

MA6926 LC-MS run 3: 6926_220709_1a2_03

Protein name	Peptide Rank	Peptide Modification	Sequence	Peptide sequence start	Peptide sequence Length	Peptide Matched Products	Peptide Score	By Matches	Precursor MH+ (Da)	Retention time (min)	Intensity	z	Precursor m/z	MH+ Error (ppm)
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	1		IAAANVPAFVSGK	70	13	24	181.33	b2b3b4b5*b5b6*b6y1y2y3y4y5y6y7°y7y8y9y10*y10y11*y11y12*y12y13	1244.69	58.328	599331	2	622.85	-6.47
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVGFGTFK	22	29	38	334.73	b2b3b4°b4b6°b6b7°b7b8b9b14b23b24b25b26b27y2y3y4y5y6y7y10y11y12*y12y14y15y19y20y21y22y23y24y25y26y29*y29	2966.57	114.152	566794	3	989.53	0.16
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	3		AALESTLAAITESLK	22	15	5	25.8	b2b3b6y5y7	1517.85	96.135	56863	2	759.43	1.93
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	4		TQLIDVIADK	3	10	5	41.68	b2y3y6y8y10	1115.62	64.819	20545	2	558.32	-5.47
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	5		EGDAVQLVGFGTFK	37	14	5	34.85	b10°b10b11b12°b12	1467.74	54.601	3189	2	734.37	-6.99
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	6		NPQTGK	61	6	1	13.62	b5	644.34	36.657	14877	1	644.34	0.66
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	7		TQLIDVIADKAELSK	3	15	23	200.8	b3b4b5°b5b6°b6°b6b12y3y4°y4y5°y5y6y7°y7y8y9°y9y10y11y12y13	1643.90	70.718	629947	3	548.64	-12.99
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	8		EGDAVQLVGFGTF	37	13	0	3.64		1339.65	54.613	32997	2	670.33	-5.29
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	1		AAADLQLQGVPAMFVNGK	158	18	31	247.11	b2b5b6°b6°b6b7°b7b8b9b10b12b14b15y2y3*y3y4y5*y5y6y7y8*y8y9*y9y10y11*y11y12y13y18	1829.96	79.867	182477	2	915.48	1.40
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	2		YQINPQGMDTSSMDVVFVQYADTVK	176	25	19	90.03	b2°b2b3b4b6°b6b15b25y2y3y4y5y6°y6y7°y7y9y12y25	2865.32	85.600	104293	3	955.78	4.26
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	3		TQTVQSAADIR	116	11	15	98.19	b2°b2b6b8b11y2y3y5y6y7°y7*y7y8y9y11	1189.61	34.089	50096	2	595.31	-4.21
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		ELTQAWAVAMALGVEDKVTVPLFEAVQK	88	28	6	26.84	b5°b5°b5b6b13b17	3043.61	115.801	3600	3	1015.21	-2.41
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	5	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	3	23.72	y3y6y8	1847.94	77.224	2345	3	616.65	11.23
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	6		PAMFVNGK	168	8	4	48.14	b3b4b5b6	863.43	79.877	4266	1	863.43	-13.64
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	7		QYADTVK	194	7	0	8.08		824.41	85.629	1984	1	824.41	-9.62
P0A1H5 EFTU_SALTY Elongation factor Tu	1		AIDKPFLLPIDVFSISGR	205	19	23	177.15	b2b4b6b7b8b12b13y1y2y3y4y5y6°y6y7y8°y8y9°y9y11y15y17y19	2117.15	103.712	687115	3	706.39	-8.88
P0A1H5 EFTU_SALTY Elongation factor Tu	2		AGENVGVLLR	270	10	17	129.45	b2b3b4b5°b5b10y2y3y4y5y6y7°y7y8y9*y9y10	1027.58	55.046	564970	2	514.29	-9.98

P0A1H5 EFTU_SALTY Elongation factor Tu	3		IELAGFLDSYIPEPER	188	17	30	284.91	b2b3b4b5b6b7b8b9b12°b12b14y1y3°y3y4y5°y5y6y7y8°y8y9y10y11y12y13y14°y14y15y17	1962.03	101.086	472059	2	981.52	6.22
P0A1H5 EFTU_SALTY Elongation factor Tu	4		TTLTAAITTVLAK	25	13	24	168.11	b1°b1b2°b2b3°b3b4°b4b5°b5b6°b6b13y2y3y4y5y6y7y8y9y10y11y13	1303.78	83.538	424505	2	652.40	0.37
P0A1H5 EFTU_SALTY Elongation factor Tu	5		ELLSQYDFPGDDTPIVR	155	17	34	264.7	b2°b2b5°b5b6°b6b7°b7b8°b8°b8b9b12b13b16y1y3y4y5y6y7y8y9°y9y10°y10y11y12y13y14°y14*y14y15y17	1964.97	75.817	423214	2	982.99	6.15
P0A1H5 EFTU_SALTY Elongation factor Tu	6		QVGVPIIVFLNK	124	13	10	76.53	b3°b3b4b13y4y5y6y9y11y13	1489.88	98.171	345893	2	745.44	-1.15
P0A1H5 EFTU_SALTY Elongation factor Tu	7		TTDVTGTIELPEGVEMVMPGDNI K	334	24	44	318.95	b1°b1b2°b2b3°b3b4b5°b5b6b7b8°b8b9°b9b10°b10b11b15b16b17°b17b18y2y3y4y6°y6*y6y7°y7*y7y8y9°y9y10y11y12y13y14°y14y15y16y24	2546.27	85.853	259819	2	1273.64	11.41
P0A1H5 EFTU_SALTY Elongation factor Tu	8		VGEEVEIVGIK	238	11	11	111.41	b2b3b5y3y4y5y7y8y9y10y11	1171.65	58.991	134140	2	586.33	-5.00
P0A1H5 EFTU_SALTY Elongation factor Tu	9	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEV	137	18	21	160.01	b2b3b4b5b8y2y3°y3y4y5°y5y6°y6y7y8°y8y11y12y13y14y18	2224.01	105.298	121572	2	1112.51	11.42
P0A1H5 EFTU_SALTY Elongation factor Tu	10	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	8	68.12	b2°b2y2y3y4y6y7y8	1187.52	51.475	120119	2	594.26	-0.82
P0A1H5 EFTU_SALTY Elongation factor Tu	11		ALEGDAEWEAK	177	11	7	47.53	b2y4y5°y5y6y9y11	1218.57	44.731	66537	2	609.79	2.00
P0A1H5 EFTU_SALTY Elongation factor Tu	12	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	4	26.22	y4y7°y7y8	1768.77	34.433	7143	3	590.26	-6.35
P0A1H5 EFTU_SALTY Elongation factor Tu	13		NMITGAAQMDGAILVVAATDGP MPQTR	90	27	4	22.55	b8b9b13y8	2729.33	126.083	2882	3	910.45	-3.85
P0A1H5 EFTU_SALTY Elongation factor Tu	14		MVVTLIHPIAMDDGLR	358	16	21	208.98	b3b5°b5b6b7°b7b13y3y4y5y6y7y8y9°y9y10°y10y11y12y13y15	1780.92	77.952	778687	3	594.31	-15.83
P0A1H5 EFTU_SALTY Elongation factor Tu	15		GITINTSHVEYDTPTR	59	16	27	208.98	b3°b3b4°b4b9b10b12°b12y3y4°y4y5y6y7y8y9°y9y10°y10y11°y11y12°y12y13°y13y14°y14	1803.86	48.274	407746	3	601.96	-15.83
P0A1H5 EFTU_SALTY Elongation factor Tu	16		TVGAGVVAK	382	9	8	79.18	b3°b3b6°b6y3y5y7y8	801.47	27.443	167900	2	401.24	-21.25
P0A1H5 EFTU_SALTY Elongation factor Tu	17		EHILLGR	117	7	5	50.68	b3°b3y3y4y5	837.48	39.481	96575	2	419.24	-18.58
P0A1H5 EFTU_SALTY Elongation factor Tu	18		GYRPQFYFR	325	9	5	59.94	b3b4b5y4y6	1233.59	58.404	64849	3	411.87	-17.81
P0A1H5 EFTU_SALTY Elongation factor Tu	19		LLDEGR	264	6	2	26.85	y4y5	702.37	25.861	20838	1	702.37	-9.21
P0A1H5 EFTU_SALTY Elongation factor Tu	20		TKPHVNVGTIGHVDHGK	8	17	6	26.15	b4°b4y3y5y7°y7	1795.92	36.555	12078	4	449.74	-18.15
P0A1H5 EFTU_SALTY Elongation factor Tu	21		GIIK	234	4	1	12.82	b3	430.30	43.602	4805	1	430.30	3.05
P0A1H5 EFTU_SALTY Elongation factor Tu	22		HTPFFK	319	6	1	13.62	b4	776.40	42.959	3298	2	388.71	-7.70

P0A1H5 EFTU_SALTY Elongation factor Tu	23	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLE LVEMEV	124	31	4	22.04	b3y5°y5y6	3694.86	126.857	16632	3	1232.29	3.83
P0A1H5 EFTU_SALTY Elongation factor Tu	24		HTPFFKGYRPQFYFR	319	15	4	18.14	b3°b3b10y3	1991.01	59.935	5328	3	664.34	1.53
P0A1H5 EFTU_SALTY Elongation factor Tu	25		ARGITINTSHVEYDTPTR	57	18	6	44.33	y5°y5y8y9y12y14	2031.01	93.047	2898	2	1016.01	-6.43
P0A1H5 EFTU_SALTY Elongation factor Tu	26		ALEGDAEWEAKIIELAGFLDSYIPE PER	177	28	5	20.52	b3b5b7y10y13	3161.56	120.862	1929	4	791.15	-1.54
P0A1H5 EFTU_SALTY Elongation factor Tu	27	Phosphoryl STY(9)	FESEVYILSK	304	10	4	42.86	b6b7y3y4	1294.61	74.400	10112	2	647.81	14.33
P0A1H5 EFTU_SALTY Elongation factor Tu	28	Oxidation+M(1)	MVVTLIHPIAMDDGLR	358	16	4	35.08	y3y7y9y10	1796.92	72.589	27837	3	599.65	-9.65
P0A1H5 EFTU_SALTY Elongation factor Tu	29	Oxidation+M()	TTDVTGTIELPEGVEMVMPGDNI K	334	24	3	12.71	b6b8y11	2562.24	77.244	3092	3	854.75	3.43
P0A1H5 EFTU_SALTY Elongation factor Tu	30		ENVGVLLR	272	8	0	2.02		899.53	55.086	3181	2	450.27	-3.66
P0A1H5 EFTU_SALTY Elongation factor Tu	31		PIEDVFSISGR	213	11	2	7.42	b6°b6	1219.62	103.705	2684	2	610.32	-6.71
P0A1H5 EFTU_SALTY Elongation factor Tu	32		IIELAGFLDSYIPEPE	188	16	0	4.85		1805.93	101.036	2243	2	903.47	6.35
P0A1H5 EFTU_SALTY Elongation factor Tu	33		QVGVPYIIVFLNK	124	13	2	7.42	b6*b6	1472.84	98.156	1802	3	491.62	-4.31
P0A1S2 HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	43	324.63	b2°b2b3°b3b4°b4b5°b5b6b7°b7b8°b8b9b10b12°b12b13b14°b14b18b21y1y2y3y4y6y7*y7y8y9y10y12*y12y13y14y15°y15y16°y16y17y18y21	2216.11	96.042	472643	2	1108.56	7.82
P0A1S2 HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	12	100.41	b2b9y2y4y5y6y7y8y9*y9y10y11	1304.56	31.741	101886	2	652.78	-2.06
P0A1S2 HNS_SALTY DNA-binding protein H-NS	3		REEESAAAAVEER	40	14	14	91.83	b2b4b7°b7b10b12b13y2y4y5°y5y7y10y14	1575.73	30.789	52753	2	788.37	5.50
P0A1S2 HNS_SALTY DNA-binding protein H-NS	4		TWTGQGR	107	7	6	69.92	b4b5b6y3*y3y6	805.39	46.460	16738	1	805.39	-9.40
P0A1S2 HNS_SALTY DNA-binding protein H-NS	5		ILNNIR	6	6	2	26.85	b4y5	742.45	27.399	4919	2	371.73	-13.56
P0A1S2 HNS_SALTY DNA-binding protein H-NS	6		SEALK	1	5	3	26.44	b3b4°b4	547.30	42.294	3971	1	547.30	-11.71
P0A1S2 HNS_SALTY DNA-binding protein H-NS	7	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEVVNER	19	21	16	153.56	b3b6y3y4y5y6y7*y7y8y13°y13y15y16y17y18y19	2563.26	123.406	152733	3	855.09	-0.67
P0A1S2 HNS_SALTY DNA-binding protein H-NS	8		YSYVDENGETKTWTGQGR	96	18	13	125.74	b8y4y5y6y8*y8y11y12*y12y14y15y16y17	2090.93	45.523	75935	3	697.65	-5.49
P0A1S2 HNS_SALTY DNA-binding protein H-NS	9		EMLIADGIDPNELLNSMAAAKSGT K	62	25	3	18.63	b4b11b15	2589.32	81.956	49639	3	863.78	9.90
P0A1S2 HNS_SALTY DNA-binding protein H-NS	10	Carbamidomethyl+C(6)	AQARECTLETLEEMLEK	15	17	3	23.31	b4b5y6	2050.95	62.226	1659	2	1025.98	-14.76
P0A1S2 HNS_SALTY DNA-binding protein H-NS	11	Oxidation+M(2)	EMLIADGIDPNELLNSMAAAK	62	21	4	20.52	y7y13°y13y16	2232.11	90.660	15238	2	1116.56	10.83
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	46	329.48	b2b3b4°b4°b4b5°b5°b5b6°b6°b6b7°b7b8°b8b10y1y2*y2y3y4y5y6°y6y7*y7y8°y8y9y10y11y14y15°y15y16°y16y17y18y19y20y21y22°y22y23y24*y24	2574.32	97.117	488491	3	858.78	-1.80

[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	2		LVSWYDNETGYSNK	307	14	20	187.17	b2b3b6b7°b7b11b12y3*y3y4*y4y5y6y7y8y9y10y11y12y14	1675.77	56.973	313475	2	838.39	8.16
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	3		AGIALNDNFVK	296	11	11	84.97	b3b4y2y3y4*y4y6y7*y7y8y11	1161.62	60.199	248285	2	581.31	-6.52
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		GASQNIIPSSTGAAK	198	15	22	141.68	b3b5°b5°b5b6°b6°b6b7°b7°b7b15y4y5°y5y6y7y8°y8y9y10y11y15	1401.73	39.699	224393	2	701.37	-2.35
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		VPTPNVSVVDLTVR	232	14	11	135.84	y3y4y5y6y7y8y9y10y11y12y14	1495.85	69.939	195894	2	748.43	2.04
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		VLDLIAHISK	321	10	6	74.35	b3y3y4y5y6y8	1108.67	63.997	137696	2	554.84	-6.17
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		AATYEQIK	249	8	9	67.31	b1b5b7b8y4*y4y5y6*y6	923.47	29.754	108219	2	462.24	-11.90
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		VLPELNGK	217	8	12	54.09	b1b2y2y3y4*y4y5*y5y6°y6°y6y8	869.50	43.554	80766	2	435.25	-10.11
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		SDIEIVAINDLLDAEYMAYMLK	24	22	25	208.19	b2b3b4b5°b5b6b7°b7b13b14y1y2y3y4y5y6y7y8y9°y9y10y11y12y14y22	2530.24	125.448	69514	3	844.08	-3.38
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		TVDGPSHKDWR	184	11	8	55.52	b1b8b9y2y4y5y6y11	1297.61	26.552	36839	3	433.21	-10.63
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11		VTAERDPANLK	73	11	6	52.51	b6b9y3y5y7y11	1213.64	27.202	19730	2	607.33	-7.64
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12		VGINGFGR	4	8	4	33.09	b5y5*y5y6	819.44	40.696	23965	2	410.23	-5.29
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13		GANFDK	132	6	1	13.62	y4	651.32	42.577	5344	1	651.32	8.62
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14		WDEVGVDDVVAEATGIFLTDETAR	84	23	9	42.94	b14°b14b15°b15y6°y6y7y14y22	2493.19	68.147	2281	4	624.05	-11.46
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15		TVDGPSHK	184	8	4	49.32	b4b6b7y3	840.41	106.992	1591	1	840.41	-11.55
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEQQDIVSNASCCTTNCL APLAK	132	28	42	335.25	b3b4b5°b5b6b7°b7°b7b8b10°b10b11°b11°b11b12°b12°b12b13b15b16b22b24°b24b26b27y3y4y5y6y8y9y10y11°y11°y11y12*y12y13y14y15*y15y16	3044.42	65.567	383551	3	1015.48	4.57
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		AGIALNDNFVKLVSWYDNETGYS NK	296	25	8	27	b4b10°b10°b10y4y5*y5y7	2818.40	99.348	12013	3	940.14	12.30
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		KHITAGAK	107	8	7	93.76	b4b6y3y4y5y6y7	825.49	12.712	9142	2	413.25	-8.87
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19		VLPELNGKLTGMAFR	217	15	3	26.22	y6y7y12	1645.89	71.868	7157	3	549.30	-11.57

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20		GGRGASQNIIPSSTGAAK	195	18	3	15.58	b11y4y8	1671.87	43.701	2564	2	836.44	-5.55
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	21		VINDNFGIIEGLMTTVHATTATQK TVDGPSHK	160	32	4	11.14	b6b8y3°y3	3395.70	118.829	2541	3	1132.57	-8.63
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	22	Oxidation+M(4)	LTGMAFR	225	7	3	40.47	y3y4y5	811.41	49.012	1740	2	406.21	-3.46
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	23		LDLIAHISK	322	9	1	8.25	b3	1009.60	63.994	46646	2	505.30	-5.80
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	24		DLIAHISK	323	8	2	20.68	b3b5	896.51	63.991	45617	2	448.76	-10.42
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	25		DGPSHKDWR	186	9	1	7.86	b7	1097.51	26.621	8770	2	549.26	-6.01
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	26		AERDPANLK	75	9	0	2.43		1013.53	27.226	3488	2	507.27	-9.70
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	27		TAERDPANLK	74	10	1	7.86	b8	1114.58	27.202	2740	2	557.79	-3.72
P25077 MDH_SALTY Malate dehydrogenase	1		NQLPSGSELSLYDIAPVTPGVAVD LSHIPTAVK	21	33	29	138.61	b1b2*b2b3*b3b4b6b7*b7b8°b8b12*b12b13b15*b15y1y2y3y5°y5y6y15y16y18y19y30y31y33	3388.81	93.114	214959	3	1130.28	3.60
P25077 MDH_SALTY Malate dehydrogenase	2		FFSQPLLLGK	262	10	8	68.12	b2y2y3y4y5y6y8y10	1149.66	74.796	187510	2	575.33	-6.16
P25077 MDH_SALTY Malate dehydrogenase	3		VAVLGAAGGIGQALALLK	2	19	30	328.39	b2b3b4b5b6b7b8b9b10b11b15b16b17b18b19y1y2y3y4y5y6y7y9y10y11y12y13y15y16y19	1735.08	119.192	183471	2	868.05	-0.42
P25077 MDH_SALTY Malate dehydrogenase	4		IQNAGTEVVEAK	205	12	27	187.92	b2*b2b3*b3b4b6*b6b8*b8b9b10b11y1y2y3°y3y4y5y6y8°y8y9y10°y10*y10y12*y12	1258.66	33.507	173200	2	629.83	-2.81
P25077 MDH_SALTY Malate dehydrogenase	5	Carbamidomethyl+C(2)	ACVGIITNPVNTTVAIAAEVLKK	111	23	18	130.98	b2b3b4b5b6b9°b9y2y4y5y6y8y15y16y18y20y21y23	2382.34	103.885	164626	3	794.78	-2.77
P25077 MDH_SALTY Malate dehydrogenase	6		DIQLGEDFINK	301	11	7	27.32	b2b3b11y2y7y8y11	1291.65	66.742	101074	2	646.33	0.85
P25077 MDH_SALTY Malate dehydrogenase	7		LFGVTTLDIIR	142	11	5	24.31	b2b3y1y3y9	1247.73	88.150	81702	2	624.37	-4.50
P25077 MDH_SALTY Malate dehydrogenase	8		AGGGSATLSMGQAAAR	217	16	27	181.96	b1b3b5b6°b6b7°b7b8°b8b11b12b13b16y6*y6y7*y7y8*y8y9*y9y10°y10*y10y11y12y16	1405.69	38.818	71520	2	703.35	2.00
P25077 MDH_SALTY Malate dehydrogenase	9		SDLFNVNAGIVK	87	12	10	75.83	b2b3b10y2y4y6y7y8y9y12	1276.69	68.597	65502	2	638.85	-0.38
P25077 MDH_SALTY Malate dehydrogenase	10		GFSGEDATPALEGADVVLISAGVAR	56	25	5	23.1	b3y4y6°y6y7	2402.23	90.115	16878	2	1201.62	5.79
P25077 MDH_SALTY Malate dehydrogenase	11		FGLSLVR	233	7	4	53.69	y3y4y5y6	791.46	65.599	97669	2	396.24	-15.96
P25077 MDH_SALTY Malate dehydrogenase	12		NGVEER	272	6	2	29.86	y3y5	703.34	30.601	14156	1	703.34	8.33

P25077 MDH_SALTY Malate dehydrogenase	13		SIGTLSAFEQHSLDAMLDTLK	279	21	3	13.88	b8b12y11	2277.17	81.548	9399	3	759.73	10.61
P25077 MDH_SALTY Malate dehydrogenase	14	Carbamidomethyl+C(2)	ACVGIITNPVNTTV AIAAEVLK	111	22	4	18.17	b4b6y6y16	2254.23	112.639	8816	3	752.08	-6.50
P25077 MDH_SALTY Malate dehydrogenase	15		ALQGEK	240	6	1	13.62	y3	645.37	44.631	6404	1	645.37	13.62
P25077 MDH_SALTY Malate dehydrogenase	16		GKLPTEVEVPVIGGHSGVTILPLLS QIPGVSFTEQEAAELTK	162	42	8	23.74	b3b27y9°y9y10y12°y12y15	4341.36	112.242	34336	4	1086.09	-0.79
P25077 MDH_SALTY Malate dehydrogenase	17		IKGFSGEDATPALEGADVVLISAG VAR	54	27	5	21.2	b9b11b14y4y6	2643.41	86.778	32586	3	881.81	4.99
P25077 MDH_SALTY Malate dehydrogenase	18		IQNAGTEVVVEAKAGGGSATLSMG QAAAR	205	28	3	17.72	b3b7b13	2645.32	95.086	7716	3	882.45	-2.95
P25077 MDH_SALTY Malate dehydrogenase	19	Carbamidomethyl+C(2)	ACVGIITNPVNTTV AIAAEVLKK	111	23	3	19.46	b3b6b13	2382.31	76.622	4457	3	794.78	-12.09
P25077 MDH_SALTY Malate dehydrogenase	20		FFSQPLLLGKNGVEER	262	16	4	17.16	b4y3y8°y8	1834.00	107.525	3105	3	612.00	6.32
P25077 MDH_SALTY Malate dehydrogenase	21	Oxidation+M(16)	SIGTLSAFEQHSLDAMLDTLK	279	21	3	20.52	b9b11b15	2293.15	76.254	6353	3	765.06	6.28
P25077 MDH_SALTY Malate dehydrogenase	22	Oxidation+M(10)	AGGGSATLSMGQAAAR	217	16	4	24.26	b5b13y5y14	1421.66	39.763	3393	2	711.34	-11.76
P06179 FLIC_SALTY Flagellin	1		AQILQQAGTSVLAQANQVPQNVLSLLR	468	27	35	237.44	b2*b2b3*b3b4b5*b5b6b7*b7b8b11°b11b12b13b14*b14b15°b15b18*b18y1y2y3y4y5y6y7y9y10y12*y12y13y14y27	2860.60	104.587	111231	3	954.20	-0.09
P06179 FLIC_SALTY Flagellin	2		AQVINTNSLSLLTQNNLNK	1	19	14	63.72	b2*b2b4b6y1y2y3y4*y4y7y8y10y15y19	2085.15	73.796	81074	2	1043.08	7.73
P06179 FLIC_SALTY Flagellin	3		FNSAITNLGNTVNNLTSAR	432	19	23	140.5	b2b3*b3b4°b4b5*b5b8b9b14y2y3y4y5y6y7°y7*y11y13*y13y14y15y19	2007.04	77.369	69287	2	1004.02	6.51
P06179 FLIC_SALTY Flagellin	4		NANDGISIAQTTEGALNEINNQLQR	66	25	14	70.86	b2b6°b6b8b13b14b15b16y2*y2y3y4y13y25	2670.34	85.772	63265	2	1335.67	10.24
P06179 FLIC_SALTY Flagellin	5		SQSALGTAIER	20	11	11	63.97	b2°b2*b2b3b8y1y5y6y7y9y11	1132.59	40.765	62201	2	566.80	-3.34
P06179 FLIC_SALTY Flagellin	6		IDAALAQVDTLR	411	12	14	127.25	b2b3b4y3y4y6y7°y7*y7y8y9y10y11y12	1285.71	59.973	53609	2	643.36	-2.85
P06179 FLIC_SALTY Flagellin	7		VSGQTQFNGVK	125	11	6	38.32	b9b10y5y9°y9y11	1164.60	32.129	52799	2	582.80	-4.51
P06179 FLIC_SALTY Flagellin	8		INSAKDDAAGQAIANR	37	16	17	89.12	b2*b2b6°b6b9°b9*b9y4y5*y5y7*y7y9y10y11*y11y12	1614.80	29.196	49410	3	538.94	-9.98
P06179 FLIC_SALTY Flagellin	9		QINSQTLGLDTLNVQQK	161	17	5	34.51	b17y10y11y12y17	1900.03	64.172	44996	2	950.52	8.03
P06179 FLIC_SALTY Flagellin	10		SDLGAVQNR	423	9	10	61.7	b2b5°b5y1y4y5y6*y6y7y9	959.48	26.697	38352	2	480.25	-7.38
P06179 FLIC_SALTY Flagellin	11		DDAAGQAIANR	42	11	3	24.31	b3b7y7	1101.52	27.062	14037	2	551.26	-5.32
P06179 FLIC_SALTY Flagellin	12		ELAVQSANSTNSQSDLDLSIQAEITQR	93	26	12	41.8	b2°b2b3b12b13b16y2*y2y7y12*y12y13	2805.36	57.789	13136	4	702.10	4.96
P06179 FLIC_SALTY Flagellin	13		AQPDLAEEAAATTENPLQK	392	19	6	23.66	b4°b4b6°b6b17y8	1969.01	59.395	9522	2	985.01	13.89
P06179 FLIC_SALTY Flagellin	14		AEGHNFK	385	7	4	37.46	b4y5y6*y6	802.40	83.978	7998	1	802.40	16.58
P06179 FLIC_SALTY Flagellin	15		TYAASK	379	6	2	26.85	b4b5	640.33	48.997	4557	1	640.33	-4.19
P06179 FLIC_SALTY Flagellin	16		LNEIDR	119	6	1	13.62	y4	759.39	27.214	4182	1	759.39	-8.44
P06179 FLIC_SALTY Flagellin	17		NVQVANADLTEAK	280	13	5	45.53	b10y4y6y7y11	1372.73	90.715	2273	2	686.87	14.14
P06179 FLIC_SALTY Flagellin	18		VSDTAATVTGYADTTIALDNSTFK	180	24	4	12.71	b10y5*y5y16	2462.17	72.777	1612	3	821.40	-8.92
P06179 FLIC_SALTY Flagellin	19		LGGADGKTEVVSIGGK	363	16	8	45.28	b5°b5b10°b10b12y3y5y9	1487.79	41.596	64005	3	496.60	-12.14
P06179 FLIC_SALTY Flagellin	20		SRIEDSDYATEVSNMSR	451	17	4	27.4	b7b8b10y4	1959.89	49.687	32728	2	980.45	8.84
P06179 FLIC_SALTY Flagellin	21		TYAASKAEGHNFK	379	13	3	28.12	b3b4b12	1423.68	91.630	28520	2	712.34	-14.23

P06179 FLIC_SALTY Flagellin	22		LNEIDRVSGQTQFNGVK	119	17	3	23.72	y5y8y10	1904.99	79.081	4690	3	635.67	3.65
P06179 FLIC_SALTY Flagellin	23		AQPDLAEEAAATTTENPLQKIDAAL AQVDTLR	392	31	4	36.37	b6b7b8*b8	3235.64	96.456	4091	3	1079.22	-12.22
P06179 FLIC_SALTY Flagellin	24		YKVSDTAATVTGYADTTIALDNS TFK	178	26	8	48.82	b16°b16y12y13°y13y14y15° y15	2753.35	136.552	3124	3	918.45	-1.51
P06179 FLIC_SALTY Flagellin	25		SDLGAVQNRFNSAITNLGNTVNN LTSAR	423	28	10	39.86	b7*b7b8b11b25y7°y7y8°y8° *y8	2947.48	136.389	2275	2	1474.24	-7.29
P06179 FLIC_SALTY Flagellin	26		QINSQTLGLDLTNVQQKYK	161	19	3	24.11	b3b5b6	2191.18	70.722	1713	2	1096.09	3.23
P06179 FLIC_SALTY Flagellin	27		MAQVINTNSLSLLTQNNLNKSQS ALGTAIER	0	31	4	16.18	b4b6b9y9	3329.76	79.099	1537	3	1110.59	2.20
P06179 FLIC_SALTY Flagellin	28		VTVTGGTGKDGYYEVSVDK	233	19	5	25.87	b7b15°b15b16y13	1974.94	91.154	1515	2	987.98	-10.63
P06179 FLIC_SALTY Flagellin	29	Phosphoryl STY(13)	TNGEVTLAGGATSPLTGGLPATA TEDVK	252	28	4	22.33	b4b12b13y11	2708.28	85.765	3348	2	1354.65	-3.34
P06179 FLIC_SALTY Flagellin	30		ELAVQSAN	93	8	1	8.49	y6	831.43	57.766	5723	2	416.22	10.86
P06179 FLIC_SALTY Flagellin	31		LDSIQAEITQR	108	11	0	8.49		1273.69	57.771	2670	2	637.35	9.20
P52616 FLJB_SALTY Phase 2 flagellin	1		AQILQQAGTSVLAQANQVPQNVL SLLR	479	27	35	237.44	b2*b2b3*b3b4b5*b5b6b7* b7b8b11°b11b12b13b14*b 14b15°b15b18*b18y1y2y3 y4y5y6y7y9y10y12*y12y1 3y14y27	2860.60	104.587	111231	3	954.20	-0.09
P52616 FLJB_SALTY Phase 2 flagellin	2		AQVINTNSLSLLTQNNLNK	1	19	14	63.72	b2*b2b4b6y1y2y3y4*y4y7° y8y10y15y19	2085.15	73.796	81074	2	1043.08	7.73
P52616 FLJB_SALTY Phase 2 flagellin	3		NANDGISIAQTTEGALNEINNNLQ R	66	25	14	70.86	b2b6°b6b8b13b14b15b16y 2*y2y3y4y13y25	2670.34	85.772	63265	2	1335.67	10.24
P52616 FLJB_SALTY Phase 2 flagellin	4		SQSALGTAIER	20	11	11	63.97	b2°b2*b2b3b8y1y5y6y7y9° y11	1132.59	40.765	62201	2	566.80	-3.34
P52616 FLJB_SALTY Phase 2 flagellin	5		YFVTIGGFTGADAAK	234	15	6	31.82	b8b9y1y3y7y15	1517.77	72.392	58203	2	759.39	1.05
P52616 FLJB_SALTY Phase 2 flagellin	6		VSGQTQFNGVK	125	11	6	38.32	b9b10y5y9*y9y11	1164.60	32.129	52799	2	582.80	-4.51
P52616 FLJB_SALTY Phase 2 flagellin	7		INSAKDDAAGQAIANR	37	16	17	89.12	b2*b2b6*b6b9°b9*b9y4y5° *y5y7*y7y9y10y11*y11y1 2	1614.80	29.196	49410	3	538.94	-9.98
P52616 FLJB_SALTY Phase 2 flagellin	8		SDLGAVQNR	434	9	10	61.7	b2b5°b5y1y4y5y6*y6y7y9	959.48	26.697	38352	2	480.25	-7.38
P52616 FLJB_SALTY Phase 2 flagellin	9		TEVVTIDGK	381	9	5	30.49	b7b9y5y6y9	961.51	51.117	25208	2	481.26	-13.58
P52616 FLJB_SALTY Phase 2 flagellin	10		DDAAGQAIANR	42	11	3	24.31	b3b7y7	1101.52	27.062	14037	2	551.26	-5.32
P52616 FLJB_SALTY Phase 2 flagellin	11		ELAVQSANSTNSQSDLSIQAEIT QR	93	26	12	41.8	b2°b2b3b12b13b16y2*y2y 7y12*y12y13	2805.36	57.789	13136	4	702.10	4.96
P52616 FLJB_SALTY Phase 2 flagellin	12		TTSYTAADGTTK	357	12	11	74.58	b1b4°b4b7b11y5y7°y7y8y1° ly12	1216.58	28.694	12503	3	406.20	7.12
P52616 FLJB_SALTY Phase 2 flagellin	13		FNSAITNLGNTVNNLSEAR	443	19	4	33.36	b7b10b12b14	2035.02	56.083	5356	4	509.51	0.00
P52616 FLJB_SALTY Phase 2 flagellin	14		NALIAGGVDATDANGAELVK	299	20	5	14.37	b1b3b16y2y16	1898.98	93.124	2132	3	633.67	0.84
P52616 FLJB_SALTY Phase 2 flagellin	15		QINSQTLGLDSLNVQK	161	16	4	25.53	b3b7b8*b8	1757.96	64.233	3920	3	586.66	12.99
P52616 FLJB_SALTY Phase 2 flagellin	16		MAQVINTNSLSLLTQNNLNK	0	20	3	23.79	b4b5b9	2216.12	94.342	3612	2	1108.57	-20.71
P52616 FLJB_SALTY Phase 2 flagellin	17		AYANNGTTLDVSLDDAAIK	189	20	3	14.37	b3b7y14	2008.95	113.347	2150	2	1004.98	-14.70
P52616 FLJB_SALTY Phase 2 flagellin	18		NGDYEYVNVATDGTVTLAAGATK	249	22	3	22.19	b15y15y16	2167.05	100.770	1551	2	1084.03	-1.13
P52616 FLJB_SALTY Phase 2 flagellin	19		FDADNNKYFVTIGGFTGADAAK	227	22	3	13.44	b11y3y6	2322.12	77.723	11983	3	774.71	8.94

P52616 FLJB_SALTY Phase 2 flagellin	20		TYNASKAAGHDFK	390	13	7	54.56	b4b8b9b12y3y9°y9	1409.66	45.617	10753	2	705.33	-13.86
P52616 FLJB_SALTY Phase 2 flagellin	21		AGDKYYAADYDEATGAIK	337	18	4	29.15	b4b5y9y11	1921.88	81.787	8291	3	641.30	-3.24
P52616 FLJB_SALTY Phase 2 flagellin	22		TEVVITDGKTYNASK	381	15	3	18.14	b7b11y10	1625.82	98.461	2821	3	542.61	-8.26
P52616 FLJB_SALTY Phase 2 flagellin	23	Phosphoryl STY()	VRELAVQSANSTNSQSDLDISIAEITQR	91	28	5	11.71	b11y7°y7y9°y9	3140.48	55.647	3032	3	1047.50	1.32
P0A1Z2 SKP_SALTY Chaperone protein skp	1		TGVSNTLENEFK	39	12	22	153.69	b3b4°b4b8b9°b9y2y4y5°y5y6y7y8°y8*y8y9°y9y10°y10y11°y11y12	1338.66	56.539	224426	2	669.83	2.55
P0A1Z2 SKP_SALTY Chaperone protein skp	2		IAIVNMGNLFQQVAQK	23	16	27	198.19	b2b3b4b6°b6b7°b7b9°b11b12b15°b15y1y2*y2y3y5*y5y6y7y8y10y11y12y13*y13y16	1773.97	89.023	195004	2	887.49	3.10
P0A1Z2 SKP_SALTY Chaperone protein skp	3		VANDQSIDLVDANTVAYNSSDVKDITADVLK	126	32	12	30.43	b2b4°b4b9°b9b11b12°b12b18y1y15y32	3392.73	89.044	63318	3	1131.58	7.84
P0A1Z2 SKP_SALTY Chaperone protein skp	4		AQAFEKDR	97	8	6	36.1	b2°b2b3y3y6y8	964.48	17.171	25851	2	482.74	-7.66
P0A1Z2 SKP_SALTY Chaperone protein skp	5		LEKDVMSQR	82	9	4	38.27	b4°b4b5b6	1105.56	47.932	4816	2	553.28	-6.40
P0A1Z2 SKP_SALTY Chaperone protein skp	6		VANDQSIDLVDANTVAYNSSDVK	126	24	8	23.61	b2b3b7°b7y2y6y9y13	2537.23	115.781	3001	3	846.41	-3.85
P0A1Z2 SKP_SALTY Chaperone protein skp	7		AAELQK	53	6	1	13.62	y3	659.38	57.191	6796	1	659.38	13.61
P0A1Z2 SKP_SALTY Chaperone protein skp	8		KVANDQSIDLVDANTVAYNSSDVK	125	25	6	23.1	b5°b5b6b10y6*y6	2665.33	91.691	6337	2	1333.17	-1.10
P0A1Z2 SKP_SALTY Chaperone protein skp	9		AAELQKMETDLQSK	53	14	3	19.29	b4b9y7	1591.80	42.212	3495	4	398.71	0.31
P0A1Z2 SKP_SALTY Chaperone protein skp	10	Oxidation+M(11)	WLLAAGGLAMVTSAQAADK	3	20	3	14.37	b18y8y13	2003.08	80.733	31510	2	1002.04	8.90
P0A1Z2 SKP_SALTY Chaperone protein skp	11		VANDQSIDL	126	10	2	9.82	y8°y8	1073.56	89.015	1741	2	537.28	9.55
P64076 ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	26	211.01	b2°b2b3°b3b4°b4b5b7°b7b13b14b15y1y2y3y4y5y6y7y8y9y10y11y12y13y15	1605.88	84.792	345691	2	803.45	-0.99
P64076 ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	41	305.13	b2b3b7°b7b8°b8b9°b9b10°b10b11b12°b12b13°b13b14°b14b16°b16b18b22y1y2y3y4y5y6y7y8°y8y9y10y12*y12y13°y13y14y15y16y17y22	2118.07	74.381	195222	2	1059.54	7.15
P64076 ENO_SALTY Enolase	3		AVGAVNGPIAQAILGK	66	16	10	60.26	b2b3b5b13y2y10y11y12y14y16	1478.87	74.137	161748	2	739.94	-2.06
P64076 ENO_SALTY Enolase	4		YSMPVPMMNIIINGGEHADNNVDIQEFMIQPVGAK	143	34	18	97.58	b2°b2b3°b3b4b5°b5b23y3y5y6*y6y7y8y9y29y31y34	3759.79	97.599	138609	3	1253.94	7.66
P64076 ENO_SALTY Enolase	5		DAGYTAVISHR	360	11	11	87.19	b2b4b11y2y3y4y5y6y7y9y11	1189.59	40.155	134876	2	595.30	-5.23
P64076 ENO_SALTY Enolase	6		GMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	200	31	24	146.77	b2b4b5°b5°b5b6°b6°b6b8b13y1y2y3y4y5y6y7y8y9y10y15y18y25y31	2989.46	94.213	134300	3	997.16	1.63
P64076 ENO_SALTY Enolase	7		GIANSILIK	333	9	11	76.17	b2b3b5°b5y1y2y3y5y6y7y9	928.57	59.293	95698	2	464.79	-10.12
P64076 ENO_SALTY Enolase	8		GMPLYEHIAELNGTPGK	126	17	6	24.97	b2y2y3y5y6y17	1826.89	66.014	94956	3	609.64	-10.96

P64076 ENO_SALTY Enolase	9		IQLVGDDLFTNTK	311	14	15	72.84	b2*b2b10y2°y2y4y5°y5*y5y6*y6y9y11y12y14	1562.85	76.617	81642	2	781.93	4.37
P64076 ENO_SALTY Enolase	10		ILKEGIEK	325	8	5	49.32	b4y4y5y6y8	929.56	28.250	28147	2	465.28	-8.47
P64076 ENO_SALTY Enolase	11		IMIDLDGTENK	92	11	9	65.52	b2y2y4y6y7y8y9°y9y11	1248.61	57.874	20394	2	624.81	-3.13
P64076 ENO_SALTY Enolase	12	Carbamidomethyl+C(8)	DITLAMDCAASEFYKDGK	239	18	4	15.58	b2b6y4y9	2034.91	77.639	10761	3	678.98	-1.80
P64076 ENO_SALTY Enolase	13		AFTSEEFTHFLEELTK	266	16	4	24.26	b9b14y5y11	1928.91	103.325	156725	3	643.64	-7.47
P64076 ENO_SALTY Enolase	14		GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	3	21.99	b3y6y7	2856.38	91.273	32186	3	952.80	9.15
P64076 ENO_SALTY Enolase	15		EIIDSR	10	6	3	40.07	b3b4b5	732.38	27.357	18229	1	732.38	-8.25
P64076 ENO_SALTY Enolase	16	Carbamidomethyl+C(8)	DITLAMDCAASEFYK	239	15	3	18.14	b12y3y5	1734.73	70.506	4404	4	434.44	-21.67
P64076 ENO_SALTY Enolase	17		QYPIVSIEDGLDESDWDGFAYQTK	282	24	5	16.87	b10b15y6*y6y9	2776.31	91.447	2761	3	926.11	16.62
P64076 ENO_SALTY Enolase	18		IEEALGEKAPYNGR	411	14	5	30.74	b7y5y6y9°y9	1546.77	38.349	26204	3	516.26	-12.39
P64076 ENO_SALTY Enolase	19		EIIDSRGNPTVEAEVHLEGGFVGMAAAPS GASTGSR	10	36	3	10.89	b5b13y5	3569.73	92.395	25382	4	893.19	0.55
P64076 ENO_SALTY Enolase	20		DQAGIDKIMIDLDGTENK	85	18	4	22.74	b6b11°b11b14	1975.96	73.821	17432	2	988.48	-3.40
P64076 ENO_SALTY Enolase	21		EAIRMGSEVFHHLAK	180	15	3	26.22	b8b12b14	1724.87	89.113	12610	3	575.63	-11.46
P64076 ENO_SALTY Enolase	22		GKGMNTAVGDEGGYAPNLGSNA EALAVIAEAVK	198	33	3	11.06	b5b11y3	3174.58	84.194	6845	3	1058.86	0.77
P64076 ENO_SALTY Enolase	23		GMNTAVGDEGGYAPNLGSNAEA LAVIAEAVKAAGYELGK	200	39	3	22.91	b6b7y5	3778.82	90.733	2608	3	1260.28	-11.18
P64076 ENO_SALTY Enolase	24	Oxidation+M(27)	YSMPVPMMNINNGEHADNNVDI QEFMIQPVGAK	143	34	4	10.98	b7b13*b13y12	3775.80	91.235	3111	3	1259.27	9.83
P64076 ENO_SALTY Enolase	25	Oxidation+M(18)	GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	6	26.38	b7b10b14b16y6y16	2872.37	74.358	2572	3	958.13	4.93
P64076 ENO_SALTY Enolase	26	Oxidation+M(2)	GMPLYEHIAELNGTPGK	126	17	3	23.72	y6y8y14	1842.90	35.189	2029	3	614.97	-0.73
P64076 ENO_SALTY Enolase	27		ANSILIK	335	7	8	38.27	b3°b3*b3b4°b4b5°b5*b5	758.47	59.289	16247	1	758.47	-3.78
P64076 ENO_SALTY Enolase	28		LKEGIEK	326	7	0	1.21		816.48	28.316	13561	2	408.74	-7.55
P0A1D5 CH10_SALTY 10 kDa chaperonin	1		VGDIVIFNDGYGVK	60	14	24	217.59	b3b4b5°b5b6b11°b11b13y1y2y3y4y5y6y7*y7y8y9y10y11y12y13*y13y14	1495.78	72.387	307394	2	748.39	-0.49
P0A1D5 CH10_SALTY 10 kDa chaperonin	2		ILDNGTVQPLDVK	47	13	32	227.98	b2b3b5*b5b7°b7b8°b8*b8b9b10b11°b11*b11b13y1y2y3°y3y4y5y6*y6y7y8y9y10y11°y11*y11y12y13	1411.78	56.211	269661	2	706.39	-0.78
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	7	42.42	b5°b5y2y3y6y8y9	1188.65	42.486	113775	2	594.83	-5.03
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIAVGK	37	8	6	54.09	y2y3y4y5y6y8	786.46	40.418	35452	2	393.74	-9.78
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		EVESK	15	5	1	13.22	b3	591.29	37.211	5138	1	591.29	-11.77
P0A1D5 CH10_SALTY 10 kDa chaperonin	6		STRGEIIAVGK	34	11	4	36.73	b5b6b8y4	1130.66	36.705	44515	2	565.83	2.05
P0A1D5 CH10_SALTY 10 kDa chaperonin	7		VGDIVIFNDGYGVKSEK	60	17	5	22.93	b3b11*b11y7y9	1839.95	96.416	5630	3	613.99	-1.53
P0A1D5 CH10_SALTY 10 kDa chaperonin	8	Oxidation+M(9)	IDNEEVLIMSES DILAIVEA	77	20	4	21.16	b7b9b12*b12	2219.09	72.820	20961	3	740.37	-2.86
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	22	141.55	b2°b2b3°b3b4°b4b13b19y1y3y4°y4y5y6y11*y11y12y13y15y16y17y19	2130.16	91.844	306410	3	710.72	-8.14

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		MVAPVDGTIGK	59	11	17	140.07	b1b2b3b4b5b7y2y3y5°y5y6y7y8y9°y9y10y11	1087.58	45.048	156933	2	544.29	-2.02
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		VGDPVIEFDLPLEEK	115	16	17	143.76	b3b4b5b6b7b10y2°y2y3°y3y4y6y9y10y11y13y16	1812.97	98.820	132578	2	906.99	2.22
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		DTGTIEIVAPLSGEIVNIEDVPDVVFAEK	16	29	7	19.9	b2b5b7y3°y3y8y11	3069.61	110.818	9278	3	1023.88	7.79
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		IVGDGIAIKPTGNK	45	14	13	126.3	b3y3y4y5°y5*y5y6*y6y7y8y10y12y13	1382.77	42.377	160442	3	461.60	-18.63
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		VKVGDPVIEFDLPLEEK	113	18	10	67.84	b5b7b9y3°y3y6y8°y8y10y13	2040.10	94.452	143982	3	680.71	-10.71
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		IAEEGQRVK	106	9	3	38.27	b3b7b8	1029.56	37.883	10593	2	515.28	-12.45
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		PVDGTIGK	62	8	5	31.29	b3b5°b5b6°b6	786.43	45.025	4398	1	786.43	-12.88
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9		STLTPVVISNMDEIKELIK	133	19	0	5.66		2113.13	91.815	2850	3	705.05	-5.66
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		VANLGSLGDQVNVK	8	14	26	190.18	b1b2b3b6b10b13*b13b14y1y3y4y5*y5y6y7y8y9y10°y10*y10y11°y11y12*y12y13y14	1413.77	55.510	142430	2	707.39	2.94
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		LADVLAANAR	57	11	10	70.96	b2b3y5*y5y6*y6y7y8y9y11	1084.60	52.114	142182	2	542.80	-11.93
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		DIADAVTAAGVDVAK	97	15	13	107.97	b2°b2b3b6b9y4y6y7y8y9y10y13y15	1415.74	65.125	110095	2	708.37	0.43
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		MQVILLDK	0	8	7	54.09	b2*b2y3y4y5y6y8	959.55	63.037	84500	2	480.28	-8.65
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		INALETVTIASK	71	12	10	87.59	b2*b2b3b4y3y5y7y10y11y12	1259.71	59.927	51132	2	630.36	-5.43
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		NFLVPK	27	6	2	26.85	b3y3	717.42	49.808	31784	1	717.42	-9.02
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		INALETVTIASKAGDEGK	71	18	4	24.5	y3°y3y4y11	1816.98	108.775	37052	2	908.99	6.25
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		DIADAVTAAGVDVAKSEVR	97	19	4	14.94	b6b9y4°y4	1886.98	102.767	1566	2	943.99	-2.98
P67093 UG_SALTY Universal stress protein G	1		TIIMPVDVFEMELSDK	3	16	22	154.06	b1°b1b2b3b4°b4b6b7y1y2°y2y3y4y5y6°y6y8y9y10y13y14y16	1866.93	103.781	81461	2	933.97	6.02
P67093 UG_SALTY Universal stress protein G	2		HATLPVLVVR	132	10	6	68.12	b2y4y6y7y8y9	1104.68	59.779	74996	2	552.84	-6.96
P67093 UG_SALTY Universal stress protein G	3		NPSITTHLLGSNASSVVR	114	18	6	24.5	b2y5y10y11y18*y18	1852.97	57.603	61470	3	618.33	-11.27
P67093 UG_SALTY Universal stress protein G	4		FEEHLQHEAETR	57	12	4	22.28	b8y8°y8y10	1525.73	41.615	7515	3	509.25	14.64
P67093 UG_SALTY Universal stress protein G	5		HAEFLLAQDQGVIIHLHLVPGSASMSLHR	22	28	4	14.91	b5b9y7y10	3063.60	95.648	5633	3	1021.87	0.24
P67093 UG_SALTY Universal stress protein G	6		LQTMVGHFSIDPSR	69	14	3	24.73	b10b11y10	1587.78	45.283	3698	2	794.39	-12.07
P67093 UG_SALTY Universal stress protein G	7		RFEHLQHEAETR	56	13	4	20.64	b6y5y7*y7	1681.78	90.970	3799	3	561.27	-11.90
P67093 UG_SALTY Universal stress protein G	8	Oxidation+M(4)	TIIMPVDVFEMELSDK	3	16	3	23.69	b7b8y10	1882.89	75.315	14100	2	941.95	-13.03

[P67093]UG_SALTY Universal stress protein G	9	Oxidation+M(24)	HAEFLAQDGVIHLLHVLPGSASMSLHR	22	28	8	54.33	b5b8b9b10b11b13°b13y6	3079.61	137.276	13087	3	1027.21	8.17
[P67093]UG_SALTY Universal stress protein G	10	Oxidation+M(11)	FGSVRDVVNEMGEELDADVVGSR	89	25	3	21.95	b3b4y14	2708.30	101.874	2870	4	677.83	-6.40
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTTQETFGNEHWAPK	135	20	19	135.47	b2b3b4y2y3y4y7°y7*y7y8y9*y9y10*y10y11y12y14y15y20	2199.07	62.232	184507	3	733.70	-4.11
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	22	154.1	b2b3°b3b4°b4b5°b5b11°b13y1y4y5°y5y6°y6y7y8y9y10y11y12y13	1425.69	54.177	127777	2	713.35	1.11
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	3	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	19	124.75	b2b3b5b10b16°b16y1y2y3y4°y4y5y6y10y12y14y15y16y20	2273.20	103.096	103961	2	1137.11	8.70
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	4		NSDIQPTVASLK	120	12	18	97.8	b1b2°b2b3°b3°b3b4y1y3y4°y4y7y8°y8°y8y9y10y12	1272.68	46.980	90433	2	636.84	-3.17
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	5		NAQGELVGFDIDLAK	42	15	5	29.44	b1b6b7b14y12	1589.83	78.544	44135	2	795.42	5.68
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	6		FGGPAVKDEK	201	10	7	61.13	b2b8y3y5y6y9y10	1047.54	25.629	43734	2	524.27	-9.44
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	7		QQEIAFTDK	99	9	6	38.27	y1y2y3y4y7y9	1079.54	41.634	35473	2	540.27	-0.90
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	8		GIEIVSYQGQDNIYSDLTAGR	155	21	5	18.93	b3b11y4y7y21	2299.14	77.809	11445	2	1150.08	10.09
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	9		LFGVGTGMGLR	211	11	5	31.29	y6°y6y7y9°y9	1107.59	71.341	78906	2	554.30	-3.20
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	10		IDAAFQDEVAASEGFLK	176	17	4	22.93	b5b13y6y11	1810.91	60.155	2173	2	905.96	10.99
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	11		IDAAFQDEVAASEGFLKQPVGK	176	22	5	38.07	b3y4y18y19y20	2320.18	77.129	74095	3	774.06	-2.10
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	12		RVGVLQGTTQETFGNEHWAPK	134	21	5	24.71	b4b5b12°b12y8	2355.19	57.768	9448	3	785.74	4.35
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	13	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLKAK	62	22	3	19.95	b11b17b19	2472.28	62.304	9118	3	824.76	-14.81
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	14		QQEIAFTDKLYAADSR	99	16	5	24.26	b4°b4b6y6y13	1855.89	68.063	5221	3	619.30	-12.96
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	15		DEKLFVGVTGMGLR	208	14	3	24.73	b6b7y9	1479.75	57.839	4215	2	740.38	-6.02
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	16		DYKFGGPAVK	198	10	4	47.91	b3b7b9y3	1081.57	49.852	3614	2	541.29	-2.03
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	17	Oxidation+M(5)	IDAIMSSLSITEK	85	13	4	34.07	b3b5b9y11	1423.74	57.799	6404	3	475.25	4.89
[Q7CQ05]GRCA_SALTY Autonomous glycy radical cofactor	1		SGFAEDEVVAVSK	35	13	11	60	b2°b2b3b4b12b13y2y8y9y10y13	1337.66	53.134	114932	2	669.33	2.92
[Q7CQ05]GRCA_SALTY Autonomous glycy radical cofactor	2		VEGGQHNLNVNVLNR	66	13	9	88.21	b3b4b9y4y5y6y7y8y13	1434.76	48.832	113274	3	478.92	-14.63
[Q7CQ05]GRCA_SALTY Autonomous glycy radical cofactor	3		EIPMEVKPEVR	55	11	7	55.97	b10y2y4y6y8y9y11	1326.70	47.354	85343	2	663.86	-3.59
[Q7CQ05]GRCA_SALTY Autonomous glycy radical cofactor	4		MITGIQITK	0	9	5	38.27	y2y3y6y7y9	1004.57	53.721	85255	2	502.79	-6.01
[Q7CQ05]GRCA_SALTY Autonomous glycy radical cofactor	5		FNSLTPEQQR	106	10	12	101.76	b2b3°b3b4y3y4°y4y5y6y7y8y10	1219.61	36.819	82208	2	610.31	-0.70
[Q7CQ05]GRCA_SALTY Autonomous glycy radical cofactor	6		LGEIEYR	48	7	8	50.68	b2b3y1y2y3y4y6y7	879.45	40.833	81106	2	440.23	-10.06
[Q7CQ05]GRCA_SALTY Autonomous glycy radical cofactor	7		AANDDLLNSFWLLDSEK	9	17	7	23.31	b2b3y2y7y8°y8y17	1950.97	87.039	40582	2	975.99	11.95
[Q7CQ05]GRCA_SALTY Autonomous glycy radical cofactor	8		VSGYAVR	99	7	5	37.46	b1b3y5y6°y6	751.40	25.954	14807	2	376.20	-14.13

Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	9		FNSLTPEQQRDVIAR	106	15	4	18.14	b5y3y6y15	1773.91	46.208	3865	3	591.97	-10.67
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	10		TFTESL	121	6	2	29.86	b3b5	697.34	54.093	52472	1	697.34	-3.94
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	11		AANDDLLNSFWLLDSEKGEAR	9	21	26	239.67	b3b5°b5b6°b6*b6b7°b7*b7b9y4y5y7y8y9°y9y10y11y12y13y14y15y16y17y18y19	2364.14	91.735	193433	3	788.72	-4.03
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	12		HPEKYPQLTIR	88	11	3	36.07	b6b7b8	1381.76	70.379	31615	3	461.26	-2.03
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	13		MITGIQITKAANDDLLNSFWLLDSEK	0	26	4	12.14	b3°b3b15y8	2936.49	104.634	11894	3	979.50	-7.48
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	14		SGFAEDVVAVSKLGEIEYR	35	20	3	14.37	b3y5y7	2198.07	77.251	4095	3	733.36	-10.77
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	15		PMEVKPEVR	57	9	3	31.29	b3b4b7	1084.57	47.335	54618	2	542.79	-6.98
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	16		TGIQITK	2	7	3	23.29	b4b5°b5	760.46	53.698	3593	1	760.46	5.94
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	17		EGGQHNLNVNVL	67	12	0	3.23		1335.69	48.860	2052	2	668.35	-14.44
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	18		EIPMEVKPEVR	55	11	2	13.3	b6y7	1308.68	47.328	16535	3	436.90	-10.26
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	1		SSIPVFGVDALPEALALVK	250	19	19	155.74	b6°b6b7°b7b10y1y2y3y4y5y8y9y10y11y12y13y14y16y19	1926.10	107.134	87899	2	963.56	5.32
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	2		SGAMAGTVLNDANNQAK	269	17	17	101.49	b2b3b5b13y2y5y8y9*y9y10y11*y11y12*y12*y12y13y17	1661.80	44.992	83882	2	831.41	8.30
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	3		ALAINLVDPAAGTVIEK	84	18	15	90.22	b2b3b4b5*b5b6y2°y2y6y10y11y13y14*y14y18	1766.01	79.623	73005	2	883.51	2.90
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	4		VPYVGVDKDNLSEFTQK	315	17	14	88.65	b3b12*b12y3y4y6°y6y8y9°y9*y9y11y13y17	1938.97	60.418	53133	3	646.99	-8.12
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	5		GQNVPPVFFNKEPSR	104	15	4	18.14	b4b5*b14y6	1717.89	56.103	16666	3	573.30	-8.03
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	6		MDAWLSGPNANK	214	12	5	29.48	y6y10*y10y11y12	1303.60	48.184	15973	2	652.30	-9.46
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	7		DNLSEFTQK	323	9	5	16.02	b6b7*b9y8y9	1081.51	32.321	2965	2	541.26	-9.14
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	8		EPSR	115	4	1	12.82	b3	488.25	33.914	20733	1	488.25	7.50
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	9		ELNDK	187	5	1	13.22	b3	618.31	79.824	17194	1	618.31	-4.44
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	10		HWQANQGWDLNK	148	12	3	29.48	b3b4b8	1496.67	48.028	16489	2	748.84	-19.66
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	11		IENK	308	4	1	12.82	y3	503.28	43.608	4512	1	503.28	2.61
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	12		TTYVVKELNDK	181	11	3	27.32	b3b4y5	1309.68	75.703	77559	2	655.34	-14.45

P23905 DGAL_SALTY D-galactose-binding periplasmic protein	13		SAPDVQLLMNDSQNDQSKQNDQI DVLLAK	52	29	6	37.64	b12b13y3y5y11y22	3227.60	77.171	41123	3	1076.54	3.86
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	14		GQNVPVVFFNKEPSR	104	15	4	29.44	b8y4y8y11	1717.88	60.270	13176	3	573.30	-13.43
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	15		ELNDKGIQTEQLALDTAMWDTAQ AK	187	25	9	52.77	b9b12°b12y5y6y7°y7*y7y8	2790.33	79.071	11453	3	930.78	-10.50
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	16		ALDSYDKAYYVGTDSK	120	16	3	17.16	b7y4y9	1795.83	50.405	10849	3	599.28	-4.62
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	17		HWQANQGWDLNKDGK	148	15	3	18.14	b4b9y3	1796.83	46.397	9038	3	599.62	-6.73
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	18		GAADGTSWKIENK	299	13	3	20.64	b12y4y10	1376.69	38.331	6631	2	688.85	5.94
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	19		MDAWLSGPNANKIEVVIANNDA MAMGAVEALK	214	32	3	11.14	b13b15y7	3343.66	102.170	3751	4	836.67	4.82
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	20		VPYVGVDKDNLSEFTQK	315	17	5	27.4	b12y6°y6y7y16	1938.98	64.179	2078	2	970.00	2.08
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	21		AWLSGPNANK	216	10	0	2.83		1057.54	48.207	2180	2	529.27	-6.12
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	1		AYPDLDAIIPDANALPAAQAEE NLKR	209	28	21	156.63	b2b6b7°b7b8b9b10°b10b1 3y3y4y6y9y10y12y16y18y 19y20y26y28	2863.50	86.791	85387	3	955.17	3.24
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	2		NNLAIVGFSTPNVMRPYVQR	237	20	13	69.48	b3b4*b4b9*b9y12y14y15* y15y16°y16y17y20	2276.17	77.196	83263	3	759.39	-11.80
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	3		VAFFYSSPTVTDQNQWVK	154	18	8	61.39	b12y5y6y8y11y12y13y18	2117.06	76.718	67532	2	1059.03	10.26
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	4		LVGVGFFTSGNGAQEAGK	35	19	17	114.14	b2b3b14b15b17y2y3y4y5° y5y12y13°y13y14y15y17y1 9	1795.91	70.612	54567	2	898.46	6.80
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	5		ISQEHPGWEIVTTQFGYNDATK	177	22	4	24.23	b9y5y7y8	2521.20	71.777	51502	3	841.07	1.26
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	6		NMPMNVGDSLDIPGIGK	284	17	8	39.75	b2b6b13b16y14y15*y15y1 7	1757.87	78.682	46592	2	879.44	5.28
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	7		VTVSPNSEQGYHYEAK	301	16	16	120.51	b3°b3b6b7°b7y2y4y5y7°y7 y8y9y10y12y13y16	1808.83	35.314	45123	3	603.61	-10.46
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	8		SYYINQGTPK	124	10	10	40.13	b2°b2b5y3y8°y8*y8y9*y9y 10	1170.58	37.195	37791	2	585.80	4.59
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	9		EFGLWDVVQQGK	261	12	7	65.16	b3b8b10°b10y7y8y9	1405.71	81.632	36201	2	703.36	-1.22
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	10		GNGIVLLPER	317	10	6	33.9	b2*b2y3y4y6y10	1067.61	60.338	29022	2	534.31	-8.69
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	11		AYPDLDAIIPDANALPAAQAEE NLK	209	27	4	11.91	b2b4y11y24	2707.41	71.942	6907	5	542.29	7.57
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	12		ISVYVANALLK	273	11	3	36.07	y6y7y8	1190.71	72.721	36893	2	595.86	-6.36
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	13		IAFIPK	29	6	1	13.62	y5	688.44	52.923	10874	2	344.72	-3.19

Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	14		DNIDK	332	5	1	13.22	b4	604.29	66.384	4319	1	604.29	-1.62
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	15	Carbamidomethyl+C(12)	ILTWSDTKPECR	111	13	3	20.64	b5b7y4	1620.80	84.058	2522	2	810.91	21.92
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	16		QLGSMLEVMAAHQVDK	134	16	6	34.77	b3b13y3y5*y5y12	1756.84	70.646	2427	3	586.28	-18.62
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	17		VTVPNSEQGYHYEAKNGIVLLPER	301	26	3	18.29	b8b10b17	2857.48	58.967	44963	4	715.13	11.62
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	18	Carbamidomethyl+C(12)	ILTWSDTKPECRSYYINQGTPK	111	23	4	17.49	b9b11y3y10	2772.33	110.732	6827	3	924.78	-0.18
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	19		AKISQEHPGWEIVTTQFGYNDATK	175	24	21	111.32	b7*b7b9*b9*b9b10b23y4y5y7y8y11*y11*y11y12*y12*y12y13*y13y14y22	2720.35	68.141	4670	3	907.45	6.19
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	20	Phosphoryl STY(12)	MIALLTAFGLASAAMTVQAAER	7	22	4	13.44	b13y6y9*y9	2316.11	78.435	1893	3	772.71	-11.81
P67091 UF_SALTY Universal stress protein F	1		TILVPIDISDSELTQR	3	16	21	154.73	b2b3*b3b4*b4b13y2*y2y3y4y6*y6y7y8y9y10y12*y12y13y14y16	1799.98	81.198	104427	2	900.50	5.09
P67091 UF_SALTY Universal stress protein F	2		FNLPADR	78	7	7	37.46	b2*b2b5b6*b6*b6y4	832.43	45.078	23618	2	416.72	-1.98
P67091 UF_SALTY Universal stress protein F	3		VQAHVAEGSPK	85	11	7	55.97	b9y2y4y6y8y9y11	1122.58	17.434	21040	2	561.79	-7.83
P67091 UF_SALTY Universal stress protein F	4		ILEMAK	98	6	2	26.85	y4y5	704.40	37.203	10760	1	704.40	-4.68
P67091 UF_SALTY Universal stress protein F	5		VQAHVAEGSPKDK	85	13	5	29.88	b4b7*b7b9*b9	1365.72	68.154	12441	2	683.36	4.29
P67091 UF_SALTY Universal stress protein F	6		SQLEAIKK	69	9	5	44.96	b4*b4b6y3y7	1029.62	43.612	3215	3	343.88	-7.35
P67091 UF_SALTY Universal stress protein F	7		QAHVAEGSPK	86	10	0	2.43		1023.52	17.432	3149	2	512.26	-0.18
P67091 UF_SALTY Universal stress protein F	8		AHVAEGSPK	87	9	0	2.43		895.45	17.441	1926	2	448.23	-10.91
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	1		TQFMGPEGVANVSLSNIAGESAEGLLVTKPK	240	31	28	178.57	b1*b1b2*b2b3b4*b4b5b10b12b15y2y3y4y5y6y8y13y14y17y19y22y26y27*y27y28y29y31	3144.64	87.602	241072	3	1048.88	3.80
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	2		NYDQVPANKPIVDAIK	271	16	12	69.51	b2*b2b3b4b11b13y2y3y5y7y11y16	1784.93	52.573	213029	3	595.65	-11.97
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	3	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTAR	92	38	21	157.81	b2b12*b12b16b23b24b25b26b27*b27y4y5y6y8y9y10y11y12y13y15y38	4078.01	88.559	155907	3	1360.01	7.60
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	4		VAVVGAMSGPVAAQYGDQEFTGA EQAIADINAK	25	32	33	236.54	b2b3b4b5b6b7b8b9b13b29y2y3*y3y4y5*y5y6*y6*y6y7y8y9*y9y10y12y13*y13y14*y14y21y25y26y32	3207.58	89.112	148477	3	1069.87	6.77
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	5		TTGLSDSQGPTAAK	137	14	20	177.93	b2*b2b3*b3b4b5b11b12b13y2y3y5y6y8y9y10*y10y11y12y14	1361.65	28.464	134190	2	681.33	-1.70
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	6		ENIDFVYYGGYHPEMGQILR	212	20	11	56.14	b2y1y2y3y8y9y10*y10y14y16y20	2401.13	79.157	128071	3	801.05	-0.31
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	7		GGVNVVFFDGITAGEKDFSTLVAR	185	24	18	131.55	b2b3b4b6b8b9b13y2y3y7y10y12y13y14y18y19y20y24	2499.29	101.324	102313	3	833.77	1.27

P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	8		GATVDTVMGPLSWDEK	326	16	6	45.95	b5b8b14y4y8y9	1705.82	77.366	13630	2	853.42	7.44
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	9		GFEFGVFDWHANGTATDAK	346	19	6	20.7	b2b3b7y4y6y19	2069.96	82.616	12180	3	690.66	12.50
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	10		QDPSGAFVWTTYAALQSLQAGLN HSDDPAEIAK	290	33	5	11.06	b2b13y6y14*y14	3501.71	108.643	12166	3	1167.91	6.27
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	11	Carbamidomethyl+C(6)	TLLAGCIALSLSHMAFADDIK	4	21	3	23.53	b6b7b13	2247.15	66.558	11498	3	749.72	-1.63
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	12		QQYGEGLAR	168	9	6	59.94	b3*b3b4y4y5y6	1021.50	31.856	5033	1	1021.50	-5.56
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	13		GGVNVVFFDGITAGEK	185	16	4	28.34	b7b14b15y9	1609.79	58.436	2673	2	805.40	-22.29
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	14		KQDPSGAFVWTTYAALQSLQAGL NHSDDPAEIAK	289	34	33	260.02	b3*b3b5*b5*b5b6b7b9*b9b11b13*b13b14b15y3y5y6y7y8y9y10y14*y14y15y16y18*y18y19y20y21y22y23y24	3629.77	101.856	318543	4	908.20	-5.78
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	15	Carbamidomethyl+C(10)	LVAVKYDDACDPK	64	13	3	25.41	b3y8y9	1493.71	38.492	35936	3	498.58	-12.18
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	16		GATVDTVMGPLSWDEKGDLK	326	20	6	38.85	b8b11y8y11y13y15	2119.03	76.622	4274	3	707.02	-2.77
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	17		GDLKGFEFGVFDWHANGTATDA K	342	23	3	13.05	b3b6y3	2483.17	91.378	3111	2	1242.09	4.23
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	18	Phosphoryl STY(12)	GGVNVVFFDGITAGEK	185	16	4	24.26	b4b11y3y12	1689.76	106.778	4860	2	845.39	-9.32
P0A1E3 CYSK_SALTY Cysteine synthase A	1		YLLQQFSNPANPEIHEK	137	18	15	134.74	b2b3b9b15y3*y3y4y6y7y9y11y12y15y16y18	2141.09	72.957	130411	3	714.37	-5.82
P0A1E3 CYSK_SALTY Cysteine synthase A	2		IQGIGAGFIPGNLDLK	226	16	16	99.63	b2*b2b3b8b9b14y2y3y7*y7y8y10*y10y12y14y16	1612.91	82.530	121147	2	806.96	3.41
P0A1E3 CYSK_SALTY Cysteine synthase A	3		YLSTALFADLFTKEKELQQ	305	18	11	51.82	b2b3b15b16y2*y2y5y11y12y14y18	2117.10	101.620	120737	2	1059.05	7.84
P0A1E3 CYSK_SALTY Cysteine synthase A	4		LTLTMPETMSIER	87	13	14	105.98	b2b5*b5b11y4y6y7y8y9*y9y10y11*y11y13	1521.77	72.935	105948	2	761.39	2.65
P0A1E3 CYSK_SALTY Cysteine synthase A	5		GVLKPGVELVEPTSGNTGIALAYV AAAR	56	28	7	29.64	b11b18y3y6y7y17y28	2753.52	80.655	77145	3	918.51	0.62
P0A1E3 CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	12	111.02	b2b3b4b5b6y6y7y8*y8y9y10y12	1283.73	62.849	69983	2	642.37	-1.14
P0A1E3 CYSK_SALTY Cysteine synthase A	7		IYEDNSLTIGHTPLVR	3	16	7	35.08	b2y4y7y8y14*y14y16	1827.95	60.492	65861	3	609.99	-6.74
P0A1E3 CYSK_SALTY Cysteine synthase A	8		LQEDESFTNK	283	10	9	43.14	b3*b3y2y6*y6y7y8*y8y10	1210.56	33.999	48117	2	605.78	2.82
P0A1E3 CYSK_SALTY Cysteine synthase A	9		AEEIVASDPQK	126	11	10	70.96	b1b2b3y2y3y6y7y8y9y11	1186.59	30.488	43748	2	593.80	-5.66
P0A1E3 CYSK_SALTY Cysteine synthase A	10		VVGITNEEAISTAR	246	14	8	60.41	b3y7y8y9y10y12*y12y14	1459.77	48.329	41049	2	730.39	-1.84
P0A1E3 CYSK_SALTY Cysteine synthase A	11		YLSTALFADLFTK	305	14	4	19.29	b5b11y12*y12	1618.84	102.573	24407	2	809.93	3.92
P0A1E3 CYSK_SALTY Cysteine synthase A	12		IGANMIWDAEK	44	11	11	66.98	b7b9*b9y1y5*y5y6y9*y9y10y11	1247.61	64.281	24403	2	624.31	0.20
P0A1E3 CYSK_SALTY Cysteine synthase A	13		TDLITVAVEPTDSPVIAQALAGEEI KPGPHK	195	31	3	11.25	b3b13y5	3196.66	84.109	51286	4	799.92	-14.28
P0A1E3 CYSK_SALTY Cysteine synthase A	14		ILAK	27	4	1	12.82	y3	444.32	44.058	6564	1	444.32	-5.29
P0A1E3 CYSK_SALTY Cysteine synthase A	15		GAIQKAEEIVASDPQK	121	16	4	25.53	y5*y5y6y10	1683.91	90.032	101765	2	842.46	9.13
P0A1E3 CYSK_SALTY Cysteine synthase A	16		GKTDLITVAVEPTDSPVIAQALAG EEIKPGPHK	193	33	5	21.93	b9y5y10y19y22	3381.79	78.751	98806	4	846.20	-9.60

[P0A1E3]CYSK_SALTY Cysteine synthase A	17		AAEIVASDPQKYLLQQFSNPANP EIHEK	126	29	7	27.22	b3b13y3y6y9y12°y12	3308.67	76.138	36056	4	827.92	-3.91
[P0A1E3]CYSK_SALTY Cysteine synthase A	18	Oxidation+M(5)	LTLTMPETMSIERR	87	14	3	19.29	b11y9y11	1693.86	77.723	5230	3	565.29	-2.09
[P0A1E3]CYSK_SALTY Cysteine synthase A	19		LTMPETMSIER	89	11	0	3.23		1307.65	72.914	6680	3	436.55	9.43
[P0A1E3]CYSK_SALTY Cysteine synthase A	20		ALFADLFTEK	309	10	0	3.64		1154.62	102.536	1569	2	577.81	7.61
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		ESSVPFSYYDNQQK	47	14	19	108.82	b2°b2b3°b3b4y1y4y5y6°y6 *y6y7°y7y8y9y10°y10*y10 y14	1691.77	54.220	202343	2	846.39	6.21
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		VVGYSQDYSNAIVEAVKK	61	18	16	152.76	b1b2b11y2y3y4y5y6y7y8y 9y10y12y14y16y18	1970.01	62.088	195512	3	657.34	-5.76
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		VVGYSQDYSNAIVEAVK	61	17	28	204.03	b2b3b6b7b11*b11b13*b13 b14b16b17y2y3y4°y4y5y6y 10*y10y11*y11y12*y12y1 3*y13y14y15y17	1841.94	66.755	148968	2	921.47	5.90
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		AVAFMMDDALLAGER	198	15	15	112.9	b3b5y2y3°y3y5y6°y6y9y10 °y10y11y12y13°y13	1609.78	83.529	124974	2	805.40	7.58
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5		LIPITSQNR	89	9	11	54.5	b2y4*y4y5°y5y6°y6*y6y7* y7y9	1041.59	41.706	59335	2	521.30	-12.07
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTTNNLER	98	22	17	101.76	b2b3b4b10b11b14°b14y1y 2y5y6y8y9°y9y10y11y22	2526.22	80.827	48671	2	1263.62	11.89
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7		QAAFSDTIFVVGTR	122	14	5	19.29	b13y1y6y12y14	1511.79	75.791	35927	2	756.40	4.68
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8		LNKPDLQVK	80	9	5	38.27	y1y4y5y6y9	1054.62	36.559	26369	2	527.81	-4.40
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9	Carbamidomethyl+C(19)	KPDNWEIVGKPKQSQEAYGCMLR	217	22	5	26.92	b7°b7b9y5y6	2606.22	60.914	19115	4	652.31	-9.37
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		LMDDTIAQAQTSGEAEK	247	17	4	22.93	b5b7y9y11	1807.85	44.953	11018	2	904.43	8.64
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11		NGVIVVGHR	38	9	3	30.49	b3y5y6	950.54	31.667	147150	2	475.77	-17.08
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTT NNLER	89	31	12	72.91	b3b14y4*y4y6y7y9y10y12 y14y21y29	3548.80	86.044	224016	3	1183.61	6.67
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	13		GGDIKDFPDLK	141	11	6	52.96	b3b4b5°b5b7y10	1204.63	69.028	30410	2	602.82	10.13
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	14		VVGYSQDYSNAIVEAVKK	61	18	8	40.68	b5b13°b13b14b15°b15y15 *y15	1970.04	93.045	12650	2	985.53	10.29
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	15		ALFKAPNDK	290	9	4	30.49	b8°b8y3y7	1003.56	37.862	12482	2	502.28	1.28
[Q9ZF60]GLTI_SALTY Glutamate/aartate periplasmic-binding protein	16		KLMDDTIAQAQTSGEAEK	246	18	3	22.98	b6y5y6	1935.92	58.944	1873	4	484.74	-5.68

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	17	Carbamidomethyl+C(21)	AKKPDNWEIVGKPQSQEAYGCMLR	215	24	4	23.43	b9y5y12y13	2805.39	58.385	1683	3	935.80	1.65
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	18	Phosphoryl STY(3)	IISAKDHGDSFR	180	12	6	62.61	b3b6y3y4y8y9	1425.65	29.731	3300	2	713.33	3.00
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	19	Carbamidomethyl+C(19) ;Phosphoryl STY(13)	KPDNWEIVGKPQSQEAYGCMLRK	217	23	3	23.14	y7y9y10	2814.32	118.783	1936	3	938.78	6.85
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	20	Carbamidomethyl+C(21) ;Oxidation+M(22)	AKKPDNWEIVGKPQSQEAYGCMLR	215	24	3	22	b9y11y12	2821.41	113.130	10797	3	941.14	10.38
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	21	Oxidation+M(2)	LMDDTIAQAQTSGEAEK	247	17	5	33.72	y3y7y8°y8y11	1823.86	55.560	4484	3	608.62	13.19
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	22		NKPDQLQVK	81	8	0	1.62		941.55	36.545	21374	2	471.28	5.38
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	23		PITSQNR	91	7	0	1.62		815.43	41.711	13219	2	408.22	-6.89
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	24		KPDNWEIVGKPQSQEA	217	16	2	21.27	y8y9	1825.90	60.938	4109	2	913.45	-6.15
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	25		GYSQDYSNAIVEAVKK	63	16	5	38.59	b3b4b5b14°b14	1771.89	62.120	3021	2	886.45	4.34
P41031 CY_SALTY Thiosulfate-binding protein	1		FGSWPEVMK	311	9	8	64.71	b2b3°b3y2y3y5y7y8	1080.52	67.547	140552	2	540.76	-0.68
P41031 CY_SALTY Thiosulfate-binding protein	2		AYLNWLYSPQAQTIIITHYYR	265	21	27	192.23	b2b3b4°b4b5°b5b6°b6b19y1y2y3y4y6°y6y7y8°y8y9y10y11y12y13°y13y14y16y21	2664.32	92.355	129290	3	888.78	-1.37
P41031 CY_SALTY Thiosulfate-binding protein	3		ELFAALNPPEQQWAK	37	16	25	143.27	b2°b2b4b5°b5b6b7°b7y1y2y4°y4y5°y5y6y8°y8y9°y9y10°y10y12y13°y13y16	1888.97	89.030	105454	2	944.99	7.95
P41031 CY_SALTY Thiosulfate-binding protein	4		LPNNSSPFYSTMGFLVR	110	17	15	108.86	b7°b7b8°b8y2y3y4y5y9y11y12y13y14°y14y17	1929.96	91.139	104247	2	965.49	5.69
P41031 CY_SALTY Thiosulfate-binding protein	5		TEQFMTQFLK	179	10	19	88.54	b1°b1b2°b2b3b4b10°b10y1y2y3y5y6y7y8°y8°y8y10°y10	1272.63	74.383	103705	2	636.82	-2.69
P41031 CY_SALTY Thiosulfate-binding protein	6		GLGDVLISFESEVNNIRK	208	18	13	96.71	b2b10b12y5y6y8°y8y10y11y12y13y16y18	1990.04	100.545	102487	3	664.02	-9.75
P41031 CY_SALTY Thiosulfate-binding protein	7		NVEVFDTGGR	189	10	7	68.12	b2y4y5y6y7y8y10	1093.53	45.970	78161	2	547.27	-0.45
P41031 CY_SALTY Thiosulfate-binding protein	8		QYEAQGFEVVIPK	226	13	12	34.07	b2°b2b3°b3b13y1y2y6y8y11°y11y13	1507.78	68.825	77267	2	754.40	2.51
P41031 CY_SALTY Thiosulfate-binding protein	9		QALAILQLK	71	10	10	88.54	b3°b3b4°b4b10y3y5y6y7y8	1054.65	73.940	67834	2	527.83	-10.07
P41031 CY_SALTY Thiosulfate-binding protein	10		VNNPEIMGK	286	9	9	67.72	b2y2y3y4y6y7°y7y8y9	1001.50	35.035	66943	2	501.25	-6.34
P41031 CY_SALTY Thiosulfate-binding protein	11		LIFPNPK	146	7	7	50.68	b5y2y4°y4y5y6y7	828.49	54.674	58144	2	414.75	-9.80
P41031 CY_SALTY Thiosulfate-binding protein	12		NIHDWSDLVR	132	10	6	28.67	b7b8y1y8°y8y10	1254.62	61.900	57176	2	627.82	1.85
P41031 CY_SALTY Thiosulfate-binding protein	13		GLGDVLISFESEVNNIR	208	17	3	24.97	y7y10y11	1861.97	106.572	22018	2	931.49	5.05

[P41031 CY_SALTY Thiosulfate-binding protein	14		GATTTFAER	199	9	5	64.71	b3y3y4y6y7	953.46	29.697	20447	2	477.23	-7.55
[P41031 CY_SALTY Thiosulfate-binding protein	15		ADVVTYNQVTDVQILHDK	81	18	6	26.58	b2b3b4b6y10y18	2058.04	62.651	16036	3	686.69	-4.51
[P41031 CY_SALTY Thiosulfate-binding protein	16		TN1LAEFPVAWVDK	239	14	13	60.41	b2°b2b13y2y4y5°y5y8y9y10°y10y14*y14	1602.86	96.501	13128	2	801.93	1.60
[P41031 CY_SALTY Thiosulfate-binding protein	17		ELFAALNPPFEQQWAKDNGGDK	37	22	3	13.44	b11y3y12	2475.22	102.015	1612	2	1238.11	9.96
[P41031 CY_SALTY Thiosulfate-binding protein	18		TN1LAEFPVAWVDKNVQANGTEK	239	23	17	153.82	b3°b3b4y4y5y6°y6y7*y7y8y9y10y13y16y18y19y20	2544.31	89.767	146877	3	848.77	0.29
[P41031 CY_SALTY Thiosulfate-binding protein	19		YTYLAAWGAADNADGGDKAK	159	20	10	62.99	b3°b3b5°b5y9y11y12y13y16y18	2057.95	60.900	74329	3	686.66	-2.85
[P41031 CY_SALTY Thiosulfate-binding protein	20		VEEKFGSWPEVMK	307	13	3	20.64	b8b10y8	1565.76	49.818	11680	2	783.38	-5.93
[P41031 CY_SALTY Thiosulfate-binding protein	21		NVEVFDTGGRGATTTFAER	189	19	3	14.94	b5y3y10	2027.97	55.374	7263	3	676.66	-3.01
[P41031 CY_SALTY Thiosulfate-binding protein	22		VNNPEIMGKQADK	286	13	3	28.12	b6b7b12	1443.72	63.589	1646	2	722.36	-3.64
[P41031 CY_SALTY Thiosulfate-binding protein	23	Oxidation+M(8)	RPLTLAAMLLLAGQAQATELLNSYDVSR	8	29	3	17.49	y9y12y15	3118.64	97.306	5242	4	780.42	-4.93
[P41031 CY_SALTY Thiosulfate-binding protein	24	Oxidation+M(12)	LPNNSSPFYSTMGFLVR	110	17	4	23.31	b4b5y11°y11	1945.95	95.011	2509	2	973.48	0.88
[P41031 CY_SALTY Thiosulfate-binding protein	25		EVFDTGGR	191	8	0	2.02		880.41	45.962	3709	1	880.41	-8.94
[P41031 CY_SALTY Thiosulfate-binding protein	26		GATTTFAER	199	9	0	1.62		935.45	29.714	12529	2	468.23	1.04
[P41031 CY_SALTY Thiosulfate-binding protein	27		QALAILQGLK	71	10	0	2.02		1037.63	73.937	2022	2	519.32	2.12
[P0A1D3 CH60_SALTY 60 kDa chaperonin	1		GYLSPYFINKPETGAVELESPFILLADKK	197	29	27	210.2	b2b3b4°b4b6°b6b11*b11b12y1y2y3y4y5y6y7y8y9y10y11y12y13y19y25y26y27y29	3239.70	94.917	317889	4	810.68	-6.63
[P0A1D3 CH60_SALTY 60 kDa chaperonin	2		EMLPVLEAVAK	231	11	13	100.41	b2°b2b3y1y2y3y4y5y6y7y8y9y11	1199.66	79.122	148727	2	600.34	-5.09
[P0A1D3 CH60_SALTY 60 kDa chaperonin	3		ANDAAGDGTTTATVLAQSIIIEGLK	80	25	21	160.45	b2°b2b3°b3b4°b4b5°b5b6y1y3y4y5y6y7y8y9y10y11y15y25	2418.23	91.274	139743	3	806.75	-3.33
[P0A1D3 CH60_SALTY 60 kDa chaperonin	4	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDLPK	501	25	19	134.4	b3b4b5°b5b10°b10y2y3y4y5y8y9°y9y10y11°y11y12y13y25	2670.32	123.976	127645	3	890.78	-0.46
[P0A1D3 CH60_SALTY 60 kDa chaperonin	5	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	14	134.91	b9°b9b13y3y4y5y6y11y12y13y14y15y16y18	1957.02	60.627	104998	2	979.01	6.11
[P0A1D3 CH60_SALTY 60 kDa chaperonin	6		AVAAAVEELK	122	10	13	100	b2b3b5y2y3°y3y4°y4y5y6y7y8y10	1000.56	46.161	104482	2	500.78	-9.09
[P0A1D3 CH60_SALTY 60 kDa chaperonin	7		QQIEEATSDYDREK	350	14	14	113.08	b7b14y3y5y6°y6y7y8y9y10°y10y12y14*y14	1711.76	32.374	89879	3	571.26	-12.27
[P0A1D3 CH60_SALTY 60 kDa chaperonin	8		GVNVLADAVK	18	10	5	33.9	b2y5y6y8y10	985.56	54.844	86686	2	493.28	-10.22
[P0A1D3 CH60_SALTY 60 kDa chaperonin	9		LAGGVAVIK	371	9	4	30.49	b5b6y7y9	827.52	43.932	78980	2	414.27	-14.01
[P0A1D3 CH60_SALTY 60 kDa chaperonin	10		SFGAPTITK	42	9	9	53.25	b2b3°b3y1y2y3y5y7y9	921.50	43.754	74311	2	461.25	-7.75
[P0A1D3 CH60_SALTY 60 kDa chaperonin	11		VVINKDTTTIIDGVGEEAAIQGR	322	23	7	28.81	y2y3y5y6y8*y8y23	2399.28	66.463	73283	3	800.43	0.51
[P0A1D3 CH60_SALTY 60 kDa chaperonin	12	Carbamidomethyl+C(6)	ALSVPCCDSK	132	10	12	74.35	b1b2b3°b3y2y4y5y6°y6y7y8y10	1063.51	34.150	68469	2	532.26	-3.44

IP0A1D3 CH60_SALTY 60 kDa chaperonin	13		GGDGNYGYNAAATEEYGNMIDMG ILDPTK	470	28	10	57.28	y2y3y4y5y7y8y12*y12y14y28	2966.32	87.469	53203	2	1483.66	13.25
IP0A1D3 CH60_SALTY 60 kDa chaperonin	14		VEDALHATR	395	9	8	74.92	b2b4y3y4y5y6y7y9	1011.51	25.200	46201	2	506.26	-9.90
IP0A1D3 CH60_SALTY 60 kDa chaperonin	15		AIAQVGTISANSDETGVGK	142	18	10	76.66	b7y4y8y9y10*y10y11y13y14y18	1760.91	47.318	45740	2	880.96	7.07
IP0A1D3 CH60_SALTY 60 kDa chaperonin	16		AVAAGMNPMDLK	105	12	13	100.14	b2b3y2y4y5*y5y6*y6y7y8y9y10y12	1217.60	57.222	39304	2	609.30	-1.80
IP0A1D3 CH60_SALTY 60 kDa chaperonin	17		AVAAGMNPMDLKR	105	13	17	119.42	b2b3b6b8y2y3y6*y6y7*y7y8*y8y9y10*y10y11y13	1373.71	49.635	35505	2	687.36	1.60
IP0A1D3 CH60_SALTY 60 kDa chaperonin	18		GQNEDQNVGIK	430	11	6	31.29	b2*b2y3y4y9y11	1201.58	26.051	26595	2	601.29	-4.06
IP0A1D3 CH60_SALTY 60 kDa chaperonin	19		ATLEDLGQAKR	311	11	8	52.96	b2b7y5y7y8*y8y9y11	1201.65	37.967	21378	2	601.33	-2.23
IP0A1D3 CH60_SALTY 60 kDa chaperonin	20		GYLSPYFINKPETGAVELESPFILL ADK	197	28	5	17.32	b2b3b5b9y4	3111.64	101.643	12528	3	1037.89	4.86
IP0A1D3 CH60_SALTY 60 kDa chaperonin	21		SFGAPTITKDGVSVAREIELEDK	42	23	4	13.05	b5y2y6y11	2462.27	93.855	4556	3	821.43	-4.07
IP0A1D3 CH60_SALTY 60 kDa chaperonin	22		FENMGAQMVKEVASK	65	15	3	18.14	b10b14y14	1668.82	72.153	1586	3	556.94	6.14
IP0A1D3 CH60_SALTY 60 kDa chaperonin	23		DGVSVAREIELEDK	51	14	3	34.85	y3y4y5	1559.77	32.512	1556	3	520.59	-14.48
IP0A1D3 CH60_SALTY 60 kDa chaperonin	24		AMEAPLR	445	7	4	37.46	b4y4y5*y5	787.40	35.772	25327	2	394.21	-11.94
IP0A1D3 CH60_SALTY 60 kDa chaperonin	25		ATLEDLGQAK	311	10	3	36.91	b5b6b7	1045.55	19.598	11425	2	523.28	1.63
IP0A1D3 CH60_SALTY 60 kDa chaperonin	26		APGFGDR	277	7	4	50.68	b4y4y5y6	719.34	26.691	7742	2	360.17	-6.70
IP0A1D3 CH60_SALTY 60 kDa chaperonin	27		FGNDAR	7	6	4	43.08	b3y3y5*y5	679.32	75.539	2126	1	679.32	7.82
IP0A1D3 CH60_SALTY 60 kDa chaperonin	28		VGAATEVEMK	380	10	5	39.34	b4b9*b9y4y6	1034.50	122.316	1966	1	1034.50	-17.46
IP0A1D3 CH60_SALTY 60 kDa chaperonin	29		EIELEDKFENMGAQMVK	58	17	9	56.85	b3*b3b8b9*b9y5y7y10y13	2010.93	72.346	197535	3	670.98	-8.50
IP0A1D3 CH60_SALTY 60 kDa chaperonin	30		IADLKGQNEDQNVGIK	425	16	11	89.12	b3b10y3y4y8*y8y9y10y11*y11y14	1741.89	38.778	122179	3	581.30	-9.88
IP0A1D3 CH60_SALTY 60 kDa chaperonin	31		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	8	41.34	b3b6b7y4y5y7y21y25	3675.88	121.707	23433	3	1225.97	3.52
IP0A1D3 CH60_SALTY 60 kDa chaperonin	32		AIAQVGTISANSDETGVGLIAEAM DK	142	26	4	22.81	y3y4y8*y8	2632.35	90.870	9482	3	878.12	1.58
IP0A1D3 CH60_SALTY 60 kDa chaperonin	33	Carbamidomethyl+C(16)	AVAAAVEELKALSVPSCDSK	122	20	3	14.37	b5y12y16	2045.04	83.524	6240	2	1023.02	-9.85
IP0A1D3 CH60_SALTY 60 kDa chaperonin	34		DGVSVAREIELEDK	51	14	4	24.73	b12b13*b13y10	1559.77	77.297	2323	2	780.39	-13.54
IP0A1D3 CH60_SALTY 60 kDa chaperonin	35	Oxidation+M(9)	AVAAGMNPMDLKR	105	13	4	25.41	b6b7y7*y7	1389.70	24.944	91943	3	463.90	1.67
IP0A1D3 CH60_SALTY 60 kDa chaperonin	36	Oxidation+M(22)	EGVITVEDGTGLQDEL DVVEGMQ FDR	171	26	3	12.14	b3b10y3	2867.33	112.859	73946	3	956.45	0.60
IP0A1D3 CH60_SALTY 60 kDa chaperonin	37		AAGMNPMDLKR	107	11	2	21.22	b3b4	1203.60	49.644	36578	2	602.30	1.62
IP0A1D3 CH60_SALTY 60 kDa chaperonin	38		EDALHATR	396	8	1	8.82	b5	912.45	25.255	29188	2	456.73	-6.09
IP0A1D3 CH60_SALTY 60 kDa chaperonin	39		AAAVEELK	124	8	2	8.25	b6*b6	830.46	46.159	15219	1	830.46	-5.81
IP0A1D3 CH60_SALTY 60 kDa chaperonin	40		AGMNPMDLKR	108	10	3	7.42	b9*b9*b9	1132.56	49.604	6278	2	566.78	-1.29
IP0A1D3 CH60_SALTY 60 kDa chaperonin	41		MNPMDLK	110	7	0	2.83		848.39	57.227	4055	2	424.70	-10.07

P0A1D3 CH60_SALTY 60 kDa chaperonin	42	Carbamidomethyl+C(4)	SVPCSDSK	134	8	0	2.02		879.39	34.157	2377	1	879.39	6.59
P0A1D3 CH60_SALTY 60 kDa chaperonin	43		DGVSVAREI	51	9	0	3.64		945.51	32.571	2303	2	473.26	8.07
P0A1D3 CH60_SALTY 60 kDa chaperonin	44		QQIEEATSDYDREK	350	14	0	3.64		1694.75	32.350	2893	3	565.59	-0.43
P0A1D3 CH60_SALTY 60 kDa chaperonin	45	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	0	2.02		1045.50	34.089	1647	2	523.25	4.90
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTASPYASYLQYGHIANIDD IIAGKKPATDLGVK	125	38	23	76.86	b1b2b3b6°b6°b6b7°b7°b7 b10°b10b11b13b20y2y3y4 y8y12y22y27y31y38	4001.03	82.284	172831	5	801.01	-9.15
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		LVEPEWFK	352	8	10	67.31	y2y3y4°y4y5°y5y6°y6y7y8	1047.55	69.955	137902	2	524.28	-5.48
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3		AEQQLDKDSAIVPVYYVYNAR	494	21	15	129.93	b3b4b5b10°b10b11b12y3y 5y7y9y11y12y20y21	2442.23	71.949	127785	3	814.75	-1.80
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4	Carbamidomethyl+C(4)	AGWCADYNEPTSFLNTMLSDSSN NTAHYK	439	29	9	62.83	b4b5y2y11y12y13y20y21y 29	3294.43	89.230	115999	3	1098.82	7.41
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		WSDGTPVTAHDFVYSWQR	107	18	15	111.55	b2b3°b3y3*y3y4y5y7y8y10 °y10y11y13y17y18	2151.99	71.233	105589	3	718.00	-1.36
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		TVINQVTYLPISSEVTDVNR	241	20	20	106.29	b2°b2b9y2*y2y3y4y5*y5y6 y9*y9y11*y11y12*y12y13 y14°y14y20	2248.20	76.236	87001	2	1124.60	7.49
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7		SGEIDMTYNNMPIELFQK	263	18	14	54.16	b2b3b5b13b15°b15y1y2*y 2y3y10y11y12°y18	2130.01	85.765	84300	2	1065.51	9.74
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		NQGDLPAYSYTPPYTDGAK	333	19	9	50.05	b5b10b11°b11°b11y8y11y 12y14	2057.97	57.930	80631	2	1029.49	10.32
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9		ALDDHTFEVTLSEPVYFYK	163	20	13	89.28	b6b7b9b10°b10b12b13y4y 5y7y9°y9y20	2371.15	85.241	73060	3	791.06	1.34
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		NLGVNVNLENQEWK	410	14	15	108.82	b1b2b3b4y3y4y7y8*y8y10 *y10y11y12*y12y14	1656.84	65.681	55219	2	828.92	2.95
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		HQGTFDVAR	430	9	4	30.49	b2b3b7y7	1030.50	31.137	41558	2	515.75	-4.15
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	8	25.13	b3b4b28y1y2y3y10y29	3091.56	87.444	38537	3	1031.19	5.84
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	13		DLFEGLLISDVEGHPSPGVAEK	67	22	7	30.67	b2b6y3y6y15y19y22	2309.17	88.328	21794	3	770.39	0.42
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	14		DPLDNIYVK	527	9	4	30.49	b3b4y3y9	1076.57	68.981	12224	2	538.79	4.65
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	15		NPQYWDNAK	232	9	4	30.49	b3y3y6°y6	1135.52	38.316	47719	2	568.26	1.40
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	16		LIADTLK	474	7	3	40.47	b6y3y5	773.47	42.290	14192	2	387.24	-15.07

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	17		IVLER	227	5	1	13.22	y4	629.39	32.558	11531	1	629.39	-13.58
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	18		TFLDTR	424	6	2	13.62	y4°y4	752.38	35.719	8116	1	752.38	-14.52
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	19		NWVVNER	220	7	4	40.47	b3b6y3*y3	916.48	37.865	2470	2	458.75	21.78
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	20		SELYAK	488	6	2	26.85	b4b5	710.38	36.186	2208	1	710.38	11.08
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	21	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYEINNQK	284	23	9	33.91	b4b9°b9*b9y7y8y14°y14y21	2920.40	75.210	55526	3	974.14	4.85
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	22		VKNQGDLPAYSYTPPYTDGAK	331	21	6	29.76	b6b12y8y9°y9y13	2285.08	68.147	47490	4	572.02	-14.32
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	23		NPQYWDNAKTVINQVTYLPISSEVTDVNR	232	29	4	24.93	b3b22y11y12	3364.72	101.106	34375	3	1122.24	10.52
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	24		TVINQVTYLPISSEVTDVNR	241	22	4	29.75	y9y13y16y20	2567.35	76.123	26973	3	856.45	0.86
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	25		NNGSEVQSLDPHKIEGVPE\$NVS\$R	43	24	10	28.74	b7y4*y4y6*y6y10°y10*y10y11*y11	2592.27	116.643	22098	3	864.76	0.19
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	26	Carbamidomethyl+C(6)	VDPYLCTYYYEINNQKAPFNDVR	291	23	4	23.8	b9y4y5y12	2882.35	75.340	16184	3	961.46	2.54
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	27		IVLERNPQYWDNAK	227	14	3	19.29	b8y6y12	1745.88	52.140	11767	3	582.63	-11.54
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	28		LKNWVVNER	218	9	7	45.47	b4*b4y4*y4y5y7°y7	1157.63	43.559	11578	2	579.32	-8.12
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	29		NQGDLPAYSYTPPYTDGAKLVEPEWFK	333	27	3	11.91	b7y4y6	3086.49	90.687	7992	3	1029.50	4.59
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	30		LVEPEWFKWSQQK	352	13	5	34.07	b7b9°b9b12y8	1704.87	83.482	5756	2	852.94	-4.58
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	31		TFLDTRHQGTFDVAR	424	15	3	18.14	b4y5y8	1763.91	74.584	4406	2	882.46	13.08
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	32		LADPNTASPYASYLQYGHIANIDDIAG	125	28	0	13.34		2963.44	82.259	4591	3	988.48	-0.99
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	33		VEGHPSPGVAEK	77	12	0	6.87		1206.62	88.319	1789	2	603.81	7.49
P65702 PGK_SALTY Phohoglycerate kinase	1	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	22	178.35	b2b3b4b5°b5b7b8b12b13b14b15°b15y2y3y4y5y8y9y13y15y16y20	2002.05	98.217	208442	2	1001.53	7.80
P65702 PGK_SALTY Phohoglycerate kinase	2		VLPAVAMLEER	373	11	14	111.41	b1b2b3b5y2°y2y3y4y5y6y7y8y9y11	1227.67	79.101	196666	2	614.34	-2.59

P65702 PGK_SALTY Phohoglycerate kinase	3		SVNDVKEDEQILDIGDASAQQLAE ILK	272	27	26	150.7	b1b2b4b5*b5b7b11b12b13°b13b14*b14b24*b24b25y1y2y3y4y5y6y10y12y13y16y27	2941.51	99.410	193624	3	981.18	3.73
P65702 PGK_SALTY Phohoglycerate kinase	4		VMVTSHLGRPTEGEYNEEFSLPV VNYLK	53	29	9	49.17	b2b13b16b17b18y2y7y8y29	3321.66	91.518	191698	4	831.17	-7.79
P65702 PGK_SALTY Phohoglycerate kinase	5	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	17	139.73	b2b6b7°b7b9b12b13y2y5y7y8y9y10y11y12°y12y14	1599.85	67.627	126879	2	800.43	6.10
P65702 PGK_SALTY Phohoglycerate kinase	6		VATEFSETAPATLK	258	14	16	111.83	b1b2b3°b3b4°b4b6y1y5y6y7y9y10y11y12y14	1464.76	51.366	99680	2	732.88	0.25
P65702 PGK_SALTY Phohoglycerate kinase	7		SLYEADLVDEAKR	231	13	11	92.77	b2°b2y1y2y4y5y6y8y9y10y11	1508.74	52.900	99093	3	503.59	-11.33
P65702 PGK_SALTY Phohoglycerate kinase	8		TILWNGPVGVFEPNFR	302	17	19	152.4	b2b6°b6b12°b12b13y3y4y5y6°y6y7*y7y10y11y12y13y14y17	1993.05	105.610	90579	2	997.03	8.64
P65702 PGK_SALTY Phohoglycerate kinase	9		ASLPTIELALK	38	11	4	31.29	y3y7y8y11	1155.69	76.291	73636	2	578.35	-6.55
P65702 PGK_SALTY Phohoglycerate kinase	10		ADLNPVKEGK	19	11	10	99.16	b3b5b9y2y3y4y6y7y8y11	1169.66	35.712	71170	2	585.33	2.71
P65702 PGK_SALTY Phohoglycerate kinase	11		LVKDYLDGVDV AEGELV VLENV R	90	23	7	28.81	y2y4*y4y6y14y16y23	2544.36	96.325	59473	3	848.79	1.54
P65702 PGK_SALTY Phohoglycerate kinase	12		MTDLDLAGKR	5	10	6	71.13	b2y3y4y5y7y9	1119.58	41.454	39049	2	560.29	-3.93
P65702 PGK_SALTY Phohoglycerate kinase	13		IADQLIVGGGIANTFVAAQGHSVG K	206	25	6	25.85	b4°b4b5y2y14y19	2423.29	77.212	36581	3	808.43	-5.84
P65702 PGK_SALTY Phohoglycerate kinase	14		TILWNGPVGVFEPNFRK	302	18	7	24.82	b1b2b14y10y12y16y18	2121.12	95.959	26527	3	707.71	-4.49
P65702 PGK_SALTY Phohoglycerate kinase	15		SLYEADLVDEAK	231	12	6	32.19	b5b10y4°y4y10y12	1352.67	57.100	14212	2	676.84	6.32
P65702 PGK_SALTY Phohoglycerate kinase	16		AQASTHGIGK	146	10	9	61.13	b1b3b5b7°b7b8°b8y2y4	969.50	22.003	6858	2	485.25	-12.59
P65702 PGK_SALTY Phohoglycerate kinase	17		LTVLDSLK	197	9	3	38.27	y5y6y8	975.56	60.704	69189	2	488.29	-7.57
P65702 PGK_SALTY Phohoglycerate kinase	18	Carbamidomethyl+C(5)	YAALCDVFVMDAFGTAHR	128	18	5	41.6	b4b5b10b11°b11	2043.93	61.937	66773	3	681.98	-6.15
P65702 PGK_SALTY Phohoglycerate kinase	19		SVNDVK	272	6	1	13.62	b5	661.36	77.700	8513	1	661.36	5.26
P65702 PGK_SALTY Phohoglycerate kinase	20		LSNPVR	84	6	3	26.85	y3y4*y4	685.39	26.685	3914	1	685.39	-8.73
P65702 PGK_SALTY Phohoglycerate kinase	21		ISYISTGGGAFLEFVEGK	355	18	7	56.08	b5b11b15y6y8y9y10	1874.97	89.041	3763	2	937.99	9.11
P65702 PGK_SALTY Phohoglycerate kinase	22		EDEQILDIGDASAQQLAEILK	278	21	4	35.83	b6b7y4y5	2299.13	76.355	2417	4	575.54	-16.35
P65702 PGK_SALTY Phohoglycerate kinase	23	Carbamidomethyl+C(5); Oxidation+M(10)	YAALCDVFVMDAFGTAHR	128	18	8	54.86	b4b5b7b8b9°b9y9°y9	2059.96	81.660	2315	3	687.32	11.14
P65702 PGK_SALTY Phohoglycerate kinase	24		DLDLAGKR	7	8	1	8.25	b3	887.49	41.521	18224	2	444.25	-0.14
P65702 PGK_SALTY Phohoglycerate kinase	25		TDLDLAGKR	6	9	1	8.25	b4	988.54	41.523	15452	2	494.77	-4.51
P65702 PGK_SALTY Phohoglycerate kinase	26		YEADLVDEAKR	233	11	2	16.45	b4b6	1308.65	52.884	14795	2	654.83	3.36
P65702 PGK_SALTY Phohoglycerate kinase	27		PAVAMLEER	375	9	2	18.87	b3b7	1015.51	79.149	10113	2	508.26	-14.79
P65702 PGK_SALTY Phohoglycerate kinase	28		DLNPVKEGK	20	10	2	7.86	b3°b3	1098.61	35.734	8480	2	549.81	-3.22

P0A1S0 IHFA_SALTY Integration host factor subunit alpha	1		TGEDIPITAR	66	10	14	103.01	b2°b2b3°b3b4°b4b5°b5y3y4y5y6y8y10	1072.56	41.760	52671	2	536.78	-3.76
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	2		LSGFGNFDLR	45	10	8	28.67	b7°b7y1y2y8y9°y9y10	1125.57	71.094	29658	2	563.29	0.22
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	3		ALENGEQVK	36	9	4	53.25	b6y4y6y8	987.53	27.995	1612	2	494.27	18.85
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	4		ALENGEQVKLSGFGNFDLR	36	19	4	14.94	b3b6°b6y6	2094.04	96.004	2160	2	1047.52	-9.33
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VVGQLGQVLGPR	122	12	14	110.05	b1b2b4b9y2y3y4y6y7y8y9y10°y10y12	1222.72	57.954	126364	2	611.86	-3.69
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VAVFTQGPNAEAAK	74	14	16	96.39	b3b7b11b14y2y4y7y8°y8y9°y9y10°y10y11°y11y14	1402.74	44.078	125666	2	701.87	2.78
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VGTVTPNVAEAVK	141	13	15	126.41	b3°b3b13y1y3y4y5y7y8y9y10y11y12°y12y13	1284.72	46.927	110994	2	642.86	-0.67
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		AAGAELVGMEDLADQIK	88	17	7	43.55	b4b6y2y10y11y12y17	1730.87	78.731	29872	2	865.94	5.01
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		GATVLPHTGR	60	11	12	76.39	b3°b3b4°b4b5b8y2y4°y4y6y7y11	1065.58	28.647	26221	2	533.29	-2.75
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		AAGAELVGMEDLADQIKK	88	18	4	34.5	b2y10y11y12	1858.94	72.008	9115	3	620.32	-12.15
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		GEMNFDVVIASPDAMR	106	16	4	23.69	b2b3y11y12	1751.81	70.606	9075	3	584.61	-1.67
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		KGEMNFDVVIASPDAMR	105	17	4	23.72	b9°b9b13b15	1879.91	107.566	4255	2	940.46	1.95
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9		TVLPHGTGR	62	9	0	2.43		937.51	28.643	19046	2	469.26	-10.09
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	13	110.76	b2b3b4b13y1y3y5y6y7y8y10y11y13	1365.68	61.893	81137	2	683.34	-0.63
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2	Carbamidomethyl+C(13)	AAQYVAAHGPEVCPAK	153	16	13	126.86	b3b4b8b10b12y3y4y5y8y9y11y12y16	1668.80	34.202	70214	3	556.94	-11.85
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		ATFVVDPQGIIAIEVTAEGIGR	120	23	24	192.24	b2b3°b3b4b5°b5b6b7°b7b8b10y2y3y4y5y6y7y8y9°y9y10y11y17y23	2384.27	128.127	50357	3	795.43	-3.99
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4	Carbamidomethyl+C(15)	WSVFFFYPADFTFVCPTELGDVA DHYEELQK	32	31	5	13.85	b3b7y12y24°y24	3757.74	118.969	16218	3	1253.25	5.20
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		DASDLLR	143	7	4	40.47	y3y4y5y7	789.41	44.458	4783	1	789.41	-5.18
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6		NGEFIEVTEKDTEGR	17	15	4	24.16	b11b12°b12y3	1723.82	63.784	4470	3	575.28	6.30
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7		LGVDVYSVSTDTHFTHK	63	17	5	43.55	b12b13b14y7y13	1905.97	71.620	2311	2	953.49	18.64
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8		EGEATLAPSLDLVGKI	171	16	4	23.69	b6b7°b7y3	1612.88	84.159	40997	2	806.94	-2.04
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9		NGEFIEVTEKDTEGR	17	15	3	18.14	b10b13y3	1723.81	85.118	5959	3	575.27	-3.68
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10		NQAFKNGEFIEVTEK	12	15	5	29.44	b5y5y10y14°y14	1753.86	70.998	3053	3	585.29	-11.62
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	1		DLVESAPAALK	85	11	7	47.53	b2b11y5y7y8y9y11	1113.61	52.298	52689	2	557.31	-7.13
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		DQIIEAVSAMSVM DVVELISAMEE K	5	25	26	224.5	b2°b2°b2b3b4b5b6b7b8b9°b9b10y2°y2y3y4y5y6y7y8y9°y9y10y11y12y25	2737.33	137.031	35340	3	913.12	-0.54
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	3		DLVESAPAALKEGVSK	85	16	8	24.86	b2°b2b3b5°b5b8y1y16	1613.86	55.485	11033	3	538.62	-11.50

[P0A299 RL7_SALTY 50S ribosomal protein L7/L12	4		SITKDKIIEAVSAMSVMDEVVELISA MEEK	1	29	5	17.49	b1y2y3y5y16	3166.60	96.409	2332	4	792.41	3.39
[P0A299 RL7_SALTY 50S ribosomal protein L7/L12	5		KSLEEAGAEVEVK	108	13	4	34.44	b7b8y3y7	1388.71	28.683	14876	3	463.58	-11.87
[P0A299 RL7_SALTY 50S ribosomal protein L7/L12	6		SITKDKIIEAVSAMSVMDEVVELISA MEEK	1	29	3	22.72	y3y4y7	3166.61	136.474	6534	3	1056.21	6.48
[P0A299 RL7_SALTY 50S ribosomal protein L7/L12	7	Oxidation+M(27)	MSITKDKIIEAVSAMSVMDEVVELI SAMEEK	0	30	6	24.78	b7°b7b11*b11y10y11	3313.59	100.597	8626	3	1105.20	-13.11
[P0A299 RL7_SALTY 50S ribosomal protein L7/L12	8		SITKDKIIEAVSAMSVMDEVV	1	20	4	26.57	y4y8y9y14	2136.12	96.412	3264	3	712.71	14.63
[P67904 RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAKR	16	15	15	147.12	b3b8y1y2y3y4y5y6y7y8y9y10y11y13y15	1673.88	50.997	97700	3	558.63	-13.56
[P67904 RS10_SALTY 30S ribosomal protein S10	2		LIDQSTAEIVETAK	16	14	12	100.37	b2b3b10y2y3y4y5y8y9y10y11y14	1517.81	54.321	77632	2	759.41	4.10
[P67904 RS10_SALTY 30S ribosomal protein S10	3		LVDIVEPTEK	72	10	5	26.91	b2b3y4y8y10	1142.62	50.629	37739	2	571.82	-5.02
[P67904 RS10_SALTY 30S ribosomal protein S10	4		GPIPLPTRK	37	9	7	45.47	b1b2b3y3y4y6y9	978.60	41.941	30966	2	489.80	-7.36
[P67904 RS10_SALTY 30S ribosomal protein S10	5		DQYEIR	62	6	2	26.85	y3y4	823.39	31.164	20460	2	412.20	-4.45
[P67904 RS10_SALTY 30S ribosomal protein S10	6		IPLPTRK	39	7	0	1.62		824.53	41.931	7178	2	412.77	-9.77
[P67904 RS10_SALTY 30S ribosomal protein S10	7		DQSTAEIVETAKR	18	13	3	14.92	b5°b5b9	1447.75	51.023	6304	2	724.38	5.23
[P0A1H3 EFG_SALTY Elongation factor G	1		IATDPFVGNLTFFR	323	14	17	129.52	b2b4b5°b5b6b13b14y1y3y4y6y7*y7y10y11y12y14	1597.84	92.444	104971	2	799.42	0.00
[P0A1H3 EFG_SALTY Elongation factor G	2		VYSGVVNSGDTVLSNVK	337	17	17	130.15	b2b4°b4b5b14*b14y3y4y5y9y10y11*y11y12y14y15y17	1737.91	61.019	91178	2	869.46	3.09
[P0A1H3 EFG_SALTY Elongation factor G	3		IHAEVPLSEMFYATQLR	653	18	5	32.75	b4b5b9y5y7	2062.03	89.361	66237	3	688.02	-5.21
[P0A1H3 EFG_SALTY Elongation factor G	4		SGPLAGYPVVDLGVR	562	15	13	74.54	b2°b2b3°b3b5b7°b7y3y4y8y10y11y15	1499.83	75.639	66234	2	750.42	2.20
[P0A1H3 EFG_SALTY Elongation factor G	5		IGEVHDDGAATMDWMEQEQR	39	20	18	95.97	b1b3b4b10b11°b11b12b14y2°y2y3°y3*y3y5y6y7y9y20	2331.99	61.014	60820	3	778.00	-2.41
[P0A1H3 EFG_SALTY Elongation factor G	6		GQYGHVVIDMYPLEPGSNPK	512	20	10	69.48	b5b10b11y5y6*y6y7°y7y9y10	2201.07	69.199	46538	3	734.36	-0.78
[P0A1H3 EFG_SALTY Elongation factor G	7		EFNVEANVGKQPQVAYR	475	16	8	35.08	b2°b2y2y3y5y6y9y16	1820.91	52.137	41871	3	607.64	-7.91
[P0A1H3 EFG_SALTY Elongation factor G	8		VEVETPEENTGDVIGDLR	618	19	14	84.61	b3b5°b5b7b9b14*b14y3y5y9°y9y14y15y19	2059.00	65.734	34854	2	1030.00	7.94
[P0A1H3 EFG_SALTY Elongation factor G	9		GQESEVTGVK	643	10	8	51.89	b2y2y4y5y6y8°y8y10	1033.51	24.507	32073	2	517.26	-10.39
[P0A1H3 EFG_SALTY Elongation factor G	10	Carbamidomethyl+C(20)	AGDIAAIGLKDVTGDTLCPENPIILER	378	30	9	33.52	b3b17b27y2y3y10*y10y11y13	3138.61	84.332	29426	3	1046.88	4.67
[P0A1H3 EFG_SALTY Elongation factor G	11		LGANPVPLQLAIGAEEGFTGVVDLVK	161	26	5	18.28	b4y3y7y14y26	2607.41	119.419	24159	3	869.81	-9.93
[P0A1H3 EFG_SALTY Elongation factor G	12		YDDAPNNVAQAVIEAR	686	16	5	25.53	y2y8y12°y12y13	1745.86	64.020	23044	2	873.43	6.99
[P0A1H3 EFG_SALTY Elongation factor G	13	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETVWR	104	24	9	27.59	b2b8°b8b14b15y1y8y15y24	2621.29	85.180	21711	3	874.43	1.21
[P0A1H3 EFG_SALTY Elongation factor G	14		GVQAMLDIVIDYLPSPVDVPAINGILDDGKDTPAER	273	36	6	30.17	b2y3y5y6y13y23	3764.93	121.911	11212	3	1255.65	6.55
[P0A1H3 EFG_SALTY Elongation factor G	15		LAASIAFKEGFK	594	12	3	22.28	b7y4y10	1281.72	46.391	9541	3	427.91	0.95
[P0A1H3 EFG_SALTY Elongation factor G	16		YLGGEELTEEEIK	236	13	4	20.64	b2b7y6y11	1509.74	56.573	5754	2	755.37	4.53

P0A1H3 EFG_SALTY Elongation factor G	17		VEVETPEENTGDVIGDLSRR	618	20	4	22.5	b1b13y12y13	2215.08	81.633	2227	3	739.03	-3.31
P0A1H3 EFG_SALTY Elongation factor G	18		MEFPEPVISIAVEPK	408	15	4	25.8	b3b9y7y12	1685.89	85.130	47030	2	843.45	5.00
P0A1H3 EFG_SALTY Elongation factor G	19		HASDDEPFSSALAFK	309	14	5	27.58	b5b12y7y12°y12	1534.72	69.370	27963	2	767.87	3.82
P0A1H3 EFG_SALTY Elongation factor G	20		ILFYTGvNHK	29	10	4	33.9	y5y7°y7y8	1191.63	53.760	21670	3	397.88	-16.80
P0A1H3 EFG_SALTY Elongation factor G	21		VVGQIK	153	6	1	13.62	b5	643.41	43.936	15744	1	643.41	-4.55
P0A1H3 EFG_SALTY Elongation factor G	22		QSGGR	507	5	1	13.22	b3	504.25	47.029	14835	1	504.25	1.45
P0A1H3 EFG_SALTY Elongation factor G	23		IAFVNK	137	6	1	13.62	b5	691.41	39.014	8878	1	691.41	-9.09
P0A1H3 EFG_SALTY Elongation factor G	24		AINWNDADQGVTFEYEDIPADMQ DLANEWHQNLISSAAEASEELME K	189	47	20	156.07	b3b6b10b11b12y3°y3y4°y4 y5y6y7y8°y8y9°y9y10°y10 y11y12	5380.44	125.428	5195	4	1345.86	9.62
P0A1H3 EFG_SALTY Elongation factor G	25		LHFGSYHDVDSSELAfK	577	17	3	23.31	b6y13y14	1951.95	83.463	4076	3	651.32	17.70
P0A1H3 EFG_SALTY Elongation factor G	26		YLGEELTEEEIKQALR	236	17	4	16.32	b8y5y10*y10	1978.00	72.429	85838	3	660.00	-8.64
P0A1H3 EFG_SALTY Elongation factor G	27		GITITSAATTAFWSGMAKQYEPHR	59	24	6	26.16	b13b22°b22y6*y6y7	2624.28	75.324	78446	4	656.82	-6.33
P0A1H3 EFG_SALTY Elongation factor G	28		ASYTMEFLKYDDAPNNVAQAVIE AR	677	25	8	39.3	b11b12b13°b13y3°y3y8*y8	2816.38	83.509	59762	3	939.47	8.84
P0A1H3 EFG_SALTY Elongation factor G	29		GGVIPGEYIPAVDKGIEQLK	541	21	3	22.33	b3b4y12	2211.20	73.343	26024	3	737.74	-2.54
P0A1H3 EFG_SALTY Elongation factor G	30		QYEPHRINIIDTPGHVDFTIEVER	77	24	4	22	b3b4y7°y7	2878.45	58.941	7245	4	720.37	0.51
P0A1H3 EFG_SALTY Elongation factor G	31		GRASYTMEFLK	675	11	4	36.73	b5b6b10y9	1302.63	33.480	1630	2	651.82	-14.06
P0A1H3 EFG_SALTY Elongation factor G	32	Phosphoryl STY(4)	LAASIAFKEGFK	594	12	3	22.28	b3b8y9	1361.69	88.220	2320	2	681.35	12.01
P0A1H3 EFG_SALTY Elongation factor G	33	Carbamidomethyl+C(10) ;Oxidation+M(7)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	7	30.35	b9b11b16°b16y10y12y20	2637.27	93.971	16744	3	879.76	-4.72
P0A1H3 EFG_SALTY Elongation factor G	34	Oxidation+M(10)	GQYGHVVIDMYPLEPGSNPK	512	20	4	19.76	b10b13y4y14	2217.10	87.103	4228	2	1109.05	14.10
P0AA28 THIO_SALTY Thioredoxin-1	1		MIAPILDEIADEYQGK	37	16	15	136.45	b2b11y2y3y4y5°y5y6y7y9y 10y11y13y14y16	1805.90	92.761	167961	2	903.46	3.24
P0AA28 THIO_SALTY Thioredoxin-1	2		LNIDQNPGTAPK	58	12	14	105.79	b2*b2b3b4b10y2y3y6y7y8 y9*y9y10y12	1267.66	37.390	130214	2	634.33	-4.33
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	13	104.37	b2b3b5°b5b6y1y2y3y4y5y 6y7y9	1001.63	89.781	63252	2	501.32	-9.38
P0AA28 THIO_SALTY Thioredoxin-1	4		MIAPILDEIADEYQGKLTVAK	37	21	4	24.71	b3y11y12y18	2318.22	93.957	59258	3	773.41	-2.74
P0AA28 THIO_SALTY Thioredoxin-1	5	Oxidation+M(1)	MIAPILDEIADEYQGK	37	16	4	28.34	b13y9y13y14	1821.91	86.636	6515	2	911.46	11.19
P0AA28 THIO_SALTY Thioredoxin-1	6		PTLLLFK	76	7	3	38.27	b3b4b5	831.52	89.784	63624	2	416.26	-14.39
P0AA28 THIO_SALTY Thioredoxin-1	7		APILDEIADEYQGK	39	14	0	4.45		1561.78	92.795	1901	2	781.40	6.49
P66038 RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	14	85.23	b3b8b10°b10b11°b11b12b 13b14y9y12y15y16y29	3110.69	97.631	83202	3	1037.57	2.67
P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	17	138.39	b3b4y2y3y4y5y6y8y9°y9y1 0y13°y13y14y15y19*y19	2109.08	100.548	60383	2	1055.04	8.91

P66038 RISB_SALTY 6	3		GAEAAALTALEMINVLK	136	16	8	45.95	b2b5b12b15y3y4y10y16	1643.91	102.257	46825	2	822.46	2.82
P66038 RISB_SALTY 6	4		ANVAAPDAR	5	9	6	38.27	b2*b2y2y5y6y7	884.45	21.649	12219	2	442.73	-7.87
P66038 RISB_SALTY 6	5		DDNITVVWVPGAYELPLATEALAK	45	24	4	19.45	b4b12b14y16	2585.39	103.997	1888	2	1293.20	16.34
P64052 EFTS_SALTY Elongation factor Ts	1		VASLEGDVLGSYQHGAR	134	17	20	122.49	b3°b3b6b8y1y3y4y5*y5y6y7°y7y8y9°y9*y9y10°y10y11*y17	1758.86	57.763	129685	3	586.96	-12.28
P64052 EFTS_SALTY Elongation factor Ts	2		ITDVEVLK	104	8	5	40.87	y2y3y6y7y8	916.52	47.447	111154	2	458.77	-11.12
P64052 EFTS_SALTY Elongation factor Ts	3		FTGEVSLTGQPFVMEPSK	222	18	8	32.75	b3b11y1y5y12°y12y13y18	1953.98	73.797	110920	2	977.49	7.68
P64052 EFTS_SALTY Elongation factor Ts	4		ALTEANGDIELAIENMRK	25	18	5	32.75	b9b10b14y14y16	1987.99	73.300	65852	3	663.34	-10.25
P64052 EFTS_SALTY Elongation factor Ts	5		IGENINIR	125	8	9	54.09	b2y2y3*y3y5*y5y6y7y8	928.51	43.328	63720	2	464.76	-8.55
P64052 EFTS_SALTY Elongation factor Ts	6		AEITASLVK	1	9	4	38.27	y4y5y6y9	931.54	47.510	63276	2	466.27	-7.93
P64052 EFTS_SALTY Elongation factor Ts	7		IGVLVAAK	151	8	7	77.52	b3b4y3y5y6y7y8	770.50	46.023	56827	2	385.75	-14.58
P64052 EFTS_SALTY Elongation factor Ts	8	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	8	40.13	b2°b2b5y2y4y5y7y10	1098.47	20.033	27926	2	549.74	-5.00
P64052 EFTS_SALTY Elongation factor Ts	9		EYQVQLDIAMQSGKPK	193	16	5	35.44	b3b5b6y4y7	1834.95	69.503	7540	3	612.32	8.71
P64052 EFTS_SALTY Elongation factor Ts	10		VETDFAAEVAAMSK	267	14	3	19.29	b5b9y3	1468.72	68.027	3768	2	734.86	12.30
P64052 EFTS_SALTY Elongation factor Ts	11		MAEITASLVKELR	0	13	4	28.12	b4°b4b6b7	1460.82	77.258	2307	3	487.61	0.75
P64052 EFTS_SALTY Elongation factor Ts	12		VLDAAVAGK	95	9	5	67.72	y3y4y5y7y8	843.48	32.605	38407	2	422.24	-15.34
P64052 EFTS_SALTY Elongation factor Ts	13		AGNVAADGVIK	52	11	3	36.07	y5y6y7	1014.55	35.642	19569	2	507.78	-3.91
P64052 EFTS_SALTY Elongation factor Ts	14		ALTEANGDIELAIENMR	25	17	7	48.2	b6*b6b13y3y4y5y11	1859.93	81.187	2461	2	930.47	7.29
P64052 EFTS_SALTY Elongation factor Ts	15		DAGFQAFADKVLDAAVAGK	85	19	4	14.94	b3b6*b6y17	1893.95	97.090	110877	3	631.99	-10.25
P64052 EFTS_SALTY Elongation factor Ts	16		KALTEANGDIELAIENMR	24	18	3	15.58	b11y6y16	1988.02	65.770	12677	2	994.52	6.51
P64052 EFTS_SALTY Elongation factor Ts	17		FEVGEGIEKVETDFAAEVAAMSK	258	23	7	33.91	b6b13°b13y6y9y12y14	2457.21	106.261	1615	2	1229.11	10.43
P64052 EFTS_SALTY Elongation factor Ts	18	Phosphoryl STY(7)	MAEITASLVKELR	0	13	4	25.41	b5°b5b6y12	1540.78	64.274	9809	2	770.89	6.18
P64052 EFTS_SALTY Elongation factor Ts	19	Phosphoryl STY(2)	ITDVEVLK	104	8	3	40.87	y4y5y6	996.49	39.848	6818	2	498.75	-4.35
P64052 EFTS_SALTY Elongation factor Ts	20	Phosphoryl STY(7)	MAEITASLVK	0	10	5	26.91	b5°b5b9°b9y4	1142.55	25.890	3352	2	571.78	1.92
P64052 EFTS_SALTY Elongation factor Ts	21	Oxidation+M(12)	VETDFAAEVAAMSK	267	14	8	60.41	b5y4y5y6y8°y8y9°y9	1484.69	76.405	15330	2	742.85	0.74
P64052 EFTS_SALTY Elongation factor Ts	22	Oxidation+M(14)	FTGEVSLTGQPFVMEPSK	222	18	10	40.82	b3°b3b5y5y6°y6y11°y11*y11y13	1969.99	82.555	5399	3	657.33	14.69
P64052 EFTS_SALTY Elongation factor Ts	23	Oxidation+M(4)	QLAMHVAASKPEFVKPEDVSADVVEK	167	26	5	22.81	b6b7°b7b10y11	2840.45	60.460	3021	3	947.49	-0.77
P64052 EFTS_SALTY Elongation factor Ts	24		GVLVAAK	152	7	0	1.21		657.43	46.019	9647	1	657.43	-5.29
P64052 EFTS_SALTY Elongation factor Ts	25	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	1	8.25	b3	997.42	20.022	6207	2	499.21	-4.83
P00924 ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	17	141.26	b2b4b5°b5b6°b6y2y3y4y5y6y7y8y9y10*y10y12	1286.71	65.044	100928	2	643.86	-1.71

P00924 ENO1_YEAST Enolase 1	2		VNQIGTLSSESIK	346	12	12	96.83	b2b6b10y3y5y8°y8y9°y9y10y11y12	1288.71	53.135	95711	2	644.86	2.56
P00924 ENO1_YEAST Enolase 1	3		SIVPSGASTGVHEALEMR	32	18	14	108.54	b8y2y3y5y6°y6y9°y9y10y11y14y15y16°y16	1840.91	60.334	80132	3	614.31	-7.43
P00924 ENO1_YEAST Enolase 1	4		AADALLLK	338	8	7	62.54	b5y2y3y4y5y6y8	814.49	52.561	79381	2	407.75	-12.51
P00924 ENO1_YEAST Enolase 1	5		TFAEALR	178	7	6	63.9	b3y3y4y5y6y7	807.43	44.320	63681	2	404.22	-9.90
P00924 ENO1_YEAST Enolase 1	6		TAGIQIVADDLTVTNPK	312	17	6	36.15	b5y8y10y11y13y17	1755.96	71.476	44242	2	878.48	7.86
P00924 ENO1_YEAST Enolase 1	7		IEEELGDNAVFAGENFHHGDK	415	21	5	18.93	b3b5y13y19y21	2328.03	56.511	41744	4	582.76	-11.01
P00924 ENO1_YEAST Enolase 1	8		AVDDFLISLDGTANK	88	15	8	47.59	b11b13y1y5y6y8y12y15	1578.81	81.312	30517	2	789.91	4.72
P00924 ENO1_YEAST Enolase 1	9		WLTGPQLADLYHSLMK	272	16	6	17.16	b6°b6b12y1y2y15	1872.98	90.739	6973	2	936.99	7.89
P00924 ENO1_YEAST Enolase 1	10		IATAIEK	330	7	8	83.14	b4°b4b6y3y4°y4y5y6	745.43	27.367	33775	2	373.22	-15.72
P00924 ENO1_YEAST Enolase 1	11		LNQLLR	409	6	4	40.07	y3y4y5°y5	756.46	41.480	29504	2	378.74	-12.67
P00924 ENO1_YEAST Enolase 1	12		AAQDSFAAGWGVMSHR	358	17	5	22.93	b3b5y3°y3y6	1789.88	49.676	18187	2	895.45	21.89
P00924 ENO1_YEAST Enolase 1	13		YDLDFK	258	6	3	29.86	y3y5°y5	800.39	99.348	8905	1	800.39	10.52
P00924 ENO1_YEAST Enolase 1	14		HLADLSK	132	7	6	66.91	b4°b4b5y3y4y5	783.42	27.354	3891	2	392.21	-19.71
P00924 ENO1_YEAST Enolase 1	15		YPIVSIEDPFAEDDWEAWSHFFK	289	23	4	19.46	b8°b8b12b16	2828.34	124.074	2811	3	943.45	17.09
P00924 ENO1_YEAST Enolase 1	16		SIVPSGASTGVHEALEMRDGDK	32	22	3	13.44	b12b14y12	2256.06	71.681	78851	4	564.77	-15.04
P00924 ENO1_YEAST Enolase 1	17	Carbamidomethyl+C(7)	VKIGLDCASSEFFK	241	14	3	24.73	b10b11y11	1600.80	48.307	5295	3	534.27	-1.14
P00924 ENO1_YEAST Enolase 1	18		VYARSVYDSR	5	10	5	54.32	b8b9y3y4y9	1215.61	48.314	4599	2	608.31	-4.72
P00924 ENO1_YEAST Enolase 1	19	Phosphoryl STY(12)	AVDDFLISLDGTANK	88	15	3	24.16	b10b11y11	1658.76	70.901	3762	3	553.59	2.65
P00924 ENO1_YEAST Enolase 1	20	Phosphoryl STY(8)	SIVPSGASTGVHEALEMR	32	18	4	22.98	b6_H3PO4 b6°b6b7y3	1920.85	103.737	1966	3	640.96	-13.73
P00924 ENO1_YEAST Enolase 1	21	Oxidation+M(15)	WLTGPQLADLYHSLMK	272	16	4	17.16	b4b13°b13y9	1888.99	84.781	39902	2	945.00	12.34
P00924 ENO1_YEAST Enolase 1	22	Oxidation+M(17)	SIVPSGASTGVHEALEMR	32	18	3	15.58	b7y3y11	1856.91	52.740	17699	3	619.64	-5.26
P00924 ENO1_YEAST Enolase 1	23		PSGASTGVHEALEMR	35	15	2	7.34	b8°b8	1541.74	60.343	5307	2	771.38	4.67
P00924 ENO1_YEAST Enolase 1	24		ADALLLK	339	7	0	1.21		743.47	52.551	5237	1	743.47	-0.66
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		VFMQPASEGTGIIAGGAMR	93	19	20	191.16	b2b3b4b6b7b10b12b13y4y5y6y7y10y11y12y13y15y16°y16y19	1892.95	67.037	139997	2	946.98	8.83
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		AVLEVAGVHNVLAK	112	14	14	114.84	b2b3b4b13y1y2y3y6y8y9y10y11y12y14	1419.81	59.344	119653	3	473.94	-14.70
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		AYGSTNPINVVR	126	12	13	93.82	b1b2b5b11y2y3y4°y4y6y7y8y10y12	1290.68	49.880	85443	2	645.84	0.19
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVA AK	138	18	16	105.95	b6°b6b11b15°b15y3y4y7°y7y10y11y12°y12y14y15y18	1890.91	62.122	71137	2	945.96	6.91
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		SVEEILGK	159	8	8	64.3	b1b6b7y1y3y4y6y8	874.47	48.987	54668	2	437.74	-15.01
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		ATIDGLENMNSPEMVA AKR	138	19	9	62.44	b4b7b10y3y4y8y11°y11y12	2046.99	57.848	39339	3	683.00	-4.41
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		IFSFTALTTVGDGNR	29	16	3	34.57	y7y8y9	1653.84	85.750	31953	2	827.42	-10.41
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		VGFGYGK	45	7	5	40.47	b2b6y2y3y5	727.37	38.402	15973	2	364.19	-10.57
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		LIAVNR	14	6	2	26.85	y4y5	685.43	31.764	12147	1	685.43	-4.01
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		AHIEK	1	5	4	39.66	b3b4y4°y4	597.33	21.941	11903	1	597.33	-11.04
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		GKSVEEILGK	157	10	3	36.91	y3y4y5	1059.60	49.861	45656	2	530.30	-2.53
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12		VFMQPASEGTGIIAGGAMRAVLE VAGVHNVLAK	93	33	5	16.83	b10°b10b13b15°b15	3293.74	111.728	7320	3	1098.58	-3.78
P0A7W4 RS5_SALTY 30S ribosomal protein S5	13		AYGSTNPINVVVRATIDGLENMNSPEMVA AK	126	30	3	22.73	b3b4b12	3162.55	77.277	3879	3	1054.85	-2.78

P0A7W4 RS5_SALTY 30S ribosomal protein S5	14		GVHTGSRVFMQPASEGTHIAGGAMR	86	26	3	12.14	b12b15y6	2587.27	136.509	3629	3	863.10	-4.81
P0A7W4 RS5_SALTY 30S ribosomal protein S5	15		GGRIFSFTALTVVGDGNR	26	19	4	22.72	b3y7y8*y8	1924.00	121.789	2006	2	962.50	-1.33
P0A7W4 RS5_SALTY 30S ribosomal protein S5	16	Oxidation+M(3)	VFMQPASEGTHIAGGAMR	93	19	3	14.94	b5b16y5	1908.94	59.018	3075	2	954.97	3.39
P0A7W4 RS5_SALTY 30S ribosomal protein S5	17		VEEILGK	160	7	2	9.66	b3*b3	787.46	49.054	2141	2	394.23	6.74
P0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	11	61.09	b2b3*b3b4*b4y2y4y8y9y10y13	1447.78	64.006	97618	2	724.39	-0.59
P0A297 RL10_SALTY 50S ribosomal protein L10	2		AAAFEGELIPASQIDR	109	16	17	124.52	b1b3b5b7b8b9b12y1y2y5y7y8*y8y9y11y12y16	1687.88	67.663	68252	2	844.44	8.46
P0A297 RL10_SALTY 50S ribosomal protein L10	3	Carbamidomethyl+C(9)	VVEGTQFECLKDTFVGPTLIAYSM EHPGAAAR	62	32	5	15.86	b3y6y8y13y32	3494.69	91.448	54398	4	874.43	-4.19
P0A297 RL10_SALTY 50S ribosomal protein L10	4		GALSAVVADSR	20	11	8	70.96	b4y2y3y4y5y7y8y11	1045.56	47.002	44526	2	523.29	0.23
P0A297 RL10_SALTY 50S ribosomal protein L10	5		QAIAEVSEVAK	8	12	9	40.27	b2b9*b9b12y8y9*y9y10y12	1243.69	56.081	22052	2	622.35	-0.59
P0A297 RL10_SALTY 50S ribosomal protein L10	6		DTFVGPTLIAYSM EHPGAAAR	73	21	8	37.58	b2b3*b3b8b12y5y6y9	2204.08	81.687	11363	3	735.36	-0.44
P0A297 RL10_SALTY 50S ribosomal protein L10	7		EAGVYMR	46	7	4	40.47	b4y3y6y7	825.39	30.660	3777	2	413.20	-2.96
P0A297 RL10_SALTY 50S ribosomal protein L10	8	Carbamidomethyl+C(9)	VVEGTQFECLK	62	11	4	36.07	b4b6b8y11	1309.63	48.900	3679	2	655.32	-10.53
P0A297 RL10_SALTY 50S ribosomal protein L10	9		GVTVDK	31	6	2	29.86	b3b5	618.35	70.458	4771	1	618.35	12.44
P0A297 RL10_SALTY 50S ribosomal protein L10	10		LMATMK	138	6	1	13.62	b4	694.37	44.059	4133	1	694.37	4.31
P0A297 RL10_SALTY 50S ribosomal protein L10	11	Carbamidomethyl+C(10)	RVVEGTQFECLK	61	12	5	22.28	b8*b8b10y9*y9	1465.73	63.382	2156	2	733.37	-11.91
P0A297 RL10_SALTY 50S ribosomal protein L10	12		DTFVGPTLIAYSM EHPGAAARL FK	73	24	3	12.71	b3b13y14	2592.36	96.561	1519	3	864.79	13.09
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	1		SDVQAAKDDAAR	52	12	9	100.14	b9y3y4y5y6y7y8y9y12	1246.60	16.973	26308	2	623.80	-3.23
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	2		VDQLSNDVNAMR	40	12	5	29.48	y2y5y7y8y12	1361.65	47.569	25607	2	681.33	3.77
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	3		IDQLSSDVQTLNAK	26	14	5	27.58	b5*b5b9y11y13	1531.80	87.221	1520	3	511.27	4.78
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	4	Phosphoryl STY()	IDQLSSDVQTLNAK	26	14	4	19.29	b4*b4y8y12	1611.76	62.837	1824	2	806.39	6.29
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	5		QAAKDDAAR	55	9	0	2.83		945.48	16.904	2871	2	473.24	4.07
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	6		VQAAKDDAAR	54	10	0	2.83		1044.53	16.910	2552	2	522.77	-9.47
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	1		DATGNTPFMLIAR	103	13	8	54.77	b2b3b5b6y4y7y10y13	1406.71	77.456	47436	2	703.86	0.00
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	2		DGTIHQFSAVEQDDQR	154	16	9	35.44	b3b9*b9y2*y2y4y5y8y16	1845.82	43.099	40579	3	615.94	-9.52
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	3		TLWFYNPFVEQATATWLK	85	18	17	125.11	b2b3b4b5*b5b9b10*b10y3y4y5y10y12*y12y13y14y18	2215.14	115.353	36374	2	1108.07	7.94
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	4		NQASDWQQYNIK	116	12	6	36.17	b1b3b11y9y10*y10	1494.70	50.967	6286	2	747.86	4.90

Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	5		FTFTPPQGVTTIDQRK	187	16	4	17.16	b4y7y10y16	1849.96	60.439	4380	2	925.48	7.85
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	6		NQASDWQQYNIKQDGDNFVLTPK	116	23	6	35.31	b3b4b12y10y14y20	2709.31	66.860	39267	3	903.77	6.85
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	7		SQQNGAVDPSKFTFTPPQGVTTIDQQR	176	26	9	52.84	b5*b5b13y5y6y7y10y12y14	2833.41	68.137	3779	3	945.14	13.10
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	8	Phosphoryl STY(11)	QFTINVGRDGTIHQFSAVEQDDQR	146	24	3	12.71	b10y8y12	2841.30	101.703	2759	3	947.77	6.19
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	9		VEQDDQR	163	7	1	7.25	b4	889.41	43.055	1987	2	445.21	4.60
P66738 RRF_SALTY Ribosome-recycling factor	1		ASPSLLDGIVVEYYGTPTPLR	31	21	7	40.78	b15y5y7y12y14y15y21	2248.20	92.605	36960	2	1124.60	6.41
P66738 RRF_SALTY Ribosome-recycling factor	2		QLASVTVEDSR	52	11	12	87.19	b3*b3y2y3y4y5y6y8*y8y9y11*y11	1204.63	38.785	30724	2	602.82	10.44
P66738 RRF_SALTY Ribosome-recycling factor	3		AIMASDLGLNPSSAGTDIR	80	19	6	36.29	b9y2y7y8y9y19	1888.96	66.424	13876	2	944.99	11.05
P66738 RRF_SALTY Ribosome-recycling factor	4		VDAALADKEAELMQF	170	15	3	18.14	b7b12y10	1650.81	84.202	5411	3	550.94	4.14
P66738 RRF_SALTY Ribosome-recycling factor	5		VDAALADK	170	8	3	36.1	b4b6y6	802.44	35.611	5055	2	401.72	11.26
P66738 RRF_SALTY Ribosome-recycling factor	6		AIMASDLGLNPSSAGTDIRVPLPLTEER	80	29	9	39.92	b4b7b11b15*b15y4y12y22y26	3020.58	85.626	52624	3	1007.53	3.31
P66738 RRF_SALTY Ribosome-recycling factor	7		IVRGAEAQAR	115	10	8	70.55	b3b6b7b8y4*y4y7*y7	1128.61	15.605	18933	2	564.81	-5.84
P66738 RRF_SALTY Ribosome-recycling factor	8		DAEVRMEK	7	8	4	51.08	b3b5y3y4	977.46	21.960	7488	2	489.24	-9.18
P66738 RRF_SALTY Ribosome-recycling factor	9		SMGPAVEKAIMASDLGLNPSSAGTDIR	72	27	4	22.55	b9y6y10y11	2688.37	66.281	5102	4	672.85	13.35
P66738 RRF_SALTY Ribosome-recycling factor	10	Phosphoryl STY(7)	VPLPLTEER	99	10	4	26.91	b8*b8y3y5_H3PO4 y5	1230.60	26.573	4567	2	615.80	-4.66
O33921 AGP_SALTY Glucose-1-phohatase	1		TPIGGQLVFQR	335	11	6	36.73	b2b6y3y8y9y11	1215.68	60.304	115557	2	608.34	-3.21
O33921 AGP_SALTY Glucose-1-phohatase	2		MGTMDPFTFNPVITDDSAAFR	141	20	19	130.81	b2b3b5b12y2y3y5y6y7y8*y8y9*y9y11y12*y12y13y15y20	2186.01	77.534	84532	2	1093.51	10.16
O33921 AGP_SALTY Glucose-1-phohatase	3		IEYVYQSAR	358	9	7	74.92	b2b3y3y5y6y7y8	1128.56	41.349	54082	2	564.79	-4.65
O33921 AGP_SALTY Glucose-1-phohatase	4		QQAVQAMEK	161	9	9	45.47	b2b3*b3b9y3y4*y4y7y9	1032.50	25.315	50624	2	516.76	-9.46
O33921 AGP_SALTY Glucose-1-phohatase	5	Carbamidomethyl+C(14)	EWLV AQGLIPSGECPAPDTVYAYANSLQR	87	29	26	131.44	b3*b3b8*b8b9*b9b12b14*b14b16y12y3y4y5*y5y6y7*y7y9y10*y10y12y13y15y29	3205.58	93.083	50051	3	1069.20	5.41
O33921 AGP_SALTY Glucose-1-phohatase	6		DTFSANYQQEPGVQGPLK	208	18	6	24.82	b2b10y8y10y12y18	1978.97	55.375	41498	2	989.99	11.29
O33921 AGP_SALTY Glucose-1-phohatase	7		VGNSLVDAFTLQYYEGFPMQVAVGGIHTDR	226	31	11	41.64	b1b8b13y1y3y4y6*y6y7y14*y14	3486.67	103.748	34814	3	1162.89	7.28
O33921 AGP_SALTY Glucose-1-phohatase	8		APLANNGSVLAQSTPNAWPAWDVPGGQLTTK	43	31	18	81.62	b2b4b6b8b9b11b14*b14b17b18y2y3y8y10y13y14*y14y31	3161.63	82.745	32950	3	1054.55	8.65
O33921 AGP_SALTY Glucose-1-phohatase	9		NGYQDSLFTSPTVAR	266	15	6	25.8	b3b13y1y5y11y15	1655.81	61.860	30083	2	828.41	5.82
O33921 AGP_SALTY Glucose-1-phohatase	10		NVAAPLVK	281	8	4	40.87	y3y4y6y8	811.50	38.992	27095	2	406.25	-9.70

O33921 AGP_SALTY Glucose-1-phohatase	11	Carbamidomethyl+C(14)	LLEQITHYQDSPSCK	182	15	7	41.48	y5°y5y8y10*y10y13y15	1818.86	50.390	26747	3	606.96	-4.70
O33921 AGP_SALTY Glucose-1-phohatase	12		GGVLEVYMGHYTR	74	13	3	25.41	b9y6y7	1481.70	63.233	23972	3	494.57	-10.87
O33921 AGP_SALTY Glucose-1-phohatase	13	Carbamidomethyl+C(16)	TVATAQFFITGAFPGCDIPVHHQE K	116	25	8	31.98	b12b14°b14y5y9y12y13*y 13	2771.41	99.982	10238	3	924.47	17.35
O33921 AGP_SALTY Glucose-1-phohatase	14	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	GCPVDANGFCPLDKFDNMNTA AK	389	24	9	63.72	b4b14y4y10y13y14y19y20 y22	2641.19	77.552	96304	3	881.07	1.94
O33921 AGP_SALTY Glucose-1-phohatase	15		LKNGYQDSLFTSPTVAR	264	17	6	42.76	b7b12y5y8y11y12	1896.96	57.618	40706	3	632.99	-8.94
O33921 AGP_SALTY Glucose-1-phohatase	16		VGNSLVDAFTLQYYEGFPMDDQVA WGGIHTDRQWK	226	34	12	36.88	b4*b4b5b8°b8b12°b12y7°y 7y8y10°y10	3928.88	83.476	15261	3	1310.30	2.36
O33921 AGP_SALTY Glucose-1-phohatase	17	Carbamidomethyl+C(24)	SQLHLDESYKLEQITHYQDSPSC K	172	25	4	18.84	b4b6b9y3	3019.45	84.047	3784	4	755.62	0.65
O33921 AGP_SALTY Glucose-1-phohatase	18		ARSQLHLDESYK	170	12	3	22.28	b5y7y9	1446.73	35.321	2497	3	482.91	-4.22
O33921 AGP_SALTY Glucose-1-phohatase	19	Oxidation+M(19)	VGNSLVDAFTLQYYEGFPMDDQVA WGGIHTDR	226	31	4	11.25	b14y5y8°y8	3502.65	83.443	12335	4	876.42	2.65
P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	17	83.77	b1b2*b2b3b4*b4b6y1y2y5 y6°y6y7°y7*y7y8y10	1129.62	37.838	70052	2	565.31	-3.24
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	14	92.08	b1b2b3y3y4y5°y5y6y7°y7y 8°y8y12y14	1452.66	56.177	59650	2	726.83	8.32
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3		SFTFVTK	65	7	5	37.46	b5y2y5y6y7	829.45	52.513	38485	2	415.23	0.59
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4	Carbamidomethyl+C(29)	LQVAAGMANPSPVGPALGQQG VNIMEFCK	10	30	3	11.38	b4b8y7	3081.56	110.285	9006	4	771.14	8.32
P0A7K0 RL11_SALTY 50S ribosomal protein L11	5		TDSIEK	45	6	2	26.85	b4b5	692.34	96.015	2740	1	692.34	-5.99
P0A7K0 RL11_SALTY 50S ribosomal protein L11	6		AQLQEIAQTKAADMTGADIEAMT R	103	24	3	22	b15y5y6	2563.28	85.156	2698	4	641.58	12.86
P0A7K0 RL11_SALTY 50S ribosomal protein L11	7	Carbamidomethyl+C(29) ;Oxidation+M(7)	LQVAAGMANPSPVGPALGQQG VNIMEFCK	10	30	9	25.58	b7*b7b11°b11*b11b13b14 *b14y10	3097.51	136.388	2787	2	1549.26	-5.04
P0A1V4 KAD_SALTY Adenylate kinase	1		LVEYHQMTAPLIGYYQK	167	17	22	111.7	b7°b7b11°b11*b11b16y1y 2*y2y5y6*y6y7y8y10y11°y 11y12°y12*y12y15y17	2054.04	68.165	57438	3	685.35	-2.73
P0A1V4 KAD_SALTY Adenylate kinase	2		VDGTQAVADVR	195	11	8	27.32	b1b3°b3b4°b4y2y4y11	1130.58	35.488	40761	2	565.79	0.86
P0A1V4 KAD_SALTY Adenylate kinase	3		YGIPQISTGDMLR	23	13	10	84.98	b2b6y3y4y7°y7y8y10y12y1 3	1450.74	71.718	38591	2	725.87	1.68
P0A1V4 KAD_SALTY Adenylate kinase	4		IILLGAPGAGK	2	11	11	100.41	b2b3y2y3y4y5y6y7y8y9y1 1	1009.63	59.989	32550	2	505.32	-7.98
P0A1V4 KAD_SALTY Adenylate kinase	5		NGFLLDGFPR	78	10	3	26.91	b3y4y6	1135.58	79.727	25324	2	568.30	-5.48
P0A1V4 KAD_SALTY Adenylate kinase	6		EAGIVVDYVLEFDVPDELIVDR	97	22	5	20.87	b4°b4b8b12y7	2505.22	110.737	4039	3	835.74	-22.22
P0A1V4 KAD_SALTY Adenylate kinase	7		IILLGAPGAGKGTQAQFIMEK	2	21	7	53.33	b3y5y9y11y12y15y17	2143.18	71.710	12439	3	715.06	-8.66
P0A1V4 KAD_SALTY Adenylate kinase	8		GTQAQFIMEKYGIPQISTGDMLR	13	23	4	20.12	b15y6y8y22	2584.26	74.585	8202	3	862.09	-10.30
P0A1V4 KAD_SALTY Adenylate kinase	9		YAKVDGTQAVADVR	192	14	4	19.29	b5b13y10°y10	1492.76	70.452	7541	2	746.88	-10.96
P0A1V4 KAD_SALTY Adenylate kinase	10		VEGKDDVTGEDLTTR	141	15	5	31.82	b7b12y10y11°y11	1634.81	70.474	4934	3	545.61	11.20
P0A1V4 KAD_SALTY Adenylate kinase	11	Oxidation+M(7)	LVEYHQMTAPLIGYYQKEAEAGN TK	167	25	4	12.41	b3b22y12*y12	2870.44	90.139	3638	3	957.49	14.46

Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	14	70.76	b2*b2b3*b3b4*b4*b4y2y3y4y12y13y14y16	1686.95	89.120	69909	2	843.98	5.64
Q7CR87 SURA_SALTY Chaperone surA	2		ITVLPQEV DALAK	149	13	14	62.73	b2*b2b3*b3y1y2y5y8*y8y9*y9*y9y10y11	1396.81	69.614	40117	2	698.91	0.35
Q7CR87 SURA_SALTY Chaperone surA	3		LIMDQIILQM GQK	73	13	7	74.77	y3y4y5y6y7y11y13	1530.84	87.272	36751	2	765.93	3.35
Q7CR87 SURA_SALTY Chaperone surA	4		LNAGQAGQQLPDDATLR	50	17	15	113.63	b2b3b4*b4y1y2y4y5y6y7y8y9y11y12y17	1767.91	49.709	31908	2	884.46	5.11
Q7CR87 SURA_SALTY Chaperone surA	5		GQSQSI SVTE VHAR	274	14	5	31.54	b3y6y8y10y14	1498.75	35.823	25397	3	500.25	-10.02
Q7CR87 SURA_SALTY Chaperone surA	6		VAAVVNNGVVLES DVDGLMQSVK	27	23	9	33.91	b1b3b4b14b17y8y11*y11y23	2343.24	90.204	24517	2	1172.13	9.06
Q7CR87 SURA_SALTY Chaperone surA	7		EYSQDPGSANQG GDLGWATPDIFDPAFR	326	28	6	22.73	b2*b2y4y11y12y28	3011.38	92.869	11411	3	1004.46	11.35
Q7CR87 SURA_SALTY Chaperone surA	8		LEEIAADIK	306	9	4	30.49	b5b7y4y9	1001.54	39.714	6038	2	501.28	-8.23
Q7CR87 SURA_SALTY Chaperone surA	9		ITDEQLDQA IANIAK	90	15	4	25.8	b4b13y5y13	1642.87	79.384	46056	2	821.94	5.57
Q7CR87 SURA_SALTY Chaperone surA	10		QAESIVEEAR	197	10	4	40.13	b8y4y5y8	1131.59	37.016	44332	2	566.30	19.42
Q7CR87 SURA_SALTY Chaperone surA	11		LAYDGLNYSTYR	117	12	4	29.48	y4*y4y7y8	1435.70	57.260	38011	2	718.35	8.76
Q7CR87 SURA_SALTY Chaperone surA	12		QIGTQNDASTE LNL SHILIALPENPTSEQVNDAQR	162	35	4	16.63	y3y5y9*y9	3816.94	87.903	28091	3	1272.99	10.62
Q7CR87 SURA_SALTY Chaperone surA	13		GQISAPVHSSFG WHLIELLDTR	362	22	4	22.19	b13*b13b14y3	2463.24	115.806	2299	4	616.57	-13.97
Q7CR87 SURA_SALTY Chaperone surA	14		LAITYSADQ QALKGGQMGWGR	214	21	3	13.88	b3y8y16	2251.12	64.087	24846	3	751.05	-2.93
Q7CR87 SURA_SALTY Chaperone surA	15		AYRMLMNR	396	8	3	33.09	b6y3y4	1054.52	49.063	18927	2	527.77	-5.09
Q7CR87 SURA_SALTY Chaperone surA	16		KFSEE AATWMQEQR	404	14	3	19.29	b6b9y10	1740.82	55.527	7646	2	870.91	11.92
Q7CR87 SURA_SALTY Chaperone surA	17		VNDLRGQSQSI SVTE VHAR	269	19	3	14.94	b4b12y3	2096.07	42.958	4866	4	524.77	-7.22
Q7CR87 SURA_SALTY Chaperone surA	18		FSEE AATWMQEQRASAYVK	405	19	3	14.94	b5y4y13	2232.06	103.839	1937	3	744.69	11.59
Q7CR87 SURA_SALTY Chaperone surA	19		LNAGQAGQQLPDDATL	50	16	1	7.28	y12	1611.78	49.758	4183	2	806.40	-8.03
Q7CR87 SURA_SALTY Chaperone surA	20		GQSQSI SVTE VHAR	274	14	0	3.64		1481.74	35.805	2629	3	494.59	7.00
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	12	111.81	b2b3b4b5y2y3y6y7y8y9y10y12	1150.68	52.195	108813	2	575.84	-4.99
P66313 RL6_SALTY 50S ribosomal protein L6	2		ALLNSM VIGVTEGFTK	69	16	10	82.01	b2b14y4y6y7y8y9y12y13y16	1679.91	93.566	52744	2	840.46	0.80
P66313 RL6_SALTY 50S ribosomal protein L6	3		RPEPYK	152	6	2	26.85	y4y5	789.42	50.466	9343	2	395.21	-9.97
P66313 RL6_SALTY 50S ribosomal protein L6	4		TLNDAVEVKHADNALT FGPR	35	20	3	14.37	b3b6y3	2168.11	62.642	2230	3	723.38	1.35
P66313 RL6_SALTY 50S ribosomal protein L6	5		GVRYADEVVR	160	10	3	26.91	b6b9y5	1163.62	69.804	2088	2	582.31	1.47
P66313 RL6_SALTY 50S ribosomal protein L6	6	Phosphoryl STY(5)	ALLNSM VIGVTEGFTKK	69	17	6	27.4	b4b12_H3PO4b12*b12b13*b13y13	1887.96	98.189	14548	2	944.49	4.14
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTDS DAVGNAVK	84	17	12	83.13	b2b3b4b5y2y9y11y12*y12y13y14y17	1739.96	69.808	92488	2	870.49	5.75
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	2		IPVITLDR	107	8	6	54.09	y1y3y4y5y6y8	926.56	60.765	69770	2	463.78	-10.87
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	3		LAATIAQLPDQIGAK	253	15	10	69.26	b2b3b4*b4y3y4y7y8y10y15	1509.87	65.321	63254	2	755.44	2.34

[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	4		ELANVQDLTVR	70	11	5	36.73	b7y5y6y8y11	1257.67	56.553	40784	2	629.34	-4.37
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	5		ADVMVVGFDGTPDGEK	231	16	7	51.52	b4b5y5y7y10y11°y11	1636.77	62.534	29318	2	818.89	12.98
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	6		VIELQGIAGTSAAR	150	14	14	92.08	b2b3y4y6y7°y7y9y10y11*y11y12°y12*y12y14	1385.78	57.875	26227	2	693.39	3.35
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	7		FNVLASQPADFDR	178	13	7	62.73	b3y3y6y8y9y10y13	1479.73	65.303	26081	2	740.37	3.71
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	8		GLNVMQNLLTAHPDVQAVFAQN DEMALGALR	193	31	13	32.74	b4*b4b6*b6b14*b14y1y4y12°y12y13y15y31	3336.70	102.038	21754	3	1112.90	3.95
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	9		IAGDYIAK	135	8	6	33.09	b7y1y2y6y7y8	850.46	34.637	16393	2	425.73	-8.11
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	10		YPVDLK	285	6	1	13.62	b4	734.40	41.212	14554	2	367.70	-14.29
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	11		LVIK	291	4	1	12.82	y3	472.35	55.185	10370	1	472.35	-3.68
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	12		EADKLGYNLVVLDSQNNPAK	50	20	5	19.76	b5b10y5y9°y9	2188.12	65.128	24910	3	730.04	-2.79
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	13		FNVLASQPADFDRTK	178	15	3	26.22	y7y10y11	1708.85	59.031	10798	3	570.29	-9.50
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	14	Oxidation+M(5)	GLNVMQNLLTAHPDVQAVFAQN DEMALGALR	193	31	5	22.04	b14*b14b15y11*y11	3352.67	83.448	2426	3	1118.23	-3.42
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	15		GLNVMQNLLTAHPDVQAVFAQN DEMALGA	193	29	1	9.58	y12	3067.52	102.098	1658	3	1023.18	8.04
[O54297]RS4_SALTY 30S ribosomal protein S4	1		VVNIASYQVSPNDVVSIR	128	18	17	122.68	b3b8b10b15b17y1y3y4y8*y9y10y11*y11y13°y13y14y18	1960.07	71.207	61346	2	980.54	10.84
[O54297]RS4_SALTY 30S ribosomal protein S4	2		GNTGENLLALLEGR	83	14	5	27.86	b3*b3b5b9°b9	1456.78	85.225	5291	2	728.89	4.52
[O54297]RS4_SALTY 30S ribosomal protein S4	3		AALELAEQR	156	9	5	45.47	b3y3y4°y4y7	1000.53	42.087	6061	1	1000.53	-8.17
[O54297]RS4_SALTY 30S ribosomal protein S4	4		IEQAPGQHGAR	33	11	10	94.39	b4b6*b6b7y4y5y6y7*y7y8	1163.57	15.482	2941	3	388.53	-15.21
[O54297]RS4_SALTY 30S ribosomal protein S4	5		SDLSADINEHLIVELYSK	188	18	6	32.75	b6b10b11y3°y3y13	2046.04	83.519	1536	3	682.68	-1.01
[O54297]RS4_SALTY 30S ribosomal protein S4	6	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	3	28.12	b8b10b11	1451.73	69.869	1817	2	726.37	10.93
[P77983]KPYK1_SALTY Pyruvate kinase I	1		GDLGVEIPVEEVIFAQK	244	17	10	83.01	b3b5b6b7b12y4y10y11y12y17	1842.99	94.049	34606	2	922.00	2.25
[P77983]KPYK1_SALTY Pyruvate kinase I	2		MLDAGMNVMR	22	10	8	51.89	b2y2y4y7y8°y8y9y10	1137.52	56.140	20073	2	569.27	3.11
[P77983]KPYK1_SALTY Pyruvate kinase I	3	Carbamidomethyl+C(13)	YPLEAVSIMATICER	319	15	5	29.44	b6°b6b10b12y12	1752.87	81.813	13341	2	876.94	4.25
[P77983]KPYK1_SALTY Pyruvate kinase I	4		IENQEGLNNFDEILEASDGIMVAR	220	24	10	28.74	b6*b6y1y2y3y4y6y9°y9y24	2677.29	95.610	13054	3	893.10	5.56
[P77983]KPYK1_SALTY Pyruvate kinase I	5		AEAGDVANAILDGTDAVMLSGES AK	292	25	7	37.69	b3b10b11y3y11y12y25	2405.18	91.330	10375	2	1203.09	11.47
[P77983]KPYK1_SALTY Pyruvate kinase I	6	Carbamidomethyl+C(6)	ITEAVCR	353	7	3	40.47	y3y5y6	848.42	24.074	9383	2	424.71	-8.49
[P77983]KPYK1_SALTY Pyruvate kinase I	7		AGQTFTFITDK	86	11	6	47.74	b4b5*b5b7y5y9	1216.58	58.370	6513	3	406.20	-5.72
[P77983]KPYK1_SALTY Pyruvate kinase I	8		VVITATQMLDSMIK	272	14	3	34.85	b10b11b12	1549.83	100.894	4830	2	775.42	-0.32
[P77983]KPYK1_SALTY Pyruvate kinase I	9	Carbamidomethyl+C(3)	IVCTIGPK	5	8	4	33.09	b5°b5y5y6	887.49	34.941	18942	2	444.25	-11.07
[P77983]KPYK1_SALTY Pyruvate kinase I	10		LNFSHGDYAEHGQR	32	14	4	31.54	b3b9b12y5	1630.76	79.580	7190	3	544.26	15.64

P77983 KPYK1_SALTY Pyruvate kinase I	11		MMIEK	261	5	1	13.22	y3	651.32	51.090	2918	1	651.32	-2.25
P77983 KPYK1_SALTY Pyruvate kinase I	12	Carbamidomethyl+C(13)	YPLEAVSIMATICERTDR	319	18	3	22.98	b5b6y14	2125.02	68.631	21534	3	709.01	-8.04
P77983 KPYK1_SALTY Pyruvate kinase I	13	Carbamidomethyl+C(15)	GKYPLEAVSIMATICER	317	17	7	32.76	b4b6°b6b16y3y7°y7	1937.98	110.929	3559	2	969.49	-3.28
P77983 KPYK1_SALTY Pyruvate kinase I	14		TDRVMNSR	334	8	5	33.09	b5b6°b6y5*y5	978.49	136.384	3248	1	978.49	10.11
P77983 KPYK1_SALTY Pyruvate kinase I	15	Carbamidomethyl+C(3)	IVCTIGPKTESEEMLSK	5	17	3	16.32	b4b11y13	1921.96	95.248	2453	3	641.33	1.33
P77983 KPYK1_SALTY Pyruvate kinase I	16	Carbamidomethyl+C(6)	MMIEKCIR	261	8	5	67.31	b3b5y3y5y6	1080.54	37.875	1705	2	540.77	3.50
P77983 KPYK1_SALTY Pyruvate kinase I	17	Oxidation+M(6)	GDVVVMVSGALVPSGTTNTASV HVL	445	25	4	12.41	b9b11y12°y12	2426.23	103.973	3546	3	809.42	-11.07
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	1		ALMIHVGGDNMSDQPKPLGGGG MR	142	24	13	91.22	b6b9b10b11y1y3y4y5y8y1 0y20y22y24	2438.14	58.484	66874	4	610.29	-12.42
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	2		SLDEVKDK	134	8	6	49.32	b2b4b6b7y6y8	933.48	20.484	11367	2	467.24	-8.96
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	3		VEMNLVTAQGVGQSIGTVVIDET EGGLK	23	28	3	11.71	b5y6y9	2844.47	98.822	5939	3	948.83	2.66
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	4	Carbamidomethyl+C(3)	YACGVIK	166	7	3	40.47	y4y5y6	810.41	33.501	69172	2	405.71	-11.07
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	5	Carbamidomethyl+C(17)	ALPPGEHGFHIIHANGSCQPAIK	57	22	3	19.95	b7b10b15	2338.13	81.977	14429	3	780.05	-9.29
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	6		AVAAEAAGGHLDPQNTGK	82	18	9	52.78	y6y7°y7*y7y8°y8y9*y9y11	1706.83	33.550	4891	3	569.62	-8.73
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	7	Carbamidomethyl+C(11)	LSLAMVTLLACAGAQAASEK	3	20	3	14.37	b5b7y9	2005.02	117.061	2406	2	1003.01	-14.06
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	8		SLDEVK	134	6	3	26.85	b3°b3y4	690.36	44.523	2263	1	690.36	-8.40
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	9		AVAAEAAGGHLDPQNTGKHGEP GQGHLDLPVLVNNNDGIASEPV TAPR	82	50	34	276.71	b3b4b5°b5b6b7b10b11°b1 1b12b13b15b30b31b33b34 b35b36b40y4y5y6y7y8y9y 11y12°y12y13y14°y14*y14 y15y24	4962.47	68.169	47146	5	993.30	-1.48
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	10	Oxidation+M(23)	ALMIHVGGDNMSDQPKPLGGGG MR	142	24	3	12.71	b5b10y3	2454.16	54.996	21810	4	614.30	-2.19
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	11	Carbamidomethyl+C(11) ;Oxidation+M(5)	LSLAMVTLLACAGAQAASEK	3	20	4	14.37	b11b14y13*y13	2021.02	80.694	14346	2	1011.02	-8.27
O68901 SODC_SALTY Superoxide dismutase [Cu-Zn] 2	12	Oxidation+M(3)	VEMNLVTAQGVGQSIGTVVIDET EGGLK	23	28	8	40.37	b6°b6b7°b7b8b11b24y10	2860.43	80.754	6744	3	954.15	-11.44
P66932 TIG_SALTY Trigger factor	1		NVALEEQAWEAVLAK	399	15	16	137.92	b2b3b4b5b11b12b13y1y2y 3y5y10y11y12y13y15	1583.87	79.143	69229	2	792.44	2.62
P66932 TIG_SALTY Trigger factor	2		ELPELTEEFIKR	243	12	12	77.59	b7°b7b8°b8b10b11y1y2y3y 7y10°y10	1503.81	70.407	39114	2	752.41	4.06
P66932 TIG_SALTY Trigger factor	3		ANDIDVPSALIDSEIDVLR	296	20	8	36.14	b2°b2b3b4°b4y4y14y16	2211.16	89.740	36154	3	737.72	-1.99
P66932 TIG_SALTY Trigger factor	4		FGVEDGSVAGLR	255	12	7	44.92	b2y1y7y8y9y11y12	1206.61	56.091	30031	2	603.81	1.11
P66932 TIG_SALTY Trigger factor	5		INPAGAPNYVPGEYK	83	15	4	26.22	b2y3y5y9	1589.80	49.779	26785	2	795.41	5.30
P66932 TIG_SALTY Trigger factor	6		ANDIDVPSALIDSEIDVLR	296	19	13	59.29	b2°b2b3b6b10°b10b14y1y 3y8y13y14y19	2055.07	93.887	19382	2	1028.04	6.18
P66932 TIG_SALTY Trigger factor	7		ELFEEQAK	334	8	4	36.1	b4°b4b7y5	993.51	40.801	31215	2	497.26	19.97

P66932 TIG_SALTY Trigger factor	8		VTITIAADSIETAVK	14	15	3	18.14	b9b11y9	1531.82	75.287	3549	2	766.42	-21.68
P66932 TIG_SALTY Trigger factor	9		MQVSVETTQGLGR	0	13	3	20.64	b4b8y9	1405.70	49.655	3084	2	703.35	-6.86
P66932 TIG_SALTY Trigger factor	10		QQATWK	146	6	1	13.62	b5	761.40	62.806	2142	1	761.40	4.17
P66932 TIG_SALTY Trigger factor	11		ATDFVLAMGQGR	181	12	3	29.48	b8b9b11	1265.63	68.136	1501	2	633.32	-4.24
P66932 TIG_SALTY Trigger factor	12		QAAQRFGGNEK	316	11	5	47.74	b3b4b8y6y8	1205.59	47.188	85963	2	603.30	-11.75
P66932 TIG_SALTY Trigger factor	13		EKINPAGAPNYVPGEYK	81	17	3	16.32	b14y9y14	1846.94	75.106	31313	3	616.32	2.12
P66932 TIG_SALTY Trigger factor	14		VTIDFTGSVDGEFEFGGKATDFVL AMGQGR	163	30	4	11.38	b8y4*y4y13	3133.47	78.368	18934	3	1045.16	-3.04
P66932 TIG_SALTY Trigger factor	15	Phosphoryl STY(8)	GLIEEMASAYEDPKEVIEFYK	368	22	4	22.19	b6b7*b7y5	2628.21	102.070	3298	3	876.74	14.96
P66932 TIG_SALTY Trigger factor	16	Oxidation+M(1)	MQVSVETTQGLGRR	0	14	3	24.73	b8b9y7	1577.80	62.248	4562	3	526.60	-6.03
P66932 TIG_SALTY Trigger factor	17		ELPELTEEFIKR	243	12	0	2.83		1485.78	70.406	18678	3	495.93	-8.54
P66170 RL29_SALTY 50S ribosomal protein L29	1		MQAASGQLQQSHLLK	29	15	24	161.44	b1b2*b2b3b5b9b15y1y2y3 y4y5y6*y6y7*y7*y10y11 y12y13*y13y14y15	1639.84	43.740	157998	3	547.28	-12.95
P66170 RL29_SALTY 50S ribosomal protein L29	2		SVEELNTELLNLLR	9	14	12	72.84	b2b4*b4y2y4y5y6y9*y9y10 y12y14	1642.91	100.242	126060	2	821.96	2.82
P66170 RL29_SALTY 50S ribosomal protein L29	3		EQFNLR	23	6	4	26.85	y3*y3y4*y4	806.41	40.718	42332	2	403.71	-7.72
P66170 RL29_SALTY 50S ribosomal protein L29	4		TLLTEK	54	6	1	13.62	y4	704.41	31.811	18260	1	704.41	-11.61
P66170 RL29_SALTY 50S ribosomal protein L29	5		QAASGQLQQSHLLK	30	14	2	14.92	b8b11	1508.82	43.746	3222	3	503.61	4.53
P66170 RL29_SALTY 50S ribosomal protein L29	6		AASGQLQQSHLLK	31	13	3	26.22	b8b11b12	1380.74	43.739	2847	2	690.88	-10.52
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	1		EITIAAAK	67	8	9	62.54	b3*b3y1y2y3y4y5y6y8	816.47	37.283	103650	2	408.74	-11.96
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	2		ALDAIIASVTESLKEGDDVALVGF GTFAVK	23	30	7	62.2	b2b4b5y6y7y8y9	3036.61	136.125	28501	3	1012.87	-1.69
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	3		IAAGADISK	9	9	8	102.61	b5b6y3y4y5y6y7y8	845.46	27.367	245299	2	423.23	-19.78
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	4		ALDAIIASVTESLKEGDDVALVGF GTFAVK	23	30	6	43.33	b3b4b5y3y8y18	3036.63	122.711	9186	3	1012.88	4.02
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	5	Phosphoryl STY(12)	ALDAIIASVTESLK	23	14	5	31.54	b3b11b13y10*y10	1510.79	114.209	11657	2	755.90	12.12
P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	6		EITIAAAK	67	8	0	1.21		798.46	37.290	24743	2	399.73	-8.71
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	23	131.2	b2*b2b3*b3b5*b5b9*b9b1 1b12*b12b13*b13b14y4y6° y6y7y8y9y10y12y23	2379.24	63.460	114030	3	793.75	-2.57
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2		AQAFTLVAK	24	9	9	79.18	b3b5y1y2y3y4y6y7y9	948.54	52.076	75384	2	474.77	-11.07
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	11	59.89	b2b3b5b13b14y2y8y10y13 y14y18	1919.02	84.417	64887	2	960.01	8.21
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	13	92.55	b2b3b4b11*b11b12b15y4y 5y6y13y15y17	1837.96	85.265	64284	2	919.48	6.97
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		NYGVEIVDGPLK	116	12	10	74.37	b2*b2b3b4*b4y4y6y8y10y 12	1303.69	63.687	50453	2	652.35	-1.12

Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		AVIVLDENDNVIFSQLVDEITHEPDYDAALNVLKA	133	35	20	134.82	b3b4b5b10b11*b11b15y3y4y5y6y7y12*y12y13*y13y18y24y28y31	3882.99	119.690	56509	3	1295.00	7.23
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		AQAFTLVAK	24	9	0	1.62		931.51	52.107	7067	2	466.26	-14.81
P26982 DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	12	90.69	b3b4b5*b5y1y2y4y7y9y12y15y19	2017.08	73.929	75430	3	673.03	-12.59
P26982 DEGP_SALTY Protease do	2		NLTSQMVEYGQVK	275	13	9	43.1	b2b6b10*b10y5y8y11*y11y13	1496.76	56.534	53653	2	748.88	9.13
P26982 DEGP_SALTY Protease do	3		GAFVSQVMPNSSAAK	313	15	11	79.1	b3b4b5y1y2y8y9y10y11*y11y15	1493.75	52.133	43906	2	747.38	4.09
P26982 DEGP_SALTY Protease do	4		VGDYTV AIGNPFLGETVTSGIVS ALGR	186	28	18	157.48	b3b5b6b7b8*b8b9y1y2y3y4y5y6y7y8y9y10y28	2750.44	115.946	35152	3	917.48	-0.09
P26982 DEGP_SALTY Protease do	5		AQVGTMPVGSK	352	11	8	52.96	b2*b2b6y5y7y8y9y11	1074.56	33.737	30797	2	537.78	-4.54
P26982 DEGP_SALTY Protease do	6		SGLNVENYENFIQTDAAINR	214	20	6	21.04	b2y2y11y12*y12y20	2268.12	76.651	29617	2	1134.56	14.10
P26982 DEGP_SALTY Protease do	7		ISLGLLR	363	7	4	53.69	y3y4y5y6	771.50	67.527	24094	2	386.26	-7.83
P26982 DEGP_SALTY Protease do	8		LADSDALR	178	8	8	49.32	b3y2y5*y5y6*y6y7y8	860.44	31.215	20675	2	430.72	-12.06
P26982 DEGP_SALTY Protease do	9		GELGIMGTELNSELAk	289	16	6	24.26	b5*b5b8y11y13*y13	1661.85	74.102	10163	2	831.43	7.05
P26982 DEGP_SALTY Protease do	10		ILDSKPSVLALNIQR	450	15	3	26.22	y3y4y10	1666.96	64.218	64893	3	556.32	-15.38
P26982 DEGP_SALTY Protease do	11		GYVVTNNHVVDNASVIK	124	17	7	55.6	b3b5b7y3y8y10y14	1828.93	48.957	43573	3	610.31	-15.35
P26982 DEGP_SALTY Protease do	12		SDIALIQINPK	160	12	4	36.17	b3b6y5y6	1339.76	62.949	42449	2	670.38	-2.10
P26982 DEGP_SALTY Protease do	13		VMPSVVSINVEGSTTVNTPR	48	20	3	21.16	y10y12y15	2087.07	102.127	8757	2	1044.04	-3.63
P26982 DEGP_SALTY Protease do	14		GDSSIYLLMQ	465	10	6	41.1	b7*b7b9y8y9*y9	1126.57	37.178	1636	2	563.79	18.31
P26982 DEGP_SALTY Protease do	15		RGELGIMGTELNSELAk	288	17	10	73	b3b4b5b6b10b12y10*y10*y10y16	1817.92	68.082	46506	3	606.65	-10.74
P26982 DEGP_SALTY Protease do	16		VDAQRGAFVSQVMPNSSAAK	308	20	3	14.37	b7y7y9	2063.04	93.699	2496	2	1032.03	4.73
P26982 DEGP_SALTY Protease do	17		GELGIMGTELNSELAkAMK	289	19	8	48.66	b6b8b14b17*b17y11*y11y12	1992.03	93.044	2473	3	664.68	8.58
P26982 DEGP_SALTY Protease do	18	Phosphoryl STY(5)	GYVVTNNHVVDNASVIK	124	17	4	29.91	b3b4y6y8	1908.91	38.803	55085	3	636.97	-2.24
P26982 DEGP_SALTY Protease do	19	Oxidation+M(2)	VMPSVVSINVEGSTTVNTPR	48	20	12	55.47	b3b4b9*b9y8*y8y10*y10*y10y11*y11y12	2103.08	136.339	2074	2	1052.04	3.60
P26982 DEGP_SALTY Protease do	20		NLTSQMVEYGQV	275	12	2	7.42	y9*y9	1368.65	56.549	343230	2	684.83	3.92
P58661 AAT_SALTY Aartate aminotransferase	1		LREEFGVYAVASGR	360	14	5	19.29	b7y1y4y11y14	1553.79	70.420	33927	2	777.40	-12.02
P58661 AAT_SALTY Aartate aminotransferase	2		MFENITAAPADPILGLADLFR	0	21	16	54.35	b2b5b6*b6b8*b8*b8b10*b10y1y2y3y5y7y13y21	2275.20	120.043	15675	2	1138.10	8.05
P58661 AAT_SALTY Aartate aminotransferase	3		NYLGIDGIPEFAR	63	13	7	45.53	b3*b3y4y5y8*y8y10	1464.75	79.890	12509	2	732.88	2.33
P58661 AAT_SALTY Aartate aminotransferase	4		TAQTPGGTGALR	96	12	9	50.18	b2*b2b4b6*b6y8y9y10y12	1129.59	28.596	10633	2	565.30	-4.97
P58661 AAT_SALTY Aartate aminotransferase	5		INLGIGVYKDETGK	28	14	6	30.74	b3b11b12*b12y11*y11	1506.80	69.830	6695	3	502.94	-13.04
P58661 AAT_SALTY Aartate aminotransferase	6	Carbamidomethyl+C(4)	VGACTLVAADAETVDR	254	16	4	17.16	b3b14y2y4	1647.81	53.644	5336	2	824.41	3.56
P58661 AAT_SALTY Aartate aminotransferase	7		ANYSNPPAHGASIVATILSNDALR	280	24	5	27.59	b11b12b15y4y9	2452.23	58.421	3387	3	818.08	-13.24
P58661 AAT_SALTY Aartate aminotransferase	8		AIWEQELTDMR	304	11	3	24.31	b7y4y7	1391.69	41.565	2983	2	696.35	18.77
P58661 AAT_SALTY Aartate aminotransferase	9		ELIVASSYSKNFLYNER	236	18	4	15.58	b9*b9b16y11	2090.05	85.386	18783	3	697.36	-0.12
P58661 AAT_SALTY Aartate aminotransferase	10		FENITAAPADPILGLADLFRADDRP GK	1	27	7	42.66	b4*b4b5b7b8y6y12	2883.47	62.207	7360	5	577.50	-11.60
P58661 AAT_SALTY Aartate aminotransferase	11		AIWEQELTDMRQR	304	13	6	32.31	b8*b8y6y8*y8y9	1675.81	68.207	2071	2	838.41	-8.45
P58661 AAT_SALTY Aartate aminotransferase	12		LREEFGVYAVASGR	360	14	3	24.73	b12y6y7	1553.79	88.311	1658	2	777.40	-10.92

P58661 AAT_SALTY Aartate aminotransferase	13		RVWVSNPSWPNHK	121	13	5	43.11	y4y7*y7y8y9	1606.80	94.065	1652	2	803.91	-11.78
P58661 AAT_SALTY Aartate aminotransferase	14		LVAADAETVDR	259	11	0	4.45		1159.60	53.642	4203	2	580.30	4.00
Q7CQV9 DPS_SALTY DNA protection during starvation protein	1		TALTDHLDTMAER	70	13	5	32.31	b9y5y7y8y13	1473.68	51.166	57450	3	491.90	-12.18
Q7CQV9 DPS_SALTY DNA protection during starvation protein	2		AIGEAKDEDTADIFTAASR	134	19	8	53.98	b12y1y3°y3y4y5y6y13	1980.94	57.177	26440	3	660.99	-3.76
Q7CQV9 DPS_SALTY DNA protection during starvation protein	3		AVQLGGVALGTTQVINSK	83	18	11	67.56	b2b3*b7b15y2y3y4y11y13y14y15	1756.01	66.436	24607	2	878.51	7.16
Q7CQV9 DPS_SALTY DNA protection during starvation protein	4		GANFIADVHEMLDGFR	55	15	6	29.44	b10*b10y3y5y6°y9	1676.81	81.675	22576	3	559.61	-8.59
Q7CQV9 DPS_SALTY DNA protection during starvation protein	5		SYPLDIHNVQDHLKELADR	105	19	3	14.94	b3b10y10	2263.12	71.719	3474	3	755.04	-12.41
Q7CQV9 DPS_SALTY DNA protection during starvation protein	6		ASNLLYTR	10	8	4	36.1	b6*b6y4y6	937.50	42.993	19710	2	469.25	-11.13
Q7CQV9 DPS_SALTY DNA protection during starvation protein	7		SYPLDIHNVQDHLK	105	14	3	24.73	b7b8y4	1678.84	43.671	3673	2	839.92	-9.02
Q7CQV9 DPS_SALTY DNA protection during starvation protein	8		SYPLDIHNVQDH	105	12	0	5.66		1437.66	71.741	13065	2	719.34	-9.00
Q7CQV9 DPS_SALTY DNA protection during starvation protein	9		ADIFTAASR	144	9	1	7.42	b5	951.48	57.111	3304	2	476.25	-5.39
P02906 SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQEIAAK	263	13	8	47.29	b2b3y2y3y9y10y11y13	1468.74	49.449	47425	2	734.87	2.16
P02906 SUBI_SALTY Sulfate-binding protein	2		NVEVLDSGAR	183	10	14	88.54	b1b2b3b4*b4y1y2y4y5y6y8y9y10*y10	1059.54	38.896	37082	2	530.27	-6.57
P02906 SUBI_SALTY Sulfate-binding protein	3		GSTNTFVER	193	9	6	38.27	y2y4y5y6*y7y9	1010.48	31.186	25689	2	505.75	-6.40
P02906 SUBI_SALTY Sulfate-binding protein	4		WNYLAAWGYALHHNNNDQAK	153	20	5	14.37	b8y2y8y13y20	2386.08	78.214	21442	4	597.28	-13.61
P02906 SUBI_SALTY Sulfate-binding protein	5		QATSVINGIEADVVTALAYDVD AIAER	66	28	7	52.86	b3b13y6y8y9y10y11	2917.52	127.636	10244	3	973.18	1.51
P02906 SUBI_SALTY Sulfate-binding protein	6		DIQLLNVSYPTR	20	13	4	28.12	y2y5y6y9	1533.77	81.746	7167	2	767.39	-13.85
P02906 SUBI_SALTY Sulfate-binding protein	7		FEIVTPSESILAEPTVSVVDK	226	21	6	37.04	b5b8b13b20y5y8	2260.24	76.347	85792	3	754.08	18.04
P02906 SUBI_SALTY Sulfate-binding protein	8		QIHDWNDLIKPGVSVITPNPK	126	21	4	22.33	b10y4y5°y5	2371.24	71.992	68803	4	593.56	-16.58
P02906 SUBI_SALTY Sulfate-binding protein	9		LFTIDEVFGGWAK	298	13	6	62.73	b7y4y5y6y7y11	1482.77	101.183	45888	2	741.89	1.65
P02906 SUBI_SALTY Sulfate-binding protein	10		NFYRPR	276	6	3	26.85	b4*b4b5	852.44	56.237	4380	2	426.72	-8.31
P02906 SUBI_SALTY Sulfate-binding protein	11		AQDFVK	173	6	3	26.85	b5*b5y5	707.36	71.150	4174	1	707.36	-12.08
P02906 SUBI_SALTY Sulfate-binding protein	12		WGVGFTLLLASTSILAKDIQLLNVSYPTR	3	30	9	62.18	b4b5b6°b6b7y5y6°y6y13	3291.76	83.500	40603	3	1097.92	-13.05
P02906 SUBI_SALTY Sulfate-binding protein	13		KYDDAFPK	288	8	3	33.09	b6y6y7	983.48	72.797	1529	2	492.24	-8.44
Q8ZP20 TREA_SALTY Periplasmic trehalase	1		WMDNPQQLSTIR	323	12	4	35.5	y8y9y10y12	1488.73	61.333	41251	2	744.87	1.23
Q8ZP20 TREA_SALTY Periplasmic trehalase	2		VAAAAQAHLQPGGLATTSVK	428	21	8	48.72	b2b3b4b5y5y10y19y21	2004.11	56.606	36944	3	668.71	-5.24
Q8ZP20 TREA_SALTY Periplasmic trehalase	3		TTTIAPVDLNALLYQLEK	335	18	8	32.75	b5°b5b8y1y2y3y13y14	2003.11	103.080	35487	2	1002.06	2.68
Q8ZP20 TREA_SALTY Periplasmic trehalase	4		TFADAIPNSDPLMILADYR	68	19	15	59.74	b2°b2b4b6°b6y2y3°y3y4y5°y5y12y13*y13y19	2123.07	100.762	32398	2	1062.04	11.04

Q8ZP20 TREA_SALTY Periplasmic trehalase	5	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPTK	534	29	7	25.99	b2b3b4b10b25y1y3	3199.57	62.877	21511	4	800.65	-4.50
Q8ZP20 TREA_SALTY Periplasmic trehalase	6		EYLPQLQKEYAYWMEGVETLQPG QQNQR	235	28	5	11.71	b9y6*y6y11*y11	3426.61	102.139	8018	3	1142.87	-9.76
Q8ZP20 TREA_SALTY Periplasmic trehalase	7		WDSLLPLPESYVVPGGR	142	17	8	42.59	b4*b4b9b12*b12y3y9y12	1884.99	90.726	7443	2	943.00	4.34
Q8ZP20 TREA_SALTY Periplasmic trehalase	8		AIEMHLWNNKEGWYADYDLK	380	20	4	34.59	b11b12b13y20	2496.18	103.387	6753	2	1248.59	5.67
Q8ZP20 TREA_SALTY Periplasmic trehalase	9		AIEMHLWNNK	380	10	5	40.13	b5y4y6y7y10	1255.64	78.296	1527	2	628.32	9.43
Q8ZP20 TREA_SALTY Periplasmic trehalase	10		EHIDGLWPVLTR	123	12	3	22.28	b3b6y5	1435.74	55.504	18283	3	479.25	-21.26
Q8ZP20 TREA_SALTY Periplasmic trehalase	11		SNPNRPATEIYR	296	12	7	36.17	b8*b8b11*b11*b11y8y9	1417.74	49.602	12233	2	709.38	17.22
Q8ZP20 TREA_SALTY Periplasmic trehalase	12		LEDGSVLNR	266	9	5	30.49	b4*b4b8y7*y7	1002.54	24.407	7241	2	501.77	15.95
Q8ZP20 TREA_SALTY Periplasmic trehalase	13		TYYLSR	206	6	2	26.85	y4y5	802.41	36.617	4368	2	401.71	3.80
Q8ZP20 TREA_SALTY Periplasmic trehalase	14		DTPRPESWVEDIATAK	280	16	5	28.34	b12y9*y9y10y13	1814.88	111.576	2744	2	907.94	-6.66
Q8ZP20 TREA_SALTY Periplasmic trehalase	15		NVEKWDSLLPLPESYVVPGGR	138	21	4	21.7	b9y4y8y10	2355.25	87.306	30246	3	785.75	5.49
Q8ZP20 TREA_SALTY Periplasmic trehalase	16		DTPRPESWVEDIATAKSNPNRPAT EIYR	280	28	3	17.72	b6b9b14	3213.61	120.694	21438	3	1071.88	5.77
Q8ZP20 TREA_SALTY Periplasmic trehalase	17		DLRSAASGWDFSSR	308	15	3	26.22	y3y5y12	1625.76	40.868	6088	3	542.59	-6.01
Q8ZP20 TREA_SALTY Periplasmic trehalase	18		WDSLLPLPESYVVPGGRFR	142	19	3	22.72	b9b10y7	2188.16	62.273	5634	3	730.06	4.02
Q8ZP20 TREA_SALTY Periplasmic trehalase	19		YWDDRDTPRPESWVEDIATAK	275	21	3	20.52	y3y8y18	2550.18	76.397	3833	4	638.30	-3.54
Q8ZP20 TREA_SALTY Periplasmic trehalase	20	Oxidation+M(9)	SQPPFFAFMVELLAQHEGDDALK	212	23	3	13.05	b8b10y5	2606.27	136.131	9728	3	869.43	5.06
Q8ZP20 TREA_SALTY Periplasmic trehalase	21		TFADAIPNSDPLMILADYR	68	19	0	5.66		2105.02	100.759	2901	3	702.35	-3.83
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	1	Carbamidomethyl+C(10)	YVIDELDQICQR	77	12	11	86.92	b2b9y1y3y6y8*y8y9y10y11y12	1551.76	67.138	33634	2	776.38	8.65
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	2	Carbamidomethyl+C(10)	YVIDELDQICQRDR	77	14	4	19.29	b5b10y11y14	1822.86	54.219	13030	2	911.93	-7.50
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	3		SLGITNPPEIDR	6	12	4	32.49	y4y6y8*y10	1343.70	80.788	8629	2	672.35	14.17
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	4		YDNLK	1	5	4	26.44	b3*b3b4*b4	652.34	25.960	8638	1	652.34	9.73
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	5		IYFQK	31	5	2	13.22	b4*b4	698.38	37.222	2458	1	698.38	-5.86
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	6		SELDLK	91	6	1	13.62	b5	704.38	27.323	1541	1	704.38	-7.97
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	7		HLESVVANKISEIEADLDK	105	19	4	25.87	b8y4y9y10	2110.09	83.938	36630	3	704.03	-7.64
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	8		SLGITNPPEIDRYSLR	6	16	5	34.77	b3b10b12y6y14	1862.95	64.336	17604	3	621.65	-7.40
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	9		ISEIEADLDKLTR	114	13	3	20.64	b4b7y8	1502.81	42.030	4079	3	501.61	1.22
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	10		YDNLKSLGITNPPEIDR	1	17	5	26.15	b7y7y10y12*y12	1977.01	109.601	3184	3	659.67	6.48
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	11		TVVADGIGQGYKEVQEISPNLR	55	22	5	26.92	b8b9y5*y5y12	2373.23	103.833	2438	2	1187.12	-5.14
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	12		MYDNLKSLGITNPPEIDR	0	18	5	32.57	y5*y5y9y10y12	2108.05	106.652	2389	2	1054.53	8.69

[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1	Carbamidomethyl+C(3)	FACGVIEK	169	8	9	54.09	b2y1y2°y2y3y5y6y7y8	923.46	39.837	138135	2	462.23	-10.18
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2		GGDNYSDKPAPLGGGGAR	151	18	16	117.71	b2b5*b5b10*b10y3y5y6y7y8y10y11y12y13°y13y18	1688.78	32.196	95407	3	563.60	-12.94
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3		EVPALMAGGHLDPEK	84	15	13	92.53	b2b3°b3b7°b7b10y3y5y7y8y9y13y15	1563.80	56.168	34678	2	782.40	11.08
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	4		GHLGDLPLGVVNADGTATYPLLA PR	110	25	4	22.89	b3b4b15y2	2517.32	84.003	3329	4	630.08	-11.25
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	5		SLSELK	137	6	1	13.62	y4	676.39	30.537	2090	1	676.39	-1.62
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	6		EVPALMAGGHLDPEKTGK	84	18	6	46.41	b7y6y8y10y11y16	1849.92	51.744	24927	3	617.31	-12.41
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	7		GHSLMIHKGGDNYSDKPAPLGGG GAR	143	26	3	22.81	b10b11b13	2592.28	75.055	18313	4	648.83	2.17
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	8	Oxidation+M(6)	EVPALMAGGHLDPEK	84	15	4	18.14	b6°b6b10y9	1579.76	64.263	17745	3	527.26	-11.28
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	9	Carbamidomethyl+C(3)	FACGVIE	169	7	0	1.21		795.38	39.816	13820	2	398.19	7.52
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	10		PALMAGGHLDPEK	86	13	3	26.22	b3b7b11	1335.68	56.180	9210	2	668.34	5.76
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	11		EVPALMAGGHLDPEK	84	15	0	4.04		1545.75	56.166	6284	3	515.92	-9.24
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	12	Carbamidomethyl+C(3)	FACGVIEK	169	8	0	1.21		905.46	39.789	2230	2	453.23	12.07
[P55900]SERC_SALTY Phohoserine aminotransferase	1	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	9	49.29	b3*b3b10y1y3y4y7y11y12	2567.17	73.083	46149	4	642.55	-14.84
[P55900]SERC_SALTY Phohoserine aminotransferase	2		ASIYNAMPIEGVK	335	13	5	20.64	b1b3b10y10y13	1392.71	58.004	40056	3	464.91	-6.66
[P55900]SERC_SALTY Phohoserine aminotransferase	3		AQVFNFSSGPAMLPAEVLK	1	19	11	57.96	b2b3y1y3y6y12y13y15*y15y16y19	2006.05	90.683	34114	2	1003.53	5.90
[P55900]SERC_SALTY Phohoserine aminotransferase	4		YGVIIYAGAQK	188	10	9	70.55	b1b2b3b7y4y5y6y9y10	1069.57	42.085	29044	2	535.29	-0.91
[P55900]SERC_SALTY Phohoserine aminotransferase	5		ALTD FMIDFERR	348	12	4	37.26	b4b6b11y5	1513.73	93.885	3204	3	505.25	-8.23
[P55900]SERC_SALTY Phohoserine aminotransferase	6		AQGGVAAMHK	257	10	3	26.91	b5y5y8	969.49	18.165	2998	2	485.25	-3.90
[P55900]SERC_SALTY Phohoserine aminotransferase	7		VFLEESFAAGLHALK	311	15	4	26.22	b2b10b11b13	1631.89	87.586	2473	3	544.63	3.96
[P55900]SERC_SALTY Phohoserine aminotransferase	8		MAQVFNFSSGPAMLPAEVLK	0	20	4	23.79	b6b7b9*b9	2137.09	102.668	1728	3	713.04	4.68
[P55900]SERC_SALTY Phohoserine aminotransferase	9	Carbamidomethyl+C(3)	KYCAPQIIDAK	111	11	4	31.29	b7b8*b8b10	1306.68	65.828	74037	2	653.84	-4.76
[P55900]SERC_SALTY Phohoserine aminotransferase	10		TTADYVDAGYWAASAIKEAK	91	20	5	22.62	b4b6b8y3°y3	2131.03	100.546	39792	3	711.02	-0.34
[P55900]SERC_SALTY Phohoserine aminotransferase	11		MNVPFQLADNTLDKVFLEESFAA GLHALK	297	29	3	11.53	b3b7y26	3218.64	108.341	24571	4	805.41	-5.84
[P55900]SERC_SALTY Phohoserine aminotransferase	12		AELLYGVIDNSDFYRNDVQAQNR	272	23	6	29.47	b14y6y10y14y19*y19	2643.29	78.344	23451	3	881.77	2.59
[P55900]SERC_SALTY Phohoserine aminotransferase	13		GQFAGVPLNLLGDKTTADYVDA GYWAASAIK	77	31	6	18.78	b3b16*b16b25y3y25	3212.64	96.435	22000	3	1071.55	4.64
[P55900]SERC_SALTY Phohoserine aminotransferase	14		ALTD FMIDFERR	348	12	4	35.5	b7b8b9°b9	1513.76	70.489	3081	3	505.26	8.23
[P55900]SERC_SALTY Phohoserine aminotransferase	15	Carbamidomethyl+C(7); Oxidation+M(17)	LAQQELCDWHGLGTSVMEISHR	20	22	3	13.44	b3b7y6	2583.19	90.860	7791	4	646.55	-6.33
[P55900]SERC_SALTY Phohoserine aminotransferase	16	Oxidation+M(1)	MNVPFQLADNTLDK	297	14	4	30.74	b3y8y10y11	1621.77	67.621	2624	4	406.20	-9.48

P55900 SERC_SALTY Phohoserine aminotransferase	17		QVFNFSGGPAMLP AEVLK	2	18	2	7.42	b13°b13	1934.99	90.625	1612	2	968.00	-5.30
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		IGSF EAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	15	73.44	b5°b5b6°b6b7b8b12b22b23y2y3y5y7y11y36	3950.88	94.596	92118	4	988.48	-1.73
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	15	62.44	b2b3b9b12y3*y3y5*y5y6y10°y10y11°y11*y11y19	2098.98	68.135	55215	3	700.33	-1.98
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3		MQLNSTEISELIK	0	13	6	28.12	b2y3y10°y10y11y13	1505.79	75.867	54546	2	753.40	-0.41
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4		DSVGAVVMGPYADLAEGMK	68	19	11	62.44	b5b8b13y1y2y3y4y7y11y12°y12	1909.92	82.697	51342	2	955.47	11.25
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		ILEVPVGR	93	8	4	40.87	y4y5y6y8	882.53	51.291	34589	2	441.77	-8.85
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6	Carbamidomethyl+C(1)	CIYVAIGQK	192	9	5	30.49	b3b4y1y5y9	1051.56	56.233	33134	2	526.28	-4.06
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		GYLADVELAK	453	10	10	68.79	b2b3b7b8y1y2y6y7y8y10	1078.57	59.304	31062	2	539.79	-4.30
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		ELAAFSQFASDLDDATR	401	17	11	73	b4°b4b10y3y4y5°y5y6y9y13y17	1856.88	87.688	30552	2	928.94	8.41
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9		QYAPMSVAQQLVFAAER	434	19	10	51.81	b3*b3b9b11b14y1y4y5y16y19	2109.09	92.427	28445	2	1055.05	6.60
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		ELAAFSQFASDLDDATRK	401	18	4	15.58	b2b8y9y11	1984.95	82.429	27036	3	662.32	-5.47
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		QSVDQPVTGYK	139	12	7	61.15	b12y4y7y8y9y10y12	1349.67	33.032	23644	2	675.34	0.27
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12		VNADYVEAFTK	303	11	10	84.97	b1b2b8b9y4y5°y5y7y8y9	1256.61	59.340	16126	2	628.81	-7.38
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		EAFPGDV FYLHSR	283	13	4	20.64	b3b11y8y13	1537.75	75.644	9245	3	513.25	3.33
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		IAQFN VVSEAHNEG TIVSVSDGVI R	15	25	6	27	b10*b10b19y5y6y22	2641.35	73.446	31879	3	881.12	-3.60
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		YAIALNLER	59	9	3	38.27	y4y5y6	1062.59	63.550	20378	2	531.80	-6.32
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16		GEDALIYDDL SK	252	13	5	46.11	b8b10b11y6y7	1451.70	55.509	16037	3	484.57	-17.91
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17		DHAPLMQEINQSGGYNDEIEGK	477	22	6	20.87	b12y3°y3y6°y6y10	2445.12	92.921	7641	4	612.04	8.29
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18		TALAQYR	394	7	3	37.46	b4y3y4	822.44	19.179	6344	2	411.72	-9.20
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	19		VNADYVEAFTKGEVK	303	15	3	18.14	b4b14y14	1669.86	100.703	68143	2	835.43	11.18
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	20		VVNTLGAPIDGKGPVDNDGFSAV EAIAPGVIDR	106	33	18	101.39	b4°b4b7°b7°b7b26y6°y6y7y8y9y10y11y13y15y17y26°y26	3263.72	83.449	59541	3	1088.58	9.80
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	21		IGSF EAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	7	25.54	b4b13°b13y5y6y11y15	3950.86	83.474	40264	3	1317.63	-6.18
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	22		DHAPLMQEINQSGGYNDEIEGKL K	477	24	4	19.02	b3b6°b6b13	2686.31	92.358	26547	3	896.11	10.18
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	23		EAFPGDV FYLHSRLLER	283	17	3	24.97	b11b13b14	2049.09	82.027	23767	3	683.70	14.77
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	24		QKQYAPMSVAQQLVFAAER	432	21	5	35.2	b5b9b11y4y5	2365.24	93.127	2309	3	789.09	4.85
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	25	Phosphoryl STY(5)	ASTISNVVRK	201	10	4	33.9	b3b4b9°b9	1154.58	40.808	9840	2	577.79	-7.19
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	26	Oxidation+M(18)	DSVGAVVMGPYADLAEGMK	68	19	4	20.7	b3b12y6y9	1925.91	89.063	1582	4	482.23	5.01
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	27		ELAAFSQFASDLDDATR K	401	18	0	5.26		1967.95	82.428	1810	3	656.65	8.13

Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTEPTWFPDSQTLAFTSDQAG RPQVYK	287	29	14	74.38	b4b5°b5b12y2y11°y11y13y 14y20y21y24y25y29	3285.56	76.715	104586	3	1095.86	4.01
Q8ZQT5 TOLB_SALTY Protein tolB	2		IEITQGVD SARPIGVV PFK	24	19	12	65.48	b2°b2b3b9y2y3y12y14y15 y16y18y19	2026.11	69.506	71617	3	676.04	-11.45
Q8ZQT5 TOLB_SALTY Protein tolB	3		LPATDGQVK	413	9	4	54.5	y4y6y7y8	928.52	26.878	59760	2	464.76	7.43
Q8ZQT5 TOLB_SALTY Protein tolB	4		WAGPGAAPEDIGGIVAADLR	43	20	14	80.12	b1b4b6b7b13b17y1y2y3y5 y6y13y14y20	1936.00	84.675	51194	2	968.50	4.60
Q8ZQT5 TOLB_SALTY Protein tolB	5		SPQPLMSPA WSPDGSK	197	16	18	116.65	b2°b2b3b6°b6b8°b8b12y1 y4y5y6y9°y9y10y13y14y16	1684.82	61.539	50193	2	842.91	11.81
Q8ZQT5 TOLB_SALTY Protein tolB	6		SALVIQTLANGAVR	223	14	5	24.73	b3b4y2y9y14	1412.83	69.839	28729	2	706.92	3.28
Q8ZQT5 TOLB_SALTY Protein tolB	7		IAYVVQTNGGQFPYELR	166	17	9	53.47	y2y3y5y8°y8y11°y11y13°y 13	1955.02	72.319	28021	2	978.01	7.37
Q8ZQT5 TOLB_SALTY Protein tolB	8		QVASFPR	237	7	4	37.46	b5y4y5y7	804.43	37.202	17064	2	402.72	-11.68
Q8ZQT5 TOLB_SALTY Protein tolB	9		TGSLNLYVMDLASGQIR	264	17	5	16.32	b9b11y2y11°y11	1837.95	88.696	12996	2	919.48	-0.40
Q8ZQT5 TOLB_SALTY Protein tolB	10		FNPLDR	67	6	1	13.62	y4	761.39	44.270	6088	2	381.20	-1.12
Q8ZQT5 TOLB_SALTY Protein tolB	11		HNGAPAFSPDGTK	244	13	4	28.12	y5°y5y7y8	1298.61	56.090	3603	2	649.81	1.13
Q8ZQT5 TOLB_SALTY Protein tolB	12		LPATDGQVKSPA WSPYL	413	17	3	24.97	b5b14b15	1829.92	91.076	5683	2	915.46	-13.94
Q8ZQT5 TOLB_SALTY Protein tolB	13		VIQTLANGAVR	226	11	0	3.64		1141.66	69.848	19157	2	571.33	-8.55
Q8ZQT5 TOLB_SALTY Protein tolB	14		WAGPGAAPEDIGGIVAAD	43	18	3	21.16	y7y11y15	1666.80	84.728	3287	3	556.27	-4.98
Q8ZQT5 TOLB_SALTY Protein tolB	15		TGSLNLYVMDLASGQIR	264	17	0	4.85		1819.95	88.718	9745	2	910.48	11.40
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		AGLGMMEGVLENVPSAR	78	17	8	43.84	b5b12b13y2y4y7y12y17	1730.87	80.934	46290	2	865.94	5.78
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		VLVLVAAPEGIAALEK	155	16	11	100.51	b2b3b4b5b6b7y8y9y11y12 y16	1592.97	85.250	30647	2	796.99	2.76
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		NEETLEPVVPYFQK	103	13	5	32.31	b2b3y5y7y8	1593.79	64.401	20745	2	797.40	4.90
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		ITVVPILR	70	8	4	40.87	b2y4y5y6	910.60	68.838	11661	2	455.81	-4.69
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		LVSNIDER	116	8	5	36.1	b5y2°y2y3y6	945.51	57.713	9839	2	473.26	10.07
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	6		ELASEVGSLLTYEATADLETEK	29	22	6	20.87	b5°b5b8b11y4y22	2369.19	108.512	3740	2	1185.10	12.78
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	7		AHPDVELYTASIDQGLNEHGYYIP GLGDAGDKIFGTK	171	37	4	21.37	b5y10y11y35	3911.95	88.188	40419	4	978.74	2.43
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	8		AGLGMMEGVLENVPSARISVVG MYR	78	25	4	12.41	b5b12y7°y7	2636.35	84.003	13228	3	879.45	3.98
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase	1		TGFYMSLIGTPDEQR	84	15	4	18.14	b3y3y7y15	1714.82	77.633	32530	2	857.92	7.40
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase	2	Carbamidomethyl+C(15)	VQDQNQIPELN VYQCGTYQM HSL SEAQDIAR	113	31	11	47.71	b2b7b10y4y8°y8y9y10y12 y24y31	3635.72	74.171	22912	3	1212.58	10.34
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase	3	Carbamidomethyl+C(2)	FCIPNKEVMPEK	39	12	5	22.28	b4y4°y4y8°y8	1491.73	37.843	3014	3	497.91	-2.45
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase	4		PLLD SFAVDHTR	1	12	3	22.28	b6y4y8	1370.72	70.477	1522	2	685.87	12.02
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase	5		VADAWKAAMADV LK	99	14	4	27.86	b3b10°b10b13	1488.79	89.698	314781	2	744.90	-0.98

[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	6	Carbamidomethyl+C(2)	FCIPNKEVMPEK	39	12	3	26.26	b8b9y4	1491.72	51.156	35518	3	497.91	-10.64
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	7	Carbamidomethyl+C(2)	FCIPNKEVM	39	10	0	2.83		1234.58	37.826	2577	3	412.20	-14.53
[Q56073]DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	15	115.45	b2b4*y1y3y5y6y9y10*y10y11y12y14y17y19y21	2215.16	74.042	56199	3	739.06	-3.86
[Q56073]DNAK_SALTY Chaperone protein dnaK	2		QAVTNPQNTLFAIKR	56	15	4	26.22	b15y3y4y6	1700.92	57.594	27923	3	567.65	-11.91
[Q56073]DNAK_SALTY Chaperone protein dnaK	3		MQELAQVSQK	587	10	7	55.57	b2b3b8y6y7y8y10	1161.59	36.070	25411	2	581.30	-1.68
[Q56073]DNAK_SALTY Chaperone protein dnaK	4		ASSGLNEEEIQK	502	12	12	100.14	b11y4y5y6*y6*y6y7y8y9y10*y10y12	1304.63	33.575	21809	2	652.82	-2.71
[Q56073]DNAK_SALTY Chaperone protein dnaK	5		NDPLAMQR	253	8	5	49.32	b5y4y5y6y8	944.46	38.200	14369	2	472.73	-5.04
[Q56073]DNAK_SALTY Chaperone protein dnaK	6		TFEVLATNGDTHLGGEDFDTR	214	21	13	57.49	b1b7*b7b8*b8b12*b12b13y4*y4y10y11y21	2295.04	64.287	12392	4	574.52	-6.17
[Q56073]DNAK_SALTY Chaperone protein dnaK	7		QAVTNPQNTLFAIK	56	14	7	39.83	b3b7*b7b10y3y11y14	1544.85	66.330	10934	2	772.93	5.53
[Q56073]DNAK_SALTY Chaperone protein dnaK	8		FQDEEVQR	76	8	5	51.08	b3b7y4*y4y5	1050.48	27.401	10837	2	525.74	-3.14
[Q56073]DNAK_SALTY Chaperone protein dnaK	9		DVSIMPYK	84	8	7	40.87	b2b8y3y6*y6y7y8	952.48	54.128	10336	2	476.74	-5.06
[Q56073]DNAK_SALTY Chaperone protein dnaK	10		VLENAEGDR	25	9	8	30.49	b2b5*b5b9y2y7y8y9	1002.49	21.950	6101	2	501.75	2.56
[Q56073]DNAK_SALTY Chaperone protein dnaK	11		DVNPDEAVAIGAAVQGGLTGDVK	363	24	4	26.16	b13b14y4y7	2295.17	101.383	2141	3	765.73	-4.79
[Q56073]DNAK_SALTY Chaperone protein dnaK	12		LINYLVEFK	235	10	4	40.13	b8y5y7y8	1253.70	40.304	29188	2	627.35	18.79
[Q56073]DNAK_SALTY Chaperone protein dnaK	13		TAEDYLGEPVTEAVITVPAYFNDAQR	125	26	3	12.14	b11y9y11	2869.39	92.783	23100	3	957.14	1.45
[Q56073]DNAK_SALTY Chaperone protein dnaK	14		LESLVEDLVNR	304	11	5	47.74	b6b7b9y6y10	1286.71	76.731	14891	2	643.86	8.54
[Q56073]DNAK_SALTY Chaperone protein dnaK	15		LPADDK	556	6	1	13.62	y4	658.33	45.135	12233	1	658.33	-12.33
[Q56073]DNAK_SALTY Chaperone protein dnaK	16		MPMVQK	345	6	1	13.62	y5	733.37	30.495	9991	1	733.37	-5.08
[Q56073]DNAK_SALTY Chaperone protein dnaK	17		GMPQIEVTFDIDADGILHVS	467	22	4	23.31	b4b5*b5b12	2356.14	93.963	3629	4	589.79	-17.41
[Q56073]DNAK_SALTY Chaperone protein dnaK	18		IELSSAQQTVDNLPYITADATGPK	270	24	3	22	b5b6y9	2532.29	73.269	3392	3	844.77	1.35
[Q56073]DNAK_SALTY Chaperone protein dnaK	19	Carbamidomethyl+C(12)	IIGIDLGTNSCVAIMDGTQAR	3	22	5	19.95	y4*y4y6*y6y13	2306.20	78.397	2989	2	1153.60	20.43
[Q56073]DNAK_SALTY Chaperone protein dnaK	20		IINEPTAAALAYGLDK	167	16	4	27.67	b6y5y8y11	1659.89	32.496	2848	2	830.45	-1.69
[Q56073]DNAK_SALTY Chaperone protein dnaK	21		IIGADNGDAWLDVK	92	14	4	19.29	b7b11*b11y12	1486.77	67.468	2154	2	743.89	10.59
[Q56073]DNAK_SALTY Chaperone protein dnaK	22		VAEFFGK	352	7	4	40.47	b4*b4b6y5	797.41	50.418	1948	2	399.21	-14.16
[Q56073]DNAK_SALTY Chaperone protein dnaK	23		TIAVYDLGGGTFDISIIEIDVDGEK	188	26	3	12.14	b14b16y6	2769.41	85.394	1894	3	923.81	15.43
[Q56073]DNAK_SALTY Chaperone protein dnaK	24		NQGDHLLHSTR	536	11	3	31.29	y4y8y9	1277.62	40.899	1870	2	639.31	-13.28
[Q56073]DNAK_SALTY Chaperone protein dnaK	25		AKIELSSAQQTVDNLPYITADATGPK	268	26	4	12.14	b13*b13y8y15	2731.40	97.996	19192	3	911.14	-7.15
[Q56073]DNAK_SALTY Chaperone protein dnaK	26		NDPLAMQRLK	253	10	4	26.91	b3*b3b5y3	1185.65	38.823	13187	2	593.33	9.68
[Q56073]DNAK_SALTY Chaperone protein dnaK	27		KTAEDYLGEPVTEAVITVPAYFND	124	27	4	25.33	b3b7y8y9	2997.52	88.248	9189	3	999.84	11.65

Q56073 DNAK_SALTY Chaperone protein dnaK	28		SLGQFNLDGINPAPRGMPIQEVTF DIDADGILHVS AK	452	37	8	23.59	b6°b6b9°b9b12b13y13°y1 3	3935.99	112.225	3785	4	984.75	-0.74
Q56073 DNAK_SALTY Chaperone protein dnaK	29		VLENAEGDRTTPSI IAYTQDGETL VGQPAK	25	30	6	16.53	b6°b6°b6b9b11y13	3173.60	69.570	3669	3	1058.54	2.38
Q56073 DNAK_SALTY Chaperone protein dnaK	30		QATKDAGR	151	8	4	36.1	b7°b7y4y6	846.45	25.882	2763	2	423.73	9.30
Q56073 DNAK_SALTY Chaperone protein dnaK	31	Phosphoryl STY(9)	IELSSAQQT D VNL PYITADATGPK	270	24	7	23.43	b7°b7b8°b8°b8b12_HPO3 b12y23	2612.22	49.587	21803	3	871.41	-7.01
Q56073 DNAK_SALTY Chaperone protein dnaK	32		TFEVLATNG	214	9	1	7.65	y8	951.47	64.343	1719	2	476.24	-13.28
Q56073 DNAK_SALTY Chaperone protein dnaK	33		VLENAEGDR	25	9	0	1.62		984.46	21.953	28207	2	492.73	-11.59
P0AA07 PTHP_SALTY Phohocarrier protein HPr	1		MFQQEVTTAPNGLHTRPAAQFV K	0	24	15	111.32	b2b3b5b6b8y3y11y12y14y 15y16y17y19y20y24	2684.37	62.394	445318	4	671.85	-9.55
P0AA07 PTHP_SALTY Phohocarrier protein HPr	2		GFTSEITVTSNGK	27	13	10	56.54	b2b4b7b10y2y5y7°y7y10° y10	1340.67	50.368	8954	2	670.84	-0.18
P0AA07 PTHP_SALTY Phohocarrier protein HPr	3		LM AELE	79	6	7	66.51	b3b4b5°b5y3°y3y4	705.34	52.945	230723	1	705.34	-5.71
P0AA07 PTHP_SALTY Phohocarrier protein HPr	4		LQTLGLTQGT VVTISAEGEDEQKA VEHLVK	49	30	24	179.61	b3°b3°b3b4°b4b6°b6°b6y3 y11y13°y13y14y15y16y17y 18y19y20y22y23y24y26y2 8	3193.67	80.572	390026	4	799.17	-7.87
P0AA07 PTHP_SALTY Phohocarrier protein HPr	5		EAKGFTSEITVTSNGK	24	16	3	25.53	b3b11b12	1668.85	66.541	18008	2	834.93	2.56
P0AA07 PTHP_SALTY Phohocarrier protein HPr	6		GFTSEITVTSNGKSASAK	27	18	4	15.58	b7°b7b9y11	1784.89	43.729	1665	3	595.63	-9.57
P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	18	135.24	b2b3b4b6y2°y2y3°y3y4y5y 6°y6y7°y7y8y9y10y12	1196.59	63.158	425148	2	598.80	-2.24
P0A9Y9 CC_SALTY Cold shock-like protein cC	2		GPAAVNVTAI	59	10	6	26.91	b2b3b6°b6y5y10	912.51	68.127	6504	1	912.51	-9.10
P0A9Y9 CC_SALTY Cold shock-like protein cC	3		DVVFHFSAIQNGGFK	27	15	7	37.1	b2b3b7b11y7y12y15	1665.86	60.886	4648	2	833.43	12.02
P0A9Y9 CC_SALTY Cold shock-like protein cC	4		TLAEGQNVEFEIQDGQK	42	17	3	23.31	b4y8y9	1905.95	65.093	1515	2	953.48	16.84
P0A9Y9 CC_SALTY Cold shock-like protein cC	5		TLAEGQNVEFEIQDGQKGPAAVN VTAI	42	27	6	17.78	b5°b5b8°b8b13y20	2799.44	99.343	13105	2	1400.22	8.29
P0A9Y9 CC_SALTY Cold shock-like protein cC	6		WFNESKGFGFITPADGSK	9	18	4	22.74	b3b7b9°b9	1987.93	71.746	10570	2	994.47	-10.38
P0A9Y9 CC_SALTY Cold shock-like protein cC	7		GQVKWFNESK	5	10	6	39.34	b6b9y5°y5y7°y7	1222.63	79.128	2615	3	408.21	3.69
P0A2B3 RS7_SALTY 30S ribosomal protein S7	1		FGSELLAK	17	8	10	51.08	b1b2b5°b5b6°b6y2y3y7y8	864.47	50.302	54117	2	432.74	-11.51
P0A2B3 RS7_SALTY 30S ribosomal protein S7	2		STAESIVYSALETLAQR	36	17	5	33.72	b8b10b11b13y17	1838.96	108.792	46575	2	919.98	6.51
P0A2B3 RS7_SALTY 30S ribosomal protein S7	3		FVNILMVDGK	25	10	6	41.1	b2b3b4y3y5y10	1135.61	74.658	21809	2	568.31	-7.31
P0A2B3 RS7_SALTY 30S ribosomal protein S7	4		LANELSDAADNK	119	12	4	32.49	b4°b4b6b10	1260.61	36.432	5262	2	630.81	3.10
P0A2B3 RS7_SALTY 30S ribosomal protein S7	5		WIVEAAR	102	7	4	40.47	y4°y4y5y6	844.46	49.075	31532	2	422.73	-12.21
P0A2B3 RS7_SALTY 30S ribosomal protein S7	6		NALAMR	96	6	1	13.62	y5	675.36	34.870	7410	1	675.36	-5.24
P0A2B3 RS7_SALTY 30S ribosomal protein S7	7		ILPDPK	11	6	2	26.85	y4y5	682.41	31.299	4142	1	682.41	-4.56
P0A2B3 RS7_SALTY 30S ribosomal protein S7	8		VGGSTYQVPVEVRPVR	79	16	4	24.86	b4b10b12°b12	1742.93	52.849	1599	3	581.65	-11.70

P0A2B3 RS7_SALTY 30S ribosomal protein S7	9		EDVHRMAEANK	138	11	4	24.31	b4b10°b10y8	1299.60	28.596	125167	2	650.31	-6.11
P0A2B3 RS7_SALTY 30S ribosomal protein S7	10		LANELSDAADNKGTAVK	119	17	17	121.7	b3b4°b4*b4b7b10y5y7y8*y8y9*y9y12*y12y13y15y16	1716.86	37.889	82829	3	572.96	-10.81
P0A2B3 RS7_SALTY 30S ribosomal protein S7	11		SGKSELEAFEVALENVRPTVEVK	53	23	4	19.46	b6°b6b9b12	2531.32	87.229	12300	3	844.44	-6.17
P63411 ACKA_SALTY Acetate kinase	1		EGTRPAVVPTNEELVIAQDASR	374	23	14	115.75	b7b8b9b12y3y4y5*y5y6y7y8y10y14y23	2465.31	68.029	40975	3	822.44	2.77
P63411 ACKA_SALTY Acetate kinase	2	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPEAR	17	26	18	117.28	b2b3b4b15y4y5y10°y10y11y12°y12y13y14°y14y18y19y22y26	2907.41	103.880	40433	3	969.81	3.11
P63411 ACKA_SALTY Acetate kinase	3		LGVLGFEVDHER	348	12	3	22.28	b3b9y3	1370.69	66.576	38007	3	457.57	-12.74
P63411 ACKA_SALTY Acetate kinase	4	Carbamidomethyl+C(7)	LVLVLNCGSSSLK	4	13	5	39.3	b3y7y8y9y13	1389.78	65.972	24847	2	695.39	-1.41
P63411 ACKA_SALTY Acetate kinase	5		YIGSYTALMDGR	312	12	4	22.28	b6b9b12y5	1346.65	60.398	18922	2	673.83	3.72
P63411 ACKA_SALTY Acetate kinase	6		NVAVFDTAFHQTMPEESYLYALPYSLYK	144	28	9	49.16	b2b11b12b13°b13y1y6y7y17	3297.61	98.038	12847	3	1099.87	8.51
P63411 ACKA_SALTY Acetate kinase	7		YGAHGTSHFYVTQEAAK	178	17	4	34.51	b2y5y6y7	1866.87	48.961	4473	3	622.96	-3.40
P63411 ACKA_SALTY Acetate kinase	8	Carbamidomethyl+C(18)	MLTKESGLLGLTEVTSDCR	268	19	3	21.9	b3b5b15	2110.04	103.655	2659	3	704.02	-6.60
P63411 ACKA_SALTY Acetate kinase	9		LDVAVFTGGIGENAAMVR	324	18	3	15.58	b4b9y11	1819.92	87.831	2229	2	910.46	-9.66
P63411 ACKA_SALTY Acetate kinase	10	Carbamidomethyl+C(14)	ESGLLGLTEVTSDCR	272	15	4	34.67	y8y9y10°y10	1636.79	70.890	33299	2	818.90	5.67
P63411 ACKA_SALTY Acetate kinase	11		YIGSYTALMDGRLDAVVFTGGIGENAAMVR	312	30	5	19.32	b3b6b9y9y12	3147.57	77.607	3780	5	630.32	3.57
P63411 ACKA_SALTY Acetate kinase	12	Carbamidomethyl+C(18);Phosphoryl STY(6)	MLTKESGLLGLTEVTSDCR	268	19	5	20.7	b9b12°b12y12y14	2190.03	66.713	3212	3	730.68	11.37
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	1		AANAGGVATSGLEMAQNAAR	370	20	15	85.33	b1b8b9b15y1y4y8y9y11y13°y13*y13y14y17y20	1859.91	58.933	26738	2	930.46	4.59
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	2		DPHQTEFAQAVR	17	12	6	22.28	b2b4*b4b8y2y3	1398.67	38.327	8580	3	466.90	-3.75
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	3		VVTASDSSGTVVDESGFTPEK	257	21	13	79.38	b5b6b7b9°b9b10b12y2y3y7y9y10y21	2112.02	51.035	8165	2	1056.51	11.21
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	4		EVMTTLWPFLQNP	29	15	5	44.7	b3b5b11b13y12	1860.94	79.931	4526	2	930.97	3.48
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	5		HGLGFEGMR	225	9	3	38.27	y5y6y8	1003.49	68.140	25834	2	502.25	7.79
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	6		HLGPDTDVPAGDIGVGGR	156	18	3	22.74	b5b7b10	1732.88	81.916	7952	2	866.94	9.30
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	7		EVGFMA GMMR	174	10	3	26.91	b5b7y9	1128.50	45.544	6159	2	564.76	3.89
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	8		VADAMLAQGV	436	11	5	31.29	b3b4b8°b8*b8	1087.56	89.006	3794	2	544.29	-17.40
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	9	Oxidation+M(14)	AANAGGVATSGLEMAQNAAR	370	20	4	22.62	b16y3y11y17	1875.88	85.269	13605	3	625.97	-8.59
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	10	Oxidation+M(23)	HLGPDTDVPAGDIGVGREVGFMA GMMR	156	28	4	14.91	b6b11y5y11	2858.36	102.566	1738	4	715.35	7.00
P15111 DHE4_SALTY NADP-ecific glutamate dehydrogenase	11		VVTASDSSGTVVDESGFTP	257	19	2	12.7	y3y9	1854.85	51.021	1704	2	927.93	-3.69
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		GIMEGEYDHLPEQAFYMVGSIDEAVEK	429	27	9	34.12	b2y6°y6y9y11°y11y12y15y27	3057.41	99.260	64573	3	1019.81	6.55

Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		QLDPLVVGQEHYDTAR	343	16	11	102.22	b2b13y3y4y5y8y9y10°y10y11y12	1840.90	56.657	56487	3	614.31	-7.82
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		YTLAGTEVSALLGR	247	14	7	24.73	b2°b2b3°b3y10y11y14	1450.79	79.081	51298	2	725.90	-0.34
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	6	58.12	b6b10y4y6y7y8	1193.60	79.743	44638	2	597.31	-0.72
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		VALTGLTMAEK	219	11	3	36.07	y7y8y9	1133.62	58.077	44088	2	567.31	-2.80
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		FLSQPFFVAEVFTGSPGK	399	18	4	22.74	y3y6y14y18	1958.02	98.985	41678	2	979.52	9.35
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		MPSAVGYQPTLAEEMGVLQER	261	21	14	88.54	b3b4b6b9y3°y3y6y7*y7y9y10y11y13y21	2306.13	80.670	38660	2	1153.57	6.14
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		TVNMMELIR	156	9	8	53.25	b2°b2b3y2y3y5y8y9	1106.57	74.927	38547	2	553.79	-3.75
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		AAPSYEELSNSQELLETGIK	112	20	10	46.68	b8b20y1y2y4y5y12y13y15y20	2179.09	72.731	38297	2	1090.05	7.62
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		VGLFGGAGVGK	145	11	7	27.32	b2b3y1y2y7y8y11	961.54	57.835	34299	2	481.27	-6.86
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		QIASLGIYPAVDPLDSTSR	324	19	8	75.95	y4y11y12y13y14y15y17y19	2003.06	79.626	34233	2	1002.04	9.69
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		DLEHPIEVPVGK	70	12	5	29.48	b4°b4b8b9y2	1332.70	54.401	10098	2	666.86	-8.70
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		NIAIEHSGYSVFAGVGER	165	18	5	15.58	b9*b9y11°y11y13	1905.95	66.739	3270	2	953.48	3.59
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		IMNVLGEPVDMK	87	12	3	22.28	b3y3y6	1345.69	65.090	1765	2	673.35	5.62
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15	Carbamidomethyl+C(26)	AAPSYEELSNSQELLETGIKVIDLMCPFAK	112	30	4	24.78	b5b6y4y9	3353.68	120.160	8454	3	1118.56	3.86
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16	Phosphoryl STY(8)	QIASLGIYPAVDPLDSTSR	324	19	4	41.14	y3y4y10y11	2082.98	69.670	8049	2	1041.99	-9.02
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17	Oxidation+M(4)	TIAMGSSDGLR	53	11	3	31.29	y6y7y10	1123.54	45.022	5419	2	562.27	0.00
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18		HSGYSVFAGVGER	170	13	0	5.26		1365.66	66.703	5637	2	683.33	5.18
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19		IAIEHSGYSVFAGVGER	166	17	1	7.34	b8	1791.89	66.786	2462	3	597.97	-5.18
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20		QLDPLVVGQEHYDTAR	343	16	0	4.45		1822.91	56.672	2608	3	608.31	1.54
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	1		AAPNTIPTAAK	149	11	9	90.2	b2b7y3y4y5y7y8y9y11	1054.58	31.137	22057	2	527.80	-4.51
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	2		AGGNYLSLLVGSEAR	160	16	5	30.8	b12b15y4y5y16	1593.80	78.200	18850	2	797.40	-13.63
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	3		EQVLSRESLYLADEVFMSGTAAEI TPVR	238	28	4	11.71	b3b13*b13y13	3111.57	93.944	9312	3	1037.86	0.71
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	4		ESLYLADEVFMSGTAAEITPVR	244	22	7	13.44	b3°b3b10°b10y13°y13y22	2399.15	117.613	2462	4	600.54	-11.09
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	5		SVDGIQVGEGR	266	11	7	35.31	b3b9*b9y6*y6y8°y8	1116.56	40.202	21441	2	558.79	0.33
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	6		EQVLSR	238	6	1	13.62	b5	731.40	31.709	15211	1	731.40	-7.09
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	7		IQQAFFGLFTGETEDK	284	16	8	45.28	b3b6b15°b15y4°y4y7y10	1830.92	89.133	2164	3	610.98	15.60
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	8	Carbamidomethyl+C(12)	SVDGIQVGEGRCGPVTK	266	17	4	39.16	b9b12b13b14	1758.89	59.398	1729	2	879.95	5.41
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	9	Phosphoryl STY()	DGVLFTPPFTSSALPGITR	204	19	5	29.42	b4b7b9y4y10	2056.02	108.322	2236	2	1028.52	9.38
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	10	Oxidation+M(11)	ESLYLADEVFMSGTAAEITPVR	244	22	6	43.64	b5b6b8b11°b11b12	2415.18	61.515	3123	5	483.84	0.40

[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	1		LAEAGIPTQMER	60	12	9	100.14	b3y3y5y6y8y9y10y11y12	1315.66	48.727	42617	2	658.33	-3.80
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	2		QSLGGLIEAYEAVHR	215	16	9	53.14	b3y1y2y3y5y6y7y13y16	1713.87	84.080	37728	3	571.96	-13.60
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	3		TVYSTENPDLLVLEFR	13	16	16	88.75	b1b2b4b6b11b12b13°b13y2y3y4y12°y12y13*y13y16	1895.99	87.691	37670	2	948.50	8.11
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	4		IEQFDR	39	6	1	13.62	b4	807.41	42.190	4624	2	404.21	10.51
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	5		FNHFIMTK	52	8	4	36.1	b3b7*b7y7	1037.51	110.765	2014	1	1037.51	-14.24
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	6		QAELYR	3	6	1	13.62	b5	779.40	27.928	1771	2	390.21	0.00
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	7		ELTYK	152	5	2	26.44	y3y4	653.34	42.313	1649	1	653.34	-10.93
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	8		ETLDKMDK	203	8	4	33.09	b4°b4y5y6	979.46	54.166	17689	2	490.24	-12.84
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	9		TVYSTENPDLLVLEFRNDTSAGD GAR	13	26	7	39.02	b10b11°b11b12°b12y3y8	2840.38	79.788	7322	3	947.46	3.09
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	10		NDTSAGDGARIEQFDR	29	16	6	28.34	b14y5y10°y10*y10y11	1751.80	84.035	2675	4	438.71	3.62
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	11		GMVNNKFNFHFIMTK	46	14	3	27.07	b7b10b11	1680.82	58.659	1810	2	840.91	-11.18
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	12	Phosphoryl STY(10)	QSLGGLIEAYEAVHR	215	16	5	17.16	b4*b4b8y7°y7	1793.83	28.682	4500	4	449.21	-10.62
[P66764]METK_SALTY S-adenosylmethionine synthetase	1		SLQEAVMEEIIPILPSEWLNSTSK	197	25	12	59.42	b5°b5b6b11*b11b12y7y9°y9y10y13y25	2856.52	110.826	51622	3	952.84	4.87
[P66764]METK_SALTY S-adenosylmethionine synthetase	2	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGR	230	15	8	29.44	b4y1y2y3°y3y12y13y15	1536.74	67.677	26963	2	768.88	8.74
[P66764]METK_SALTY S-adenosylmethionine synthetase	3	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGRK	230	16	5	28.34	b6b12b13y13y16	1664.82	58.649	21869	2	832.91	-3.74
[P66764]METK_SALTY S-adenosylmethionine synthetase	4		ADPLEQQAGDQGLMFGYATNET DVLMPAPITYAHR	109	35	7	21.45	b6°b6b7°b7b14y9y35	3749.79	90.179	7643	3	1250.60	7.42
[P66764]METK_SALTY S-adenosylmethionine synthetase	5		NGTLPWLRPDAK	154	12	5	34.25	b3*b3b4b6y5	1367.71	46.436	40861	3	456.58	-21.51
[P66764]METK_SALTY S-adenosylmethionine synthetase	6		ETAAYGHFGR	353	10	4	39.34	b4b7y7y9	1108.51	54.177	36880	2	554.76	-6.17
[P66764]METK_SALTY S-adenosylmethionine synthetase	7		HLFTSESVSEGHDPK	3	15	4	18.14	b11°b11y5y11	1669.79	52.242	4337	2	835.40	7.60
[P66764]METK_SALTY S-adenosylmethionine synthetase	8		NIVAAGLADR	284	10	3	26.91	b4y4y7	999.58	68.101	3730	2	500.29	19.05
[P66764]METK_SALTY S-adenosylmethionine synthetase	9	Carbamidomethyl+C(16)	EIGYVHSDMGFDANSCAVLSAIG K	74	24	6	23.61	b3b11y4y14*y14y16	2541.22	99.903	2149	3	847.75	19.60
[P66764]METK_SALTY S-adenosylmethionine synthetase	10		MAKHLFTSESVSEGHDPK	0	18	5	24.82	b13°b13y4y7y9	1999.96	101.102	133351	3	667.32	1.65
[P66764]METK_SALTY S-adenosylmethionine synthetase	11		ETAAYGHFGRENFPWEK	353	17	4	36.94	b11y6y7y8	2038.94	123.273	2864	3	680.32	-2.45

[P66764]METK_SALTY S-adenosylmethionine synthetase	12	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGRK	230	16	4	27.67	b7b9b13y13	1664.84	124.629	2828	2	832.92	7.48
[P66764]METK_SALTY S-adenosylmethionine synthetase	13		HLFTSESVSEGHPDKIADQISDAVLDAILQQDPK	3	34	5	24.28	b6b8b10b11y5	3703.87	77.548	2551	4	926.72	5.41
[P66764]METK_SALTY S-adenosylmethionine synthetase	14	Carbamidomethyl+C(10) ;Oxidation+M(7)	FVIGGPMGDCGLTGR	230	15	4	26.22	y3°y3y6y13	1552.72	69.672	5316	2	776.87	-0.79
[P66764]METK_SALTY S-adenosylmethionine synthetase	15	Oxidation+M(9)	IIVDTYGGMAR	246	11	3	24.31	b8b10y5	1211.60	61.530	2404	2	606.30	-10.78
[P66764]METK_SALTY S-adenosylmethionine synthetase	16		VLMPAPITYAHR	132	12	0	12.13		1368.76	90.158	11996	2	684.88	11.95
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	1		GFGVPTLIAVHPENDPQGEGMAIAK	167	25	10	41.52	b2b3b4y1y2y7y8y14y21y25	2548.29	76.370	57804	3	850.10	2.97
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	2		DGAALGYSHGFNIVEVGEQIRK	123	22	6	20.87	b2b3b13b15y17y22	2360.19	71.517	45729	3	787.40	-3.00
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	3		ANYFNTLNL	1	10	5	40.13	b3y4y6y7y10	1225.64	66.844	35733	2	613.32	2.59
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	4		TAFETAPQYEGK	336	12	8	65.92	b4y4y6y7y8°y8y9y12	1341.63	40.707	19508	2	671.32	-0.91
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	5		FMGRDEFADGASYLQGK	21	17	5	27.4	b3y2y7y8y10	1891.89	76.482	17531	3	631.30	13.10
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	6		LIQFGWETITEALK	252	14	5	19.29	b6b8y1y3y14	1648.89	105.246	17330	2	824.95	-2.00
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	7		LVAEGTDPAYAEK	239	13	4	20.64	b3b11°b11y9	1363.67	46.398	6336	3	455.23	0.27
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	8	Carbamidomethyl+C(6)	VVIVGCGAQLNQGLNMR	39	18	3	15.58	b3y5y10	1885.99	63.353	6183	2	943.50	8.41
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	9		DGAALGYSHGFNIVEVGEQIR	123	21	4	13.88	b5y7y12y21	2232.08	87.446	3634	3	744.70	-12.80
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	10		LSNPAK	276	6	1	13.62	b3	629.37	39.595	11948	1	629.37	7.95
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	11		VGTYEELIPQADLVVNLTDPK	88	21	4	18.93	b6b8y8y12	2314.23	114.056	3471	3	772.08	3.38
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	12		VGTYEELIPQADLVVNLTDPKQHS DVVR	88	28	3	11.71	b3b11y20	3135.62	80.892	40413	4	784.66	-5.06
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	13	Carbamidomethyl+C(11)	DITVVMVAPKCPGTEVR	145	17	4	29.91	b3b14y7y8	1871.98	56.729	24729	2	936.49	1.96
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	14	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21))	SDLMGEQTILCGMLQAGSLLCFDKLVAEGTDPAYAEK	215	37	9	34.37	b3y3y4y6°y6y9y11°y11y13	4031.95	117.474	19833	3	1344.66	10.48
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	15		QGGITLMDRLSNPAK	266	16	5	41.31	b4b7b14y4y5	1731.88	70.712	10039	3	577.96	-7.19
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	16		IGEQEYFDKGVLMIAMVK	348	18	3	22.74	b3b6b12	2071.06	90.187	7094	2	1036.04	1.53
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	17		ANYFNTLNLRQQLAQLGK	1	18	6	52.43	b3b6b9b11b14y3	2092.13	89.012	5570	2	1046.57	-2.22
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	18	Carbamidomethyl+C(7)	KVVIVGCGAQLNQGLNMR	38	19	3	24.11	y5y9y10	2014.10	57.807	1949	2	1007.55	14.12
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	19		AWAAATGGHRAGVLESSFVAEVK	192	23	3	22.08	b9b10y9	2314.21	94.035	1631	3	772.07	5.17
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	20	Phosphoryl STY(6)	LVAEGTDPAYAEK	239	13	3	20.64	b5y4y6	1443.63	38.811	10591	3	481.88	-1.94
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	21	Phosphoryl STY(4)	KDITVVMVAPK	144	11	3	24.31	b3b9y9	1280.67	56.100	4874	3	427.56	6.86
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	22	Oxidation+M(6)	SVQPLMKDGAALGYSHGFNIVEVGEQIR	116	28	5	14.91	b7b13y3*y3y24	3031.56	132.436	91507	3	1011.19	8.54
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	23	Oxidation+M(21)	GFGVPTLIAVHPENDPQGEGMAIAK	167	25	4	12.41	b4b14y12°y12	2564.26	112.290	15909	3	855.42	-8.47

[P05989]ILVC_SALTY Ketol-acid reductoisomerase	24	Oxidation+M()	HMDDIISGEFSSGMMADWANDDKK	302	24	4	16.87	b6b8y4y7	2716.14	78.310	13880	3	906.05	3.60
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	25	Oxidation+M(6)	DITVVMVAPK	145	10	6	58.12	b3°b3b4b5b7y7	1088.61	28.657	3180	3	363.54	5.05
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		VTDIEPLVGGETESSVR	171	18	15	100.81	b1b2b5°b5b6b14y6°y6y7y8y9y11°y11y12y13	1862.96	68.171	21833	2	931.98	4.98
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		AVLPGMVER	115	9	6	30.49	b2b8y2°y2y5y7	971.54	57.834	21169	2	486.27	7.35
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		GHIINIGSTAGSWPYAGGNVYGATK	126	25	3	12.41	b13y11y13	2491.26	63.841	17397	4	623.57	7.55
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4		AAIEEMMASLPAQWR	58	15	3	24.16	b12b13y5	1703.85	89.704	12311	2	852.43	13.04
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		TYENTTALTPEDITEAVVWVATLPAHVNINTVEMMPVTQSFAGLSVHR	199	48	3	11.36	b9b11y9	5340.68	136.422	5504	4	1335.93	9.23
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		ASVEDWETMIDTNNK	93	15	5	29.44	b5y5y8*y8y9	1752.81	70.967	11913	2	876.91	17.69
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		DIDVLVNNAGLALGLEPAHK	73	20	3	23.79	b3b4b14	2059.07	69.451	1968	3	687.03	-21.58
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	8		GLIYMTRAVLPGMVER	108	16	3	17.16	b3y8y10	1805.96	82.733	14536	4	452.25	-9.13
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	9		NRGHIINIGSTAGSWPYAGGNVYGATK	124	27	10	36.23	b3b10b13*b13b14y9°y9y12°y12y26	2761.36	99.307	4498	2	1381.18	-8.31
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	10	Carbamidomethyl+C(15)	MIVLVTGATAGFGECIARR	0	19	3	22.72	b14y9y10	2022.05	53.765	2006	3	674.69	-5.01
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	11	Phosphoryl STY(8)	GHIINIGSTAGSWPYAGGNVYGATK	126	25	4	18.84	b6b8b14y24	2571.19	101.275	2361	4	643.55	-0.85
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	12	Oxidation+M(9)	ASVEDWETMIDTNNK	93	15	3	18.14	b3y3y5	1768.76	33.445	29283	4	442.95	-4.07
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	13	Oxidation+M(6)	AVLPGMVER	115	9	3	30.49	b8y3y4	987.54	49.721	8871	2	494.27	10.57
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	14	Oxidation+M()	AAIEEMMASLPAQWRDIDVLVNNAGLALGLEPAHK	58	35	3	23	b4b5b11	3759.88	135.604	2515	3	1253.96	-10.71
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	1		AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	8	35	24	176.79	b2b3b6b7b8b9b10b11y4y6y7°y7y9y11y19y24y25°y25y26y27y28*y28y29y35	3487.83	106.948	71768	3	1163.28	6.65
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	2	Carbamidomethyl+C(3)	FICIADASK	112	9	6	38.27	y1y2y4y5y7y9	1024.51	49.900	26038	2	512.76	-2.86
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	3		GADVALIGTPDGVK	201	14	8	52.26	b5b6y1y2y5y6y7y14	1312.71	56.245	24242	2	656.86	0.28
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	4		GQIEGAVSSSDASTEK	43	16	5	24.86	y4°y4y6y8y16	1565.74	32.470	17024	2	783.37	7.64
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	5		GLGIHVFDLNEVDSLGIYVDGADEINGHMQMIK	61	33	7	21.93	b3b5b11b21y10°y10*y10	3599.79	95.494	7165	3	1200.60	12.21

[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	6		TQDELKK	1	7	4	37.46	b1b3y4y5	861.46	19.593	2072	2	431.23	-9.14
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	7		TIVK	215	4	1	12.82	y3	460.31	51.913	6201	1	460.31	-1.86
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	8		GGGAALTR	94	8	5	49.32	b5y3y4°y4y6	702.38	27.340	5661	1	702.38	-19.12
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	9		QVDILGKFPLPEVIPMAR	121	19	3	14.94	b3y4y7	2122.19	99.399	31046	3	708.07	-7.82
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	10		GQIEGAVSSSDASTEKLK	43	18	4	22.98	b3y9°y9y10	1806.89	37.824	5731	3	602.97	-8.85
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	11	Oxidation+M(34)	AVGWAAALQYVQPGTIVGVGTGST AAHFIDALGTMK	8	35	4	12.84	b3b11y8y13	3503.76	86.855	3626	3	1168.59	-12.05
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	12		LGIHVFDLNEVDSLGIYVDGADEI NGHMQMIK	62	32	0	11.32		3542.77	95.434	145496	5	709.36	11.16
[P62405 RL5_SALTY 50S ribosomal protein L5	1		LLDNAAADLTAISGQKPLITK	48	21	11	45.83	b3b5*b5b6b8b11y1y5y19y 21*y21	2153.21	74.407	43014	3	718.41	-5.44
[P62405 RL5_SALTY 50S ribosomal protein L5	2		LMTEFNYSVMQVPR	15	15	10	63.24	b10*b10b13°b13y2y3y4y5 y8y13	1828.86	75.205	6083	3	610.29	-5.07
[P62405 RL5_SALTY 50S ribosomal protein L5	3		ITLNMGVGEAIADK	33	14	5	19.29	b5b7b8°y11y14	1431.76	64.263	4647	2	716.39	8.53
[P62405 RL5_SALTY 50S ribosomal protein L5	4		ITLNMGVGEAIADKK	33	15	4	10.48	b1b6*b6y11	1559.84	61.020	4240	3	520.62	-5.09
[P62405 RL5_SALTY 50S ribosomal protein L5	5		LHDYYKDEVVNK	3	12	7	52.7	b3°b3y5y6y8*y8y9	1522.75	37.154	2614	3	508.26	-1.44
[P62405 RL5_SALTY 50S ribosomal protein L5	6		LHDYYK	3	6	1	13.62	y5	838.42	74.550	2485	1	838.42	13.18
[P62405 RL5_SALTY 50S ribosomal protein L5	7		DEVVNKLMTFNYSVMQVPR	9	21	9	54.48	b4b5b8*b8b9*b9y7y10y13	2513.21	113.196	3655	3	838.41	-3.30
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	1		VLSEDFQVNQLLDILR	49	17	13	53.84	b2b9b12b14°b14*b14b15° b15y2y3y4y13y17	1989.08	103.923	30765	2	995.04	7.43
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	2		GIEGASLDVPDEFVHSGK	72	18	7	41.99	b3b7b14y6°y6y12y13	1856.88	58.422	16642	3	619.63	-10.32
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	3		PSFDIVSEVDLQEAR	1	15	12	96.67	b7°b7b10y3°y3y5y6y7°y7y 8y9y10	1704.84	58.460	11754	2	852.92	-2.15
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	4		TWYVEAK	90	7	6	37.46	b1b4°b4b5y3y7	896.45	46.358	9564	2	448.73	-1.29
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	5		GGDLGQPFQFK	148	11	3	24.31	b3b9y6	1193.60	62.525	19068	2	597.30	5.42
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	6		VQAQIQGEEIR	120	11	3	24.31	b4y6y8	1270.69	84.016	3794	3	424.23	11.91
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	7		MPSFDIVSEVDLQEAR	0	16	4	28.34	b6y3y4y9	1835.87	48.294	2312	3	612.63	-7.85
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	8		RGIEGASLDVPDEFVHSGK	71	19	4	23.66	b6y5y8y17	2013.03	34.443	17044	3	671.68	13.46
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	9		FDFRGVEATIELNDANK	29	17	3	16.32	b5y7y12	1938.95	94.812	1654	2	969.98	-0.50
[Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	10	Phosphoryl STY(5)	GVEATIELNDANK	33	13	4	28.12	y4°y4y8y9	1453.64	36.492	22792	3	485.22	-4.62
[P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	1		VALDPLTGMPYQGR	146	15	7	58.59	b13y5y8y9y10y11y15	1614.84	69.956	42872	2	807.92	6.73
[P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	2	Carbamidomethyl+C(11)	YGLPAPVGYACTTPR	14	15	7	51.57	b5b10y4y10y11y12y15	1622.81	60.411	30657	2	811.91	4.89
[P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	3		DLALIEINPLVITK	191	14	8	45.27	b2b4b5y2y3y6y9y14	1551.94	96.908	19889	2	776.47	1.73

P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	4		LVTYQTDANGQPVNQILVEAATDI GKELYLGAVVDR	80	36	13	63.13	b2b7b8°b8b10b13y1y3y4y6y7y8y36	3874.05	120.889	19598	3	1292.02	6.74
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	5		IILSDDNVK	303	9	7	38.27	b2y5°y5y6y7°y7y9	1016.56	42.919	19356	2	508.78	-5.16
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	6		LHGGEPANFLDVGGGATK	277	18	4	13.5	b7°b10*b10b15	1739.85	58.312	11527	3	580.62	-10.45
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	7		LEGNNAELGAK	348	11	3	31.29	y5y9y10	1115.57	28.191	20814	2	558.29	-0.22
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	8		LGADGNALFR	215	10	5	40.13	b4°b4b8b9y8	1033.54	31.200	9786	2	517.28	1.65
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	9		VAEETPHLIHK	135	11	3	36.07	b5b7b10	1273.68	59.969	2199	3	425.23	-4.98
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	10		AFAENWL GK	70	9	7	61.7	b3b4b5*b5b6y6*y6	1035.51	38.369	1547	2	518.26	-17.92
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	11		LHGGEPANFLDVGGGATKER	277	20	4	30.75	b4b10b12b13	2025.00	79.619	15460	3	675.67	-8.20
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	12	Oxidation+M(4)	VVFMASTEGGVEIEK	120	15	4	24.16	b11y9y10°y10	1611.77	86.413	2251	3	537.93	-13.10
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	13		LHGGEPANFLDVGGGAT	277	17	1	7.34	y12	1611.78	58.365	2628	2	806.39	-0.23
P0A1P6 GLNA_SALTY Glutamine synthetase	1		LVPGYEAPVMLAYSAR	322	16	6	51.89	b15y4y5y9y11y14	1736.92	76.659	53230	2	868.96	6.89
P0A1P6 GLNA_SALTY Glutamine synthetase	2	Carbamidomethyl+C(1)	CDILEPGTLQGYDRDPR	89	17	8	36.73	b2b3b10b12*b12b15y1y2	2004.94	58.891	50177	3	668.98	-2.80
P0A1P6 GLNA_SALTY Glutamine synthetase	3		AINALANPTTNSYKR	307	15	9	59.35	b3*b3b11y7°*y7y8y9y10y15	1633.86	41.584	35548	3	545.29	-2.24
P0A1P6 GLNA_SALTY Glutamine synthetase	4		GGYFPVPPVDSAQDIR	177	16	10	56.16	b2b3b4b6b14y2y6y10y11y16	1717.87	69.060	33567	2	859.44	7.96
P0A1P6 GLNA_SALTY Glutamine synthetase	5		EIPQVAGSLEEALNALDLDR	406	20	5	14.37	b11y10y13°y13y20	2153.09	95.066	24339	3	718.37	-6.69
P0A1P6 GLNA_SALTY Glutamine synthetase	6		ATGIADTVLFGPEPEFFLDDIR	117	23	16	64.53	b3°b3b4°b4b6b13°b13y1y2y4y5y8y9°y9y13y23	2570.28	116.642	17352	3	857.43	-0.76
P0A1P6 GLNA_SALTY Glutamine synthetase	7		FGASISGSHVAIDDIEGAWNSSTK	140	24	7	32.9	b4b14y5y6y8y12y24	2449.15	75.788	16449	3	817.05	-6.98
P0A1P6 GLNA_SALTY Glutamine synthetase	8		GINESDMVLPDASTAVIDPFFADSTLIIR	59	30	11	52.84	b9°b9b10*b10y2y3y4y7y8y11y30	3238.62	112.941	16358	3	1080.21	4.98
P0A1P6 GLNA_SALTY Glutamine synthetase	9		AINALANPTTNSYK	307	14	3	27.86	y7y9y13	1477.76	46.712	12099	2	739.39	-0.91
P0A1P6 GLNA_SALTY Glutamine synthetase	10		EIPQVAGSLEEALNALDLREFLK	406	24	11	47.75	b2b5b8b10°b10b12b13°b13y11y13y20	2670.40	111.642	12034	3	890.80	-0.91
P0A1P6 GLNA_SALTY Glutamine synthetase	11		MTPHPVEFELYYSV	455	14	3	19.29	b5y4y12	1711.83	66.423	7144	3	571.28	13.12
P0A1P6 GLNA_SALTY Glutamine synthetase	12		AGGVFTDEAIDAYIALR	430	17	3	23.72	b9b12b16	1781.90	91.597	4535	2	891.45	-3.15
P0A1P6 GLNA_SALTY Glutamine synthetase	13		ADEIQIYK	232	8	5	40.87	b4°b4b5°b5b6	979.52	60.911	17257	2	490.26	6.29
P0A1P6 GLNA_SALTY Glutamine synthetase	14		YAGLSEQALYYIGGVIK	287	17	3	24.97	b4b5b13	1845.01	77.141	10608	2	923.01	16.34

[P0A1P6 GLNA_SALTY Glutamine synthetase	15	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	7	27.59	b15°b15*b15b16b23y4y6	2565.32	136.534	10256	2	1283.16	12.56
[P0A1P6 GLNA_SALTY Glutamine synthetase	16		MSAEHVLTMLNEHEVK	0	16	4	17.16	b8°b8y5y8	1867.92	86.893	8138	2	934.46	7.71
[P0A1P6 GLNA_SALTY Glutamine synthetase	17		IHPGEAMDK	386	9	3	30.49	b8y3y6	997.45	26.670	5246	2	499.23	-22.33
[P0A1P6 GLNA_SALTY Glutamine synthetase	18		SAEHVLTMLNEHEVK	1	15	3	18.14	b3y5y10	1736.84	55.579	4570	4	434.97	-13.35
[P0A1P6 GLNA_SALTY Glutamine synthetase	19		EQHVTIPAHQVNAEFFEEGK	28	20	4	14.37	b4y5°y5y19	2310.13	60.974	2983	4	578.29	7.29
[P0A1P6 GLNA_SALTY Glutamine synthetase	20		FNTMTK	225	6	1	13.62	b5	741.35	30.405	2440	1	741.35	-13.50
[P0A1P6 GLNA_SALTY Glutamine synthetase	21		FGASISGSHVAIDIEGAWNSSTK YEGGNK	140	30	4	21.97	b5b7b8y3	3097.46	51.018	37198	3	1033.16	4.65
[P0A1P6 GLNA_SALTY Glutamine synthetase	22		EFLKAGGVTFDEAIDAYIALR	426	21	3	13.88	b7b13y11	2299.17	73.341	16163	3	767.06	-12.00
[P0A1P6 GLNA_SALTY Glutamine synthetase	23		GKEQHVTIPAHQVNAEFFEEGK	26	22	3	19.95	y5y9y20	2495.23	106.342	15995	3	832.42	0.29
[P0A1P6 GLNA_SALTY Glutamine synthetase	24		NGTNLFSGDKYAGLSEQALYYIG GVIK	277	27	5	25.89	b3*b3b5b10b14	2878.49	110.869	11397	3	960.17	8.31
[P0A1P6 GLNA_SALTY Glutamine synthetase	25		VRMTPHPVEFELYYSV	453	16	3	23.69	b8b9y11	1966.97	61.350	3005	2	983.99	-4.16
[P0A1P6 GLNA_SALTY Glutamine synthetase	26		MSAEHVLTMLNEHEVKFVDLR	0	21	4	22.33	b11*b11b12y10	2498.28	133.722	2404	3	833.43	10.65
[P0A1P6 GLNA_SALTY Glutamine synthetase	27	Phosphoryl STY(7)	SAEHVLTMLNEHEVK	1	15	4	18.14	b5b12_HPO3 b12y7°y7	1816.82	69.071	35357	2	908.91	-1.48
[P0A1P6 GLNA_SALTY Glutamine synthetase	28	Phosphoryl STY(6)	AGGVTFDEAIDAYIALR	430	17	3	16.32	b3b5y11	1861.87	69.730	2015	3	621.29	2.82
[P0A1P6 GLNA_SALTY Glutamine synthetase	29	Carbamidomethyl+C(4); Oxidation+M()	SEMCLVMEQMGLVVEAHHHEVA TAGQNEVATR	193	32	5	16.96	y9y11°y11y14°y14	3579.69	96.535	5866	3	1193.90	12.96
[P0A1P6 GLNA_SALTY Glutamine synthetase	30	Carbamidomethyl+C(11);Oxidation+M(17)	FPDPAANPYLCFAALLMAGLDGIK	360	24	3	23	b5b6b8	2581.29	85.384	4620	3	861.10	1.99
[P0A1P6 GLNA_SALTY Glutamine synthetase	31		AINALANPTTNSY	307	13	0	4.04		1349.69	41.640	23544	3	450.57	12.75
[P0A1P6 GLNA_SALTY Glutamine synthetase	32		NALANPTTNSYKR	309	13	1	7.26	b8	1449.75	41.554	3105	2	725.38	0.84
[P0A1P6 GLNA_SALTY Glutamine synthetase	33	Carbamidomethyl+C(1)	CDILEPGTLQGYDRDPR	89	17	0	4.85		1986.93	58.887	2818	3	662.98	-0.61
[P60446 RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	11	74.35	b2°b2b4°b4y2y3y5y6y7y8y10	1115.64	55.374	84796	2	558.32	-5.03
[P60446 RL3_SALTY 50S ribosomal protein L3	2		IFTEDGVSIPTVIEVEANR	13	20	12	60.32	b2b5b7b9y4y5y6°y6y11y13*y13y20	2188.17	87.413	46586	2	1094.59	10.26
[P60446 RL3_SALTY 50S ribosomal protein L3	3	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	7	37	b12y1y4y6y8y15y18	1738.93	52.876	27889	3	580.32	-10.46
[P60446 RL3_SALTY 50S ribosomal protein L3	4		VTKPEAGHFAK	59	11	5	36.73	b2b7b8b10y6	1184.63	23.397	3551	2	592.82	-11.33
[P60446 RL3_SALTY 50S ribosomal protein L3	5		LAEGEETYVGQSIGVELFADV K	83	22	3	13.44	b6b11y9	2384.20	136.273	2736	3	795.41	7.07
[P60446 RL3_SALTY 50S ribosomal protein L3	6		LAEGEETYVGQSIGVELFADV K K	83	23	3	19.46	b8b11b14	2512.27	89.489	1789	4	628.82	-5.64
[P60446 RL3_SALTY 50S ribosomal protein L3	7		NLLLVK	184	6	3	40.07	b3y3y4	699.48	55.187	22536	1	699.48	-1.05
[P60446 RL3_SALTY 50S ribosomal protein L3	8		GLWEFR	77	6	1	13.62	y4	807.41	68.778	16819	2	404.21	-6.58
[P60446 RL3_SALTY 50S ribosomal protein L3	9		VGMTR	8	5	1	13.22	y3	563.29	48.976	16343	1	563.29	-4.77
[P60446 RL3_SALTY 50S ribosomal protein L3	10		TQDATHGNSLSHR	128	13	5	58.54	y3y4y5y7y11	1423.65	14.799	14277	3	475.22	-13.55

[P60446]RL3_SALTY 50S ribosomal protein L3	11		MAGQMGNER	160	9	4	38.27	y4y6°y6y7	993.44	19.676	8596	2	497.22	14.19
[P60446]RL3_SALTY 50S ribosomal protein L3	12		VDAER	179	5	1	13.22	y4	589.29	66.420	1691	1	589.29	-14.60
[P60446]RL3_SALTY 50S ribosomal protein L3	13	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	9	74.65	b3b8b9y5y7y8y12y13y16	1809.98	55.112	65174	3	604.00	-7.22
[P60446]RL3_SALTY 50S ribosomal protein L3	14		IFTEDGVSPVTVIEVEANRVTVK	13	25	3	12.41	b7y16y18	2743.49	94.226	22946	3	915.17	0.27
[P60446]RL3_SALTY 50S ribosomal protein L3	15		VTVQSLDVVRVDAER	169	15	5	18.14	b5°b5b7y3°y3	1685.91	103.741	3355	2	843.46	-6.37
[P60446]RL3_SALTY 50S ribosomal protein L3	16		WNFRTQDATHGNSLSHR	124	17	4	16.32	b8y8y10°y10	2026.94	51.797	2540	3	676.32	-11.50
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	1		NLTGFWIMPDTGFSDDADLK	491	21	8	13.88	b2b6b8°b8°b8y2y13y21	2390.13	106.184	36878	2	1195.57	10.52
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	2		DIGFHPVGTGPYQLETWNQTDV K	176	24	7	50.35	b9b10b11y7y9y10y24	2749.35	82.334	23236	3	917.12	7.81
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	3		FQDGADFNAAVK	97	13	8	50.3	b2b3y5y6y10y11°y11y13	1353.65	48.405	20335	2	677.33	3.34
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	4		ITAMDAGQR	379	9	4	30.49	b2b4y7y8	962.47	28.192	16956	2	481.74	-6.47
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	5		LDSITWRPVTDNNT	214	15	6	36.71	y4°y4y11°y11y13y14	1787.90	55.624	15958	3	596.64	-2.05
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	6		TEVVDPATVK	134	10	12	75.32	b1b2°b2b6°b6b7y2y5y6y8y 9y10	1058.57	37.904	15781	2	529.79	-4.04
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	7		AAMLQTGEAQFAPIPYEAALLA K	229	25	4	27.87	b3b4b6b9	2679.40	96.355	15588	3	893.80	4.10
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	8		ELLKEAGYPDGFSTTLWSSHNS TAQK	335	27	3	21.91	b9b10y6	3004.41	65.232	10042	4	751.86	-10.24
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	9		NLELVASPSIMQR	256	13	5	20.64	b1b3°b3y6y12	1457.76	59.337	5849	3	486.59	-11.97
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	10		NVLAEGYTVSDDGLTYTITLR	72	21	6	20.52	b5°b5b7b10°b10°b10	2301.17	86.824	2341	4	576.05	2.55
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	11		YISMNVTQKPFDNPK	269	15	7	52.36	b4b5b9°b9b10°b10b12	1781.92	75.273	12171	3	594.64	15.21
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	12		FAGYWQQGLPK	203	11	5	38.32	b3b4y6°y6y10	1294.64	43.603	1667	3	432.22	-16.59
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	13		QALVKVAFAGYATPATGVVPPSI AYAQSYQPWPYPDAK	295	38	4	16.47	y5y8y12°y12	4023.05	82.287	12747	4	1006.52	-5.70
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	14		DIGFHPVGTGPYQLETWNQTDV KVK	176	26	3	12.14	b7b12y10	2976.48	55.594	9830	4	744.88	-2.71
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	15		QGVKFQDGADFNAAVK	93	17	3	16.32	b10y5y12	1765.87	78.261	9284	2	883.44	-7.95
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	16		SFYQGLFGLDKDMK	56	14	11	91.83	b3b4°b4b8b10b12°b12y3y 7y8y13	1648.80	68.201	7015	2	824.90	-1.78
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	17		ASNPDNHLKR	115	10	3	33.9	y3y6y7	1151.59	14.517	4770	2	576.30	-3.39
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	18		QVDSDLAAALKTNDPQEK	442	18	6	26.58	b3y8°y8y9°y9y13	1942.97	82.739	2068	3	648.33	-0.57
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	19		YGKDIGHFPVGTGPYQLETWNQT DFVK	173	27	4	15.33	b4b7y5y10	3097.47	132.457	1602	3	1033.16	-12.53
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	20	Phosphoryl STY(15)	YGKDIGHFPVGTGPYQLETWNQT DFVK	173	27	3	11.91	b8b13y12	3177.43	78.385	4250	3	1059.81	-10.68
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	21	Phosphoryl STY(8)	TEVVDPATVK	134	10	4	28.67	b6°b6y4y5	1138.53	96.034	3922	1	1138.53	1.50
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	22	Phosphoryl STY(7)	NLELVASPSIMQR	256	13	4	20.64	b3b6°b6y6	1537.73	52.114	2177	2	769.37	-0.08
[Q8ZQM3]GSIB_SALTY Glutathione-binding protein gSiB	23	Oxidation+M(13)	SFYQGLFGLDKDMK	56	14	4	19.29	b12y3y12°y12	1664.80	136.530	4517	1	1664.80	1.76

P66593 RS6_SALTY 30S ribosomal protein S6	1		AHYVLMNVEAPQEVIDELETTFR	56	23	7	23.8	b2b10y2y4y5°y5y13	2704.32	110.039	160701	3	902.11	-1.99
P66593 RS6_SALTY 30S ribosomal protein S6	2		YSAAITGAEGK	24	11	12	73.97	b2°b2b3°b3b11y2y3y4y5y7y9y11	1067.53	32.331	90118	2	534.27	-6.29
P66593 RS6_SALTY 30S ribosomal protein S6	3		FNDAVIR	79	7	6	63.9	b5y3y4y5y6y7	834.44	40.868	79762	2	417.72	-10.24
P66593 RS6_SALTY 30S ribosomal protein S6	4		HYEIVFMVHPDQSEQVPGMIER	2	22	5	23.31	b6°b6b8b9°b9	2641.22	37.305	3656	3	881.08	-13.31
P66593 RS6_SALTY 30S ribosomal protein S6	5		LEDWGR	38	6	3	43.08	b3y3y5	775.38	37.249	2630	1	775.38	13.70
P66593 RS6_SALTY 30S ribosomal protein S6	6		SMVMR	86	5	2	13.22	b4°b4	623.30	94.030	1952	1	623.30	-0.88
P66593 RS6_SALTY 30S ribosomal protein S6	7		HYEIVFMVHPDQSEQVPGMIERYSAAITGAEGK	2	33	5	11.06	b7°b7b22°b22y3	3689.72	101.845	8433	4	923.19	-13.70
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	1		TAGLDSSQGPTAAK	139	14	12	80.95	b5°b5b10b12y5y6°y6y8y10°y10y12y14	1303.65	27.851	40919	2	652.33	0.75
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	2		TQFMGPEGVGNASLSNIAGGAAEGMLVTMPK	242	31	13	38.38	b2°b2b3b4°b4b9y1y2y3y4y10y13y31	3035.47	91.889	31994	3	1012.49	2.25
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	3		GYQYIMR	132	7	5	40.47	b3y2y4y6*y6	930.46	46.395	29491	2	465.73	9.77
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	4		LQKENIDFVYYGGYYPEMGMLR	211	23	7	28.24	b9°b9b12°b12y9y10y12	2814.34	84.169	26198	3	938.79	5.90
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	5		QGNANIVFFDGITAGEK	186	17	4	23.72	b8b12°b12b16	1780.87	66.810	4941	2	890.94	-8.84
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	6		VAIVGAMSGPVAQWGDMEFNGAR	27	23	6	31.63	b3b8b15y5y7y15	2363.17	86.656	52136	3	788.40	19.63
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	7	Carbamidomethyl+C(10)	LVGVEYDDACDPK	66	13	3	20.64	b6y9y11	1480.67	45.784	22900	2	740.84	5.77
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	8		ENIDFVYYGGYYPEMGMLR	214	20	4	23.79	y7*y7y8y12	2445.13	89.821	11006	2	1223.07	15.58
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	9		SASHAPLDLVK	316	11	4	36.07	b4b7b9°b9	1137.60	36.429	4581	2	569.30	-22.32
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	10		WDEK	342	4	1	12.82	y3	577.26	74.717	4229	1	577.26	1.16
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	11		GFEFGVFQWHADGSSTVAK	350	19	3	24.11	y8y11y12	2069.97	57.858	2357	3	690.66	-1.06
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	12		RYDQDPANK	273	9	3	30.49	b3b5y4	1106.52	15.266	7740	2	553.76	-6.51
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	13		LQKENIDFVYYGGYYPEMGMLR	211	23	3	13.05	b10b12y6	2814.35	86.558	4165	3	938.79	6.85
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	14		QQYGEGLARSVQDGLK	170	16	3	25.53	b3b8b9	1748.91	78.285	3473	2	874.96	9.21
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	15		ANGADTVIGPLKWDEK	330	16	6	41.31	b5b8b10°b10y5y6	1713.86	40.851	1582	2	857.43	-13.25
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	1		TQNAPVATPQELADYDAIIFGTPT R	54	25	9	33.43	b2b9°b9b11b24y6y7y21y25	2689.36	89.162	20447	3	897.12	4.45
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	2		LGSVFSSTGTGGGQEQTITSTWTT LAHHGMVIVPIGYAAQELFDVSQ VR	106	49	22	116.24	b2b4b7b11b12b14y2y3y4y5y6y7°y7y8*y8y9*y9y10*y10y12°y12y49	5134.57	115.779	16647	4	1284.40	2.95
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	3		FGNMSGQMR	79	9	8	45.47	b2b3°b3y2y4y5y6y9	1027.46	37.173	11113	2	514.23	12.59
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	4		VPETMPPEIFAK	38	12	4	35.5	b5b6°b6b7	1358.70	47.003	9923	2	679.85	-2.96
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	5		TFLDQTGGLWASGSLYGK	88	18	5	24.82	b5°b5y3y7y10	1900.95	71.907	9751	3	634.32	0.96
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	6		GGTPYGATTIAGGDGSR	155	17	5	34.01	b5b6b14y6y10	1537.72	39.573	2755	2	769.37	-0.40

Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	7		GGTPYGATTIAGGDGSRQPSQEEL SIAR	155	28	4	22.33	b14y3y8y9	2776.31	136.440	2597	2	1388.66	-12.49
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	8		TQNAPVATPQELADYDAI	54	18	0	8.08		1916.93	89.177	4046	3	639.65	2.23
Q7CPZ4 GRPE_SALTY Protein grpE	1		FVNELLPVIDSLDR	90	14	5	33.02	b4b6*b6y8y9	1629.89	96.157	31142	2	815.45	1.35
Q7CPZ4 GRPE_SALTY Protein grpE	2		IANLEVQLAEAQTR	43	14	8	45.27	b1b10b11y5°y5y10y12	1555.85	62.245	11793	2	778.43	6.83
Q7CPZ4 GRPE_SALTY Protein grpE	3		TPEGQAPEEIIIMDQHEEVEAVEPN DSAEQVDPR	7	33	6	17.82	b10b15y3°y3y7y9	3688.66	101.864	8364	5	738.54	1.39
Q7CPZ4 GRPE_SALTY Protein grpE	4		AAMVTVAK	186	8	3	33.09	b6y6y7	790.43	31.194	6957	2	395.72	-22.24
Q7CPZ4 GRPE_SALTY Protein grpE	5		ALEVADKANPDMAAMVEGIELTL K	104	24	3	12.71	b11b15y13	2529.31	96.451	9535	3	843.78	7.43
Q7CPZ4 GRPE_SALTY Protein grpE	6		IKAEMENLR	64	9	5	44.96	b6°b6b7y5y7	1103.60	45.605	8263	2	552.30	10.40
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	1		AIPNYNVMLAK	151	12	7	34.25	b7*b7b9*b9b10y3y12	1290.69	56.689	27863	2	645.85	3.78
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	2		FDGFVHSIGFAPGDQLDGDYVNA VTR	84	26	8	32.61	b2b3°b3b11b14y9y10y12	2797.34	81.615	14250	3	933.12	4.89
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	3		VNAISAGPIR	183	10	4	28.67	b2b3y6y7	997.57	43.084	12720	2	499.29	-5.81
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	4		LSIAYGIAQAMHR	17	13	7	46.12	b2°b2b13y3y4y7y8	1430.74	69.725	8321	3	477.59	-8.79
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	5		VAHDISSYSFVAMAK	114	15	4	25.8	b4b10y4y8	1625.78	75.999	3743	2	813.39	-12.84
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	6	Carbamidomethyl+C(5)	MLAHCEAVTPIR	205	12	4	22.28	b4b11y10y12	1397.69	65.317	1849	3	466.57	-7.16
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	7		YMANAMGPEGVR	171	12	4	34.25	b3b4b8y4	1295.58	85.855	6183	2	648.29	-3.86
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	8		TMLNPGSALLTLSYLGAER	132	19	7	35.11	b8y4°y4y7°y7y9y15	2007.05	100.434	3256	3	669.69	-5.41
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	9		LSIAYGIAQAMHREGAELAFYQNDK	17	26	6	22.81	b6b12°b12b13y8°y8	2897.45	106.224	98603	4	725.12	6.99
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	10		EGFKVAHDISSYSFVAMAK	110	19	6	23.66	b8°b8b10b13°b13y13	2087.00	122.353	2096	2	1044.00	-12.63
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	11	Carbamidomethyl+C(17)	VAHDISSYSFVAMAKACR	114	18	4	15.58	b8°b8b12y11	2012.96	102.230	2041	2	1006.98	-2.91
P16657 FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	12	Oxidation+M(11)	LSIAYGIAQAMHR	17	13	3	25.41	b9y7y8	1446.74	42.123	4091	2	723.87	-11.48
P61179 RL22_SALTY 50S ribosomal protein L22	1		IFVDEGPSMK	73	10	8	51.89	b2y5y7y8°y8y9°y9y10	1122.55	49.828	42066	2	561.78	-3.48
P61179 RL22_SALTY 50S ribosomal protein L22	2		LVADLIR	18	7	6	40.47	b2b3y2y3y5y7	799.49	56.123	24714	2	400.25	-11.15
P61179 RL22_SALTY 50S ribosomal protein L22	3		IFVDEGPSMKR	73	11	3	36.07	y7y8y9	1278.66	43.596	8711	2	639.83	7.06
P61179 RL22_SALTY 50S ribosomal protein L22	4		VLESAIANAEHNDGADIDDLK	49	21	3	13.88	b3y3y5	2210.04	60.066	4407	3	737.35	-9.61
P61179 RL22_SALTY 50S ribosomal protein L22	5	Phosphoryl STY(5)	TSHITVVVSDR	99	11	4	24.31	b3°b3b10y5	1293.59	54.176	351514	2	647.30	-14.53
P61179 RL22_SALTY 50S ribosomal protein L22	6		IFVDEGPSMKR	73	11	1	7.86	b8	1260.64	43.543	5540	2	630.82	1.36
Q7CPL4 RL16_SALTY 50S ribosomal protein L16	1		VLYEMDGVPEELAR	100	14	11	84.14	b1b4b8y3y6y8y9y10y11°y11y14	1620.80	68.766	67886	2	810.91	6.10
Q7CPL4 RL16_SALTY 50S ribosomal protein L16	2		GNVEYWVALIQPGK	86	14	7	24.73	b2b4°b4b5y2y3y14	1573.83	86.373	9606	2	787.42	-3.65
Q7CPL4 RL16_SALTY 50S ribosomal protein L16	3		TTFVTK	127	6	1	13.62	b5	696.40	21.951	8430	1	696.40	9.82

Q7CPL4 RL16_SALTY 50S ribosomal protein L16	4		GNVEYWVALIQPGKVLVEMDGV PEELAR	86	28	11	54.19	b5b8*b8b9y6°y6y8y9°y9y1y12	3175.58	89.010	2424	4	794.65	-11.76
P65882 PURA_SALTY Adenylosuccinate synthetase	1	Carbamidomethyl+C(7)	LLLSEACPLILDYHVALDNAR	97	21	12	79.05	b2b3b8b19y3y5y6y11y12*y12y14y19	2396.25	90.884	31172	3	799.42	-4.79
P65882 PURA_SALTY Adenylosuccinate synthetase	2		GVEPIYETMPGWSESTFGVK	367	20	11	63.66	b3b4°b4b7b8°b8b9b13y7°y7y13	2214.07	99.291	22470	2	1107.54	14.22
P65882 PURA_SALTY Adenylosuccinate synthetase	3		GNNVVVLGTQWGDEGK	1	16	4	17.16	b5*b5b10y6	1672.82	81.131	14072	3	558.28	-2.99
P65882 PURA_SALTY Adenylosuccinate synthetase	4		VLDDTMAVADILTSMVVDVSDLL DQAR	186	27	11	68.38	b5b6b8b11y3y4y5y7y8°y8y27	2905.47	138.242	6350	3	969.16	4.20
P65882 PURA_SALTY Adenylosuccinate synthetase	5		EVMEYHNFQLVNYYK	163	15	5	37.84	b10*b10b11y9y10	1976.94	83.542	3534	3	659.65	10.06
P65882 PURA_SALTY Adenylosuccinate synthetase	6		VGDLFDKETFAEK	148	13	7	47.29	b4b5b6°b6b10y2y5	1498.74	51.044	3451	3	500.25	0.33
P65882 PURA_SALTY Adenylosuccinate synthetase	7		GVEPIYETMPGWSESTFGVKDR	367	22	3	22.19	b11b12y9	2485.19	81.514	2350	2	1243.10	8.84
P65882 PURA_SALTY Adenylosuccinate synthetase	8		EVTTTPLAADDWK	354	13	3	29.88	b4b8b11	1446.71	75.253	32850	2	723.86	2.62
P65882 PURA_SALTY Adenylosuccinate synthetase	9		IEELTGVPIDIISTGPDR	402	18	6	26.58	b7b8°b8b13y6°y6	1924.99	86.906	19573	3	642.33	-17.69
P65882 PURA_SALTY Adenylosuccinate synthetase	10	Carbamidomethyl+C(19)	VGAGPFPTELFDETGEFLCK	273	20	4	14.37	b13y5y10°y10	2214.08	114.907	2195	4	554.28	18.42
P65882 PURA_SALTY Adenylosuccinate synthetase	11	Carbamidomethyl+C(2)	LCVAYR	343	6	2	26.85	b5y3	781.40	41.676	2112	2	391.20	-3.12
P65882 PURA_SALTY Adenylosuccinate synthetase	12		ETFAEK	155	6	1	13.62	y5	724.34	98.433	1790	1	724.34	-10.36
P65882 PURA_SALTY Adenylosuccinate synthetase	13		EVTTTPLAADDWKGVVEPIYETMP GWSESTFGVK	354	33	4	24.43	b4b5y6y11	3641.76	92.404	6035	3	1214.59	7.31
P65882 PURA_SALTY Adenylosuccinate synthetase	14		GIGPAYEDKVAR	132	12	4	22.28	b3b9y10°y10	1275.66	70.457	5195	2	638.33	-5.84
P65882 PURA_SALTY Adenylosuccinate synthetase	15	Carbamidomethyl+C(2)	LCVAYRMPDGR	343	11	3	24.31	b4y4y10	1337.66	61.640	4655	2	669.33	11.13
P65882 PURA_SALTY Adenylosuccinate synthetase	16		LKEVMEYHNFQLVNYYK	161	17	4	22.93	b10b12y6y9	2218.13	46.872	2572	2	1109.57	14.64
P65882 PURA_SALTY Adenylosuccinate synthetase	17		YVVRYQGGHNAGHTLVINGEK	29	21	4	23.53	b7b9b10°b10	2312.18	99.879	1605	3	771.40	-5.60
P65882 PURA_SALTY Adenylosuccinate synthetase	18	Phosphoryl STY(14)	ENVTSIIGNGVVLSPSALMK	62	20	4	14.37	b10°b10b14y5	2109.05	102.107	3203	3	703.69	-2.08
P65882 PURA_SALTY Adenylosuccinate synthetase	19	Oxidation+M(19)	ENVTSIIGNGVVLSPSALMKEMK	62	23	4	20.12	b10y3y5y12	2433.24	87.456	21008	2	1217.12	-14.65
P65882 PURA_SALTY Adenylosuccinate synthetase	20	Oxidation+M(1)	MPDGREVTTTPLAADDWK	349	18	5	24.82	b10b14°b14b17y9	2018.95	66.792	8402	3	673.66	1.33
P65882 PURA_SALTY Adenylosuccinate synthetase	21	Oxidation+M(2)	EMKELEDR	82	8	6	67.31	b3b4b6y3°y3y6	1065.49	22.019	7967	2	533.25	1.49
P65882 PURA_SALTY Adenylosuccinate synthetase	22	Oxidation+M(1)	MGNNVVVLGTQWGDEGK	0	17	3	16.32	b6b9y4	1819.86	58.906	5593	3	607.29	-3.09
P65882 PURA_SALTY Adenylosuccinate synthetase	23	Oxidation+M(15)	VLDDTMAVADILTSMVVDVSDLL DQAR	186	27	3	22.76	b4b7b8	2921.49	122.076	5372	3	974.50	13.37
Q8ZR01 RLPA_SALTY Rare lipoprotein A	1		LSQQFSVPGR	329	10	7	71.8	b4°b4b5b6y4y5y6	1118.59	46.484	15710	2	559.80	-0.44
Q8ZR01 RLPA_SALTY Rare lipoprotein A	2		LQTEAQLQSFIASAQ	366	15	6	14.92	b3°b3°b3b9°b9b10°	1634.84	64.289	2910	2	817.93	2.69
Q8ZR01 RLPA_SALTY Rare lipoprotein A	3		YEPLNPTANQDYQR	51	14	4	27.86	y4y6y9*y9	1708.80	45.781	3594	2	854.90	5.57
Q8ZR01 RLPA_SALTY Rare lipoprotein A	4		INDRGPYGTDR	135	11	3	31.29	b5b9b10	1263.61	41.993	17909	2	632.31	4.06
Q8ZR01 RLPA_SALTY Rare lipoprotein A	5		AAADRLNTSNNTK	152	13	3	20.64	b8b12y11	1375.67	77.758	5688	2	688.34	-14.64

[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	1		SFELPALPYAK	1	11	4	24.31	b3y2y4y7	1235.67	78.192	56553	2	618.34	-0.69
[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	2		SLEEIVR	51	7	6	50.68	b3°b3y4y5y6y7	845.47	47.239	25982	2	423.24	-9.02
[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	3	Carbamidomethyl+C(22)	TSEGGIFNNAAQVWNHTFYWNCL APNAGGEPTGK	58	34	14	29.38	b2°b2b10°b10*b10y2y4y7° y7y9y10y13*y13y34	3708.72	95.551	24190	3	1236.91	6.58
[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	4		NARPNYLEHFWALVNWEFVAK	168	21	10	36.24	b2b3b4*b4b6b14y1y8y15y 21	2604.30	103.770	14116	3	868.77	-4.59
[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	5		DALAPHISAETLEYHYGK	12	18	3	22.98	b3b4y7	2014.96	86.797	17893	2	1007.99	-11.63
[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	6		LADAIAASFGSFAEFK	92	16	3	17.16	b11b14y11	1644.85	64.884	17809	2	822.93	16.92
[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	7		HHQTYVTNLNLIKGTAFEGK	30	21	3	13.88	b5y3y7	2385.20	85.775	10235	3	795.74	-14.13
[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	8		SFELPALPYAKDALAPHISAETLEY HYGK	1	29	6	14.52	b6°b6b26y6y12°y12	3231.64	93.932	3782	4	808.66	0.23
[P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	9		GTAFEGKSLEEIVR	44	14	3	27.86	b4b7b11	1535.83	90.665	2172	3	512.61	13.59
[P60726 RL4_SALTY 50S ribosomal protein L4	1		DATGIDPVSLIAFDK	170	15	7	25.8	b2b3b5y1y3y10y15	1561.82	87.344	31439	2	781.41	5.55
[P60726 RL4_SALTY 50S ribosomal protein L4	2		VVMTADAVK	185	9	6	54.5	b2y4y5°y5y6y7	933.50	35.571	26562	2	467.26	-3.07
[P60726 RL4_SALTY 50S ribosomal protein L4	3		DFNEALVHQVVVAYAAGAR	21	19	5	31.63	b7b11y4y6y7	2030.04	82.726	21466	3	677.35	-2.04
[P60726 RL4_SALTY 50S ribosomal protein L4	4		QVEEMLA	194	7	6	40.47	b4°b4b6*b6y5y7	819.39	50.367	17622	1	819.39	-4.25
[P60726 RL4_SALTY 50S ribosomal protein L4	5		SGGVTFARPQDHSQK	79	16	4	30.8	b3b8y10y11	1685.81	59.359	25708	3	562.61	-12.89
[P60726 RL4_SALTY 50S ribosomal protein L4	6		MELVLK	0	6	2	26.85	b3y4	732.43	54.151	9201	2	366.72	-9.75
[P60726 RL4_SALTY 50S ribosomal protein L4	7		SGGVTFARPQDHSQKVNK	79	19	3	14.94	b3b6y11	2027.02	135.287	116020	2	1014.01	-11.20
[P60726 RL4_SALTY 50S ribosomal protein L4	8		DATGIDPVSLIAFDKVVMTADAV K	170	24	8	42.2	b3°b3b4°b4y3y6y7y19	2476.31	101.316	32753	3	826.11	4.54
[P60726 RL4_SALTY 50S ribosomal protein L4	9		SPIWRSGGVTFARPQDHSQK	74	21	4	18.93	b7b10y4y13	2325.20	56.721	3831	2	1163.10	4.62
[P60726 RL4_SALTY 50S ribosomal protein L4	10		MELVLKDAQSALTVSETTFGR	0	21	3	13.88	b7y9y12	2296.16	99.265	1688	2	1148.58	-12.23
[P60726 RL4_SALTY 50S ribosomal protein L4	11	Phosphoryl STY(13)	VDVRDATGIDPVSLIAFDK	166	19	5	20.7	b7°b7b11y5y13	2111.06	47.298	2425	3	704.36	13.76
[P66541 RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAEUNK	45	14	8	19.29	b1b2b8*b8b10y12°y12*y1 2	1576.81	83.609	79523	2	788.91	5.03
[P66541 RS2_SALTY 30S ribosomal protein S2	2		WLGGMMLTNWK	95	10	6	28.67	b1b6y7y8°y8y10	1205.61	84.626	52528	2	603.31	-3.95
[P66541 RS2_SALTY 30S ribosomal protein S2	3		EANNLGIPVFAIVDNTSDPDGVDF VIPGNDDAIR	174	34	17	65.97	b5b7°b7°b7b8°b8b15°b15 y1y4y6y7y8y11y14y16y34	3569.76	103.815	24160	3	1190.59	6.09
[P66541 RS2_SALTY 30S ribosomal protein S2	4		LENSLGGIKDMGGLPDALFVIDAD HEHIAIK	143	31	3	22.04	b3b4y13	3288.70	100.188	1572	3	1096.90	0.59
[P66541 RS2_SALTY 30S ribosomal protein S2	5		DMGGLPDALFVIDADHEHIAIK	152	22	4	37.15	b6b10b11b12	2377.15	98.068	181754	2	1189.08	-13.76
[P66541 RS2_SALTY 30S ribosomal protein S2	6		AGVHFHGQTR	11	10	6	40.13	b8y3°y3y4y8*y8	1109.58	55.322	10593	2	555.30	22.11
[P66541 RS2_SALTY 30S ribosomal protein S2	7	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	4	24.73	b4y8°y8y9	1694.77	65.677	10556	3	565.60	21.97
[P66541 RS2_SALTY 30S ribosomal protein S2	8		SQDLASQAEEESFVEAE	225	16	4	17.16	b8°b8y10y12	1739.78	72.249	9846	2	870.39	9.61

P66541 RS2_SALTY 30S ribosomal protein S2	9		LENSLGGIK	143	9	3	30.49	b4b8y3	930.51	65.242	1641	2	465.76	-17.12
P66541 RS2_SALTY 30S ribosomal protein S2	10	Carbamidomethyl+C(6)	EAANSCDQFFVNHRWLGGMLTNWK	81	24	3	12.71	b5y7y9	2881.35	93.034	7179	3	961.12	5.85
P66541 RS2_SALTY 30S ribosomal protein S2	11	Oxidation+M(11)	LENSLGGIKDMGGLPDALFVIDADHEHIAIK	143	31	4	11.25	b7°b7b10y12	3304.69	102.170	30145	4	826.93	0.81
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	1		SPFVTSGIR	354	9	6	54.5	b1y3y5y6y7y9	963.52	47.886	58407	2	482.26	-3.74
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	2		LNSAVFPSAQGGPLMHVIAGK	251	21	7	45.55	b16y3y4y13y15y16y21	2094.11	77.409	58355	3	698.71	-4.20
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	3		VMQAQGSQTLNK	42	12	12	83.91	b2b3y2y3y4y7*y7y9y10*y10y11y12	1304.66	28.777	44391	2	652.83	-1.50
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	4		EMNIADYDAELWQAMEQEK	4	19	8	56.2	y4y6y7y9y12*y12y13y19	2314.03	91.779	31888	2	1157.52	11.18
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	5	Carbamidomethyl+C(7)	ELAGWMCDVLDNINDEATIER	380	21	9	45.55	b5°b5y4y5y8y11y12°y12y21	2464.14	100.757	28610	2	1232.58	12.58
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	6		AVALKEAMEPEFK	272	13	8	43.1	b3b9b11y1y4°y4y9y13	1462.75	58.363	27506	2	731.88	-6.18
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	7		YAEGYPGKR	54	9	4	38.27	y4y6y7y9	1040.51	22.795	12485	2	520.76	-6.10
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	8		MIIGGFSAYSGVVDWAK	168	17	4	23.72	b2y8y12y15	1800.88	102.107	4477	3	600.97	-8.54
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	9	Carbamidomethyl+C(5)	VLDICAR	405	7	3	40.47	y4y5y6	846.44	43.431	30326	2	423.72	-12.33
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	10		LYNIVPYGIDESGK	138	14	5	27.58	b3b8y4°y4y7	1567.81	72.922	12036	2	784.41	7.24
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	11		QEEHIELIASENYTSR	25	17	7	48.2	b6b8b9b10y10y14°y14	2016.00	96.489	2386	2	1008.50	15.74
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	12	Carbamidomethyl+C(5)	YYGGCEYVDVVEQLAIDR	63	18	3	22.98	b4y10y11	2149.03	90.675	1932	2	1075.02	17.15
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	13		YAEGYPGK	54	8	4	33.09	b6°b6y6y7	884.40	25.876	1772	2	442.70	-22.43
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	14		GYKVVSGGTENHLFLDLVDK	305	21	4	13.88	b10°b10y11y15	2304.21	100.561	69181	2	1152.61	-3.92
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	15		LYNIVPYGIDESGKIDYDEMAK	138	22	6	44.55	b3y4y11y17y18y19	2533.22	75.558	51944	3	845.08	1.54
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	16		QEEHIELIASENYTSRPMQAQGSQTLNK	25	29	5	38.35	b11b17y11y12y13	3301.63	83.442	38128	4	826.16	6.66
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	17		NSVPNDPKSPFVTSGIR	346	17	4	16.32	b3°b3b12y8	1814.92	51.099	20956	3	605.65	-9.08
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	18		VMQAQGSQTLNKYAEGYPGK	42	20	4	36.02	b10b11y6y7	2170.06	66.597	16537	4	543.27	1.80
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	19		EHKPKMIIGGFSAYSGVVDWAK	163	22	6	25.6	b3b6°b6y9y11y14	2420.24	103.871	6942	4	605.82	0.61
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	20		EADAALGRANITVNK	331	15	3	18.14	b7b13y4	1542.80	69.547	1771	2	771.90	-14.32
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	21		MIIGGFSAYSGVVDWAKMR	168	19	5	31.63	b7b12y6y8y9	2088.06	99.429	1637	2	1044.53	9.94
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	22	Oxidation+M(1)	MIIGGFSAYSGVVDWAK	168	17	4	22.93	b5b8y3y6	1816.90	65.306	7960	3	606.30	3.09
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	23	Oxidation+M(8)	AVALKEAMEPEFK	272	13	3	20.64	b4y6y12	1478.76	70.815	5123	2	739.88	3.22
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	1		AESFTTTNR	1	9	9	45.47	b2b4y2y5y6°y6y7°y7y9	1026.48	26.520	23557	2	513.74	-5.23
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	2		HGHAFNDLDLGK	37	12	4	22.28	b3b12y4y7	1323.66	54.145	14230	2	662.34	14.76
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	3		MAESFTTTNR	0	10	5	26.91	b8y5°y5*y5y9	1157.55	96.433	9773	2	579.28	22.25

Q7CPD8 YIFE_SALTY UPF0438 protein yifE	4		EPVTD AER	68	8	3	33.09	b3y4y5	916.43	43.560	5677	2	458.72	-6.06
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	5		FHTLSGGKPKVEGAEDYTEADD	90	22	6	28.96	b4b8y4y5°y5y14	2366.05	60.889	5548	3	789.35	2.58
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	6	Carbamidomethyl+C(14)	EPVTEEEKLFVAVCR	50	15	3	18.14	b3y4y6	1805.88	61.574	5574	2	903.45	-14.80
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	7		HGHAFNDLDLGKR	37	13	7	54.56	b3b8°b8y3y4y7y9	1479.73	35.419	2765	3	493.91	-10.56
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	8		GFSRHGDFTIK	19	11	3	31.29	y5y6y8	1264.63	54.198	1635	3	422.21	-14.19
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	17	109.61	b3b7y1y2y3y5y7y8y10*y10y11°y11y12y13°y13y14y19	2032.91	36.491	73150	3	678.31	-5.94
P02936 OMPA_SALTY Outer membrane protein A	2		IGSDAYNQGLSEKR	267	14	8	52.42	b5y1y6y7y8*y8y9y14	1537.74	33.335	33236	3	513.25	-12.22
P02936 OMPA_SALTY Outer membrane protein A	3		LGYPITDDLDVYTR	103	14	5	31.54	b10y4y9y11y14	1640.83	75.165	16399	2	820.92	7.07
P02936 OMPA_SALTY Outer membrane protein A	4	Carbamidomethyl+C(6)	AALIDCLAPDR	321	11	5	36.07	b2y3y8°y8y10	1214.62	68.075	11828	2	607.81	0.20
P02936 OMPA_SALTY Outer membrane protein A	5		STLKPEGQQALDQLYSQSLNDPK	231	24	6	12.71	b1b6b8y1y9y24	2673.33	81.200	7947	3	891.78	-14.52
P02936 OMPA_SALTY Outer membrane protein A	6		FGQQEAAPVVAPAPAPAEVQTK	194	23	7	33.91	b3b6y6°y6y8y10y12	2303.25	52.828	9879	2	1152.13	20.14
P02936 OMPA_SALTY Outer membrane protein A	7		GDNINGAYK	85	9	5	64.71	b3b5b6b8y3	951.47	68.129	3236	2	476.24	19.24
P02936 OMPA_SALTY Outer membrane protein A	8		DGSVVVLGFTDRIGSDAYNQGLSEK	255	25	5	23.1	b5y7y8°y8y15	2627.27	82.680	12218	3	876.43	-7.81
P02936 OMPA_SALTY Outer membrane protein A	9	Carbamidomethyl+C(17)	ISARGMGESNPVTGNTCDNVKPR	298	23	3	13.05	b4b8y4	2460.19	68.887	4017	3	820.74	9.33
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	1		VILVGNLQGDPEVR	8	14	12	68.7	b3b6y1y2y4y5y8y9°y9y10°y10y14	1508.84	64.734	26227	2	754.93	0.16
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	2		YTTEINVPQIGGVMQMLGGR	97	20	9	28.01	b2b7°b7b10y10y13*y13y15y20	2164.11	95.804	22588	2	1082.56	10.49
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	3		GSQVYIEGQLR	74	11	8	41.5	b4b7b10*b10y2y6*y6y11	1249.66	79.131	15216	2	625.33	1.47
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	4		YMPSGGAVANLTLATSESWR	22	20	4	30.75	y5y11y12y15	2111.02	103.996	1658	2	1056.01	-3.47
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	5		QTGEMK	44	6	1	13.62	y3	693.33	48.121	11122	1	693.33	13.56
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	6		WTDQSGQER	88	9	5	30.49	b3°b3y5°y5y8	1106.50	39.716	3225	2	553.75	12.80
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	7	Oxidation+M(2)	YMPSGGAVANLTLATSESWR	22	20	4	25.25	b14y13y14y17	2127.05	96.215	11568	2	1064.03	13.31
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	8	Oxidation+M(16)	YTTEINVPQIGGVMQMLGGR	97	20	5	19.76	b6°b6b13y5y18	2180.10	78.344	4452	3	727.37	8.96
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	9		GGVMQMLGGR	107	10	0	6.06		1005.49	95.835	1787	1	1005.49	-4.92
O68926 BFR_SALTY Bacterioferritin	1		ILFLEGIPNLQDLGK	61	15	8	43.12	b2b3b4y3y6y8*y8y15	1669.95	100.008	9840	2	835.48	-1.17
O68926 BFR_SALTY Bacterioferritin	2		DLREAIAYADSVHDYVSR	99	18	6	21.75	b5°b5b7y5y11y18	2080.02	74.390	7703	2	1040.51	2.82
O68926 BFR_SALTY Bacterioferritin	3		LGIGEDVEEMLR	76	12	7	34.25	b1b11b12y2y6y7y9	1360.68	81.687	6418	2	680.84	1.17
O68926 BFR_SALTY Bacterioferritin	4		LGMQNYLQSQIK	143	12	6	36.17	b9°b9b11y10y11*y11	1422.76	62.788	19250	2	711.89	15.87
O68926 BFR_SALTY Bacterioferritin	5		SDLRLELEGAK	88	11	4	24.31	b5b10y5°y5	1230.68	38.850	9323	3	410.90	11.90
O68926 BFR_SALTY Bacterioferritin	6		DLREAIAYADSVHDYVSR	99	18	3	15.58	b3b5y11	2080.03	81.955	5138	2	1040.52	10.80

O68926 BFR_SALTY Bacterioferritin	7		YADSVHDYVSR	106	11	1	7.34	b3	1311.61	74.429	2048	2	656.31	6.51
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	1		MYAVFQSGGK	0	10	12	91.55	b2b3b5b8y4°y4y6y7y8°y8*y8y10	1087.52	51.061	48607	2	544.26	-2.47
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	2		IGVPPFVDGGVIK	48	12	5	32.49	y2y5y7y9y12	1200.69	75.920	41671	2	600.85	-5.69
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	3		ITGISA	97	6	1	13.62	b3	561.32	46.181	12841	1	561.32	-0.11
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	4		YAVFQSGGK	1	9	5	44.96	b5b7°b7y6y7	956.46	89.105	9186	1	956.46	-19.97
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	5		LDIATGETIEFAEVLMIANGEEVK	24	24	3	12.71	b11b13y6	2592.32	87.308	6414	3	864.78	4.80
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	6		YAVFQSGGKQHR	1	12	3	26.26	b11y9y10	1377.72	71.694	9064	2	689.36	9.57
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	7		AEVVAHGRGEK	60	11	4	41.5	b3y5y6y7	1152.61	13.555	3693	2	576.81	-2.86
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	8		QQGHRQWFTDVK	85	12	3	22.28	b4b8y8	1529.75	33.370	1776	4	383.19	-4.15
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	9	Oxidation+M(16)	LDIATGETIEFAEVLMIANGEEVK	24	24	10	55.67	b10°b10b11°b11b12y4y6y7y12*y12	2608.34	75.329	80241	3	870.12	14.32
P0A7V6 RS3_SALTY 30S ribosomal protein S3	1		LVADSITSQLER	114	12	11	61.15	b2b12y2y5°y5y6°y6y8y9y10y12	1331.72	59.408	62534	2	666.36	-0.46
P0A7V6 RS3_SALTY 30S ribosomal protein S3	2		ADIDYNTSEAHTTYGVIGVK	179	20	8	42.21	b13y2y3y4y17°y17y18y20	2154.04	55.175	37429	3	718.68	1.59
P0A7V6 RS3_SALTY 30S ribosomal protein S3	3		LGIVKPWNSTWFANTK	11	16	6	42.86	y2y4y5y7y8y16	1861.98	78.188	35847	3	621.33	-7.28
P0A7V6 RS3_SALTY 30S ribosomal protein S3	4		VVADIAGVPAQINIAEVR	89	18	4	15.58	b8y1y5y10	1835.03	75.837	25393	2	918.02	-6.72
P0A7V6 RS3_SALTY 30S ribosomal protein S3	5		GEILGGMAAVEQPEKPAAQPKK	204	22	4	29.37	b3b10b11b14	2249.18	109.585	2463	2	1125.10	-4.88
P0A7V6 RS3_SALTY 30S ribosomal protein S3	6		LGIVKPWNSTWFANTK	11	16	0	4.45		1843.97	78.188	6533	2	922.49	-3.24
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	14	79.81	b2b3b4b12y1y2y3y4y6°y9y10y11*y11y12	1377.65	77.247	96986	2	689.33	1.33
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AVVESIQR	69	8	8	49.32	b2b5y1y4*y4y5y6y8	901.50	31.702	62650	2	451.25	-11.37
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3		AAVTMPSSK	22	9	7	57.51	y2y3y4°y4y6y7y9	891.46	30.354	56584	2	446.23	2.05
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4		VEGDTKPELELTlk	50	14	3	27.07	b3b4b13	1571.86	68.151	8348	2	786.43	5.44
P0A7X0 RS8_SALTY 30S ribosomal protein S8	5		VEGDTKPELELTlkyFQGK	50	19	4	22.72	b7b8y5*y5	2195.14	102.652	19430	3	732.39	-7.12
P0A7X0 RS8_SALTY 30S ribosomal protein S8	6	Carbamidomethyl+C(13)	AARQAQLGGEIICYVA	114	16	4	17.16	b10°b10y5y14	1648.87	102.157	1546	3	550.29	11.70
P0A7X0 RS8_SALTY 30S ribosomal protein S8	7		VTMPSSK	24	7	1	8.82	b4	749.38	30.306	9918	1	749.38	-7.25
O68883 CISY_SALTY Citrate synthase	1	Carbamidomethyl+C(12)	TAGSSGANPFACIAAGIASLWGPAHGGANEAAALK	240	34	26	92.32	b1°b1b2b4°b4b6b7°b7b8°b8°b8b9y1y2y3y9*y9y12*y12y13*y13y14y26y27y34*y34	3195.58	115.675	45028	3	1065.87	5.73
O68883 CISY_SALTY Citrate synthase	2		YSIGQPFVYPR	178	11	4	36.07	y3y6y8y11	1326.69	67.584	32829	2	663.85	2.21
O68883 CISY_SALTY Citrate synthase	3	Carbamidomethyl+C(18)	NDLSYAGNFLNMMFSTPCETYEVNPVLER	189	29	12	64.2	b2b3b4y2y3y5y6y11y12°y12y13y29	3411.55	110.904	13954	3	1137.85	3.58
O68883 CISY_SALTY Citrate synthase	4		AMGIPSSMFTVIFAMAR	371	17	4	22.93	b5b11y5y13	1829.92	119.171	10753	2	915.47	6.40
O68883 CISY_SALTY Citrate synthase	5	Carbamidomethyl+C(10)	RDSHPMAVMCGITGALAAFYHDSL DVNNPR	126	30	5	14.17	b5b16y10y13°y13	3315.54	94.918	7952	5	663.91	-1.47

O68883 CISY_SALTY Citrate synthase	6	Carbamidomethyl+C(15)	GVFTFDPGFTSTASCESK	38	18	3	15.58	b3b10y11	1937.89	73.093	3274	3	646.63	14.36
O68883 CISY_SALTY Citrate synthase	7		ILILHADHEQNASTSTVR	222	18	3	13.5	y4y8*y12	2005.07	43.682	1667	2	1003.04	11.20
O68883 CISY_SALTY Citrate synthase	8		HTMIHEQITR	110	10	4	28.67	b4*b4b5y5	1265.63	21.995	47086	3	422.55	-10.22
O68883 CISY_SALTY Citrate synthase	9	Carbamidomethyl+C(9)	DSHPMAVMCGITGALAAFYHDSL DVNNPR	127	29	4	22.72	y5*y5y6y10	3159.42	108.374	11490	4	790.61	-8.89
O68883 CISY_SALTY Citrate synthase	10		GTLGQDVIDIR	22	11	5	24.31	b7*b7y3y8*y8	1186.66	103.949	1762	2	593.83	12.34
O68883 CISY_SALTY Citrate synthase	11		HTMIHEQITRLFHAFR	110	16	3	25.53	b4b5b7	2037.06	70.928	29013	3	679.69	1.56
O68883 CISY_SALTY Citrate synthase	12	Carbamidomethyl+C(3)	ETCHEVLKELGTK	320	13	3	20.64	b7b11y3	1543.76	72.939	18211	2	772.38	-14.55
O68883 CISY_SALTY Citrate synthase	13		DDLLEVAMELEHIALNDPYFIEKK	333	24	10	64.83	b6b8*b8b9b10*b10b11*b11 b12y22	2845.40	136.387	3441	2	1423.20	-12.01
O68883 CISY_SALTY Citrate synthase	14	Carbamidomethyl+C(8)	ATVMRETCHVLK	315	13	3	20.64	b7b11y3	1573.78	84.451	2317	2	787.39	-1.47
O68883 CISY_SALTY Citrate synthase	15		IARPRQLYTGYDK	405	13	5	58.54	y3y6y7y8y10	1580.84	123.355	1796	2	790.92	-9.73
O68883 CISY_SALTY Citrate synthase	16		NYDPRATVMR	310	10	3	33.9	b5b6b9	1222.60	120.751	1712	1	1222.60	-0.40
O68883 CISY_SALTY Citrate synthase	17	Oxidation+M(15)	AMGIPSSMFTVIFAMAR	371	17	4	22.93	b4b14y5y11	1845.91	98.829	54496	3	615.97	0.46
O68883 CISY_SALTY Citrate synthase	18	Oxidation+M(8)	DDLLEVAMELEHIALNDPYFIEKK	333	24	3	23	b4b5b10	2861.39	79.858	2239	3	954.47	-13.65
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	1	Carbamidomethyl+C(11)	IAAVAEDGEPCTVYIGADGAGHY VK	158	25	8	32.28	b2b3b4y1y5y10y21y25	2563.22	59.309	35705	3	855.08	0.95
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	2		AAVLPANLIQAQR	432	13	7	20.64	b2b3y2y4*y4y9y13	1364.80	63.505	15761	2	682.90	-2.68
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	3		IVSYAQGFSQLR	329	12	6	37.26	b2b5y6y8y10y12	1368.73	61.418	12727	2	684.87	0.71
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	4		WTSQSALDLGEPLSLITESVFAR	264	23	7	37.6	b7y2y3y5y6y7y23	2520.32	116.684	12170	2	1260.66	9.69
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	5		TDKEGIFHTEWLE	455	13	9	66.99	b2*b2b9*b9b10b11y8y9y10	1604.75	51.031	3613	2	802.88	-3.42
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	6		DVVAYAVQNGIPVPTFSAAVAYY DSYR	405	27	5	11.91	b4*b4y8*y8y14	2936.42	136.456	2925	2	1468.72	-7.48
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	7		ELSAEGFNFIGTGVSGGEEGALK	113	23	13	70.44	b3*b3b7b9b11*b11*b11b1 3y3y9y10y13y19	2269.14	68.155	51940	3	757.05	17.65
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	8		GDIIDGGNTFFQDTIR	93	17	4	16.32	b6b11*b11y8	1881.91	35.229	21126	3	627.98	-10.70
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	9		MVHNGIEYGDMQLIAEAYSLLK	183	22	5	13.44	b3b7*b7y12*y12	2495.26	112.206	17296	3	832.42	10.57
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	10		IADEYQQALR	395	10	4	26.91	b4y3y6*y6	1206.62	46.328	9505	2	603.81	9.31
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	11		GGLNLSNEELANTFTTEWNNGELS SYLIDITK	205	31	7	24.42	b3b10*b10b11y9y12*y12	3442.65	94.965	4631	3	1148.22	-5.39
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	12		AGAGTDAAIIDSLKPYLEK	75	18	3	24.5	b7b10b11	1819.91	80.319	3360	3	607.31	-18.98
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	13		ITDAYAENADIANLLLAPYFK	373	21	3	22.33	b20y4y5	2326.22	105.616	3219	2	1163.61	9.87
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	14		DEDGNYLVDVILDEAANK	242	18	5	22.98	b14y5*y5y6*y6	1992.92	85.739	2273	2	996.97	-8.45
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	15		AQPAGDKAEFIEK	307	13	4	34.07	b8y3y9y11	1403.72	34.842	11605	2	702.36	1.83
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	16		ELSAEGFNFIGTGVSGGEEGALKG PSIMPGGQK	113	33	6	21.6	b10b13*b13b14y7*y7	3221.56	82.743	7638	3	1074.53	-4.77

[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	17		IVSYAQGFSQLRAASDEYHWDLN YGEIAK	329	29	4	24.81	y7y9y20y24	3331.63	111.725	6309	4	833.66	9.23
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	18		AGAGTDAAIDSLKPYLEKGDIIIDG GNTFFQDTIR	75	35	4	23	b9b10b12°b12	3682.85	98.111	3464	4	921.47	-3.71
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	19		QQIGVVGMMAVMGRNLALNIESR	3	22	4	13.44	b4*b4b8y13	2356.26	88.334	1503	2	1178.63	1.45
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	20	Phosphoryl STY(8)	DYFGAHTYKR	445	10	3	28.67	b6_H3PO4 b6b7y4	1337.54	28.597	25213	3	446.52	-14.33
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	21	Phosphoryl STY(15)	AGAGTDAAIDSLKPYLEK	75	18	4	24.82	b3b14b16y3	1899.89	57.815	17574	3	633.97	-5.65
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	22	Oxidation+M(11)	QQIGVVGMMAVMGR	3	13	3	25.41	b10y8y9	1361.70	36.362	3234	3	454.57	-1.43
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	1	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLALASGAK	257	25	12	73.85	b2b3b6y4y5y7y12y17y19y20y23y25	2684.45	127.260	35305	3	895.49	1.46
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	2		LTVVPAQTSAAEVLK	215	15	7	29.44	b1b14y8y11°y11y12y15	1584.89	62.283	23395	2	792.95	2.62
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	3		EVTTAETYR	160	9	5	46.05	b2y3y5y7y9	1069.51	27.395	6547	2	535.26	-7.76
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	4		AFPGLNGMDLAKEVTTAETYR	148	21	8	47.87	b2b3b6b10b12y4y8y9	2284.13	108.962	5336	3	762.05	0.21
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	5		QIVTLTYPHIGNVGTNK	50	17	6	45.09	b3b4b11y3y7y8	1854.97	51.968	46248	3	619.00	-17.97
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	6		AFPGLNGMDLAK	148	12	3	22.28	b4y3y6	1233.61	36.227	3831	2	617.31	-12.07
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	7	Carbamidomethyl+C(18)	MNPDGIFLSNGPGDPAPCDYAITA IQK	230	27	5	21.2	b10b14y11y13y19	2862.40	82.139	2843	2	1431.70	18.42
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	8		NVVMITAQNHGFAVDEDESLPANL R	302	24	4	12.71	b4b8°b8y14	2611.24	68.934	2475	2	1306.12	-20.48
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	9		SEDDLPHFVVAYDFGAK	185	17	4	33.72	y3y5y6y11	1909.86	45.143	1688	3	637.29	-17.38
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	10		EVTTAETYRWTQGSWTLK	160	18	3	24.5	b3b6b7	2157.08	81.695	50450	2	1079.04	7.13
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	11		QIVTLTYPHIGNVGTNKADEESSQ VHAQGLVIR	50	33	3	11.06	b17b25y19	3574.84	136.334	31941	4	894.46	-7.38
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	12		AFPGLNGMDLAKEVTTAETYR	148	21	4	21.7	b3b7b11y4	2284.15	79.884	29862	3	762.06	11.65
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	13		MKFGHHGGNHPVK	285	13	4	34.07	b3b5b7y11	1445.73	58.403	6093	3	482.58	7.35
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	14	Carbamidomethyl+C(8)	EKGAQNGCIIAGDSPDAK	123	18	4	21.75	b5b13y5y9	1830.86	62.728	2893	4	458.47	-1.40
[P14845]CARA_SALTY Carbamoyl-phohate synthase small chain	15	Oxidation+M(8)	AFPGLNGMDLAK	148	12	3	29.48	b3b4b9	1249.63	38.857	2071	2	625.32	0.59
[P15171]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	1		AGLVAPDETTFNYSVK	229	15	6	29.44	b5y4*y4y10y11y15	1624.83	64.516	17290	2	812.92	3.91
[P15171]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	2	Carbamidomethyl+C(4)	MTLCNMAIEMGAK	216	13	6	58.54	y4y9y10y11y12y13	1469.67	70.538	7952	2	735.34	8.14
[P15171]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	3		AEEIAPQVTWGTNPGQVISVTDIIP DPASFSDPVER	280	36	4	10.89	b12°b12y4y6	3835.93	101.808	2798	3	1279.32	7.26
[P15171]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	4		IQMQELIK	80	8	3	36.1	b3y3y6	1002.56	58.405	9969	2	501.78	-7.00
[P15171]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	5		LNPGER	417	6	1	13.62	y3	685.35	72.379	5948	1	685.35	-13.89

P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	6		IFIEAGFEWR	393	10	5	47.91	b5y3y7°y7y9	1267.66	38.761	5377	2	634.33	12.23
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	7		ALAYMGLQPGVPLTDVAIDK	321	20	3	14.37	b7y6y8	2072.07	105.856	4695	2	1036.54	-18.50
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	8		TFATMDHNVSTQTK	56	14	3	19.29	b3y5y7	1580.75	36.655	4577	2	790.88	7.49
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	9		ALSMGR	209	7	4	37.46	b5°b5b6y6	763.39	20.530	2694	2	382.20	20.39
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	10		THLVSPAMAAAAVTGHFADIR	441	22	6	28.96	b9b11°b11b12y8y11	2207.13	90.684	2217	2	1104.07	-2.77
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	11		AQAEAEGLDK	383	10	6	41.1	b4°b4b9y5°y5y6	1031.48	98.202	1635	2	516.24	-22.13
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	12	Carbamidomethyl+C(14) ;Carbamidomethyl+C(17))	IFIEAGFEWRLPGCSMCLAMNDR	393	24	4	19.02	b7b9°b9b11	2887.30	85.599	116125	3	963.11	-4.23
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	13	Carbamidomethyl+C(26)	ALAYMGLQPGVPLTDVAIDKVFI GSCTNSR	321	30	7	31.66	b6y4*y4y7y8y11y22	3193.65	94.663	7085	3	1065.22	4.05
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	14		AGLVAPDETTFNyVKGR	229	17	6	26.15	b3b7b9°b9y9°y9	1837.93	37.243	3802	3	613.31	-8.57
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	15		TMKIEVTGNAAPGITAK	164	17	5	26.15	b3b9b12*b12y14	1701.93	88.278	2436	3	567.98	7.60
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	16	Oxidation+M()	TFATMDHNVSTQTKDINASGEMAR	56	24	4	16.87	b3b11y4y8	2641.21	35.449	40094	3	881.07	4.53
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	17	Oxidation+M(8)	THLVSPAMAAAAVTGHFADIR	441	22	4	13.44	b6b12°b12y7	2223.11	68.041	4120	3	741.71	-11.42
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	1		TGYLPITTAAYELTR	343	15	11	87.25	b1b3b4y1y5y6y7y8y9y11y15	1669.89	84.044	56214	2	835.45	3.80
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	2		TIVDEELESVWTGKK	397	15	3	18.14	b5y4y13	1733.88	74.625	27437	3	578.63	-10.63
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	3		LGNMPQIR	389	8	3	40.87	y4y5y7	928.50	46.538	24430	2	464.75	-6.05
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	4		FNyGVGMMPYDADIK	282	15	4	26.22	b2y5y7y10	1720.79	73.624	16866	2	860.90	8.65
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	5		TIVDEELESVWTGK	397	14	6	58.28	b8b11b12y10y11y12	1605.81	81.516	14930	2	803.41	8.36
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	6	Carbamidomethyl+C(6)	FYNGDCAMTTASSGLANIR	258	20	5	23.79	y4*y4y11y12y20	2135.97	59.990	11942	2	1068.49	10.63
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	7		FLDFLAKPENAAEWHQK	326	17	3	16.32	b11b13y6	2044.03	73.144	40900	3	682.01	-1.25

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	8		QMLNKPPLPFTK	374	12	3	26.26	b6y3y4	1413.78	60.451	32210	3	471.93	-5.53
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	9		HTALGLALSIAFTGQALAVTTIPF WHSMEGELGK	5	34	3	22.92	y7y8y10	3567.87	101.151	12039	4	892.72	0.96
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	10		FNQANPDYK	47	9	4	30.49	b3*b3b5y3	1096.50	50.994	6415	3	366.17	-6.68
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	11		NNGFDGTDAVLEFNKPEQVK	212	20	7	42.42	b4y4y6y9°y9y10y18	2222.10	64.375	4675	2	1111.55	13.07
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	12		GAPQNAIIGGASLWVMQGK	297	19	8	39.11	b3b4b6b12*b12y6y14*y14	1897.99	85.190	2918	3	633.34	-0.26
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	13		EVDSLAQR	39	8	4	51.08	b4b6y5y6	917.49	42.077	2761	1	917.49	18.63
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	14		SGHLLSQPFNSSTPVLYYNK	132	20	5	36.04	b6y3*y3y4y5	2252.18	65.331	2512	4	563.80	18.43
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	15		TWQELADYTAK	167	11	6	47.74	b6°b6b10y5y6y9	1325.63	37.837	1586	2	663.32	-3.87
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	16		SGHLLSQPFNSSTPVLYYNKDAFK	132	24	4	16.87	b6b11y4y7	2713.33	105.863	20243	4	679.09	-10.53
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	17		KGDFSIVGR	242	9	7	44.96	b4°b4b5°b5y6°y6y7	1028.51	62.245	4346	2	514.76	-6.29
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	18		EVDSLAQRFNQANPDYK	39	17	4	27.4	b3y3y12y13	1994.93	117.635	2891	2	997.97	-11.56
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	19		ETYTGVAKFDFLAKPENAAEWH QK	318	25	3	21.95	b3b4y10	2893.48	115.643	2796	3	965.16	8.18
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	20		HIALLEEMNKK	232	11	3	24.31	b8b10y6	1325.73	83.556	2228	3	442.58	0.55
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	21		AGLDPEQPPKTWQELADYTAK	157	21	4	13.88	b9b12°b12y6	2358.14	83.544	1873	3	786.72	-10.35
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	22	Oxidation+M()	TGNAPAILQVYEVGTATMMASK	77	22	3	13.44	b5b11y12	2269.13	106.757	2217	3	757.05	3.01
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	1		GVDVVAYANQDLIYSDLTAGR	155	21	4	13.88	b6y8y13y21	2240.12	71.701	81891	3	747.38	0.54
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	2	Carbamidomethyl+C(1)	CTWVASDFDALIPSLK	66	16	7	34.77	b3b5b12°b12y4y11y16	1822.91	97.497	36852	2	911.96	5.42
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	3		YFGDGTGVGLR	211	11	4	24.31	b9y7y9y11	1141.57	54.644	33679	2	571.29	6.20
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	4		IGTDTTYAPFSSK	29	13	3	29.88	y3y5y12	1387.68	51.976	36271	2	694.34	2.46

P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	5		QQEIAFSDK	99	9	3	30.49	b6y5y6	1065.52	39.650	11048	2	533.26	-1.83
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	6		QPAGK	193	5	1	13.22	y3	500.28	44.316	9783	1	500.28	1.77
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	7		GSPIQPTLESLK	120	12	4	22.28	b5y4y8*y8	1269.69	42.415	5309	2	635.35	-7.79
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	8		ALTELR	234	6	1	13.62	y5	702.41	34.293	5284	1	702.41	-9.65
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	9		LDAALQDEVAASEGFLK	176	17	3	24.97	y10y11y14	1776.90	89.811	4295	2	888.95	-0.96
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	10		ALTELRQDGTYDK	234	13	5	53.32	b9y3y5y9y11	1509.76	37.864	18486	2	755.38	4.69
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	11		QPAGKEYAFAGPSVK	193	15	5	31.82	b3b4*b4y10y14	1549.81	73.956	14147	2	775.41	7.33
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	12		RQQEIAFSDK	98	10	6	73.56	b3b5b6b8y6y8	1221.62	79.110	11328	2	611.32	0.70
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	13		IGTDTTYAPFSSKDAK	29	16	8	70.18	b4b5b8b11b13y8y9y11	1701.82	46.447	2419	3	567.94	-9.40
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	14	Carbamidomethyl+C(15) ;Oxidation+M(14)	GEFIGFDIDLGEMCK	45	16	4	24.26	b7b11y5y7	1860.81	25.953	5627	3	620.94	-3.15
P0A1P8 GLRX1_SALTY Glutaredoxin-1	1	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14)	MFTVIFGRPGCPYCVR	0	16	5	17.16	b2b3y3y9y16	1959.93	75.554	38549	3	653.98	-7.16
P0A1P8 GLRX1_SALTY Glutaredoxin-1	2		TVGKPVETVPQIFVDQK	50	17	12	55.52	b3b8*b8y1y2*y2y3y5y6y8y13y17	1885.02	63.821	35628	3	629.01	-11.40
P0A1P8 GLRX1_SALTY Glutaredoxin-1	3		ENLNLFA	80	7	3	37.46	b5y4y5	820.43	46.350	64533	2	410.72	11.83
P0A1P8 GLRX1_SALTY Glutaredoxin-1	4	Carbamidomethyl+C(10) ;Carbamidomethyl+C(13)	FTVIFGRPGCPYCVRAK	1	17	4	29.91	b10b11y10y12	2028.01	71.932	3024	3	676.67	-10.95
P0A1P8 GLRX1_SALTY Glutaredoxin-1	5	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14)	MFTVIFGRPGCPYCV	0	15	0	4.45		1803.83	75.503	22824	3	601.95	-2.64
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	1		IQVTGSEGELGIYPGHAPLLTAIKP GMIR	23	29	12	49.8	b2*b2b3b10b15b16y5y12y13y16y27y29	3018.62	81.221	92236	4	755.41	-7.52
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	2		AMTYHLDVVSAEQQMFSGLVEK	1	22	8	36.39	b2b6*b6b9b11y8y10y11	2483.19	89.611	32710	3	828.40	-0.88
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	3		SSHGDVDYAQASAEAK	107	17	6	41.59	b7y2y5y7y8y9	1748.80	44.112	18167	3	583.60	-7.33
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	4		AEEHIKSSHGDVDYAQASAEAK	101	23	3	13.05	b12y14y20	2456.18	91.270	65912	3	819.40	3.38
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	1		QTFNTAIAAIMELMNK	719	16	11	56.16	b4b6b7*b7y1y3y6y7*y7y9y16	1795.93	89.023	87310	3	599.31	11.01
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	2		NWVSPVDAIVERDEK	583	15	4	26.22	b3b8b9*b9	1756.89	55.433	9654	2	878.95	0.07
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	3	Carbamidomethyl+C(3)	YYCLSMLPYPSGR	34	13	4	28.12	y5y6y12*y12	1606.76	75.114	8511	2	803.88	13.83
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	4		ITAYADELLRDLDK	194	14	6	19.29	b2*b2b3b6y4y14	1635.86	50.995	6948	3	545.96	1.64

Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	5	Carbamidomethyl+C(15)	AAANNAELAAFIDECR	270	16	3	17.16	b4b7y10	1735.80	75.601	3041	3	579.27	-4.64
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	6		YGLTIKPVILAADGSEPDLSSEQALT EK	351	27	3	17.99	y3y6y11	2858.46	80.391	2723	3	953.49	-13.58
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	7		MQEQRPEEIESK	0	13	4	20.64	b7y6y8°y8	1666.79	36.630	2302	3	556.27	12.23
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	8		GVLFNSGEFDGLAFEAAFNAIADK	378	24	7	23.61	b6b8°b8b14*b14y5y14	2503.19	71.955	9969	3	835.07	-8.10
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	9		NNTAPAPWTYDNIAYMK	92	17	4	16.32	b4y9°y9y13	1969.94	72.688	9153	2	985.48	16.30
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	10		NVLQPIGWDAFGLPAEGAAVK	71	21	3	13.88	b11b14y16	2153.13	80.821	7930	2	1077.07	-3.29
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	11		YWGAPIPMVTLEDGTVLPTPEDQ LPVILPEDVVMGDITSPIK	426	42	5	28.92	b4b7b9b10b15	4546.28	101.974	6413	4	1137.33	-11.92
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	12		NWVSPVDAIVER	583	12	4	29.48	b4b6b7°b7	1384.75	35.399	4847	2	692.88	19.04
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	13		NNGIDPQVMVER	624	12	4	34.25	b9y4y7y8	1371.64	31.640	3111	2	686.32	-20.65
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	14		TLGFGYDWSR	113	10	5	26.91	b3°b3b7y5°y5	1201.58	85.785	2400	2	601.29	9.45
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	15		LVYEHTAK	675	8	3	36.1	b4b6y7	960.50	25.388	2089	2	480.75	-17.60
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	16		TTVNGMPALR	475	10	6	41.1	b8°b8b9y7y9*y9	1059.55	40.305	2085	2	530.28	-8.06
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	17		VQLHWDEK	13	8	5	67.31	b3b4b6y3y5	1054.51	120.863	2047	1	1054.51	-21.30
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	18	Carbamidomethyl+C(3)	YTCPQYQEGMLDSK	502	14	4	38.74	y3y5y6y12	1719.75	70.581	1954	4	430.69	9.44
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	19	Carbamidomethyl+C(5)	EKYYCLSMPLPYPSGR	32	15	3	18.14	b4b14y9	1863.87	68.116	16890	3	621.96	-4.39
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	20		YGADTVRLFMMFASPADMTLEW QESGVEGANR	636	32	6	13.56	b4b7°b7y6y9*y9	3579.67	116.670	13097	3	1193.89	9.82
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	21		NNGIDPQVMVERYGADTVR	624	19	5	36.26	b10b11y6°y6y7	2134.05	107.039	6136	3	712.02	4.92
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	22		NWIGRSEGVEITFDVK	221	16	5	30.8	b6b7y4°y4y14	1849.93	95.050	5443	2	925.47	-9.30
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	23		DAAGHELVYTGMKMSK	605	17	4	22.93	b5b14y9y11	1824.88	79.667	2431	2	912.94	11.30
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	24		ITVPVDATEEQVRER	813	15	4	18.14	b11y3y10*y10	1741.89	80.708	2238	2	871.45	-7.64
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	25	Oxidation+M(0)	YWGAPIPMVTLEDGTVLPTPEDQ LPVILPEDVVMGDITSPIK	426	42	3	16.46	b6b10b13	4562.38	112.519	19536	5	913.28	9.42
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	26	Carbamidomethyl+C(4); Oxidation+M(7)	QLLCQGMVLADAFYYVGENGER	561	22	5	13.44	b11°b11b16*b16y5	2549.19	81.702	5486	3	850.40	4.88
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	27	Oxidation+M(9)	NNGIDPQVMVER	624	12	3	26.26	b8b9y9	1387.66	87.516	2078	2	694.33	-5.37
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	28	Oxidation+M(16)	NNTAPAPWTYDNIAYMK	92	17	4	23.72	b4°b4b6b9	1985.91	45.208	1679	3	662.64	2.89
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	1		LFAGNATPELAQR	5	13	6	46.12	y5y6*y6y10y11°y11	1387.74	52.737	18966	2	694.37	4.57
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	2		ITAVIPYFGYAR	84	12	4	26.26	b4y2y6y7	1370.75	79.673	16669	2	685.88	1.42
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	3		VFAYATHPIFSGNAANNLR	243	19	9	31.63	b1b9°b9b11b12°b12y8y12 *y12	2063.02	64.273	15079	3	688.35	-10.65
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	4		LYTSLGDAAVGR	22	12	3	35.5	y5y6y7	1222.64	51.377	10845	2	611.82	-1.30

[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	5		LLNDTDMAIIDK	182	12	5	37.26	b4b9b11y3y12	1361.70	90.126	4301	2	681.35	3.05
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	6		AAEALK	231	6	2	13.62	b4*b4	602.34	30.644	14837	1	602.34	-10.13
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	7	Carbamidomethyl+C(10)	NSVIDEVVVCDTIPTDEIK	262	20	8	49.73	b12*b12b13b15y4y7y10y14	2259.18	87.517	9640	2	1130.09	16.10
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	8		RISNEESISAMFEH	301	14	4	31.54	b11y3y7y9	1649.77	38.895	4089	2	825.39	8.73
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	9	Carbamidomethyl+C(18) ;Carbamidomethyl+C(32))	ANVSQVMHIIGDVAGRDCVLVDD MIDTGGTLCK	198	33	4	24.43	b3b23y9y10	3559.68	89.028	3373	4	890.68	-4.80
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase	10	Oxidation+M(7)	ANVSQVMHIIGDVAGR	198	16	4	27.67	b4b9b13y6	1682.87	58.462	72081	2	841.94	2.97
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	1		LIQQEGEDGYFHGK	132	14	7	41.75	b1b2y4y5y6y12y14	1620.74	48.972	44853	3	540.92	-14.01
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	2		AMEAIGKPFDK	187	11	4	13.3	b8b9*y6y11	1206.63	38.978	16664	2	603.82	12.24
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	3		MLGSAMDK	400	8	6	33.09	b5*b5b6y6*y6y8	852.41	39.767	9311	2	426.71	12.67
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	4		AAWDAGATDAEMKPILNDIR	355	20	3	14.37	b3b15y13	2158.05	61.526	4977	3	720.02	-6.45
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	5		LYTDHK	296	6	3	40.07	b3b4y3	776.40	41.623	89224	2	388.70	4.09
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	6	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	TAEDGPLMACWSCK	111	15	3	24.16	b6y3y4	1722.76	61.566	10201	3	574.92	18.14
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	7		FFSLIFPFFFITSVYAEQTPESAK	10	24	4	16.87	b10b13y11y17	2816.40	99.262	3801	2	1408.70	-7.02
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	8		GITHEIPLDISTKEK	423	16	4	25.53	b3*b3b5b6	1777.97	105.541	60669	3	593.33	1.51
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	9		IKVEDQLVHAHFEAK	340	15	4	24.16	b14y11*y11y12	1763.93	96.541	36752	2	882.47	-8.44
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	10		TPMLKAQHPEYETWSAGIHGK	256	21	4	20.52	y4y9*y9y15	2381.17	94.492	8832	2	1191.09	-2.36
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	11		AMEAIGKPFDKAGR	187	14	4	30.74	b5b7b8y7	1490.79	90.738	6622	2	745.90	5.24
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	12		VQNAEGKLYTDHK	289	13	8	43.1	b3b5*b5b11y5*y5y11*y11	1502.74	38.886	2246	2	751.88	-11.05
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	13		DYNKPRGHAYAVTDVR	86	16	7	55.49	b5b6b10b12y4y6y12	1861.91	62.255	2047	4	466.23	-10.75
[Q8ZKF5]NRFA_SALTY Cytochrome c-552	14	Phosphoryl STY(12)	FFSLIFPFFFITSVYAEQTPESAK	10	24	3	22	b4y11y12	2896.37	136.439	2851	2	1448.69	-2.78
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	1		EGGIFWMDSLAIPANAK	249	17	6	29.91	b2b11b12y5y13y17	1819.91	92.897	31441	2	910.46	4.09
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	2		LGYSGNTTDPKEIEAA YEELK	179	21	6	35.85	b4*b4b5b6y2y11	2328.12	49.860	12457	3	776.71	-1.57
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	3		VIYSTYESNETMYAK	53	15	6	36.71	y2y5y6y10*y10y12	1798.83	50.357	5928	2	899.92	6.99
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	4		NSLLLTDDAREVFQMALR	160	18	6	15.58	b13*b13y3y12*y12*y12	2092.06	97.554	4516	3	698.02	-13.65
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	5		EGMIQK	92	6	1	13.62	b5	705.36	29.162	10636	1	705.36	-2.94

P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	6		LTNFHNLDPEMLNKPFDPNNDYS VPYIWGATAIGVNSDAIDPK	103	43	4	10.99	b5y3y11*y11	4803.31	94.199	10634	4	1201.58	1.52
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	7		TITSWADLWKPEYK	146	14	4	30.74	b11y3y9y10	1737.85	80.539	4855	2	869.43	-17.28
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	8		EVFQMALR	170	8	3	40.87	b3b4b6	993.54	24.140	4056	3	331.85	17.57
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	9		GEWQNDVGDAIYEEYYQKLK	323	22	4	13.44	b15y9°y9y21	2606.19	85.859	61419	3	869.40	-5.81
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	10		VIYSTYESNETMYAKLK	53	17	7	54.63	b7b8b11y11y12°y12y13	2040.01	92.978	3652	3	680.68	5.86
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	11		TITSWADLWKPEYKNSLLLTDDA R	146	24	3	12.71	b12y3y12	2836.43	136.430	2685	2	1418.72	-8.69
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	12		KLGYSGNTTDPK	178	12	5	22.28	b5b11y11°y11*y11	1280.65	65.790	2077	3	427.56	4.10
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	1		LGPLSGEVSAGEILHLVGPNGAGK	15	24	5	16.87	b2b3b12y4y9	2272.22	85.694	27295	3	758.08	-5.37
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	2		MSQLMQLKDVAESTR	0	15	5	18.14	b5b11°b11y5°y5	1736.85	79.126	8652	2	868.93	-9.42
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	3		AYLAQQQNPPFAMPVWHYTLH QPKD	75	26	4	12.14	b10y2y7y10	3093.57	102.210	7163	4	774.15	9.31
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	4	Carbamidomethyl+C(4)	LIACGRR	210	7	3	37.46	b5y3y4	845.46	29.220	1928	2	423.24	-15.02
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	5		SVNQLSGGEWQR	122	12	8	40.27	b4°b4y3y4*y4y5°y5*y5	1360.65	24.933	39401	2	680.83	-7.54
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	6	Carbamidomethyl+C(6)	VLHHLQAGIAIVMSSHDLNHTLR	174	24	5	23	y7*y7y9y10*y10	2722.36	62.387	9701	3	908.12	-16.32
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	7	Carbamidomethyl+C(4)	LIACGR	210	6	1	13.62	y5	689.38	43.713	6635	1	689.38	0.53
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	8		EEVLTPSYLAQAYGLRFR	217	18	4	22.74	b6b12b15°b15	2113.09	99.688	19458	3	705.04	-6.47
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	9		RLDVEGHPMLISAT	235	14	3	24.73	b6b7y10	1538.78	67.090	13721	3	513.60	-11.11
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	10		TRTQQLNEVADMLGLGDK	101	18	7	32.75	b9b10°b10b13°b13y5y14	1918.00	72.821	3472	3	640.00	14.51
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	11	Phosphoryl STY(6)	REEVLTPSYLAQAYGLR	216	17	6	22.93	b10b13y10y13°y13*y13	2046.02	78.547	4822	4	512.26	13.13
P63351 BTUD_SALTY Vitamin B12 import ATP-binding protein btuD	12	Oxidation+M(4)	SQLMQLKDVAESTR	1	14	3	19.29	b3b6y11	1621.81	63.861	6823	2	811.41	-7.38
P65215 KDSA_SALTY 2-dehydro-3- deoxyphosphooctonate aldolase	1		AGMAVGLAGLFLESHDPANAK	226	22	5	35.67	b3b4y1y17y18	2166.10	87.452	26211	3	722.70	-0.79

[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	2		VANDLPFVFLGGMNVLESR	12	19	9	33.35	b2b5y2y7°y7y9y10y14y19	2078.08	109.671	19464	2	1039.54	3.64
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	3	Carbamidomethyl+C(17)	VSGNSPVIFDVTHALQCR	189	18	5	21.75	b5b12°b12y10y17	1999.99	78.484	12577	3	667.33	-6.41
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	4	Carbamidomethyl+C(17)	VSGNSPVIFDVTHALQCRDPFGAA SGGR	189	28	4	35.74	b5°b5b6b7	2915.41	84.747	5946	4	729.61	-2.76
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	5		DLAMR	31	5	1	13.22	y4	605.30	41.055	20777	1	605.30	-10.18
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	6	Carbamidomethyl+C(4)	VILCDR	162	6	1	13.62	y4	775.40	27.278	6621	1	775.40	-11.26
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	7		VITDVHEASQAQPVADVVDVIQL PAFLAR	91	29	8	28.98	b6b9b10b12°b12*b12y6y8	3101.63	103.905	5228	4	776.16	-12.20
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	8	Carbamidomethyl+C(1)	CDGPSALPLAK	248	11	4	31.29	b4b9°b9b10	1128.56	99.347	4170	1	1128.56	-10.06
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	9		KPQFVSPGQMGNIVDKFHEGGND K	138	24	4	22	b11b12°b12y8	2629.25	58.509	5423	3	877.09	-11.61
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	10		GQVTELARAGMAVGLAGLFLESH PDPANAK	218	30	5	11.38	b4°b4*b4y3y6	3020.53	110.634	2231	3	1007.51	-11.48
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	11		AIDDLVKSFDELDTEN	268	16	3	23.69	b11y9y10	1823.85	38.802	1578	2	912.43	-1.47
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	12	Oxidation+M(10)	KPQFVSPGQMGNIVDK	138	16	5	17.16	b8y10°y10y13*y13	1760.88	76.717	6581	2	880.94	-13.17
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	13	Oxidation+M(19)	GANFGYDNLVVDMLGFSVMKK	168	21	3	13.88	b5b13y5	2321.13	80.918	2255	3	774.38	-0.32
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	14	Oxidation+M(3)	AGMAVGLAGLFLESHDPANAK	226	22	4	13.44	b11y8y21*y21	2182.11	117.967	1695	2	1091.56	4.36
[Q8ZL56]GPMI_SALTY 2	1		TFFANPVLTAVDQAK	91	16	6	24.26	b1b3b5y4y11y16	1735.90	75.753	33762	2	868.45	0.21
[Q8ZL56]GPMI_SALTY 2	2	Carbamidomethyl+C(8)	AVEALDNCIEQVTK	416	14	7	39.04	b6b13y6*y6y7y9y14	1589.79	60.150	17272	2	795.40	5.30
[Q8ZL56]GPMI_SALTY 2	3		TPVMDALWAK	31	10	3	14.48	b5°b5y8	1131.59	70.579	15361	2	566.30	3.45
[Q8ZL56]GPMI_SALTY 2	4		LSDIAPTMSLMGMEIPQEMTGKP LFIVE	485	29	13	49.42	b2b3b4b5°b5b12°b12b13y 1y2°y2y13y29	3191.62	120.695	14115	3	1064.54	1.84
[Q8ZL56]GPMI_SALTY 2	5		AVESVGGQLLITADHGNAEQMR	430	22	7	35.02	b3b6y3y5y12y13*y13	2296.15	81.600	9709	3	766.05	6.27
[Q8ZL56]GPMI_SALTY 2	6		IVYQDLTR	75	8	5	40.87	y3y5y6y8*y8	1007.55	45.297	7104	2	504.28	-1.88
[Q8ZL56]GPMI_SALTY 2	7		AFVNADFDGFARK	272	13	6	29.67	b6°b6b10y6y10y13	1457.72	55.495	4085	2	729.36	2.18
[Q8ZL56]GPMI_SALTY 2	8		YAHVTFFFNGGVVEPFAGEER	336	21	3	23.53	b3b4b12	2403.13	94.472	3056	3	801.71	10.36
[Q8ZL56]GPMI_SALTY 2	9		FAALGK	172	6	2	26.85	y3y4	606.35	39.615	30282	1	606.35	-10.17
[Q8ZL56]GPMI_SALTY 2	10		VATYDLQPEMSSAELTEK	364	18	8	61.82	b9b10b11*b11y9y11y12y1 7	2011.99	62.124	19659	2	1006.50	17.84
[Q8ZL56]GPMI_SALTY 2	11		IYLHAFLDGR	145	10	3	26.91	b4y3y8	1204.66	52.042	14652	2	602.83	9.83
[Q8ZL56]GPMI_SALTY 2	12		AFVNADFDGFGAR	272	12	5	52.7	b11y4y5y9y10	1329.65	70.490	12654	2	665.33	18.64
[Q8ZL56]GPMI_SALTY 2	13		DPATGQAHTAHTNLPVPLIYVGE K	452	24	4	12.71	b8b11y5°y5	2529.26	46.315	12266	3	843.76	-18.05
[Q8ZL56]GPMI_SALTY 2	14		TAVAYPPASLANTFGEWMAK	303	20	4	22.5	b14°b14y9y10	2125.06	95.016	11395	2	1063.04	10.11
[Q8ZL56]GPMI_SALTY 2	15		LDVEIK	83	6	1	13.62	y3	716.41	35.332	4964	1	716.41	-13.80
[Q8ZL56]GPMI_SALTY 2	16		TAVAYPPASLANTFGEWMAKND K	303	23	10	51.45	b11°b11y7y8°y8y9y11y12° y12*y12	2482.23	68.162	64867	3	828.08	8.16
[Q8ZL56]GPMI_SALTY 2	17		DPATGQAHTAHTNLPVPLIYVGE KNVK	452	27	5	22.55	b7°b7b9b10y3	2870.50	109.480	51038	3	957.50	-6.89
[Q8ZL56]GPMI_SALTY 2	18		EEQQDNAILNAKTPVMDALWAK	19	22	4	13.44	b13y7y13*y13	2485.25	80.745	6816	2	1243.13	2.85
[Q8ZL56]GPMI_SALTY 2	19	Oxidation+M(3)	KPMVLVILDGYGYR	5	14	3	27.86	y5y7y10	1639.87	73.254	20155	3	547.29	-10.57
[Q8ZL56]GPMI_SALTY 2	20	Oxidation+M(5)	AYDLMTLAQGEFQADTAVAGLQ AAYARDENDEFVK	202	35	4	21.45	b7b8b20y9	3837.83	90.135	14350	3	1279.95	8.91
[Q8ZL56]GPMI_SALTY 2	21	Oxidation+M(1)	MSVSKKPMVLVILDGYGYR	0	19	4	14.94	b5°b5y5y7	2172.14	78.375	2057	3	724.72	-7.98
[Q8ZL56]GPMI_SALTY 2	22	Carbamidomethyl+C(1)	CIEQVTK	423	7	1	7.32	b3	877.45	60.116	4501	1	877.45	6.61

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1	Carbamidomethyl+C(7)	LWVNPDCGLK	719	10	9	74.35	b2b3b10y4y5y6y7y8y10	1201.60	59.471	46168	2	601.31	0.20
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2		WFNTNYHYIVPEFSK	117	15	6	43.7	y5y6y12°y12y13y15	1944.92	77.262	38811	3	648.98	-3.70
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	3		QAGIDLLPVGDFAWYDHLVLTSL LLGNVPAR	52	31	11	38.6	b5*b5b6°b6*b6b31y3y6y7 y24y31	3351.79	118.864	28489	3	1117.94	6.12
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	4		LTWTQLLEEVDEALALGHK	137	19	8	20.7	b5°b5b11°b11y1y3y12y19	2166.12	118.525	26778	3	722.71	-8.90
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	5		LAAITAQDSQRENPYEV	395	18	7	50.22	b2b3y2y13y14y15y16	2061.02	46.250	25720	3	687.68	-6.04
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	6		SWFAFALQK	343	9	7	53.25	b3b5b7°b7y1y7y9	1097.56	84.685	25410	2	549.29	-13.79
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	7	Carbamidomethyl+C(1)	CVKPPVVIGDISRPAPITVEWAK	515	23	6	23.14	b2b4b6b7y2y23	2532.41	74.895	22870	3	844.81	2.22
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8		DALNSGETAALKEEWSAPIQAR	360	21	6	24.71	b3°b3b12b13°b13y7	2229.11	79.259	21616	2	1115.06	13.25
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	9		LAAITAQDSQR	395	11	9	90.2	b2b3y3y5y6y7y8y10y11	1173.62	33.052	15518	2	587.31	-1.46
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	10	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPREDVTR	549	21	4	20.52	y7y10y17y21	2435.22	91.960	2952	3	812.41	-0.90
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	11	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETR	315	22	3	19.95	b3b7b14	2441.24	102.799	43309	4	611.07	-2.30
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	12		LPVDWLLSAGLINGR	279	15	3	18.14	b6y3y12	1623.93	100.798	20684	2	812.47	2.41
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	13		HQNNDGSVDIDLFR	83	15	3	18.14	b8b11y7	1730.83	68.931	14699	2	865.92	14.18
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	14		AQESYWAGNTTR	21	12	3	26.26	b8b9y5	1383.63	39.582	11424	2	692.32	3.09
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	15		ETIAK	570	5	1	13.22	b3	561.32	27.369	10065	1	561.32	-5.65
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	16		GQQFR	132	5	1	13.22	y3	635.32	40.689	5966	1	635.32	-5.67
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	17		NDMVEYFGEHLDFVFTQNGWV QSYGSR	487	28	6	22.33	b4y5y8y9°y9*y9	3282.50	93.035	3079	3	1094.84	13.39
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	18	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	4	25.53	y8y10°y10y11	1834.90	83.626	3037	3	612.30	-20.69
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	19		GWPETR	731	6	3	29.86	y3°y3y5	745.36	78.160	1784	1	745.36	-3.11

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	20		FKLPAWPTTTIGSFPQTTEIR	420	21	3	22.33	b14y6y7	2391.27	87.286	42714	3	797.76	-1.43
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	21	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPREDVTR	549	21	3	20.52	y3y6y16	2435.22	96.918	20917	3	812.41	-1.50
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	22		GNLDANHYRTGIAEHK	449	17	3	24.97	b7b10b11	1908.95	74.472	3789	2	954.98	-8.19
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	23		LAAITAQDSQRENPYEVR	395	18	3	15.58	b13y6y10	2061.02	95.772	1855	2	1031.01	-6.52
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	24	Oxidation+M(12)	APTGEPAAAAEMTK	103	14	6	48.44	b8y4y8°y8y11y13	1360.65	56.558	28828	2	680.83	4.49
P0A275 MUCA_SALTY Protein mucA	1	Carbamidomethyl+C(13)	SLTASHGSIVVACIHNEFTVK	78	21	11	36.24	b2°b2b8°b8b13y8y9y13°y13y19y21	2270.15	76.239	58335	3	757.39	-2.26
P0A275 MUCA_SALTY Protein mucA	2		VDIFESSGASR	2	11	6	55.97	b6b7b8b9y6°y6	1167.57	37.843	4100	2	584.29	1.57
P0A275 MUCA_SALTY Protein mucA	3		HPSATYFLR	48	9	3	30.49	b5b8y6	1091.55	83.481	19698	2	546.28	-9.06
P0A275 MUCA_SALTY Protein mucA	4		HPSATYFLRVSGSSMEDGR	48	19	3	14.94	b4b8y11	2096.96	70.582	5215	3	699.66	-11.06
P0A275 MUCA_SALTY Protein mucA	5	Carbamidomethyl+C(13) ;Phosphoryl STY(8)	SLTASHGSIVVACIHNEFTVK	78	21	3	22.33	b6b7y9	2350.12	102.195	1528	2	1175.57	3.22
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	1		EAPEGTVKDIKEQEVYMGEIPLMT DNGTFVINGTER	107	36	10	34.2	b3b9b10b12b17y1y3y9y14 y36	4010.89	93.923	101004	4	1003.48	-12.11
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	2		SVFPIQSYSGNSELQYVSyr	54	20	5	22.62	b12*b12y11y14y16	2324.15	56.748	19392	3	775.39	12.92
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	3		LSLGDLDTLMPQDMINAKPISAAV K	478	25	4	22.89	b10b11b24y25	2641.39	92.531	14953	3	881.13	-2.22
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	4		NIVDGNHQMEPGMPESFNVLLK	1306	22	7	49.21	b10b11°b11b12b13y2y12	2469.19	79.933	11714	3	823.74	0.99
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	5		MNIGQILETHLGMAAK	1106	16	3	24.86	b6b8b14	1726.91	71.273	10273	2	863.96	6.72
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	6		ADKPLVGTGMER	694	12	6	32.19	b4b6y2y3y9y12	1273.64	51.911	9515	2	637.33	-10.06
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	7		KDLSEELQILEAGLFSR	957	17	3	9.71	b5°b5y7	1948.04	82.576	7765	2	974.52	-1.75
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	8		FIEQDPEGQYGLEAAFR	37	17	5	16.32	b4b13y1y2y12	1969.94	107.026	7051	3	657.32	4.40
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	9		EFFGSSQLSQFMDQNNPLSEITHK R	503	25	3	22.89	y10y11y13	2940.37	71.635	6804	4	735.85	-7.06
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	10		VNEDEMYPGEAGIDIYNLTk	735	20	3	14.37	b10b13y14	2271.03	65.623	6221	3	757.68	-6.77
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	11	Carbamidomethyl+C(11)	LGEPVFDVQECQIR	74	14	3	19.29	b7b10y6	1689.82	65.962	6118	2	845.41	-3.40

[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	12		INPIEDMPYDENGTPVDIVLNPLG VPSR	1078	28	4	17.72	b1y3y5y7	3064.56	97.458	5444	3	1022.19	8.52
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	13		VDLSTFSDDDEVLR	1158	13	5	20.64	b3b13y9y12y13	1495.71	67.570	4480	3	499.24	-8.65
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	14		DLSEELQILEAGLFSR	958	16	5	28.34	b7b8b13y3°y3	1819.92	81.884	1881	2	910.46	-12.01
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	15	Carbamidomethyl+C(11)	FTTIHIQELACVSRDTK	827	17	6	23.31	b1b2b8y8y9y17	2019.04	50.286	1598	3	673.68	2.24
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	16		IQPGDK	1059	6	4	26.85	b5°b5*b5y3	657.35	43.552	65544	1	657.35	-4.64
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	17		LGDLPTSGQITLFDGR	1200	16	3	17.16	b9b12y4	1689.88	66.420	24010	2	845.44	-1.73
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	18		LSQSGHK	324	7	5	37.46	b3y5*y5y6*y6	756.40	98.080	19202	1	756.40	-4.12
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	19		WLELGLTDEEK	996	11	4	24.31	b3y6y9°y9	1332.66	49.614	9509	2	666.83	-7.14
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	20		MMRPGEPPTR	368	10	4	28.67	b5y8y9°y9	1171.58	50.384	8622	2	586.30	10.63
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	21		EFFGSSQLSQFMDQNNPLSEITHK	503	24	5	28.31	b3b9°b9b11b12	2784.29	95.139	7445	3	928.77	-1.32
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	22		GETQLTPEEK	890	10	4	26.91	b5*b5y3y5	1131.58	25.950	6067	2	566.29	20.28
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	23		STGSYSLVTTQQLGGK	1246	16	5	17.16	b3b12°b12*b12y13	1622.81	67.615	5663	3	541.61	-19.18
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	24		GSWLDFEFDPK	180	11	4	35.31	b4b6y4y9	1340.64	46.370	5459	2	670.82	17.94
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	25		ASDVK	909	5	2	13.22	b3°b3	519.27	63.982	4823	1	519.27	-8.23
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	26		GDVLADGPSTDLGELALGQNMR	779	22	3	34.77	b8b9b10	2229.11	77.763	3263	3	743.71	12.92
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	27	Carbamidomethyl+C(11)	FTTIHIQELACVSR	827	14	4	27.07	b7°b7b9b10	1674.87	63.420	2960	3	558.96	1.53
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	28		DVHPHYGR	548	9	3	30.49	b7y4y5	1081.53	73.745	2903	2	541.27	7.22
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	29		VTPK	886	4	1	12.82	y3	444.28	103.113	2680	1	444.28	-12.23
[P06173]RPOB_SALTY DNA-directed RNA polymerase subunit beta	30		QNQLEQLAEQYDELK	1007	15	3	26.22	b3b4b6	1848.89	58.400	2635	2	924.95	-3.57

P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	31		FGEMEVWALEAYGAAYTLQEML TVK	1269	25	5	27	b11b13y6y13y14	2850.36	82.736	2555	3	950.79	-3.68
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	32		SPGVFFDS DK	151	10	6	40.13	b8°b8y3°y3y4y7	1098.53	93.992	1595	1	1098.53	18.00
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	33		GMPIATPVFDGAKEAEIK	1178	18	5	38.59	b4b5b6°b6b13	1873.95	51.317	83678	3	625.32	-11.33
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	34	Carbamidomethyl+C(17)	VVQEDRFTTIIHQELACVSR	821	20	3	14.37	b3b11y11	2401.21	73.367	16901	2	1201.11	-8.64
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	35		INAMLKQQQEVAK	1127	13	5	43.1	b4b12y4y7y12	1500.80	70.539	9524	2	750.90	-13.75
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	36		VDLSTFSDDDEVLR LAENLR	1158	19	3	21.9	b3b7b13	2192.15	72.392	9193	2	1096.58	11.69
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	37		EAAESLFENLFFSEDRYDLSAVGR	378	24	4	16.87	b7b13y12y19	2765.32	74.235	5626	4	692.09	4.77
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	38		VIVSQLHRSPGVFFDS DK	143	18	3	24.5	y9y12y13	2031.08	82.752	3183	2	1016.05	9.20
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	39		QKVDLSTFSDDDEVLR	1156	15	3	26.22	y7y10y14	1751.87	63.906	3064	2	876.44	-7.80
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	40		AGFEVRDVHPH YGR	542	15	4	29.44	b3y3y4y6	1740.87	58.355	2926	2	870.94	10.52
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	41		EFIQRAYDLGADV R	1142	14	3	19.29	b4b11y11	1652.83	51.235	2462	3	551.61	-7.16
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	42		KGMPIATPVFDGAK	1177	14	3	27.07	b6b11b12	1431.78	76.254	2344	2	716.39	9.46
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	43		MVYSYTEKK	0	9	3	30.49	b3b4y8	1148.58	81.648	2103	1	1148.58	10.20
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	44		VAFMPWNGYNFEDSILVSE RVVQ EDR	801	26	4	35.36	b7b8b9y7	3100.53	69.835	1852	3	1034.18	14.80
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	45	Carbamidomethyl+C(11)	FTTIIHQELACVSRDTK	827	17	5	33.72	y4y6y9y10°y10	2019.02	101.205	1771	2	1010.01	-6.65
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	46		MNIGQILETHLGMAAKGIGDK	1106	21	3	20.52	b3b5b12	2197.12	102.650	1579	4	550.04	-11.22
P06173 RPOB_SALTY DNA-directed RNA polymerase subunit beta	47	Oxidation+M(7)	ALEIEEMQLK	944	10	4	40.13	b3y5y7y8	1219.63	65.203	14756	2	610.32	4.30