

MA6926 + Zn(II) LC-MS run 2: 6926_Zn_220709_1a2_02

Protein name	Peptide Rank	Peptide Modification	Peptide Sequence	Peptide sequence start	Peptide sequence Length	Peptide Matched Products	Peptide Score	By Matches	Precursor MH+ (Da)	Retention time (min)	Intensity	z	Precursor m/z	MH+ Error (ppm)
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	1		IAAANVPAFVSGK	70	13	23	180.93	b2b3b4b5*b5b6*b6y2y3y4*y4y5y6y7*y7y8y9y10*y10y11*y11y12y13	1244.69	60.155	663691	2	622.85	-6.47
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVGFGTFK	22	29	43	370.35	b2b3b4b5*b5b6*b6b7*b7b8*b8b9b12b18b19b23b24b25b26b27b29y1y2y3y4*y4y6y7y8y10y11y12*y12y15y17y18y19y21y22y23y25y27y29	2966.58	114.529	424485	3	989.53	2.55
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	1		DQIIEAVSAMSVM DVVELISAMEEK	5	25	27	190.02	b2*b2b3b4b5b6b7b8b9*b9b10y2*y2y3y4y5*y5y6*y6y7y9*y9y10y11y13*y13y25	2737.34	137.012	26298	3	913.12	1.25
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		DLVESAPAALK	85	11	4	31.22	y4y5y9y11	1113.60	54.153	17224	2	557.30	-12.61
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	3		EAKDLVESAPAALKEGVSK	82	19	9	41.05	b3b4*b4b7*b7b8*b8y1y19	1942.04	55.728	15876	3	648.02	-2.77
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	4		EGVSKDDAEALK	96	12	7	34.15	b3b12y5*y5y6y9y12	1261.64	36.129	11352	2	631.32	8.22
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	5		EAKDLVESAPAALK	82	14	7	30.65	b3*b3b4b11y2y3y14	1441.80	60.967	8138	2	721.40	7.62
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	6		SLEEAGAEVEVK	109	12	4	22.21	b9y2y3y9	1260.63	45.995	2768	2	630.82	-4.45
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	7		AAGANKVAVIK	60	11	8	81.76	b3b7*b7b8b9b10y4y9	1041.63	29.792	34009	2	521.32	-11.95
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	8		SITKDQIIEAVSAMSVM DVVELISAMEEK	1	29	14	88.28	b6b7b15*b15b23b27y4y5y6y7y12y13*y13y27	3166.61	136.429	8535	3	1056.21	6.01
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	9		EAKDLVESAPAALK	82	14	4	27.79	b3b5*b5b8	1441.80	105.802	2515	2	721.40	3.81
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	10		FGVSAAA AVAAGPAEAAEEKT EFDVILK	30	30	5	25.5	b3b10b11b13y17	2932.55	137.144	1601	3	978.19	6.74
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	11	Oxidation+M(1)	MSITKDQIIEAVSAMSVM DVVELISAMEEK	0	30	5	16.47	b5b10*b10b16y22	3313.60	101.283	7203	3	1105.20	-9.65
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	12		SLEEAGAE	109	8	0	2.85		805.35	45.961	6025	2	403.18	-7.96
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	13		EAKDLVESAPAAL	82	13	1	7.43	y4	1313.68	55.668	1646	3	438.57	-10.22
P0A1H5 EFTU_SALTY Elongation factor Tu	1		AIDKPFLLPIDVFSISGR	205	19	23	195.12	b2b4b6b7b8b9b12y2y3y4y5y6*y6y7y8y9*y9y10*y10y11y14y15y19	2117.15	104.316	373288	3	706.39	-6.23
P0A1H5 EFTU_SALTY Elongation factor Tu	2		ELLSQYDFPGDDTPIVR	155	17	21	160.76	b2*b2b7b9b13b16b17y1y2y3y4y5y6y8y9*y9y10y11y12y14y17	1964.97	77.096	316030	2	982.99	4.47
P0A1H5 EFTU_SALTY Elongation factor Tu	3		AGENVGVLLR	270	10	6	67.98	y3y4y5y6y7y10	1027.58	56.986	255214	2	514.29	-14.02
P0A1H5 EFTU_SALTY Elongation factor Tu	4		GITINTSHVEYDTPTR	59	16	20	169.89	b2b3*b3b9b12y3y4y6y7y8y9*y9y10y11y12*y12y13y14*y14y16	1803.86	50.228	239791	3	601.96	-12.38

P0A1H5 EFTU_SALTY Elongation factor Tu	5		TTDVTGTIELPEGVEMVMPGDNI K	334	24	34	223.48	b1b2°b2b3°b3b4b5°b5b7°b7b8°b8b9°b9b10°b10b14°b14b16y3y5y6°y6*y6y7y8y9y10y11y13y14y15y16y24	2546.26	86.762	234542	2	1273.63	9.97
P0A1H5 EFTU_SALTY Elongation factor Tu	6		TTLTAAITTVLAK	25	13	15	126.7	b2°b2b4b5°b5b13y2y3y4y6y7y8y9y10y11	1303.78	84.541	203301	2	652.39	-3.75
P0A1H5 EFTU_SALTY Elongation factor Tu	7		IELAGFLDSYIPEPER	188	17	27	250.9	b2b3b4b5b6b7b11°b11b12b14y1y3°y3y4y5y6y7°y7y8y9°y9y10y11y12y13y14y17	1962.03	101.844	172049	2	981.52	5.10
P0A1H5 EFTU_SALTY Elongation factor Tu	8		QVGVPYIIVFLNK	124	13	8	47.74	b3b4*b4b13y4y9y11y13	1489.88	98.954	167098	2	745.44	1.15
P0A1H5 EFTU_SALTY Elongation factor Tu	9		ALEGDAEWEAK	177	11	10	64.77	b4b6°b6b10b11y2y4y9y10°y10	1218.56	46.934	107505	2	609.78	-1.10
P0A1H5 EFTU_SALTY Elongation factor Tu	10	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	6	51.78	y2y4y6y7y8y10	1187.51	53.516	71189	2	594.26	-6.27
P0A1H5 EFTU_SALTY Elongation factor Tu	11	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEV	137	18	9	50.42	b2b3b4y2y3y6y8y12y18	2224.00	106.006	37850	2	1112.51	10.21
P0A1H5 EFTU_SALTY Elongation factor Tu	12		NMITGAAQMDGAILVVAATDGP MPQTR	90	27	11	39.53	b3b7°b7b8°b8b9y7*y7y11*y11y27	2729.31	105.659	16831	3	910.44	-10.64
P0A1H5 EFTU_SALTY Elongation factor Tu	13		GYRPQFYFR	325	9	5	45.36	b3b4b5y3y9	1233.61	59.252	16644	2	617.31	-8.41
P0A1H5 EFTU_SALTY Elongation factor Tu	14		VGEEVEIVGIK	238	11	13	55.84	b2b4°b4b5°b5b9°b9b10°b10b11y2y3y11	1171.66	45.615	16512	2	586.33	2.08
P0A1H5 EFTU_SALTY Elongation factor Tu	15		FESEVYILSKDEGGR	304	15	4	29.35	b3b8b11y6	1728.84	86.084	11278	2	864.93	0.35
P0A1H5 EFTU_SALTY Elongation factor Tu	16		MVVTLIHPIAMDDGLR	358	16	21	187.85	b3b4°b4b5°b5b7°b7y3y4y5°y5y6y7y9°y9y10°y10y11y12y13y15	1780.91	79.040	686962	3	594.31	-17.82
P0A1H5 EFTU_SALTY Elongation factor Tu	17		LLDEGR	264	6	3	39.98	y3y4y5	702.37	27.507	7890	2	351.69	-13.03
P0A1H5 EFTU_SALTY Elongation factor Tu	18		EHILLGR	117	7	3	37.37	b3y4y5	837.48	42.164	4406	2	419.24	-16.25
P0A1H5 EFTU_SALTY Elongation factor Tu	19		GSALKALEGDAEWEAK	172	16	4	17.1	b3°b3b14y7	1674.84	35.349	75798	4	419.47	4.08
P0A1H5 EFTU_SALTY Elongation factor Tu	20		GTVVTGRVER	224	10	6	73.39	b6b9y3y5y7y8	1073.60	26.344	50770	2	537.30	-10.12
P0A1H5 EFTU_SALTY Elongation factor Tu	21	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLE LVEMEV	124	31	7	48.76	b3y3°y3y4y5y6°y6	3694.85	127.295	14145	3	1232.29	2.58
P0A1H5 EFTU_SALTY Elongation factor Tu	22		GYRPQFYFRTTDVTGTIELPEGVE MVMPGDNIK	325	33	4	11.04	b20y9°y9y15	3760.79	97.388	8757	3	1254.27	-12.98
P0A1H5 EFTU_SALTY Elongation factor Tu	23		HTPFKGYRPQFYFR	319	15	4	26.16	b8°b8b9b12	1990.98	93.052	6691	2	995.99	-13.98
P0A1H5 EFTU_SALTY Elongation factor Tu	24	Carbamidomethyl+C(23)	GITINTSHVEYDTPTRHYAHVDCP GHADYVK	59	31	4	11.23	b14y9°y9y13	3553.70	117.047	5476	3	1185.24	11.95
P0A1H5 EFTU_SALTY Elongation factor Tu	25		ARGITINTSHVEYDTPTR	57	18	4	22.69	y6y11y13*y13	2031.00	91.594	3698	2	1016.00	-14.61
P0A1H5 EFTU_SALTY Elongation factor Tu	26		ALEGDAEWEAKIELAGFLDSYIPE PER	177	28	4	17.27	b6b11b13y3	3161.52	88.788	2097	3	1054.51	-13.75
P0A1H5 EFTU_SALTY Elongation factor Tu	27		TYGGAARAFDQIDNAPEEK	38	19	5	25.79	b3°b3b4b14y4	2052.98	83.180	1995	3	685.00	10.35
P0A1H5 EFTU_SALTY Elongation factor Tu	28	Phosphoryl STY(9)	TKPHVNVGTIGHVDH GK	8	17	6	36.03	b4b8°b8b9b11_H3PO4 b11y11	1875.92	49.762	2229	3	625.98	3.25
P0A1H5 EFTU_SALTY Elongation factor Tu	29	Oxidation+M(1)	MVVTLIHPIAMDDGLR	358	16	4	27.58	b3y3y5y9	1796.91	73.899	38899	3	599.64	-14.61
P0A1H5 EFTU_SALTY Elongation factor Tu	30	Oxidation+M(23)	NMITGAAQMDGAILVVAATDGP MPQTR	90	27	4	17.72	b4b14b17y13	2745.36	96.863	2732	4	687.10	9.07

P0A1H5 EFTU_SALTY Elongation factor Tu	31		INTSHVEYDTPTR	62	13	4	14.32	b3b10°b10*b10	1532.74	50.235	1933	2	766.87	3.27
P0A1H5 EFTU_SALTY Elongation factor Tu	32		PIEDVFSISGR	213	11	1	7.43	b10	1219.63	104.300	1511	2	610.32	-3.50
P0A1H5 EFTU_SALTY Elongation factor Tu	33		GITINTSHVEYDTPTR	59	16	2	10.03	b10y5	1785.87	50.210	12667	3	595.96	-0.55
P0A1H5 EFTU_SALTY Elongation factor Tu	34		GYRPQFYFR	325	9	0	1.63		1216.58	59.256	1982	3	406.20	-6.62
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	50	314.88	b2b3b4°b4*b4b5*b5b6°b6*b6b7°b7*b7b12y1y2*y2y3y4y6°y6*y6y7°y7*y7y8*y8y9y10y11°y11y13y14y15°y15*y15y16*y16y17y18°y18y19y20y21y22°y22*y22y23y24*y24	2574.32	97.906	508317	3	858.78	0.09
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	2		AGIALNDNFVK	296	11	17	110.36	b1b3b4b8y1y2y3y4*y4y5*y5y6y7*y7y8*y8y11	1161.62	61.965	229832	2	581.31	-9.35
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	3		GASQNIIPSSTGAAK	198	15	21	141.35	b3°b3b5°b5°b5b6°b6°b6b7°b7*b7y1y4y5y6y7y8y9y10y11y15	1401.73	41.645	183390	2	701.37	-4.09
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		LVSWYDNETGYSNK	307	14	17	145.71	b2b6b11*b11b12y2y3y4y5°y5y6y8y9y10y11y12y14	1675.77	58.988	172191	2	838.39	3.13
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		VLDLIAHISK	321	10	8	74.18	b2b3y2y3y4y5y6y8	1108.66	65.499	116265	2	554.83	-10.46
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		AATYEQIK	249	8	17	93.55	b1b5b6b7°b7b8°b8y2y4°y4*y4y5y6°y6y7y8*y8	923.47	31.609	102254	2	462.24	-13.48
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		SDIEIVAINDLLDAEYMAYMLK	24	22	25	170.52	b2b3°b3b4b5°b5b6°b6b7b8b10°b10*b10y2y3y4y5y6y7y9y10°y10y11y13y22	2530.25	125.734	84118	3	844.09	1.06
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		VPTPNVSVVDLTVR	232	14	7	56.6	y5y6y10y11y12°y12y14	1495.85	71.370	72808	2	748.43	-1.47
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		VVLTGPSKDNTPMFVK	116	16	6	28.25	b2b3y3y13y14y16	1732.91	58.182	48151	3	578.31	-12.68
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		FDGTVEVKDGLHIVNGK	53	17	8	27.31	b8b9°b9b11°b11y1y9y17	1827.97	60.904	20715	2	914.49	3.87
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11	Carbamidomethyl+C(12);Carbamidomethyl+C(16)	YEQDIVSNASCTTNCLAPLAK	138	22	3	19.91	b7b9b13	2412.12	72.791	9419	3	804.71	1.21
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12		VLPELNGK	217	8	8	53.98	y3y4*y4y5°y5*y5y6°y6	869.49	45.500	57092	2	435.25	-16.78
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13		GANFDK	132	6	1	13.6	b5	651.31	44.579	4707	1	651.31	6.65
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14		WDEVGVDVVAEATGIFLTDETAR	84	23	5	17.42	b8b12y6y14°y14	2493.19	69.512	3020	4	624.05	-11.46

[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEGQDIVSNASCTTNCL APLAK	132	28	38	302.49	b4b5*b5b6*b6b7*b7b8b9b10b11*b11b12*b12b13*b13b16b17b24*b24b26b27y3y4y5y6y8y9y10y11*y11y12*y12*y12y14*y14y15y16	3044.42	67.103	331645	3	1015.48	3.69
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		TVDGPSHKDWR	184	11	4	24.23	b5b9°b9y9	1297.62	71.947	24283	2	649.32	-4.42
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		AGIALNDNFVKLVSWYDNETGYS NK	296	25	4	23.03	b4b8b9y4	2818.39	96.376	17108	3	940.13	7.10
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		VLPELNGKLTGMAFR	217	15	5	36.62	y5y10y11y13*y13	1645.89	73.195	16103	3	549.30	-13.72
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19		GGRGASQNIPSSSTGAAK	195	18	6	40.04	b8b9y3y8y9°y9	1671.88	37.330	10145	2	836.44	1.31
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20		SDIEIVAINDLLDAEYMayMLKYD STHGR	24	29	8	27.11	b7b10*b10b13°b13b15y5y8	3346.62	82.162	3099	3	1116.21	7.37
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	21	Phosphoryl.STY(6)	TVDGPSHKDWR	184	11	3	24.23	b5b10y4	1377.57	56.648	22639	3	459.86	-9.66
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	22		DLIAHISK	323	8	4	51.78	b3b4b5b6	896.51	65.491	35637	2	448.76	-13.55
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	23		LDLIAHISK	322	9	2	20.63	b3b6	1009.60	65.494	32790	2	505.30	-9.01
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	24		AATYEQIK	249	8	0	1.22		905.46	31.607	36276	2	453.23	-6.67
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	46	346.62	b2°b2b3°b3b4°b4b5°b5b6°b6b7°b7b8°b8b9°b9b10b12°b12b13°b13b14°b14°b14b15b21y2y3y4y5y6y7y8y9y10y12*y12y13y14°y14*y14y15y16y17y18y21	2216.11	96.856	591269	2	1108.56	9.14
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	8	35.99	b1y2y8*y8y9y10*y10y11	1304.56	33.796	43492	2	652.78	-5.90
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	3	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	5	28.05	b2y8y10y11y13	1624.76	92.718	19124	2	812.88	6.91
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	4		LQQYREMLIADGIDPNELLNSMAAAK	57	26	10	55.45	b3b6b11b12y5y7°y7y13y18y20	2904.48	99.801	11413	4	726.88	8.07
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	5		YSYVDENGETKTWTGQGR	96	18	16	145.61	y3y4*y4y5y6°y6y7*y7y8y10*y10y11°y11y14y15y17	2090.92	47.516	139305	3	697.65	-8.06
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	6	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEV VVNER	19	21	9	86.16	b7y3y4y5y6y8y15y16y17	2563.26	123.641	103046	3	855.09	-0.29
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	7		LQQYREMLIADGIDPNELLNSMAAAK	57	26	9	37.13	b3b8°b8b9b14y3y5y13*y13	2904.49	92.922	31932	3	968.84	10.84
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	8		AARPAKYSYVDENGETK	90	17	4	29.83	b9b12y8y9	1898.90	71.919	12222	2	949.95	-11.64
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	9	Oxidation+M(2)	EMLIADGIDPNELLNSMAAAK	62	21	5	26.64	b3b5b12y7y12	2232.12	91.525	17999	2	1116.56	11.81
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	10	Oxidation+M(22)	LQQYREMLIADGIDPNELLNSMAAAK	57	26	6	27.39	b6y5y7y9y10*y10	2920.49	105.255	14866	3	974.17	12.96

P0A1S2 HNS_SALTY DNA-binding protein H-NS	11		MLIADGIDPNELLNSMAAAK	63	20	3	20.47	b4b13b17	2087.05	96.837	5319	2	1044.03	-2.57
P0A1S2 HNS_SALTY DNA-binding protein H-NS	12		QQYREMLIADGIDPNELLNSMAAAK	58	25	6	22.78	b9*b9b10*b10*b10b19	2791.39	99.830	3349	4	698.60	3.67
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	1		AAADLQLQGVPMAMFVNGK	158	18	27	196.97	b1b2b4b5b6*b6b7b8b10b14b16b18y2y3*y3y5*y5y6y7y8*y8y10y11*y11y12y13y18	1829.96	80.961	234275	2	915.49	2.67
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	2		YQINPQGMDTSSMDVVFQQYADTVK	176	25	20	104.45	b2*b2b3b4b5*b5b10b11b15y1y2y3y5y6y7*y7y9y11y12y25	2865.32	86.547	122288	3	955.78	3.83
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	3		TQTVQSAADIR	116	11	9	55.84	b2b3*b3y2y6y7y8y9y11	1189.61	36.019	46306	2	595.31	-8.52
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		ELTQAWAVAMALGVEDK	88	17	4	23.25	b13y4y5°y5	1831.92	86.889	1711	2	916.47	-1.67
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	5		IWLALAGMVLAFSASAAQISDGK	3	23	5	37.25	y6y9y12y14y15	2320.20	85.788	2273	3	774.07	-16.84
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	6	Oxidation+M(21)	YHVEFLGPLGKELTQAWAVAMALGVEDK	77	28	3	17.69	y5y9y11	3088.57	78.672	4293	4	772.90	-2.85
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	1		MITGIQITK	0	9	6	38.19	b2y2y3y6y7y9	1004.57	55.587	124424	2	502.79	-11.12
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	2		SGFAEDEVVAVSK	35	13	11	83.21	b3b4b9y2y4y5y8y9°y9y10y13	1337.66	55.200	82745	2	669.33	-1.28
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	3		LGEIEYR	48	7	10	63.75	b2b3y2y3°y3y4y5y6°y6y7	879.45	42.896	58419	2	440.23	-11.52
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	4		FNSLTPEQQRDV1AR	106	15	13	53.46	b2*b2b3°b3b4y2y3y4y10°y10*y10y13y15	1773.90	48.108	55858	3	591.97	-11.15
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	5		FNSLTPEQQR	106	10	13	88.34	b2*b2b3°b3b4°b4y3y5*y5y6y7y8y10	1219.60	38.758	52724	2	610.30	-7.81
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	6		VEGGQH1NVNVLR	66	13	11	59.84	b3b9*b9b10°b10y1y6*y6y7y8y13	1434.76	50.688	45359	3	478.93	-12.76
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	7		EIPMEVKPEVR	55	11	8	70.79	b5y2y4y6y7y8y9y11	1326.71	49.132	34122	2	663.86	3.59
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	8		AANDDLLNSFWLLDSEK	9	17	4	23.25	b3y4°y4y5	1950.95	77.286	2714	3	650.99	4.76
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	9		TFTESL	121	6	4	39.98	b4°b4b5y5	697.33	56.216	37277	1	697.33	-8.84
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	10		AANDDLLNSFWLLDSEKGEAR	9	21	27	260.08	b3b4b5°b5*b5b6*b6b7*b7b14y3y4y5y7y8y9y10y11°y11y12y13y14°y14y15y16y18y19	2364.14	92.588	194786	3	788.72	-4.03
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	11	Carbamidomethyl+C(1)	CIVAKSGFAEDEVVAVSK	30	18	3	22.93	b5b6y13	1908.96	75.818	5111	2	954.98	-8.44
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	12		ETLEDAVKHPEK	80	12	3	29.41	b5b6b9	1395.71	96.879	4082	2	698.36	-3.50
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	13		SGFAEDEVVAVSKLGEIEYR	35	20	4	37.66	b3b4b5b14	2198.11	100.661	2891	2	1099.56	4.89
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	14	Phosphoryl.STY(9)	AANDDLLNSFWLLDSEK	9	17	3	23.25	b8y7y8	2030.89	87.761	17191	3	677.63	-6.97
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	15		PMEVKPEVR	57	9	2	21.83	b3b4	1084.58	49.156	31599	2	542.79	-5.40
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	16		TGIQITK	2	7	3	23.24	b4*b4b5	760.45	55.573	4945	1	760.45	-9.87
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	17		EIPMEVKPEVR	55	11	0	2.44		1308.68	49.160	10043	3	436.90	-11.10

[P0A1D5]CH10_SALTY 10 kDa chaperonin	1		VGDIVIFNDGYGVK	60	14	19	162.12	b3b4°b4b5°b5b6b13°b13y1y3y5y6y7y8y9y10y12°y12y14	1495.78	73.840	212623	2	748.39	-1.55
[P0A1D5]CH10_SALTY 10 kDa chaperonin	2		ILDNGTVQPLDVK	47	13	33	209.52	b2b6°b6°b6b7°b7b8°b8b9°b9b10b11°b11°b11b13y1y2y3y4y5y6°y6°y6y7y8y9y10y11°y11°y11y12°y12y13	1411.77	58.086	183904	2	706.39	-3.11
[P0A1D5]CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	15	121.09	b2b4°b4b6°b6y2y3y4y6y7y8y9y11y12y14	1188.65	44.439	119252	2	594.83	-8.83
[P0A1D5]CH10_SALTY 10 kDa chaperonin	4		GEIIAVGK	37	8	5	62.4	b3y3y4y5y6	786.46	42.251	21387	2	393.73	-18.94
[P0A1D5]CH10_SALTY 10 kDa chaperonin	5		EVESK	15	5	1	13.19	y4	591.30	28.945	2547	1	591.30	-0.10
[P0A1D5]CH10_SALTY 10 kDa chaperonin	6		IDNEEVLIMSESDILAIVEA	77	20	3	14.32	b9b12y10	2203.09	83.944	2253	3	735.03	-6.87
[P0A1D5]CH10_SALTY 10 kDa chaperonin	7		STRGEIIAVGK	34	11	4	50.43	b5b6b8b9	1130.65	38.428	62178	2	565.83	-6.15
[P0A1D5]CH10_SALTY 10 kDa chaperonin	8		EVESKSAGGIVLTGSAAGK	15	19	6	38.04	b4°b4b7°b7b8b9	1760.94	68.579	2413	3	587.65	2.43
[P0A1D5]CH10_SALTY 10 kDa chaperonin	9		VGDIVIFNDGYGVKSEK	60	17	4	23.25	b9°b9b10y10	1839.94	137.609	2047	2	920.48	-2.72
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	1		TQFMGPEGVANVSLSNAGESAEGLLVTKPK	240	31	25	181.94	b1°b1b2°b2b3b4b5°b5b12y3y4y5y6y8y13y14y16y17y19y22y26y27y28y29y31	3144.64	88.456	227633	3	1048.88	4.35
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	2		NYDQVPANKPIVDAIK	271	16	14	95.86	b2°b2b3°b3b4b5y2y3y5y7y10y11y12y16	1784.93	54.387	215411	3	595.65	-11.63
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	3		TTGLDSDQGPTAAK	137	14	28	179.29	b2°b2b3°b3b4b5°b5b8°b8b10b12°b12y2y3y5°y5y6°y6y8°y8y9°y9y10°y10°y10y11y12y14	1361.65	30.211	132870	2	681.33	-3.94
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	4		GGVNVVFFDGITAGEKDFSTLVAR	185	24	16	88.08	b3b4b6°b6b7°b7b13b24y7y12y13°y13y18y19y20y24	2499.29	101.913	107405	3	833.77	-1.07
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	5	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTAR	92	38	16	106.01	b2b10b11°b11b12°b12b24b25b26y6y8y11y12y13y14y38	4078.01	89.376	96438	3	1360.01	8.62
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	6		VAVVGAMSGPVAQYGDQEFTGAEQAIADINAK	25	32	15	56.2	b2b3b6b8°b8b14y3y5y6°y6°y6y12y13y25y32	3207.58	90.003	63871	3	1069.87	5.86
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	7		QQYGEGLAR	168	9	8	45.36	b7b9y5y6°y6y7y9°y9	1021.50	33.741	46028	2	511.25	-10.34
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	8		GATVDVTVMGPLSWDEK	326	16	4	24.17	b6b9y4y9	1705.83	65.222	6872	3	569.28	9.30
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	9		ENIDFVYYGGYHPMGQILR	212	20	4	14.32	b9b12y9°y9	2401.12	86.564	9195	4	601.03	-4.88
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	10	Carbamidomethyl+C(6)	TLLAGCIALSLSHMAFADDIK	4	21	4	29.94	y6y7y9y13	2247.12	104.687	1711	2	1124.06	-15.32
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	11		DFSTLVAR	201	8	3	40.79	b3b6b7	908.48	125.702	1703	1	908.48	-0.20
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	12		KQDPSGAFVWTTYAALQSLQAGLNHSDDPAEIAK	289	34	37	226.88	b3°b3b5°b5b7°b7b8°b8b9°b9b11°b11b13°b13b15b18y3y6y9y11y12°y12y13°y13y14y15°y15y17°y17y18°y18y19y20y21y22y24y25	3629.77	102.459	331752	4	908.20	-4.04

P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	13	Carbamidomethyl+C(6); Oxidation+M(14)	TLLAGCIALSLSHMAFADDIK	4	21	5	38.1	b6b7y5y6y9	2263.15	63.747	4501	3	755.06	2.70
P25077 MDH_SALTY Malate dehydrogenase	1	Carbamidomethyl+C(2)	ACVGIITNPVNTTVAIAAEVLKK	111	23	19	137.32	b2b3b4b5b6b8b9b13*b13y1y3y12y13y15y16y18y20y21y23	2382.34	104.538	213809	3	794.78	-2.97
P25077 MDH_SALTY Malate dehydrogenase	2		NQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVK	21	33	26	83.04	b1*b1b2*b2b3*b3b5b8b10*b10b12b13*b13b15*b15y1y2y3y5*y5y15y18y19y24y30y33	3388.81	93.864	174351	3	1130.27	1.66
P25077 MDH_SALTY Malate dehydrogenase	3		VAVLGAAGGIGQALALLK	2	19	24	247.52	b2b3b5b6b7b8b9b10b17y1y2y3y4y5y6y7y9y10y11y12y13y15y17y19	1735.09	119.595	138314	2	868.05	1.83
P25077 MDH_SALTY Malate dehydrogenase	4		FFSQPLLLGK	262	10	9	61	b2b3*b3y2y3y4y6y8y10	1149.66	76.120	123683	2	575.33	-8.18
P25077 MDH_SALTY Malate dehydrogenase	5		IQNAGTEVVEAK	205	12	28	166.54	b2*b2b3b4*b4b9*b9b10*b10*b10y1y2y3*y3y4y5y6y7y8*y8y9*y9y10*y10y11*y11y12*y12	1258.65	35.351	100360	2	629.83	-7.18
P25077 MDH_SALTY Malate dehydrogenase	6		NLVQQIAK	99	8	6	36.02	b1b3*b3y3y6y8	913.53	49.762	77672	2	457.27	-13.90
P25077 MDH_SALTY Malate dehydrogenase	7		DIQLGEDFINK	301	11	7	36.63	b3y1y5*y5y7y8y11	1291.65	68.419	67581	2	646.33	-3.87
P25077 MDH_SALTY Malate dehydrogenase	8		AGGGSATLSMGQAAAR	217	16	18	106.75	b1b7*b7b16y5y6*y6y7*y7y8y9*y9*y9y10y11*y11y12y16	1405.69	40.756	61887	2	703.35	1.56
P25077 MDH_SALTY Malate dehydrogenase	9		SIGTLSAFEQHSLDAMLDTLKK	279	22	7	50.94	b2b9b10*b10b13b14b15	2405.23	94.874	44688	3	802.42	-1.32
P25077 MDH_SALTY Malate dehydrogenase	10		SDLFNVNAGIVK	87	12	5	34.15	b3y6y8y9y12	1276.69	70.077	37144	2	638.85	-2.87
P25077 MDH_SALTY Malate dehydrogenase	11		KDIQLGEDFINK	300	12	5	40.17	b7b8b9y2y5	1419.75	49.789	14513	3	473.92	0.00
P25077 MDH_SALTY Malate dehydrogenase	12		FGLSLVR	233	7	4	53.57	y3y4y5y6	791.46	67.140	74781	2	396.23	-19.51
P25077 MDH_SALTY Malate dehydrogenase	13		SNTFVAELKGK	153	11	4	31.22	b5b6*b6b8	1193.64	26.316	27549	3	398.55	-11.15
P25077 MDH_SALTY Malate dehydrogenase	14		IKGFSGEDATPALEGADVVLISAGVAR	54	27	4	48.93	y3y4y5y6	2643.40	87.103	25632	3	881.80	-1.20
P25077 MDH_SALTY Malate dehydrogenase	15	Carbamidomethyl+C(11)	ALQGEKGVVECAAYVEGDGQYAR	240	22	7	52.64	b12b13y3y5y7y9y10	2399.13	52.659	23584	3	800.38	-1.02
P25077 MDH_SALTY Malate dehydrogenase	16		AGGGSATLSMGQAAARFGLSLVR	217	23	3	23.09	b7b8b15	2178.11	78.595	2330	3	726.71	-15.02
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	23	135.17	b1b2*b2b3*b3b4*b4b13b19y2y3y4*y4y5y6y9y11*y11y12y13y15y16y19	2130.16	92.552	284414	3	710.72	-6.99
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		MVAPVDGTIGK	59	11	18	144.52	b1b2b3b7b8*b8b9b10y2y5*y5y6y7y8y9*y9y10y11	1087.57	46.914	140270	2	544.29	-9.99
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		VGDPVIEFDLPLLEEK	115	16	7	37.76	b5y2y3y6y10y11y16	1812.97	99.632	87998	2	906.99	5.25
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		STLTPVVISNMDEIK	133	15	4	18.08	b1b11b13y9	1646.85	86.390	6573	2	823.93	-11.49

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		DTGTIEIVAPLSGEIVNIEDVPDVV FAEK	16	29	3	11.5	b4y3y8	3069.60	111.314	3677	3	1023.87	3.74
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		LSGSVTVGETPVIR	152	14	4	32.92	b4b5y7y13	1414.79	56.193	25495	2	707.90	-1.04
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		VKVGDPVIEFDLPLEEK	113	18	12	92.38	b3b5b6b7y3°y3y4y6y8°y8y9y10	2040.11	95.124	118587	3	680.71	-7.30
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		VGDPVIEFDLPLEEKAK	115	18	3	24.45	b3b6b7	2012.07	91.585	17527	3	671.36	-12.86
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9		LSGSVTVGETPVIRIK	152	16	3	24.8	b7b10b12	1655.95	58.553	12684	3	552.66	-8.70
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	10	Phosphoryl STY(10)	LSGSVTVGETPVIR	152	14	4	19.22	b3b8°b8y3	1494.74	50.714	3391	2	747.88	-2.37
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	11		STLTPVVISNMDEIKELIK	133	19	0	5.7		2113.13	92.530	3136	3	705.05	-7.05
P64076 ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	25	186.36	b2*b2b3*b3b4*b4b5b7°b7°b7b9b12°b12b13°b13b15y3y4y6y7y8y11y12y13y15	1605.89	85.736	320193	2	803.45	0.46
P64076 ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	32	257.06	b2b4b8b11b12°b12b13°b13b14°b14b15b16b18b22y2y4y5y6y7y8y9°y9y12°y12y13y14°y14y15y16y17y18y22	2118.07	75.725	226900	2	1059.54	5.65
P64076 ENO_SALTY Enolase	3		DAGYTAVISHR	360	11	15	110.36	b2b3°b3b7b8y1y2y3y4y5y6y7y9°y9y11	1189.59	42.127	114440	2	595.30	-6.98
P64076 ENO_SALTY Enolase	4		GMNTAVGDEGGYAPNLGSNAEA LAVIAEAVK	200	31	23	126.77	b2b3°b3b4°b4b5°b5b6°b6b12b16y1y2y4y5y6y7y8y10y14y15y18y31	2989.47	94.998	109309	3	997.16	4.41
P64076 ENO_SALTY Enolase	5		AVGAVNGPIAQAILGK	66	16	6	28.25	b3y2y5y10y11y16	1478.87	75.472	77377	2	739.94	-2.31
P64076 ENO_SALTY Enolase	6		YSMPVPMMNIIINGGEHADNNVDI QEFMIQPVGAK	143	34	11	41.97	b2°b2b3°b3b4b5°b5y5y13y29y34	3759.79	98.382	72696	3	1253.94	7.92
P64076 ENO_SALTY Enolase	7		IQLVGDDLFTVNTNK	311	14	8	27	b2y2y4°y4y11°y11y12y14	1562.85	77.846	36300	2	781.93	1.64
P64076 ENO_SALTY Enolase	8		ILKEGIEK	325	8	9	53.98	b2y1y3°y3y4y5°y5y6y8	929.56	29.736	26850	2	465.28	-12.15
P64076 ENO_SALTY Enolase	9	Carbamidomethyl+C(16)	AAGYELGKIDITLAMDCAASEFYK DGK	231	26	10	36.55	b2b3b5°b5b7b9b11°b11y2y6	2824.30	97.878	23241	4	706.83	-7.00
P64076 ENO_SALTY Enolase	10		GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	5	38.51	b3y11y12y16y17	2856.34	87.453	10322	3	952.78	-6.75
P64076 ENO_SALTY Enolase	11		GMPLYEHIAELNGTPGK	126	17	4	36.85	b15y3y4y5	1826.88	67.564	86184	3	609.63	-16.10
P64076 ENO_SALTY Enolase	12		GIANSILIK	333	9	4	54.39	y3y5y6y7	928.57	61.037	81496	2	464.79	-16.04
P64076 ENO_SALTY Enolase	13		AFTSEEFTHFLEELTK	266	16	4	30.7	b3b4y4y7	1928.92	103.067	49125	3	643.64	-5.63
P64076 ENO_SALTY Enolase	14		IEEALGEK	411	8	4	49.21	b3b5b6y4	888.47	48.808	23283	1	888.47	6.66
P64076 ENO_SALTY Enolase	15		EIIDSR	10	6	1	13.6	y4	732.39	27.368	12979	1	732.39	2.92
P64076 ENO_SALTY Enolase	16		SNFGANAILAVSLANAK	103	17	6	23.66	b3b5°b5°b5b11°b11	1660.89	78.664	4005	2	830.95	-9.04
P64076 ENO_SALTY Enolase	17		VLGDKIQLVGDDLFTVNTNK	306	19	11	73.4	b4°b4b5b8b9y4°y4y5y6y10°y10	2075.12	79.673	102474	3	692.38	-7.29
P64076 ENO_SALTY Enolase	18		GMPLYEHIAELNGTPGKYSPMPVPMNIIINGGEHADNNVDIQEFMIQP VGAK	126	51	15	52.64	b6b8b10°b10b14b20b22y5y6°y6y8y9y13°y13y24	5567.66	97.884	88843	5	1114.34	1.05
P64076 ENO_SALTY Enolase	19		DGKYVLAGEGNK	254	12	6	37.16	b11y3y6°y6y9°y9	1250.62	44.376	67886	2	625.82	-11.13

P64076 ENO_SALTY Enolase	20		GKGMNTAVGDEGGYAPNLGSNA EALAVIAEAVK	198	33	4	21.56	b4b5b15y5	3174.59	89.865	28430	3	1058.87	5.23
P64076 ENO_SALTY Enolase	21		EIIDSRGNPTVEAEVHLEGGFVGM AAAPSGASTGSR	10	36	8	27.03	b5°b5b7b8°b8y9y15y17	3569.77	104.502	13262	3	1190.59	10.40
P64076 ENO_SALTY Enolase	22		SGETEDATIADLAVGTAAGQIKTG SMSR	371	28	5	38.91	b15y5y6y11y12	2737.34	74.283	11544	3	913.12	4.73
P64076 ENO_SALTY Enolase	23		IEEALGEKAPYNGR	411	14	6	45.3	b9y4y5y6y9°y9	1546.76	40.307	6156	3	516.26	-14.44
P64076 ENO_SALTY Enolase	24		AAAAAKGMPLYEHIAELNGTPGK	120	23	5	20.05	b3b8b12y8*y8	2310.16	106.952	4677	2	1155.58	-14.80
P64076 ENO_SALTY Enolase	25		YVLAGEGNKAFSTSEEFTHFLELT K	257	25	4	21.91	b12b13°b13y9	2860.42	109.371	2442	3	954.15	6.57
P64076 ENO_SALTY Enolase	26	Oxidation+M(1)	MAKDAGYTAVISHR	357	14	3	19.22	b3b10y11	1535.78	51.284	1950	2	768.39	12.24
P64076 ENO_SALTY Enolase	27		GYTAVISHR	362	9	3	18.82	b3°b3b8	1003.53	42.150	44605	2	502.27	-3.10
P64076 ENO_SALTY Enolase	28		AGYTAVISHR	361	10	4	35.99	b3b5°b5b9	1074.57	42.122	20158	2	537.79	-3.29
P64076 ENO_SALTY Enolase	29		LKEGIEK	326	7	0	1.22		816.47	29.758	20062	2	408.74	-14.28
P64076 ENO_SALTY Enolase	30		NTAVGDEGGYAPNLGSNAEALAV IAEAVK	202	29	3	12.19	b3°b3b16	2801.43	95.018	4605	3	934.48	12.11
P64076 ENO_SALTY Enolase	31		DAGYTAVISHR	360	11	0	2.44		1171.58	42.131	1795	3	391.20	1.15
P0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAIR	125	13	13	101.17	b2b3°b3b10b12y2y4y7y8y 9y10y11y13	1447.78	65.750	78423	2	724.39	-2.61
P0A297 RL10_SALTY 50S ribosomal protein L10	2	Carbamidomethyl+C(9)	VVEGTQFECCLKDTFVGPTLIAYSM EHPGAAAR	62	32	7	27.18	b3b8y7y10y11y17y32	3494.70	92.244	53856	4	874.43	-2.72
P0A297 RL10_SALTY 50S ribosomal protein L10	3		AAAFEGELIPASQIDR	109	16	9	86.57	b4y5y7y8y9y10y11y12y16	1687.88	69.207	51297	2	844.44	6.08
P0A297 RL10_SALTY 50S ribosomal protein L10	4		GALSAVVADSR	20	11	9	70.79	b6y4y5y6°y6y7y8°y8y11	1045.58	48.977	29515	2	523.29	12.26
P0A297 RL10_SALTY 50S ribosomal protein L10	5		AGREAGVYMR	43	10	6	73.39	b4b8y3y6y7y9	1109.56	46.919	11727	2	555.28	3.52
P0A297 RL10_SALTY 50S ribosomal protein L10	6		QAIVAEVSEVAK	8	12	4	35.43	b12y8y9y10	1243.68	57.947	10667	2	622.35	-3.83
P0A297 RL10_SALTY 50S ribosomal protein L10	7		DTFVGPTLIAYSMHPGAAAR	73	21	3	13.83	b7b12y5	2204.08	82.634	5673	3	735.37	0.11
P0A297 RL10_SALTY 50S ribosomal protein L10	8		EAGVYMR	46	7	4	40.38	b5y3y6y7	825.39	32.985	5606	2	413.20	-5.40
P0A297 RL10_SALTY 50S ribosomal protein L10	9		LMATMK	138	6	2	26.79	b5y4	694.37	41.635	13930	1	694.37	11.78
P0A297 RL10_SALTY 50S ribosomal protein L10	10		EFAK	97	4	1	12.78	b3	494.26	42.144	2976	1	494.26	5.62
P0A297 RL10_SALTY 50S ribosomal protein L10	11		ALNLQDKQAIVAEVSEVAK	1	19	3	22.67	b9y8y9	2026.09	71.777	30344	3	676.04	-12.47
P0A297 RL10_SALTY 50S ribosomal protein L10	12		AAAFEGELIPASQIDRLATLPTYEE AIAIR	109	29	12	55.92	b3b5b6b10°b10b14y4y9°y9 y10y20y25	3116.64	92.923	27194	3	1039.55	3.53
P0A297 RL10_SALTY 50S ribosomal protein L10	13		FEVKAAAFEGELIPASQIDR	105	20	3	21.11	b4b6b9	2191.12	96.417	14840	2	1096.07	-7.13
P0A297 RL10_SALTY 50S ribosomal protein L10	14		LMATMKEASAGK	138	12	4	26.19	b8°b8y8y9	1237.63	98.749	9672	1	1237.63	1.48
P0A297 RL10_SALTY 50S ribosomal protein L10	15		AGREAGVYMR	43	10	5	40.02	b4b5°b5b9y6	1109.55	74.936	5702	2	555.28	-1.32
P0A297 RL10_SALTY 50S ribosomal protein L10	16	Phosphoryl.STY(6)	LATLPTYEEAIAIR	125	13	3	28.05	y6y7y11	1527.74	73.834	11796	2	764.37	2.96
P0A297 RL10_SALTY 50S ribosomal protein L10	17	Phosphoryl.STY(4)	GALSAVVADSR	20	11	5	50.61	b7b8y6y7y9_H3PO4 y9_HPO3 y9	1125.53	46.905	10855	2	563.27	10.52
P0A297 RL10_SALTY 50S ribosomal protein L10	18	Oxidation+M(13)	DTFVGPTLIAYSMHPGAAAR	73	21	4	35.77	b14y8y9y10	2220.07	70.419	18749	3	740.69	-3.41
P0A297 RL10_SALTY 50S ribosomal protein L10	19	Oxidation+M()	LMATMKEASAGK	138	12	8	47.04	b5°b5b9y4°y4y6°y6y8	1253.61	31.681	6318	2	627.31	-13.63

P02910 HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTTQETFGNEHWAPK	135	20	21	184.71	b1b2b3b4y1y2y3y4y5y8y9y10y11*y11y12y14y15y16y17y19y20	2199.06	63.906	184466	3	733.69	-8.33
P02910 HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPITYAPFESK	29	13	20	146.76	b2b3*b3b4b8b13y2*y2y4y5*y5y6y7y8*y8y9y10y11y12y13	1425.69	56.199	123976	2	713.35	0.09
P02910 HISJ_SALTY Histidine-binding periplasmic protein	3		NSDIQPTVASLK	120	12	19	123.96	b2*b2b3*b3b4*b4b5b11*b11*b11y3y4y5y8*y8y9y10*y10y12	1272.68	48.911	102188	2	636.84	-1.25
P02910 HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALISLK	62	20	21	113.72	b2b3*b3b8*b8b10*b10b14b16*b16y1y2y3y4*y4y5y6y7y10y13y20	2273.21	103.735	94035	2	1137.11	11.49
P02910 HISJ_SALTY Histidine-binding periplasmic protein	5		FGGPAVKDEK	201	10	7	43.03	b2b8*b8y3y4y5y10	1047.54	27.289	25224	2	524.27	-6.06
P02910 HISJ_SALTY Histidine-binding periplasmic protein	6		GIEIVSYQGQDNIYSDLTAGR	155	21	3	13.83	b3b8y3	2299.15	79.012	12035	2	1150.08	10.94
P02910 HISJ_SALTY Histidine-binding periplasmic protein	7		NAQGELVGFDIDLAK	42	15	5	43	b5b11b13y7y8	1589.82	79.654	29809	2	795.41	3.07
P02910 HISJ_SALTY Histidine-binding periplasmic protein	8		QQEIAFTDK	99	9	3	30.41	b5y3y7	1079.54	43.624	16742	2	540.27	1.81
P02910 HISJ_SALTY Histidine-binding periplasmic protein	9		AFAEMR	234	6	1	13.6	y4	724.34	36.792	7472	1	724.34	-5.31
P02910 HISJ_SALTY Histidine-binding periplasmic protein	10		FGGPAVK	201	7	4	56.58	b4b6y5y6	675.37	44.282	5360	1	675.37	-17.71
P02910 HISJ_SALTY Histidine-binding periplasmic protein	11		IDAAFQDEVAASEGFLK	176	17	4	33.63	b4b7b14b15	1810.93	97.920	2914	2	905.97	22.45
P02910 HISJ_SALTY Histidine-binding periplasmic protein	12		QPVGKDYK	193	8	5	33.01	b3y4*y4y5*y5	934.50	50.657	17736	2	467.76	5.36
P02910 HISJ_SALTY Histidine-binding periplasmic protein	13		IGTDPITYAPFESKNAQGLVGFDIDLAK	29	28	3	11.68	b9b14y15	2996.52	85.053	11160	3	999.51	11.16
P02910 HISJ_SALTY Histidine-binding periplasmic protein	14		QQEIAFTDKLYAADSR	99	16	3	17.1	b9b14y11	1855.91	84.469	3658	3	619.31	-5.99
P02910 HISJ_SALTY Histidine-binding periplasmic protein	15		DEKLFGVGTGMGLR	208	14	4	27	b7b9b10*b10	1479.75	59.766	3604	2	740.38	-8.91
P02910 HISJ_SALTY Histidine-binding periplasmic protein	16		GGPAVKDEK	202	9	0	2.04		900.47	27.281	9196	2	450.74	-9.69
P06179 FLIC_SALTY Flagellin	1		AQILQQAGTSVLAQANQVPQNVLSLLR	468	27	26	182.68	b2*b2b3b4b5*b5b6b7*b7b11*b11b12b13b17b18y1y2y3y4y5y6y9y10y12y13y27	2860.61	105.253	87276	3	954.21	2.90
P06179 FLIC_SALTY Flagellin	2		FNSAITNLGNVTNNLTSAR	432	19	20	137.13	b2b4b5b6*b6b12*b12b13*b13b14y2y3y4y7*y7y8y13y14y17y19	2007.03	78.579	46600	2	1004.02	4.01
P06179 FLIC_SALTY Flagellin	3		NANDGISIAQTTEGALNEINNNLQR	66	25	8	12.37	b6*b6*b6b14*b14*b14y14y25	2670.34	86.747	45033	2	1335.67	11.25
P06179 FLIC_SALTY Flagellin	4		AQVINTNSLSLLTQNNLNK	1	19	8	22.67	b2*b2b7*b7b8y1y15y19	2085.14	75.112	44705	2	1043.08	6.44
P06179 FLIC_SALTY Flagellin	5		SQSALGTAIER	20	11	9	36.63	b2*b2b10y1y6*y6y7y9y11	1132.59	42.781	41795	2	566.80	-6.79
P06179 FLIC_SALTY Flagellin	6		ELAVQSANSTNSQSDLDLSIAEITQR	93	26	10	21.85	b2b6*b6*b6b13*b13y6y10y12y26	2805.36	70.929	16642	3	935.79	2.87
P06179 FLIC_SALTY Flagellin	7		QINSQTLGLDVLNVQQK	161	17	7	34.45	b4*b4*b4b5*b5b6*b6	1900.03	94.935	11879	3	634.02	10.60
P06179 FLIC_SALTY Flagellin	8		IDAALAQVDTLR	411	12	4	29.41	b4*b4b6b7	1285.71	84.698	8814	2	643.36	2.85
P06179 FLIC_SALTY Flagellin	9		LNEIDR	119	6	4	39.98	b3b4b5*b5	759.40	96.887	14100	1	759.40	-4.82
P06179 FLIC_SALTY Flagellin	10		TYAASK	379	6	1	13.6	y5	640.34	50.868	4153	1	640.34	12.49
P06179 FLIC_SALTY Flagellin	11		NVQVANADLTEAK	280	13	4	25.34	b9b10y5*y5	1372.71	42.138	2275	3	458.24	1.87
P06179 FLIC_SALTY Flagellin	12		ASATGLGGTDQK	204	12	3	26.19	b10y5y6	1105.54	104.614	1914	1	1105.54	-6.51
P06179 FLIC_SALTY Flagellin	13		AQPDLAEEAAATTENPLQK	392	19	6	50.62	b10b11b12y7y9y12	1968.99	67.931	1649	2	985.00	-0.74

P06179 FLIC_SALTY Flagellin	14		VSDTAATVTGYADTTIALDNSTF K	180	24	5	19.38	b9°b9y6y11y16	2462.19	74.104	1624	3	821.40	-3.27
P06179 FLIC_SALTY Flagellin	15		LGGADGKTEVVSIGGK	363	16	5	45.54	b7b8b10b11y9	1487.79	43.541	38645	3	496.60	-14.28
P06179 FLIC_SALTY Flagellin	16		TYAASKAEGHNFK	379	13	4	20.57	b3°b3b6y9	1423.71	41.646	31768	2	712.36	7.55
P06179 FLIC_SALTY Flagellin	17		IDAALAQVDTLRSDLGAVQNR	411	21	5	23.48	y9°y9*y9y10y18	2226.19	63.870	15781	3	742.73	1.43
P06179 FLIC_SALTY Flagellin	18		FNSAITNLGNTVNNLTSARSR	432	21	7	31.09	b3b7b10*b10b11°b11y13	2250.18	112.150	6203	2	1125.59	7.60
P06179 FLIC_SALTY Flagellin	19		YKVSDTAATVTGYADTTIALDNS TFK	178	26	6	32.48	b6b10b12y5y6y16	2753.37	98.813	4868	3	918.46	5.05
P06179 FLIC_SALTY Flagellin	20		AEGHNFKAQPDLAEEAAATTTENP LQK	385	26	5	39.46	b7b8b10b11*b11	2752.32	126.414	2677	3	918.11	-13.22
P06179 FLIC_SALTY Flagellin	21	Phosphoryl STY(6)	QINSQTLGLDTLNVQQK	161	17	6	26.06	b5y8*y8y12*y12y15	1979.97	99.755	27223	3	660.66	-2.03
P06179 FLIC_SALTY Flagellin	22	Phosphoryl STY(13)	AQPDLAEEAAATTTENPLQK	392	19	5	41.05	b4b5b11*b11b12	2048.94	62.034	2202	3	683.65	-1.07
P06179 FLIC_SALTY Flagellin	23	Phosphoryl STY(13)	TNGEVLTAGGATSPLTGGLPATA TEDVK	252	28	4	14.85	b8b12y7y16	2708.32	102.518	1831	4	677.84	10.10
P06179 FLIC_SALTY Flagellin	24	Phosphoryl STY(11)	FNSAITNLGNTVNNLTSAR	432	19	5	31.52	b7b10y9y10y14	2086.98	67.039	1804	4	522.50	-0.70
P06179 FLIC_SALTY Flagellin	25		IDAALAQVDTLR	411	12	0	2.85		1267.69	84.674	1743	2	634.35	-5.78
P02906 SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQEIAAK	263	13	22	129.77	b2b3b4°b4b7°b7b10°b10b1 1y1y2y3y7y8°y8*y8y9y10* y10y11°y11y13	1468.73	51.438	66060	2	734.87	-0.08
P02906 SUBI_SALTY Sulfate-binding protein	2		NVEVLDSGAR	183	10	9	57.98	b2*b2b6*b6y4y6y7y8y10	1059.54	40.784	50282	2	530.27	-5.41
P02906 SUBI_SALTY Sulfate-binding protein	3		GIGDVLIAWENEALLATNELGK	202	22	6	13.39	b4b13y1y7°y7y22	2326.21	91.234	35727	2	1163.61	-7.35
P02906 SUBI_SALTY Sulfate-binding protein	4		QATSVINGIEADVVTALAYDVD AIAER	66	28	12	129.37	b2b11y3y4y5y6y7y8y9y10 y11y12	2917.52	127.948	13647	3	973.18	0.25
P02906 SUBI_SALTY Sulfate-binding protein	5		QETGDNVVIR	48	10	5	39.23	b3°b3b6y3y8	1130.58	36.141	12608	2	565.79	-3.78
P02906 SUBI_SALTY Sulfate-binding protein	6		WNYLAAWGYALHHNNNDQAK	153	20	5	14.32	b2*b2b11y7y10	2386.12	78.722	7748	3	796.05	5.01
P02906 SUBI_SALTY Sulfate-binding protein	7		LPDNSAPYTSTIVFLVR	104	17	5	24.91	b4b6°b6b7°b7	1893.02	86.344	2642	2	947.01	2.51
P02906 SUBI_SALTY Sulfate-binding protein	8		QIHDWNLIKPGVSVITPNPK	126	21	6	51.59	b5b6b9y4y5y6	2371.23	73.104	83315	4	593.56	-18.43
P02906 SUBI_SALTY Sulfate-binding protein	9		FEIVTPSESILAEPVSVDK	226	21	5	24.63	b8b13b14y5°y5	2260.23	77.422	74904	3	754.08	13.07
P02906 SUBI_SALTY Sulfate-binding protein	10		LFTIDEVFGGWAK	298	13	4	20.57	b3°b3b8y8	1482.76	101.981	55990	2	741.88	-1.15
P02906 SUBI_SALTY Sulfate-binding protein	11		NFYRPR	276	6	1	13.6	b5	852.44	30.199	11055	2	426.72	-11.74
P02906 SUBI_SALTY Sulfate-binding protein	12		VVEK	247	4	1	12.78	b3	474.30	67.129	8744	1	474.30	7.08
P02906 SUBI_SALTY Sulfate-binding protein	13		DIQLLNVSYPTR	20	13	6	33.97	b3y4y9y11°y11*y11	1533.77	82.798	8428	2	767.39	-13.93
P02906 SUBI_SALTY Sulfate-binding protein	14		GSTNTFVER	193	9	4	54.39	y3y4y5y7	1010.49	32.979	3038	1	1010.49	-1.87
P02906 SUBI_SALTY Sulfate-binding protein	15		RLPDNSAPYTSTIVFLVR	103	18	5	26.5	b7b9b10°b10y5	2049.09	82.763	30468	3	683.70	-9.77
P02906 SUBI_SALTY Sulfate-binding protein	16		ELYEQYNKAFAHWK	33	15	4	18.08	b9y5y11*y11	1913.92	98.282	4081	2	957.46	-0.06
P02906 SUBI_SALTY Sulfate-binding protein	17		AVAEAYLKLYSPEGQEIAAK	255	21	6	49.24	b11b12y8y9y10°y10	2314.23	114.593	2311	3	772.08	13.50
P02906 SUBI_SALTY Sulfate-binding protein	18		QETGDNVVIRQSHGGSGK	48	18	11	56.24	b4*b4b8y6y7°y7y8°y8y9°y 9*y9	1868.90	35.332	1792	3	623.64	-12.34

[P41031 CY_SALTY Thiosulfate-binding protein	1		AYLNWLYSPQAQTIIHHYYR	265	21	25	259.17	b2b3b4b5*b5b6y2y3y4y5y6y7y8y9*y9y10y11y12y13y14y15y16y17y18y21	2664.32	93.121	194702	3	888.78	-2.75
[P41031 CY_SALTY Thiosulfate-binding protein	2		GLGDVLISFESEVNNIRK	208	18	14	103.55	b2b3b4b5y2y5y6y8*y8y9y11y13y16y18	1990.04	101.229	137259	3	664.02	-11.53
[P41031 CY_SALTY Thiosulfate-binding protein	3		LPNNSSPFYSTMGFLVR	110	17	14	80.83	b2b4b7b8*b8y1y2y3y5y6y11y12y13y17	1929.97	92.038	119017	2	965.49	7.40
[P41031 CY_SALTY Thiosulfate-binding protein	4		FGSWPEVMK	311	9	10	61.56	b2b3*b3y1y2y5y6y7y8y9	1080.51	69.135	113458	2	540.76	-5.76
[P41031 CY_SALTY Thiosulfate-binding protein	5		QYEAQGFEVVIPK	226	13	19	102.93	b2*b2b3*b3b10*b10*b10b11*b11*b11b12b13y2y3y5y8y10y11y13	1507.77	70.349	96798	2	754.39	-4.61
[P41031 CY_SALTY Thiosulfate-binding protein	6		VNNPEIMGK	286	9	16	74.75	b1b2*b2b3*b3y2y3y4y6y7*y7*y7y8*y8y9*y9	1001.50	36.904	96714	2	501.25	-11.34
[P41031 CY_SALTY Thiosulfate-binding protein	7		TEQFMTQFLK	179	10	14	74.18	b1b2b3*b3y2y3y5y6y7*y7y8*y8*y8y10	1272.63	75.765	95602	2	636.82	-1.44
[P41031 CY_SALTY Thiosulfate-binding protein	8		ELFAALNPPFEQQWAK	37	16	12	63.76	b3b6b7*b7y1y8y9*y9y12y13*y13y16	1888.97	89.846	78829	2	944.99	5.95
[P41031 CY_SALTY Thiosulfate-binding protein	9		NVEVFDTGGR	189	10	12	83.57	b2b4*b4b5b8*b8y4y6y7y8*y8y10	1093.53	47.938	63586	2	547.27	-1.90
[P41031 CY_SALTY Thiosulfate-binding protein	10		QALAILQLK	71	10	8	74.18	b3*b3b10y3y5y6y7y8	1054.65	75.300	54210	2	527.83	-9.95
[P41031 CY_SALTY Thiosulfate-binding protein	11		ADVVTYNQVTDVQILHDK	81	18	9	32.49	b2*b2b3b4b6b10*b10y1y18	2058.03	64.360	9399	3	686.68	-11.15
[P41031 CY_SALTY Thiosulfate-binding protein	12		TNLAIEFPVAWVDK	239	14	6	31.44	b2b8y4y9y11y14	1602.85	97.284	9357	2	801.93	-1.52
[P41031 CY_SALTY Thiosulfate-binding protein	13		GATTTFAER	199	9	6	30.41	b7*b7b8*b8y7*y7	953.47	123.341	3755	1	953.47	5.76
[P41031 CY_SALTY Thiosulfate-binding protein	14		THFASGGELDK	320	11	6	60	b4b5b9y4y6y7	1161.55	80.928	1512	2	581.28	-4.20
[P41031 CY_SALTY Thiosulfate-binding protein	15		TNLAIEFPVAWVDKNVQANGTEK	239	23	28	210.73	b3*b3b4b5*b5b6*b6*b6b7*b7y4y6*y6y7*y7y8*y8*y8y9y10y12y13*y13y16y17y18y19y20	2544.31	90.580	265982	3	848.77	-1.15
[P41031 CY_SALTY Thiosulfate-binding protein	16		LIPADWQSRPLNNSSPFYSTMGFLVR	101	26	7	56.1	y3y5y9y11y12y21y24	2996.52	95.815	72047	3	999.51	3.99
[P41031 CY_SALTY Thiosulfate-binding protein	17		NVEVFDTGGRGATTTFAER	189	19	20	170.29	b3b5*b5*b5b6b8b9b10b11b13*b13y3y4y5y6y9*y9y13y15y17	2027.96	57.288	48439	3	676.66	-7.10
[P41031 CY_SALTY Thiosulfate-binding protein	18		VEEKFGSWPEVMK	307	13	3	25.34	b3b4y8	1565.77	47.515	2009	2	783.39	-0.55
[P41031 CY_SALTY Thiosulfate-binding protein	19	Phosphoryl STY(8)	GLGDVLISFESEVNNIR	208	17	3	16.26	b3b8y8	1941.95	60.826	5299	4	486.24	12.95
[P41031 CY_SALTY Thiosulfate-binding protein	20	Oxidation+M(7)	VNNPEIMGK	286	9	5	38.19	b3b4*b4b8*b8	1017.49	74.371	3120	2	509.25	-10.80
[P41031 CY_SALTY Thiosulfate-binding protein	21		DVLISFESEVNNIRK	211	15	1	7.34	b7	1762.93	101.244	3146	2	881.97	-1.73
[P41031 CY_SALTY Thiosulfate-binding protein	22		NPEIMGK	288	7	2	8.8	b4*b4	788.41	36.895	2983	1	788.41	13.94
[P41031 CY_SALTY Thiosulfate-binding protein	23		EVFDTGGR	191	8	0	2.04		880.41	47.921	2667	1	880.41	-4.78
[P41031 CY_SALTY Thiosulfate-binding protein	24		QALAILQLK	71	10	0	2.04		1037.63	75.303	1553	2	519.32	-4.35
[P67093 UG_SALTY Universal stress protein G	1		HATLPVLVVR	132	10	4	51.78	y5y7y8y9	1104.68	61.277	81439	2	552.84	-12.27

P67093 UG_SALTY Universal stress protein G	2		TIIMPVDVFEMELSDK	3	16	16	131.78	b2°b2b3°b3b4y1y3y4y7y8y9y10y12y13y14y16	1866.94	104.471	69241	2	933.97	8.50
P67093 UG_SALTY Universal stress protein G	3		LQTMVGHFSDPSR	69	14	5	27.79	b7b9°b9b11°b11	1587.80	67.865	2480	2	794.41	5.30
P67093 UG_SALTY Universal stress protein G	4		NPSITTHLLGSNASSVVR	114	18	5	24.45	y5y11°y11y12°y12	1852.96	59.270	41624	3	618.32	-17.26
P67093 UG_SALTY Universal stress protein G	5		FEEHLQHEAETR	57	12	3	22.21	b6b8y3	1525.72	43.553	4117	3	509.25	11.60
P67093 UG_SALTY Universal stress protein G	6		FAADVRR	50	6	1	13.6	y4	678.35	30.576	1928	2	339.68	-2.97
P67093 UG_SALTY Universal stress protein G	7		TIIMPVDVFEMELSDKAIR	3	19	8	59.54	b3y4y9y10°y10y11y15y16	2207.13	100.564	47979	3	736.38	-6.64
P67093 UG_SALTY Universal stress protein G	8		MYKTIIMPVDVFEMELSDK	0	19	6	40.73	b3b12y3y5y9y13	2289.09	98.764	6182	3	763.70	-13.86
P67093 UG_SALTY Universal stress protein G	9	Oxidation+M(24)	HAEFLLAQDQGVHLLHVLPGSASMSLHR	22	28	3	11.68	b8b12y7	3079.62	137.270	13523	3	1027.21	9.51
P67093 UG_SALTY Universal stress protein G	10	Oxidation+M(4)	TIIMPVDVFEMELSDK	3	16	3	25.47	y6y9y10	1882.94	60.146	3953	3	628.32	11.35
P67093 UG_SALTY Universal stress protein G	11	Oxidation+M(4)	LQTMVGHFSDPSR	69	14	4	24.66	b12y9y10°y10	1603.80	71.811	2761	2	802.40	5.25
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		VFMQPASEGTHIAGGAMR	93	19	31	236.15	b2b3b4b7°b7b10°b10°b10b11b12°b12°b12b13°b13b14b17y4y5y6y7y11y12y13°y13y14y15°y15y16°y16y17y19	1892.95	68.563	112117	2	946.98	5.35
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		AYGSTNPINVVRR	126	12	19	153.35	b2b3b4b5b6°b6b11y1y2y3y4°y4y5y6y7y8y10y12°y12	1290.68	51.783	92714	2	645.84	-2.46
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		ATIDGLENMNSPEMVAAK	138	18	18	112.19	b11b12°b12b15y1y2y3y7y8y9°y9°y9y10y11y12y14°y14°y14	1890.91	63.837	55982	2	945.96	6.71
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVAAKR	138	19	15	102.44	b2°b2b4b7y1y3y4y8y9y10°y10y11y12y13°y13	2046.98	59.709	53668	3	683.00	-8.95
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		AREVPAAIQK	52	10	5	39.23	b4b6y4y6y10	1082.62	29.251	5858	2	541.81	-8.91
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		SVEEILGK	159	8	7	33.01	b1b2b5y2y6y7y8	874.48	31.775	4189	2	437.74	-8.72
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		AVLEVAGVHNVLAK	112	14	10	106.99	b4b6b11b12y6y8y9y10y11y12	1419.80	60.983	112372	3	473.94	-21.84
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		IFSFTALTTVGDGNRR	29	16	11	79.47	b5b7b13b14y3y6y10°y10y11°y11y14	1653.83	70.901	6209	2	827.42	-20.59
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		QAGELQEK	6	8	4	36.02	b5b7y7°y7	902.44	52.154	2844	2	451.73	-15.56
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		IFSFTALTTVGDGNRRVGFYGYK	29	23	3	22.04	b4y4y5	2362.23	73.301	344637	4	591.31	4.65
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		MAHIEKQAGELQEK	0	14	6	19.22	b8°b8b12y6°y6°y6	1611.80	55.735	17517	2	806.40	-12.87
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12		AYGSTNPINVVRRATIDGLENMNSPEMVAAK	126	30	6	25.5	b9°b9y6y7y11y14	3162.59	117.954	3093	3	1054.87	10.27
P0A7W4 RS5_SALTY 30S ribosomal protein S5	13		GVHTGSRVFMQPASEGTHIAGGAMR	86	26	3	12.11	b14b16y15	2587.26	72.488	1847	3	863.09	-8.49
Q8ZM79 YQFB_SALTY UPF0267 protein yqfB	1		VIAEIYPNQTQFYVIDFK	83	18	6	26.5	b2b8b9b13y12y18	2188.16	88.787	19549	2	1094.58	11.05
Q8ZM79 YQFB_SALTY UPF0267 protein yqfB	2		MQPNDITFFQR	0	11	16	84.77	b2°b2b9b10°b10b11y5°y5y7°y7y8y9°y9y10y11°y11	1396.67	69.585	12003	2	698.84	1.31

[Q8ZM79]YQFB_SALTY UPF0267 protein yqfB	3		QPN DITFFQR	1	10	6	26.83	b6*b6b8y5°y5*y5	1265.63	24.026	35043	3	422.55	-0.58
[Q8ZM79]YQFB_SALTY UPF0267 protein yqfB	4		HAQQENMSLDELKR	69	14	4	24.66	b4*b4b5y11	1698.81	63.845	2251	2	849.91	-5.60
[P65702]PGK_SALTY Phohoglycerate kinase	1		SVNDVKEDEQILDIGDASAQQLAE ILK	272	27	21	105.7	b2°b2b4°b4b5b11*b11b13*b13b14b25b26y1y2y3y4y5y7y8y10y27	2941.51	100.133	198923	3	981.17	2.41
[P65702]PGK_SALTY Phohoglycerate kinase	2		VLPAVAMLEER	373	11	12	94.77	b2y1y2y3y4°y4y5y6y7y8y9y11	1227.67	80.313	152734	2	614.34	-5.97
[P65702]PGK_SALTY Phohoglycerate kinase	3	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	21	170.79	b2b3b4b5b7b12b13y2y3y4y5°y5y6y8y9y13y14y15y16°y16y20	2002.05	99.008	134425	2	1001.53	6.95
[P65702]PGK_SALTY Phohoglycerate kinase	4		VATEFSETAPATLK	258	14	19	144.16	b1b2b3°b3b5b6b7y1y2y3y5y6y7y9°y9y10y11y12y14	1464.76	53.270	93420	2	732.88	-0.33
[P65702]PGK_SALTY Phohoglycerate kinase	5	Carbamidomethyl+C(5)	LLTTC DIPVPTDVR	244	14	15	106.99	b2b5b6°b6b7°b7b9y2y5y7y8y10y11y12y14	1599.84	69.132	87822	2	800.43	1.30
[P65702]PGK_SALTY Phohoglycerate kinase	6		VMVTSHLGRPTEGEYNEEFSLLPV VNYLK	53	29	9	30.39	b1b2b13b17b18y4y7y17y29	3321.66	92.201	84978	4	831.17	-6.69
[P65702]PGK_SALTY Phohoglycerate kinase	7		TILWNGPVGVFEPNFR	302	17	18	102.8	b2°b2b13°b13*b13y2y4*y4y5y6°y6y7*y7y11y12y13y14y17	1993.05	106.315	81561	2	997.03	9.49
[P65702]PGK_SALTY Phohoglycerate kinase	8		ADLNV PVKEGK	19	11	11	70.79	b1b5y1y2y3y5y6y7y8*y8y11	1169.65	37.519	55109	2	585.33	-5.95
[P65702]PGK_SALTY Phohoglycerate kinase	9		ASLPTIELALK	38	11	8	65.38	y1y2y3y4y5y7y8y11	1155.69	77.513	50802	2	578.35	-9.61
[P65702]PGK_SALTY Phohoglycerate kinase	10		IADQLIVGGGIANTFVAAQGH SVG K	206	25	7	16.24	b1b3b5y2y5y9°y9	2423.29	78.317	41781	3	808.43	-7.46
[P65702]PGK_SALTY Phohoglycerate kinase	11		TILWNGPVGVFEPNFRK	302	18	5	22.69	b2y5y10y12y18	2121.12	96.716	38467	3	707.71	-4.72
[P65702]PGK_SALTY Phohoglycerate kinase	12		MTDL DLAGKR	5	10	10	86.58	b2b6b9°b9y1y3y4y5y6y7	1119.58	43.359	36169	2	560.29	-3.82
[P65702]PGK_SALTY Phohoglycerate kinase	13		SLYEADLVDEAK	231	12	4	26.19	b11y4y5y12	1352.65	59.020	13415	2	676.83	-3.25
[P65702]PGK_SALTY Phohoglycerate kinase	14	Carbamidomethyl+C(5)	YAALCDVFVMDAFGTAHR	128	18	4	22.93	b9b10°b10y13	2043.92	90.389	4838	2	1022.46	-11.05
[P65702]PGK_SALTY Phohoglycerate kinase	15		VTSDAR	30	6	1	13.6	y4	648.32	65.253	11595	1	648.32	-13.56
[P65702]PGK_SALTY Phohoglycerate kinase	16		AQASTHGIGK	146	10	3	33.82	y4y7y8	969.50	16.572	5907	2	485.26	-8.88
[P65702]PGK_SALTY Phohoglycerate kinase	17		DYLDGVDVAEGELVVLENVR	93	20	4	25.17	b7y4y5y7	2204.11	115.431	4425	3	735.37	-1.11
[P65702]PGK_SALTY Phohoglycerate kinase	18		ISYISTGGGAFLEFVEGK	355	18	6	26.5	b5°b5b7b8°b8y14	1874.94	97.868	1826	2	937.97	-8.72
[P65702]PGK_SALTY Phohoglycerate kinase	19		EDEQILDIGDASAQQLAEILK	278	21	4	21.62	b4b7b9y13	2299.13	82.005	1717	3	767.05	-14.97
[P65702]PGK_SALTY Phohoglycerate kinase	20		TDL DLAGKR	6	9	0	2.04		988.53	43.394	15663	2	494.77	-7.84
[P65702]PGK_SALTY Phohoglycerate kinase	21		PAVAMLEER	375	9	2	18.82	b3b5	1015.52	80.314	7948	2	508.26	-6.79
[P65702]PGK_SALTY Phohoglycerate kinase	22		DLNV PVKEGK	20	10	1	7.85	b4	1098.60	37.523	7025	2	549.81	-10.78
[P0AA28]THIO_SALTY Thioredoxin-1	1		LNIDQNPGTAPK	58	12	25	179.09	b2*b2b3b4*b4b6°b6b7°b7b9°b9b10y1y2y4y6y7y8*y8y9*y9y10*y10y11y12	1267.65	39.286	144672	2	634.33	-11.07
[P0AA28]THIO_SALTY Thioredoxin-1	2		MIAPILDEIADEYQGK	37	16	9	64.07	b2y2y3y4y7y10y13y14y16	1805.91	93.645	103927	2	903.46	6.35

P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLLFK	74	9	9	74.75	b3y1y2y3y4y5y6y7y9	1001.63	90.616	88761	2	501.32	-10.91
P0AA28 THIO_SALTY Thioredoxin-1	4		MIAPILDEIADEYQGKLTVAK	37	21	12	113.33	b3y5y7y11y12y13y14y15* y15y16y18y19	2318.22	94.697	119517	3	773.41	-5.37
P0AA28 THIO_SALTY Thioredoxin-1	5		MSDKIHLTDDSFDTDVLK	0	19	5	14.89	b11y9*y9y12*y12	2193.06	104.406	1775	3	731.69	-5.12
P0AA28 THIO_SALTY Thioredoxin-1	6		GIPTLLLLFK	74	9	0	1.63		983.63	90.619	1903	2	492.32	2.05
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	1		SSIPVFGVDALPEALALVK	250	19	17	172.34	b4b5b6b10y2y3y4y5y6y8y 10y11y13y14y15y16y19	1926.11	107.740	90609	2	963.56	7.16
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	2		ALAINLVDPAAGTVIEK	84	18	12	66.38	b3b5*b5b6y2*y2y6y7y10y 11y14y18	1766.01	80.648	76496	2	883.51	2.42
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	3		SGAMAGTVLNDANNQAK	269	17	23	132.16	b2*b2b3b4b9*b9b13b17*b1 7y2y5y6y7y8y9*y9y10y11* y11y12*y12*y12y17	1661.80	46.980	70023	2	831.40	2.57
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	4		VPYVGVDKDNLEFTQK	315	17	4	16.26	b3y11y13y17	1938.96	62.209	40547	3	646.99	-9.88
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	5		GQNPVVFFNKEPSR	104	15	5	29.35	b11y4y5y8*y8	1717.89	67.916	18840	3	573.30	-9.73
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	6		YDDNFMSVVR	34	10	3	33.82	y5y6y9	1245.56	67.038	13235	2	623.29	5.29
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	7		MDAWLSGPNANK	214	12	4	22.21	b11*b11y8y10	1303.60	50.147	11875	2	652.31	-5.24
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	8		SAPDVQLLMNDSQNDQSK	52	18	3	15.53	b9b11y5	1989.95	62.813	1532	2	995.48	15.15
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	9		SAPDVQLLMNDSQNDQSKQNDQI DVLLAK	52	29	5	48.69	b5y3y4y5y6	3227.61	78.283	41758	3	1076.54	7.26
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	10		GQNPVVFFNKEPSR	104	15	3	18.08	b4y4y8	1717.88	62.016	14685	3	573.30	-11.80
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	11		DGKSAPDVQLLMNDSQNDQSK	49	21	4	23.48	b3b7*b7b8	2290.07	77.830	12224	3	764.03	3.09
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	12		AIEKD GK	45	7	5	37.37	b4b5*b5y4*y4	760.43	72.079	7482	1	760.43	10.19
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	13		SGAMAGTVLNDANNQAKATFDL AK	269	24	3	12.67	b9b12y3	2408.17	58.557	5182	2	1204.59	-8.21
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	14		MDAWLSGPNANKIEVVIANNDA MAMGAVEALK	214	32	4	22.1	b12*b12y11y12	3343.60	92.186	4332	5	669.53	-14.31
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	15		IGVTIYKYDDNFMSVVR	27	17	5	16.26	b5y8*y8*y8y11	2020.05	57.247	3378	3	674.02	13.05
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	16	Phosphoryl STY(11)	AYYVGTDSESGVIQGDLIAK	127	21	5	35.75	b9b10y11*y11y12	2294.07	68.350	1747	3	765.36	-6.28

P23905 DGAL_SALTY D-galactose-binding periplasmic protein	17	Oxidation+M()	IEVVIANN DAMAMGAVEALK	226	20	4	14.32	b9y10°y10y15	2075.05	66.999	18437	3	692.35	-2.82
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	18	Oxidation+M(8)	VLTL SAVMASLLFGAHAHAADTR	4	23	3	23.09	y6y7y9	2368.23	78.689	14101	3	790.08	-5.36
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	19		GQNV PVVFFNKEPSR	104	15	0	4.07		1699.91	67.866	7364	3	567.31	14.65
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTASPYASYLQYGHIANIDD IIAGKKPATDLGVK	125	38	38	205.61	b2b3b5°b5*b5b6°b6*b6b7° b7*b7b8°b8*b8b9°b9b10° b10b11b13b26b34y1y3y4y 8y11y12y16y22y25y26y27 y28y30y31y38*y38	4001.02	83.123	265338	5	801.01	-10.50
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		AEQQLDKDSAIVPVYYYVNAR	494	21	14	107.89	b3b5b10°b10b11b12b13y3 y4y5y7y9y10y21	2442.23	73.401	133949	3	814.75	-1.80
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3		WSDGTPVTAHDFVYSWQR	107	18	17	134.58	b2b3b7°b7y3y4y5y6y7y8y9° y9y11y12y13y18*y18	2151.97	72.655	129606	3	718.00	-6.58
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4	Carbamidomethyl+C(4)	AGWCADYNEPTSLNTMLSDSSN NTAHYK	439	29	8	41.26	y2y4y11y15y20y23y24y29	3294.43	90.167	121709	3	1098.82	6.52
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		LVEPEWFK	352	8	10	67.17	y2y3y4°y4y5°y5y6°y6y7y8	1047.54	71.484	112722	2	524.27	-10.84
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		ALDDHTFEVTLSEPVYFYK	163	20	10	52.67	b6b7b8b10°b10y5y7y9°y9y20	2371.15	86.057	97197	3	791.06	0.72
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7		SGEIDMTYNNMPIELFQK	263	18	11	52.4	b2b3b13y2y3y5y7y11y12* y12y18	2130.00	86.675	85069	2	1065.51	6.76
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		TVINQVTYLPISSEVTDVNR	241	20	21	130.14	b8°b8*b8b9b10b12y2*y2y3y4y5y6y8°y8*y8y11y12y14° y14y15y20	2248.20	77.395	78912	2	1124.61	9.45
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9		NQGDLPAYSYTPPYTDGAK	333	19	7	46.75	b10b11y3y11y13y14y19	2057.96	59.933	76453	2	1029.48	7.83
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		NLGVN NVLENQEWK	410	14	7	38.91	b2b3b10y8y11y12y14	1656.84	67.294	54914	2	828.93	5.30
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		NPQYWDNAK	232	9	9	57.4	b2y1y3*y3y4y6y8*y8y9	1135.51	40.322	34678	2	568.26	-3.98
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		NWVVNER	220	7	10	37.37	b1b4*b4b7y3*y3y4°y4y7* y7	916.46	44.284	31994	2	458.73	-7.93
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	13		HQGTFDVAR	430	9	6	45.36	b6y1y3y4y8y9	1030.50	32.952	26913	2	515.75	-4.15
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	14		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	8	25.91	b2b13°b13y3y4y10y22y29	3091.56	88.347	25305	3	1031.19	6.95
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	15		VWTFHLRENAK	96	11	4	36.63	b4b5b9y3	1400.75	61.957	5699	2	700.88	2.79

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	16		LLAEAGFTADKPLTFDLLYNTSDLHK	372	26	3	22.78	b5b9b10	2893.50	88.304	3044	3	965.17	-0.17
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	17		NEEAK	366	5	1	13.19	b4	590.28	64.346	2524	1	590.28	10.86
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	18		TVINQVTYLPISSEVTDVNRYS	241	22	11	84.75	b3y5y13°y13*y13y14y16y17y18y19y20	2567.34	77.239	116211	3	856.45	-2.76
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	19		IVLERNPQYWDNAK	227	14	3	19.22	b11y4y12	1745.88	54.129	54892	3	582.63	-11.82
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	20		FGDKWTQPANIVTNGAYK	200	18	3	24.45	y6y7y11	2009.99	63.611	41751	3	670.67	-7.41
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	21	Carbamidomethyl+C(13)	EIPNEVRVDPYLCITYYYEINNQK	284	23	8	66.69	y4y6y7y8°y8y9y11y21	2920.38	76.449	29974	3	974.13	0.75
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	22		NQGDLPAYSYTPPYTDGAKLVPEEWFK	333	27	4	17.72	b5y5y7y22	3086.49	84.700	18544	3	1029.50	4.83
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	23		VKNQGDLPAYSYTPPYTDGAK	331	21	6	38.49	b6*b6y3y8y9y10	2285.11	55.758	18182	3	762.37	-1.07
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	24		LKNWVVNER	218	9	3	38.19	y4y5y7	1157.63	45.406	17312	2	579.32	-14.02
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	25		NPQYWDNAKTVINQVTYLPISSEVTDVNR	232	29	6	25.91	b12y7*y7y11y12y15	3364.69	101.756	16427	3	1122.23	1.81
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	26		SELYAKAEQQLDK	488	13	4	20.57	b8y6y10*y10	1522.76	68.864	4739	2	761.88	-10.66
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	27		KNLGVNVNLENQEWK	409	15	4	41.39	y4y6y8y13	1784.92	80.338	3082	3	595.65	-4.58
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	28		DSAIVPVYYYVNARLVKPWVGGYTGK	501	26	4	15.73	b8b13y5y8	2915.52	84.502	1944	4	729.63	-9.88
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	29		TFLDTRHQGTDFVAR	424	15	4	18.08	b5y4y7°y7	1763.89	111.701	1739	2	882.45	2.91
P52616 FLJB_SALTY Phase 2 flagellin	1		AQILQQAGTSVLAQANQVPQNVLSLLR	479	27	26	182.68	b2*b2b3b4b5*b5b6b7*b7b11°b11b12b13b17b18y1y2y3y4y5y6y9y10y12y13y27	2860.61	105.253	87276	3	954.21	2.90
P52616 FLJB_SALTY Phase 2 flagellin	2		NANDGISIAQTTEGALNEINNLR	66	25	8	12.37	b6°b6*b6b14°b14*b14y14y25	2670.34	86.747	45033	2	1335.67	11.25
P52616 FLJB_SALTY Phase 2 flagellin	3		AQVINTNSLSLLTQNNLNK	1	19	8	22.67	b2*b2b7°b7b8y1y15y19	2085.14	75.112	44705	2	1043.08	6.44
P52616 FLJB_SALTY Phase 2 flagellin	4		SQSALGTAIER	20	11	9	36.63	b2*b2b10y1y6°y6y7y9y11	1132.59	42.781	41795	2	566.80	-6.79
P52616 FLJB_SALTY Phase 2 flagellin	5		AYANNGTTLDVSGLDAAIK	189	20	10	62.79	b3b6b10b11b12°b12b15y2y6y14	2009.00	78.617	19669	3	670.34	7.96
P52616 FLJB_SALTY Phase 2 flagellin	6		ELAVQSANSTNSQSDLDLSIAEITQR	93	26	10	21.85	b2b6°b6*b6b13°b13y6y10y12y26	2805.36	70.929	16642	3	935.79	2.87
P52616 FLJB_SALTY Phase 2 flagellin	7		YFVTIGGFTGADAAK	234	15	4	29.35	b7b8b11y6	1517.76	73.847	40422	2	759.38	-2.09

P52616 FLJB_SALTY Phase 2 flagellin	8		AQPELAEAAAK	403	11	3	24.23	b3b8y10	1098.56	87.872	4039	2	549.79	-13.56
P52616 FLJB_SALTY Phase 2 flagellin	9		NALIAGGVDATDANGAELVK	299	20	7	27.9	b3b14°b14b16y15°y15y18	1898.99	93.871	2616	3	633.67	3.34
P52616 FLJB_SALTY Phase 2 flagellin	10		QINSQTLGLDSLNVQK	161	16	5	17.1	b4°b4*b4b12y8	1757.93	30.253	1562	3	586.65	-4.44
P52616 FLJB_SALTY Phase 2 flagellin	11		AYANNGTTLDVSGLDDAAIKAAT GGTNGTASVTGGAVK	189	38	3	10.86	b3y13y18	3509.78	107.572	23528	4	878.20	11.55
P52616 FLJB_SALTY Phase 2 flagellin	12		TIEGGYALKAGDK	328	13	5	32.21	b4b5°b5b7y7	1322.69	38.245	19403	3	441.57	-6.74
P52616 FLJB_SALTY Phase 2 flagellin	13		TEVVTIDGKTYNASK	381	15	10	36.97	b6b10°b10y5°y5°y5y8y11° y11°y11	1625.83	70.955	11168	2	813.42	-4.05
P52616 FLJB_SALTY Phase 2 flagellin	14		AATGGTNGTASVTGGAVKFDAD NNK	209	25	3	35.16	y11y12y13	2324.13	97.229	9922	2	1162.57	7.04
P52616 FLJB_SALTY Phase 2 flagellin	15		QINSQTLGLDSLNVQKAYDVK	161	21	5	29.94	b6*b6b12b13b15	2334.22	89.799	6125	3	778.74	-4.29
P52616 FLJB_SALTY Phase 2 flagellin	16		SDLGAVQNRNSAITNLGNTVNN LSEAR	434	28	8	53.63	b3b4°b4y3y10y11y12y14	2975.47	93.728	5795	3	992.49	-7.88
P52616 FLJB_SALTY Phase 2 flagellin	17		LNEIDRVSGQTQFNGVK	119	17	3	16.26	b3b11y4	1905.01	60.124	4323	3	635.67	13.78
P52616 FLJB_SALTY Phase 2 flagellin	18		TYNASKAAGHDFK	390	13	3	20.57	b8b12y3	1409.67	60.891	3903	2	705.34	-6.32
P52616 FLJB_SALTY Phase 2 flagellin	19		TTMPAGATTKTEVQELK	271	17	4	22.84	b3b7y3y9	1805.93	43.647	3371	3	602.65	-0.81
P52616 FLJB_SALTY Phase 2 flagellin	20		TTSYTAADGTTKTAANQLGGVD GK	357	24	4	16.8	b3b12y5y13	2328.17	61.901	2458	2	1164.59	14.89
P52616 FLJB_SALTY Phase 2 flagellin	21		AYDVKDTAVTTK	177	12	5	37.16	b7b9b11°b11y7	1311.68	67.875	2346	2	656.34	-0.09
P52616 FLJB_SALTY Phase 2 flagellin	22		AQPELAEAAAKTTENPLQK	403	19	6	20.62	b10°b10b14y7y13°y13	2010.06	108.449	1674	3	670.69	4.13
P52616 FLJB_SALTY Phase 2 flagellin	23		VRELAVQSANSTNSQSDLSIQAE ITQR	91	28	4	17.69	b5b11°b11b14	3060.52	114.476	1559	4	765.89	0.00
P0A1Z2 SKP_SALTY Chaperone protein skp	1		TGVSNTLENEFK	39	12	20	137.15	b2b3b6°b6b8°b8b9°b9y2y 3y4°y4°y4y5y6y7y8°y8y10 y12	1338.66	58.485	141170	2	669.83	1.09
P0A1Z2 SKP_SALTY Chaperone protein skp	2		IAIVNMGNLFQQVAQK	23	16	19	126.52	b1b2b3b4b8b12b15y1y2°y 2y3y4y6°y6y7y11y12y13y 16	1773.97	89.882	127829	2	887.49	1.31
P0A1Z2 SKP_SALTY Chaperone protein skp	3		VANDQSIDLVDANTVAYNSSDV KIDITADV LK	126	32	17	71.76	b2b6b9°b9b10°b10b11b12 °b12°b12b15b18y1y2y24y 25y32	3392.72	89.893	73222	3	1131.58	4.61
P0A1Z2 SKP_SALTY Chaperone protein skp	4		AQAFEKDR	97	8	7	33.01	b2°b2b3y2y5y6y8	964.48	18.587	35410	2	482.74	-7.85
P0A1Z2 SKP_SALTY Chaperone protein skp	5		KVANDQSIDLVDANTVAYNSSD VK	125	25	4	12.37	b5b14°b14y15	2665.33	92.525	13087	2	1333.17	-1.92
P0A1Z2 SKP_SALTY Chaperone protein skp	6		IAIVNMGNLFQQVAQKTGVSNTL ENEFK	23	28	5	20.44	b8b11y5y8y12	3093.58	102.846	11402	4	774.15	-8.60
P0A1Z2 SKP_SALTY Chaperone protein skp	7		MQRLQSMK	67	8	3	33.01	b6y4y5	1021.52	65.170	6685	2	511.27	-3.29
P0A1Z2 SKP_SALTY Chaperone protein skp	8		AAELQKMETDLQSK	53	14	3	27.79	b4b6b11	1591.78	66.134	3185	3	531.27	-9.51
O33921 AGP_SALTY Glucose-1- phohatase	1		TPIGGQLVFQR	335	11	13	70.79	b1°b1b2°b2b6°b6°b6y3y4y 8y9y10y11	1215.68	62.065	123689	2	608.34	-7.33
O33921 AGP_SALTY Glucose-1- phohatase	2		MGTMDPTEFNPVITDDSAAFR	141	20	18	137.85	b2b5y2y3y5y6y7y8y9°y9y1 1y12y13°y13y14y15°y15y 20	2186.01	78.715	98733	2	1093.51	7.71
O33921 AGP_SALTY Glucose-1- phohatase	3		IEYVYQSAR	358	9	12	90.95	b2b3b6b7b9y1y5y6y7°y7y 8y9	1128.56	43.415	62058	2	564.79	-3.35

O33921 AGP_SALTY Glucose-1-phohatase	4		QQAVQAMEK	161	9	9	67.58	b2*b2y3y4y5y6y7y9*y9	1032.51	27.013	57239	2	516.76	-8.16
O33921 AGP_SALTY Glucose-1-phohatase	5	Carbamidomethyl+C(14)	EWLV AQGLIPSGECPAPDTVYAY ANSLQR	87	29	22	155.08	b4b7°b7b8b9b16y2*y2y3y4y5y6y7*y7y9y10y11*y11y12y13y20y29	3205.58	93.910	42614	3	1069.20	4.11
O33921 AGP_SALTY Glucose-1-phohatase	6		NGYQDSLFTSPTVAR	266	15	7	43.79	b14y1y3y9y10y11y15	1655.80	63.689	37623	2	828.41	0.29
O33921 AGP_SALTY Glucose-1-phohatase	7		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDR	226	31	5	13.8	b8b10*b10y5y16	3486.68	104.508	35955	3	1162.90	10.43
O33921 AGP_SALTY Glucose-1-phohatase	8		APLANNGSVLAQSTPNAWPAWD VPGGQLTTK	43	31	18	60.93	b2b3b7b9°b9b14*b14b17b18y2y3y8*y8y10y13°y13y14y31	3161.62	83.717	30409	3	1054.55	6.41
O33921 AGP_SALTY Glucose-1-phohatase	9		DTFSANYQQEPGVQGPLK	208	18	15	64.62	b2b3°b3b10b12*b12y1y8y11y12y13°y13*y13y15y18	1978.97	57.319	29258	2	989.99	7.96
O33921 AGP_SALTY Glucose-1-phohatase	10	Carbamidomethyl+C(16)	TVATAQFFITGAFPGCDIPVHHQE K	116	25	3	12.37	b13y7y12	2771.32	79.210	27141	4	693.59	-13.92
O33921 AGP_SALTY Glucose-1-phohatase	11	Carbamidomethyl+C(14)	LLEQITHYQDSPSCKEK	182	17	5	29.83	b10b11y7y10y17	2075.99	48.592	14905	3	692.67	-6.70
O33921 AGP_SALTY Glucose-1-phohatase	12	Carbamidomethyl+C(3)	HQCSLIDAK	199	9	6	30.41	b2*b2b5y2y4y7	1071.52	32.930	9836	2	536.26	-2.73
O33921 AGP_SALTY Glucose-1-phohatase	13		VTVLVGHDNSNIASLLTALDFKPYQ LHDQYER	304	31	16	91.74	b4b10*b10b12°b12b14y4°y4*y4y5y6y7y10y15y16y17	3542.77	96.021	196078	5	709.36	-17.02
O33921 AGP_SALTY Glucose-1-phohatase	14		SQLHLDSEYK	172	10	4	26.83	b8y3y6°y6	1219.59	41.102	14596	2	610.30	-1.50
O33921 AGP_SALTY Glucose-1-phohatase	15		GGVLEVYMGHYTR	74	13	4	34.34	b11b12y8y10	1481.69	57.263	2060	2	741.35	-19.94
O33921 AGP_SALTY Glucose-1-phohatase	16		LKNGYQDSLFTSPTVAR	264	17	12	122.65	b9*b9b10b11b12y4y5y6y7y8y12y15	1896.96	59.423	83484	3	632.99	-13.06
O33921 AGP_SALTY Glucose-1-phohatase	17	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	GCPVDANGFCPLDKFDNMNTA AK	389	24	9	39.31	b4y3y10y14°y14*y14y20y22°y22	2641.19	78.688	73112	3	881.07	1.39
O33921 AGP_SALTY Glucose-1-phohatase	18		HNLRAPLANNGSVLAQSTPNAWP AWDVPGGQLTTK	39	35	3	22.99	b12b13b22	3681.86	78.255	68859	4	921.22	-7.36
O33921 AGP_SALTY Glucose-1-phohatase	19		MGTMDPTFNPNVITDDSAAFRQQA VQAMEK	141	29	10	58.96	b3b5b13y3y4y5°y5y21y24y25	3199.51	81.952	42296	3	1067.17	7.48
O33921 AGP_SALTY Glucose-1-phohatase	20		NAEALTLSKSPAQR	370	13	4	49.03	y4y5y6y7	1398.77	42.082	38810	2	699.89	-2.79
O33921 AGP_SALTY Glucose-1-phohatase	21		QQAVQAMEKAR	161	11	4	24.23	b7b10°b10y8	1259.66	64.397	15577	2	630.33	6.11
O33921 AGP_SALTY Glucose-1-phohatase	22	Oxidation+M(8)	GGVLEVYMGHYTR	74	13	4	20.57	b5°b5b12y12	1497.71	96.965	1722	2	749.36	-3.67
O33921 AGP_SALTY Glucose-1-phohatase	23		QQAVQAMEK	161	9	0	1.63		1015.48	27.004	1713	2	508.24	-4.69
P00924 ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	17	126.97	b2*b2b3*b3b4b6b7y2y3y5y6y7y8y10*y10y12*y12	1286.71	66.650	97116	2	643.86	-3.23
P00924 ENO1_YEAST Enolase 1	2		VNQIGTLESSEIK	346	12	7	49.56	b2b8y5y8y9y10y12	1288.71	55.091	95583	2	644.86	-3.88
P00924 ENO1_YEAST Enolase 1	3		SIVPSGASTGVHEALEMR	32	18	16	125.37	b2b9°b9b12b13y2y3y5y6y9y10y11°y11y14y15y16	1840.90	61.998	71620	3	614.31	-9.68
P00924 ENO1_YEAST Enolase 1	4		TAGIQIVADDLTVTNPK	312	17	10	66.39	b3b14b15y6y8y10*y10y11y13y17	1755.95	72.882	57129	2	878.48	3.06
P00924 ENO1_YEAST Enolase 1	5		IEEELGDNAVFAGENFHHGDK	415	21	7	36.11	b7b8b10b12*b12y8y13	2328.04	81.342	6710	4	582.77	-3.88
P00924 ENO1_YEAST Enolase 1	6		IGSEVYHNLK	185	10	5	40.99	b5°b5b6y3y7	1159.59	55.564	2659	2	580.30	-14.21
P00924 ENO1_YEAST Enolase 1	7		AADALLLK	338	8	7	93.55	b3b6y3y4y5y6y7	814.49	54.378	71318	2	407.75	-16.11

P00924 ENO1_YEAST Enolase 1	8		IATAIEK	330	7	5	53.57	y3y4y5y6°y6	745.43	29.004	27993	2	373.22	-20.88
P00924 ENO1_YEAST Enolase 1	9		NVPLYK	126	6	3	26.79	b3*b3y4	733.42	37.600	19038	1	733.42	-8.57
P00924 ENO1_YEAST Enolase 1	10		YGASAGNVGDEGGVAPNIQTAEELDLDLIVDAIK	201	33	4	11.04	b7b16°b16y3	3257.68	101.619	9947	3	1086.56	17.76
P00924 ENO1_YEAST Enolase 1	11		YDLDFK	258	6	5	56.18	b4b5y3y5°y5	800.39	99.847	9036	1	800.39	6.48
P00924 ENO1_YEAST Enolase 1	12		HLADLSK	132	7	3	37.37	b4y3y4	783.43	30.340	3619	1	783.43	-13.17
P00924 ENO1_YEAST Enolase 1	13		SGETEDTFIADLVVGLR	375	17	3	16.26	b8b14y14	1821.90	87.581	3408	2	911.46	-10.92
P00924 ENO1_YEAST Enolase 1	14		WLTGPQLADLYHSLMK	272	16	3	25.47	b3b8b9	1872.99	91.637	3389	2	937.00	10.04
P00924 ENO1_YEAST Enolase 1	15		WMGK	56	4	1	12.78	y3	521.26	24.780	1946	1	521.26	2.11
P00924 ENO1_YEAST Enolase 1	16		AAQDSFAAGWGVMSVSHR	358	17	3	23.66	b3b11b15	1789.84	95.450	1789	2	895.42	-3.55
P00924 ENO1_YEAST Enolase 1	17		SKWLTGPQLADLYHSLMK	270	18	4	15.53	b3y6°y6y9	2088.11	84.733	330419	3	696.71	7.48
P00924 ENO1_YEAST Enolase 1	18		WMGKGVLHAVK	56	11	3	24.23	b5b7y3	1225.70	40.775	28655	3	409.24	11.55
P00924 ENO1_YEAST Enolase 1	19		IEEELGDNVAFAGENFHHGDKL	415	22	5	40.32	b3b4b5y7y12	2441.13	64.592	16883	3	814.38	-1.70
P00924 ENO1_YEAST Enolase 1	20		AAQDSFAAGWGVMSVSHRSGETE DTFIADLVVGLR	358	34	3	22.28	b8b9y31	3592.77	99.784	14936	4	898.95	5.91
P00924 ENO1_YEAST Enolase 1	21		DQKAVDDFLISLDGTANK	85	18	6	29.06	b5°b5*b5b10y5y6	1950.00	74.325	5497	3	650.67	7.89
P00924 ENO1_YEAST Enolase 1	22		VYARSVYDSR	5	10	4	28.59	b6°b6b7y3	1215.63	26.324	2024	2	608.32	12.95
P00924 ENO1_YEAST Enolase 1	23	Phosphoryl STY(12)	TAGIQIVADDLTVTNPKR	312	18	7	48.08	b5*b5b10b12b13y11y12	1992.00	93.812	2286	3	664.67	-4.60
P00924 ENO1_YEAST Enolase 1	24	Oxidation+M(17)	SIVPSGASTGVHEALEMR	32	18	3	15.53	b7y11y15	1856.91	54.554	15282	3	619.64	-6.38
P00924 ENO1_YEAST Enolase 1	25		PSGASTGVHEALEMR	35	15	2	13.48	b8b13	1541.74	61.986	4132	2	771.37	2.53
P00924 ENO1_YEAST Enolase 1	26		ADDLTVTNPK	319	10	0	4.88		1073.54	72.923	1647	2	537.27	-11.37
P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	19	126.15	b2*b2b3*b3b4b6y2y3°y3*y3y4y5y6y7*y7y8*y8y9y10	1129.61	39.770	78024	2	565.31	-8.32
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	5	27.79	y2y4y7y9y14	1452.65	58.177	53074	2	726.83	2.44
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3		TPPAAVLLK	72	9	4	38.19	y5y7y8y9	909.57	55.003	41494	2	455.29	-11.07
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4		GLPIPVITVYADR	51	14	5	19.22	b4y1y5y10y14	1512.88	91.259	28673	2	756.94	0.16
P0A7K0 RL11_SALTY 50S ribosomal protein L11	5		AQLQEIAQTKAADMTGADIEAMTR	103	24	5	23.36	b9y5y6°y6y9	2563.27	75.877	3846	3	855.10	8.95
P0A7K0 RL11_SALTY 50S ribosomal protein L11	6		SGSGKPNKDK	87	10	3	33.82	b6b8b9	1017.52	33.953	1998	2	509.26	-14.10
P0A7K0 RL11_SALTY 50S ribosomal protein L11	7		PAAVLLK	74	7	0	1.63		711.48	54.959	1837	1	711.48	9.09
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTSDSAVGNAVK	84	17	16	142.37	b2b3b4b5y5y7y8y9y10y11y12*y12y13*y13y14y17	1739.95	71.264	110910	2	870.48	-0.28
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	2		LAATIAQLPDQIGAK	253	15	12	88.8	b2b4°b4y3y4y6y7y8y9*y9y10y15	1509.87	66.932	52652	2	755.44	1.94
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	3		VIELQGIAGTSAAR	150	14	11	112.83	b1b3y4y5y6y7y9y10y11y12y14	1385.78	59.734	40088	2	693.39	1.94
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	4		GLNVMQNLLTAHPDVQAVFAQNDEMALGALR	193	31	6	22.91	b11y4y6y8y11y31	3336.71	102.670	35552	3	1112.91	7.02
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	5		ADVMMVVGFDGTPDGEK	231	16	6	42.53	b5°b5y7y10y11y12	1636.78	64.281	20066	2	818.89	14.69
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	6		FNVLASQPADEFDR	178	13	7	54.4	b3b7*b7y3y6y9y10	1479.72	66.998	11355	2	740.37	0.91
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	7		GDVVSHIASDNVLGGK	119	16	4	24.17	b13b15y4y15	1567.82	74.302	9805	2	784.41	5.45
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	8		DTIALVISTLNNPFFVSLKDGAQKEADK	26	28	8	25.27	b2°b2y1y4y8*y8y19y25	3034.57	114.497	9222	4	759.40	-13.03
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	9		IPVITLDR	107	8	3	33.01	b3y5y6	926.55	62.487	59821	2	463.78	-16.34
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	10		ELANVQDLTVR	70	11	11	89.54	b3°b3b4°b4b6b8°b8b10y6*y6y8	1257.67	58.486	14591	2	629.34	-8.35

[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	11		LVIK	291	4	1	12.78	y3	472.35	57.004	10197	1	472.35	-7.69
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	12		MANQAK	101	6	1	13.6	b5	662.34	54.220	5613	1	662.34	15.02
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	13		GEGFQQAVAAHK	166	12	9	59.44	b3°b3b5b7b8°b8°b8y4y9	1242.61	35.295	3527	2	621.81	-6.68
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	14		GTKILLINPTSDAVGNAVK	81	20	7	23.74	y9*y9y10*y10y12°y12*y12	2026.10	58.464	17728	3	676.04	-10.54
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	15		FNVLASQPADFRTK	178	15	4	31.72	b11b12y7y10	1708.84	60.807	14451	3	570.29	-13.64
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	16		ADVMVVGFDGTPDGEKAVK	231	19	13	75.21	b3°b3b5b6°b6b9b12b14°b14y3y12y13°y13	1934.94	60.887	9071	3	645.65	-9.08
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	17	Phosphoryl STY(9)	ILLINPTSDAVGNAVK	84	17	3	16.26	b9b13y8	1819.90	91.140	4102	3	607.30	-7.04
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	1		NNLAIVGFSTPNVMRPYVQR	237	20	16	88.11	b2°b2b3°b3b4°b4b5°b5y5y12°y12y14y15y16y17y20	2276.18	78.232	124280	3	759.40	-5.26
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	2		AYPDLDAIHAPDANALPAAAQAAE NLKR	209	28	13	87.37	b2b7b8°b8b9b10y9y12y18y19y20y23y28	2863.50	87.659	121405	3	955.17	1.36
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	3		ISQEHPGWEIVTTQFGYNDATK	177	22	14	98.02	b5b9b11b13°b13y4y5*y5y6y7y8y9*y9y22	2521.20	73.234	80802	3	841.07	1.07
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	4		VAFFYSSPTVTDQNQWVK	154	18	11	79.86	b5b6b9b12y8°y8y11y12y13y14y18	2117.05	77.964	60179	2	1059.03	7.38
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	5	Carbamidomethyl+C(12)	ILTWSDTKPECR	111	13	10	62.57	b1b2b9y2y4y6y7y8y9y13	1620.75	50.912	59771	3	540.92	-10.02
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	6		LVGVGFFTSGGNGAQEAGK	35	19	19	96.36	b1b2b4b6b12b16y1y3y4y5*y5y7°y7*y7y11y12°y12y17y19	1795.92	89.885	59644	3	599.31	12.23
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	7		ISVYVANALLK	273	11	8	65.38	b2y2y3y5y6y7y8y11	1190.71	74.019	57897	2	595.86	-5.74
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	8		SLQTAEGIIK	199	10	5	33.82	y2y4y6y7y10	1059.60	51.762	48897	2	530.30	-6.80
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	9		NMPMNVGDSLDIPGIGK	284	17	12	44.94	b2b6b12b13°b13y2y11y14*y14y15*y15y17	1757.87	79.768	43550	2	879.44	5.56
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	10		VTVSPNSEQGYHYEAK	301	16	14	121.19	b8y2y4°y4y5y7y8°y8y9y10y12y14y15y16	1808.82	37.215	43272	3	603.61	-14.51
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	11		GTVKEFGLWDVVQQGK	257	16	8	28.25	b7°b7y4*y4y7*y7y8y16	1790.92	76.507	36753	3	597.64	-13.97
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	12		EFGLWDVVQQGK	261	12	11	63.42	b3b4b5°b5b10y1y2y3*y3y4y12	1405.71	82.740	27758	2	703.36	-1.13
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	13		VIFNKDNIDK	327	10	5	28.59	b1b9y7y8y10	1205.67	77.867	4071	2	603.34	11.85
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	14		NGGIVLLPER	317	10	4	51.78	y3y4y5y6	1067.61	62.097	26008	2	534.31	-9.95
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	15		AYPDLDAIHAPDANALPAAAQAAE NLK	209	27	4	27.08	b3b11b12b14	2707.38	65.482	3457	3	903.13	-3.97
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	16		AKISQEHPGWEIVTTQFGYNDAT K	175	24	4	12.67	b7b12°b12y7	2720.33	69.469	12304	3	907.45	-1.35
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	17		AKVAFFYSSPTVTDQNQWVK	152	20	3	21.11	y8y10y12	2316.18	82.978	10333	2	1158.59	7.06
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	18	Carbamidomethyl+C(12)	ILTWSDTKPECRSYIINQGTPK	111	23	3	13.01	b11y3y6	2772.34	111.202	3573	3	924.79	4.67
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	19	Oxidation+M(5)	QLGSMLEVMAAHQVDK	134	16	5	44.35	b5b11y8y9y10	1772.87	115.296	5317	2	886.94	1.93
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	20	Oxidation+M(9)	QLGSMLEVMAAHQVDKEK	134	18	4	22.93	b4°b4b5y6	2030.01	67.741	2212	3	677.34	1.80
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	21		AYPDLDAI	209	8	0	9.36		877.43	87.614	1678	1	877.43	-3.62

P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	19	187.51	b2b3b4b5b6b8b10y3°y3y4y5y6°y6y7°y7y8y9y10y12	1196.58	65.005	260922	2	598.80	-8.98
P0A9Y9 CC_SALTY Cold shock-like protein cC	2		GFGFITPADGSKDVFVHFSAIQGN GFK	15	27	8	38.99	b2b3b4y4y6y10y21y27	2843.38	87.388	64831	4	711.60	-10.99
P0A9Y9 CC_SALTY Cold shock-like protein cC	3		DVFVHFSAIQNGGFK	27	15	5	18.08	b6y4*y4y11y15	1665.85	54.761	4995	3	555.95	6.08
P0A9Y9 CC_SALTY Cold shock-like protein cC	4		TLAEGQNVEFEIQDGQK	42	17	4	16.26	b4b10*b10y9	1905.93	56.160	1730	2	953.47	3.97
P0A9Y9 CC_SALTY Cold shock-like protein cC	5		WFNESKGFGFITPADGSK	9	18	5	32.63	b3b5b6y4y7	1987.96	73.217	5097	2	994.48	0.74
Q8ZQT5 TOLB_SALTY Protein tolB	1		VSDYDGYNQFVVHR	183	14	4	27.79	y2y4y7y9	1698.77	54.642	110864	3	566.93	-10.06
Q8ZQT5 TOLB_SALTY Protein tolB	2		SNNTEPTWFPDSQTLAFTSDQAG RPQVYK	287	29	16	69.21	b4°b4b5°b5*b5y2y11*y11y12y14°y14y20y21y22y24y29	3285.56	77.886	93508	3	1095.86	4.38
Q8ZQT5 TOLB_SALTY Protein tolB	3		IEITQGVSARPIGVVPPFK	24	19	13	56.41	b2b8*b8b9b11°b11y1y2y3y14y15y16y19	2026.11	70.907	65015	3	676.04	-13.25
Q8ZQT5 TOLB_SALTY Protein tolB	4		WAGPGAAPEDIGGIVAADLR	43	20	13	90.64	b4b6b7b13b14°b14y2y4y5y6y13y14y20	1935.99	85.637	48742	2	968.50	0.95
Q8ZQT5 TOLB_SALTY Protein tolB	5		LPATDGQVK	413	9	5	54.39	y5y6y7y8y9	928.51	28.635	47968	2	464.76	2.70
Q8ZQT5 TOLB_SALTY Protein tolB	6		MNINGGAAQR	316	10	12	88.34	b2*b2b3b4y1y3y6y7*y7y8y9y10	1031.49	28.728	44319	2	516.25	-11.12
Q8ZQT5 TOLB_SALTY Protein tolB	7		SPQPLMSPA WSPDGSK	197	16	4	38.79	y3y5y9y13	1684.81	63.324	44069	2	842.91	6.45
Q8ZQT5 TOLB_SALTY Protein tolB	8		IAYVVQTNGGQFPYELR	166	17	10	60.8	y2y5°y5y6y9y11y12*y12y13*y13	1955.02	73.725	40956	2	978.01	6.87
Q8ZQT5 TOLB_SALTY Protein tolB	9		SALVIQTLANGAVR	223	14	9	73.95	b3b4y2y5y7y8y9y10y14	1412.82	71.265	38150	2	706.91	-2.07
Q8ZQT5 TOLB_SALTY Protein tolB	10		TGSLNLYVMDLASGQIR	264	17	3	16.26	b12y3y9	1837.95	89.572	15471	2	919.48	-0.33
Q8ZQT5 TOLB_SALTY Protein tolB	11		LAFALSK	257	7	4	50.56	b4y3y5y6	749.44	57.093	10230	2	375.22	-17.51
Q8ZQT5 TOLB_SALTY Protein tolB	12		HNGAPAFSPDGTK	244	13	3	20.57	b5y4y6	1298.61	67.898	8109	2	649.81	0.94
Q8ZQT5 TOLB_SALTY Protein tolB	13		QITDGR	281	6	1	13.6	y3	689.35	82.298	3456	1	689.35	-13.28
Q8ZQT5 TOLB_SALTY Protein tolB	14		HNGAPAFSPDGTKLAFALSK	244	20	9	88.58	b3b4b5b6b7b9b11b14y3	2029.04	67.075	32737	3	677.02	-6.08
Q8ZQT5 TOLB_SALTY Protein tolB	15		SPQPLMSPA WSPDGSKLAYVTFES GR	197	26	5	27.39	b12y5y6y15y23	2808.37	81.271	31533	3	936.80	3.04
Q8ZQT5 TOLB_SALTY Protein tolB	16		VSDYDGYNQFVVHRSPQPLMSPA WSPDGSK	183	30	3	11.36	b3y3y8	3364.54	70.466	4419	4	841.89	-7.98
Q8ZQT5 TOLB_SALTY Protein tolB	17		QVASFPRHNGAPAFSPDGTK	237	20	5	35.96	b12y6°y6y7y8	2084.01	88.706	1963	2	1042.51	-7.97
P66932 TIG_SALTY Trigger factor	1		NVALEEQA VEAVLAK	399	15	19	134.57	b1*b1b2b3b4b8°b8b12b13b14y1y2y3y4y5y11y12y13y15	1583.86	80.286	54690	2	792.43	-1.62
P66932 TIG_SALTY Trigger factor	2		ANDIDVPSALIDSEIDLRR	296	20	10	63.46	b2b3b4b5b7b13b14y1y14y16	2211.16	90.613	43228	3	737.72	-1.77
P66932 TIG_SALTY Trigger factor	3		GLIEEMASAYEDPKEVIEFYK	368	22	7	37.61	b2b6b7y5y6y8y22	2548.18	81.897	27561	3	850.06	-14.75
P66932 TIG_SALTY Trigger factor	4		ELPELTEEFIKR	243	12	5	22.21	b7°b7y4y10y12	1503.79	71.797	16903	3	501.93	-13.47
P66932 TIG_SALTY Trigger factor	5		FGVEDGSVAGLR	255	12	8	47.04	b2b3b9b11y1y7y9y12	1206.61	58.026	14753	2	603.81	-4.35
P66932 TIG_SALTY Trigger factor	6		INPAGAPNYVPGEYK	83	15	7	48.25	b9b10b12y3y8*y8y10	1589.79	62.040	13160	2	795.40	-5.22

P66932 TIG_SALTY Trigger factor	7		VTIDFTGSVDGEEFEGGK	163	18	5	22.93	b2°b2b9y5y6	1886.87	53.288	9696	4	472.47	2.52
P66932 TIG_SALTY Trigger factor	8		ANDIDVPSALIDSEIDVLR	296	19	11	40.21	b4°b4*b4b6°b6b15*b15y3y13y14y19	2055.07	94.681	9392	2	1028.04	6.18
P66932 TIG_SALTY Trigger factor	9		ATSFNELMNQQA	420	12	3	26.19	b8b9y11	1353.61	50.686	4725	3	451.87	-2.34
P66932 TIG_SALTY Trigger factor	10		ELFEEQAK	334	8	7	50.97	b2b5b7y2y5y6y8	993.50	63.845	4713	2	497.26	14.74
P66932 TIG_SALTY Trigger factor	11		NKELMDNMR	390	9	6	30.41	b1b3°b3*b3b4y7	1150.53	36.214	4685	2	575.77	-5.84
P66932 TIG_SALTY Trigger factor	12		MQVSVETTQGLGR	0	13	3	20.57	b7b10y6	1405.71	59.304	3030	2	703.36	-2.26
P66932 TIG_SALTY Trigger factor	13		MIPGFEDGVK	193	10	4	40.02	b3b4b6y7	1092.52	59.150	9539	2	546.76	-19.11
P66932 TIG_SALTY Trigger factor	14		ATDFVLAMGQGR	181	12	9	82.17	b4b5°b5b8°b8y4y6y8y11	1265.62	57.453	2758	2	633.31	-9.26
P66932 TIG_SALTY Trigger factor	15		VTITIAADSIETAVK	14	15	4	24.1	b11°b11b12y9	1531.83	76.552	2669	2	766.42	-20.24
P66932 TIG_SALTY Trigger factor	16		VTIDFTGSVDGEEFEGGKATDFVLAMGQGR	163	30	8	26.26	b10b13°b13y4y8*y8y12y14	3133.48	79.501	16094	3	1045.16	-1.01
P66932 TIG_SALTY Trigger factor	17		AGEEFTIDVTFPEEYHAENLK GK	206	23	4	34.85	b9b10b11°b11	2624.27	62.590	11636	3	875.43	8.56
P66932 TIG_SALTY Trigger factor	18		EKINPAGAPNYVPGEYK	81	17	3	16.26	b11b14y11	1846.92	76.365	11089	3	616.31	-6.08
P66932 TIG_SALTY Trigger factor	19		RFGVEDGSVAGLR	254	13	3	35.04	b6b7b8	1362.69	49.859	6043	3	454.90	-13.08
P66932 TIG_SALTY Trigger factor	20	Phosphoryl.STY(6)	ELPELTEEFIKR	243	12	4	36.07	b4b10y7_H3PO4 y7y8	1583.76	70.394	4769	2	792.39	1.39
P66932 TIG_SALTY Trigger factor	21	Oxidation+M()	GLIEEMASAYEDPKEVIEFYSK	368	22	5	20.79	b3b6b10°b10y11	2564.22	82.158	4328	2	1282.61	4.28
P66932 TIG_SALTY Trigger factor	22	Oxidation+M(1)	MQVSVETTQGLGR	0	13	4	39.2	b4b5b6y8	1421.71	73.814	1849	2	711.36	0.00
P0A1E3 CYSK_SALTY Cysteine synthase A	1		YLSTALFADLFTEKELQQ	305	18	18	105.57	b2b4°b4b5°b5b8b11b15b16y2y5y6y7°y7*y7y8y12y18	2117.10	102.319	86257	2	1059.05	8.30
P0A1E3 CYSK_SALTY Cysteine synthase A	2		GVLKPGVELVEPTSGNTGIALAYVAAAR	56	28	5	26.78	y3y4y7y17y28	2753.52	81.521	78100	3	918.51	1.33
P0A1E3 CYSK_SALTY Cysteine synthase A	3		IQGIGAGFIPGNLDLK	226	16	9	41.18	b2*b2b3b4y2y3y7y10y16	1612.91	83.530	74085	2	806.96	0.23
P0A1E3 CYSK_SALTY Cysteine synthase A	4		YLLLQQFSNPANPEIHEK	137	18	11	49.88	b2b3b5b12°b12b13°b13y3y7y9y18	2141.09	74.374	63620	3	714.37	-5.02
P0A1E3 CYSK_SALTY Cysteine synthase A	5		LTLTMPETMSIER	87	13	12	58.41	b2°b2b13°b13y1y6y8y9°y9y10y12y13	1521.77	74.339	58557	2	761.39	2.41
P0A1E3 CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	9	77.4	b2b3b4b5y6y8y9y10y12	1283.72	64.657	30816	2	642.36	-7.61
P0A1E3 CYSK_SALTY Cysteine synthase A	7		ALGANLVLTEGAK	105	13	5	29.82	b2y5y7y11y13	1256.72	61.850	23892	2	628.86	0.49
P0A1E3 CYSK_SALTY Cysteine synthase A	8		IYEDNSLTIGHTPLVR	3	16	3	17.1	b8y7y14	1827.93	62.295	46535	3	609.98	-13.89
P0A1E3 CYSK_SALTY Cysteine synthase A	9		IGNGR	22	5	2	26.38	b4y4	516.28	37.506	43796	1	516.28	-14.30
P0A1E3 CYSK_SALTY Cysteine synthase A	10		AEEIVASDPQK	126	11	3	24.23	b5b7y8	1186.62	64.268	4272	2	593.81	19.44
P0A1E3 CYSK_SALTY Cysteine synthase A	11		VVGITNEEAISTAR	246	14	7	50.55	b9b11y3y7y12y13°y13	1459.78	53.200	1837	2	730.39	4.77
P0A1E3 CYSK_SALTY Cysteine synthase A	12		IGANMIWDAEK	44	11	3	35.99	b5b6b7	1247.62	59.313	1704	2	624.31	6.46
P0A1E3 CYSK_SALTY Cysteine synthase A	13		TDLITVAVEPTDSPVIAQALAGEEIKPGPHK	195	31	4	13.8	b6b11y10y14	3196.72	106.351	1584	4	799.93	2.21

[P0A1E3]CYSK_SALTY Cysteine synthase A	14		LIDKVVGITNEEAISTAR	242	18	5	47.23	y4y5y10y12y13	1929.07	60.326	66283	2	965.04	3.29
[P0A1E3]CYSK_SALTY Cysteine synthase A	15		GKTDLTITVAVEPTDSPVIAQALAG EEIKPGPHK	193	33	5	21.85	b14y5y11y20y22	3381.79	79.641	64305	4	846.20	-10.61
[P0A1E3]CYSK_SALTY Cysteine synthase A	16		AEEIVASDPQKYLLLLQQFSNPANP EIHEK	126	29	7	43.61	b3b4b5°b5y7y9y11	3308.66	77.261	31887	4	827.92	-7.31
[P0A1E3]CYSK_SALTY Cysteine synthase A	17		RLMEEEGILAGISSGA AVAAALK	260	23	4	19.41	b7b9b12°b12	2257.20	90.528	6953	3	753.07	-11.36
[P0A1E3]CYSK_SALTY Cysteine synthase A	18		LMEEEGILAGISSGA AVAAALKLQ EDESFTNK	261	32	3	11.13	b8b10y11	3292.65	126.387	2381	3	1098.22	-3.41
[P0A1E3]CYSK_SALTY Cysteine synthase A	19	Phosphoryl STY(11)	TDLITVAVEPTDSPVIAQALAGEEI KPGPHK	195	31	3	11.23	b9y5y22	3276.70	128.618	31740	3	1092.90	9.16
[P0A1E3]CYSK_SALTY Cysteine synthase A	20	Phosphoryl STY(8)	NIVVILPSSGER	293	12	4	26.19	b10y3°y3y4	1363.68	70.514	1636	2	682.34	-9.31
[P0A1E3]CYSK_SALTY Cysteine synthase A	21		LTMPETMSIER	89	11	1	7.42	b4	1307.64	74.336	10445	3	436.55	6.91
[P0A1D3]CH60_SALTY 60 kDa chaperonin	1		GYLSPYFINKPETGAVELESPFILL ADKK	197	29	21	136.22	b2b3b4°b4b7b11y1y2y3y4 y5y6y7y9y11y13y19y22y25y26y29	3239.71	95.619	138769	4	810.68	-3.17
[P0A1D3]CH60_SALTY 60 kDa chaperonin	2		EMLPVLEAVAK	231	11	12	86.99	b2°b2b3y1y2y3y4y5y6y7y8y11	1199.66	80.236	110698	2	600.33	-6.72
[P0A1D3]CH60_SALTY 60 kDa chaperonin	3		ANDAAGDGT TTATVLAQSIITEGL K	80	25	20	158.44	b2b3°b3b4°b4°b4b5b6b14 b15°b15y3y4y5y6y7y8y9y10y25	2418.22	92.160	93635	3	806.75	-4.85
[P0A1D3]CH60_SALTY 60 kDa chaperonin	4	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDL PK	501	25	18	139.52	b4b5°b5b6b7°b7b8b9b10b13y2y3y4y5y6y8y11°y11	2670.32	124.224	69495	3	890.78	0.91
[P0A1D3]CH60_SALTY 60 kDa chaperonin	5		VVINKD TTTIIDGVGEEAAIQGR	322	23	18	114.55	b1b13b14y2y3y4y5y6y7°y7y8°y8y9°y9y13°y13y17y23	2399.27	67.953	66061	3	800.43	-1.22
[P0A1D3]CH60_SALTY 60 kDa chaperonin	6		GVNVLADAVK	18	10	7	54.79	b2y3y4y6y8°y8y10	985.55	56.732	54145	2	493.28	-13.87
[P0A1D3]CH60_SALTY 60 kDa chaperonin	7		AVAAAVEELK	122	10	7	57.98	b2b3y5y6y7y8y10	1000.56	48.035	43277	2	500.78	-7.02
[P0A1D3]CH60_SALTY 60 kDa chaperonin	8		QQIEEATSDYDREK	350	14	7	38.91	b6°b6b8y5y7y8y14	1711.75	34.296	41651	3	571.26	-14.98
[P0A1D3]CH60_SALTY 60 kDa chaperonin	9	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	7	46.69	b9b13y5y13y14y15y18	1957.02	62.420	39284	2	979.01	5.05
[P0A1D3]CH60_SALTY 60 kDa chaperonin	10		VEDALHATR	395	9	6	67.58	y3y4°y4y6y7y8	1011.51	26.880	30963	2	506.26	-9.29
[P0A1D3]CH60_SALTY 60 kDa chaperonin	11	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	7	40.02	b3°b3y2y5y6y8y10	1063.50	36.061	29475	2	532.25	-5.97
[P0A1D3]CH60_SALTY 60 kDa chaperonin	12		SFGAPTITK	42	9	8	53.14	b2b3y1y2y3y5y7y9	921.49	45.654	28934	2	461.25	-13.25
[P0A1D3]CH60_SALTY 60 kDa chaperonin	13		AVAAGMNPMDLK	105	12	12	112.81	b2b4b8y3y5y7y8y9y10y11°y11y12	1217.60	59.133	26351	2	609.30	-3.01
[P0A1D3]CH60_SALTY 60 kDa chaperonin	14		AIAQVGTISANSDETVGK	142	18	9	52.67	y2y9y10°y10y11y13°y13y14y18	1760.91	49.183	25075	2	880.96	4.85
[P0A1D3]CH60_SALTY 60 kDa chaperonin	15		GGDGNYGYNAAATEEYGNMIDMG ILDPTK	470	28	6	49.97	y3y4y5y10y11y28	2966.32	88.462	12731	2	1483.66	11.77
[P0A1D3]CH60_SALTY 60 kDa chaperonin	16		GQNEQNVGKIK	430	11	7	24.23	b2°b2b9y3y9°y9y11	1201.58	27.823	9916	2	601.29	-0.91
[P0A1D3]CH60_SALTY 60 kDa chaperonin	17		GYLSPYFINKPETGAVELESPFILL ADK	197	28	7	25.44	b2b4b12y2y3y4y24	3111.65	102.209	3478	3	1037.89	5.65
[P0A1D3]CH60_SALTY 60 kDa chaperonin	18		AMEAPLR	445	7	8	40.38	b1b2b6°b6y2y4y6°y6	787.41	37.550	3265	1	787.41	-10.23
[P0A1D3]CH60_SALTY 60 kDa chaperonin	19		EGVITVEDGTGLQDEL DVVEGMQ FDR	171	26	7	27.96	b8°b8b12b14y3y10y12	2851.37	104.738	3230	3	951.13	12.50

[P0A1D3]CH60_SALTY 60 kDa chaperonin	20		DTTTHIDGVGEEAAIQGR	327	18	5	15.53	b5b12°b12y12°y12	1845.90	87.685	2272	2	923.45	-11.11
[P0A1D3]CH60_SALTY 60 kDa chaperonin	21		LAGGVAVIK	371	9	3	30.41	b4y7y8	827.52	45.742	54740	2	414.26	-17.78
[P0A1D3]CH60_SALTY 60 kDa chaperonin	22		ATLEDLGQAK	311	10	3	26.83	b6b9y9	1045.55	44.917	12104	2	523.28	-4.79
[P0A1D3]CH60_SALTY 60 kDa chaperonin	23		FENMGAQMVK	65	10	4	26.83	b3b6y7*y7	1154.54	36.365	1902	3	385.52	4.23
[P0A1D3]CH60_SALTY 60 kDa chaperonin	24		FGNDAR	7	6	1	13.6	y4	679.32	77.189	1824	1	679.32	0.18
[P0A1D3]CH60_SALTY 60 kDa chaperonin	25		IADLKGQNEQNVGIK	425	16	15	153.69	b3b9b10b11y3y4y6y7y8y9y11*y11y14y15*y15	1741.88	40.712	82822	3	581.30	-13.81
[P0A1D3]CH60_SALTY 60 kDa chaperonin	26	Carbamidomethyl+C(16)	AVAAAVEELKALSVP CSDSK	122	20	6	38.71	b5b8y4y6y10y18	2045.04	72.413	40366	3	682.35	-7.34
[P0A1D3]CH60_SALTY 60 kDa chaperonin	27		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	18	118.53	b3b4b6b8b10*b10b13y5y6y7y10y16y20y21y24y25y26y29	3675.89	122.015	32389	3	1225.97	4.91
[P0A1D3]CH60_SALTY 60 kDa chaperonin	28		GGDGNYGYNAAATEEYGNMIDMG ILDPTKVTR	470	31	3	17.09	y6y16y25	3322.53	86.679	31057	3	1108.18	8.01
[P0A1D3]CH60_SALTY 60 kDa chaperonin	29	Carbamidomethyl+C(13)	AMEAPLRQIVLNCGEEPSVVANT VK	445	25	10	50.18	b3b4b7b9b16y4*y4y5y12°y12	2725.41	74.392	25422	3	909.14	2.96
[P0A1D3]CH60_SALTY 60 kDa chaperonin	30		AVAAGMNPMDLKR	105	13	10	95.55	b8b11y3y4y6y7*y7y9y10*y10	1373.70	51.497	13509	2	687.35	-0.44
[P0A1D3]CH60_SALTY 60 kDa chaperonin	31		LIAEAMDKV GK	160	11	4	24.23	b3y7y9°y9	1174.64	46.703	12085	2	587.83	-5.09
[P0A1D3]CH60_SALTY 60 kDa chaperonin	32		ANDAAGDGTTTATVLAQSIITEGL KAVAAGMNPMDLK	80	37	4	21.34	b7y6y8y9	3616.83	131.557	7184	3	1206.28	4.19
[P0A1D3]CH60_SALTY 60 kDa chaperonin	33		EVASKANDAAGDGTTTATVLAQS IITEGLK	75	30	3	11.36	b10b13y3	2932.49	87.543	6289	3	978.17	-6.99
[P0A1D3]CH60_SALTY 60 kDa chaperonin	34	Carbamidomethyl+C(6)	ALSVP CSDSKAIAQVGTISANSDE TVGK	132	28	3	11.68	b11y7y13	2805.38	59.542	1779	3	935.80	-5.05
[P0A1D3]CH60_SALTY 60 kDa chaperonin	35	Phosphoryl STY(6)	SFGAPTITKDGVS VAR	42	16	4	24.17	b4b14y12y14	1685.83	74.391	1651	2	843.42	8.40
[P0A1D3]CH60_SALTY 60 kDa chaperonin	36	Carbamidomethyl+C(18) ;Oxidation+M(13)	SALQYAASVAGLMITTECMVTDL PK	501	25	3	12.37	b8b11y9	2686.35	107.916	1723	4	672.34	15.00
[P0A1D3]CH60_SALTY 60 kDa chaperonin	37		DALHATR	397	7	0	1.63		783.42	26.832	65096	2	392.21	8.88
[P0A1D3]CH60_SALTY 60 kDa chaperonin	38		EDALHATR	396	8	2	8.8	b6°b6	912.44	26.877	25828	2	456.72	-12.78
[P0A1D3]CH60_SALTY 60 kDa chaperonin	39	Carbamidomethyl+C(4)	SVPCSDSK	134	8	0	2.04		879.38	36.043	2127	1	879.38	-3.19
[P0A1D3]CH60_SALTY 60 kDa chaperonin	40		EMLPVLEAVAK	231	11	0	2.44		1181.65	80.245	5192	2	591.33	-3.51
[P0A1D3]CH60_SALTY 60 kDa chaperonin	41		QQIEEATSDYDREK	350	14	0	3.66		1694.75	34.280	1843	3	565.59	2.74
[P66313]RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	13	127.76	b2b3b4b5y3y5y6y7°y7y8y9y10y12	1150.68	54.028	60701	2	575.84	-6.47
[P66313]RL6_SALTY 50S ribosomal protein L6	2		DGYADGWAQAGTAR	55	14	4	19.22	b3y6y11y14	1438.64	50.763	46020	2	719.82	5.35
[P66313]RL6_SALTY 50S ribosomal protein L6	3		TLNDAVEVK	35	9	10	54.39	b2°b2y1y3°y3y6y7°y7y8y9	988.52	39.174	43927	2	494.76	-12.90
[P66313]RL6_SALTY 50S ribosomal protein L6	4		INGQVITIK	18	9	4	30.41	b3y7y8y9	985.59	49.155	42959	2	493.30	-9.29
[P66313]RL6_SALTY 50S ribosomal protein L6	5		LQLVGVGYR	86	9	7	38.19	b2*b2y2y4y5y7y9	1004.58	60.245	32213	2	502.79	-8.32
[P66313]RL6_SALTY 50S ribosomal protein L6	6		HADNALTFGPR	44	11	8	47.6	b3°b3b5y4y9*y9y10y11	1198.59	46.925	20014	2	599.80	-3.97

[P66313]RL6_SALTY 50S ribosomal protein L6	7		HADNALTFGPRDGYADGWAQAG TAR	44	25	3	35.16	b10b11b12	2618.19	56.554	2418	3	873.40	-10.26
[P66313]RL6_SALTY 50S ribosomal protein L6	8		ALLNSMVIGVTEGFTK	69	16	6	44.83	b7b15y6y8y12y13	1679.90	94.349	48182	2	840.45	-3.34
[P66313]RL6_SALTY 50S ribosomal protein L6	9		RPEPYK	152	6	1	13.6	y4	789.43	39.121	5586	2	395.22	9.97
[P66313]RL6_SALTY 50S ribosomal protein L6	10		NGELTRTLNDAVEVK	29	15	3	24.1	b5y7y8	1658.85	38.187	4364	3	553.62	-12.58
[P66313]RL6_SALTY 50S ribosomal protein L6	11	Phosphoryl STY(14)	HADNALTFGPRDGYADGWAQAG TAR	44	25	4	12.37	b7b12y11°y11	2698.18	84.944	2842	4	675.30	4.98
[Q8ZP20]TREA_SALTY Periplasmic trehalase	1		VAAAAQAHLQPGLATTSVK	428	21	13	78.66	b2b3b4b5b9b11b17*b17y5y8y10y19y21	2004.11	58.463	85590	3	668.71	-7.00
[Q8ZP20]TREA_SALTY Periplasmic trehalase	2		TTTIAPVDLNALLYQLEK	335	18	19	85.88	b2°b2b3°b3b4°b4b5°b5b8°b8y1y3y4°y4*y4y5y13y14y18	2003.12	103.706	56158	2	1002.07	9.38
[Q8ZP20]TREA_SALTY Periplasmic trehalase	3		WMDNPQQLSTIR	323	12	9	54.33	b2b11y2y8y9y10*y10y11y12	1488.73	63.130	48527	2	744.87	-0.33
[Q8ZP20]TREA_SALTY Periplasmic trehalase	4		TFADAIPNSDPLMILADYR	68	19	13	73.05	b5°b5b6y2y3y4°y4y5°y5y9y10y13y19	2123.07	101.541	48029	2	1062.04	9.77
[Q8ZP20]TREA_SALTY Periplasmic trehalase	5		FLTNVQHTYDR	486	11	5	24.23	b4b7°b7y2y9	1393.67	44.100	10561	3	465.23	-8.06
[Q8ZP20]TREA_SALTY Periplasmic trehalase	6		WDSLLPLPESYVVPGGR	142	17	5	29.83	b4b5y4y12y17	1884.99	91.570	7532	2	943.00	3.11
[Q8ZP20]TREA_SALTY Periplasmic trehalase	7		AIEMHLWNNK	380	10	6	26.83	b7b9y2*y2y6y10	1255.62	43.522	3493	2	628.31	-3.89
[Q8ZP20]TREA_SALTY Periplasmic trehalase	8		SAAASGWDFSSR	311	12	3	32.42	y6y8y11	1241.57	54.626	32545	2	621.29	12.88
[Q8ZP20]TREA_SALTY Periplasmic trehalase	9		SNPNRPATEIYR	296	12	8	29.41	b8*b8b9°b9*b9b11°b11*b11	1417.74	51.497	11196	2	709.37	14.03
[Q8ZP20]TREA_SALTY Periplasmic trehalase	10		VADMVANFGYEIDAWGHIPNGNR	183	23	5	20.05	b8b11b13*b13y12	2546.19	81.289	4315	3	849.40	1.63
[Q8ZP20]TREA_SALTY Periplasmic trehalase	11	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPK	534	29	3	17.46	y3y12y14	3199.59	64.544	3387	3	1067.20	3.36
[Q8ZP20]TREA_SALTY Periplasmic trehalase	12		LEDGSVLNR	266	9	4	45.36	b4b5b7y3	1002.51	24.006	2355	2	501.76	-14.19
[Q8ZP20]TREA_SALTY Periplasmic trehalase	13		DTPRPESWVEDIATAK	280	16	7	55.98	b4b5b10y5y9y11y12	1814.92	111.491	2283	2	907.96	12.71
[Q8ZP20]TREA_SALTY Periplasmic trehalase	14		SQPPFFAFMVELLAQHEGDDALK	212	23	3	34.85	b7b8b9	2590.21	98.043	2253	4	648.31	-20.45
[Q8ZP20]TREA_SALTY Periplasmic trehalase	15		NVEKWDSLLPLPESYVVPGGR	138	21	9	61.86	b9b11y4y5y8y10°y10y11y12	2355.24	88.061	58983	3	785.75	3.21
[Q8ZP20]TREA_SALTY Periplasmic trehalase	16	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPKTPSAATQ	534	36	10	39.13	b3b4b5b10*b10b26y10°y10y13*y13	3855.88	64.463	50930	4	964.73	-2.98
[Q8ZP20]TREA_SALTY Periplasmic trehalase	17		DLRSAAASGWDFSSR	308	15	3	18.08	b7b14y4	1625.79	62.266	8461	3	542.60	12.01
[Q8ZP20]TREA_SALTY Periplasmic trehalase	18		LVEKNDVSSTGTGGGGGEYPLQD GFGWTVNGVTLK	500	34	4	22.91	y11y12*y12y14	3440.71	111.095	3359	4	860.93	13.69
[Q8ZP20]TREA_SALTY Periplasmic trehalase	19	Phosphoryl STY(11)	SNPNRPATEIYRDLR	296	15	5	43.61	b6b7°b7b9b10	1881.88	60.881	3897	3	627.96	-4.86
[Q8ZP20]TREA_SALTY Periplasmic trehalase	20	Oxidation+M(9)	SQPPFFAFMVELLAQHEGDDALK	212	23	4	34.85	b6°b6b7b8	2606.27	136.191	12608	3	869.43	3.00
[Q8ZP20]TREA_SALTY Periplasmic trehalase	21	Oxidation+M(4)	VADMVANFGYEIDAWGHIPNGNR	183	23	3	13.01	b11b19y4	2562.19	73.373	10406	3	854.74	3.81
[P65882]PURA_SALTY Adenylosuccinate synthetase	1	Carbamidomethyl+C(7)	LLLSEACPLILDYHVALDNAR	97	21	10	54.11	b2b19b20*b20y3y9y11y12y19y21	2396.25	91.688	26201	3	799.42	-4.99
[P65882]PURA_SALTY Adenylosuccinate synthetase	2		IVDLLTER	19	8	4	36.02	b2b3b7y6	958.54	62.515	12037	2	479.77	-14.96

P65882 PURA_SALTY Adenylosuccinate synthetase	3		VLDDTMAVADILTSMVVDVSDLLDQAR	186	27	21	176.28	b2b4b5b6b7b8°b8b10b23y2y3y4y5y6y7y8°y8y9y10y11y27	2905.46	138.207	9784	3	969.16	1.09
P65882 PURA_SALTY Adenylosuccinate synthetase	4		EVTTTPLAADDWK	354	13	5	29.57	b7b11y4y12y13	1446.69	80.356	5708	3	482.90	-11.39
P65882 PURA_SALTY Adenylosuccinate synthetase	5	Carbamidomethyl+C(11)	AVQLNSLSGFCLTK	318	14	4	19.22	b11y7°y7y10	1537.79	74.464	4594	2	769.40	-7.46
P65882 PURA_SALTY Adenylosuccinate synthetase	6		EVMEYHNFLVNYK	163	15	3	18.08	b5y9y11	1976.90	62.216	2123	4	494.98	-8.64
P65882 PURA_SALTY Adenylosuccinate synthetase	7		TETMILRDPFDA	420	12	3	32.42	b3b5b8	1408.67	80.819	1938	3	470.23	-4.59
P65882 PURA_SALTY Adenylosuccinate synthetase	8	Carbamidomethyl+C(2)	LCVAYR	343	6	2	29.8	y3y5	781.40	31.592	21950	1	781.40	0.00
P65882 PURA_SALTY Adenylosuccinate synthetase	9		MGNNVVVLGTQWGDEGK	0	17	3	24.91	y8y9y14	1803.83	76.795	19825	3	601.95	-20.84
P65882 PURA_SALTY Adenylosuccinate synthetase	10		ENVTSIINGNVVLSPSALMK	62	20	3	14.32	b4b15y14	2029.07	72.885	3329	3	677.03	-14.50
P65882 PURA_SALTY Adenylosuccinate synthetase	11		AEAVDYQK	178	8	3	33.01	b4b5y7	923.44	32.944	1973	2	462.23	-3.37
P65882 PURA_SALTY Adenylosuccinate synthetase	12		ENVTSIINGNVVLSPSALMKEMK	62	23	4	20.05	b3b14b17y10	2417.26	97.904	9081	2	1209.13	-7.57
P65882 PURA_SALTY Adenylosuccinate synthetase	13		MGNNVVVLGTQWGDEGKGK	0	19	3	22.67	b5b6y3	1988.98	43.601	8132	4	498.00	-4.23
P65882 PURA_SALTY Adenylosuccinate synthetase	14		AIGTTGRGIGPAYEDK	125	16	11	81.8	b4°b4y3y6y7y8°y8y9°y9y11y12	1605.82	69.546	5424	3	535.94	-3.65
P65882 PURA_SALTY Adenylosuccinate synthetase	15		EVTTTPLAADDWKGVPIYETMPGWSESTFGVK	354	33	3	11.04	b5y6y12	3641.76	93.214	2797	3	1214.59	5.50
P65882 PURA_SALTY Adenylosuccinate synthetase	16	Carbamidomethyl+C(2)	LCVAYRMPDGR	343	11	4	27.24	b3b4y6°y6	1337.63	89.844	1957	2	669.32	-14.14
P65882 PURA_SALTY Adenylosuccinate synthetase	17	Oxidation+M()	ENVTSIINGNVVLSPSALMKEMKELEDR	62	28	3	11.68	b9b11y10	3075.59	95.312	6708	3	1025.87	5.40
P65882 PURA_SALTY Adenylosuccinate synthetase	18	Oxidation+M(15)	VLDDTMAVADILTSMVVDVSDLLDQAR	186	27	4	22.73	b7b9°b9b10	2921.44	122.470	3210	3	974.48	-3.18
P66593 RS6_SALTY 30S ribosomal protein S6	1		AHYVLMNVEAPQEVIDELETTFR	56	23	20	150.28	b2b3b4b5b6b8b14y2y3y4y5°y5y6y7°y7y8y9y11y13y23	2704.34	110.352	125372	3	902.12	2.71
P66593 RS6_SALTY 30S ribosomal protein S6	2		YSAAITGAEGK	24	11	6	47.42	y2y5y6y7y9y11	1067.53	34.172	71240	2	534.27	-7.32
P66593 RS6_SALTY 30S ribosomal protein S6	3		FNDAVIR	79	7	8	63.75	b5y1y3y4y5y6*y6y7	834.44	42.774	55809	2	417.72	-10.61
P66593 RS6_SALTY 30S ribosomal protein S6	4		HAVTEASPMVK	93	11	3	35.99	y6y7y8	1169.59	31.203	33244	2	585.30	-6.47
P66593 RS6_SALTY 30S ribosomal protein S6	5		LEDWGR	38	6	1	13.6	y4	775.37	39.086	6543	2	388.19	-6.14
P66593 RS6_SALTY 30S ribosomal protein S6	6		AHYVLMNVEAPQEVIDELETTFRFNDAVIR	56	30	8	43.38	b3b8b9b10°b10y4y12y15	3519.75	115.409	46826	4	880.69	-1.80
P66593 RS6_SALTY 30S ribosomal protein S6	7		RHYEIVFMVHPDQSEQVPGMIER	1	23	4	17.42	b7b9y10y12	2797.35	96.356	3964	4	700.09	-3.58
P66593 RS6_SALTY 30S ribosomal protein S6	8		HYEIVFMVHPDQSEQVPGMIERYSAAITGAEGK	2	33	9	34.58	b3b4b8°b8y3°y3y8y12y16	3689.78	119.578	3143	5	738.76	1.19
P66593 RS6_SALTY 30S ribosomal protein S6	9		YSAAITGAEGKIHR	24	14	4	44.66	b7b8b11b12	1473.80	136.398	2263	2	737.40	12.42
P66593 RS6_SALTY 30S ribosomal protein S6	10	Oxidation+M(9)	HAVTEASPMVK	93	11	3	24.23	b4b7y5	1185.61	63.681	4547	2	593.31	12.87
P67091 UF_SALTY Universal stress protein F	1		TILVPIDISDSELTQR	3	16	24	149.75	b2b3°b3b4°b4y2*y2y3y4y6*y6y7°y7y8°y8y9*y9y10y12°y12*y12y13y14y16	1799.98	82.210	130626	2	900.49	4.00

[P67091]UF_SALTY Universal stress protein F	2	Carbamidomethyl+C(4)	HAECSVLVVR	134	10	9	47.81	b2b3°b3y1y4y6y8°y8y10	1169.60	42.199	45781	2	585.30	-6.05
[P67091]UF_SALTY Universal stress protein F	3		IDDAKVHFLTVPISLPYYASLG LAYSALPAMDDLK	29	36	3	16.56	y5y7y9	3936.98	112.761	2458	4	985.00	-13.08
[P67091]UF_SALTY Universal stress protein F	4		MNRTLVPIDISDSELTQR	0	19	3	22.67	b5y7y8	2201.15	69.548	2375	2	1101.08	-3.44
[P67091]UF_SALTY Universal stress protein F	5	Carbamidomethyl+C(2)	ECSVLVVR	136	8	1	8.24	b5	961.51	42.156	4249	2	481.26	-0.25
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	1		LQKENIDFVYGGYYPEMGQMLR	211	23	8	42.3	b9b14y6y8y9y11y13y23	2814.34	85.037	47562	3	938.78	3.04
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	2		QGNANIVFFDGITAGEKDFSALIA R	186	25	9	23.03	b2b6°b6b7°b7b14°b14y13 y25	2654.36	104.468	47164	3	885.46	1.29
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	3		TAGLDSSQGPTAAK	139	14	12	100.12	b3°b3b5y5y6y8y9°y9y10y1 1y12y14	1303.64	29.582	46534	2	652.32	-5.62
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	4		QQYGEGLAR	170	9	8	45.36	b7b9y5y6°y6y7y9°y9	1021.50	33.741	46028	2	511.25	-10.34
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	5		TQFMGPEGVGNASLSNIAGGAEE GMLVTMPK	242	31	11	46.39	b2b3b9b17y2y4y5y8y12y1 3y31	3035.48	92.683	33211	3	1012.50	5.63
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	6	Carbamidomethyl+C(14)	IVNDGIQYVIGHLCSSSTOPASDIY EDEGLMISPGATNPFLTQR	87	45	6	21.54	b8°b8y11°y11y12y14	4889.40	97.326	11323	3	1630.47	8.39
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	7		GFEFGVFQWHADGSSTVAK	350	19	6	29.3	b4b8b12y8y12°y12	2069.98	83.667	2403	2	1035.50	5.78
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	8		YILETVKPQR	153	10	4	54.79	y3y4y6y7	1246.69	46.001	63814	3	416.24	-20.17
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	9		ENIDFVYGGYYPEMGQMLR	214	20	4	19.68	b4b9y9y11	2445.14	102.288	2732	3	815.72	20.77
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	10		DPSGPVYWITYAAVQSLATAMTR	293	23	4	28.73	b9b11b16b17	2498.29	133.863	2719	3	833.44	21.40
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	11		IAIIHDKQQYGEGLAR	163	16	6	68.85	y6y7y8y9y10y12	1811.96	47.001	124370	3	604.66	-11.79
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	12		DINAKGGIK	54	9	5	38.19	b5°b5b6°b6b7	915.53	26.342	28074	2	458.27	1.27
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	13		TAGLDSSQGPTAAKYILETVKPQR	139	24	3	22.96	b8b12b13	2531.33	86.498	16825	3	844.45	-5.79
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	14		GYQYIMRTAGLDSSQGPTAAK	132	21	5	24.63	b5b12b13y14°y14	2215.07	100.162	7771	2	1108.04	-4.74
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	15		LQKENIDFVYGGYYPEMGQMLR	211	23	3	13.01	b11y9y12	2814.37	90.023	6945	3	938.79	14.66
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	16		RYDQDPANK	273	9	3	30.41	b3b5y4	1106.52	16.144	3975	2	553.76	-3.53
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	17		GDLKGFEFGVFQWHADGSSTVA K	346	23	6	23.73	b9b13°b13°b13b14y9	2483.18	92.160	1982	2	1242.09	-8.65
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	18	Phosphoryl STY(15)	TQFMGPEGVGNASLSNIAGGAEE GMLVTMPK	242	31	5	18.7	b7b12b14y8y16	3115.44	136.454	2529	2	1558.23	7.44
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	19	Oxidation+M()	LQKENIDFVYGGYYPEMGQMLR	211	23	3	13.01	b11b13y11	2830.35	69.447	3946	3	944.12	11.30
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein	20		QQYGEGLAR	170	9	0	1.63		1003.49	33.781	2748	2	502.25	0.36
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	16	82.58	b1b2b7b12y1y2y4y5°y5y1 0y12°y12y14y16y17y18	1970.00	63.818	169158	3	657.34	-11.03
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		AVAFMMDDALLAGER	198	15	14	96.42	b1b3b5y2°y2y3°y3y4y5y7y 10y11y12y15	1609.78	84.578	133629	2	805.39	4.17
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		ESSVPFSYYDNQQK	47	14	12	83.92	b2b4°b4b11y4y6y7y8y9y1 0°y10y14	1691.76	56.276	130319	2	846.38	2.16

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		VVGYSQDYSNAIVEAVK	61	17	14	111.19	b2b3b8b14b16y3y4y5y11y12y13*y13y15y17	1841.94	68.362	117323	2	921.47	4.44
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5		NGVIVVGHR	38	9	3	38.19	y3y5y6	950.54	33.183	62817	2	475.77	-13.48
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTNNLER	98	22	10	49.12	b3b10y2y6y8y10y11y12*y12y22	2526.22	81.906	31976	2	1263.61	10.34
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7		LIPITSQNR	89	9	6	38.19	b2y5y6y7*y7y9	1041.59	43.604	29611	2	521.30	-10.08
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8		NGVIVVGHRESSVPFSYYDNQK	38	23	7	29.37	b2b3y4y8y10y11y23	2623.30	58.420	27640	3	875.10	3.72
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9		LNKPDLQVK	80	9	6	38.19	y2y3y4y6*y6y9	1054.61	38.357	21832	2	527.81	-11.69
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		LMDDTIAQAQTSGEAEK	247	17	6	36.85	b2b3*b3y6y7y8	1807.83	75.812	12359	3	603.28	-2.36
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11	Carbamidomethyl+C(19)	KPDNWEIVGKPKSQEAYGCMLR	217	22	6	37.96	b5*b5b6b7b12y5	2606.23	76.573	6274	5	522.05	-7.12
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12		LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	4	21.91	b10y8y9y16	2869.45	67.847	5885	3	957.16	2.64
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	13	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTNNLER	89	31	16	130.53	b3y4*y4y6*y6y7y8y9y10y11y12y13y14*y14y21y27	3548.80	86.887	273430	3	1183.60	4.88
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	14		LMDDTIAQAQTSGEAEKWFDK	247	21	5	29.94	y3*y3y4y8y13	2384.09	88.868	50493	4	596.78	-8.81
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	15		KLTTAMLVMGLSAGLAHAEDGA PAAGSTLDK	4	31	4	24.59	b5b10y14y15	2997.50	85.735	18873	3	999.84	-13.68
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	16		VVGYSQDYSNAIVEAVKK	61	18	3	22.69	b5b14b16	1970.04	93.809	12924	2	985.52	8.12
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	17		TLESGRAVAFMMDDALLAGER	192	21	4	13.83	b5*b5b7y13	2253.09	73.260	2675	4	564.03	-5.42
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	18	Carbamidomethyl+C(19) ;Oxidation+M(20)	KPDNWEIVGKPKSQEAYGCMLR	217	22	4	23.27	b3b4*b4b8	2622.26	74.422	7362	4	656.32	7.54
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	19		NKPDLQVK	81	8	0	1.63		941.54	38.329	19577	2	471.27	-3.05
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	20		PITSQNR	91	7	2	8.8	b5*b5	815.43	43.602	11998	2	408.22	-13.62
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	21		KPDNWEIVGKPKS	217	13	1	7.8	y5	1497.76	76.586	9718	2	749.38	-8.64
P0A1V4 KAD_SALTY Adenylate kinase	1		YGIPQISTGDMLR	23	13	9	54.4	b2b3b6y5y7y8y10y13*y13	1450.74	73.138	37723	2	725.87	-0.42
P0A1V4 KAD_SALTY Adenylate kinase	2		LVEYHQMTAPLIGYYQK	167	17	14	56.67	b2b3b7*b7b9*b9b11y1y2*y2y5y6y8y17	2054.03	69.633	37529	3	685.35	-7.25

P0A1V4 KAD_SALTY Adenylate kinase	3		NGFLLDGFPR	78	10	7	55.43	b3b9b10y4y5y6y10	1135.58	80.874	26456	2	568.30	-5.05
P0A1V4 KAD_SALTY Adenylate kinase	4		IILLGAPGAGK	2	11	7	47.42	b1b2y5y6y7y9y11	1009.63	61.788	21446	2	505.32	-11.12
P0A1V4 KAD_SALTY Adenylate kinase	5		LVEYHQMTAPLIGYYQKEAEGN TK	167	25	6	22.64	b5b7b13y6*y6y11	2854.38	97.366	7622	3	952.13	-10.78
P0A1V4 KAD_SALTY Adenylate kinase	6		VDGTQAVADVR	195	11	9	24.23	b1b5*b5b11y2y4y10*y10y1 1	1130.57	60.912	6905	1	1130.57	-11.12
P0A1V4 KAD_SALTY Adenylate kinase	7		FNPPK	136	5	2	26.38	b3y4	602.32	56.564	42469	1	602.32	-11.75
P0A1V4 KAD_SALTY Adenylate kinase	8		IILLGAPGAGKGTQAQFIMEK	2	21	9	68.99	b3y3y5y9y15y17y18*y18y 19	2143.18	73.082	27047	3	715.07	-6.27
P0A1V4 KAD_SALTY Adenylate kinase	9	Carbamidomethyl+C(6)	IAQEDCRNGFLLDGFPR	71	17	5	16.26	b4*b4b10y5*y5	2007.98	89.112	23208	2	1004.49	4.26
P0A1V4 KAD_SALTY Adenylate kinase	10		DIMDAGKLVTDDELVIALVK	50	19	4	28.4	b9b12y4y5	2043.13	116.171	20464	3	681.71	-5.97
P0A1V4 KAD_SALTY Adenylate kinase	11		QAKDIMDAGK	47	10	4	26.83	b4b9y9*y9	1076.54	70.521	4731	2	538.77	0.00
P0A1V4 KAD_SALTY Adenylate kinase	12		NGFLLDGFPRTIPQADAMK	78	19	6	14.89	b6*b6*b6b8*b8y9	2091.05	58.474	2701	3	697.69	-8.06
P0A1V4 KAD_SALTY Adenylate kinase	13		VEGKDDVTGEDLTTR	141	15	8	66.07	b7*b7b11b12b13b14y8y11	1634.79	71.905	2211	3	545.60	-0.90
P0A1V4 KAD_SALTY Adenylate kinase	14	Oxidation+M(7)	LVEYHQMTAPLIGYYQK	167	17	3	16.26	b9y3y6	2070.05	70.859	2149	3	690.69	6.37
P0A1V4 KAD_SALTY Adenylate kinase	15	Oxidation+M(6)	QAKDIMDAGK	47	10	3	26.83	b6b8y3	1092.54	32.904	1502	2	546.77	0.67
P0A1V4 KAD_SALTY Adenylate kinase	16		LVEYHQMTAPLIG	167	13	0	4.88		1471.76	69.685	1652	2	736.38	-3.48
P26982 DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	8	60.33	b3b4y4y7y9y12y15y20	2017.09	75.195	101983	3	673.03	-11.20
P26982 DEGP_SALTY Protease do	2		SDIALIQIQNPK	160	12	12	110.77	b3b4*b4b5b6y2y3y5y6y7y 9y12	1339.75	64.660	68496	2	670.38	-4.28
P26982 DEGP_SALTY Protease do	3		GYVVTNNHVVDNASVIK	124	17	11	63.2	b2b3y1y2y7y8y10y12y14y 15y17	1828.94	50.803	55903	3	610.32	-9.54
P26982 DEGP_SALTY Protease do	4		NLTSQMVEYGQVK	275	13	17	84.97	b1b2b6b8*b8b11*b11y6*y 6y7*y7y8y9y11*y11y13*y1 3	1496.75	58.454	48566	2	748.88	3.34
P26982 DEGP_SALTY Protease do	5		GAFVSQVMPNSSAAK	313	15	13	92.29	b3b4b5b8b11b13y2y8y10° y10y11*y11y15	1493.74	54.008	39748	2	747.38	1.47
P26982 DEGP_SALTY Protease do	6		VGDYTVAINPPFGLGETVTSGIVS ALGR	186	28	19	92.87	b2b3b5*b5b6*b6b7b8*b8b1 4y1y2y4y5y6y8y10y14y28	2750.44	116.470	35313	3	917.48	1.51
P26982 DEGP_SALTY Protease do	7		AQVGTMPVGSK	352	11	8	68.39	b2*b2y3y5y6y8y9y11	1074.55	35.544	30398	2	537.78	-7.27
P26982 DEGP_SALTY Protease do	8		SGLNVENYENFIQTDAAINR	214	20	9	30.53	b2b7*b7b11y1y5y11y12*y12 y20	2268.11	77.849	22003	2	1134.56	8.50
P26982 DEGP_SALTY Protease do	9		LADSDALR	178	8	5	53.98	y3y5y6y7y8	860.44	33.023	18289	2	430.72	-11.99
P26982 DEGP_SALTY Protease do	10		GDSSIYLLMQ	465	10	4	26.83	b7y2y3y9	1126.54	99.825	1785	1	1126.54	-0.11
P26982 DEGP_SALTY Protease do	11		FMALGSGVIIDAAK	110	14	3	19.22	b3y4y10	1392.75	76.649	39446	2	696.88	-6.84
P26982 DEGP_SALTY Protease do	12		ISLGLLR	363	7	4	50.56	b4y4y5y6	771.50	69.016	26186	2	386.25	-15.74
P26982 DEGP_SALTY Protease do	13		ANSPAAQIGLK	418	11	5	35.99	b5b6*b6b7*b7	1069.62	33.000	19703	3	357.21	14.38
P26982 DEGP_SALTY Protease do	14		NIAELR	443	6	1	13.6	b5	715.41	34.329	2882	2	358.21	-5.63
P26982 DEGP_SALTY Protease do	15		RGELGIMGTELNSELAK	288	17	12	99.46	b4b5b6b8b9b10b13°b13y1 0*y10y11y16	1817.93	69.496	57722	3	606.65	-8.26
P26982 DEGP_SALTY Protease do	16		LADSDALRVGDYTVAINPPFGLG ETVTSGIVSALGR	178	36	7	36.59	b3b5b8*b8b13b14b25	3591.83	99.781	35325	3	1197.95	-10.60
P26982 DEGP_SALTY Protease do	17		VDAQRGAFVSQVMPNSSAAK	308	20	4	22.45	b5b6*b6y8	2063.02	48.906	7463	4	516.51	-5.21
P26982 DEGP_SALTY Protease do	18	Phosphoryl STY(14)	GYVVTNNHVVDNASVIK	124	17	5	36.85	b12y3y4*y4y5	1908.90	40.789	29622	3	636.97	-6.14
P26982 DEGP_SALTY Protease do	19	Phosphoryl STY(5)	AQVGTMPVGSK	352	11	4	35.2	b3b9_H3PO4 b9y6y9	1154.52	42.147	2464	3	385.51	0.42

P26982 DEGP_SALTY Protease do	20		NLTSQMVEYGQV	275	12	6	41.24	y5y6°y6y9°y9y11	1368.64	58.485	292053	2	684.82	-2.76
P26982 DEGP_SALTY Protease do	21		VVTNNHVVDNASVIK	126	15	3	23.66	b4b6b11	1608.86	50.740	3355	2	804.93	-7.21
P26982 DEGP_SALTY Protease do	22		GAFVSQVMPNSSAAK	313	15	1	7.26	y4	1476.71	54.057	3293	2	738.86	-0.25
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VVGQLGQVLGPR	122	12	9	49.56	b2b4y2y3y7y8y10*y10y12	1222.72	59.811	119127	2	611.86	-7.79
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VAVFTQGPNAEAAK	74	14	11	66.27	b11*b11y7y8*y8y9*y9y10y11°y11y14	1402.73	45.978	92544	2	701.87	-2.35
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VGTVTPNVAEAVK	141	13	17	105.73	b2b3°b3b7°b7y3y7y8*y8y9y10y11y12*y12*y12y13*y13	1284.72	48.837	82801	2	642.86	0.00
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		GATVLPHGTR	60	11	7	50.43	y2y4y5y6°y6y7y11	1065.57	30.262	13727	2	533.29	-10.88
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		AAGAELVGMEDLADQIK	88	17	5	22.84	b10b15y7y16y17	1730.88	65.301	3063	3	577.63	9.24
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		FNESVDVAVNLGIDAR	37	16	5	17.1	b5°b5b12y5°y5	1718.88	77.271	5412	3	573.63	3.34
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		SDQNVR	54	6	2	26.79	b4y5	718.35	49.295	4365	1	718.35	2.46
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		VSISTTMGAGVAVDQAGLSASAN	211	23	5	20.05	b7y3°y3y7y11	2107.04	86.181	2373	3	703.02	3.59
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9		KGEMNFDVVIASPDAMR	105	17	5	29.83	b9°b9b10y5y8	1879.91	108.092	7767	2	940.46	4.09
P0A2A3 RL1_SALTY 50S ribosomal protein L1	10		NDKNGIIHTTIGK	164	13	4	28.05	b4°b4b10b11	1410.77	108.733	7631	2	705.89	0.87
P0A2A3 RL1_SALTY 50S ribosomal protein L1	11		KVSISTTMGAGVAVDQAGLSASAN	210	24	7	60.73	y3y7y8y9y14y15y18	2235.14	74.364	5731	4	559.54	5.90
P0A2A3 RL1_SALTY 50S ribosomal protein L1	12		SDQNVRGATVLPHGTR	54	17	3	16.26	b7b12y5	1764.91	60.362	2624	2	882.96	-1.18
P0A2A3 RL1_SALTY 50S ribosomal protein L1	13	Oxidation+M(7)	VSISTTMGAGVAVDQAGLSASAN	211	23	5	17.42	b14b18y4°y4y11	2123.06	75.112	13648	3	708.36	13.91
P0A2A3 RL1_SALTY 50S ribosomal protein L1	14	Oxidation+M(9)	AAGAELVGMEDLADQIK	88	17	3	16.26	b3b5y4	1746.85	63.742	9756	3	582.95	-5.87
P0A2A3 RL1_SALTY 50S ribosomal protein L1	15		GATVLPHGTR	60	11	0	2.44		1047.55	30.238	5808	3	349.86	-9.32
Q7CQV9 DPS_SALTY DNA protection during starvation protein	1		GANFIHAVHEMLDGFR	55	15	6	39.81	b4y3y4°y4y6y9	1676.80	82.565	26260	3	559.60	-14.49
Q7CQV9 DPS_SALTY DNA protection during starvation protein	2		AVQLGGVALGTTQVINSK	83	18	11	85.59	b2b3b7y3y4y9y10y11y13y14y18	1756.01	67.986	25242	2	878.51	5.28
Q7CQV9 DPS_SALTY DNA protection during starvation protein	3		AIGEAKDEDTADIFTAASR	134	19	6	44.13	b12y4y5y7y10y13	1980.92	59.068	23088	3	660.98	-14.42
Q7CQV9 DPS_SALTY DNA protection during starvation protein	4		ASNLLYTR	10	8	5	49.21	b3y3y4y5y8	937.50	44.954	20067	2	469.25	-11.00
Q7CQV9 DPS_SALTY DNA protection during starvation protein	5		TALTDHLDTMAER	70	13	3	20.57	b9b11y8	1473.68	53.066	39388	3	491.90	-13.17
Q7CQV9 DPS_SALTY DNA protection during starvation protein	6		ELADR	119	5	1	13.19	b3	603.31	43.622	3722	1	603.31	1.32
Q7CQV9 DPS_SALTY DNA protection during starvation protein	7		ASNLLYTRNDVSESDK	10	16	6	48.97	y4°y4y5y7y10y14	1811.89	89.886	22722	3	604.64	7.95
Q7CQV9 DPS_SALTY DNA protection during starvation protein	8		DLDKFLWFIESNIE	153	14	3	19.22	b10b12y12	1768.88	100.633	4286	2	884.95	3.11
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	19	112.95	b2b4*b4b6b7y1y5y6*y6y7°y7y9*y9y10y11y12y17y19y21	2215.16	75.345	44973	3	739.06	-4.96
Q56073 DNAK_SALTY Chaperone protein dnaK	2		SLGQFNLDGINPAPR	452	15	8	25.7	b3b11°b11*b11y4y10*y10y15	1598.83	72.413	19066	2	799.92	3.36
Q56073 DNAK_SALTY Chaperone protein dnaK	3		TAEDYLGEVPTEAVITVPAYFNDAQR	125	26	7	26.42	b1b16y7°y7y9y11y23	2869.41	93.617	17924	3	957.14	6.81
Q56073 DNAK_SALTY Chaperone protein dnaK	4		ASSGLNEEEIQK	502	12	6	29.41	b1y2y7y9y10y12	1304.62	35.490	12446	2	652.82	-7.02

Q56073 DNAK_SALTY Chaperone protein dnaK	5		TAIESALNALETALK	562	15	3	18.08	b6b9y5	1544.85	67.957	6116	2	772.93	-5.22
Q56073 DNAK_SALTY Chaperone protein dnaK	6		MAPPQISAEVLK	109	12	4	35.43	b5b6*b6b7	1283.70	82.698	3756	2	642.35	-4.85
Q56073 DNAK_SALTY Chaperone protein dnaK	7		LMEIAQQQHAQQAGSADASANNAK	597	25	5	21.91	b12°b12y12y13°y13	2610.26	67.096	2099	3	870.76	11.69
Q56073 DNAK_SALTY Chaperone protein dnaK	8		EVGNR	183	5	2	13.19	y4*y4	574.29	42.195	12084	1	574.29	-14.56
Q56073 DNAK_SALTY Chaperone protein dnaK	9		IIGADNGDAWLDDVK	92	14	3	19.22	b6b13y11	1486.73	67.754	3125	2	743.87	-15.68
Q56073 DNAK_SALTY Chaperone protein dnaK	10		DVNPDEAVAIGAAVQGGVLTGDVK	363	24	7	16.8	b11°b11b13°b13y4°y4y13	2295.21	79.549	2862	3	765.74	12.66
Q56073 DNAK_SALTY Chaperone protein dnaK	11		MPMVQK	345	6	1	13.6	b4	733.37	32.312	1907	1	733.37	-8.07
Q56073 DNAK_SALTY Chaperone protein dnaK	12		IELSSAQQTDVNLPLYTADATGPK	270	24	7	42.07	b5°b5b7b12b13y10y11	2532.29	108.847	1749	3	844.77	3.86
Q56073 DNAK_SALTY Chaperone protein dnaK	13		GMPQIEVTFDIDADGILHVS AK	467	22	4	19.91	b10°b10b13b21	2356.16	57.319	1706	3	786.06	-11.50
Q56073 DNAK_SALTY Chaperone protein dnaK	14	Carbamidomethyl+C(12)	IIGIDLTNTNSCVAIMDGTQAR	3	22	5	22.14	b15°b15y13°y13y14	2306.18	79.440	1614	2	1153.59	14.72
Q56073 DNAK_SALTY Chaperone protein dnaK	15		AKIELSSAQQTDVNLPLYTADATGPK	268	26	6	41.4	y7y9°y9y10y11y13	2731.40	98.813	38212	3	911.14	-4.47
Q56073 DNAK_SALTY Chaperone protein dnaK	16		MQELAQVSQKLMEIAQQQHAQQQAGSADASANNAK	587	35	4	24.26	b3b4y4y9	3752.86	67.458	34662	5	751.38	14.70
Q56073 DNAK_SALTY Chaperone protein dnaK	17		IELSSAQQTDVNLPLYTADATGPKH MN IK	270	29	3	11.5	b12b20y11	3155.58	88.024	23437	4	789.65	-6.50
Q56073 DNAK_SALTY Chaperone protein dnaK	18		DVSIMPYKIIGADNGDAWLDDVK	84	22	4	13.39	b15°b15y8y11	2420.25	104.533	9630	4	605.82	12.41
Q56073 DNAK_SALTY Chaperone protein dnaK	19		TAEDYLGEPVTEAVITVPAYFNDAQRQATK	125	30	3	11.36	b10b13y8	3297.64	98.797	8292	3	1099.89	4.81
Q56073 DNAK_SALTY Chaperone protein dnaK	20		KTAEDYLGEPVTEAVITVPAYFNDAQR	124	27	5	36.37	b6b7°b7b8b13	2997.52	89.059	5688	3	999.84	11.73
Q56073 DNAK_SALTY Chaperone protein dnaK	21		IIGADNGDAWLDDVKGQK	92	17	3	16.26	b3b9y3	1799.91	60.972	3019	3	600.64	-8.41
Q56073 DNAK_SALTY Chaperone protein dnaK	22		DQGIDLRNDPLAMQR	246	15	3	18.08	b5b8y3	1741.85	48.275	2756	2	871.43	-5.89
Q56073 DNAK_SALTY Chaperone protein dnaK	23	Phosphoryl STY(17)	IELSSAQQTDVNLPLYTADATGPK	270	24	6	23.51	b7°b7b10y7y9y12	2612.24	97.910	57497	4	653.81	-1.59
Q56073 DNAK_SALTY Chaperone protein dnaK	24	Oxidation+M(2)	LMEIAQQQHAQQQAGSADASANNAKDDDVDAEFEEVKDK	597	40	4	10.88	b9°b9b12y14	4359.94	103.558	2973	6	727.50	-11.09
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	1		TFDTPPTYPNLSALSADGK	308	18	11	59.68	b2b3b4b7b13y2y6y7y11y14y18	1897.93	66.281	27911	2	949.47	4.89
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	2		QAGQVSVIDAK	291	11	10	65.38	b11y2y3y4°y4y7y8y9°y9y11	1115.60	38.345	16704	2	558.30	-6.35
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	3		EQEATQPDDVIR	338	12	12	60.35	b1b3°b3b12°b12y2y3y6°y6y8y10y12	1400.67	40.261	14539	2	700.84	0.78
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	4		LLDDGKEHFFINLSLDTAGHR	223	21	5	18.85	b5°b5b7y6y9	2398.19	66.028	11622	3	800.07	-9.87
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	5		ELVADAATNTIYISGVGKESAIWVVDGETIK	144	31	8	25.13	b7°b7b10b11b14°b14y7°y7	3249.73	104.328	3125	3	1083.92	13.30
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	6		EHFFINLSLDTAGHR	229	15	6	18.08	b7°b7y11°y11y13°y13	1756.90	95.935	7779	2	878.96	15.36
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	7		ESAIWVVDGETIK	162	13	4	20.57	b12y6y9°y9	1446.74	71.797	7755	2	723.88	-1.77
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	8		IAAPASLAVLFNPTR	268	15	4	24.1	b3y4°y4y5	1540.87	89.944	4744	2	770.94	-6.42
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	9		TGDVK	119	5	1	13.19	b3	519.27	65.668	2339	1	519.27	-13.05

Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	10		AFITDSK	244	7	4	40.38	b6°b6y3y5	781.40	35.384	2296	1	781.40	-7.73
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	11		ELVADAATNTIYISGVGK	144	18	5	15.53	b5b12°b12y14°y14	1821.98	67.901	1714	2	911.49	9.11
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	12		MSTGLALDSKAQR	185	13	4	20.57	b4b7°b7y6	1377.72	45.541	12951	2	689.37	6.03
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	13		AQRLYTTNADGEFITIDTASNK	195	22	6	20.79	b5b10°b10b12°b12y4	2429.23	93.743	3867	2	1215.12	14.27
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	14	Phosphoryl STY(14)	LLDDGKEHFFINLSLDTAGHR	223	21	5	24.63	b5b11b12y6°y6	2478.16	92.183	9435	3	826.72	-5.42
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	15	Oxidation+M(5)	GAYEMAWSQQENALWLATSQSR	41	22	4	13.39	b5y3°y3y5	2543.13	62.677	2131	4	636.54	-13.25
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		NVEYFEAR	42	8	8	56.99	y2y3y4y6°y6y7°y7y8	1027.48	47.445	70032	2	514.24	-7.37
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGSGLDQVNVK	8	14	12	103.13	b2b3b6y3y7y9y10°y10y11y12y13y14	1413.77	57.411	69287	2	707.39	0.35
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		DIADAVTAAGVDVAK	97	15	6	39.81	b13y3y4°y4y6y9	1415.74	66.803	58086	2	708.37	-1.12
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		INALETVTIASK	71	12	6	22.21	b2b3°b3y7y11y12	1259.71	61.683	34253	2	630.36	-7.17
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		MQVILLDK	0	8	3	40.79	y3y4y5	959.55	64.808	56238	2	480.28	-12.28
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		TTGEHEVNFQVHSEVFAK	123	18	4	15.53	b5b13°b13y10	2059.01	80.418	8383	3	687.01	11.98
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		LADVLAANAR	57	11	7	66.81	b4b7y4y5°y5y8y9	1084.60	54.003	7192	1	1084.60	-7.20
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	1		AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	8	35	22	153.73	b2b3b6b7b8b9b10b11y2y3y4y7y9°y9y10y15y17y19y20y24y28y35	3487.83	107.575	56211	3	1163.28	7.98
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	2	Carbamidomethyl+C(3)	FICIADASK	112	9	8	76	b5b7y2y4y5y6y7y9	1024.51	51.799	20854	2	512.76	-3.81
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	3		GADVALIGTPDGVK	201	14	4	38.43	b12y5y6y7	1312.70	58.140	26275	2	656.85	-7.44
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	4		GGGAALTR	94	8	3	33.01	b3b4y5	702.40	42.296	23184	1	702.40	21.46
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	5		GQIEGAVSSSDASTEK	43	16	4	27.58	b11y3y5y12	1565.73	32.431	1618	2	783.37	2.34
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	6		QVDILGKFPLPVEVIPMAR	121	19	3	34.48	y5y6y7	2122.19	100.033	36686	3	708.07	-7.36
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	7		GQIEGAVSSSDASTEKLK	43	18	5	22.93	b3°b3b4°b4y11	1806.89	39.814	7498	3	602.97	-7.36
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	8		AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMKQGIEGAVSSSDASTEK	8	51	4	11.71	b3b12°b12y6	5034.45	111.116	3052	4	1259.37	-12.12
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	1		SFELPALPYAK	1	11	8	47.6	b3b4°b4b6y2y4y7y11	1235.66	79.424	25135	2	618.34	-1.88
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	2	Carbamidomethyl+C(22)	TSEGGIFNNAQVWNHTFYWNCLAPNAGGEPTGK	58	34	14	50.58	b1°b1b2°b2b6b11y2y3y4y8y9y10°y10°y10	3708.70	96.372	19238	3	1236.91	2.90
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	3		NARPNYLEHFWALVNWEFVAK	168	21	8	29.94	b1b2b3b5°b5b6b10y1	2604.31	104.451	11215	3	868.77	-2.81
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	4		DALAPHISAETLEYHYGK	12	18	5	30.87	b8b10b15y5y10	2014.95	87.769	21733	2	1007.98	-18.36
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	5		SFELPALPYAKDALAPHISAETLEYHYGK	1	29	3	11.5	b5b12y7	3231.62	81.347	25224	4	808.66	-6.50
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	6		HHQTYVTNLNLIKGTAFEGK	30	21	4	18.85	b4b8y3y6	2385.20	86.573	10230	3	795.74	-13.82
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		QLDPLVVGQEHYDTAR	343	16	11	115.41	b2°b2y3y4y5y6y9y10y11y13y14	1840.89	58.529	56927	3	614.30	-14.06

Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		VALTGLTMAEK	219	11	7	84.59	y3y5y7y8y9y10y11	1133.62	59.967	51079	2	567.31	-6.89
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		GLDVKDLHPiEVPVGK	65	17	6	16.26	b3b9°b9y2y3y17	1844.99	67.877	47835	3	615.67	-12.50
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4		YTLAGTEVSALLGR	247	14	8	24.66	b2b8°b8b9°b9y2y11y14	1450.79	80.221	40569	2	725.90	-0.76
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		TVNMMELIR	156	9	5	38.19	y1y3y4y5y9	1106.56	76.303	38250	2	553.78	-8.05
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		FLSQPFFVAEVFTGSPGK	399	18	6	24.74	b2b17y3y7y13y18	1958.02	99.744	38073	2	979.51	7.36
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	5	22.73	b2y6y7y9y27	3057.41	99.953	37845	3	1019.81	6.95
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	5	51.78	y4y5y6y8y10	1193.60	80.990	31408	2	597.30	-5.11
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		QIASLGIYPAVDPLDSTSR	324	19	5	25.79	b3y4y5y11y19	2003.06	80.671	30208	2	1002.03	6.16
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		MPSAVGYQPTLAEEMGVLQER	261	21	6	24.63	b7b21y3y4y11y21	2306.14	81.765	25094	2	1153.57	9.53
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		AAPSYEELSNSQELLETGIK	112	20	5	21.11	y1y3y12y18y20	2179.10	74.128	21638	2	1090.05	10.31
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		GVQSILQR	359	8	4	40.79	y3y5y6y8	900.52	48.664	15125	2	450.76	-11.05
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		VYDALEVQNGNEK	25	13	5	20.57	b2b3b9y11y13	1478.72	45.235	9552	2	739.86	4.54
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		TGSITSVQAVYVPADDLTDPSPAT TFAHLDATVVLRS	287	37	5	35.96	b7°b7b8b9y19	3815.98	89.104	7673	5	764.00	12.54
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15		TREGNDFYHEMTDSNVIDK	183	19	5	25.79	b3b4b8y9y19	2271.01	68.470	6856	4	568.51	4.09
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16		TIAMGSSDGLR	53	11	3	27.24	b6y9y10	1107.54	44.091	5383	2	554.27	-7.49
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17		IMNVLGEPVDMK	87	12	4	34.15	b6y8y9y11	1345.70	58.067	11214	2	673.35	8.16
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18		DLEHPiEVPVGK	70	12	4	32.42	b5b7b9°b9	1332.70	56.284	6358	2	666.85	-10.17
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19		VSLVYQGMNEPPGNR	202	15	8	36.97	b9°b9b13y4*y4y6y8°y8	1660.80	46.955	1635	3	554.27	-5.59
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20		ATGKIVQVIGAVVDVEFPQDAVP R	1	24	5	23.36	b4y5y6y8°y8	2508.37	44.461	44567	4	627.85	-3.02
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	21	Carbamidomethyl+C(26)	AAPSYEELSNSQELLETGIKVIDLM CPFAK	112	30	18	141.67	b4b5b6b7b8°b8b20b24y4y5y6y7y8°y8y13y22y25y28	3353.69	120.575	37959	3	1118.57	6.41
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	22		VSLVYQGMNEPPGNRLR	202	17	4	39.07	b8b11b12b13	1930.01	84.421	14000	2	965.51	8.35
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	23	Carbamidomethyl+C(6)	VIDLMCPFAKGGK	132	13	3	20.57	b8y3y10	1435.73	57.407	9423	3	479.25	-10.37
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	24	Oxidation+M(17)	GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	4	17.72	b7y8y10y13	3073.40	92.679	27301	4	769.10	5.48
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	25	Oxidation+M(4)	TIAMGSSDGLRR	53	12	5	36.07	b6b7y8y10°y10	1279.65	57.326	4261	2	640.33	7.54
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	26		FLSQPFFVAEVFT	399	13	1	7.34	y5	1531.77	99.730	4670	1	1531.77	-10.84
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	27		DVKDLHPiEVPVGK	67	15	2	7.28	b8°b8	1674.88	67.846	4635	3	558.97	-13.63
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	28		GVQSILQ	359	7	1	9.64	y6	744.42	48.677	1942	2	372.72	-3.12
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		AGLGMMEGVLENVPSAR	78	17	8	43.69	b11b13b14y1y4y6y12y17	1730.87	81.984	47685	2	865.94	5.29
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		VLVLVAAPEGIAALEK	155	16	8	71.82	b2b3b4b5b6b7y9y11	1592.97	86.111	24116	2	796.99	1.84

[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	3		ITVVPILR	70	8	4	53.98	y4y5y6y7	910.60	70.248	10931	2	455.80	-10.86
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	4		NEETLEPVYPYFQK	103	13	3	20.57	b7y5y7	1593.80	66.178	17643	2	797.41	14.71
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	5		ELASEVGSLLTYEATADLETEK	29	22	4	13.39	b6°b6y12y14	2369.21	88.843	3364	2	1185.11	20.92
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	6		AHPDVELYTASIDQGLNEHGYIIP GLGDAGDKIFGTK	171	37	5	16.21	b8b11y3y11y14	3911.93	88.884	21857	4	978.74	-3.99
[P0A2M5]UPP_SALTY Uracil phohoribosyltransferase	7		AGLGMMEGVLENVPSARISVVG MYR	78	25	3	12.37	b15y6y23	2636.35	84.922	18792	3	879.46	6.95
[P55900]SERC_SALTY Phohoserine aminotransferase	1		AQVFNFSSGPAMLPAEVLK	1	19	7	31.52	b6b7°b7b14y13y16y19	2006.06	91.512	26181	2	1003.53	7.55
[P55900]SERC_SALTY Phohoserine aminotransferase	2		GKEFIQVAEEAEQDFRDLNIPSN YK	42	26	8	18.22	b3b9°b9b12°b12y1y4y26	3053.55	132.657	20281	3	1018.52	8.16
[P55900]SERC_SALTY Phohoserine aminotransferase	3		ASIYNAMPIEGVK	335	13	7	39.2	b11y1y8y9*y9y10y13	1392.72	65.399	19567	2	696.86	-0.61
[P55900]SERC_SALTY Phohoserine aminotransferase	4		YGVIIYAGAQK	188	10	8	61	b2b3b4b7b9*b9y4y10	1069.55	44.123	14126	2	535.28	-12.55
[P55900]SERC_SALTY Phohoserine aminotransferase	5		GKEFIQVAEEAEQDFR	42	16	4	24.8	y3y5y7y16	1895.92	53.205	12266	3	632.65	4.44
[P55900]SERC_SALTY Phohoserine aminotransferase	6		ALTDFMIDFER	348	11	7	55.38	b2b5b6y4°y4y5y6	1357.65	90.590	9967	2	679.33	-0.27
[P55900]SERC_SALTY Phohoserine aminotransferase	7	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	4	18.1	b3b12y6y10	2567.22	118.862	3587	3	856.41	1.33
[P55900]SERC_SALTY Phohoserine aminotransferase	8		AELLYGVIDNSDFYR	272	15	3	26.16	y3y4y12	1774.86	107.593	1786	2	887.93	-1.31
[P55900]SERC_SALTY Phohoserine aminotransferase	9		MNVPFQLADNTLDK	297	14	5	27.48	b3b5°b5y5y13	1605.82	58.498	22075	2	803.41	14.98
[P55900]SERC_SALTY Phohoserine aminotransferase	10		GQFAGVPLNLLGDK	77	14	3	19.22	b3b10y6	1428.77	65.224	7911	3	476.93	-9.83
[P55900]SERC_SALTY Phohoserine aminotransferase	11		TTADYVDAGYWAASAIKEAK	91	20	3	14.32	b6y4y16	2131.03	101.292	43987	3	711.01	-1.95
[P55900]SERC_SALTY Phohoserine aminotransferase	12		AELLYGVIDNSDFYRNDVAQANR	272	23	10	56.95	b6b13°b13y4y8y10y12y13 y14°y14	2643.26	79.479	13232	3	881.76	-7.02
[P55900]SERC_SALTY Phohoserine aminotransferase	13	Carbamidomethyl+C(3)	KYCAPQIIDAK	111	11	4	36.63	b3b5b6y10	1306.69	48.843	6600	2	653.85	6.07
[P55900]SERC_SALTY Phohoserine aminotransferase	14		WLKAQGGVAAMHK	254	13	3	28.05	y5y9y10	1396.77	88.732	3400	2	698.89	12.41
[P55900]SERC_SALTY Phohoserine aminotransferase	15		SRMNVPFQLADNTLDK	295	16	3	17.1	b4b8y7	1848.92	69.485	3000	3	616.98	-2.57
[P55900]SERC_SALTY Phohoserine aminotransferase	16		ASIYNAMPIEGVKALTDFMIDFER	335	24	3	12.67	b3b5y7	2731.36	119.615	2146	3	911.12	3.22
[P55900]SERC_SALTY Phohoserine aminotransferase	17		GKEFIQVAEEAEQDFR	42	16	8	55.31	b3°b3b5b10b11y4y7y9	1895.90	42.162	2111	3	632.64	-8.43
[P55900]SERC_SALTY Phohoserine aminotransferase	18		ALTDFMIDFERR	348	12	3	32.42	y3y7y10	1513.77	82.018	1669	2	757.39	13.31
[P55900]SERC_SALTY Phohoserine aminotransferase	19	Phosphoryl.STY(6)	VFLEESFAAGLHALK	311	15	3	24.1	b4y10y11	1711.83	49.844	15227	2	856.42	-2.57
[P55900]SERC_SALTY Phohoserine aminotransferase	20	Carbamidomethyl+C(7); Oxidation+M(17)	LAQQELCDWHGLGTSVMEISHR	20	22	7	30.56	b3b5°b5b9b11°b11y5	2583.20	91.662	9783	4	646.56	-1.70
[P55900]SERC_SALTY Phohoserine aminotransferase	21	Oxidation+M(1)	MNVPFQLADNTLDK	297	14	4	30.65	b3b4b11y10	1621.79	80.244	5183	3	541.27	2.26
[Q8ZRP4]DAPD_SALTY 2	1		EAVNQVISLLDSGALR	28	16	12	81.8	b2°b2b14y2y4y5y6y7y9y12 y13y16	1684.93	92.145	46443	2	842.97	2.61
[Q8ZRP4]DAPD_SALTY 2	2		MQQLQNVIETAER	0	14	9	50.55	b4°b4b12y3y9y11°y11y12 y14	1706.86	86.081	41245	2	853.93	3.93
[Q8ZRP4]DAPD_SALTY 2	3		INDNQVIDGAESR	68	13	4	43.01	y5y6y7y10	1430.69	42.050	22510	2	715.85	0.09
[Q8ZRP4]DAPD_SALTY 2	4		FADYDEAR	89	8	5	53.98	y2y4y5y6y7	986.42	35.332	10739	2	493.71	-6.50

Q8ZRP4 DAPD_SALTY 2	5		IDGQWVTHQWLK	48	12	3	26.19	b3y9y10	1510.76	114.852	4187	3	504.26	-10.26
Q8ZRP4 DAPD_SALTY 2	6		EGFR	100	4	1	12.78	b3	508.26	37.573	11935	1	508.26	13.51
Q8ZRP4 DAPD_SALTY 2	7	Carbamidomethyl+C(28)	NVHLSGGVGIGGVLEPLQANPTIE DNCFIGAR	154	33	6	24.49	b7y3y6y7*y7y10	3417.69	96.016	6380	5	684.34	-21.00
Q8ZRP4 DAPD_SALTY 2	8		AVLLSFR	61	7	3	40.38	y3y4y5	805.49	66.492	4782	2	403.25	-9.02
Q8ZRP4 DAPD_SALTY 2	9		ADITPANVDTVTR	15	13	6	63.19	b4b6b8b9*b9b11	1372.73	91.648	3403	2	686.87	13.34
Q8ZRP4 DAPD_SALTY 2	10		SEVVEGVIVEEGSVISMGVYLGS TK	187	26	4	15.73	b3b10y7y12	2696.40	101.112	3101	3	899.47	10.14
Q8ZRP4 DAPD_SALTY 2	11		IYDRETGEVHYGR	213	13	3	20.57	b7b9y3	1594.78	68.618	4477	2	797.89	9.49
P60446 RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	12	86.58	b1b5*b5b7y1y2y3y5y6y7y 8y10	1115.63	57.258	58269	2	558.32	-10.39
P60446 RL3_SALTY 50S ribosomal protein L3	2		TQDATHGNSLSHR	128	13	4	28.05	y3y6y7y13	1423.65	15.574	6245	3	475.22	-13.55
P60446 RL3_SALTY 50S ribosomal protein L3	3		IFTEDGVSIPVTVIEVEANR	13	20	4	22.45	b13y4y5*y5	2188.14	97.416	2800	3	730.05	-3.12
P60446 RL3_SALTY 50S ribosomal protein L3	4		LAEGEETYVGQSSISVELFADVKK	83	23	5	28.73	b3b6b11*b11b14	2512.29	118.304	1783	3	838.10	4.86
P60446 RL3_SALTY 50S ribosomal protein L3	5		GLWEFR	77	6	2	26.79	b5y4	807.42	46.231	54601	2	404.21	6.35
P60446 RL3_SALTY 50S ribosomal protein L3	6		NLLLVK	184	6	3	39.98	y3y4y5	699.47	56.996	24328	1	699.47	-5.58
P60446 RL3_SALTY 50S ribosomal protein L3	7	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	4	21.66	b5b9y4y15	1738.91	54.679	12654	3	580.31	-21.34
P60446 RL3_SALTY 50S ribosomal protein L3	8	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	6	57.81	y5y6y7y9y12y16	1809.97	56.908	59758	3	603.99	-11.94
P60446 RL3_SALTY 50S ribosomal protein L3	9		IFTEDGVSIPVTVIEVEANRVTQVK	13	25	5	22.64	b3b8y16y18y20	2743.49	94.995	58648	3	915.17	1.33
P60446 RL3_SALTY 50S ribosomal protein L3	10		WNFRTQDATHGNSLSHR	124	17	5	26.06	b6b9b12y7*y7	2026.93	73.867	9069	2	1013.97	-13.49
P60446 RL3_SALTY 50S ribosomal protein L3	11	Phosphoryl STY(6)	AVQVTTGAKK	46	10	4	26.83	b5y6*y6y8	1082.56	26.385	5274	2	541.78	5.75
P60446 RL3_SALTY 50S ribosomal protein L3	12	Phosphoryl STY(10)	VPGSIGQNQTPGK	141	13	3	20.57	b7b9y5	1362.61	58.540	1588	3	454.88	-13.71
O54297 RS4_SALTY 30S ribosomal protein S4	1		VVNIASYQVSPNDVVSIR	128	18	11	76.45	b3y1y2y3y8y9y10y11y13y 14y18	1960.06	72.603	35065	2	980.53	4.42
O54297 RS4_SALTY 30S ribosomal protein S4	2		LSDYGVQLR	47	9	6	45.36	b7y2y5y7y8y9	1050.56	51.737	21377	2	525.78	-1.86
O54297 RS4_SALTY 30S ribosomal protein S4	3		AALELAEQREKPTWLEVDAGK	156	21	6	21.62	b3b7*b7b10y6*y6	2354.25	95.067	6103	3	785.42	6.95
O54297 RS4_SALTY 30S ribosomal protein S4	4		VVNIASYQVSPNDVVSIREK	128	20	3	21.11	b6b8b12	2217.20	96.153	4102	3	739.74	5.62
O54297 RS4_SALTY 30S ribosomal protein S4	5		SDLSADINEHLIVELYSK	188	18	3	15.53	b6b17y3	2046.05	84.509	2634	3	682.69	4.83
O54297 RS4_SALTY 30S ribosomal protein S4	6		GNTGENLLALLEGR	83	14	5	42.29	b5b8b12b13y3	1456.79	70.964	23460	2	728.90	8.97
O54297 RS4_SALTY 30S ribosomal protein S4	7		EAAR	77	4	1	12.78	b3	446.23	45.536	2224	1	446.23	-7.32
O54297 RS4_SALTY 30S ribosomal protein S4	8		IEQAPGQHGARKPR	33	14	5	19.22	b3*b3b8*b8y10	1544.85	54.724	7333	3	515.62	9.09
O54297 RS4_SALTY 30S ribosomal protein S4	9		ASYQVSPNDVVSIREK	132	16	3	21.11	b4b10b12	1791.90	96.128	3893	2	896.46	-11.65
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	1		LNSAVFPSAQGGPLMHVIAGK	251	21	6	22.28	b2b3*b3y3y4y21	2094.10	78.504	39322	3	698.71	-6.76
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	2		SPFVTSGIR	354	9	7	59.8	b1b6b7y4y5y7y9	963.52	49.763	30494	2	482.26	-4.56
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	3		VMQAQGSQLTNK	42	12	8	64.03	b2y2y3y4y6y7y9y12	1304.66	30.544	20542	2	652.83	-2.43
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	4		AVALKEAMEPEFK	272	13	10	76.34	b2b8b9y2y3y4y5y8y9y13	1462.75	56.666	7596	2	731.88	-4.59

P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	5		EAMEPEFK	277	8	5	36.02	b3b5y2y4y8	980.44	44.195	3379	2	490.72	-2.49
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	6	Carbamidomethyl+C(7)	ELAGWMCDVLDNINDEATIER	380	21	4	23.48	y5y10y11*y11	2464.15	101.499	13479	2	1232.58	15.46
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	7		YAEGYPGK	54	8	4	33.01	b3°b3b4y4	884.42	61.033	4976	2	442.71	7.87
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	8		MIIGGFSAYSGVVDWAK	168	17	5	43.43	b7b10y3y4y5	1800.94	106.128	1565	3	600.98	21.56
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	9		GYKVVSOGGTENHLFLDLVDK	305	21	3	13.83	b10y11y14	2304.21	101.320	41470	2	1152.61	-4.98
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	10		LYNIVPYGIDESGKIDYDEMAK	138	22	6	34.88	b3b14y5y11y17y18	2533.21	76.774	37667	3	845.08	-1.06
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	11		VVSGGTENHLFLDLVDKNLTGK	308	23	5	13.01	b10y3y21°y21*y21	2469.30	92.113	31548	4	618.08	-14.73
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	12		NSVPNDPKSPFVTS GIR	346	17	7	53.66	b3b10b11y8y9y11y14	1814.92	52.997	22877	3	605.64	-11.64
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	13		QEEHIELIASENYTSPRVMAQGS QLTNK	25	29	3	11.5	b8y10y12	3301.64	89.491	6577	4	826.16	7.10
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	14		EMNIADYDAELWQAMEQE KVR	4	21	3	23.48	y6y9y10	2569.20	88.238	4883	3	857.07	10.55
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	15	Oxidation+M(15)	LNSAVFPSAQGGPLMHVIAGK	251	21	7	35.09	b3°b3b4°b4y3y14y18	2110.09	84.733	85447	3	704.04	-9.37
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	16	Carbamidomethyl+C(12) ;Oxidation+M(11)	EAEVKELAGWMCDVLDNINDEAT IER	375	26	3	12.11	b4y6y9	3036.39	79.558	10735	4	759.85	-1.77
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	17	Oxidation+M(16)	REMNIADYDAELWQAMEQE K	3	20	3	14.32	b5b12y7	2486.13	30.695	10548	3	829.38	12.47
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	18		SPFVTSGI	354	8	0	1.63		807.43	49.709	2138	2	404.22	1.13
P66038 RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	22	156.13	b3b4b8b9b10°b10b11°b11°b11b12°b12b13°b13b14y3y4y9y11y12y15y16y29	3110.69	98.371	87748	3	1037.57	5.57
P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	18	186.4	b3b4b5b12b13y3y4y5y6y8y9y10y12y14*y14y15y16y19	2109.08	101.294	66139	2	1055.04	9.49
P66038 RISB_SALTY 6	3		GAEAALTALEMINVLK	136	16	7	41.85	b6b7°b7b12°b12y3y4	1643.90	102.943	27494	2	822.46	0.30
P66038 RISB_SALTY 6	4		ANVAAPDAR	5	9	8	54.39	b2°b2y2y3y5y6y7y9	884.45	23.576	13660	2	442.73	-10.35
P66038 RISB_SALTY 6	5		VAIT IAR	14	7	4	53.57	y3y4y5y6	743.47	44.942	11117	2	372.24	-15.11
P66038 RISB_SALTY 6	6		AGNKGAEAAALTALEMINVLK	132	20	3	21.11	b6b8b16	2014.09	97.165	31624	3	672.03	-6.79
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	1		SVDGIQVGEGR	266	11	14	76.2	b1b3b4b7°b7y2y4°y4y5y6°y6y9°y9y11	1116.56	42.189	17570	2	558.78	-1.86
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	2		AAPNTIPTAAK	149	11	8	36.63	b3y1y2y3y8*y8y9y11	1054.58	32.930	16099	2	527.79	-9.49
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	3		ELGIEVR	231	7	4	37.37	b3y2y4y5	815.47	51.787	4654	2	408.24	4.12
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	4		EQVLSR	238	6	1	13.6	y3	731.40	33.494	15852	1	731.40	-5.84
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	5		ADYIWFNGEMVR	5	12	6	36.07	b4b9y7°y7y8°y8	1500.69	60.143	10130	3	500.90	-2.44
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	6		DGVLFTPPFTSSALPGITR	204	19	3	24.06	b4b5b12	1976.02	111.751	2556	2	988.52	-12.66
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	7		IQQAFFGLFTGETEDK	284	16	3	17.1	b8y7y9	1830.85	64.442	1898	4	458.47	-20.00
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	8	Phosphoryl STY(12)	DGVLFTPPFTSSALPGITR	204	19	6	42.78	b5b6b9b10°b10y8	2056.03	105.299	4482	2	1028.52	14.01
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	9	Oxidation+M(11)	ESLYLADEVFMSGTAAEITPVR	244	22	5	28.85	b4b5b10y10y13	2415.14	106.989	24830	3	805.72	-12.84

Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		MQLNSTEISELIK	0	13	11	32.21	b2b12°b12*b12y2y8y10°y10y11*y11y13	1505.79	77.154	44065	2	753.40	-0.49
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	13	60.77	b2b3b8b9b12b14y4y11°y11*y11y12°y12y19	2098.97	69.526	37766	3	700.33	-6.16
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3		ASTISNVVR	201	9	6	53.14	b5y1y3y5y7y9	946.52	38.122	25265	2	473.76	-12.38
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4		ELAAFSQFASDLDDATR	401	17	5	50.5	b6y3y4y5y6	1856.88	88.683	22430	2	928.94	7.89
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		DSVGAVVMGPYADLAEGMK	68	19	8	51.64	b5b7b8y7y10y12y14y19	1909.92	83.783	22150	2	955.47	10.35
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6		QLNSTEISELIK	1	12	9	34.15	b4b7°b9b10*b10y10°y10*y10y12	1374.74	81.364	20675	2	687.87	-7.55
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		QYAPMSVAQQLVLFAAER	434	19	6	25.79	b3y5°y5y6y16y19	2109.10	93.273	19539	2	1055.05	10.07
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		QSVDQPVPQTGYK	139	12	7	35.43	b12°b12y2y7y8y9y12	1349.66	34.898	17492	2	675.33	-5.34
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9	Carbamidomethyl+C(1)	CIYVAIGQK	192	9	5	38.19	b3b5b6y1y9	1051.55	58.136	17329	2	526.28	-5.57
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		ELAAFSQFASDLDDATRK	401	18	5	30.87	b8b13y6y9y11	1984.95	83.473	13035	3	662.32	-7.20
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		DHAPLMQEINQSGGYNDEIEGK	477	22	3	13.39	b4b6y6	2445.12	90.709	6679	2	1223.07	10.58
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12		GPVDNDGFSAVEAIAPGVDR	118	21	3	20.47	b5b13b16	2099.05	82.150	2442	2	1050.03	6.63
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		ILEVPVGR	93	8	3	33.01	b3y5y6	882.53	53.143	43832	2	441.77	-12.73
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		IGSFEAALLAYVDRDHAPLMQEINQSGGYNDEIEGK	463	36	3	10.89	b8b22y11	3950.89	95.362	89799	4	988.48	1.92
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		VVNTLGAPIDGKGPPVDNDGFSAVEAIAPGVDR	106	33	9	26.69	b7*b7b27°b27y6°y6y7y9y15	3263.71	84.366	44076	3	1088.57	5.69
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16		EAFPGDVFLHSRLER	283	17	4	16.26	b3b16°b16y11	2049.04	77.366	2418	3	683.69	-5.96
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17	Oxidation+M(17)	YAIALNLERDSVGAVVMGPYADLAEGMK	59	28	3	11.68	b11b23y12	2969.52	123.010	2032	3	990.51	14.06
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18	Carbamidomethyl+C(1)	CIYVAIGQ	192	8	0	1.63		923.47	58.125	1710	2	462.24	5.88
P64052 EFTS_SALTY Elongation factor Ts	1		ITDVEVLK	104	8	6	56.99	y2y3y4y6y7y8	916.52	49.342	122961	2	458.77	-13.19
P64052 EFTS_SALTY Elongation factor Ts	2		AEITASLVK	1	9	5	54.39	y4y5y6y7y9	931.54	49.383	83904	2	466.27	-9.89
P64052 EFTS_SALTY Elongation factor Ts	3		ALTEANGDIELAIENMRK	25	18	3	22.69	y9y14y16	1988.00	74.663	40412	3	663.34	-7.25
P64052 EFTS_SALTY Elongation factor Ts	4	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	7	57.98	b2b4y2y3y4y5y7	1098.47	21.759	21798	2	549.74	-4.67
P64052 EFTS_SALTY Elongation factor Ts	5		VLDAAVAGK	95	9	4	38.19	y6y7y8y9	843.48	34.421	19724	2	422.24	-14.40
P64052 EFTS_SALTY Elongation factor Ts	6		DAGFQAFADK	85	10	3	41.6	y3y6y8	1069.50	54.646	8893	2	535.25	2.17
P64052 EFTS_SALTY Elongation factor Ts	7		VETDFAAEVAAMSK	267	14	7	58.49	b4b5b10b12b13°b13y4	1468.70	60.342	4624	3	490.24	1.91
P64052 EFTS_SALTY Elongation factor Ts	8		VASLEGDVLGSYQHGAR	134	17	18	144.97	b3°b3b4°b4y3y4y5y7y8°y8*y8y10*y10y11*y11y12y13y15	1758.85	59.639	139748	3	586.95	-17.07
P64052 EFTS_SALTY Elongation factor Ts	9		IGVLVAAK	151	8	3	36.02	b3y3y7	770.50	47.822	49928	2	385.75	-18.69
P64052 EFTS_SALTY Elongation factor Ts	10		IGENINIR	125	8	6	53.98	y3y5y6°y6y7*y7	928.51	45.233	46170	2	464.76	-15.38

[P64052]EFTS_SALTY Elongation factor Ts	11		EYQVQLDIAMQSGKPK	193	16	5	28.25	b5y4y7y8*y8	1834.91	70.912	12309	3	612.31	-15.70
[P64052]EFTS_SALTY Elongation factor Ts	12		ALTEANGDIELAIENMR	25	17	4	22.84	b5b11y5y13	1859.91	60.878	11403	2	930.46	-2.10
[P64052]EFTS_SALTY Elongation factor Ts	13		SVGQLLK	240	7	5	37.37	b5°b5*b5b6y5	744.45	45.586	7675	2	372.73	-18.28
[P64052]EFTS_SALTY Elongation factor Ts	14		QLAMHVAASKPEFVKPEDVSADV VEK	167	26	3	12.11	b13y7y11	2824.41	109.798	3579	3	942.14	-15.99
[P64052]EFTS_SALTY Elongation factor Ts	15		MVEGR	214	5	1	13.19	y4	591.30	39.043	3359	1	591.30	7.43
[P64052]EFTS_SALTY Elongation factor Ts	16		VALVAK	119	6	2	26.79	b4y5	600.41	47.802	3030	1	600.41	3.86
[P64052]EFTS_SALTY Elongation factor Ts	17		FEVGEGIEK VETDFAAEVAAMSK	258	23	8	49.34	b3b5b13y3y4y7y12y14	2457.18	106.179	45736	3	819.73	-0.20
[P64052]EFTS_SALTY Elongation factor Ts	18		DAGFQAFADKVLDAAVAGK	85	19	5	20.62	b3b15*b15y6y15	1893.98	77.251	17676	3	632.00	3.29
[P64052]EFTS_SALTY Elongation factor Ts	19	Phosphoryl STY(12)	EYQVQLDIAMQSGKPK	193	16	6	24.17	b5°b5*b5b10y5y13	1914.90	68.573	60712	3	638.97	3.44
[P64052]EFTS_SALTY Elongation factor Ts	20	Oxidation+M(12)	VETDFAAEVAAMSK	267	14	4	19.22	b4y5y12°y12	1484.70	77.725	13574	2	742.85	1.32
[P64052]EFTS_SALTY Elongation factor Ts	21	Oxidation+M(4)	QLAMHVAASKPEFVKPEDVSADV VEK	167	26	5	15.73	b5b11y9°y9y22	2840.47	101.254	3962	3	947.49	5.59
[P64052]EFTS_SALTY Elongation factor Ts	22		ITASLVK	3	7	2	8.8	b4°b4	731.46	49.394	8655	1	731.46	-14.60
[P64052]EFTS_SALTY Elongation factor Ts	23	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	0	2.04		997.42	21.767	5897	2	499.21	-6.49
[P64052]EFTS_SALTY Elongation factor Ts	24	Carbamidomethyl+C(6)	AGMMDCKK	17	8	0	2.04		940.40	21.740	2711	2	470.70	-3.05
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	1		TMNTPHGDITVFDLR	23	16	11	60.06	b1b2b3b10y2y3y4y6y10y11y16	1787.85	71.618	48892	3	596.62	-13.79
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	2	Carbamidomethyl+C(15)	VQDQNQIPELN VYQCGTYQMHS LSEAQDIAR	113	31	7	37.91	b7b10y4y9y10y11y31	3635.71	75.435	22233	3	1212.57	5.71
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	3	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCR	65	19	5	36.2	b2b11b12b13y13	2097.00	76.472	1504	2	1049.01	8.96
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	4		PLLD SFAVDHTR	1	12	3	35.43	b8b9b10	1370.69	53.269	1507	2	685.85	-11.67
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	5		VADAWKAAMADV LK	99	14	3	27.79	b3b8b12	1488.79	90.641	232310	2	744.90	-1.39
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	6		TGFYMSLIGTPDEQ RVADAWK	84	21	5	21.62	b4y4y9*y9y11	2385.14	85.842	3580	3	795.72	-7.68
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	7	Carbamidomethyl+C(18)	TMNTPHGDITVFDLRFCIPNK	23	22	6	18.1	b5b10y5*y5y19°y19	2547.23	136.287	2388	2	1274.12	-6.71
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	8	Carbamidomethyl+C(15) ;Oxidation+M(20)	VQDQNQIPELN VYQCGTYQMHS LSEAQDIAR	113	31	6	38.35	b4b5b12b13y6*y6	3651.72	99.884	7458	3	1217.91	10.56
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	9	Carbamidomethyl+C(2); Oxidation+M(9)	FCIPNKEVMPEK	39	12	3	35.43	y3y4y5	1507.73	47.476	2341	3	503.25	4.21
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	10	Oxidation+M(2)	TMNTPHGDITVFDLR	23	16	3	17.1	b12y5y11	1803.88	83.177	1542	2	902.45	8.53
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	11		TMNTPHGDITVFDL	23	15	0	4.48		1631.78	71.624	2070	2	816.39	4.86
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	1		TGYLPITTAAYELTR	343	15	11	102.45	b3b4y5y6y7y9°y9y10y11y12y15	1669.88	85.026	95487	2	835.44	1.10
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	2		FLD FLAKPENAAEWHQK	326	17	9	26.06	b2b3y2y4*y4y6°y6y8y17	2044.02	74.062	47301	3	682.01	-2.21

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	3		LGNMPQIR	389	8	5	49.21	b6y4y5y7*y7	928.50	48.445	41818	2	464.75	-8.15
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	4		TGNAPAILQVYEVGTATMMASK	77	22	5	20.79	b3y3y6y15y22	2253.15	94.131	26852	2	1127.08	10.19
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	5		FNQANPDYK	47	9	8	38.19	b2y2y4°y4y7*y7y8y9	1096.50	29.456	15745	2	548.75	-3.56
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	6		NNGFDGTDAVLEFNKPEQVK	212	20	6	45.41	y5y10y12y16y18y20	2222.10	66.096	7248	2	1111.55	12.64
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	7		SGHLLSQPFNSSTPVLYYNKDAFK	132	24	3	12.67	b9b16y6	2713.39	118.865	2125	3	905.13	9.72
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	8		TGYLPITTAAYELTREQGYDDK	343	22	3	13.39	b14y3y11	2553.22	85.578	1577	3	851.75	-10.81
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	9		QMLNKPPLPFTK	374	12	6	32.09	b4*b4b9y4°y4y7	1413.76	61.972	53833	3	471.93	-20.29
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	10		TWQELADYTAK	167	11	6	41.4	b3°b3b5*b5b7y8	1325.64	53.246	15892	2	663.32	-1.47
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	11		TIVDEELESVWTGK	397	14	3	27.79	y3y7y12	1605.81	82.568	15224	2	803.41	5.17
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	12	Carbamidomethyl+C(6)	FYNGDCAMTTASSGLANIR	258	20	4	23.74	y4y11y12°y12	2135.96	61.859	11859	2	1068.48	5.49
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	13		GAPQNAIIGGASLWVMQGK	297	19	4	14.89	b4b14*b14y9	1898.01	84.406	7490	2	949.51	6.43
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	14		DAGINFDESQFVPTVAGYYTDAK	109	23	5	20.05	b12y5°y5y8y12	2508.21	123.385	3880	3	836.74	20.05
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	15		GNYEQNLSAGIAAFR	62	15	6	45.43	b9b10°b10b11y4y11	1610.78	47.501	3453	2	805.89	-9.47
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	16		EVDSLAQR	39	8	4	33.01	b6y6*y6y7	917.49	69.050	2074	2	459.25	19.82
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	17		AGLDPEQPPKTWQELADYTAK	157	21	5	26.64	b4b15y11y14y17	2358.16	73.058	87781	3	786.72	-2.07
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	18		EQGYDKNPGADIATR	358	16	5	42.77	y3y4°y4y8y9	1797.82	41.115	51211	3	599.94	-11.88
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	19		TPQQALDTAVDRGNQLLR	412	18	5	21.66	b3°b3b12y3y12	1996.04	68.930	40178	3	666.02	-7.95
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	20		EVDSLAQRFNQANPDYK	39	17	3	16.26	b7b13y8	1994.98	102.876	13978	2	997.99	11.38
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	21		TWQELADYTAKLR	167	13	5	43.01	b4b5°b5b6b9	1594.81	79.425	9500	2	797.91	-9.03

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	22		GNYEQNL\$AGIAAFRTGNAPAILQVYEVGTATMMASK	62	37	6	16.21	b9b15y5°y5y10y13	3844.89	80.864	6369	6	641.66	-1.52
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	23		LGNMPQIRTIVDEELESVWTGK	389	22	7	28.85	b5b6b14y7°y7y16°y16	2515.29	62.642	2218	4	629.58	2.14
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	24	Phosphoryl.STY(8)	TGYLPITTAAYELTREQGYDYK	343	22	4	18.1	b7b9y4y10	2633.20	51.474	3678	3	878.41	-1.11
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	25	Oxidation+M()	TGNAPAILQVYEVGTATMMASK	77	22	5	20.79	b5y4y13°y13y16	2269.13	69.611	53324	3	757.05	3.55
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	26	Oxidation+M(16)	GAPQNAIIGGASLWVMQGKDK	297	21	3	13.83	b4y6y10	2157.13	65.868	2829	3	719.71	7.24
P0A1P6 GLNA_SALTY Glutamine synthetase	1		AINALANPTTNSYKR	307	15	5	26.16	y5y8°y8y9*y9	1633.86	43.539	29961	3	545.29	-5.16
P0A1P6 GLNA_SALTY Glutamine synthetase	2		LVPGYEAPVMLAYSAR	322	16	7	52.99	b15y2y4y5y9y13y14	1736.91	77.897	27518	2	868.96	2.11
P0A1P6 GLNA_SALTY Glutamine synthetase	3		GGYFPVPPVDSAQDIR	177	16	7	44.83	b3b13y2y4y7y11y12	1717.86	70.501	12474	2	859.43	4.19
P0A1P6 GLNA_SALTY Glutamine synthetase	4		MSAEHVLTMLNEHEVK	0	16	5	24.17	b7b12°b12y9y11	1867.91	87.832	6738	2	934.46	1.05
P0A1P6 GLNA_SALTY Glutamine synthetase	5		ATGIADTVLFGPEPEFFLFDDIR	117	23	8	29.37	b3°b3b4b8°b8b14y2y6	2570.28	117.132	4033	3	857.43	0.19
P0A1P6 GLNA_SALTY Glutamine synthetase	6	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	4	23.36	b6b9b10y4	2565.32	108.405	2252	3	855.78	10.75
P0A1P6 GLNA_SALTY Glutamine synthetase	7	Carbamidomethyl+C(1)	CDILEPGTLQGYDR	89	14	4	19.22	b4b9°b9y7	1636.78	71.442	1823	3	546.27	10.44
P0A1P6 GLNA_SALTY Glutamine synthetase	8		AGGVFTDEAIDAYIALR	430	17	3	23.25	b5y11y12	1781.88	76.802	62637	2	891.44	-16.17
P0A1P6 GLNA_SALTY Glutamine synthetase	9		FNTMTK	225	6	2	26.79	b4y3	741.35	66.000	21194	1	741.35	-7.66
P0A1P6 GLNA_SALTY Glutamine synthetase	10		NLYDLPPEEAK	395	11	3	24.23	b5b7y8	1288.65	45.157	6076	3	430.22	3.98
P0A1P6 GLNA_SALTY Glutamine synthetase	11		AINALANPTTNSYK	307	14	4	32.92	b9b10y6y9	1477.76	48.687	5890	2	739.38	-1.65
P0A1P6 GLNA_SALTY Glutamine synthetase	12		GINESDMVLPDASTAVIDPFFADSTLIIR	59	30	5	24.67	b4b9b10y6y11	3238.63	113.448	5302	3	1080.21	7.76
P0A1P6 GLNA_SALTY Glutamine synthetase	13		SAEHVLTMLNEHEVK	1	15	5	29.35	b5°b5b7b11y5	1736.83	60.919	2915	2	868.92	-16.87
P0A1P6 GLNA_SALTY Glutamine synthetase	14		MTPHPVEFELYYSV	455	14	4	19.22	b4b6y3°y3	1711.82	37.159	2627	3	571.28	12.05
P0A1P6 GLNA_SALTY Glutamine synthetase	15		YAGLSEQALYYIGGVIK	287	17	6	33.63	b4b7°b7b9°b9b10	1845.02	130.043	2156	2	923.01	21.24
P0A1P6 GLNA_SALTY Glutamine synthetase	16		IHPGEAMDKNLYDLPPEEAK	386	20	3	14.32	b6b12y8	2267.12	98.768	76658	3	756.38	9.15
P0A1P6 GLNA_SALTY Glutamine synthetase	17		ATGIADTVLFGPEPEFFLFDDIRFGASISGSHVAIDDIEGAWNSSTK	117	47	9	35.97	b4°b4y6y8y9°y9y10*y10y17	5000.39	69.527	22616	6	834.24	-6.93
P0A1P6 GLNA_SALTY Glutamine synthetase	18		NGTNLFSGDKYAGLSEQALYYIGGVIK	277	27	4	17.95	b5°b5b12b14	2878.47	111.240	9250	3	960.16	3.14
P0A1P6 GLNA_SALTY Glutamine synthetase	19		GKEQHVTIPAHQVNAEFFEFGK	26	22	4	29.67	y3y5y12y15	2495.27	101.733	4259	2	1248.14	13.80
P0A1P6 GLNA_SALTY Glutamine synthetase	20	Phosphoryl STY(13)	LVPGYEAPVMLAYSAR	322	16	6	44.83	b9b11b13b14y3y10	1816.85	58.468	3809	3	606.29	-5.85
P0A1P6 GLNA_SALTY Glutamine synthetase	21	Oxidation+M(1)	MSAEHVLTMLNEHEVK	0	16	5	30.7	b11°b11b12y6y12	1883.91	82.750	22689	2	942.46	8.16

P0A1P6 GLNA_SALTY Glutamine synthetase	22	Oxidation+M(8)	SAEHVLTMLNEHEVK	1	15	4	29.35	b3b5b9y6	1752.84	82.782	3520	3	584.95	-10.59
P0A1P6 GLNA_SALTY Glutamine synthetase	23		NALANPTTNSYKR	309	13	0	4.07		1449.73	43.529	3110	2	725.37	-8.25
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	1		DGTIHQFSAVEQDDQR	154	16	7	27.58	b9*b9y3°y3y5y9y16	1845.85	45.115	36017	3	615.96	9.19
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	2		TLWFYNPFVEQATATWLK	85	18	13	94.15	b3b4b5b6b7*b7b14y2y5y12y13y16y18	2215.15	115.936	24882	2	1108.08	13.34
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	3		FTFTPPQGVTTIDDQR	187	15	5	25.7	b5b9y6y10y15	1721.87	64.455	13284	3	574.63	11.06
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	4		VTDGSGAAVQEGQGDLWVKRPN LFNWHMTQPDESILVSDGK	44	41	3	38.91	b3b4b5	4482.20	83.424	8588	4	1121.31	5.23
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	5		TLWFYNPFVEQATATWLKDATG NTPFMILIAR	85	31	8	37.96	b4b5°b5b6*b6y5y11y31	3602.84	129.266	8365	3	1201.62	7.12
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	6		VTDGSGAAVQEGQGDWVK	44	19	4	14.89	b5°b5b13y7	1916.95	58.001	8028	2	958.98	5.92
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	7		RPNLFNWHMTQPDESILVSDGK	63	22	3	13.39	b11y6y12	2584.23	77.997	10804	3	862.08	-12.00
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	8		ASNGNLK	139	7	6	40.38	b3b5°b5y6°y6*y6	703.38	29.682	4071	1	703.38	12.58
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	9		VSSFHATFTQK	33	11	3	24.23	b6b10y8	1252.61	56.053	3667	2	626.81	-17.35
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	10		NQASDWQQYNIKQDGDNFVLTP K	116	23	5	24.46	b3b21y9y12y20	2709.30	68.484	76068	3	903.77	2.88
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	11		SQQNGAVDPSKFTFTPPQGVTTIDD QR	176	26	8	37.01	b5b6b14y5°y5y6°y6y10	2833.41	86.850	2292	2	1417.21	13.79
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	12		SAYQLKSQQNGAVDPSK	170	17	3	16.26	b10y5y12	1820.89	87.199	1858	4	455.98	-12.60
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	17	62.23	b2°b2b7°b7b9b11y4y6°y6*y6y7y9y10*y10y12*y12y23	2379.23	65.142	133920	3	793.75	-5.03
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	7	29.06	b2b3b5y2y13y14y18	1919.02	85.340	64780	2	960.01	5.34
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3		AQAFTLVAK	24	9	7	59.8	b3b4b5y2y3y7y9	948.54	53.948	56764	2	474.77	-12.74
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	12	52.41	b2b3b11*b11b13b14°b14y4y6y15*y15y17	1837.96	86.166	36471	2	919.48	6.91
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		DLSDVSLSQYAGK	33	13	5	20.57	b2b5b8y1y12	1382.68	60.092	33355	2	691.84	-0.09
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		DLSDVSLSQYAGKR	33	14	10	38.91	b2°b2b4b11*b11b12°b12y7*y7y9	1538.78	55.638	9082	2	769.89	-2.06
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		AVIVLDENDNVIFSQVLVDEITHEPD YDAALNVLK	133	34	3	22.28	b31y12y13	3811.96	118.318	3889	3	1271.32	8.33
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8	Carbamidomethyl+C(15)	FNQLATEVENTVVLCSADLPFA QSR	67	26	6	15.73	b5b7y4°y4y11°y11	2908.42	102.829	1760	3	970.14	-10.74

Q8ZP65 TPX_SALTY Probable thiol peroxidase	9		AVIVLDENDNVIFSQLVDEITHEPDYDAALNVLKA	133	35	21	150.54	b3b4b5b8b10*b10b11°b11y3y5y6y7y12y13y16y19y20y22y24y30y31	3883.01	120.081	77860	3	1295.01	10.81
Q8ZP65 TPX_SALTY Probable thiol peroxidase	10		SQTVHFQGNPV	1	11	4	21.4	y9°y9*y9y10	1213.60	65.085	1639	2	607.31	5.83
P26976 PHON_SALTY Non-ecific acid phohatase	1		NGSYPSGHTAYGTLLALVLSEARPER	150	26	11	18.22	b2*b2b3°b3y1y2y3°y3y8y2y26	2759.38	96.357	57229	4	690.60	-12.30
P26976 PHON_SALTY Non-ecific acid phohatase	2		IFSPVVGAK	85	9	7	61.56	b2b3y3y6y7y8y9	917.54	51.875	40284	2	459.27	-9.98
P26976 PHON_SALTY Non-ecific acid phohatase	3		NLLTMGGYYATASAK	108	15	4	24.1	b10y12y13°y13	1560.77	70.319	39387	2	780.89	0.78
P26976 PHON_SALTY Non-ecific acid phohatase	4		LQTIPAFQK	215	9	6	45.97	b2*b2y3y5y7y9	1045.60	55.801	38738	2	523.30	-7.71
P26976 PHON_SALTY Non-ecific acid phohatase	5		QAAEDADVSVENIAR	70	15	10	63.48	b3b8b10*b10b13°b13y4y9y10y15	1587.76	51.390	7982	2	794.38	1.00
P26976 PHON_SALTY Non-ecific acid phohatase	6	Carbamidomethyl+C(3)	VICGAHWQSDVDAGR	191	15	3	18.08	b8y3y5	1670.77	46.090	4504	2	835.89	0.80
P26976 PHON_SALTY Non-ecific acid phohatase	7		INPK	94	4	1	12.78	y3	471.29	70.498	12545	1	471.29	-13.92
P26976 PHON_SALTY Non-ecific acid phohatase	8	Carbamidomethyl+C(12)	TRPFVLFNHSTCRPEDENTLR	128	21	3	23.48	y8y11y12	2589.30	90.602	8383	3	863.77	15.09
P26976 PHON_SALTY Non-ecific acid phohatase	9		EELNDK	230	6	1	13.6	y5	747.35	33.815	1507	1	747.35	2.37
P26976 PHON_SALTY Non-ecific acid phohatase	10		DTPETWNMLKNLLTMGGYYATASAK	98	25	4	23.03	b4y9y10y17	2776.30	93.811	18685	2	1388.65	-12.05
P26976 PHON_SALTY Non-ecific acid phohatase	11		NNLSKEDHPK	236	11	3	24.23	b10y5y7	1294.66	48.938	11581	2	647.83	-12.35
P26976 PHON_SALTY Non-ecific acid phohatase	12		RGWEFGQSR	182	9	6	54.39	b4b5°b5b6°b6b7	1122.53	97.874	4621	1	1122.53	-10.00
P26976 PHON_SALTY Non-ecific acid phohatase	13		WKQAAEDADVSVENIAR	68	17	4	16.26	b7°b7b15y13	1901.95	73.339	2188	3	634.66	9.50
P26976 PHON_SALTY Non-ecific acid phohatase	14	Oxidation+M(5)	NLLTMGGYYATASAKK	108	16	3	17.1	b8b12y10	1704.88	64.557	11303	3	568.96	8.74
P26976 PHON_SALTY Non-ecific acid phohatase	15	Oxidation+M(12)	INPKDTPETWNMLK	94	14	3	19.22	b11y5y10	1702.83	100.870	2186	2	851.92	-11.90
P26976 PHON_SALTY Non-ecific acid phohatase	16		IFSPVVGAK	85	9	0	1.63		899.53	51.869	4016	2	450.27	-0.34
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		VTDIEPGLVGGTEFSSVR	171	18	7	55.41	b5b13y5y6y7y9y13	1862.95	69.692	24596	2	931.98	2.56
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		AAIEEMMASLPAQWR	58	15	7	36.97	b4°b4b13b15y4y5y11	1703.85	90.666	10205	2	852.43	12.25
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		TYENTTALTPEDITEAVVWWVATLPAHVNIINTVEMMPVTQSFAGLSVHR	199	48	9	35.93	b2b5b8b9b13°b13b14y21y48	5340.63	136.426	5615	4	1335.91	-1.28
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4		GHIINIGSTAGSWPYAGGNVYGATK	126	25	3	12.37	b13y9y19	2491.24	65.310	50581	4	623.57	2.25
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		ASVEDWETMIDTNNK	93	15	3	18.08	b4b7y8	1752.81	72.469	5917	2	876.91	17.48
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6	Oxidation+M()	AAIEEMMASLPAQWR	58	15	4	18.08	b5y8y10°y10	1719.84	93.714	23926	2	860.42	10.08
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7	Oxidation+M(9)	ASVEDWETMIDTNNK	93	15	3	26.16	y4y5y7	1768.76	35.172	8296	4	442.94	-8.01

P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	8	Carbamidomethyl+C(15) ;Oxidation+M(1)	MIVLVTGATAGFGECIAR	0	18	5	21.66	b3b13y5°y5y11	1881.94	81.890	3374	2	941.47	-10.96
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	9	Oxidation+M()	AAIEEMMASLPAQWRDIDLNN AGLALGLEPAHK	58	35	5	39.24	b3b4b10b11b13	3759.92	136.364	2664	3	1253.98	-0.06
P66955 TALB_SALTY Transaldolase B	1	Carbamidomethyl+C(5)	EGINCNLTLFSFAQAR	148	17	6	33.89	b9°b9b10b13y3y16	1953.98	75.146	75102	2	977.49	-4.12
P66955 TALB_SALTY Transaldolase B	2		ELAESEGAIER	250	11	6	41.4	b9°b9y7y8y9y11	1203.59	51.503	35519	2	602.30	5.17
P66955 TALB_SALTY Transaldolase B	3		LSYDTEASIAK	100	11	4	35.99	y8y9y10y11	1197.59	45.107	13598	2	599.30	-5.30
P66955 TALB_SALTY Transaldolase B	4		ISTEVDAR	92	8	5	40.79	y2y3y6y7y8	890.45	28.910	13574	2	445.73	-14.12
P66955 TALB_SALTY Transaldolase B	5		QHGYETVVMGASFR	214	14	5	19.22	b7y5°y5y9y14	1581.76	56.660	10979	2	791.38	5.63
P66955 TALB_SALTY Transaldolase B	6	Carbamidomethyl+C(11)	NVGEILELAGCDR	228	13	6	34.34	b3b7y2y11y12y13	1445.73	74.301	10285	2	723.37	13.76
P66955 TALB_SALTY Transaldolase B	7		LYNDAGISNDR	117	11	7	64.77	b5b8b9y3y7y10y11	1237.59	80.251	6798	3	413.20	6.41
P66955 TALB_SALTY Transaldolase B	8		LASTWQGIR	132	9	6	59.8	b5b6b7y3y5*y5	1031.57	59.441	5176	2	516.29	8.64
P66955 TALB_SALTY Transaldolase B	9		QFTTVVADTGDIAAMK	9	16	3	17.1	b10y6y11	1667.81	59.419	1780	2	834.41	-11.34
P66955 TALB_SALTY Transaldolase B	10		LIDDAVAWAKQSSDR	50	16	3	17.1	b5y11y13	1802.90	79.044	60090	3	601.64	-2.91
P66955 TALB_SALTY Transaldolase B	11		LSFSGEVKARPER	262	13	4	20.57	b6y4°y4y8	1475.79	49.773	29299	2	738.40	-7.20
P66955 TALB_SALTY Transaldolase B	12	Oxidation+M(15)	ITEAEFLWQHHQDPMAYDK	275	19	3	22.67	b7y4y5	2311.06	47.757	1930	4	578.52	-10.14
P66955 TALB_SALTY Transaldolase B	13		STEVDAR	93	7	0	1.22		777.38	28.892	1646	1	777.38	5.42
P0AA07 PTHP_SALTY Phohocarrier protein HPr	1		MFQQEVTITAPNGLHTRPAAQFV K	0	24	14	89.77	b2b3b7b10y1y10y12y13y1 4y16y18y19y20y24	2684.36	63.894	393612	4	671.84	-14.82
P0AA07 PTHP_SALTY Phohocarrier protein HPr	2		GFTSEITVTSNGK	27	13	10	67.8	b4b6°b6b10y5°y5y8y9y11 y13	1340.67	51.308	20442	2	670.84	0.27
P0AA07 PTHP_SALTY Phohocarrier protein HPr	3		LMAELE	79	6	5	53.17	b3b4b5°b5y4	705.34	54.888	191139	1	705.34	-11.60
P0AA07 PTHP_SALTY Phohocarrier protein HPr	4		LQTLGLTQGTVVTTISAEGEDEQKA VEHLVK	49	30	28	185.32	b3°b3*b3b4°b4b5°b5*b5b6 °b6b11*b11b25y3y8y11y1 3°y13*y13y14y15y16y17y1 8y19y20y22y28	3193.67	81.464	509618	4	799.17	-7.87
P0A6B1 ACP_SALTY Acyl carrier protein	1		IIGEQLGVK	10	9	10	64.57	b2b8y1y3y4y7*y7y8*y8y9	956.57	49.805	86972	2	478.79	-9.95
P0A6B1 ACP_SALTY Acyl carrier protein	2		ITTVQAAIDYINGHQA	62	16	8	59.98	b13°b13y4y6y8y11°y11y1 4	1714.88	82.647	20845	2	857.94	3.35
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	11	83.72	b2b4y3y4y6°y6y8y9y10°y1 0y12	1377.65	78.495	105176	2	689.33	-2.48
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AVVESIQR	69	8	13	49.21	b2b5y2*y2y4°y4*y4y5°y5* y5y6*y6y8	901.50	33.502	67480	2	451.25	-13.47
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3	Carbamidomethyl+C(10)	QAGLGGEIICYVA	117	13	3	29.82	b3b5b8	1350.67	81.362	4347	1	1350.67	-2.26
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4	Oxidation+M(5)	AAVTMPSSK	22	9	3	30.41	b5b8y4	907.45	106.512	2648	1	907.45	-3.63
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	1		LLEQEMVSFLFEGK	64	14	7	19.22	b5°b5b7°b7°b7y1y10	1669.87	101.289	31428	2	835.44	9.21

P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	2	Carbamidomethyl+C(4)	TIFCTYLQRDAEGQDFQLYPGELGK	3	25	5	18.77	b7b11*b11b13y7	2949.41	136.400	4168	2	1475.21	1.66
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	3	Carbamidomethyl+C(4)	TIFCTYLQR	3	9	3	30.41	b6y7y8	1201.59	62.056	1944	2	601.30	-8.03
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	4		IYNEISK	29	7	4	40.38	y3y4y6*y6	866.45	39.668	10076	2	433.73	-9.44
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	5		DAWAQWQHK	36	9	4	38.19	b4°b4b6b7	1169.57	60.119	1831	2	585.29	16.39
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	6		IYNEISKDAWAQWQHK	29	16	4	17.1	b9°b9y4y7	2016.97	96.425	1508	3	672.99	-13.31
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	7	Oxidation+M(6)	LLEQEMVSFLFEGKDVHIEGYTPEDK	64	26	3	22.78	y5y6y9	3069.46	102.277	2298	5	614.70	-4.69
Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	9	30.7	b2b3°b3*b3b4*b4y12y14y16	1686.94	90.006	60023	2	843.98	1.01
Q7CR87 SURA_SALTY Chaperone surA	2		ITDEQLDQAIANIAK	90	15	5	25.7	b9b14y5y13y15	1642.87	80.577	50752	2	821.94	3.94
Q7CR87 SURA_SALTY Chaperone surA	3		LAYDGLNYSTYR	117	12	5	22.21	b8°b8y4y10y12	1435.69	59.245	44904	2	718.35	3.49
Q7CR87 SURA_SALTY Chaperone surA	4		LIMDQIILQMGQK	73	13	5	32.21	b5y3y5*y5y6	1530.84	88.139	37033	2	765.92	0.96
Q7CR87 SURA_SALTY Chaperone surA	5		LNAGQAGQQLPDDATLR	50	17	6	33.63	y2y5y7y11y12y17	1767.91	51.653	33616	2	884.46	6.70
Q7CR87 SURA_SALTY Chaperone surA	6		QIGTQNDASTELNLSHILALPENPTSEQVNDAQR	162	35	8	50.03	b2*b2y4y5y6y12y13y35	3816.94	88.786	23487	3	1272.98	10.11
Q7CR87 SURA_SALTY Chaperone surA	7		GQSQSISVTEVHAR	274	14	5	27	y2y6y8y9y14	1498.74	37.685	13726	3	500.25	-13.11
Q7CR87 SURA_SALTY Chaperone surA	8		VAAVVNNGVVLESVDGLMQSVK	27	23	8	50.94	b3b4y7y8y9y13*y13y23	2343.24	91.104	10684	2	1172.12	8.34
Q7CR87 SURA_SALTY Chaperone surA	9		TTFAAAAKEYSQDPGSANQGDDLGWATPDIFDPAFRDALTK	318	41	4	14.08	b9b11b13y14	4301.05	91.627	9728	4	1076.02	2.16
Q7CR87 SURA_SALTY Chaperone surA	10		FSEEAATWMQEQR	405	13	7	58.41	b2y3°y3y4y5y7y8	1612.72	60.064	9179	2	806.86	9.76
Q7CR87 SURA_SALTY Chaperone surA	11		GQISAPVHSSFGWHLIELLDTR	362	22	5	13.39	b10*b10b12*b12y11	2463.31	116.260	2096	3	821.77	12.59
Q7CR87 SURA_SALTY Chaperone surA	12		ITVLPQEVDALAK	149	13	6	52.97	b3°b3b4y9y10y11	1396.80	71.060	46772	2	698.90	-3.15
Q7CR87 SURA_SALTY Chaperone surA	13		QAESIVVEAR	197	10	4	28.59	b7y4°y4y5	1131.58	27.771	4922	2	566.29	12.19
Q7CR87 SURA_SALTY Chaperone surA	14		LAITYSADQQALKGGQMGWGR	214	21	9	64.83	y4y5y8y9y11*y11y14*y14y18	2251.12	65.732	28624	3	751.04	-3.90
Q7CR87 SURA_SALTY Chaperone surA	15		QIGTQNDASTELNLSHILALPENPTSEQVNDAQRQAESIVVEAR	162	45	3	24.37	y4y5y24	4929.47	94.225	7717	4	1233.12	4.06
Q7CR87 SURA_SALTY Chaperone surA	16		KFSEEAATWMQEQR	404	14	6	50.34	b5b6b10y5y6y11	1740.79	57.252	5486	3	580.94	-4.98
Q7CR87 SURA_SALTY Chaperone surA	17		EMIISEVRNNEVR	134	13	3	20.57	b7b12y10	1588.83	71.222	4420	2	794.92	12.29
Q7CR87 SURA_SALTY Chaperone surA	18	PhosphorylSTY(4)	LAITYSADQQALK	214	13	3	28.05	y9y11y12	1501.71	136.405	1871	1	1501.71	-5.45
Q7CR87 SURA_SALTY Chaperone surA	19		PVHSSFGWHLIELLDTR	367	17	1	7.8	b10	2007.06	116.320	4777	3	669.69	6.81
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	1		TLFEPGEMVR	125	10	6	51.78	b2°b2y5y6y7y8	1178.58	65.518	26044	2	589.79	-8.29
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	2		VMGFIGGTSDRPAPISDKVDAIMNR	88	26	6	21.85	b4b8y3y6y13y26	2776.36	55.777	17910	3	926.12	-6.60

[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	3		LHNMEELFGEVMVPTEEVVEIR	31	22	8	43.64	b3b5*b5b8*b8b9y9y10	2600.24	38.245	12108	3	867.42	-13.33
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	4		SEAPK	1	5	1	13.19	b3	531.28	31.143	5925	1	531.28	9.77
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	5		WYVVQAFSGFEGR	8	13	5	32.21	b5*b5y5y6y9	1545.76	58.065	3221	3	515.92	4.34
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	6		VMGFIGGTSDRPAPISDK	88	18	3	22.93	b4y3y4	1847.92	102.260	2367	2	924.46	-7.99
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	7		ATPVELDFSQVEK	167	13	9	47.74	b6b9*b9b11y8*y8y9*y9*y9	1462.71	136.376	1891	1	1462.71	-22.20
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	8		VMGFIGGTSDRPAPISDKVDAIM NR	88	26	5	26.42	b3y5y7y15y21	2776.35	73.417	38261	4	694.84	-9.76
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	9		ATPVELDFSQVEKA	167	14	3	19.22	b7b11y13	1533.78	70.251	14245	2	767.39	-0.40
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	10		TLFEPGEMVRVNDGPFADFNGVV EEVDYEK	125	30	6	19.23	b7b10y4y9y13*y13	3402.61	99.767	8492	4	851.41	6.67
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	11		VNDGPFADFNGVVEEVDYEKSR	135	22	4	13.39	b5y5*y5y10	2486.12	77.308	6698	4	622.29	-10.02
[P0AA02]NUSG_SALTY Transcription antitermination protein nusG	12	Oxidation+M(2)	VMGFIGGTSDRPAPISDK	88	18	5	34.54	b6b8b9b12y11	1863.91	111.139	2934	2	932.46	-9.10
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	1	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLALASGAK	257	25	20	140.77	b2b3b4b5*b5b6*b6b16b25 y3y6y7y8y9y14y16y19y22 y23y25	2684.45	127.573	52770	3	895.49	-0.73
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	2		AFPGLNGMDLAKEVTTAETYR	148	21	5	13.83	b2b8y5*y5y11	2284.13	81.935	6541	3	762.05	2.99
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	3		SEDDLPHFVVAYDFGAK	185	17	5	27.31	b11*b11y6y11y12	1909.89	81.889	2058	3	637.30	-1.85
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	4		SALLVLEDGTQFHGR	3	15	4	24.1	b12b13y2y14	1642.84	60.980	1788	3	548.28	-10.25
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	5		QIVTLTYPHIGNVGTNK	50	17	6	33.89	b4*b4b7b8y7y10	1854.98	55.637	2760	2	927.99	-16.98
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	6		FGHHGGNHPVK	287	11	4	38.21	b6b10y9y10	1186.58	70.459	1712	3	396.20	-3.09
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	7	Carbamidomethyl+C(6)	GAQNGCIIAGDSPDAK	125	16	5	24.17	b5b10*b10y7y12	1573.75	47.556	1548	2	787.38	16.52
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	8		SEDDLPHFVVAYDFGAKR	185	18	3	24.45	y8y12y13	2066.00	97.382	21321	2	1033.51	2.72
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	9	Carbamidomethyl+C(7)	MLVDRGCR	207	8	5	53.98	y3y5y6*y6y7	1006.48	27.727	8970	2	503.74	-12.13
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	10		FGHHGGNHPVKMDMR	287	15	5	36.62	y6*y6y7y11y13	1703.77	73.826	5295	3	568.59	-9.74
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	11	Carbamidomethyl+C(8)	EKGAQNGCIIAGDSPDAK	123	18	4	24.74	b5b10b12y11	1830.89	81.963	2456	3	610.97	13.93
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	12		AFPGLNGMDLAKEVTTAETYR	148	21	4	21.62	b4y3y6y10	2284.12	84.109	1525	3	762.05	-3.10
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	13	Carbamidomethyl+C(18);Oxidation+M(1)	MNPDGIFLSNGPGDPAPCDYAITA IQK	230	27	3	11.88	b8y3y11	2878.37	92.102	5728	3	960.13	12.38

P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	14	Oxidation+M(18)	AIGATGSAGVEVVNTSMTGYQEILTDPSSYSR	18	32	4	24.48	b13b16y9y10	3337.56	96.789	5148	3	1113.19	-9.44
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	15	Oxidation+M(4)	NVVMITAQNHGFAVDEDSL PANLR	302	24	4	19.38	b3b12b17y15	2627.25	97.939	4708	4	657.57	-13.10
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	16		AYDFGAK	195	7	0	4.88		771.37	81.944	2274	1	771.37	4.04
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	17		LAKEVTTAETYR	157	12	0	6.51		1381.74	81.879	2078	2	691.37	2.30
P0A1H3 EFG_SALTY Elongation factor G	1		VYSGVVNSGDTVLSNVK	337	17	14	68.61	b1b2b4b5°b5b14*b14y5y10y11*y11y12y14y17	1737.91	62.811	64372	2	869.46	1.90
P0A1H3 EFG_SALTY Elongation factor G	2		IATDPFVGNLTFFR	323	14	9	50.55	b2b4b10y3y6y7y10y14*y14	1597.84	93.309	53897	2	799.42	2.29
P0A1H3 EFG_SALTY Elongation factor G	3		SGPLAGYPVVDLGVR	562	15	13	74.33	b2b3°b3b6°b6b7°b7y3y4y8y10y11y15	1499.82	76.889	36921	2	750.42	1.47
P0A1H3 EFG_SALTY Elongation factor G	4		ILFYTG VNHK	29	10	5	20.63	y2y6°y6y8y10	1191.64	55.556	35139	2	596.32	-12.91
P0A1H3 EFG_SALTY Elongation factor G	5		IGEVHDDGAATMDWMEQE QER	39	20	9	51.9	b7b8b10b12b13y2y5y9y20	2332.00	62.802	24918	3	778.00	-0.63
P0A1H3 EFG_SALTY Elongation factor G	6		EFNVEANVGK PQVAYREAIR	475	20	6	21.11	b4°b4*b4b7b11y20	2290.18	81.317	23021	2	1145.60	-4.05
P0A1H3 EFG_SALTY Elongation factor G	7		LGANPVPLQLAIGAEEGFTGVVDLVK	161	26	5	18.22	b4y4y10y12y26	2607.42	119.890	21075	3	869.81	-8.33
P0A1H3 EFG_SALTY Elongation factor G	8		GQYGHVVIDMYPLEPGSNPK	512	20	7	32.1	b11y4y6y9°y9*y9y10	2201.05	70.616	19269	3	734.36	-7.21
P0A1H3 EFG_SALTY Elongation factor G	9	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETVWR	104	24	4	18.98	b2y3y6y9	2621.29	86.085	15752	3	874.43	1.02
P0A1H3 EFG_SALTY Elongation factor G	10	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTGDTLCDPENPIILER	378	30	6	16.47	b3b9b25y11*y11y30	3138.62	85.197	13714	3	1046.88	6.38
P0A1H3 EFG_SALTY Elongation factor G	11		NIGISAHIDAGK	11	12	4	29.41	b2y5y6y9	1195.63	45.521	5725	2	598.32	-11.74
P0A1H3 EFG_SALTY Elongation factor G	12		VEVETPEENTGDVIGDLSR	618	19	3	22.67	b11y12y13	2058.98	73.369	2074	2	1030.00	0.83
P0A1H3 EFG_SALTY Elongation factor G	13		EFNVEANVGK PQVAYR	475	16	5	23.63	b4*b4y5*y5y6	1820.91	54.105	28134	3	607.64	-10.39
P0A1H3 EFG_SALTY Elongation factor G	14		YLGGEELTEEEIK	236	13	3	35.04	b10b11b12	1509.73	89.313	10660	2	755.37	-2.26
P0A1H3 EFG_SALTY Elongation factor G	15		VVGQIK	153	6	1	13.6	b4	643.41	45.741	9979	1	643.41	-11.48
P0A1H3 EFG_SALTY Elongation factor G	16	Carbamidomethyl+C(11)	VLNNEILVTCGSAFK	255	16	3	17.1	b5y3y9	1777.92	33.631	6847	3	593.31	-17.85
P0A1H3 EFG_SALTY Elongation factor G	17		LHFGSYHDVDSSELA FK	577	17	4	22.84	b5b13y8y10	1951.95	84.441	5822	3	651.32	15.95
P0A1H3 EFG_SALTY Elongation factor G	18		MEFPEPVISIAVEPK	408	15	5	52.24	b3b4b7b9b10	1685.91	70.498	5751	2	843.46	17.02
P0A1H3 EFG_SALTY Elongation factor G	19		IHAEVPLSEMFYATQLR	653	18	3	24.45	b10b14b15	2062.05	90.131	5021	2	1031.53	1.42
P0A1H3 EFG_SALTY Elongation factor G	20	Carbamidomethyl+C(9)	DVTTGDTLCDPENPIILER	389	19	4	14.89	b8°b8b12y17	2158.05	63.108	3225	3	720.02	6.22
P0A1H3 EFG_SALTY Elongation factor G	21		INIIDTPGHVDFTIEVER	83	18	3	22.69	y8y10y12	2068.04	91.882	2638	2	1034.52	-14.87
P0A1H3 EFG_SALTY Elongation factor G	22		YLGGEELTEEEIKQALR	236	17	4	23.66	b3b5°b5b8	1977.99	73.763	45545	3	660.00	-13.27
P0A1H3 EFG_SALTY Elongation factor G	23		GMLKGQSEVTGVK	639	14	4	19.22	b7b12y13*y13	1462.75	60.172	37045	2	731.88	-4.09
P0A1H3 EFG_SALTY Elongation factor G	24		NIGISAHIDAGKTTTTER	11	18	4	15.53	b9°b9y14y16	1884.95	84.470	7479	2	942.98	-14.57
P0A1H3 EFG_SALTY Elongation factor G	25		AKPVLLEPIMKVEVETPEENTGDVIGDLSR	607	30	4	17.26	y5y11*y11y13	3278.72	84.024	7090	3	1093.58	1.71

[P0A1H3]EFG_SALTY Elongation factor G	26		INIIDTPGHVDFTIEVERSMR	83	21	5	38.1	b11b12y8y10y11	2442.25	96.423	4947	4	611.32	3.20
[P0A1H3]EFG_SALTY Elongation factor G	27		LAKEDPSFR	437	9	4	44.85	b5b8y4y8	1062.55	31.717	3659	2	531.78	-5.40
[P0A1H3]EFG_SALTY Elongation factor G	28	Carbamidomethyl+C(13)	SMRVLDGAVMVYCAVGGVQPQS ETVWR	101	27	14	37.18	b9°b9b12y3y5°y5y7°y7*y7 y8°y8*y8y12°y12	2995.48	136.368	3631	2	1498.24	7.50
[P0A1H3]EFG_SALTY Elongation factor G	29	Phosphoryl STY(8)	YLGGEELTEEEIK	236	13	3	20.57	b5b9y5	1589.71	54.178	22704	3	530.57	12.75
[P0A1H3]EFG_SALTY Elongation factor G	30	Oxidation+M(10)	IHAEVPLSEMGFYATQLR	653	18	5	26.5	b10y4y9*y9y10	2078.04	108.884	1511	2	1039.52	0.35
[P0A1H3]EFG_SALTY Elongation factor G	31		FYTGTVNHK	31	8	0	2.04		965.48	55.571	12117	2	483.25	-0.44
[P0A1H3]EFG_SALTY Elongation factor G	32		EFNVEANVGKPVAYR	475	16	0	6.11		1820.94	81.287	2078	3	607.65	7.37
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	1	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	6	12.67	b2b4°b4y4y11y24	2589.31	82.907	50182	3	863.77	1.51
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	2		SATPAQAQAVHK	176	12	18	99.92	b2b3°b3b12y1y2y3y4y5*y 5y6*y6y7*y7y8y9*y9y12	1208.63	19.690	44492	2	604.82	-6.46
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	3		TQGAAAFEGAVIAYEPVWAIGTG K	152	24	11	47.56	b1°b1b3b4b8b12b16y4y7y 12y24	2407.26	93.738	36141	2	1204.13	12.27
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	4	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	6	28.14	b5b14y3y9y10y23	2433.24	88.330	10068	2	1217.12	13.45
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	5		HMVNELVANLRK	16	12	7	44.82	b3b4b5b7°b7°b7y12	1423.76	58.064	6586	3	475.26	-13.72
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	6		AAAGSHIMLG AQNVDLNLSGAFT GETSAEMLK	52	32	4	13.51	b5b10y5y9	3204.63	62.788	2763	4	801.91	21.10
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	7		HMVNELVANLR	16	11	3	31.22	b3b4b10	1295.68	41.627	1918	2	648.34	-5.09
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	8	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAENEAGKTEE VCAR	117	28	17	154.97	b4b14y3y4y5y6y7y10y11y 12°y12y13y20y21y23y24y 26	3090.44	72.706	111079	3	1030.82	2.29
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	9		HMVNELVANLRK	16	12	4	32.42	b5b9b11°b11	1423.77	63.721	10659	2	712.39	-11.40
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	10		TQGAAAFEGAVIAYEPVWAIGTG KSATPAQAQAVHK	152	36	8	36.59	b5°b5b6°b6°b6b7b10°b10	3596.81	136.277	6937	4	899.96	-12.29
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	11	Oxidation+M(5)	HPLVMGNWK	2	9	3	45.97	y3y5y7	1097.55	67.786	2206	2	549.28	-5.67
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	12		TPAQAQAVHK	178	10	8	61.02	b3°b3b4b5°b5b8°b8b9	1050.56	19.693	17714	2	525.78	-8.60
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	13		PAQAQAVHK	179	9	8	78.98	b3b4b5b6°b6b7°b7b8	949.51	19.693	14110	2	475.26	-13.11
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase	14		ATPAQAQAVHK	177	11	4	17.47	b3°b3b5°b5	1121.59	19.720	1857	2	561.30	-10.23
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	8	45.4	b1b2b3y1y3y7y8y10	1365.68	63.651	44827	2	683.34	-3.04
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2		ATFVVDPPQGIIQAEVTAEGIGR	120	23	14	58.27	b2b3°b3b4b6b10°b10y1y2 y4y5y6y8y23	2384.27	128.477	25447	3	795.43	-5.94
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTELGDVA DHYEELQK	32	31	6	35.38	b2b6°b6b7y7y8	3757.76	119.493	7498	3	1253.26	10.53
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4	Carbamidomethyl+C(13)	AAQYVAAHPEVCPAK	153	16	10	92.69	b3b4b5°b5b6y3y5y8y11y1 2	1668.79	36.053	33219	3	556.93	-16.02
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		LGVDVYSVSTDTHFTHK	63	17	6	27.31	b4°b4b6b7y3°y3	1905.95	67.093	3416	2	953.48	8.97
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6		DTEGR	27	5	2	26.38	y3y4	577.27	74.920	1986	1	577.27	12.79
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7		NGEFIEVTEKDTEGR	17	15	6	36.97	b4b5b7°b7y3y9	1723.81	85.982	2583	3	575.27	-3.47

[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8		YAMIGDPTGALTRNFDNMR	93	19	4	31.51	b3b6b7b10	2143.00	84.704	2407	4	536.50	-4.67
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9		YAMIGDPTGA	93	10	1	7.42	y7	995.44	63.708	6983	2	498.23	-7.60
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	1		VLSEDFQVNQLLDILR	49	17	10	39.63	b8b11*b11b13*b13*b13y2y3y4y17	1989.08	104.639	34496	2	995.04	8.65
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	2		GIEGASLDVPDEFVHSGK	72	18	7	46.69	b4b15y6y10y11y12y18	1856.89	67.515	30308	3	619.63	-7.89
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	3		GGDLGQPQFK	148	11	9	52.37	b3b5b8*b8y1y5y7*y7y11	1193.59	64.331	14916	2	597.30	-1.53
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	4		SRDDLQSVMALVR	135	13	4	29.82	b5b7b11*b11	1489.79	73.807	7893	2	745.40	9.67
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	5		VQAQIQGEEIR	120	11	13	81.58	b1b2*b2y2y4y6*y6y7*y7y8y9*y9y10	1270.67	40.260	4413	2	635.84	-1.73
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	6		GVEATIELNDANK	33	13	3	20.57	b9y5y7	1373.68	92.497	6471	2	687.35	-4.98
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	7		PSFDIVSEVDLQEAR	1	15	7	52.21	b6*b6b12y3y7y10y13	1704.87	84.463	2047	2	852.94	16.40
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	8		DDLQSVMALVRGGDLGQPQFK	137	22	6	34.73	y9*y9*y9y10y11*y11	2421.25	67.972	35275	3	807.76	12.00
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	9		SRDDLQSVMALVR	135	13	4	29.82	b3b8b11*b11	1489.79	108.859	14706	2	745.40	5.49
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	10		GIEGASLDVPDEFVHSGKTWYVEAK	72	25	3	12.37	b4b10y3	2734.35	57.508	12304	3	912.12	5.00
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	11		MPSFDIVSEVDLQEARNGVDNAVR	0	24	4	12.67	b3b12*b12y8	2661.30	58.572	10154	4	666.08	1.74
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	12		RGIEGASLDVPDEFVHSGK	71	19	3	14.89	b3b10y9	2013.01	36.247	9666	3	671.67	1.33
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	13		PSFDIVSEVDLQEARNGVDNAVR	1	23	4	13.01	b11b15y5*y5	2530.25	88.674	5400	4	633.32	0.10
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	14	Phosphoryl STY(5)	GVEATIELNDANK	33	13	6	29.57	b3b6y5*y5y9*y9	1453.64	38.177	22925	3	485.22	-2.94
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	15		GIEGASLDVPDEFVHSGK	72	18	0	5.29		1838.88	67.478	15166	3	613.63	-4.38
[P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	1		LGVQSTEIQASPVAGMK	32	17	10	67.79	b9*y1y6y7y11*y11y12y13y14y17	1715.91	58.102	32477	2	858.46	5.26
[P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	2		QGLESQAEQDMK	146	12	13	87.58	b2*b2b7*b7*b7b8b11y4y7y8*y8y9y10	1363.62	43.493	21658	2	682.31	-0.63
[P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	3	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	HVITVFTDITCGYCHK	108	16	3	17.1	b10y3y5	1950.96	87.987	66064	2	975.98	21.71
[P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	4		TVLTHSGVLYVTDDGK	49	16	4	24.17	b5b7y3y9	1704.84	60.340	18005	2	852.93	-21.41
[P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	5		FMMFTLLAAVFSGVAHADDAAIR	4	23	4	28.73	b6b8b9b11	2454.27	97.831	6635	3	818.76	15.12
[P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	6		YLAFPRQGLESQAEQDMK	140	18	4	21.66	b11b13y3y10	2111.00	72.361	16320	3	704.34	-12.61
[P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	7		FMMFTLLAAVFSGVAHADDAAIR QSLAK	4	28	4	36.32	b9b11b12b13	2981.50	108.863	2532	3	994.50	-12.61
[P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	8	Carbamidomethyl+C(16) ;Carbamidomethyl+C(19))	APDEKHVITVFTDITCGYCHK	103	21	5	24.63	b5*b5y4y11y12	2491.18	92.144	1724	2	1246.09	2.16

P55890 DSBC_SALTY Thiol:disulfide interchange protein dsbC	9	Phosphoryl STY(6)	LGVQSTEIQASPVAGMK	32	17	4	39.07	b3b4b5b8	1795.87	38.199	1590	3	599.30	8.22
P66541 RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAE LNK	45	14	10	30.65	b2b3°b3y2y9y10*y11y12*y12y14	1576.81	84.575	58741	2	788.91	4.65
P66541 RS2_SALTY 30S ribosomal protein S2	2		WLGGMLTNWK	95	10	4	33.82	y4y8y9y10	1205.61	85.574	42963	2	603.31	-2.53
P66541 RS2_SALTY 30S ribosomal protein S2	3		MATVSMR	0	7	4	40.38	b5°b5y4y6	795.40	99.815	8264	1	795.40	13.66
P66541 RS2_SALTY 30S ribosomal protein S2	4		AGVHFHGHQTR	11	10	3	36.83	y3y4y5	1109.55	47.453	2142	1	1109.55	-11.44
P66541 RS2_SALTY 30S ribosomal protein S2	5		DMGGLPDALFVIDADHEHIAIK	152	22	4	22.14	b12°b12b13y12	2377.17	65.196	1660	3	793.06	-8.11
P66541 RS2_SALTY 30S ribosomal protein S2	6		WLGGMLTNWKTVR	95	13	3	29.82	b4b9b11	1561.84	73.193	5876	2	781.43	8.91
P66541 RS2_SALTY 30S ribosomal protein S2	7		YWNPKMKPFIFGAR	21	14	3	27	b7b8b11	1754.92	83.089	5582	2	877.97	2.16
P66541 RS2_SALTY 30S ribosomal protein S2	8		DLETQSQDGTFEKLTK	115	16	3	17.1	b3b13y13	1839.89	77.667	3959	2	920.45	-5.57
P63411 ACKA_SALTY Acetate kinase	1		LDVVFTGGIGENAAMVR	324	18	8	36.88	b2b3b8b12b15°b15y8y18	1819.92	93.761	44587	2	910.46	-11.00
P63411 ACKA_SALTY Acetate kinase	2	Carbamidomethyl+C(19)	FAIDAVNGDEYLSGLAECFHLPEAR	17	26	13	59.69	b2b3b12y4°y4y5y10y12°y12y14y19y22y26	2907.41	104.589	29325	3	969.81	4.37
P63411 ACKA_SALTY Acetate kinase	3		EGTRPAVVIPTNEELVIAQDASR	374	23	11	59.17	b13°b13b15y6y7y11°y11*y11y13y14y15	2465.30	69.493	28928	3	822.44	0.89
P63411 ACKA_SALTY Acetate kinase	4		DSASFAPLHNPAHLIGIAEALK	114	22	5	24.15	b9b13b14y8y22	2272.23	86.500	28761	3	758.08	10.96
P63411 ACKA_SALTY Acetate kinase	5	Carbamidomethyl+C(18)	MLTKESGLLGLEVTSDCR	268	19	5	25.79	b6b7b13°b13y9	2110.02	67.037	4763	4	528.26	-14.69
P63411 ACKA_SALTY Acetate kinase	6		LGVLGFEVDHER	348	12	5	34.15	b10y3y6°y6y7	1370.70	63.812	3699	2	685.85	-6.95
P63411 ACKA_SALTY Acetate kinase	7	Carbamidomethyl+C(1)	CVDTSMGLTPLEGLVMGTR	224	19	8	61.33	b12°b12b13y4y5y10y11y13	2037.02	94.851	21920	2	1019.02	21.39
P63411 ACKA_SALTY Acetate kinase	8	Carbamidomethyl+C(14)	MLNKPVEELNIITCHLGNNGSVSAR	195	26	3	12.11	b9y9y11	2822.46	105.784	2963	3	941.49	-3.37
P63411 ACKA_SALTY Acetate kinase	9		LGVLGFEVDHERNLAAR	348	17	4	27.31	b3b13b14y13	1895.98	88.623	21212	2	948.50	-13.07
P63411 ACKA_SALTY Acetate kinase	10		MDGSKQEAALGAGAAHSEALNFI VNTILAQKPELSAQLTAIGHR	47	44	3	23.73	b5y12y13	4529.33	102.154	14282	5	906.67	-7.01
P63411 ACKA_SALTY Acetate kinase	11	Phosphoryl STY(11)	EGTRPAVVIPTNEELVIAQDASR	374	23	4	13.01	b12_H3PO4 b12°b12b15_HPO3 b15y12	2545.29	91.671	48169	3	849.10	14.68
P63411 ACKA_SALTY Acetate kinase	12	Phosphoryl STY(25)	NVAVFDATAFHQTMPEESYLYALP YSLYKEHGVR	144	33	4	16.82	y5°y5y7y9	3955.85	81.352	3721	4	989.72	5.80
P63411 ACKA_SALTY Acetate kinase	13		DSASFAPLHNPAHLIGIAE	114	19	0	6.92		1959.98	86.480	2254	3	654.00	-8.35
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	12	72.27	b5y2y5y7y8*y8y10y11*y11y13y17y19	2032.90	38.379	66586	3	678.30	-10.33
P02936 OMPA_SALTY Outer membrane protein A	2		STLKPEGQQALDQLYSQLSNLDPK	231	24	4	12.67	b12y2y6y10	2673.38	89.681	26365	3	891.80	3.11
P02936 OMPA_SALTY Outer membrane protein A	3		SDVLFNFNK	222	9	4	44.85	b3b6y5y6	1083.53	69.227	25187	2	542.27	-14.53
P02936 OMPA_SALTY Outer membrane protein A	4		FGQQEAAPV VAPAPAPEVQTK	194	23	8	42.81	b10b11°b11y6y8y10y13y23	2303.23	54.706	8010	2	1152.12	13.36
P02936 OMPA_SALTY Outer membrane protein A	5		LEYQWTNNIGDANTIGTRPDNGL LSVGVSYR	163	31	4	17.09	b2y5y12y16	3423.70	112.855	3893	4	856.68	3.42
P02936 OMPA_SALTY Outer membrane protein A	6		DVVTQPQA	342	8	4	33.01	b6b7y4*y4	857.45	53.190	3186	2	429.23	10.82

[P02936]OMPA_SALTY Outer membrane protein A	7		AQSVVDYLSK	281	11	4	36.63	b6y6y7y9	1222.66	72.543	34087	2	611.83	-4.39
[P02936]OMPA_SALTY Outer membrane protein A	8		LGYPITDDLDVYTR	103	14	4	34.78	y9y10*y10y11	1640.82	76.442	12284	2	820.91	0.67
[P02936]OMPA_SALTY Outer membrane protein A	9		LGYPITDDLDVYTRLGGMVWR	103	21	4	13.83	b13*b13b19y5	2440.21	92.163	104427	3	814.08	-8.20
[P02936]OMPA_SALTY Outer membrane protein A	10	Carbamidomethyl+C(17)	ISARGMGESNPVTGNTCDNVKPR	298	23	4	13.01	b3*b3y8y10	2460.18	70.389	8712	3	820.73	4.56
[P02936]OMPA_SALTY Outer membrane protein A	11		MPYKGDNINGAYK	81	13	5	20.57	b6*b6b11*b11y9	1470.69	136.443	2428	1	1470.69	-10.62
[P02936]OMPA_SALTY Outer membrane protein A	12	Phosphoryl STY(7)	AQSVVDYLSK	281	11	4	27.24	b5*b5y5y6	1302.64	51.515	2263	3	434.88	11.53
[P0A1G5]DKSA_SALTY DnaK suppressor protein	1		TVTHMQDEAANFPDPVDR	57	18	6	40.56	b6y4y6y7y8y18	2042.91	56.429	23508	3	681.64	-7.65
[P0A1G5]DKSA_SALTY DnaK suppressor protein	2	Carbamidomethyl+C(10) ;Carbamidomethyl+C(13))	LEARPTADLCIDCK	125	14	4	27	y6y8y9y14	1661.80	40.964	3215	2	831.40	-0.44
[P0A1G5]DKSA_SALTY DnaK suppressor protein	3		ILEAWR	42	6	2	26.79	b3y3	787.45	36.899	60176	2	394.23	7.13
[P0A1G5]DKSA_SALTY DnaK suppressor protein	4		AAQEEFSLELRNR	75	14	7	45.3	b3b11b12*b12b13*b13y13	1691.81	136.480	2333	1	1691.81	-11.91
[P0A1G5]DKSA_SALTY DnaK suppressor protein	5	Phosphoryl STY(23)	TSSLSILAIGVEPYQEKPGEEYM NEAQLSHFK	8	33	4	22.18	b15y9y10*y10	3746.71	96.343	2391	3	1249.57	-12.71
[P58661]AAT_SALTY Aartate aminotransferase	1		ANYSNPPAHGASIVATILSNDALR	280	24	5	32.81	b3b8b12y6y7	2452.25	86.321	14001	3	818.09	-2.29
[P58661]AAT_SALTY Aartate aminotransferase	2	Carbamidomethyl+C(4)	VGACTLVAADAETVDR	254	16	4	17.1	b3b7y10y16	1647.81	43.571	10580	2	824.41	3.04
[P58661]AAT_SALTY Aartate aminotransferase	3		MFENITAAPADPILGLADLFR	0	21	9	43.9	b2b3b5b7b8y2y3y7y14	2275.20	120.475	10237	2	1138.10	7.62
[P58661]AAT_SALTY Aartate aminotransferase	4		VWVSNPSWPNHK	122	12	4	22.21	b6b8y4*y4	1450.71	54.336	4362	3	484.24	-6.06
[P58661]AAT_SALTY Aartate aminotransferase	5		INLGIGVYKDETGK	28	14	6	38.43	b2b10y7y8y9*y9	1506.82	44.982	2585	2	753.91	2.19
[P58661]AAT_SALTY Aartate aminotransferase	6		GWLPLFD FayQG FAR	204	15	4	10.45	b10*b10y2y13	1787.90	89.948	2254	2	894.45	3.21
[P58661]AAT_SALTY Aartate aminotransferase	7		TAQTPGGTGALR	96	12	3	22.21	b6b8y8	1129.59	42.260	1956	3	377.20	-2.59
[P58661]AAT_SALTY Aartate aminotransferase	8		AIWEQELTDMR	304	11	14	79.21	b4*b4b6*b6b8*b8b9*b9y3° y3y6°y6y7*y7	1391.69	42.216	3412	3	464.57	21.49
[P58661]AAT_SALTY Aartate aminotransferase	9		QNGMFSFSGLTK	343	12	3	22.21	b3b10y11	1316.61	73.182	2675	3	439.54	-19.19
[P58661]AAT_SALTY Aartate aminotransferase	10		EEFGVYAVASGR	362	12	6	44.03	b3b8y6y9*y9y10	1284.62	91.667	2100	2	642.81	-4.66
[P58661]AAT_SALTY Aartate aminotransferase	11		NFGLYNER	246	8	4	36.02	b6y4y7*y7	1012.49	103.023	1634	1	1012.49	2.95
[P58661]AAT_SALTY Aartate aminotransferase	12		ELIVASSYSKNFGLYNER	236	18	6	29.06	b9*b9b11y8y9*y9	2090.06	86.138	41968	3	697.36	1.52
[P58661]AAT_SALTY Aartate aminotransferase	13	Carbamidomethyl+C(27)	EEFGVYAVASGRVNVAGMTPDN MAPLCEAIVAVL	362	34	3	22.28	b12b13y4	3550.76	80.199	26838	4	888.45	7.08
[P58661]AAT_SALTY Aartate aminotransferase	14	Carbamidomethyl+C(4)	VGACTLVAADAETVDRAFSQMK	254	22	5	30.18	b8b10b11b14y4	2340.14	85.856	8142	3	780.72	1.77
[P58661]AAT_SALTY Aartate aminotransferase	15		QLFVNTLQEKGANR	322	14	6	46.69	b4b5b6y4y7°y7	1617.89	36.124	7538	3	539.97	13.66
[P58661]AAT_SALTY Aartate aminotransferase	16		MFENITAAPADPILGLADLFRADD RPGK	0	28	3	11.68	b7b11y11	3014.52	107.382	3075	3	1005.51	-8.10
[P58661]AAT_SALTY Aartate aminotransferase	17		RVWVSNPSWPNHK	121	13	6	66.96	b10b11y8y9y10y11	1606.82	94.883	2314	2	803.91	-5.01
[P58661]AAT_SALTY Aartate aminotransferase	18		AIWEQELTDMRQR	304	13	3	29.82	b6b8b12	1675.82	94.750	1878	2	838.42	1.46

P58661 AAT_SALTY Aartate aminotransferase	19		VWVSNPSWPNH	122	11	1	7.59	y4	1322.63	54.331	16017	3	441.55	2.77
P58661 AAT_SALTY Aartate aminotransferase	20		NLGIGVYKDETGK	29	13	1	7.31	b11	1393.72	44.927	3459	2	697.37	-5.26
P67904 RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAK	16	14	11	78.18	b2b6b9b10y2y3y5y8y9y10y14	1517.81	56.235	63725	2	759.41	2.09
P67904 RS10_SALTY 30S ribosomal protein S10	2		LVDIVEPTEK	72	10	7	61	b2b3y3y4y6y8y10	1142.62	52.519	32116	2	571.82	-5.02
P67904 RS10_SALTY 30S ribosomal protein S10	3		DQYEIR	62	6	2	13.6	y5°y5	823.39	33.006	16270	2	412.20	-1.41
P67904 RS10_SALTY 30S ribosomal protein S10	4		RLVDIVEPTEK	71	11	7	50.61	b4b5b7y4°y4y5°y5	1298.72	51.481	34157	2	649.87	-5.83
P67904 RS10_SALTY 30S ribosomal protein S10	5		GPIPLPTRK	37	9	4	54.39	y3y4y5y6	978.60	43.815	28917	2	489.80	-9.29
P67904 RS10_SALTY 30S ribosomal protein S10	6		AFDHLRIDQSTAEIVETAK	11	19	4	22.67	b12*b12y12y13	2144.07	78.723	2859	3	715.36	-12.64
P67904 RS10_SALTY 30S ribosomal protein S10	7		LIDQSTAEIVE	16	11	3	15.57	y5y7°y7	1217.61	56.187	8223	2	609.31	-11.13
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1		SLTEIKDVLASR	298	12	7	52.57	b4°b4y3y4y6y7y12	1331.73	63.817	56753	2	666.37	-14.85
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2		VTLEPLER	25	8	6	40.79	y1y4°y4y6y7y8	956.53	52.821	34737	2	478.77	-9.32
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3	Carbamidomethyl+C(6)	LLVDACYPVER	170	12	6	61.02	y5y6y7y8y10y12	1421.71	60.042	29090	2	711.36	0.00
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4		LVIEMETNGTIDPEEAIR	200	18	8	32.63	b9°b9*b9b10b12*b12y10y12	2030.03	83.726	11733	3	677.35	8.36
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5		EGVQEDILEILLNLK	71	15	10	79.08	b6b7b8b9*b9b10y2y4y5y15	1725.97	122.103	9731	2	863.49	4.46
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		GFGHTLGNALRR	33	12	3	12.33	b8*b11y5	1298.72	63.854	6305	2	649.86	9.40
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		LVDIEQVSSTHAK	12	13	4	32.21	b3y4y5y11	1426.73	46.120	52744	3	476.25	-18.05
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8		QPEVK	238	5	1	13.19	b4	600.34	31.762	11782	1	600.34	4.58
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9		AEAIHYIGDLVQR	271	13	4	20.57	b11y6y10*y10	1484.76	63.684	9240	3	495.59	-13.98
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	10	Carbamidomethyl+C(10)	RILLSSMPGCAVTEVEIDGVLHEY STK	44	27	4	15.27	b12b18y5y12	3004.50	114.525	114377	4	751.88	-4.71
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	11	Carbamidomethyl+C(18)	IHSEEDERPIGRLLVDACYPVER	158	24	4	19.38	b5b8b10y7	2840.40	62.109	13752	4	710.85	-0.95
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	12		VEQRTDLDK	191	9	3	45.97	b3b6b8	1103.55	39.787	1722	2	552.28	-13.94
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	13	Phosphoryl STY(10)	LVIEMETNGTIDPEEAIIR	200	19	4	28.4	b8b9y10y13	2266.05	90.652	9264	2	1133.53	-9.80

[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	14	Phosphoryl STY(6)	MQGSVTEFLKPR	0	12	3	22.21	b5y7y11	1472.68	73.132	1612	3	491.57	-2.49
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	15	Oxidation+M(5)	LVIEMETNGTIDPEEAIR	200	18	6	32.63	b7b9b10°b10y3y12	2046.02	79.531	2699	4	512.26	4.83
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	16		TEIKDVLASR	300	10	0	2.85		1131.63	63.759	14955	2	566.32	-10.46
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	17	Carbamidomethyl+C(6)	LLVDACYSPVER	170	12	0	2.85		1403.69	60.015	72084	3	468.57	-5.39
[P65692 K6PF_SALTY 6-phohofructokinase	1		IGVLTSGGDAPGMNAAIR	4	18	6	43.57	b3y8y9y12y13y18	1699.89	62.905	23438	2	850.45	3.95
[P65692 K6PF_SALTY 6-phohofructokinase	2	Carbamidomethyl+C(1)	CVGIQNEQLVHHDIIDAENMK	283	22	8	43.89	b3b10y5y8y12°y12y13y20	2576.27	81.519	13078	3	859.43	2.94
[P65692 K6PF_SALTY 6-phohofructokinase	3		FPEFRDENIR	73	10	7	57.98	b2b3b4°b4b5b8y6	1322.65	48.835	8419	3	441.55	-0.09
[P65692 K6PF_SALTY 6-phohofructokinase	4		GGSPVPYDR	253	9	3	30.41	b4y4y5	947.46	33.896	7808	2	474.23	2.51
[P65692 K6PF_SALTY 6-phohofructokinase	5		AALTEGLEVMGIYDGYLGLYEDR	26	23	6	20.05	b5°b5b11b13y2y9	2548.23	83.030	3211	4	637.81	0.57
[P65692 K6PF_SALTY 6-phohofructokinase	6		MGAYAIDLLLEGHGGR	267	16	11	99.35	b3b11b12b13y3y4y6y7y10y13°y13	1672.82	82.126	17073	3	558.28	-16.64
[P65692 K6PF_SALTY 6-phohofructokinase	7	Carbamidomethyl+C(8)	LTEMGFPCIGLPGTIDNDIK	112	20	4	21.11	y5y9y11*y11	2191.12	84.993	6294	3	731.04	18.05
[P65692 K6PF_SALTY 6-phohofructokinase	8		FPEFR	73	5	1	13.19	b3	695.34	48.125	3691	1	695.34	-10.01
[P65692 K6PF_SALTY 6-phohofructokinase	9		GVVRAALTEGLEVMGIYDGYLGLYEDR	22	27	4	25.83	y3y6y8y10	2959.47	56.163	29916	4	740.62	-4.54
[P65692 K6PF_SALTY 6-phohofructokinase	10	Carbamidomethyl+C(11)	HAIVAITEHMC DVDELAHFIEKET GR	215	26	3	22.78	y6y7y17	3021.46	51.354	14751	3	1007.83	2.91
[P65692 K6PF_SALTY 6-phohofructokinase	11		AALTEGLEVMGIYDGYLGLYEDR MVQLDR	26	29	3	21.92	b8y9y10	3290.59	89.020	3670	5	658.92	-5.19
[P65692 K6PF_SALTY 6-phohofructokinase	12	Carbamidomethyl+C(1); Oxidation+M(21)	CVGIQNEQLVHHDIIDAENMK	283	22	3	13.39	b5y5y15	2592.26	117.147	5391	3	864.76	3.86
[P65692 K6PF_SALTY 6-phohofructokinase	13	Oxidation+M(10)	AALTEGLEVMGIYDGYLGLYEDR	26	23	3	13.01	b11y5y7	2564.23	123.724	4243	4	641.81	2.86
[P65692 K6PF_SALTY 6-phohofructokinase	14		GGSPVPYDR	253	9	0	1.63		929.46	33.910	2158	2	465.23	14.25
[P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	1		TSDFIESREYEKPLNVYGYSK	123	21	4	21.62	b7b10b14y7	2525.21	86.878	9968	3	842.41	-2.13
[P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	2		QILPEANSQIVGFR	152	14	5	32.92	b3b13y11*y11y12	1571.86	69.645	8637	2	786.43	2.56
[P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	3		EYEKPLNVYGYSK	131	13	6	29.57	b9b12y5°y5y7°y7	1589.79	48.848	7254	2	795.40	4.30
[P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	4		AESFQAVADATLAYHKK	239	17	6	27.31	b3b4°b4b13y10y17	1849.96	60.907	2142	2	925.48	6.00
[P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	5		GSMASVAFHLNTQLNNGESPK	178	21	3	20.47	b7b9b15	2202.03	75.401	5472	2	1101.52	-15.30
[P67912 HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	6		TSDFIESR	123	8	4	47.96	b6b7y6y7	954.44	76.485	3259	1	954.44	-8.70

[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	7		GSIEYIPFPDK	256	11	3	24.23	b5b7y3	1265.66	93.959	3153	2	633.33	13.50
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	8		FVNLVDLNIADYMDK	38	15	5	41.39	y3y6y9y12°y12	1769.87	92.310	1647	2	885.44	-5.86
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	9		AESFQAVADATLAYHK	239	16	8	35.32	b7*b7b9b10°b10y3y13°y13	1721.85	85.008	1614	2	861.43	0.43
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	10		NAGYDKPFKTV AEGVTEYMAWL NR	284	24	3	22.96	b6b11b12	2760.38	101.023	20404	3	920.80	13.71
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	11		TVAEGVTEYMAWLN RDA	293	17	5	16.26	b8b12°b12y9°y9	1925.89	67.103	4544	2	963.45	-7.16
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	12		YQAFQTQADLTNLRNAGYDKPFK	271	22	4	20.79	b11y6y10y13	2561.30	94.826	2330	3	854.44	8.77
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	13	Oxidation+M(13)	FVNLVDLNIADYMDK	38	15	3	18.08	b12y9y11	1785.89	80.651	1626	4	447.23	11.48
[P11003]METF_SALTY 5	1		EVADFDISVAAYPEVHPEAK	140	20	15	55.86	b1b2b3b9°b9b12b20y1y5y 7°y7y11y12y19y20	2187.03	81.405	100666	3	729.68	-13.28
[P11003]METF_SALTY 5	2	Carbamidomethyl+C(11)	TGLEAAPHLTCIDATRDEL R	80	20	3	21.11	b3b5b9	2239.10	59.873	26892	3	747.04	-6.00
[P11003]METF_SALTY 5	3		FVSVTYGANSGERDR	54	15	6	43	b8b9*b9y5y8y11	1657.79	42.191	6178	3	553.27	-4.27
[P11003]METF_SALTY 5	4		TSEMEQTLWNSIDR	33	14	5	38.36	b3b4y2y9y10	1709.81	77.865	5796	2	855.41	14.99
[P11003]METF_SALTY 5	5		GDLPPGSGKPEMYAADLVGLLK	118	22	5	24.15	b2b3b4b6y13	2228.14	109.384	4082	2	1114.57	-10.19
[P11003]METF_SALTY 5	6		EALNQSLAEVQGQINVSFEFFPPR	9	24	6	23.51	b6b12y1y6y8y18	2720.38	112.114	3922	2	1360.69	3.68
[P11003]METF_SALTY 5	7		GDLPPGSGKPEMYAADLVGLLKE VADFDISVAAYPEVHPEAK	118	42	9	34.83	b3b7b8°b8b9°b9y2y7°y7	4396.27	113.226	2650	3	1466.09	13.55
[P11003]METF_SALTY 5	8		AITQFFFDVESYLR	179	14	3	19.22	b12y8y13	1735.87	99.837	2345	3	579.30	1.55
[P11003]METF_SALTY 5	9	Carbamidomethyl+C(11)	TGLEAAPHLTCIDATR	80	16	3	23.63	b11y11y12	1725.89	101.503	4300	2	863.45	20.09
[P11003]METF_SALTY 5	10		IPSWMSLMFEGLDNDAETR	230	19	3	22.67	b8y4y5	2212.04	111.084	3320	2	1106.52	16.67
[P11003]METF_SALTY 5	11		EGVKDFHFYTLNR	266	13	4	20.57	b4b6y8°y8	1625.82	43.579	80535	2	813.41	6.38
[P11003]METF_SALTY 5	12		AITQFFFDVESYLRFR	179	16	7	60.06	b7b8b9b11b13y8y10	2039.04	58.467	12102	3	680.35	0.24
[P11003]METF_SALTY 5	13		PPGSGKPEMYAADLVGLLK	121	19	1	7.8	b9	1943.05	109.436	6943	2	972.03	7.73
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	1		LFAGNATPELAQR	5	13	8	52.85	b3b4b8y6y10*y10y11y13	1387.74	54.625	21785	2	694.37	1.85
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	2		ITAVIPYFGYAR	84	12	5	32.09	b4b11y5y7y12	1370.74	80.785	14589	2	685.87	-5.43
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	3		VFAYATHPIFSGNAANNLR	243	19	6	29.3	b2b3b16y8y13y16	2063.02	65.818	12070	3	688.34	-14.08
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	4		LYTSLGDAAVGR	22	12	4	29.41	b3°b3b4b10	1222.65	80.288	4334	2	611.83	8.49
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	5	Carbamidomethyl+C(10)	NSVIDEVVVCDTIPLTDEIK	262	20	4	27.81	b4b7y9y10	2259.15	49.789	61084	3	753.72	3.35
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	6		ANVSQVMHIIGDVAGR	198	16	5	35.32	b3b7y5y6y15	1666.86	79.508	2603	2	833.93	-7.84
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	7	Carbamidomethyl+C(11)	GGDIFIQSTCAPTNDNLMELVVM VDALR	49	29	8	25.91	b5b9°b9°b9b10°b10b14y2 1	3192.63	136.379	1550	4	798.91	17.13
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	8		LLNDTDMAIIDKR	182	13	6	32.21	b3b6°b6b7°b7y4	1517.79	40.243	19201	3	506.60	-5.87

P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	9	Phosphoryl STY(5)	TLTLSGMLAEAIRR	288	14	3	24.66	b5y9y10	1611.81	56.644	3927	3	537.94	-6.89
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	10		YATHPIFSGNAANNLR	246	16	3	20.94	b10°b10b11	1745.86	65.816	8341	2	873.43	-8.88
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	11		THPIFSGNAANNLR	248	14	1	7.43	b12	1511.75	65.772	3820	2	756.38	-14.78
P22107 TRAT_SALTY TraT complement resistance protein	1		NTSDKDMSDLQSLIAK	58	16	5	17.1	b9y2y3y5y16	1765.84	66.254	67016	3	589.29	-12.17
P22107 TRAT_SALTY TraT complement resistance protein	2		FEEAKPVLEEQLAK	223	14	8	27.48	b2b3°b3b10y2y6y9y14	1630.86	54.055	42442	3	544.29	-7.63
P22107 TRAT_SALTY TraT complement resistance protein	3		ATVTTDNVAALR	177	12	9	68.77	b9y1y3y5y8°y8y9y10y12	1231.65	46.294	41079	2	616.33	-7.43
P22107 TRAT_SALTY TraT complement resistance protein	4		GYTVVTSPDK	79	10	10	70.38	b2b7b9y2°y2y4y5y6y7y10	1066.53	36.946	10424	2	533.77	-8.24
P22107 TRAT_SALTY TraT complement resistance protein	5	Carbamidomethyl+C(16)	LMMVTLVSSTLALSGCGAMSTAIK	5	24	3	22.96	b3b9b10	2442.28	81.958	19269	3	814.77	14.30
P22107 TRAT_SALTY TraT complement resistance protein	6		IQTSTETGNQHK	196	12	3	29.41	y5y6y10	1343.63	15.159	9771	3	448.55	-21.62
P22107 TRAT_SALTY TraT complement resistance protein	7		DIQAKGYTVVTSPDK	74	15	4	26.16	b3°b3b7b9	1621.83	90.570	4064	2	811.42	-11.21
P22107 TRAT_SALTY TraT complement resistance protein	8	Carbamidomethyl+C(16)	LMMVTLVSSTLALSGCGAMSTAIKK	5	25	3	12.37	b10y10y14	2570.32	76.020	3991	4	643.33	-9.97
P22107 TRAT_SALTY TraT complement resistance protein	9		IQTSTETGNQHKEYQTR	196	16	7	27.58	b8°b8y7°y7°y7y9y11	1891.91	86.458	2501	3	631.31	-10.90
P22107 TRAT_SALTY TraT complement resistance protein	10		GYTVVTSPDKAYYWIQANVLK	79	21	5	21.62	b4°b4b10b14y11	2416.28	103.628	2143	2	1208.64	9.70
P06196 USHA_SALTY Silent protein ushA(0)	1	Carbamidomethyl+C(20)	SLPAGSLAMIVGHSQDPVCMAS ENKK	238	27	9	22.49	b2b16y1y2y9y10°y10°y10y25	2784.31	70.909	31637	4	696.83	-14.99
P06196 USHA_SALTY Silent protein ushA(0)	2		EVAQEGGSVLLLSGGDINTGVPESDLQDAEPDFR	68	34	5	10.97	b2b3y4y9y34	3514.69	80.256	29344	3	1172.24	3.33
P06196 USHA_SALTY Silent protein ushA(0)	3		IAVIGLTTDDTAK	164	13	4	32.21	b3y9y10y12	1317.72	61.374	21912	2	659.36	-3.06
P06196 USHA_SALTY Silent protein ushA(0)	4		GMNLIGYDAMAVGNHEFDNPLTVLR	102	25	8	31.85	b6°b6b8b9b14y1y12y14	2747.36	98.815	20326	3	916.46	11.37
P06196 USHA_SALTY Silent protein ushA(0)	5		VLYTPEIAENPQMLSLLTPFQNK	332	23	6	26.45	b2b9b12y2y5y6	2646.38	101.018	10306	3	882.80	-1.38
P06196 USHA_SALTY Silent protein ushA(0)	6		VQPFGNIVVYADMSGK	425	16	3	17.1	b3b11y13	1724.85	87.011	6624	3	575.62	-9.41
P06196 USHA_SALTY Silent protein ushA(0)	7		IGSVNGLLEGDR	363	12	5	29.41	y5°y5y10y11y12	1229.66	54.337	6065	2	615.34	13.00
P06196 USHA_SALTY Silent protein ushA(0)	8		IGNPEYFTDIEFR	177	13	3	25.34	b3y8y9	1600.76	77.850	4878	3	534.26	-0.76
P06196 USHA_SALTY Silent protein ushA(0)	9		DSIEAGDITYK	410	11	7	47.6	b3b4b9°b9y3y6y11	1211.59	42.176	4802	2	606.30	5.74
P06196 USHA_SALTY Silent protein ushA(0)	10		MATLSFNATGGDGYPR	492	16	5	41.18	b6b7y3y6y13	1657.76	81.443	3675	2	829.38	-4.71
P06196 USHA_SALTY Silent protein ushA(0)	11		ITILHTNDHHGHFWR	33	15	4	29.35	b12y5y7y8	1883.96	67.117	2627	3	628.66	12.12
P06196 USHA_SALTY Silent protein ushA(0)	12		EFIQNSPLDAAFTPNGEVSWL	527	23	4	13.01	b9y2y5y14	2534.25	107.955	1506	2	1267.63	10.69
P06196 USHA_SALTY Silent protein ushA(0)	13		VVIQELNMNEKPDVIAHTTHMGHYDNGDHGSNAPGDVEMAR	197	41	8	15.09	b8°b8°b8b21y4y12°y12y14	4475.04	69.532	23419	6	746.68	-9.49
P06196 USHA_SALTY Silent protein ushA(0)	14	Carbamidomethyl+C(10)	QVNYVPGTPCAPDK	265	14	6	39.7	b7b10b12y5°y5y10	1545.71	70.352	12811	3	515.91	-18.80
P06196 USHA_SALTY Silent protein ushA(0)	15		ADFEFR	297	6	1	13.6	b3	784.37	79.896	2959	1	784.37	7.86
P06196 USHA_SALTY Silent protein ushA(0)	16		FVQTNMGR	379	8	5	40.79	b4°b4b5°b5b6	952.48	70.949	2581	2	476.74	14.67

[P06196]USHA_SALTY Silent protein ushA(0)	17		STGER	145	5	1	13.19	b4	549.26	58.513	2090	1	549.26	-4.33
[P06196]USHA_SALTY Silent protein ushA(0)	18		ADFEFRNGEMK	297	11	5	35.2	b3b8y5y7°y7	1343.62	63.787	2811	3	448.54	9.63
[P06196]USHA_SALTY Silent protein ushA(0)	19		FPFLYANIYQKSTGER	134	16	5	24.8	y4°y4y6y8*y8	1934.00	137.633	2134	2	967.50	8.84
[P06196]USHA_SALTY Silent protein ushA(0)	20	Carbamidomethyl+C(11)	KQVNYVPGTPCAPDK	264	15	8	85.61	y3y7°y7y9y10y12y13y14	1673.84	88.671	1701	2	837.42	3.21
[P06196]USHA_SALTY Silent protein ushA(0)	21	Phosphoryl STY(7)	IAVIGLTTDDTAK	164	13	3	20.57	b7y5y12	1397.68	58.447	7358	2	699.34	-5.41
[P06196]USHA_SALTY Silent protein ushA(0)	22	Phosphoryl STY(5)	TLVDSIRK	60	8	4	40.79	y3y4y6°y6	1011.51	55.667	2916	2	506.26	-8.81
[P06196]USHA_SALTY Silent protein ushA(0)	23	Oxidation+M(12)	EVVDYLTAVAQMKPDSGAYPQL ANVSFVAKEGK	441	33	3	22.18	b11b12y5	3541.81	94.597	1816	4	886.21	7.44
[P06196]USHA_SALTY Silent protein ushA(0)	24		SLPAGSLAMIVGGHSQDPV	238	19	5	17.95	y4*y4y8y13°y13	1835.95	70.907	8162	2	918.48	12.43
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	1	Carbamidomethyl+C(19)	LQDGLPVELVDVVEGLDGCHSAN ITPDNR	110	29	10	52.66	b2b3b4b5y4°y4y8y9y24y29	3132.56	102.498	18626	3	1044.86	10.52
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	2	Carbamidomethyl+C(8)	NPHGEIECVQTLDMMPADFSDTR	206	23	7	39.9	b2b9b10b11y5y7y23	2663.17	78.692	15088	3	888.40	7.61
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	3		YAVGQGPMWVVVNAY	316	15	4	25.7	b5b8y3y5	1653.78	41.148	34111	3	551.93	-20.30
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	4		WAADIHTPDGR	229	12	4	32.42	y3y5°y5y7	1351.66	93.134	22184	2	676.33	-13.55
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	5	Carbamidomethyl+C(2)	ICLFTLSDDGHLVAQEPAEVNTVE GAGPR	150	29	5	22.08	b12b13°b13b19y11	3095.52	79.677	6750	3	1032.51	1.74
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	6		SHHIAVYEITGTQGLLTEK	295	19	3	21.84	b6b10b12	2097.06	84.640	6215	2	1049.04	-15.60
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	7	Carbamidomethyl+C(5)	QYAYCVNELNSSVDVWQLK	187	19	3	24.06	b3b4b13	2316.08	69.589	3971	4	579.78	-6.22
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	8		TASLITVFSVSEDSGVSLSVEGFQPT EAQPR	248	30	3	11.36	b11y5y7	3151.58	117.741	2491	3	1051.20	-1.39
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	9		FVFVGSYNAGNVSVTR	94	16	8	55.31	b3b7b10°b10y6y9y12y13	1716.90	113.264	2143	2	858.96	19.27
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	10	Carbamidomethyl+C(2)	ICLFTLSDDGHLVAQEPAEVNTVE GAGPRHMFHPNR	150	37	4	10.87	b8°b8b13y8	4113.96	97.390	171144	5	823.60	-11.16
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	11	Carbamidomethyl+C(5)	QDRICLFTLSDDGHLVAQEPAEVN TVEGAGPR	147	32	3	11.13	b7b10y9	3494.69	64.292	6633	4	874.43	-0.84
[Q8ZQR4]6PGL_SALTY 6-phohogluconolactonase	12		VLAYRIAPDDGALTFAAESALPGS PTHISTDHHGR	59	35	3	10.92	b5y6y14	3643.88	101.193	3565	4	911.73	14.74
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	1		NFVDYVNSGFYNNTTFHR	54	18	9	47.23	b2y8y10*y10y11y12*y12y16y18	2194.99	75.012	40885	3	732.33	-1.89
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	2		TADKDSATSQFFINVADNAFLDH GQR	116	26	5	22.78	b1y4y10y11°y11	2868.33	86.081	27978	4	717.84	-7.06
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	3		VIPGFMIQGGGFNEQMQQK	72	19	9	33.24	b2b6b9b13b14y1y5*y5y19	2109.00	70.381	15286	2	1055.00	-12.27
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	4		TADKDSATSQFFINVADNAFLDH GQRDFGYAVFGK	116	35	6	34.75	b6b7y3y12*y12y13	3852.80	95.481	13771	5	771.37	-5.26
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	5		GDPHVLLTTSAGNIELENSQK	26	22	4	22.14	b13y8*y8y9	2336.19	110.572	2564	2	1168.60	-9.30
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	6		GMDVADKISQVPTHDVGPYQNV PTKPVVILSAK	154	33	7	31.99	b3b10y3y5y8y11y31	3503.84	68.876	104617	4	876.72	-3.97
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	7		DSATSQFFINVADNAFLDHGQRD FGYAVFGK	120	31	3	11.23	b9b13y6	3437.64	91.735	3385	3	1146.55	7.10
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	8		APVSVKNFVDYVNSGFYNNTTFH R	48	24	3	21.96	b12b13y8	2776.32	100.957	2600	4	694.83	-11.08
[P20753]PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	9		TADKDSATSQFFINVADNAFLDH GQR	116	26	9	55.4	b3b9b11*b11b12b13b14y8*y8	2868.35	92.139	1969	3	956.79	-1.19

P66764 METK_SALTY S-adenosylmethionine synthetase	1		SLQEAVMEEIIPILPSEWLNSTK	197	25	15	75.59	b1b2b3*b3b4*b4b5b6b8b11y3y8y9y12*y12	2856.52	111.216	28695	3	952.84	4.53
P66764 METK_SALTY S-adenosylmethionine synthetase	2	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGR	230	15	4	18.08	b5y3y5y15	1536.74	69.251	18291	2	768.88	8.58
P66764 METK_SALTY S-adenosylmethionine synthetase	3	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGRK	230	16	3	17.1	b6y6y9	1664.81	62.655	15204	3	555.61	-8.07
P66764 METK_SALTY S-adenosylmethionine synthetase	4		ADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHR	109	35	5	10.92	b1b9b15y10°y10	3749.76	84.505	10284	4	938.19	-0.46
P66764 METK_SALTY S-adenosylmethionine synthetase	5		IIVDTYGGMAR	246	11	5	55.84	b9y5y6y7y8	1195.61	53.255	6810	2	598.31	-6.43
P66764 METK_SALTY S-adenosylmethionine synthetase	6		HLFTSESVSEGHDPK	3	15	6	18.08	b3y2y5°y6y10°y10	1669.79	43.547	3479	2	835.40	4.75
P66764 METK_SALTY S-adenosylmethionine synthetase	7		FFINPTGR	222	8	4	33.01	b7*b7y4y5	951.50	60.973	23954	2	476.26	-1.60
P66764 METK_SALTY S-adenosylmethionine synthetase	8	Carbamidomethyl+C(16)	EIGYVHSDMGFDANSCAVLSAIGK	74	24	3	21.96	b14y11y12	2541.18	87.968	6516	3	847.73	2.79
P66764 METK_SALTY S-adenosylmethionine synthetase	9	Carbamidomethyl+C(1)	CEIQVSYAIGVAEPTSIMVETFGTEK	294	26	6	36.15	b5b6°b6b13y3y4	2859.36	93.884	5063	3	953.79	-7.60
P66764 METK_SALTY S-adenosylmethionine synthetase	10		QSPDINQGVDR	98	11	5	24.23	b4b9*b9y9°y9	1228.59	44.121	4594	2	614.80	-4.47
P66764 METK_SALTY S-adenosylmethionine synthetase	11		SAAYAARYVAK	273	11	3	24.23	b7b10y8	1170.64	44.310	20379	2	585.82	9.70
P66764 METK_SALTY S-adenosylmethionine synthetase	12		QSPDINQGVDRADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHR	98	46	3	24.55	y4y9y10	4959.36	88.283	17233	4	1240.60	5.81
P66764 METK_SALTY S-adenosylmethionine synthetase	13		SLQEAVMEEIIPILPSEWLNSTKFFINPTGR	197	33	5	21.56	b3°b3b7b8y13	3788.96	113.187	9465	4	948.00	-8.57
P66764 METK_SALTY S-adenosylmethionine synthetase	14		SQVTFQYDDGKIVIGIDAVVLSTQHAEDIDQK	166	31	3	11.23	b11b17y14	3419.74	79.632	4094	4	855.69	13.56
P66764 METK_SALTY S-adenosylmethionine synthetase	15		TGMVLVGGEITTSAWVDIEETRNTVR	47	27	4	27.08	b7b9b11b12	2947.51	106.103	3712	3	983.18	-1.74
P66764 METK_SALTY S-adenosylmethionine synthetase	16	Carbamidomethyl+C(20)	NTVREIGYVHSDMGFDANSCAVLSAIGK	70	28	5	22.7	b9°b9b12*b12b13	3011.40	93.760	2489	2	1506.20	-12.65
P66764 METK_SALTY S-adenosylmethionine synthetase	17		MAKHLFTSESVSEGHDPK	0	18	5	26.5	b12°b12y4y5y10	1999.96	105.664	2027	3	667.33	4.76
P66764 METK_SALTY S-adenosylmethionine synthetase	18	Phosphoryl STY(8)	EFFDLRPYGLIQLDLLHPIYK	331	22	3	34.73	b5b6b7	2801.39	99.815	2352	4	701.10	-6.80
P66764 METK_SALTY S-adenosylmethionine synthetase	19	Oxidation+M(13)	EFFDLRPYGLIQLDLLHPIYK	331	22	4	13.39	b12°b12y11y13	2737.46	97.013	3035	3	913.16	5.08
P66764 METK_SALTY S-adenosylmethionine synthetase	20	Oxidation+M(14)	ADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHR	109	35	3	16.63	y5y10y12	3765.79	99.822	1691	3	1255.93	9.21
O54296 RS11_SALTY 30S ribosomal protein S11	1		STPFAAQVAAER	57	12	5	29.41	y6y8y9y12*y12	1247.64	50.351	18946	2	624.33	5.48
O54296 RS11_SALTY 30S ribosomal protein S11	2		ALNAAGFR	98	8	5	40.79	y4y5y6*y6y8	819.45	42.675	14566	2	410.23	2.53
O54296 RS11_SALTY 30S ribosomal protein S11	3		QVSDGVAHIHASFNNITIVTITDR	14	23	5	23.09	b3*b3b6b7°b7	2495.27	112.728	11292	3	832.43	0.78
O54296 RS11_SALTY 30S ribosomal protein S11	4	Carbamidomethyl+C(15)	ITNITDVTPIPHNGCRPPK	106	19	6	35	b3*b3y5y7y11y13	2130.12	89.725	1869	3	710.71	3.21
O54296 RS11_SALTY 30S ribosomal protein S11	5	Carbamidomethyl+C(15)	ITNITDVTPIPHNGCRPPKK	106	20	5	22.54	b4b6°b6b12y6	2258.18	90.587	6308	2	1129.59	-12.76
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	1		NIANPIAQILSLALLLR	293	17	9	42.61	b2b3b6y1y5y7y8y13y17	1833.14	137.281	6223	2	917.08	5.93
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	2	Carbamidomethyl+C(9)	LYQGLEAFCPLR	112	12	6	51.02	b5b9b11°b11y5y6	1466.74	62.938	5508	3	489.58	-5.66
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	3		TYPDVELAHMYIDNATMQLIK	214	21	3	12.68	b4°b4b9	2466.20	99.851	2306	2	1233.60	-1.88
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	4		ITTSHYDVGGIAIDNHHGHLPK	37	22	5	28.85	b9b12b13y11y19	2342.24	55.641	65747	5	469.25	20.95

P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	5		AFDTEVYHR	160	9	3	30.41	b5b7y3	1137.53	58.049	13253	2	569.27	-5.37
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	6		GAAAVSTDEMGDIAR	341	16	4	23.63	b3b4y11°y11	1576.78	62.642	6021	2	788.89	10.14
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	7		NYHIAVLPGDGIGPEVMAQALK	3	22	4	18.1	b4b6y6y13	2293.15	108.743	3742	3	765.06	-20.97
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	8		VMDAVR	25	6	1	13.6	y5	690.35	32.986	3078	1	690.35	-11.94
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	9	Carbamidomethyl+C(6)	ATVEGCEQADAILFGSVGGPK	59	21	3	20.47	b4b6b15	2106.02	76.612	2459	3	702.68	1.39
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	10	Carbamidomethyl+C(12)	ADIAANGFDILCVR	124	14	6	30.65	b3°b3b10b11°b11y10	1534.74	73.217	2420	2	767.87	-18.69
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	11		ALEEGVRTGDLAR	328	13	3	20.57	b3b11y6	1386.75	49.758	7531	3	462.92	8.63
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	12		TGDLARGAAAVSTDEMGDIAR	335	22	4	29.3	b4b14b16b17	2190.09	92.541	2390	3	730.70	2.34
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	13		WENLPPESQPERGALLPLR	80	19	8	38.04	b3°b3b7°b7°b7b8°b8b9	2202.16	69.565	2249	3	734.72	-3.77
P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	14		DVELAHMYIDNATMQLIK	217	18	2	12.68	b7b9	2105.07	99.803	5074	2	1053.04	12.99
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	1		IQVTGSEGELGIYPGHAPLLTAIKP GMIR	23	29	18	69.52	b2°b2b3b4b8°b8b16°b16y1y2y5y12y13y16y19y26y27y29	3018.62	82.063	91891	4	755.41	-8.98
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	2		AMTYHLDVVSAEQQMFSGLVEK	1	22	8	32.9	b5b8b11y3y8°y8y13y22	2483.19	90.397	27158	3	828.40	-1.47
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	3		MAMTYHLDVVSAEQQMFSGLVE K	0	23	4	22.04	b10y10°y10y11	2614.27	117.183	1525	3	872.09	12.89
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	4		SSHGDVDYAQASAELAK	107	17	4	22.84	b5b15y6y8	1748.79	46.062	15270	3	583.60	-10.26
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	5	Oxidation+M()	AMTYHLDVVSAEQQMFSGLVEK	1	22	3	22.14	b10b11y5	2499.20	97.967	1767	3	833.74	3.71
O86090 PPK_SALTY Polyphohate kinase	1		IIDSMIAAHNGK	381	13	9	59.17	b5b9y7°y7y8°y8y10y11y13	1406.71	78.700	27816	2	703.86	-9.81
O86090 PPK_SALTY Polyphohate kinase	2		VLQEAADK	20	8	9	49.21	b1b4°b4y3y4°y4y5°y5y8	873.47	32.470	15511	2	437.24	-2.93
O86090 PPK_SALTY Polyphohate kinase	3		YHNFKDFINFPNVGK	293	15	4	18.08	b2b6b11y7	1839.92	66.130	11026	3	613.98	-1.46
O86090 PPK_SALTY Polyphohate kinase	4		VFNFIENPYRPVTFDYLMVSPQNS RR	486	26	11	57.01	b1b3b4°b4b7b8b12b24y5y12y22	3189.62	109.352	7115	3	1063.88	8.42
O86090 PPK_SALTY Polyphohate kinase	5		DMPAALVDVLREK	266	13	3	29.82	b4b6b11	1456.79	94.721	4079	2	728.90	4.86
O86090 PPK_SALTY Polyphohate kinase	6		VFNFIENPYRPVTFDYLMVSPQNS R	486	25	6	18.77	b13°b13y3y6y9°y9	3033.44	94.998	14292	3	1011.82	-18.59
O86090 PPK_SALTY Polyphohate kinase	7		FLGIYSNNLDEFYK	37	14	3	19.22	b6y3y6	1722.86	74.189	11412	3	574.96	11.76
O86090 PPK_SALTY Polyphohate kinase	8		VQAQLAIYDYIK	670	12	5	26.19	b9b10y11°y11°y11	1424.80	66.622	11378	2	712.91	17.91
O86090 PPK_SALTY Polyphohate kinase	9		ADQEFDGLYNELLEMAR	86	18	5	26.5	b13y5y6y13°y13	2127.04	96.990	10458	2	1064.02	16.30
O86090 PPK_SALTY Polyphohate kinase	10		VYIFENGSDK	594	10	5	33.82	b5°b5b6b8°b8	1141.56	56.643	9354	2	571.28	7.06
O86090 PPK_SALTY Polyphohate kinase	11		QLSVNQSWLR	113	11	3	35.99	b5b6b7	1358.72	47.456	4873	2	679.86	1.80
O86090 PPK_SALTY Polyphohate kinase	12		YDSIVPGGR	284	9	4	45.36	b4b5b8y7	963.47	105.270	3202	1	963.47	-15.90
O86090 PPK_SALTY Polyphohate kinase	13		HLWFDK	320	6	1	13.6	y3	845.44	42.648	2160	1	845.44	12.49
O86090 PPK_SALTY Polyphohate kinase	14		DAEYDLVHEMESSLMELMSSSLK	229	23	3	13.01	b6b9y7	2644.21	136.193	1830	4	661.81	8.49

O86090 PPK_SALTY Polyphohate kinase	15		GDTINYALLEIPSDK	163	15	3	18.08	b3y3y5	1648.81	56.687	1750	2	824.91	-17.77
O86090 PPK_SALTY Polyphohate kinase	16		IIDSMIHAAHNGKK	381	14	3	24.66	b13y11y12	1534.79	85.365	25831	2	767.90	-13.68
O86090 PPK_SALTY Polyphohate kinase	17		TARLYTDYSLLTADAR	463	16	3	17.1	b5b10y10	1829.96	90.077	14979	2	915.48	9.67
O86090 PPK_SALTY Polyphohate kinase	18		LYTDYSLLTADARITNEVR	466	19	7	37.08	b3b7b11°b11y4°y4y5	2214.17	73.292	9749	2	1107.59	12.24
O86090 PPK_SALTY Polyphohate kinase	19		IIISEEQGSNSHSRHLLGK	60	19	6	39.77	b9b11b12b13y14°y14	2105.08	103.207	6810	3	702.37	-13.22
O86090 PPK_SALTY Polyphohate kinase	20		DSRIIDSMIHAAHNGK	378	16	3	23.63	b10b11y9	1764.89	84.320	4237	2	882.95	5.26
O86090 PPK_SALTY Polyphohate kinase	21		LYIEKELSWLAFNER	5	15	5	46.8	b10y4y5y7y8	1911.01	59.646	3285	3	637.67	3.26
O86090 PPK_SALTY Polyphohate kinase	22		ELSWLAFNERVLQEADK	10	18	8	38.27	b5b7b11°b11*b11y4°y4y5	2119.10	114.499	2783	2	1060.05	6.22
O86090 PPK_SALTY Polyphohate kinase	23		YLEHDRVYIFENGSDK	588	16	3	17.1	b4b11y12	1954.92	80.388	2114	2	977.96	-4.87
O86090 PPK_SALTY Polyphohate kinase	24	Phosphoryl STY(11)	EIANAQQGLPSGITLK	520	16	9	52.99	b3b6*b6b7*b7b10*b10b11y6	1719.84	57.334	4030	3	573.95	-9.23
O86090 PPK_SALTY Polyphohate kinase	25	Oxidation+M(18)	VFNFIENPYRPVTFDYL MVSPQNSRR	486	26	4	12.11	b8y4*y4y18	3205.54	83.736	7799	4	802.14	-13.71