	10	29.12	b6°b6b13°b13b16y2y5°y5y13*y13	2123.06	101.976	15275	2	1062.03	6.90
Q8ZP20 TREA_SALTY Periplasmic trehalase	3		SNPNRPATEIYR	296	12	3	26.07	b8y6y7	1417.72	33.471	4789	2	709.37	3.87
Q8ZP20 TREA_SALTY Periplasmic trehalase	4		TTTIAPVDLNALLYQLEK	335	18	3	15.44	b6b11y8	2003.07	85.425	8667	2	1002.04	-20.05
Q8ZP20 TREA_SALTY Periplasmic trehalase	5		SQPPFFAFMVELLAQHEGDDALK	212	23	3	12.94	b9y10y13	2590.22	128.303	3563	3	864.08	-16.12
Q8ZP20 TREA_SALTY Periplasmic trehalase	6		DTPRPESWVEDIATAK	280	16	3	17	b12y8y10	1814.90	112.727	3523	2	907.95	5.18
Q8ZP20 TREA_SALTY Periplasmic trehalase	7		TYYLSR	206	6	1	13.55	b4	802.41	37.886	1825	1	802.41	-1.06
Q8ZP20 TREA_SALTY Periplasmic trehalase	8		FLTNVQHTYDREK	486	13	3	20.46	b4b11y5	1650.83	83.536	25414	3	550.95	3.99
Q8ZP20 TREA_SALTY Periplasmic trehalase	9		ASAAAGDRAK	357	10	3	33.7	y4y5y9	917.49	19.985	10103	2	459.25	5.65
Q8ZP20 TREA_SALTY Periplasmic trehalase	10		DTPRPESWVEDIATAKSNPNRPAT EIYR	280	28	4	22.18	b7b9b10y13	3213.62	125.755	7654	3	1071.88	7.98
Q8ZP20 TREA_SALTY Periplasmic trehalase	11		SNPNRPATEIYRDLR	296	15	4	26.06	b5b7*b7b8	1801.90	90.128	2784	2	901.46	-14.29
Q8ZP20 TREA_SALTY Periplasmic trehalase	12	Phosphoryl STY(4)	DQLTAAALFLYVNAAAK	405	18	3	22.84	b13_H3PO4 b13y14y15	1956.97	122.331	2853	2	978.99	-3.12
Q8ZP20 TREA_SALTY Periplasmic trehalase	13	Oxidation+M(13)	TFADAIPNSDPLMILADYR	68	19	3	21.76	b4b7b13	2139.04	102.916	35704	3	713.68	-1.37
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	1		AESFTTTNR	1	9	5	54.21	y4y5y6y7y9	1026.49	27.404	33771	2	513.75	0.48
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	2		GEREPVTD AER	65	11	7	24.11	b2°b2b6°b6y3°y3y5	1258.61	22.523	3264	2	629.81	6.89

[Q7CPD8]YIFE_SALTY UPF0438 protein yifE	3		MAESFTTTNR	0	10	3	28.47	b9y6y7	1157.54	97.296	11360	2	579.28	15.50
[Q7CPD8]YIFE_SALTY UPF0438 protein yifE	4		AESFTTTNR	1	9	0	1.65		1008.48	27.428	2406	2	504.74	8.23
[P66541]RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAE LNK	45	14	5	27.69	b2y3y5y12y14	1576.81	84.646	118032	2	788.91	3.87
[P66541]RS2_SALTY 30S ribosomal protein S2	2		MATVSMR DMLK	0	11	7	24.11	b4y1y6°y6y10°y10y11	1282.63	59.256	48018	3	428.21	-3.33
[P66541]RS2_SALTY 30S ribosomal protein S2	3	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	5	30.49	b4y1y3y7y8	1694.72	47.369	41103	3	565.58	-9.65
[P66541]RS2_SALTY 30S ribosomal protein S2	4		EANNLGIPVFAIVD TNSDPDG VDF VIPGNDDAIR	174	34	13	30.89	b5°b5*b5b7°b7*b7y3y8*y8y11y14y16y34	3569.75	104.757	26771	3	1190.59	2.94
[P66541]RS2_SALTY 30S ribosomal protein S2	5		LKDLETQSQDGT FEK	113	15	5	25.55	b7b9y4y6y15	1738.87	39.073	4459	2	869.94	14.04
[P66541]RS2_SALTY 30S ribosomal protein S2	6		YWNPK	21	5	1	13.14	b3	707.34	34.529	16942	2	354.18	-9.41
[P66541]RS2_SALTY 30S ribosomal protein S2	7		ILFVGTK	66	7	3	40.25	y3y5y6	777.48	57.215	13841	2	389.24	-13.50
[P66541]RS2_SALTY 30S ribosomal protein S2	8		AGVHF GHQTR	11	10	3	28.47	b6b7y4	1109.56	109.770	1598	1	1109.56	-1.21
[P66541]RS2_SALTY 30S ribosomal protein S2	9		DLETQSQDGT FEK LTK	115	16	4	17	b3b13y14°y14	1839.90	89.916	21252	2	920.45	2.45
[P66541]RS2_SALTY 30S ribosomal protein S2	10		TVPMFNEALAE LNKISAR	45	18	4	24.6	b9b12b17y3	2004.03	107.473	6261	2	1002.52	-14.07
[P66541]RS2_SALTY 30S ribosomal protein S2	11		NEALAE LNK	50	9	0	3.7		1001.52	84.629	3199	2	501.26	-9.45
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	1		GIEGASLDVPDEFV HSGK	72	18	5	26.36	b2b11y3y10y11	1856.89	67.059	40313	3	619.64	-5.13
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	2		VLSESD FQVNQLLDILR	49	17	4	33.49	y3y4y13y15	1989.08	105.366	31117	2	995.04	6.87
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	3		TWYVEAK	90	7	4	37.24	b6y3y4y7	896.44	23.825	16708	2	448.72	-11.10
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	4		PSFDIVSEVD LQEAR	1	15	5	36.47	y6y7°y7y10y12	1704.86	84.494	5098	2	852.93	7.73
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	5		QGIESAVQK	99	9	4	30.28	b4y4*y4y6	959.53	30.100	19554	2	480.27	17.05
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	6		GVEATIELNDANK	33	13	3	20.46	b7b10y5	1373.70	97.225	3945	2	687.35	7.29
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	7		GIEGASLDVPDEFV HSGKTWYVEAK	72	25	10	61.15	b4b9b12b13y3y4y6°y6y7y10	2734.35	90.024	6175	3	912.12	6.79
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	1		YGH DIPSAVSLAINSR	112	17	5	27.17	b5b6b15y11y17	1814.92	52.247	34389	3	605.65	11.77
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	2	Carbamidomethyl+C(11)	SQDHLHIHISCI RPDVREQLDNDLTR	132	26	3	21.83	b7y8y9	3167.58	93.514	6934	4	792.65	1.39
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	3		HGPLQYLLMPTYR	68	13	7	39.04	b2b6y2y3y4°y4y5	1588.84	70.644	6284	2	794.92	5.92
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	4		SPFMMLAE EVPEAR	188	14	5	30.49	b7b11b12y11y14	1606.77	73.308	3020	2	803.89	6.00
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	5	Carbamidomethyl+C(7); Carbamidomethyl+C(20)	EIVLEQCLPDQLQHQNPA PCAEVKPR	33	26	6	15.63	b8°b8b10°b10y10y22	3069.51	133.868	18036	3	1023.84	-4.37
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	6		INGTESPLLEPATPNFFW LAWQAR	81	25	3	12.31	b3b5y11	2871.49	97.473	4897	4	718.63	3.66
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	7		GYMSK	106	5	1	13.14	y4	585.28	79.583	4671	1	585.28	11.78
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	8	Carbamidomethyl+C(18)	NLLTFNRASAE EIQDHSCAILSSR	227	24	3	22.9	y10y12y13	2732.34	98.925	2375	4	683.84	0.80
[P26219]CDH_SALTY CDP-diacylglycerol pyrophohatase	9	Oxidation+M()	SPFMMLAE EVPEAR DHMGR	188	19	3	14.8	b6b11y7	2218.98	97.013	8415	4	555.50	-10.89

[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	1		SLNFLDFEQPIAELEAK	1	17	3	24.82	y5y14y15	1964.02	108.333	10469	3	655.34	9.45
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	2		FNMPIITFIDTPGAYPGVGAEER	152	23	7	41.7	b5b10y8°y8y11y12y13	2495.25	113.848	9392	3	832.42	10.18
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	3		LAFDEFDELAGDR	80	13	3	20.46	b5y3y9	1497.68	40.099	9507	2	749.35	-1.96
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	4		APLAAEAMGIIAPR	243	14	3	19.11	b8b10y13	1380.75	45.051	4891	2	690.88	-11.49
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	5	Carbamidomethyl+C(17)	VNMLQYSTYSVISPEGCASILWKS ADK	216	27	14	79.4	b3b4b6b8b9b10*b10b11*b11y3°y3y5y6°y6	3047.50	133.852	36176	4	762.63	5.61
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	6		FNMPIITFIDTPGAYPGVGAEERGQ SEAIAR	152	31	3	11.2	b6b14y15	3307.66	80.350	9112	4	827.67	4.28
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	7		NFGMPAPEGYRK	130	12	3	29.29	b3b4b6	1366.65	14.710	5799	3	456.22	-3.57
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	8		SLNFLDFEQPIAELEAKIDSLTAVS R	1	26	8	47.02	b6b7*b7b10b13b22b23y8	2906.49	71.992	4654	3	969.50	-7.06
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	9		QDEKLDINIDEEVHR	27	15	4	40.45	b5b6b7b12	1852.90	78.664	2112	2	926.96	-0.07
[P0A1C3]ACCA_SALTY Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	10	Oxidation+M(3)	FNMPIITFIDTPGAYPGVGAEER	152	23	7	31.29	b5b10°b10b15y6y8y16	2511.24	87.847	19368	2	1256.12	6.71
[P10503]PUTA_SALTY Bifunctional protein putA	1		EAVDFLHYIYAGQVR	744	14	6	30.49	b3b4b13*b13y8y14	1667.84	67.502	37680	2	834.42	13.03
[P10503]PUTA_SALTY Bifunctional protein putA	2		DIVGWGREATESEVEQALQNAVN QAPVWFATPPQER	670	36	6	12.55	b6b10y5*y5y10*y10	4022.99	107.508	12569	4	1006.50	6.49
[P10503]PUTA_SALTY Bifunctional protein putA	3	Carbamidomethyl+C(3)	TVCEAVAAREGAIVSVQG FAR	1266	21	4	29.81	b8b12b16b17	2191.15	88.777	12349	3	731.06	10.59
[P10503]PUTA_SALTY Bifunctional protein putA	4		QFADLAQAGTQR	1161	12	8	35.9	b9°b9b11*b11y6y7°y7y12	1305.67	62.969	11871	2	653.34	9.44
[P10503]PUTA_SALTY Bifunctional protein putA	5		GETVGAQLTADAR	834	13	7	29.41	b2b5°b5b9y3y8y13	1288.67	64.810	6843	2	644.84	12.31
[P10503]PUTA_SALTY Bifunctional protein putA	6		GVMFTGSTEVATLLQR	849	16	5	34.84	b5b7°b7b11b12	1709.90	90.136	6554	3	570.64	4.07
[P10503]PUTA_SALTY Bifunctional protein putA	7		WQAKPVLEQPVADGEMTPVINPA EPK	644	26	5	25.41	b3b15y5y6y26	2844.43	106.131	6420	3	948.81	-11.24
[P10503]PUTA_SALTY Bifunctional protein putA	8		LLENGANTSFVNR	556	13	4	20.46	b4y2y5y8	1434.72	54.769	4996	2	717.87	-7.57
[P10503]PUTA_SALTY Bifunctional protein putA	9	Carbamidomethyl+C(10)	VYTDVSYLACAK	459	12	6	40	b4y7°y7y8y9y12	1389.67	62.925	4049	3	463.89	-4.92
[P10503]PUTA_SALTY Bifunctional protein putA	10		DALIR	181	5	1	13.14	y3	587.35	57.447	22266	1	587.35	-8.42
[P10503]PUTA_SALTY Bifunctional protein putA	11		LTTDIGPVIDSEAK	951	14	3	19.11	b7y4y6	1458.74	76.419	8458	2	729.87	-20.42
[P10503]PUTA_SALTY Bifunctional protein putA	12		SLSVNTAAAGGNASLMTIG	1301	19	4	23.98	b6°b6b8b9	1734.87	123.527	7457	2	867.94	1.13
[P10503]PUTA_SALTY Bifunctional protein putA	13		RPETDAVSMLMEQAR	100	15	4	17.98	b3°b3b7y10	1733.80	48.668	4786	3	578.61	-17.18
[P10503]PUTA_SALTY Bifunctional protein putA	14	Carbamidomethyl+C(5)	LNRPCR	532	6	1	13.55	y5	815.44	47.071	3619	2	408.22	10.78

P10503 PUTA_SALTY Bifunctional protein putA	15		DLYGEGR	609	7	3	37.24	b4b5y3	809.40	84.540	2765	1	809.40	20.06
P10503 PUTA_SALTY Bifunctional protein putA	16	Carbamidomethyl+C(3)	VLCLQDDIAEHTLKMLR	921	17	5	25.92	b8*b8b10b12y12	2055.08	94.883	25093	2	1028.04	2.14
P10503 PUTA_SALTY Bifunctional protein putA	17		DLYGEGRINSAGLDLANEHR	609	20	3	22.37	b7y6y7	2200.10	88.864	8238	2	1100.55	12.10
P10503 PUTA_SALTY Bifunctional protein putA	18		AETLMAQPFDAVIFHGSDSKLR	1244	22	5	17.98	b7*b7b11y6y9	2461.22	111.253	6671	3	821.08	2.08
P10503 PUTA_SALTY Bifunctional protein putA	19		SPSLFVNAATWGLLFTGRLVSTH NEANLSR	200	30	3	11.32	b7y7y15	3258.70	88.263	2529	3	1086.91	0.15
P10503 PUTA_SALTY Bifunctional protein putA	20		MGNPGRLTTDIGPVIDSEAK	945	20	3	14.24	b3b10y10	2071.07	91.990	1634	3	691.03	10.61
P10503 PUTA_SALTY Bifunctional protein putA	21	Oxidation+M(5)	AETLMAQPFDAVIFHGSDK	1244	20	4	14.24	b6y11*y11y13	2208.04	54.996	34807	3	736.69	7.08
P10503 PUTA_SALTY Bifunctional protein putA	22		MFTGSTEVATLLQR	851	14	1	7.25	b3	1553.80	90.230	8867	2	777.41	3.06
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	1	Carbamidomethyl+C(16)	ELDGLSYEEIAAIMDCPVGTVR	149	22	4	17.98	b13b15y10y12	2438.15	102.065	3851	3	813.39	-1.30
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	2		RPPSSDVDAIEAENFESGGALKEIS NPENLMLSEELR	91	37	8	26.53	b6b9*b9b14*b14y6y13y14	4043.96	102.332	3180	3	1348.66	1.75
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	3		RPPSSDVDAIEAENFESGGALK	91	22	3	13.32	b4b13y8	2289.10	64.376	2125	2	1145.05	-0.64
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	4	Oxidation+M(9)	EISNPENLMLSEELR	113	15	7	44.38	b3b5*b5b8b10*b10y6	1789.87	50.464	15945	3	597.29	0.95
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	5	Carbamidomethyl+C(11)	SYEEIAAIMDCPVGTVR	154	17	1	7.83	b14	1910.91	102.046	1683	3	637.64	4.86
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		MQLNSTEISELIK	0	13	6	27.94	b2y3y10y11y13*y13	1505.79	76.871	37649	2	753.40	3.89
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2		QSVDQPVTGYK	139	12	6	44.65	b12y7y8y9y11y12	1349.67	33.828	21213	2	675.34	2.71
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3		ELAAFSQFASDLDDATR	401	17	11	67.02	b2b4b8b11y1y4*y4y9y13y14y15	1856.88	88.897	20377	2	928.94	5.85
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4		DSVGAVVMGPYADLAEGMK	68	19	3	14.8	b4b6y14	1909.92	83.667	39756	2	955.47	10.10
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		ILEVPVGR	93	8	3	40.66	y4y5y6	882.53	52.393	35859	2	441.77	-6.57
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6		QYAPMSVAQQLVFAAER	434	19	4	20.48	b3b15y6y15	2109.09	93.387	26233	2	1055.05	4.86
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		GYLADVELAK	453	10	4	26.71	b4b8y6*y6	1078.56	68.552	25656	2	539.79	-12.11
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		AVDSMIPIGR	151	10	3	26.71	b4b8y9	1058.57	38.782	12906	2	529.79	7.61
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9		DHAPLMQEINQSGGYNDEIEGK	477	22	3	23.2	y7y8y11	2445.10	100.389	9346	3	815.71	1.90
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		VTELLK	426	6	1	13.55	y4	702.43	40.189	7039	2	351.72	-9.56
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		EAFPGDVFYLSHR	283	13	5	29.41	b4*b4b8y8y12	1537.75	78.143	4796	2	769.38	1.19
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12	Carbamidomethyl+C(1)	CIYVAIGQK	192	9	3	38.06	b5b6b7	1051.54	74.158	4598	2	526.27	-21.59
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		GEDALIYYDLSK	252	13	3	20.46	b7b10y5	1451.74	99.881	1801	2	726.38	11.27
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		QLDHGQK	419	7	5	40.25	b3b6*b6y6*y6	825.42	62.980	1704	2	413.21	-6.21
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		VVNTLGAPIDGKGPVDNDGFSAV EAIAPGVIDR	106	33	6	24.37	b27y6*y6y7y10y28	3263.70	84.243	43882	3	1088.57	3.07
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16		IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	4	22.5	b21y11y12*y12	3950.88	97.013	4472	3	1317.63	-0.74

Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17		GEDALIYYDDL SKQAVAYR	252	19	3	23.98	b8b13b14	2140.06	77.804	4301	2	1070.53	-13.80
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18		DSVGAVVMGPYADLAEGMKVK	68	21	4	13.75	b6°b6y7y17	2137.04	70.662	2379	2	1069.02	-12.80
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	19		RPPGREAFPGDV FYLHSR	278	18	5	39.85	b9b10y10y12y13	2101.09	79.515	2342	2	1051.05	8.83
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	20		AARVNADYVEAFTK	300	14	17	107.33	b5*b5b6*b6b8°b8b9°b9b11y4y5°y5y7°y7y8°y8y9	1554.79	136.278	1962	2	777.90	0.79
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	21	Phosphoryl STY(10)	ELAAFSQFASDLDDATRK	401	18	8	39.85	b5b6°b6b8°b8y6y7°y7	2064.95	136.234	1677	3	688.99	14.66
P66643 RS9_SALTY 30S ribosomal protein S9	1		SLEQYFGR	33	8	5	40.66	y2y3y4y6y8	999.48	60.629	72372	2	500.25	-5.86
P66643 RS9_SALTY 30S ribosomal protein S9	2		GGGISGQAGAIR	68	12	6	33.98	b2b3y5y7y8y12	1043.56	33.370	57413	2	522.28	-3.51
P66643 RS9_SALTY 30S ribosomal protein S9	3		AENQYYGTGR	1	10	6	33.7	b2°b2y4y5y8y10	1158.52	26.879	45229	2	579.76	0.32
P66643 RS9_SALTY 30S ribosomal protein S9	4		IVINQR	27	6	1	13.55	y4	742.45	28.488	12900	2	371.73	-8.71
P66643 RS9_SALTY 30S ribosomal protein S9	5		AGFVTRDAR	100	9	3	30.28	b4y7y8	992.53	85.452	16557	2	496.77	-1.91
P66643 RS9_SALTY 30S ribosomal protein S9	6		ALMEYDESLRGELR	85	14	3	19.11	b5b12y11	1681.84	90.034	1699	3	561.28	10.31
P66643 RS9_SALTY 30S ribosomal protein S9	7		HGITRALMEYDESLR	80	15	3	26.06	b10b13b14	1790.88	104.538	1619	2	895.95	-0.55