

SA123 + Zn(II) LC-MS run 1: 123_Zn_220709_1a2_01

Protein name	Peptide Rank	Peptide Modification	Peptide Sequence	Peptide sequence start	Peptide sequence Length	Peptide Matched Products	Peptide Score	By Matches	Precursor MH+ (Da)	Retention time (min)	Intensity	z	Precursor m/z	MH+ Error (ppm)
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	51	307.3	b2 ° b2b3 ° b3b4 ° b4b5 ° b5b6 ° b6b7 ° b7b8 ° b8b9b10b12 ° b12b14 ° b14b17b18b21 ° b21y1y2y3y4y5y6 ° y6y7 ° y7y8y9y10y11y12y13 ° y13y14y15*y15y16 ° y16*y16y17 ° y17*y17y18y21	2216.11	97.460	467949	2	1108.56	6.17
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	8	57.01	y2y6y7y8y9y10*y10y11	1304.56	33.525	124687	2	652.78	-2.25
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	3		REEESAAAAEVEER	40	14	11	65.45	b6b8 ° b8b10y1y3y4y5y7y11y14	1575.74	32.948	58807	2	788.37	6.82
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	4		TWTGQGR	107	7	8	32	b3 ° b3b7y5y6 ° y6y7*y7	805.39	23.151	4059	2	403.20	-10.38
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	5		QLEDFLIK	128	8	3	35.64	b3b4b5	1005.56	25.956	2596	2	503.28	-2.19
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	6	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	6	37.48	b8y4y5y8*y8y11	1624.76	47.884	2907	3	542.26	10.22
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	7		ILNNIR	6	6	4	23.13	b4*b4y5*y5	742.46	28.963	1915	1	742.46	0.58
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	8		YSYVDENGETKTWTGQGR	96	18	4	33.63	y4y12y13y14	2090.92	47.605	131921	3	697.65	-8.06
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	9		REEESAAAAEVEER	40	14	3	23.17	y3y4y10	1575.73	33.665	11945	2	788.37	4.34
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	10		AARPAKYSYVDENGETK	90	17	3	13.09	b7b12y9	1898.95	54.280	6720	3	633.66	14.98
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	11		TWTGQGRTPAVIK	107	13	4	24.01	b3b10b11*b11	1414.76	62.660	4434	2	707.88	-14.50
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	12	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEVVNER	19	21	6	28.93	b5b8b11y3*y3y4	2563.23	125.581	3804	4	641.56	-12.86
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	13		KAMEEQGK	120	8	3	30.87	b3b5y7	920.44	70.863	3070	1	920.44	-9.15
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	14	Oxidation+M(17)	EMLIADGIDPNELLNSMAAAK	62	21	4	20.41	b15y7y12y13	2232.11	97.306	17877	2	1116.56	9.73
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	15	Oxidation+M(7)	LQQYREMLIADGIDPNELLNSMAAAK	57	26	3	17.08	b4b10b12	2920.47	105.852	6077	3	974.16	5.52
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	16		ADGIDPNELLNSMAAAK	66	17	4	18.19	b3 ° b3b5b10	1729.86	97.429	3031	2	865.43	9.95
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	1		YQINPQGMdTSSMDVFVQQYADTVK	176	25	21	84.91	b2*b2b3b4*b4b6*b6b10b12b14b16y1y4y5y6y7*y7y9*y9y14y25	2865.30	87.130	96740	3	955.77	-1.19
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	2		AAADLQLQGVPMFVNGK	158	18	25	141.67	b2b4b5 ° b5b6*b6b7*b7b10b15y2y3y4*y4y5*y5y6y7y8y10y11*y11y12*y12y18	1829.96	81.356	87099	2	915.48	2.40
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	3		TQTVQSAADIR	116	11	12	56.5	b2b3 ° b3*b3b8y2y4y5y7*y7y9y11	1189.61	35.779	40413	2	595.31	-4.82
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		ELTQAWAVAMALGVEDK	88	17	4	20.96	b4y3y6y8	1831.92	61.048	7582	2	916.47	-0.80
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	5		YHVEFLGPLGK	77	11	3	22.75	b8y5y6	1259.69	74.130	6635	2	630.35	5.33

P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	6	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	5	13.09	b14°b14*b14y7y11	1847.91	70.006	4874	3	616.64	-7.86
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	7	Oxidation+M(13)	YQINPQGMDTSSMDVVFVQQYAD TVK	176	25	7	26.09	b3b7b11y8y9*y9y15	2881.28	74.102	1908	2	1441.14	-9.15
P0A1D5 CH10_SALTY 10 kDa chaperonin	1		ILDNGTVQPLDVK	47	13	22	125.27	b2b8*b8b10*b10b11b13y2y3y5y6°y6*y6y7y8y9y10y11°y11*y11y12y13	1411.77	57.893	344098	2	706.39	-3.20
P0A1D5 CH10_SALTY 10 kDa chaperonin	2		VGDIVIFNDGYGVK	60	14	30	200.39	b2b3b4b5°b5b6b10°b10b11*b11b13*b13y1y2y3y4y5y6°y6y7y8y9y10*y10y11*y11y12y13*y13y14	1495.78	74.169	206209	2	748.39	-0.82
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	16	84.66	b2b3°b3b5°b5b14°b14y2y3y6y7y8y9y11y12y14	1188.65	44.162	160184	2	594.83	-7.91
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIAVGK	37	8	9	42.12	b2°b2b3°b3y2y3y4y6y8	786.47	41.684	7740	1	786.47	-8.77
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		IDNEEVLIMSESDILAIVEA	77	20	8	25.72	b3b4b7°b7°b7b11y11°y11	2203.10	136.439	3146	2	1102.06	-0.33
P0A1D5 CH10_SALTY 10 kDa chaperonin	6		SIRPLHDR	1	8	6	49.9	b3°b3b5b7y5°y5	993.55	28.964	2407	2	497.28	-8.97
P0A1D5 CH10_SALTY 10 kDa chaperonin	7		SAGGIVLTGSAAGK	20	14	1	7.36	b4	1170.64	44.114	29992	2	585.83	-0.10
P0A1H5 EFTU_SALTY Elongation factor Tu	1		AIDKPFLPIEDVFSISGR	205	19	19	113.26	b2b4b6b7b8b13y1y2y3y4y5y6°y6y7y8°y8y9°y9y11	2117.15	105.745	614047	3	706.39	-6.80
P0A1H5 EFTU_SALTY Elongation factor Tu	2		TTLTAAITTVLAK	25	13	15	97.25	b2°b2b3°b3b13y2y3y5y6y7y8y9y10y11y13	1303.78	85.311	404512	2	652.39	-5.80
P0A1H5 EFTU_SALTY Elongation factor Tu	3		IIELAGFLDSYIPEPER	188	17	28	168.47	b2b3b5b6b7b11°b11b12°b12b14y1y2y3°y3y4°y4y5y6y8°y8y9y10y11y12°y12y13°y13y17	1962.03	102.600	347104	2	981.52	4.48
P0A1H5 EFTU_SALTY Elongation factor Tu	4		GITINTSHVEYDTPTR	59	16	22	157.1	b2b3°b3b12°b12b13y2y3y4y5y6y7y8y9°y9y10°y10y11y12y13y14y16	1803.87	50.092	342064	3	601.96	-11.30
P0A1H5 EFTU_SALTY Elongation factor Tu	5		TTDVTGTIELPEGVEMVMPGDNI K	334	24	37	191.81	b2°b2b3°b3b4b5°b5b8°b8b10°b10b11b13b14b16y3y4y5y6°y6°y6y7°y7y8y9°y9*y9y10°y10y12°y12y14°y14y15y16y20y24	2546.24	87.290	294106	2	1273.62	2.21
P0A1H5 EFTU_SALTY Elongation factor Tu	6		QVGVPYIIVFLNK	124	13	10	64.54	b3b4°b4b13y4y5y6y9y11y13	1489.87	99.768	291844	2	745.44	-1.97
P0A1H5 EFTU_SALTY Elongation factor Tu	7		ELLSQYDFPGDDTPIVR	155	17	20	154.72	b2b3°b3b5°b5b6b7y1y3y4y5y6y8y9y10y11y12y13y14y17	1964.96	77.410	255876	2	982.98	-1.86
P0A1H5 EFTU_SALTY Elongation factor Tu	8		ALEGDAEWEAK	177	11	17	86	b1b2b4°b4y1y2y4°y4y5y6y7y8y9°y9y10°y10y11	1218.56	46.826	161333	2	609.78	-5.11
P0A1H5 EFTU_SALTY Elongation factor Tu	9	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	9	59.4	b1b2y2y3y4y6y7y8y10	1187.51	53.409	111210	2	594.26	-4.93
P0A1H5 EFTU_SALTY Elongation factor Tu	10	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEV	137	18	9	37.51	b2b3y2y3y5y6y8y11y18	2224.00	106.657	70110	2	1112.51	10.21

P0A1H5 EFTU_SALTY Elongation factor Tu	11		VGEEVEIVGIK	238	11	6	31.78	b7b10y2y3y4y11	1171.66	45.490	9476	2	586.33	4.27
P0A1H5 EFTU_SALTY Elongation factor Tu	12	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	6	20.49	b2b4y2y4y5°y5	1768.78	37.149	7099	3	590.26	-5.25
P0A1H5 EFTU_SALTY Elongation factor Tu	13		MVVTLIHPIAMDDGLR	358	16	18	164.67	b3b5°b5b6b11y3y4y5y7y8y9y10°y10y11y12y13y14y15	1780.91	79.829	693116	3	594.31	-17.55
P0A1H5 EFTU_SALTY Elongation factor Tu	14		AGENVGVLLR	270	10	16	112.64	b4°b4b5°b5°b5b6b7°b7°b7y3y4y5y6y7y9*y9	1027.57	56.838	297453	2	514.29	-16.87
P0A1H5 EFTU_SALTY Elongation factor Tu	15		TVGAGVVAK	382	9	8	81.27	b3b4°b4b7y3y5y7y8	801.47	28.902	191193	2	401.24	-19.88
P0A1H5 EFTU_SALTY Elongation factor Tu	16		NMITGAAQMDGAILVVAATDGPMPQTR	90	27	6	12.37	b16b22y7°y7y9°y9	2729.40	97.703	30466	4	683.11	22.45
P0A1H5 EFTU_SALTY Elongation factor Tu	17		LLDEGR	264	6	3	34.38	y3y4y5	702.37	27.102	10748	1	702.37	-6.60
P0A1H5 EFTU_SALTY Elongation factor Tu	18		GYRPQFYFR	325	9	4	41.04	b3b5°b5b8	1233.61	60.660	8764	2	617.31	-3.86
P0A1H5 EFTU_SALTY Elongation factor Tu	19		TKPHVNVGTIGHVDHGK	8	17	7	54.83	y3y5y6°y6y7y8y12	1795.92	38.122	1735	2	898.46	-19.71
P0A1H5 EFTU_SALTY Elongation factor Tu	20		GTVVTGRVER	224	10	3	22.12	b3b5y6	1073.60	26.626	46178	2	537.30	-10.35
P0A1H5 EFTU_SALTY Elongation factor Tu	21	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLE LVEMEV	124	31	12	60.43	b4°b4b6°b6b16y4y5y6y7y8y12y27	3694.86	127.777	45053	3	1232.29	3.57
P0A1H5 EFTU_SALTY Elongation factor Tu	22		ELLSQYDFPGDDTPIVRGSALK	155	22	3	11.33	b6b9y13	2421.26	68.468	21413	3	807.76	11.70
P0A1H5 EFTU_SALTY Elongation factor Tu	23		DEGGRHTPFKK	314	11	3	19.74	b3b10y3	1290.63	59.806	7391	2	645.82	3.50
P0A1H5 EFTU_SALTY Elongation factor Tu	24		HTPFFKGYRPQFYFR	319	15	5	23.8	b4°b4b7b9y4	1991.02	74.172	3078	3	664.35	8.15
P0A1H5 EFTU_SALTY Elongation factor Tu	25		ARGITINTSHVEYDTPTR	57	18	5	21.61	b10y9y11°y11y12	2031.02	67.889	1916	3	677.68	-4.63
P0A1H5 EFTU_SALTY Elongation factor Tu	26	Phosphoryl STY(9)	GQVLAKPGTIKPTK	289	15	4	23.8	b9y5y8y11	1654.91	58.447	35449	3	552.31	9.96
P0A1H5 EFTU_SALTY Elongation factor Tu	27	Oxidation+M(1)	MVVTLIHPIAMDDGLR	358	16	3	22.09	y3y9y10	1796.91	74.297	22441	3	599.64	-14.81
P0A1H5 EFTU_SALTY Elongation factor Tu	28	Oxidation+M(18)	TTDVTGTIELPEGVEMVMPGDNI K	334	24	4	13.24	b3b12y4y8	2562.25	80.048	3840	2	1281.63	8.58
P0A1H5 EFTU_SALTY Elongation factor Tu	29		TINTSHVEYDTPTR	61	14	4	29.66	b4b10b11b13	1633.79	50.064	19045	2	817.40	4.03
P0A1H5 EFTU_SALTY Elongation factor Tu	30		GITINTSHVEYDTPTR	59	16	1	7.74	y11	1785.87	50.090	21472	3	595.96	-3.42
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	1		SGFAEDEVVAVSK	35	13	7	37.48	b3y2y3y4y8y10y13	1337.65	54.885	215051	2	669.33	-2.83
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	2		LGEIEYR	48	7	7	54.5	b3y2y3y4y5y6y7	879.44	42.732	169371	2	440.23	-13.81
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	3		FNSLTPEQQR	106	10	25	123.89	b2°b2b3°b3°b3b4°b4b5b8°b8y2*y2y3*y3y4°y4y5*y5y6y7°y7y8°y8y9y10	1219.60	38.583	111298	2	610.31	-2.30
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	4		EIPMEVKPEVR	55	11	13	79.97	b2b5b9b10y1y2y4y6y7y8°y8y9y11	1326.71	48.893	59877	2	663.86	2.58
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	5		VSGYAVR	99	7	5	32	b4y2y5y6y7	751.40	27.733	40491	2	376.20	-14.54
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	6		FNSLTPEQQRDVIA	106	15	15	47.34	b2°b2b3°b3b7b8°b8°b8y6y8*y8y10*y10y11y15	1773.90	47.940	34680	3	591.97	-12.94
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	7		LGEIEYREIPMEVKPEVR	48	18	5	16.78	b9b12y4y11y18	2187.15	64.437	25829	3	729.72	-0.22

Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	8		MITGIQITK	0	9	4	33.25	y3y4*y4y6	1004.57	55.480	211127	2	502.79	-15.19
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	9		VEGGQHNLNVNVLRR	66	13	6	50.49	y4*y4y6y7y8y12	1434.76	50.846	151307	3	478.92	-17.44
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	10		TFTESL	121	6	1	11.88	y4	697.34	41.344	5425	1	697.34	-0.26
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	11		ETLEDAVK	80	8	4	35.64	y4y6y7°y7	904.45	54.319	4255	2	452.73	-9.99
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	12		AANDDLLNSFWLLDSEKGEAR	9	21	24	213.14	b3b4b5°b5*b5b7*b7y3y4y5y7y8°y8y9y10y11y12y13y14y15y16y17y18y19	2364.14	93.386	381989	3	788.72	-2.48
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	13		RETLEDAVK	79	9	5	37.97	b3b5y5°y5y8	1060.57	32.876	28365	2	530.79	5.76
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	14	Carbamidomethyl+C(5)	GEARCIVAK	26	9	3	25.47	b4b7y3	1003.55	39.677	17162	2	502.28	12.35
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	15		VEGGQHNLNVNVLRR	66	14	8	50.61	b4b5b6b7°b7b9°b9y3	1590.88	46.824	9225	2	795.94	-3.53
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	16		LGEIEYREIPMEVKPEVR	48	18	3	19.99	b7b8y11	2187.18	109.397	4827	3	729.73	13.73
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	17		SGFAEDEVVAVSKLGEIEYR	35	20	4	11.82	b4b12y3°y3	2198.10	101.281	3912	2	1099.55	1.56
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	18		FNSLTPEQQRDVIAAR	106	15	6	23.8	b3b4*b4b6y11*y11	1773.93	69.070	2262	3	591.98	1.65
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	19		VSGYAVRFNSLTPEQQR	99	17	5	20.96	b4b6b13*b13y11	1951.99	103.368	2166	3	651.33	-6.13
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	20	Phosphoryl STY(2)	ITGIQITK	1	8	4	27.86	b6y6y7*y7	953.49	32.034	12293	2	477.25	-5.95
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	21		PMEVKPEVR	57	9	1	7.24	b3	1084.58	48.928	42237	2	542.79	-5.40
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	22		EIPMEVKPEVR	55	11	0	3.77		1308.67	48.916	12768	3	436.90	-14.92
P64076 ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	30	186.76	b2*b2b3*b3b4*b4b5*b5b6*b6b7°b7*b7b9*b9b14y1y2y3y4y5y6y7y8y10y11y12y13y15*y15	1605.88	86.397	344419	2	803.44	-1.90
P64076 ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	28	177.88	b2b3b4b9°b9b11b14°b14b15b16b18y1y2y4y5*y5y6y7y8y9y10y12y13*y13y14y16y17y22	2118.06	75.939	201569	2	1059.53	2.42
P64076 ENO_SALTY Enolase	3		AVGAVNGPIAQAILGK	66	16	9	48.92	b2b3b5y3y5y10y11y12y16	1478.86	75.749	175090	2	739.94	-3.38
P64076 ENO_SALTY Enolase	4		GMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	200	31	18	111.16	b2b4b5°b5b13y2y3y4y5y6y7y8y9y10y14y18y19y31	2989.46	95.608	171689	3	997.16	2.53
P64076 ENO_SALTY Enolase	5		GIANSILIK	333	9	5	33.25	b2y3y6y7y9	928.57	61.321	169153	2	464.79	-12.36
P64076 ENO_SALTY Enolase	6		YSMPVPMNINIINGEHADNNVDIQEFMIQPVGAK	143	34	17	86.27	b2°b2b3°b3b4b5b23y3y5y6y7y8y9y13y29y31y34	3759.77	99.031	108861	3	1253.93	2.79
P64076 ENO_SALTY Enolase	7	Carbamidomethyl+C(16)	AAGYELGKIDITLAMDCAASEFYKDGK	231	26	10	33.48	b2b4b6b9b15y3y6y9y11y26	2824.29	100.624	74715	4	706.83	-10.98
P64076 ENO_SALTY Enolase	8		IQLVGDDLFTVNTNK	311	14	14	50.61	b2*b2b3b14y2y4°y4y5°y5*y5y10y11y12y14	1562.85	78.221	65825	2	781.93	4.06
P64076 ENO_SALTY Enolase	9		GMPLYEHIAELNGTPGK	126	17	7	28.53	b2y2y3y6*y6y7y9	1826.89	67.950	50772	3	609.64	-9.02
P64076 ENO_SALTY Enolase	10		DAGYTAVISHR	360	11	12	94.24	b2b3b4b7y3y4y5y6y7°y7y9y11	1189.59	42.362	46686	2	595.30	-2.67

P64076 ENO_SALTY Enolase	11		QYPIVSIEDGLDESDWDGFAYQTK	282	24	9	34.09	b6°b6b10b11y1y4y6y8y9	2776.28	94.397	46000	2	1388.64	6.68
P64076 ENO_SALTY Enolase	12		ILKEGIEK	325	8	10	53.37	b2b7y2°y2y3y4y5°y5y6y8	929.56	30.240	37958	2	465.28	-11.36
P64076 ENO_SALTY Enolase	13		GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	10	35.33	b6b8b10y5°y5y6y7°y7y24y 30	2856.37	92.652	25329	3	952.80	4.36
P64076 ENO_SALTY Enolase	14		AAGYELGK	231	8	9	55.13	b1b3b4b5b8y2y6°y6y7	808.41	31.999	12079	2	404.71	-12.76
P64076 ENO_SALTY Enolase	15		EALELRDGDK	46	10	4	22.12	b7y2y3y6	1145.58	34.579	11573	2	573.29	-3.52
P64076 ENO_SALTY Enolase	16		SNFGANAILAVSLANAK	103	17	5	20.5	b2°b2b4b8b11	1660.88	79.160	3232	2	830.94	-11.98
P64076 ENO_SALTY Enolase	17		IMIDLDGTENK	92	11	7	30.2	b7y5y8°y8y9°y9*y9	1248.64	59.682	23523	2	624.82	17.70
P64076 ENO_SALTY Enolase	18		AFTSEEFTHFLEELTK	266	16	3	13.71	b6y5y11	1928.91	58.259	4385	3	643.64	-8.16
P64076 ENO_SALTY Enolase	19		IEEALGEK	411	8	6	58.14	b4°b4b6y3y4y7	888.46	60.580	3835	1	888.46	-3.02
P64076 ENO_SALTY Enolase	20		APYNGR	419	6	1	11.88	b4	677.33	46.731	2198	1	677.33	-9.82
P64076 ENO_SALTY Enolase	21		VLGDKIQLVGDDLFVTNTK	306	19	8	50.85	b3b4y4y5y6y10°y10y13	2075.12	80.579	58304	3	692.38	-9.29
P64076 ENO_SALTY Enolase	22		GKGMNTAVGDEGGYAPNLGSNA EALAVIAEAVK	198	33	10	56.39	b4b7b9b14b15y3y4y5y25y 26	3174.58	90.598	48617	3	1058.87	2.31
P64076 ENO_SALTY Enolase	23		EIIDSRGNPTVEAEVHLEGGFVGMA AAPSGASTGSR	10	36	4	17.59	y4y11°y11y21	3569.75	93.685	21948	4	893.19	4.51
P64076 ENO_SALTY Enolase	24		DQAGIDKIMIDLDGTENK	85	18	6	27.72	b5y4°y4y5y7y11	1975.96	75.349	19686	2	988.48	-2.72
P64076 ENO_SALTY Enolase	25		AAAAAKGMPLYEHIAELNGTPGK	120	23	3	11.17	b11y5y13	2310.23	67.919	3672	2	1155.62	15.01
P64076 ENO_SALTY Enolase	26		EALELRDGDK	46	10	5	34.34	b7b8y5°y5y7	1145.57	66.247	2020	2	573.29	-4.80
P64076 ENO_SALTY Enolase	27		DGKYVLAGEGNK	254	12	5	17.94	b9°b9b11°b11y3	1250.65	46.009	1714	3	417.56	12.98
P64076 ENO_SALTY Enolase	28		ANSILIK	335	7	3	7.74	b3°b3*b3	758.48	61.328	29714	1	758.48	-0.97
P64076 ENO_SALTY Enolase	29		GYTAVISHR	362	9	0	3.77		1003.53	42.357	16304	2	502.27	-1.58
P64076 ENO_SALTY Enolase	30		YSMPVPMMNININGGEHA	143	17	2	26.24	y13y14	1860.84	99.032	3109	3	620.95	-4.13
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	47	282.53	b2b3b4°b4*b4b5°b5*b5b6 *b6b7°b7*b7b8*b8b14y3y 4y5y6y7°y7*y7y8°y8*y8y9 y10y11y13y14*y14y15°y15 *y15y16*y16y17y18°y18y2 0y21y22°y22y23y24*y24	2574.32	98.645	578353	3	858.78	-1.61
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	2		AGIALNDNFVK	296	11	17	97.25	b3b4b8b10y1y2y3y4*y4y6 *y6y7*y7y8*y8y11*y11	1161.62	61.938	295826	2	581.31	-6.83
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	3		GASQNIIPSSTGA AK	198	15	19	138.23	b3b5*b5b6*b6b7*b7b13b1 4y2y3y4y5y7y8y9y10y11y 15	1401.73	41.353	222665	2	701.37	-4.09
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		AATYEQIK	249	8	17	80.64	b1b3b7°b7y2y3*y3y4*y4y 5*y5y6°y6*y6y7*y7y8	923.47	31.524	190707	2	462.24	-13.42
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		SDIEIVAINDLLDAEY MAYMLK	24	22	13	54.77	b2b5b6b7b10*b10y3y4y9y 11°y11y14y22	2530.24	127.188	127056	3	844.09	-1.93
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		VPTPNVSVVDLTVR	232	14	10	78.34	b3y2y4y5y6y7y8y11y12y1 4	1495.84	71.538	112222	2	748.42	-4.24
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		VVLTGPSKDNTMPFVK	116	16	9	50.78	b1b2b3y5y7y9y11y14y16	1732.91	58.141	69223	3	578.31	-14.16
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		VLDLIAHISK	321	10	7	59.4	b2y2y3y4y5y6y8	1108.66	66.190	51401	2	554.84	-7.93
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		TVDGPSHKDWR	184	11	9	54.46	b1b4b5b9y3y5y8°y8y11	1297.63	29.012	8573	2	649.32	-0.66

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		VLPELNGK	217	8	6	42.12	b3y3y4*y4y6°y6	869.49	45.307	65844	2	435.25	-17.69
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11		DNTPMFVK	124	8	3	35.64	y5y6y7	951.46	48.869	41894	2	476.24	4.23
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12	Carbamidomethyl+C(12) ;Carbamidomethyl+C(16))	YEGQDIVSNASCTTNCLAPLAK	138	22	4	20.15	b9y7y10y11	2412.13	73.301	8461	3	804.71	4.76
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13		LVSWYDNETGYSNK	307	14	5	23.17	y4*y4y6*y6y7	1675.78	41.161	7575	2	838.39	11.07
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEGQDIVSNASCTTNCLAPLAK	132	28	35	223.1	b4*b4b5b7b8b10*b10b11° b11*b11b12*b12b13b15b1 6*b16b24*b24b26b27y3y4 y5y6y8y9y10y11y12°y12y1 4*y14y15*y15y16	3044.41	67.391	312262	3	1015.48	0.80
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15		VINDNFGIIEGLMTTVHATTATQK TVDGPSHK	160	32	3	22.24	b5b6y13	3395.72	79.548	6020	4	849.69	-0.86
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		TVDGPSHKDWR	184	11	5	30.2	b9y4y5°y5y9	1297.62	30.706	5530	3	433.21	-6.59
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		GGRGASQNIIPSSTGAAK	195	18	16	98.95	b5b6b7b8°b8*b8b9*b9b11 b15y3y4y8y9°y9y13	1671.88	37.178	4893	2	836.45	4.38
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		KHITAGAK	107	8	3	43.42	y3y5y7	825.48	12.671	4601	2	413.25	-13.38
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19		DNTPMFVKGANFDK	124	14	3	15.39	b8y5y12	1583.77	88.799	4338	3	528.60	11.72
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20		AGIALNDNFVKLVSWYDNETGYS NK	296	25	3	17.2	b4b7b9	2818.37	110.170	4105	3	940.13	2.25
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	21		YDSTHGRFDGTVEVK	46	15	4	20.49	b10y7y8°y8	1710.80	47.855	2269	2	855.90	-3.92
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	22	Oxidation+M(13)	VINDNFGIIEGLMTTVHATTATQK	160	24	3	11.05	b8b10y9	2590.32	42.491	2868	6	432.56	1.41
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	23	Oxidation+M(4)	LTGMAFR	225	7	6	71.77	b4b6y3y4y5y6	811.41	32.886	2011	2	406.21	-6.62
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	24	Oxidation+M(20)	SDIEIVAINDLLDAEYMAYMLK	24	22	6	43.2	b16b17b18y10y15y16	2546.22	136.879	1547	2	1273.61	-7.38
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	25		LNDNFVK	300	7	3	16.27	b3b5*b5	849.44	61.867	19150	1	849.44	-9.63
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	26		LDLIAHISK	322	9	2	7.4	b6°b6	1009.59	66.191	14206	2	505.30	-9.49
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	27		VVLTGPSKDNTPMFVK	116	16	0	6.91		1715.89	58.096	2400	3	572.63	-5.62

P0A299 RL7_SALTY 50S ribosomal protein L7/L12	1		DQIIEAVSAMSVMDEVVELISAMEEK	5	25	33	181.9	b2°b2*b2b3b4b5*b5b6b7*b7b8°b8b9°b9*b9b10y2°y2y3y4y5°y5y6°y6y7°y7y8y9°y9y10°y10y11y25	2737.33	137.118	77028	3	913.12	-0.71
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		SITKDKIIEAVSAMSVMDEVVELISAMEEK	1	29	8	19.63	b1b10*b10y3y4y12°y12y29	3166.58	89.040	49936	4	792.40	-3.32
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	3		EAKDLVESAPAALKEGVSK	82	19	7	21.13	b7°b7b11b12°b12y7y19	1942.05	55.489	40664	3	648.02	-1.26
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	4		DLVESAPAALK	85	11	4	26.73	y4y5y8y11	1113.60	54.178	22208	2	557.30	-14.58
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	5		MSITKDKIIEAVSAMSVMDEVVELISAMEEK	0	30	6	19.33	b7y3y9y13°y13y15	3297.61	99.698	13860	3	1099.87	-8.29
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	6		EGVSKDDAEALK	96	12	6	28.15	b2°b2b4b6b11b12	1261.64	74.100	2671	1	1261.64	6.97
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	7		SLEEAGAEVEVK	109	12	7	71.39	b3b11y3y5y7y9y10	1260.63	46.003	6673	2	630.82	-1.65
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	8		FGVSAAAAVAVAAGPAEAAEEK	30	22	15	79.75	b3b5b6b7b9°b9b12y3°y3y4°y4y5y10y15y17	1987.03	45.979	6583	5	398.21	9.46
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	9		EGVSKDDAEALK	96	12	4	33.96	b3y6y7y8	1261.64	54.312	5712	2	631.32	10.45
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	10		FGVSAAAAVAVAAGPAEAAEECT EFDVILK	30	30	6	28.16	b3b5b6b8°b8b10	2932.51	136.343	4586	3	978.18	-6.58
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	11		MSITKDKIIEAVSAMSVMDEVVELISAMEEK	0	30	3	11.06	b3b21y9	3297.61	110.655	3862	3	1099.88	-6.81
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	12	Phosphoryl STY(5)	DLVESAPAALK	85	11	5	42.24	b3b4y7y8y10	1193.57	48.795	4336	2	597.29	-2.86
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	13	Phosphoryl STY(5)	DLVESAPAALKEGVSK	85	16	3	22.09	b3b4b13	1693.82	67.583	3582	2	847.41	-9.51
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	14	Phosphoryl STY(15)	DLVESAPAALKEGVSKDDAEALK	85	23	7	42.97	b4b7b8y6y7°y7y8	2436.20	136.322	1825	2	1218.60	5.81
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	15	Oxidation+M(1)	MSITKDKIIEAVSAMSVMDEVVELISAMEEK	0	30	3	21.67	b7b8y3	3313.64	85.010	15787	4	829.17	3.39
P65702 PGK_SALTY Phohoglycerate kinase	1	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	20	154.25	b2b3b4b5b7b8y1y2y3y4y5y8y9y10y12y13y14y15y16y20	2002.04	99.720	247558	2	1001.52	4.82
P65702 PGK_SALTY Phohoglycerate kinase	2		SVNDVKEDEQILDIGDASAQQLAEILK	272	27	10	32.14	b9b13°b13b14y1y5y6y10y12y27	2941.51	101.304	177656	3	981.17	2.41
P65702 PGK_SALTY Phohoglycerate kinase	3		VATEFSETAPATLK	258	14	25	148.4	b1b2b3°b3b4°b4b6°b6b7b9y1y2y3y5°y5y6y7y9°y9y10y11°y11y12y13y14	1464.76	53.048	163755	2	732.88	1.83
P65702 PGK_SALTY Phohoglycerate kinase	4	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	15	113.18	b2b6b7°b7b9y2y3y5y7y8y9y10y11y12y14	1599.84	69.152	121223	2	800.43	2.06
P65702 PGK_SALTY Phohoglycerate kinase	5		TILWNGPVGVFEPNFR	302	17	18	115.28	b2y1y4y5y6°y6y7°y7y8°y8y10y11y12y13°y13°y13y14y17	1993.04	107.046	113327	2	997.02	4.29
P65702 PGK_SALTY Phohoglycerate kinase	6		MTDLDLAGKR	5	10	8	70.65	b2y3y4y5y6y7y9y10	1119.58	43.500	83170	2	560.29	-5.56
P65702 PGK_SALTY Phohoglycerate kinase	7		LTVLDSLSK	197	9	10	47.52	b2°b2y2y4y5y6°y6y7°y7y9	975.56	62.595	70840	2	488.29	-8.70
P65702 PGK_SALTY Phohoglycerate kinase	8		KDDEALSK	119	8	5	14.84	b2b3b7°y6y8	905.46	31.515	67321	2	453.23	1.82
P65702 PGK_SALTY Phohoglycerate kinase	9		VLPAVAMLEER	373	11	6	40.99	y5y7°y7y8°y8y9	1227.67	81.085	61592	2	614.34	-2.09
P65702 PGK_SALTY Phohoglycerate kinase	10		ADLNVPVKEGK	19	11	14	66.96	b2°b2b5°b5b9b10°b10y1y2y4y6y8y9y11	1169.65	37.265	56330	2	585.33	-4.80
P65702 PGK_SALTY Phohoglycerate kinase	11		LVKDYLDGVDVAEGELVVLENV R	90	23	5	22.67	b14b15y2y3y6	2544.36	98.259	56027	3	848.79	0.29

P65702 PGK_SALTY Phohoglycerate kinase	12		MTDLDLAGK	5	9	7	25.47	b2b6y2y3y8°y8y9	963.48	48.872	35036	2	482.24	-4.43
P65702 PGK_SALTY Phohoglycerate kinase	13		AQASTHGIGK	146	10	11	63.66	b2*b2b3*b3y2y4y5y6y7y8y10	969.50	16.372	18310	2	485.26	-8.18
P65702 PGK_SALTY Phohoglycerate kinase	14		ASLPTIELALK	38	11	4	28.77	b5b7y4y8	1155.69	77.924	71407	2	578.35	-6.34
P65702 PGK_SALTY Phohoglycerate kinase	15	Carbamidomethyl+C(5)	YAALCDVFMDFAGTAHR	128	18	6	24.05	b9b13y7°y7y9y11	2043.98	92.110	13659	3	682.00	16.54
P65702 PGK_SALTY Phohoglycerate kinase	16		ISYISTGGGAFLEFVEGK	355	18	5	35.81	b8b9b10y8y11	1874.99	62.505	8242	2	938.00	17.25
P65702 PGK_SALTY Phohoglycerate kinase	17		LSNPVR	84	6	4	34.38	y3y4*y4y5	685.39	28.369	7727	2	343.20	-11.75
P65702 PGK_SALTY Phohoglycerate kinase	18		VTSDAR	30	6	1	11.88	y4	648.33	65.392	3271	1	648.33	-1.22
P65702 PGK_SALTY Phohoglycerate kinase	19		VMVTSHLGRPTEGEYNEEFSLPVVNYLK	53	29	7	40.67	b4b5b6°b6b9b13b16	3321.67	136.297	2242	3	1107.89	-4.41
P65702 PGK_SALTY Phohoglycerate kinase	20		SLYEADLVDEAK	231	12	10	85.95	b4b5°b5b7b8°b8b9b10b11y4	1352.66	46.765	2152	3	451.56	4.87
P65702 PGK_SALTY Phohoglycerate kinase	21		IADQLIVGGGIANTFVAAQGHSVGK	206	25	3	10.97	b3y9y19	2423.25	111.368	1657	3	808.42	-21.76
P65702 PGK_SALTY Phohoglycerate kinase	22		VTSDARIR	30	8	3	27.86	b4y5y6	917.51	48.865	69514	2	459.26	-6.85
P65702 PGK_SALTY Phohoglycerate kinase	23		VATEFSETAPATLKSVNDVK	258	20	3	21.24	b5b9b10	2107.09	75.324	40619	3	703.03	-1.04
P65702 PGK_SALTY Phohoglycerate kinase	24		ISYISTGGGAFLEFVEGKVLPVAMLEER	355	29	4	21.4	b11y6°y6y7	3083.64	136.435	3098	4	771.66	8.23
P65702 PGK_SALTY Phohoglycerate kinase	25	Oxidation+M(7)	VLPVAMLEER	373	11	4	28.77	b3b5y3y9	1243.66	80.904	11388	2	622.34	-5.59
P65702 PGK_SALTY Phohoglycerate kinase	26		TDLDLAGK	6	8	6	33.25	b3°b3b4°b4b5°b5	832.45	48.831	42674	2	416.73	13.93
P65702 PGK_SALTY Phohoglycerate kinase	27		TDLDLAGKR	6	9	0	3.14		988.54	43.461	17173	2	494.77	-6.42
P65702 PGK_SALTY Phohoglycerate kinase	28		LNVPVKEGK	21	9	3	19.28	b3*b3b4	983.58	37.234	13969	2	492.29	-11.67
P65702 PGK_SALTY Phohoglycerate kinase	29		DLNVPVKEGK	20	10	5	44	b3b4b5°b5b6	1098.60	37.248	8530	2	549.80	-11.78
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	18	96.65	b2°b2b3°b3b4b14b16y1y3y4y11y12y13°y13y15y16y17y19	2130.16	93.577	254100	3	710.72	-5.96
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		VGDPVIEFDLPLEEK	115	16	16	99.67	b4b5b6b7°b7b10y2°y2y6y9°y9y10y11y12y13y16	1812.97	100.239	148048	2	906.99	1.21
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		MVAPVDGTIGK	59	11	23	138.78	b1b2b3b5b6b8°b8b9b10°b10b11°b11y1y2y3y6y7y8°y8y9°y9y10y11	1087.57	46.728	143415	2	544.29	-12.12
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		STLTPVVISNMDEIK	133	15	4	14.47	b3°b3y5y11	1646.87	67.897	2432	2	823.94	0.37
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		LSGSVTVGETPVIR	152	14	3	20.83	b4b5y7	1414.79	55.809	39296	2	707.90	-1.90
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		VKVGDPVIEFDLPLEEK	113	18	9	51.73	b5b7b9b11°b11y3y6y8y10	2040.11	96.459	128149	3	680.71	-6.64
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7	Phosphoryl STY(8)	MVAPVDGTIGK	59	11	7	39.23	b3b6°b6y4°y4y5y10	1167.53	47.847	2197	2	584.27	-4.81

[P0A283]PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8	Oxidation+M(11)	STLTPVVISNMDEIK	133	15	3	20.49	b5y5y6	1662.89	59.787	6053	2	831.95	14.98
[P0A283]PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9		SNMDEIK	141	7	0	6.28		836.38	67.871	1901	1	836.38	3.21
[P0A1E3]CYSK_SALTY Cysteine synthase A	1		IQGIGAGFIPGNLDLK	226	16	15	72.69	b2*b2b3b8b9b14y1y2y3y7°y7y10y12y14y16	1612.91	84.142	99750	2	806.96	1.14
[P0A1E3]CYSK_SALTY Cysteine synthase A	2		YLSTALFADLFTEKELQQ	305	18	10	33.08	b2b8b12°b12b16y7*y7y11y12y18	2117.09	103.131	96722	2	1059.05	5.30
[P0A1E3]CYSK_SALTY Cysteine synthase A	3		YLLLQQFSNPANPEIHEK	137	18	21	120.21	b2b3b12°b12b13*b13y2y3°y3y4y6y7y8y9°y9*y9y11y12y13y15y18	2141.09	74.859	81407	3	714.37	-7.18
[P0A1E3]CYSK_SALTY Cysteine synthase A	4		NIVVILPSSGER	293	12	10	79.63	b2b4b6y3y6y7y8y9y10y12	1283.73	64.633	59320	2	642.37	-4.47
[P0A1E3]CYSK_SALTY Cysteine synthase A	5		AEEIVASDPQK	126	11	17	108.04	b1b3b5°b5b7b10y1y2y3y5°y5*y5y6y7°y7y8y11	1186.59	32.004	48796	2	593.80	-4.22
[P0A1E3]CYSK_SALTY Cysteine synthase A	6		GVLKPGVELVEPTSGNTGIALAYVAAAR	56	28	6	45.36	y1y4y5y6y7y17	2753.52	82.309	38703	3	918.51	-1.15
[P0A1E3]CYSK_SALTY Cysteine synthase A	7		LQEDESFTNK	283	10	5	23.88	b3y7y8°y8y10	1210.57	35.725	33320	2	605.79	5.45
[P0A1E3]CYSK_SALTY Cysteine synthase A	8		NPSFSVK	35	7	10	46.26	b1b2b5b6y2y5y6°y6y7*y7	778.40	38.079	30208	2	389.70	-12.94
[P0A1E3]CYSK_SALTY Cysteine synthase A	9		YLSTALFADLFTEK	305	14	6	31.99	b2b5b7b13y8y12	1618.84	104.098	12823	2	809.92	0.23
[P0A1E3]CYSK_SALTY Cysteine synthase A	10		LTLTMPETMSIER	87	13	3	25.77	y4y8y11	1521.76	74.662	70361	2	761.39	-1.04
[P0A1E3]CYSK_SALTY Cysteine synthase A	11		IGANMIWDAEK	44	11	5	47.47	b7y5y6y8y10	1247.61	66.222	8914	2	624.31	3.72
[P0A1E3]CYSK_SALTY Cysteine synthase A	12		LIDK	242	4	1	10.62	b3	488.31	64.000	3941	1	488.31	7.44
[P0A1E3]CYSK_SALTY Cysteine synthase A	13		LIDKVVGITNEEAISTAR	242	18	3	12.58	b5y5y12	1929.04	60.684	42394	3	643.69	-11.64
[P0A1E3]CYSK_SALTY Cysteine synthase A	14		GYKLTLTMPETMSIER	84	16	5	22.92	b13y5°y5y10y11	1869.92	78.083	36450	2	935.47	-10.64
[P0A1E3]CYSK_SALTY Cysteine synthase A	15		AEEIVASDPQKYLLLQQFSNPANPEIHEK	126	29	8	20.78	b3b14y3y6y10y13°y13*y13	3308.67	77.819	35288	4	827.92	-3.84
[P0A1E3]CYSK_SALTY Cysteine synthase A	16		SKIYEDNSLTIGHTPLVR	1	18	3	21.5	b6b7b11	2043.07	59.793	21141	3	681.70	-8.01
[P0A1E3]CYSK_SALTY Cysteine synthase A	17		MSKIYEDNSLTIGHTPLVR	0	19	4	18.91	b4b10b13y13	2174.15	90.074	12200	2	1087.58	11.57
[P0A1E3]CYSK_SALTY Cysteine synthase A	18		LTLTMPETMSIERR	87	14	7	37.59	b5°b5b8b9°b9b10y3	1677.87	49.625	2097	2	839.44	-0.58
[P0A1E3]CYSK_SALTY Cysteine synthase A	19	Phosphoryl STY(12)	IYEDNSLTIGHTPLVR	3	16	6	22.09	b4b10*b10b11°b11*b11	1907.92	74.920	68704	3	636.65	2.43
[P0A1E3]CYSK_SALTY Cysteine synthase A	20	Phosphoryl STY(11)	VVGITNEEAISTARR	246	15	3	14.47	b10y6y9_H3PO4 y9	1695.84	54.278	3260	2	848.42	2.16
[P0A1E3]CYSK_SALTY Cysteine synthase A	21	Oxidation+M(5)	IGANMIWDAEKR	44	12	4	28.15	b4b7b9°b9	1419.70	57.669	2856	2	710.35	-4.99
[P0A1E3]CYSK_SALTY Cysteine synthase A	22	Oxidation+M(5)	LTLTMPETMSIER	87	13	3	16.52	b9y5y8	1537.76	71.320	2429	3	513.26	-0.24
[P0A1E3]CYSK_SALTY Cysteine synthase A	23		QFSNPANPEIHEK	142	13	6	45.85	b3b4b5b6°b6b8	1510.71	74.903	6658	3	504.24	-11.39
[P0A1E3]CYSK_SALTY Cysteine synthase A	24		NPSFSVK	35	7	0	1.26		761.38	38.086	3927	2	381.19	-0.08

P0A1E3 CYSK_SALTY Cysteine synthase A	25		AEEIVASDPQK	126	11	0	3.77		1169.57	31.988	1807	3	390.53	5.32
P0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	14	81.81	b2b3°b3b4°b4y6y7°y7y8°y8y9y10y11y13	1447.78	65.716	84655	2	724.39	-2.45
P0A297 RL10_SALTY 50S ribosomal protein L10	2	Carbamidomethyl+C(9)	VVEGTQFECLKDFTVGPTLIAYSM EHPGAAAR	62	32	10	25.1	b1b2b3b8y4y6y13y15y16y32	3494.70	92.953	67756	4	874.43	-1.47
P0A297 RL10_SALTY 50S ribosomal protein L10	3		AAAFEGELIPASQIDR	109	16	7	37.44	b1y2y7y8y11y12y16	1687.87	69.324	62217	2	844.44	5.35
P0A297 RL10_SALTY 50S ribosomal protein L10	4		EAGVYMR	46	7	7	43.25	b1b4b7y3y5y6y7	825.40	31.995	10824	2	413.20	4.44
P0A297 RL10_SALTY 50S ribosomal protein L10	5		DTFVGPTLIAYSM EHPGAAAR	73	21	10	61.4	b4b5b8b10b12y5y8y9y10y12	2204.10	83.323	9564	3	735.37	7.20
P0A297 RL10_SALTY 50S ribosomal protein L10	6		LMATMKEASAGK	138	12	5	27.94	b9y8°y8y10y11	1237.63	61.997	8527	2	619.32	3.65
P0A297 RL10_SALTY 50S ribosomal protein L10	7	Carbamidomethyl+C(9)	VVEGTQFECLK	62	11	7	30.2	b1b3b4b10°b10y4y11	1309.66	86.871	6269	2	655.34	13.70
P0A297 RL10_SALTY 50S ribosomal protein L10	8		GALSAVVADSR	20	11	7	59.51	b5b6y4y5y6y7y11	1045.58	30.176	5823	2	523.29	12.61
P0A297 RL10_SALTY 50S ribosomal protein L10	9		MTELR	37	5	3	22.5	b4°b4y3	649.33	41.616	24177	1	649.33	-7.99
P0A297 RL10_SALTY 50S ribosomal protein L10	10		LMATMK	138	6	4	34.38	b4b5y5°y5	694.37	41.548	12171	1	694.37	14.94
P0A297 RL10_SALTY 50S ribosomal protein L10	11		QAIVAEVSEVAK	8	12	4	17.94	b3°b3y3y6	1243.71	41.606	10245	2	622.36	16.98
P0A297 RL10_SALTY 50S ribosomal protein L10	12		EASAGK	144	6	1	11.88	b3	562.29	44.255	2979	1	562.29	6.84
P0A297 RL10_SALTY 50S ribosomal protein L10	13		AAAFEGELIPASQIDRLATLPTYEE AIAR	109	29	6	29.28	b9b10b13y6y9y10	3116.64	93.577	13156	3	1039.55	4.31
P0A297 RL10_SALTY 50S ribosomal protein L10	14		LMATMKEASAGK	138	12	12	76.62	b4b6°b6b10y6y8°y8y9y10°y10y11°y11	1237.63	59.761	6341	2	619.32	-1.97
P0A297 RL10_SALTY 50S ribosomal protein L10	15	Carbamidomethyl+C(9)	VVEGTQFECLKDFTVGPTLIAYSM EHPGAAAR	62	32	3	22.24	b10y12y13	3494.69	64.310	3570	3	1165.57	-5.59
P0A297 RL10_SALTY 50S ribosomal protein L10	16	Carbamidomethyl+C(10)	RVVEGTQFECLK	61	12	4	29.86	b9b10y5y11	1465.75	71.243	2279	2	733.38	-0.92
P0A297 RL10_SALTY 50S ribosomal protein L10	17		AGREAGVYMR	43	10	3	23.88	b8y6y7	1109.55	37.149	1914	2	555.28	0.00
P0A297 RL10_SALTY 50S ribosomal protein L10	18	Phosphoryl STY(12)	AAAFEGELIPASQIDR	109	16	6	22.92	b5b10b11°b11y4°y4	1767.82	46.736	1777	2	884.41	-3.38
P0A297 RL10_SALTY 50S ribosomal protein L10	19	Oxidation+M(9)	AGREAGVYMR	43	10	6	43.83	b5b8b9y3y8°y8	1125.55	42.452	8518	2	563.28	2.28
P0A297 RL10_SALTY 50S ribosomal protein L10	20	Oxidation+M(5)	LMATMKEASAGK	138	12	4	38.61	b4b7b9b10	1253.63	42.424	5724	2	627.32	2.43
P52616 FLJB_SALTY Phase 2 flagellin	1		AQILQQAGTSVLAQANQVPQNVLSLLR	479	27	13	28.47	b2°b2b3°b3b4b7°b7b9b11y2y4y9y27	2860.60	105.872	87537	3	954.20	-0.34
P52616 FLJB_SALTY Phase 2 flagellin	2		SQSALGTAIER	20	11	9	47.47	b2b8y1y6y7y8y9°y9y11	1132.59	42.564	68904	2	566.80	-2.91
P52616 FLJB_SALTY Phase 2 flagellin	3		AQVINTNSLSLLTQNNLNK	1	19	12	43.06	b2°b2b4b8y2y5y7y8y9y15°y15y19	2085.13	75.335	42970	2	1043.07	-1.41
P52616 FLJB_SALTY Phase 2 flagellin	4		TIEGGYALK	328	9	4	25.47	b3b8y7y9	951.51	44.189	36563	2	476.26	-9.88
P52616 FLJB_SALTY Phase 2 flagellin	5		SDLGAVQNR	434	9	12	64	b1b2b5°b5y2y3y5y6y7y8y9°y9	959.48	28.303	27853	2	480.24	-10.18
P52616 FLJB_SALTY Phase 2 flagellin	6		TTSYTAADGTTK	357	12	6	45.88	b8b10b11y3y5y6	1216.58	31.371	16648	3	406.20	5.52
P52616 FLJB_SALTY Phase 2 flagellin	7		TAANQLGGVDGK	369	12	15	66.62	b2°b2b4b5b7°b7b9°b9b10°b10y2y6°y6y8y12	1130.57	60.608	15733	2	565.79	-5.07

P52616 FLJB_SALTY Phase 2 flagellin	8		INSAKDDAAGQAIANR	37	16	24	150.11	b2b4°b4b5°b5b6b9°b9b11 b12y1y3°y3y4y5y6y7°y7y 8y9y10°y10y11y16	1614.80	30.755	13485	3	538.94	-14.82
P52616 FLJB_SALTY Phase 2 flagellin	9		AAGHDFK	396	7	4	32	b3y1y4y5	745.35	112.123	3602	1	745.35	-13.92
P52616 FLJB_SALTY Phase 2 flagellin	10		ELAVQSANSTNSQSDLDLSIQAEIT QR	93	26	5	19.63	b8b9b13°b13y13	2805.36	71.046	3240	2	1403.18	2.35
P52616 FLJB_SALTY Phase 2 flagellin	11		DTPAVVSADAK	288	11	3	19.74	b7y3y7	1073.56	83.476	2849	1	1073.56	9.67
P52616 FLJB_SALTY Phase 2 flagellin	12		NANDGISIAQTTEGALNEINNQL R	66	25	4	12.9	b13b16y6y9	2670.32	125.761	80234	3	890.78	4.21
P52616 FLJB_SALTY Phase 2 flagellin	13		YFVTIGGFTGADAAK	234	15	6	23.8	b3y5y6°y6y8°y8	1517.76	74.168	41426	2	759.38	-2.09
P52616 FLJB_SALTY Phase 2 flagellin	14		FNSAITNLGNTVNNLSEAR	443	19	4	12.16	b4y4°y4y7	2034.98	80.074	13635	3	679.00	-18.12
P52616 FLJB_SALTY Phase 2 flagellin	15		IDAALAQVDALR	422	12	5	27.94	b3b4b9y6°y6	1255.70	68.553	4425	3	419.24	-3.99
P52616 FLJB_SALTY Phase 2 flagellin	16		QINSQTLGLDSLNVQK	161	16	8	27.39	b3°b3b7b11°b11°b11y4y9	1757.95	45.987	3133	3	586.66	7.22
P52616 FLJB_SALTY Phase 2 flagellin	17		VLAQDNTLTIQVGANDGETIDIDL K	136	25	3	10.97	b6y9y13	2656.41	115.677	1826	2	1328.71	16.27
P52616 FLJB_SALTY Phase 2 flagellin	18		DDAAGQAIANR	42	11	5	22.75	b9°b9°b9b10y10	1101.55	65.180	1609	2	551.28	19.28
P52616 FLJB_SALTY Phase 2 flagellin	19		DTAVTTKAYANNGTTLDVSGLD DAAIK	182	27	6	22.01	b7°b7y6y11y12y24	2725.39	74.836	19006	3	909.14	14.51
P52616 FLJB_SALTY Phase 2 flagellin	20		FDADNNKYFVTIGGFTGADAAK	227	22	3	11.33	b13y6y12	2322.12	79.482	6694	3	774.71	5.78
P52616 FLJB_SALTY Phase 2 flagellin	21		AKTTSYTAADGTTK	355	14	5	24.88	b6b7b9°b9y8	1415.72	48.821	5251	2	708.36	13.88
P52616 FLJB_SALTY Phase 2 flagellin	22		AATGGTNGTASVTTGGAVKFDAD NNK	209	25	6	12.9	b7b12°b12y5°y5y19	2324.14	88.273	2957	3	775.39	13.45
P52616 FLJB_SALTY Phase 2 flagellin	23		QINSQTLGLDSLNVQKAYDVK	161	21	5	14.63	b3b6°b6y5y13	2334.24	68.945	2554	2	1167.62	4.50
P52616 FLJB_SALTY Phase 2 flagellin	24		TYNASKAAGHDFK	390	13	9	73.27	b7°b7b8b9b10y4y7y8y10	1409.67	32.928	2433	3	470.56	-5.98
P52616 FLJB_SALTY Phase 2 flagellin	25		AAGHDFKAQPELAEAAAK	396	18	3	21.5	b8b9b14	1824.94	89.152	2294	3	608.98	6.09
P52616 FLJB_SALTY Phase 2 flagellin	26	Phosphoryl STY(5)	DTAVTTK	182	7	4	35.01	b3y4°y4y6	815.35	42.432	1837	2	408.18	11.90
P52616 FLJB_SALTY Phase 2 flagellin	27		SQSALGT	20	7	0	3.77		663.33	42.513	9821	1	663.33	5.43
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	1		MKPDIHVPYR	0	10	6	22.12	b3y2y4y7°y7y10	1255.65	41.588	70003	3	419.22	-7.29
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	2		TFDSESSAAR	62	10	17	74.91	b1°b1b2°b2b4°b4y1y2y3y5 y6y7°y7y8°y8y9y10	1070.47	25.528	38012	2	535.74	-6.27
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	3		TVVFHDTSANEYVK	10	14	3	20.83	b8y10y11	1609.77	56.240	1524	2	805.39	-12.51
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	4		FGHFIGAK	76	8	5	58.14	b3b6b7y3y7	876.46	45.997	13940	2	438.73	-19.15
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	5		SHPFYTGRR	52	8	6	42.12	b4°b4b6°b6b7y7	964.47	90.595	3023	1	964.47	2.03
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	6		VGSTIKTER	24	9	4	33.25	y3°y3y4y5	990.55	18.326	4904	2	495.78	-12.75
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	7		QKTFDSESSAAR	60	12	3	21.92	b6y7y8	1326.62	35.238	2786	2	663.81	-6.81
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	8		SHPFYTGRRQK	52	10	7	48.14	b3b4b8°b8b9°b9°b9	1220.62	42.425	2214	3	407.55	3.80

P06179 FLIC_SALTY Flagellin	1		AQILQQAGTSVLAQANQPQNVLSLLR	468	27	13	28.47	b2*b2b3*b3b4b7*b7b9b11y2y4y9y27	2860.60	105.872	87537	3	954.20	-0.34
P06179 FLIC_SALTY Flagellin	2		SQSALGTAIER	20	11	9	47.47	b2b8y1y6y7y8y9°y9y11	1132.59	42.564	68904	2	566.80	-2.91
P06179 FLIC_SALTY Flagellin	3		AQVINTNSLSLLTQNNLNK	1	19	12	43.06	b2*b2b4b8y2y5y7y8y9y15°y15y19	2085.13	75.335	42970	2	1043.07	-1.41
P06179 FLIC_SALTY Flagellin	4		FNSAITNLGNTVNNLTSAR	432	19	9	41.16	b4b5°b5b11y2y3y6y11y14	2007.04	79.195	31242	2	1004.02	7.97
P06179 FLIC_SALTY Flagellin	5		SDLGAVQNR	423	9	12	64	b1b2b5°b5y2y3y5y6y7y8y9°y9	959.48	28.303	27853	2	480.24	-10.18
P06179 FLIC_SALTY Flagellin	6		IDAALAQVDTLR	411	12	5	27.94	b11y3y6y7*y7	1285.71	61.714	24616	2	643.36	-4.37
P06179 FLIC_SALTY Flagellin	7		INSAKDDAAGQAIANR	37	16	24	150.11	b2b4°b4b5°b5b6b9*b9b11b12y1y3*y3y4y5y6y7*y7y8y9y10*y10y11y16	1614.80	30.755	13485	3	538.94	-14.82
P06179 FLIC_SALTY Flagellin	8		VSDTAATVTGYADTTIALDNSTFK	180	24	5	23.15	b3b6b7b15y6	2462.16	72.248	12637	3	821.39	-13.88
P06179 FLIC_SALTY Flagellin	9		ELAVQSANSTNSQSDDLDSIQAEITQR	93	26	5	19.63	b8b9b13*b13y13	2805.36	71.046	3240	2	1403.18	2.35
P06179 FLIC_SALTY Flagellin	10		AQPDLAEEAAATTENPLQK	392	19	6	18.91	b9°b9*b9y10y12y17	1968.98	95.342	123790	2	985.00	-1.55
P06179 FLIC_SALTY Flagellin	11		TEVVSIGGK	370	9	3	33.25	b6b7b8	889.48	78.084	7282	1	889.48	-18.32
P06179 FLIC_SALTY Flagellin	12		QINSQTLGLDTLNVQQK	161	17	13	68.97	b3b4°b4*b4b5°b5b6b8°b8°b8b10b16y12	1899.98	74.123	3324	2	950.50	-15.03
P06179 FLIC_SALTY Flagellin	13		DGSISINTTK	339	10	3	29.11	b4b5b9	1035.52	68.998	1639	2	518.26	-9.55
P06179 FLIC_SALTY Flagellin	14		INSAKDDAAGQAIANR	37	16	12	48.92	b3*b3b4°b4*b4b7°b7b8b11y7*y7y11	1614.80	31.425	20399	3	538.94	-10.89
P06179 FLIC_SALTY Flagellin	15		LGADGKTEVVSIGGK	363	16	5	27.39	b3b12y3y7y13	1487.79	58.702	17615	3	496.60	-7.79
P06179 FLIC_SALTY Flagellin	16		FDDTTGKYAK	222	11	6	60.48	b8y4y7y8y9y10	1308.61	32.039	6762	2	654.81	2.99
P06179 FLIC_SALTY Flagellin	17		FNSAITNLGNTVNNLTSARSR	432	21	5	31.55	b9b10b11°b11y9	2250.13	109.789	4931	2	1125.57	-14.54
P06179 FLIC_SALTY Flagellin	18		AQPDLAEEAAATTENPLQKIDAALAQVDTLR	392	31	3	17.02	b3b10b16	3235.66	104.780	4528	3	1079.22	-6.87
P06179 FLIC_SALTY Flagellin	19		YKVSDTAATVTGYADTTIALDNSTFK	178	26	4	12.62	b7b14y7y10	2753.38	111.371	3762	3	918.46	10.37
P06179 FLIC_SALTY Flagellin	20		AEGHNFKAQPDLAEEAAATTENPLQK	385	26	4	10.93	b10b12°b12y10	2752.37	111.944	1543	4	688.85	4.61
P06179 FLIC_SALTY Flagellin	21	Phosphoryl STY()	AQVINTNSLSLLTQNNLNK	1	19	6	42.08	b8b10b14y10y11y12	2165.07	81.789	78485	2	1083.04	-9.81
P06179 FLIC_SALTY Flagellin	22	Phosphoryl STY(10)	IDAALAQVDTLR	411	12	7	45.88	b5b6b8y3_HPO3y3y9y10*y10	1365.68	67.033	4480	2	683.34	5.90
P06179 FLIC_SALTY Flagellin	23	Phosphoryl STY(9)	DGSISINTTK	339	10	8	33.37	b4_H3PO4b4°b4b7°b7*b7b8y5°y5	1115.51	47.825	3959	2	558.26	14.88
P0AA28 THIO_SALTY Thioredoxin-1	1		LNIDQNPGTAPK	58	12	29	154.13	b2*b2b4*b4b5b6°b6°b6b7b10y1y2y3y4y5y6°y6y7y8°y8*y8y9°y9*y9y10°y10y11*y11y12	1267.66	39.046	191279	2	634.33	-4.43
P0AA28 THIO_SALTY Thioredoxin-1	2		MIAPILDEIADEYQGK	37	16	22	143.93	b2b3b4b5b12y2y3*y3y4y5°y5y6y10y11°y11y12°y12y13y14°y14y15y16	1805.91	94.327	161269	2	903.46	6.62
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	9	58.77	b2y1y2y3y4y5y6y7y9	1001.63	91.543	117951	2	501.32	-10.48
P0AA28 THIO_SALTY Thioredoxin-1	4		NGEVAATK	83	8	7	42.12	b1b2b5y4y6°y6y7	789.42	45.975	8102	1	789.42	11.06
P0AA28 THIO_SALTY Thioredoxin-1	5		EFLDANLA	101	8	6	58.14	b3b6y5y6y7*y7	892.43	70.901	20656	1	892.43	-7.73
P0AA28 THIO_SALTY Thioredoxin-1	6		MIAPILDEIADEYQGKLTVAK	37	21	17	110.12	b3b4b5b13°b13b15°b15°b15y4y5y7y13y14y15y18y19y20	2318.23	95.420	145299	3	773.41	-2.42

P0AA28 THIO_SALTY Thioredoxin-1	7	Phosphoryl STY(4)	GIPTLLLLFK	74	9	3	33.25	b3b5b6	1081.61	44.437	6992	2	541.31	13.88
P0AA28 THIO_SALTY Thioredoxin-1	8	Oxidation+M(1)	MIAPILDEIADEYQGK	37	16	4	13.71	b4b7y5*y5	1821.90	88.229	6790	2	911.46	6.03
P25077 MDH_SALTY Malate dehydrogenase	1		NQLPSGSELSLYDIAPVTPGVAVD LSHIPTAVK	21	33	24	66.92	b1b2*b2b3*b3b4b9*b9b10 b10*b10b12*b12b13b15*b 15y1y3y5y6y15y18y30y33	3388.81	94.445	228176	3	1130.27	2.38
P25077 MDH_SALTY Malate dehydrogenase	2	Carbamidomethyl+C(2)	ACVGIITNPVNTTVAIAAEVLKK	111	23	18	90.79	b2b3b4b5b6b8*b8b13y1y2 y3y4y6y8y15y18y20y23	2382.34	105.503	202328	3	794.78	-3.18
P25077 MDH_SALTY Malate dehydrogenase	3		VAVLGAAGGIGQALALLK	2	19	18	134.21	b3b6b8b9b10y1y2y3y4y5y 6y7y9y11y12y13y15y19	1735.08	120.379	198554	2	868.05	-0.28
P25077 MDH_SALTY Malate dehydrogenase	4		FFSQPLLLGK	262	10	7	41.15	b2b6y2y3y6y8y10	1149.65	76.630	122404	2	575.33	-10.62
P25077 MDH_SALTY Malate dehydrogenase	5		IQNAGTEVVEAK	205	12	17	106.91	b2*b2b3b7b9y2y3*y3y4y5 y7y8y9y10*y10*y10y12	1258.66	35.081	102379	2	629.83	-4.56
P25077 MDH_SALTY Malate dehydrogenase	6		DIQLGEDFINK	301	11	10	75.54	b3b6b7b9*b9b10y8y9*y9y 11	1291.65	68.501	91201	2	646.33	-2.46
P25077 MDH_SALTY Malate dehydrogenase	7		AGGGSATLSMGQAAAR	217	16	21	138.86	b3b6b7b9*b9b12b13b16y5 y6*y6y7y8y9*y9y10*y10*y 10y11y12y16	1405.68	40.546	65693	2	703.35	-1.13
P25077 MDH_SALTY Malate dehydrogenase	8		FGLSLVR	233	7	5	35.01	b2y2y4y5y6	791.47	67.618	56082	2	396.24	-14.57
P25077 MDH_SALTY Malate dehydrogenase	9	Carbamidomethyl+C(5)	GVVECAYVEGDGQYAR	246	16	4	13.71	b8y7y11*y11	1772.81	50.346	5207	2	886.91	12.60
P25077 MDH_SALTY Malate dehydrogenase	10		SNTFV AELK	153	9	3	25.47	b3y4y7	1008.53	55.140	48729	2	504.77	-10.53
P25077 MDH_SALTY Malate dehydrogenase	11		KPGMDR	81	6	1	11.88	b4	703.35	44.024	13543	1	703.35	-1.74
P25077 MDH_SALTY Malate dehydrogenase	12		GFSGEDATPALEGADVVLISAGVA R	56	25	6	24.64	b3b4b11b16y4y14	2402.23	91.531	8701	2	1201.62	3.66
P25077 MDH_SALTY Malate dehydrogenase	13		NGVEER	272	6	3	23.13	y3*y3y4	703.34	32.017	7006	1	703.34	9.20
P25077 MDH_SALTY Malate dehydrogenase	14		AGVYDK	134	6	4	34.38	b4y3*y3y4	652.32	45.977	3966	1	652.32	-14.03
P25077 MDH_SALTY Malate dehydrogenase	15	Carbamidomethyl+C(11)	ALQGEKGVVECAYVEGDGQYAR	240	22	4	11.33	b5*b5y3y7	2399.11	99.646	96507	3	800.38	-7.94
P25077 MDH_SALTY Malate dehydrogenase	16		IQNAGTEVVEAKAGGGSATLSMG QAAAR	205	28	6	26.43	b3b4b7b9b14y14	2645.34	120.467	6686	4	662.09	3.88
P25077 MDH_SALTY Malate dehydrogenase	17	Phosphoryl STY(6)	IQNAGTEVVEAK	205	12	3	17.94	b4y7y11	1338.62	37.214	4272	3	446.88	0.91
P25077 MDH_SALTY Malate dehydrogenase	18	Oxidation+M(16)	SIGTLSAFEQHSLDAMLDTLK	279	21	3	11.55	b11y4y11	2293.15	103.234	5782	3	765.05	5.22
P64052 EFTS_SALTY Elongation factor Ts	1		VASLEGDVLGSYQHGAR	134	17	24	112.21	b2b8*b8b9*b9b14y1y2y3y4 y5*y5y6*y6y8y9*y10*y10y 11y12*y12*y12y13y17	1758.85	59.688	141661	3	586.96	-12.98
P64052 EFTS_SALTY Elongation factor Ts	2		FTGEVSLTGQPFVMEPSK	222	18	8	40.94	b3*b3b4b8b9y3y10y18	1953.97	75.389	78047	2	977.49	3.69
P64052 EFTS_SALTY Elongation factor Ts	3		AEITASLVK	1	9	7	52.75	b1b5y3y4y5y6y9	931.53	49.519	34958	2	466.27	-13.63
P64052 EFTS_SALTY Elongation factor Ts	4		ALTEANGDIELAIENMRK	25	18	7	16.78	b2b6b9y1y13*y13y16	1988.00	75.017	33203	3	663.34	-6.32
P64052 EFTS_SALTY Elongation factor Ts	5	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	3	23.88	b3y7y8	1098.47	21.618	26214	2	549.74	-2.44

[P64052 EFTS_SALTY Elongation factor Ts	6		AGNVAADGVIK	52	11	11	79.97	b4*b4b8b9y2y4y5y6y7y8y11	1014.55	37.195	21407	2	507.78	-7.58
[P64052 EFTS_SALTY Elongation factor Ts	7		MAEITASLVKELR	0	13	4	25.77	b3b5*b5b7	1460.80	69.867	3689	3	487.60	-12.03
[P64052 EFTS_SALTY Elongation factor Ts	8	Carbamidomethyl+C(13)	IDGNVAFILEVNCQTDFVAK	65	20	6	19.95	b13*b13b14*b14y10y20	2253.11	69.874	2258	4	564.03	-5.63
[P64052 EFTS_SALTY Elongation factor Ts	9		VETDFAAEVAAMSK	267	14	7	25.67	b1b2*b2b3b5b7y7	1468.69	22.323	1928	3	490.23	-6.98
[P64052 EFTS_SALTY Elongation factor Ts	10		IGVLVAAK	151	8	5	53.37	b3y4y5y6y7	770.50	47.775	42276	2	385.75	-19.41
[P64052 EFTS_SALTY Elongation factor Ts	11		VLDAAVAGK	95	9	4	50.53	y3y4y7y8	843.48	34.221	39667	2	422.24	-17.66
[P64052 EFTS_SALTY Elongation factor Ts	12		ALTEANGDIELAIENMR	25	17	4	13.09	b11y5*y5y13	1859.92	60.664	23355	2	930.46	0.72
[P64052 EFTS_SALTY Elongation factor Ts	13		SVGQLLK	240	7	6	35.01	b3*b3b4*b4b5*b5	744.45	20.558	14298	2	372.73	-18.69
[P64052 EFTS_SALTY Elongation factor Ts	14		MVEGR	214	5	1	11.25	y4	591.29	39.164	8957	1	591.29	-5.26
[P64052 EFTS_SALTY Elongation factor Ts	15		EYQVQLDIAMQSGKPK	193	16	5	46.93	b3b5b6b7b8	1834.94	71.414	5343	3	612.32	-0.27
[P64052 EFTS_SALTY Elongation factor Ts	16		DAGFQAFADK	85	10	6	51.61	b6b8y3y6*y6y8	1069.49	47.871	4100	2	535.25	-1.71
[P64052 EFTS_SALTY Elongation factor Ts	17		QLAMHVAASKPEFVKPEDVSADVVEK	167	26	6	43.13	b4b6b7b8b9y12	2824.43	48.796	3535	6	471.58	-10.11
[P64052 EFTS_SALTY Elongation factor Ts	18		FEVGEGIEK	258	9	4	33.25	b3b4*b4b8	1007.49	96.621	2034	1	1007.49	-16.84
[P64052 EFTS_SALTY Elongation factor Ts	19		KALTEANGDIELAIENMR	24	18	4	27.6	y6y9y14y15	1988.03	67.483	15067	2	994.52	7.92
[P64052 EFTS_SALTY Elongation factor Ts	20		FEVGEGIEKVETDFAAEVAAMSK	258	23	5	13.64	b5b9*b9y4y13	2457.18	92.617	4997	2	1229.09	-3.97
[P64052 EFTS_SALTY Elongation factor Ts	21		KFTGEVSLTGQPFVMEPSK	221	19	9	47.17	b6b7y5y6*y6y9*y9y11y13	2082.07	79.194	3180	2	1041.54	4.81
[P64052 EFTS_SALTY Elongation factor Ts	22		EIAEKMVEGR	209	10	5	22.12	b6*b6y3y8*y8	1161.60	46.793	2944	2	581.30	2.31
[P64052 EFTS_SALTY Elongation factor Ts	23	Oxidation+M(14)	FTGEVSLTGQPFVMEPSK	222	18	9	40.94	b4*b4b5b14y5*y5y8y13y14	1969.95	74.214	3791	2	985.48	-5.52
[P64052 EFTS_SALTY Elongation factor Ts	24	Oxidation+M(16)	ALTEANGDIELAIENMRK	25	18	5	31.45	b9b10y4y11y13	2004.03	72.863	2836	2	1002.52	9.75
[P64052 EFTS_SALTY Elongation factor Ts	25	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	0	3.14		997.42	21.581	9308	2	499.21	-9.00
[P64052 EFTS_SALTY Elongation factor Ts	26		VASLEGDLVLS	134	11	0	7.54		1046.52	59.655	4605	2	523.77	-11.66
[P64052 EFTS_SALTY Elongation factor Ts	27		AEITASLV	1	8	0	2.51		803.44	49.506	2438	1	803.44	-12.08
[P41031 CY_SALTY Thiosulfate-binding protein	1		AYLNWLYSPQAQTIIHHYYR	265	21	7	20.48	b2b5b10y11y13y15y21	2664.33	94.261	87239	3	888.78	3.21
[P41031 CY_SALTY Thiosulfate-binding protein	2		ELFAALNPPFEQQWAK	37	16	22	92.68	b2*b2b3*b3b5*b5b6b7b11*b11b15y1y2y4y9*y9y10*y10y12*y12y13y16	1888.97	90.590	86678	2	944.99	5.95
[P41031 CY_SALTY Thiosulfate-binding protein	3		VNNPEIMGK	286	9	10	64	b2b3y2y3y4y6y7y8*y8y9	1001.50	36.704	84561	2	501.25	-9.20
[P41031 CY_SALTY Thiosulfate-binding protein	4		LPNNSSPFYSTMGFLVR	110	17	15	102.51	b5b6b7b8b15y2y3y5y8y9y11y12y13*y13y17	1929.97	92.708	71402	2	965.49	6.83
[P41031 CY_SALTY Thiosulfate-binding protein	5		NVEVFDTGGR	189	10	18	101.39	b2b3b4*b4b5b8b10y1y2y4*y4y5y6y7*y7y8*y8y10	1093.52	47.803	57966	2	547.27	-3.35

[P41031 CY_SALTY Thiosulfate-binding protein	6		LIPADWQSR	101	9	14	81.27	b2b6°b6b7°b7b8°b8y3°y3y4°y4y6y7y9	1085.58	53.551	54339	2	543.30	9.56
[P41031 CY_SALTY Thiosulfate-binding protein	7		QALAILQGLK	71	10	5	36.38	b3°b3y5y6y7	1054.65	75.740	51233	2	527.83	-8.45
[P41031 CY_SALTY Thiosulfate-binding protein	8		TEQFMTQFLK	179	10	7	22.12	b2b3b10y3y6y10°y10	1272.63	76.308	46115	2	636.82	-1.25
[P41031 CY_SALTY Thiosulfate-binding protein	9		FGSWPEVMK	311	9	6	25.47	b2b4b7y2y5y9	1080.52	69.708	40994	2	540.76	-2.37
[P41031 CY_SALTY Thiosulfate-binding protein	10		GATTTFAER	199	9	6	38.49	b3°b3y4y5y6y9	953.46	31.465	30570	2	477.23	-8.58
[P41031 CY_SALTY Thiosulfate-binding protein	11		RPLTAAMLLLAGQAQATELLNS SYDVSRELF AALNPPFEQQWAKD NGGDK	8	51	3	29.87	y4y5y8	5558.85	102.633	15981	4	1390.47	2.02
[P41031 CY_SALTY Thiosulfate-binding protein	12		LIFPNPK	146	7	5	43.25	b5y4y5°y5y6	828.48	56.513	77366	2	414.75	-16.21
[P41031 CY_SALTY Thiosulfate-binding protein	13		GLGDVLISFESEVNNIR	208	17	7	37.44	b13y6y7°y7°y7y9y10	1861.93	59.785	41017	3	621.31	-21.11
[P41031 CY_SALTY Thiosulfate-binding protein	14		QYEAQGFEVVIPK	226	13	3	16.52	b5b10y11	1507.76	71.530	13312	2	754.39	-10.36
[P41031 CY_SALTY Thiosulfate-binding protein	15		NVQANGTEK	253	9	12	89.51	b3b7b8°b8y3y5y6y7°y7°y7y8°y8	960.49	32.869	4341	2	480.75	19.06
[P41031 CY_SALTY Thiosulfate-binding protein	16		TSGNAR	153	6	1	11.88	b5	605.29	28.910	3310	1	605.29	-14.62
[P41031 CY_SALTY Thiosulfate-binding protein	17		TNILAEFPVAVVDKNVQANGTEK	239	23	18	97.99	b3b5b6y4y5°y5y6°y6°y6y8°y8°y8y12y13y16y18y19y20	2544.31	91.493	156702	3	848.77	-0.86
[P41031 CY_SALTY Thiosulfate-binding protein	18		YTYLAAWGAADNADGGDKAK	159	20	3	11.82	b9y7y14	2057.96	59.615	44601	2	1029.48	0.83
[P41031 CY_SALTY Thiosulfate-binding protein	19		NVEVFDTGGRGATTTFAER	189	19	10	51.44	b3b12°b12b13°b13b14y5y6y9y14	2027.98	69.041	25659	3	676.66	-0.18
[P41031 CY_SALTY Thiosulfate-binding protein	20		TSGNARYTYLAAWGAADNADGGDK	153	24	6	13.24	b6°b6b11°b11y4y6	2445.13	91.489	5094	2	1223.07	9.19
[P41031 CY_SALTY Thiosulfate-binding protein	21		VNNPEIMGKQADK	286	13	6	37.48	b5y5y7°y7y8y10	1443.71	63.201	4720	2	722.36	-11.58
[P41031 CY_SALTY Thiosulfate-binding protein	22		GNPKNIHDWSDLVR	128	14	3	15.39	b3y6y9	1650.81	96.777	3976	2	825.91	-15.08
[P41031 CY_SALTY Thiosulfate-binding protein	23		VEEKFGSWPEVMK	307	13	3	16.52	b10y9y11	1565.76	60.564	1654	3	522.59	-3.12
[P41031 CY_SALTY Thiosulfate-binding protein	24	Oxidation+M(7)	VNNPEIMGK	286	9	5	38.49	b4y4y7°y7y8	1017.50	38.096	5559	2	509.25	-7.32
[P41031 CY_SALTY Thiosulfate-binding protein	25		EVFDTGGR	191	8	3	19.62	b3°b3b4	880.41	47.841	3278	1	880.41	-1.94
[P41031 CY_SALTY Thiosulfate-binding protein	26		GATTTFAER	199	9	0	2.51		935.45	31.495	14577	2	468.23	-3.26
[P0A1P8 GLRX1_SALTY Glutaredoxin-1	1		TVGKPVETVPQIFVDQK	50	17	10	51.41	b3b9y2°y2y3y4y5y6y8y17	1885.02	65.611	40941	3	629.01	-12.63
[P0A1P8 GLRX1_SALTY Glutaredoxin-1	2	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	MFTVIFGRGPCPYCVR	0	16	7	40.4	b7°b7b9y5y10y11y12	1959.93	78.067	28354	3	653.98	-5.73
[P0A1P8 GLRX1_SALTY Glutaredoxin-1	3		ENLNLFA	80	7	6	35.01	b3°b3b5°b5y6°y6	820.43	39.674	8222	2	410.72	12.87
[P0AA07 PTHP_SALTY Phohocarrier protein HPr	1		MFQQEVTITAPNGLHTRPAAQFVK	0	24	7	23.15	b2b3b5b6b7°b22y15	2684.37	64.162	132434	4	671.85	-8.91
[P0AA07 PTHP_SALTY Phohocarrier protein HPr	2		GFTSEITVTSNGK	27	13	16	95.95	b2b3°b3b8b9b10b11°b11y3y5y6°y6°y6y9°y9y10	1340.67	51.278	20826	2	670.84	-0.91
[P0AA07 PTHP_SALTY Phohocarrier protein HPr	3		LMAELE	79	6	5	34.38	y3°y3y4y5°y5	705.36	41.634	5536	1	705.36	14.10

P0AA07 PTHP_SALTY Phohocarrier protein HPr	4		LQTLGLTQGTVVTTISAEGEDEQKA VEHLVK	49	30	23	134.63	b3°b3b4°b4b5b6°b6b10°b10b11°b11y3y11y13y16y17y18y19y20y22°y22y24y26	3193.67	82.258	409249	4	799.17	-9.33
P0AA07 PTHP_SALTY Phohocarrier protein HPr	5		GFTSEITVTSNGKSASAK	27	18	9	39.18	b3°b3b4b6b12y10y12°y12y15	1784.92	62.674	2527	2	892.97	12.11
P0AA07 PTHP_SALTY Phohocarrier protein HPr	6		EAKGFTSEITVTSNGK	24	16	3	13.71	b8b10y4	1668.83	74.920	1683	3	556.95	-6.73
P0AA07 PTHP_SALTY Phohocarrier protein HPr	7	Phosphoryl STY(3)	GFTSEITVTSNGK	27	13	6	35.26	y3y6°y6y9y10°y10	1420.61	59.783	14392	3	474.21	-8.68
P0A1Z2 SKP_SALTY Chaperone protein skp	1		IAIVNMGNLFFQVVAQK	23	16	17	90.63	b2b3b4b6°b6b8y1y2y3y6y7y9y11y12y13°y13y16	1773.97	90.582	171714	2	887.49	1.65
P0A1Z2 SKP_SALTY Chaperone protein skp	2		TGVSNTLENEFK	39	12	13	71.69	b1b3y1y2y5°y5y6y7°y7y8y9y10y12	1338.65	58.576	127219	2	669.83	1.00
P0A1Z2 SKP_SALTY Chaperone protein skp	3		VANDQSIDL VVDANTVAYNSSDV K DITADVLK	126	32	15	33.12	b1b2b5b8b10°b10b12°b12b18b31°b31y1y15y17y32	3392.70	90.544	83981	3	1131.57	-0.58
P0A1Z2 SKP_SALTY Chaperone protein skp	4		AQAFEKDR	97	8	13	69.39	b2°b2b3b6y1y2°y2y3°y3y4y5y6y8	964.47	18.265	9780	2	482.74	-10.88
P0A1Z2 SKP_SALTY Chaperone protein skp	5		AAELQK	53	6	4	34.38	b4b5°b5y5	659.38	32.018	6941	1	659.38	14.90
P0A1Z2 SKP_SALTY Chaperone protein skp	6		VANDQSIDL VVDANTVAYNSSDV K	126	24	4	22.54	b10b12y7y8	2537.19	99.946	3943	2	1269.10	-17.42
P0A1Z2 SKP_SALTY Chaperone protein skp	7		WLLAAGLGLAMVTSQAADK	3	20	5	20.73	b17y13y14y16°y16	1987.03	87.208	1571	3	663.02	-17.82
P0A1Z2 SKP_SALTY Chaperone protein skp	8		TGVSNTLENEFKGR	39	14	4	15.39	b5°b5b8y5	1551.76	68.943	28809	2	776.39	-8.10
P0A1Z2 SKP_SALTY Chaperone protein skp	9		LEKDVMSQR	82	9	5	25.47	b4y3°y3°y3y7	1105.55	48.828	4779	2	553.28	-13.47
P0A1Z2 SKP_SALTY Chaperone protein skp	10		MQRLQSMK	67	8	6	27.86	b5b6°b6°b6y3°y3	1021.52	30.167	3286	2	511.27	-3.47
P0A1Z2 SKP_SALTY Chaperone protein skp	11		LQSMKAGSDR	70	10	8	51.61	b7°b7b9°b9y5y7y9°y9	1092.54	32.805	2037	2	546.77	-10.50
P0A1Z2 SKP_SALTY Chaperone protein skp	12	Phosphoryl STY(13)	WLLAAGLGLAMVTSQAADK	3	20	5	18.1	b13y7y12_H3PO4 y12y15°y15	2067.04	69.018	8430	2	1034.02	6.02
P0A1Z2 SKP_SALTY Chaperone protein skp	13	Oxidation+M(11)	WLLAAGLGLAMVTSQAADK	3	20	5	21.24	y5°y5y9y10°y10	2003.06	86.281	14895	2	1002.04	-0.12
P0A1Z2 SKP_SALTY Chaperone protein skp	14		QAFEKDR	98	7	1	8.36	b4	893.45	18.297	2936	2	447.23	3.42
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		NVEYFEAR	42	8	5	46.89	y2y3y4y5y6	1027.48	47.466	95324	2	514.24	-4.40
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGLSGDQVNVK	8	14	11	94.36	b3y3y4y6y7y8°y8y9y10y11y14	1413.77	57.034	86958	2	707.39	-1.47
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		DIADAVTAAGVDVAK	97	15	15	129.99	b2b3b4b5°b5b6b10y4y5y6y7y9y10y11y13	1415.74	66.951	82116	2	708.37	0.69
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		INALETVTIASK	71	12	4	17.94	b3y9y11y12	1259.72	61.620	62128	2	630.36	-3.97
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		MQVILLDK	0	8	3	35.64	y3y4y5	959.55	64.880	80145	2	480.28	-13.93
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		TTGEHEVNFQVHSEVFAK	123	18	3	12.58	b5y11y13	2058.96	95.502	8486	3	686.99	-13.40
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		INALETVTIASKAGDEGK	71	18	4	33.63	y5y6y7y9	1816.94	63.240	11070	2	908.97	-14.78
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		RAELEAK	50	7	4	52.28	b3b6y3y6	816.45	54.301	8880	1	816.45	-13.68
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	9		NVEYFEARR	42	9	4	37.97	b3b5y5y7	1183.58	54.298	3392	2	592.29	-7.22

Q8ZK80 RL9_SALTY 50S ribosomal protein L9	10		KNVEYFEAR	41	9	11	81.27	b5b6°b6°b6b7°b7y3y4y6y7°y7	1155.56	46.744	2728	2	578.29	-13.42
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	11	Phosphoryl STY(7)	DIADAVTAAGVDVAK	97	15	8	38.01	b4b6°b6y8y9_HPO3y9y11°y11y13_HPO3 y13	1495.69	48.743	10055	2	748.35	-1.22
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	12	Phosphoryl STY(6)	VANLGSLGDQVNVK	8	14	12	62.95	b9b13°b13y7°y7*y7y8y9_H3PO4 y10_H3PO4 y9*y9y10y11_H3PO4 y11°y11	1493.72	45.978	5496	3	498.58	-5.31
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	1		TGEDIPITAR	66	10	8	61.62	b3°b3b4y5y6y7y8y10	1072.56	43.488	87725	2	536.78	-6.49
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	2		LSGFGNFDLR	45	10	4	29.11	y2y3y8y9	1125.56	73.103	19120	2	563.29	-4.66
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	3		ELVELFFEEIR	24	11	11	39.23	b2b4b9°b9y2y4y7°y7y8°y8 y11	1423.74	59.732	15212	3	475.25	-4.20
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	4		ALENGEQVK	36	9	9	37.97	b5b8°b8°b8b9°b9y4*y4y7	987.52	45.996	7464	2	494.26	7.54
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	5		ELVELFFEEIRR	24	12	8	38.61	b1b3b8°b8b9°b9b10y2	1579.84	54.291	5333	4	395.71	-6.49
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	6		AEMSEYLFDK	5	10	4	22.12	b9y3y9°y9	1232.54	54.345	4127	3	411.52	-11.79
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	7		LSGFGNFDLRDK	45	12	8	29.86	b6°b6b10y7°y7*y7y8*y8	1368.67	59.743	19492	3	456.90	-12.58
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	8		MALTKAEMSEYLFDK	0	15	3	22.55	b3b7b9	1776.86	77.255	4017	3	592.96	0.96
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	9		ALENGEQVKLSGFGNFDLR	36	19	5	21.13	b5b13°b13b14y7	2094.05	67.225	2483	3	698.69	-4.78
P02906 SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQELAAK	263	13	10	51.07	b3b4°b4y2y6y9y10y11°y11 y13	1468.73	51.224	91750	2	734.87	0.58
P02906 SUBI_SALTY Sulfate-binding protein	2		FEIVTPSESILAEPTVSVVDK	226	21	8	25.72	b2b5b8b13b14°b14y1y21	2260.22	78.052	53755	3	754.08	12.53
P02906 SUBI_SALTY Sulfate-binding protein	3		NVEVLDSGAR	183	10	11	74.12	b2b3°b3b6y4y5y6y7y8y10*y10	1059.54	40.712	50539	2	530.27	-5.88
P02906 SUBI_SALTY Sulfate-binding protein	4		AVAEAYLK	255	8	8	46.89	b1b2b4b6y2y4y6y8	864.47	41.559	42037	2	432.74	-14.19
P02906 SUBI_SALTY Sulfate-binding protein	5		GSTNTFVER	193	9	5	33.25	y3y5y6*y6y9	1010.48	32.983	38137	2	505.75	-5.50
P02906 SUBI_SALTY Sulfate-binding protein	6		DIQLLNVSYPDTRELYEQYNK	20	21	8	23.49	b9b13°b13y2y4y10y11*y11 l	2601.32	78.123	10087	3	867.78	12.39
P02906 SUBI_SALTY Sulfate-binding protein	7		QATSVINGIEADVVTALAYDVD AIAER	66	28	7	26.62	b3b5b11y3y7y10y11	2917.51	129.068	9896	3	973.17	-3.10
P02906 SUBI_SALTY Sulfate-binding protein	8		AQKDHFANGGTFDQISK	311	17	6	22.21	b5y2y10°y10y12y13	1863.90	70.822	7122	2	932.45	1.31
P02906 SUBI_SALTY Sulfate-binding protein	9		AFSAHWK	41	7	3	35.01	b6y3y6	846.42	103.199	5923	1	846.42	-1.95
P02906 SUBI_SALTY Sulfate-binding protein	10		NFYRPRDADVAK	276	12	5	29.86	b8b9°b9y3y11	1451.73	74.231	2306	2	726.37	-5.89
P02906 SUBI_SALTY Sulfate-binding protein	11		QIHDWNDLIKPGSVITPNPK	126	21	12	35.63	b3°b3b5°b5b6b12°b12°b12b15y4*y4y19	2371.24	74.173	29185	4	593.57	-15.86
P02906 SUBI_SALTY Sulfate-binding protein	12		DIQLLNVSYPDTR	20	13	3	21.29	b11y7y8	1533.76	77.235	2294	2	767.38	-18.94
P02906 SUBI_SALTY Sulfate-binding protein	13		IDKNWIK	96	7	3	35.01	b5y4y6	916.52	49.498	21861	2	458.77	-1.73
P02906 SUBI_SALTY Sulfate-binding protein	14		AFSAHWKQETGDNVVIR	41	17	3	21.75	b7b8b10	1957.97	68.489	10592	3	653.33	-11.41
P02906 SUBI_SALTY Sulfate-binding protein	15		NVEVLDSGARGSTNTFVER	183	19	7	28.4	b4b6°b6b9°b9b11y9	2051.02	54.289	2278	4	513.51	4.64

P0A2A7 RL30_SALTY 50S ribosomal protein L30	1		ATLLGLGLR	21	9	6	52.75	b5y3y5y6y7y9	913.57	74.795	47887	2	457.29	-12.29
P0A2A7 RL30_SALTY 50S ribosomal protein L30	2		GMVNAVSMFMVK	45	11	19	111.51	b2b4b6b7b9y1y2y4y5y7y8*y8y9*y9y10*y10y11*y11	1182.60	74.141	33850	2	591.80	-0.93
P0A2A7 RL30_SALTY 50S ribosomal protein L30	3		EDTPAVRGMVNAVSMFMVK	38	18	3	12.58	b12y11y13	1950.97	101.660	7252	2	975.99	-3.44
P0A2A7 RL30_SALTY 50S ribosomal protein L30	4		GMVNAVSMFMKVEE	45	14	5	25.67	b4b8b13*b13y12	1539.77	96.478	2112	2	770.39	8.40
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		VFMQPASEGTGIIAGGAMR	93	19	21	197.3	b2b3b4b5b11b12b13b14y3y4y5y6y7y10y11y12y13y14y15y17y19	1892.95	68.716	163757	2	946.98	5.48
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		AYGSTNPINVVVR	126	12	13	79.63	b1b2b3b8y2y4*y4y6y7y8y9y10y12	1290.68	51.648	138714	2	645.84	-3.88
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		ATIDGLENMNSPEMVA AK	138	18	18	111.08	b2b5*b5b11b14b15*b15y2y3y4y7y10y11y12y13y14y15y18	1890.90	63.873	85530	2	945.95	4.58
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVA AKR	138	19	9	69.86	b11y3y4y9y10y11y12y13*y13	2046.98	59.550	82474	3	683.00	-6.32
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		EVPA AIQK	54	8	6	35.64	y2*y2y3y5y6y8	855.48	30.281	27040	2	428.24	-12.70
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		VGFGYGK	45	7	4	35.01	y2y3y5y6	727.37	40.473	21694	2	364.19	-11.50
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		NMINVALNNGTLQHPVK	69	17	3	13.09	b7b11y10	1862.97	63.749	15336	3	621.66	-10.75
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		AVLEVAGVHNVLAK	112	14	11	97.16	b3b4b11y3y6y8y9y10y11*y11y12	1419.80	61.251	216782	3	473.94	-20.38
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		LIAVNR	14	6	2	23.13	y4y5	685.43	33.513	22418	1	685.43	-5.34
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		AMEK	62	4	1	10.62	y3	478.23	54.918	4584	1	478.23	-3.77
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		RNMINVALNNGTLQHPVK	68	18	3	12.58	b3b5y17	2019.06	59.678	18099	3	673.69	-14.87
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12		GVHTGSRVFMQPASEGTGIIAGGAMR	86	26	7	16.79	b7b14*b14b16y13*y13y22	2587.30	101.521	9321	3	863.10	4.62
P0A7W4 RS5_SALTY 30S ribosomal protein S5	13		ATIDGLENMNSPEMVA AKR	138	19	4	19.12	b5b7*b7b13	2047.01	86.267	4311	3	683.01	8.71
P0A7W4 RS5_SALTY 30S ribosomal protein S5	14		MAHIEKQAGELQEK	0	14	6	15.39	b4y5*y5y7*y7*y7	1611.82	61.932	3090	4	403.71	2.95
P0A7W4 RS5_SALTY 30S ribosomal protein S5	15		AYGSTNPINVVVRATIDGLENMNSPEMVA AK	126	30	3	11.06	b7y7y10	3162.53	78.803	2312	3	1054.85	-8.03
P0A7W4 RS5_SALTY 30S ribosomal protein S5	16	Oxidation+M(18)	VFMQPASEGTGIIAGGAMR	93	19	4	12.16	b3y12y16*y16	1908.95	121.348	19825	2	954.98	11.96
P0A7W4 RS5_SALTY 30S ribosomal protein S5	17	Oxidation+M(14)	ATIDGLENMNSPEMVA AKR	138	19	6	15.95	b4*b4b11*b11y10y16	2062.99	46.750	3022	4	516.50	-1.54
O54297 RS4_SALTY 30S ribosomal protein S4	1		AALELAEQR	156	9	14	65.25	b2b3b7y1y2*y2y4y5y6*y6*y6y7*y7y9	1000.54	43.885	115024	2	500.77	-4.76
O54297 RS4_SALTY 30S ribosomal protein S4	2		VVNIASYQVSPNDVVSIR	128	18	15	112.63	b3b6*b6b8b13b15y3y4y5y9y11y12y13y14y18	1960.05	72.845	79451	2	980.53	2.37
O54297 RS4_SALTY 30S ribosomal protein S4	3		LSDYGVQLR	47	9	4	25.47	b3b5y2y5	1050.55	51.597	46774	2	525.78	-5.11
O54297 RS4_SALTY 30S ribosomal protein S4	4		LDNVVYR	97	7	5	17.74	b6*b6y2y6y7	878.47	30.675	11880	2	439.74	1.25
O54297 RS4_SALTY 30S ribosomal protein S4	5		IEQAPGQHGAR	33	11	5	31.78	b4b5y2y6y10	1163.58	106.961	2116	1	1163.58	-7.97
O54297 RS4_SALTY 30S ribosomal protein S4	6		EKPTWLEVDAGKMEGTYK	165	18	5	43.21	b5b6b7y4y5	2082.02	66.216	11399	3	694.68	-1.76

O54297 RS4_SALTY 30S ribosomal protein S4	7	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	4	16.52	b5b10y5*y5	1451.73	38.048	1527	3	484.58	11.69
O54297 RS4_SALTY 30S ribosomal protein S4	8	Carbamidomethyl+C(6)	AIDTKCK	26	7	4	46.26	b3b4y5y6	835.42	29.018	1505	2	418.22	-12.42
O54297 RS4_SALTY 30S ribosomal protein S4	9		ALELAEQR	157	8	2	7.74	b3*b3	929.51	43.954	7020	2	465.26	4.14
Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	14	49.61	b2*b2b3*b3b4*b4b15y1y2y4*y4y12y13y14	1686.94	90.647	42518	2	843.97	-0.65
Q7CR87 SURA_SALTY Chaperone surA	2		ITVLPQEVDALAK	149	13	9	21.29	b2b3*b3y1y2y9*y9y10y13	1396.80	71.329	36489	2	698.90	-3.76
Q7CR87 SURA_SALTY Chaperone surA	3		ITDEQLDQAIAIAK	90	15	4	22.55	b2b3b4b13	1642.87	81.106	33685	2	821.94	1.04
Q7CR87 SURA_SALTY Chaperone surA	4		LNAGQAGQQLPDDATLR	50	17	13	98.74	b4b8b9y4y6y7*y7y8y9y10y11y12*y12	1767.90	51.336	27578	2	884.45	2.35
Q7CR87 SURA_SALTY Chaperone surA	5		QIGTQNDASTELNLSHILIALPENP TSEQVNDAQR	162	35	5	17.44	y5y9y14*y14y35	3816.90	89.331	19293	3	1272.97	0.45
Q7CR87 SURA_SALTY Chaperone surA	6		VAAVVNNGVVLESDDVDGLMQSV K	27	23	5	31.78	b3y8y12y13y14	2343.23	91.656	15530	2	1172.12	1.46
Q7CR87 SURA_SALTY Chaperone surA	7		LAYDGLNYSTYR	117	12	10	49.35	b2b4b5b6b10*b10y2y3y8*y8	1435.70	49.628	11530	2	718.36	12.50
Q7CR87 SURA_SALTY Chaperone surA	8		LAITYSADQQALK	214	13	4	24.01	y2y5y8y9	1421.76	54.952	6063	2	711.39	0.34
Q7CR87 SURA_SALTY Chaperone surA	9		HILLKPSPIMNDQQAR	288	16	6	13.71	b2b11*b11y5y10*y10	1861.03	53.509	4901	2	931.02	9.05
Q7CR87 SURA_SALTY Chaperone surA	10		LEEIAADIK	306	9	8	64	b4b5*b5b6b7*b7b8y7	1001.53	46.788	4407	2	501.27	-20.42
Q7CR87 SURA_SALTY Chaperone surA	11		LIMDQIILQMGQK	73	13	4	16.52	b4*b4b7y12	1530.83	78.159	4052	2	765.92	-8.61
Q7CR87 SURA_SALTY Chaperone surA	12		GQSQISVTEVHAR	274	14	10	66.12	b4*b4b6b9*b9b10y5y6y10y11	1498.77	37.241	3256	3	500.26	6.19
Q7CR87 SURA_SALTY Chaperone surA	13		EYSQDPGSANQGGLGWATPDIF DPAFR	326	28	7	36.06	y3y4y5*y5y8y11*y11	3011.34	94.367	3099	2	1506.17	-1.95
Q7CR87 SURA_SALTY Chaperone surA	14		TDAAQK	388	6	1	11.88	y3	633.33	118.837	2150	1	633.33	12.72
Q7CR87 SURA_SALTY Chaperone surA	15		QAESIVEEARNGADFGK	197	17	11	46.64	b4b13y4*y4y6y9y10*y10*y10y11*y11	1820.88	60.586	4976	2	910.94	1.81
Q7CR87 SURA_SALTY Chaperone surA	16		AYRMLMNR	396	8	4	42.12	b4b5b7y3	1054.52	48.835	4393	3	352.18	-8.10
Q7CR87 SURA_SALTY Chaperone surA	17		LNAGQAGQQLPDDATLRHQILER	50	23	4	24.96	b7b8b11b15	2544.33	89.704	4369	3	848.78	1.63
Q7CR87 SURA_SALTY Chaperone surA	18		SRLAYDGLNYSTYR	115	14	7	48.84	b4b5b7b8b10y4*y4	1678.80	45.471	3306	2	839.90	-10.83
Q7CR87 SURA_SALTY Chaperone surA	19	Oxidation+M(19)	VAAVVNNGVVLESDDVDGLMQSV K	27	23	3	11.17	b3b16y8	2359.21	115.737	5519	3	787.07	-3.52
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	30	157.26	b2*b2*b2b3b5b7*b7b9b10b11*b11b12*b12b13*b13*b13b16y4y6*y6y7*y7y8y9y10y11y12*y12y17y23	2379.22	65.115	193917	3	793.75	-7.08
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	9	46.93	b2b3b7b12y4y5y6y15y17	1837.95	86.832	96406	2	919.48	1.46
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(13)	VLNIFPSIDTVGCAASVR	48	18	11	53.74	b2b3b5y2y3y7y9y10y13y14y18	1919.02	85.925	88014	2	960.01	6.36
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4		AQAFTLVAK	24	9	9	50.53	b2*b2y2y3y4y6y7y9*y9	948.54	53.629	47741	2	474.77	-11.45
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		NYGVEIVDGPLK	116	12	11	48.89	b1*b1b2b3*b3b10b11y4y8y10y12	1303.68	65.452	28531	2	652.34	-7.49
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6	Carbamidomethyl+C(15)	FNQLATEVENTVVLCVSADLPFA QSR	67	26	3	21.6	b7b9b10	2908.45	110.539	5974	3	970.15	-0.50

Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		NNEFLK	110	6	1	11.88	b5	764.39	37.127	6126	1	764.39	-2.40
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8		AVIVLDENDNVIFSQVLVDEITHEPDYDAALNVLKA	133	35	23	127.73	b3b4b5b10b11*b11b13*b13y3y4y5y6y7y12y13°y13*y13y14y16y18y24y30y31	3882.97	120.889	163477	3	1294.99	0.75
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9	Carbamidomethyl+C(13);Phosphoryl STY(10)	VLNIFPSIDTGVCASVRK	48	19	3	12.16	b8y11_HPO3 y11y14	2127.07	48.880	39924	3	709.70	6.66
Q8ZP65 TPX_SALTY Probable thiol peroxidase	10	Phosphoryl STY(10)	DLSDVSLSQYAGKR	33	14	5	38.89	b3°b3b4b8b9	1618.73	42.418	4430	3	540.25	-5.88
Q8ZP65 TPX_SALTY Probable thiol peroxidase	11	Carbamidomethyl+C(15)	FNQLATEVENTVVL CVSADLPFAQSR	67	26	0	13.19		2891.46	110.573	7693	3	964.49	14.69
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	12	77.38	b2y1y2y3y4y6y7y8y12y14y16y18	1970.00	63.971	133482	3	657.34	-10.97
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		ESSVPFSYYDNQKK	47	14	8	43.92	b3°b3b11y5y6y7y10y14	1691.76	55.916	125881	2	846.38	0.94
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		VVGYSQDYSNAIVEAVK	61	17	17	102.51	b2b3b4b8b13b14°b14y3y4y5y11y12*y12y13°y13y15y17	1841.94	68.545	102800	2	921.47	7.16
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		AVAFMMDDALLAGER	198	15	8	61.02	b3b5b10y3y4y8y11y13	1609.78	85.224	78140	2	805.39	4.55
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTTNNLER	98	22	9	27.39	b3b13y1y2y3y5y7y10y22	2526.20	82.347	18991	3	842.74	1.84
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6		QAAFSDTIFVVGTR	122	14	4	15.39	b7b12*b12y13	1511.77	74.136	15565	2	756.39	-12.11
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7		LMDDTIAQAQTSGEAEK	247	17	12	59.86	b3b11°b11*b11y9y10*y10y11°y11*y11y12y13	1807.84	46.721	7898	2	904.42	2.03
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8	Carbamidomethyl+C(19)	KPDNWEIVGK PQSQEAYGCMLR	217	22	5	24.24	b3b4b12b14y8	2606.24	76.814	5618	5	522.05	-5.15
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9		TLESGR	192	6	2	23.13	b4b5	662.34	54.264	5510	1	662.34	-8.02
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		LNEEQK	170	6	1	11.88	b5	760.39	33.952	2464	1	760.39	7.55
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11		DHGD SFTLESGR	185	13	3	16.52	b9b12y4	1476.68	43.849	853201	3	492.90	1.24
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTTNNLER	89	31	8	35.38	b3y6y9y10y13°y13y14y21	3548.78	87.539	206629	3	1183.60	0.34
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	13		WFDKWFK	264	7	5	32	b5b6°b6y5°y5	1056.54	30.759	5657	2	528.77	7.63
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	14		AVAFMMDDALLAGERAK	198	17	3	13.09	b3b5y6	1808.90	54.340	5347	3	603.64	-4.25
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	15		DFPDLK GK	146	8	6	56.38	b3°b3b4b6b7y5	919.48	24.742	5016	2	460.24	-6.44

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	16		KLMDDTIAQAQTSGEAEK	246	18	3	12.58	b4b14y4	1935.93	82.988	4729	2	968.47	-1.58
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	17		LNEEQKMGMR	170	10	3	36.89	b5b7b9	1235.58	65.951	2876	2	618.30	-2.07
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	18	Oxidation+M(5)	LTTAMLVMGLSAGLAHAEDGAP AAGSTLDDK	5	30	5	25.67	b5b6y10y12y15	2885.41	110.547	7695	3	962.47	-10.83
P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	18	121.17	b2b3b4b5y2°y2y3°y3y4y5y6°y6y7°y7y8y9y10y12	1196.59	64.983	435371	2	598.80	-7.45
P0A9Y9 CC_SALTY Cold shock-like protein cC	2		DVVFVHFSAIQNGGFK	27	15	13	79.48	b7°b7b8°b8b9y1y5y7y9*y9y11y13y15	1665.82	74.242	29332	3	555.94	-12.16
P0A9Y9 CC_SALTY Cold shock-like protein cC	3		TLAEGQNVEFEIQDGQK	42	17	8	17.73	b6*b6b8y2*y2y8y10*y10	1905.94	70.030	2499	2	953.48	13.13
P0A9Y9 CC_SALTY Cold shock-like protein cC	4		GPAAVNVTAI	59	10	6	48.14	b3b6*b6b7b9*b9	912.51	60.518	9674	1	912.51	-7.76
P0A9Y9 CC_SALTY Cold shock-like protein cC	5		GFGFITPADGSKDVFVHFSAIQGN GFK	15	27	3	10.92	b25y9y11	2843.39	66.095	5263	3	948.47	-9.19
P0A9Y9 CC_SALTY Cold shock-like protein cC	6		GQVKWFNESH	5	10	10	58.09	b4b5*b5b8°b8*b8y4y5*y5y6	1222.61	32.027	2795	3	408.21	-12.68
P0A9Y9 CC_SALTY Cold shock-like protein cC	7		ITPADGSK	19	8	0	4.4		788.43	65.043	4399	1	788.43	14.63
P0A9Y9 CC_SALTY Cold shock-like protein cC	8		GFITPADGSK	17	10	0	4.4		992.50	65.053	1574	1	992.50	-5.90
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	11	47.3	b11y2y5y6y10y11°y11*y11y13y17y19	2032.91	38.292	99166	3	678.31	-4.74
P02936 OMPA_SALTY Outer membrane protein A	2		GVKDVVTQPQA	339	11	10	44.46	b6b7b8°b8b10°b10y1y4*y4y11	1141.61	38.051	32506	2	571.31	-8.02
P02936 OMPA_SALTY Outer membrane protein A	3		STLKPEGQQALDQLYSQLSNLDP K	231	24	8	15.82	b14y1y2y9°y9y12y14*y14	2673.40	90.651	32031	3	891.80	8.77
P02936 OMPA_SALTY Outer membrane protein A	4	Carbamidomethyl+C(6)	AALIDCLAPDR	321	11	13	105.49	b2b3b7°b7b8y3y4y5°y5y6y7y8y9	1214.62	62.602	17342	2	607.81	-1.11
P02936 OMPA_SALTY Outer membrane protein A	5		IGSDAYNQGLSEKR	267	14	5	15.39	b2b5°b5y3y6	1537.75	35.149	14495	3	513.26	-6.27
P02936 OMPA_SALTY Outer membrane protein A	6		LGGMVWR	117	7	7	35.01	b2b3b5b7y2y5y7	818.43	38.026	11136	2	409.72	-7.53
P02936 OMPA_SALTY Outer membrane protein A	7		FGQQEAAPVVAPAPAPEVQTK	194	23	8	26.12	b5b10y6y9°y9y10y12y23	2303.18	54.252	8828	3	768.40	-9.33
P02936 OMPA_SALTY Outer membrane protein A	8		LGYPITDDLVDYTR	103	14	7	37.59	b2b11°b11y7y9y10y11	1640.81	76.765	7764	2	820.91	-2.98
P02936 OMPA_SALTY Outer membrane protein A	9		AQSVVDYLISK	281	11	4	30.2	b7y6y7y9	1222.66	72.907	23682	2	611.84	-2.90
P02936 OMPA_SALTY Outer membrane protein A	10		DGSVVVLGFTDR	255	12	6	41.41	b11y3°y3y6y7y10	1264.63	55.042	7000	3	422.21	-20.27
P02936 OMPA_SALTY Outer membrane protein A	11		GDNINGAYK	85	9	8	65.25	b4°b4b7°b7y4y6y7y8	951.47	49.659	4044	2	476.24	19.50
P02936 OMPA_SALTY Outer membrane protein A	12		IGSDAYNQGLSEK	267	13	15	62.02	b8°b8b9b10°b10*b10b11°b11y6°y6*y6y8*y8y9*y9	1381.65	42.462	3612	3	461.22	-4.42
P02936 OMPA_SALTY Outer membrane protein A	13		SDVLFNFNK	222	9	4	25.47	b3°b3b6y7	1083.54	31.988	3492	2	542.27	-9.80
P02936 OMPA_SALTY Outer membrane protein A	14		GIPSDK	292	6	1	11.88	b3	616.32	46.868	3244	1	616.32	-10.79
P02936 OMPA_SALTY Outer membrane protein A	15		SNVPGGPSTK	128	10	4	41.15	b3b6b9y7	943.50	74.895	1759	2	472.25	17.79
P02936 OMPA_SALTY Outer membrane protein A	16	Carbamidomethyl+C(6)	AALIDCLAPDRR	321	12	6	42.87	b3b7b11y5°y5y6	1370.70	56.850	13511	3	457.57	-13.27

[P02936]OMPA_SALTY Outer membrane protein A	17		LGGMVWRADTK	117	11	3	31.5	y6y8y10	1233.62	38.101	3423	2	617.32	-14.25
[P02936]OMPA_SALTY Outer membrane protein A	18		GDNINGAYKAQGVQLTAK	85	18	6	21.5	b9°b9*b9b12°b12b13	1847.95	63.214	2610	3	616.65	-6.01
[P02936]OMPA_SALTY Outer membrane protein A	19		HFTLKSDVLFNFNK	217	14	5	15.39	b4b7y9°y9*y9	1709.88	95.377	2459	2	855.44	-11.14
[P02936]OMPA_SALTY Outer membrane protein A	20	Carbamidomethyl+C(13) ;Oxidation+M(2)	GMGESNPVTGNTCDNVKPR	302	19	3	12.16	b17y9y13	2048.89	74.201	9977	3	683.63	-13.35
[P02936]OMPA_SALTY Outer membrane protein A	21		DAYNQGLSEKR	270	11	0	5.65		1280.64	35.095	7376	2	640.82	14.58
[P02936]OMPA_SALTY Outer membrane protein A	22		PAPAPAEVQTK	205	12	3	12.47	b6b11*b11	1205.64	54.285	6107	2	603.32	-13.26
[P66541]RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAELENK	45	14	7	23.96	b2b3°y4y9y12°y12y14	1576.81	85.284	143045	2	788.91	3.25
[P66541]RS2_SALTY 30S ribosomal protein S2	2		EANNLGIPVFAIVDTNSDPDGVDF VIPGNDDAIR	174	34	16	36.76	b5°b5*b5b7°b7*b7b26y3y 4y7y8°y8y11y16*y16y34	3569.75	104.971	33504	3	1190.59	2.26
[P66541]RS2_SALTY 30S ribosomal protein S2	3	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	10	50.61	b4y3*y3y4*y4y5*y5y7*y7 y8	1694.72	47.892	28670	3	565.58	-10.52
[P66541]RS2_SALTY 30S ribosomal protein S2	4		AGVHFGHQTR	11	10	14	85.37	b1b3b5b6b7b8*b8y2y4°y4 y7y8*y8y10	1109.55	46.732	22871	2	555.28	-8.36
[P66541]RS2_SALTY 30S ribosomal protein S2	5		ATVSMRDLK	1	10	5	29.11	b4°b4b8b9y10	1151.60	39.538	12980	2	576.30	5.09
[P66541]RS2_SALTY 30S ribosomal protein S2	6		LKDLETQSQDGTFEK	113	15	8	23.8	b10y4°y4y9*y9y10*y10y15	1738.87	39.680	8773	2	869.94	9.34
[P66541]RS2_SALTY 30S ribosomal protein S2	7		MATVSMR	0	7	5	49.27	b4b5b7y3y6	795.39	59.780	6603	1	795.39	2.76
[P66541]RS2_SALTY 30S ribosomal protein S2	8		SQDLASQAEESFVEAE	225	16	3	13.71	b8b10y9	1739.77	73.552	4829	2	870.39	7.72
[P66541]RS2_SALTY 30S ribosomal protein S2	9		DLETQSQDGTFEK	115	13	5	28.35	b3b4y4y10*y10	1497.69	134.775	1659	2	749.35	14.02
[P66541]RS2_SALTY 30S ribosomal protein S2	10		DMGGLPDALFVIDADHEHIAIK	152	22	4	22.85	b6b9y7y8	2377.14	99.640	124603	2	1189.07	-18.79
[P66541]RS2_SALTY 30S ribosomal protein S2	11		ILFVGTK	66	7	3	35.01	y3y5y6	777.48	57.726	20395	2	389.24	-14.76
[P66541]RS2_SALTY 30S ribosomal protein S2	12		RAASEAVK	73	8	8	58.14	b4°b4b5b6°b6y5y7°y7	831.46	31.467	15356	2	416.23	-8.74
[P66541]RS2_SALTY 30S ribosomal protein S2	13		AGVHFGHQTRYWNPK	11	15	3	20.49	b10y11y12	1797.90	100.658	9784	2	899.45	3.26
[P66541]RS2_SALTY 30S ribosomal protein S2	14		LKDLETQSQDGTFEK	113	15	11	69.55	b4b10°b10b11°b11b13y4y 6y7y9y10	1738.85	60.633	9485	3	580.29	-0.07
[P66541]RS2_SALTY 30S ribosomal protein S2	15		TVPMFNEALAELENKISAR	45	18	7	21.5	b5b10°b10°b10b11°b11*b 11	2004.03	45.988	1717	2	1002.52	-12.91
[P66541]RS2_SALTY 30S ribosomal protein S2	16		YWNPKMKPFIFGAR	21	14	3	23.96	b6b8b12	1754.91	71.310	1564	2	877.96	-5.70
[P66541]RS2_SALTY 30S ribosomal protein S2	17	Oxidation+M(2)	DMGGLPDALFVIDADHEHIAIK	152	22	4	22.85	b13b15y10y11	2393.16	83.324	2697	2	1197.08	-9.90
[P66541]RS2_SALTY 30S ribosomal protein S2	18	Oxidation+M(1)	MATVSMRDLK	0	11	5	30.2	b4°b4b8b9y9	1298.63	46.792	2303	3	433.55	-0.09
[P66541]RS2_SALTY 30S ribosomal protein S2	19		AGVHFGHQQT	11	9	2	17.86	y5y7	953.47	46.784	2450	2	477.24	10.88
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	1		TQFMGPEGVANVSLNAGESAE GLLVTKPK	240	31	17	75.8	b2°b2*b2b3b4b5°b5b6b15 y4y6y8y19y27y28y29y31	3144.63	89.061	104862	3	1048.88	1.24
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	2	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILM ITPAATAPELTAR	92	38	13	75.9	b12b23b25b26b27y6y9y10 y11y12y13y15y38	4077.98	90.128	81267	3	1360.00	-0.42

P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	3		TTGLDSDQGPTAAK	137	14	10	94.36	b4y5y6y7y8y9y10y11y12y14	1361.65	29.890	80116	2	681.33	-1.88
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	4		VAVVGAMSGPV AQYGDQEFTGA EQAIADINAK	25	32	15	78.59	b2b3b4b14b15b26y1y3*y3y4y5*y5y6y7y32	3207.56	90.559	67881	3	1069.86	-0.84
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	5		QQYGEGLAR	168	9	7	38.49	b3b9y2y4y6y7y9	1021.50	33.603	38310	2	511.25	-5.38
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	6		ENIDFVYYGGYHPMGQILR	212	20	4	20.73	b7y7y12y13	2401.13	81.303	23584	3	801.05	2.54
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	7		GGVNVVFFDGITAGEK	185	16	5	28.06	b9b15y3y4y10	1609.82	110.196	7948	2	805.41	-1.97
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	8		QDPSGAFVWTTYAALQSLQAGLN HSDDPAEIAK	290	33	7	17.19	b2y1y2y8y14°y14y24	3501.71	109.834	6439	3	1167.91	4.46
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	9	Carbamidomethyl+C(6)	TLLAGCIALSLSHMAFADDIK	4	21	4	14.63	b9b14y6y14	2247.14	69.920	163625	3	749.72	-3.04
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	10		GATVDTVMGPLSWDEK	326	16	10	35.93	b3°b3b5°b5b9°b9y3°y3y5y12	1705.84	62.624	22078	2	853.42	15.39
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	11		LVLRTTGLDSDQGPTAAK	133	18	8	21.61	b14°b14y10°y10y12°y12*y12y13	1842.99	95.479	28037	2	922.00	0.93
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	12		VAVVGAMSGPV AQYGDQEFTGA EQAIADINAKGGIK	25	36	4	24.55	b3b7b8b13	3562.74	123.719	20284	4	891.44	-13.09
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	13		KQDPSGAFVWTTYAALQSLQAGLN HSDDPAEIAK	289	34	6	22.59	b4b10b14y8y9y12	3629.75	100.325	11797	3	1210.59	-8.88
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	14		IAIHDKQQYGEGLAR	161	16	7	42.95	y4y6y7°y7y10y11°y11	1811.99	48.724	5003	2	906.50	6.06
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	15		YLKGATVDTVMGPLSWDEK	323	19	3	21.34	y5y6y16	2110.06	66.244	2960	3	704.03	4.98
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	16		GDLKGFEFGVFDWHANGTATDAK	342	23	7	22.42	b8b12°b12y9y10*y10y13	2483.16	92.705	2443	2	1242.08	-1.08
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	17	Oxidation+M(16)	KENIDFVYYGGYHPMGQILR	211	21	4	11.55	b4b7y8*y8	2545.25	38.032	1792	3	849.09	14.48
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	18		QQYGEGLAR	168	9	0	2.51		1003.49	33.664	5220	2	502.25	3.35
P66170 RL29_SALTY 50S ribosomal protein L29	1		SVEELNTELLNLLR	9	14	12	63.11	b1b4b5°b5b6b12y3y4*y4y9y11y14	1642.90	102.063	161437	2	821.96	2.01
P66170 RL29_SALTY 50S ribosomal protein L29	2		SVEELNTELLNLLREQFNLR	9	20	4	26.23	b4b10b11b13	2430.28	113.716	7092	3	810.77	-6.03
P66170 RL29_SALTY 50S ribosomal protein L29	3		EQFNLR	23	6	3	23.13	y3*y3y4	806.41	42.706	80862	2	403.71	-9.46
P66170 RL29_SALTY 50S ribosomal protein L29	4		TLLTEK	54	6	1	11.88	y4	704.41	33.021	5822	1	704.41	-12.74
O33921 AGP_SALTY Glucose-1-phohatase	1		MGTMDPTFNPNVITDDSAAFR	141	20	10	56.66	b3y2y4y6y8y9y12y13y15y20	2186.01	79.115	40500	2	1093.51	7.59
O33921 AGP_SALTY Glucose-1-phohatase	2		IEYVYQSAR	358	9	7	64	b6y3y5y6y7y8y9	1128.57	43.275	29640	2	564.79	-2.92
O33921 AGP_SALTY Glucose-1-phohatase	3	Carbamidomethyl+C(14)	EWLVAQGLIPSGECPAPDTVYAY ANSLQR	87	29	10	20.78	b3°b3b15y2y5y7*y7y9y20y29	3205.58	94.522	24111	3	1069.20	5.33
O33921 AGP_SALTY Glucose-1-phohatase	4		DTFSANYQQEPGVQGPLK	208	18	5	12.58	b13°b13y8y13y18	1978.96	56.965	14767	2	989.98	5.61
O33921 AGP_SALTY Glucose-1-phohatase	5		APLANNGSVLAQSTPNAWPAWD VPGGQLTTK	43	31	12	21.81	b6b7°b7b9°b9b14°b14y1y8y11°y13y31	3161.59	84.149	12692	3	1054.54	-3.32
O33921 AGP_SALTY Glucose-1-phohatase	6		SQLHLDSEYK	172	10	8	29.11	b1b2°b2y2y4°y4y5y7	1219.59	22.291	5521	3	407.20	-4.50
O33921 AGP_SALTY Glucose-1-phohatase	7		NGYQDSLFTSPTVAR	266	15	8	43.96	b1b8°b8b9b10°b10y6y7	1655.82	42.432	4894	3	552.61	9.07
O33921 AGP_SALTY Glucose-1-phohatase	8	Carbamidomethyl+C(14)	LLEQITHYQDSPSCKEK	182	17	6	31.71	b2b10°b10b11y6y7	2076.00	48.765	4068	3	692.67	-1.65
O33921 AGP_SALTY Glucose-1-phohatase	9	Carbamidomethyl+C(14)	LLEQITHYQDSPSCK	182	15	5	13.22	b9°b9b11°b11y2	1818.86	59.740	2182	2	909.93	-4.70

O33921 AGP_SALTY Glucose-1-phohatase	10		VLVADR	293	6	3	23.13	y3y4°y4	672.39	46.073	54178	1	672.39	-13.43
O33921 AGP_SALTY Glucose-1-phohatase	11		TPIGGQLVFQR	335	11	4	19.74	b7y3*y3y8	1215.66	64.154	10014	2	608.33	-21.79
O33921 AGP_SALTY Glucose-1-phohatase	12		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDR	226	31	3	11.16	b3y7y9	3486.70	84.562	4060	3	1162.91	17.02
O33921 AGP_SALTY Glucose-1-phohatase	13		GGVLEVYMGHYTR	74	13	3	16.52	b4b8y11	1481.70	73.545	2390	2	741.35	-14.01
O33921 AGP_SALTY Glucose-1-phohatase	14		QQAQVAMEK	161	9	6	50.99	b3b4*b4b6y4y7	1032.53	19.337	1890	3	344.85	13.00
O33921 AGP_SALTY Glucose-1-phohatase	15	Carbamidomethyl+C(8); Carbamidomethyl+C(16)	VTLELKGPCVDANGFCPLDK	383	20	7	37.27	b12b13*b13y6y7y9y14	2233.09	68.970	65746	3	745.03	-6.12
O33921 AGP_SALTY Glucose-1-phohatase	16	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	GCPVDANGFCPLDKFDNMNTA AK	389	24	6	39.43	y3y6y7y12y14y22	2641.20	79.193	45323	3	881.07	5.55
O33921 AGP_SALTY Glucose-1-phohatase	17		IEYVYQSARQLR	358	12	4	21.92	b6*b6b7y4	1525.83	45.969	29389	3	509.28	11.04
O33921 AGP_SALTY Glucose-1-phohatase	18		QQAQVAMEKAR	161	11	5	31.78	b7*b7b8y7y9	1259.64	49.644	13010	3	420.55	-13.86
O33921 AGP_SALTY Glucose-1-phohatase	19	Carbamidomethyl+C(5)	EKHQCSLIDAK	197	11	6	44	b4b8y4y7°y7y10	1328.65	50.301	3291	2	664.83	-7.81
O33921 AGP_SALTY Glucose-1-phohatase	20	Carbamidomethyl+C(24)	SQLHLDSEYKLEQITHYQDSPSC K	172	25	8	21.63	b4b6*b6b7°b7y3°y3y12	3019.47	94.398	2281	4	755.62	8.00
O33921 AGP_SALTY Glucose-1-phohatase	21	Phosphoryl STY(6)	NAEALTLK	370	8	6	30.87	b5_H3PO4 b5*b5b7_H3PO4 b7°b7y3°y3	939.44	42.430	3990	2	470.22	-6.76
O33921 AGP_SALTY Glucose-1-phohatase	22		LLEQITHYQDSP	182	12	2	13.22	y9y11	1443.70	59.781	13217	2	722.36	-4.74
O33921 AGP_SALTY Glucose-1-phohatase	23		NYQQEPGVQGPLK	213	13	0	8.16		1457.73	56.956	7930	2	729.37	-6.87
O33921 AGP_SALTY Glucose-1-phohatase	24		APLANNGSVLAQSTPNAWPAWD VP	43	24	2	13.43	y5°y5	2476.20	84.097	1616	2	1238.60	-10.06
O33921 AGP_SALTY Glucose-1-phohatase	25		SQLHLDSEY	172	9	0	3.14		1091.51	22.327	1503	2	546.26	7.38
P0A1V4 KAD_SALTY Adenylate kinase	1		LVEYHQMTAPLIGYYQK	167	17	9	34.43	b2b8°b8y2y3y5y6y7y17	2054.02	70.058	42948	3	685.35	-8.08
P0A1V4 KAD_SALTY Adenylate kinase	2		VDGTQAVADV R	195	11	6	19.74	b4b11y2y4y9y11	1130.57	37.106	42622	2	565.79	-7.45
P0A1V4 KAD_SALTY Adenylate kinase	3		IILLGAPGAGK	2	11	7	58.26	b2b3y2y3y5y7y9	1009.63	61.666	35238	2	505.32	-9.07
P0A1V4 KAD_SALTY Adenylate kinase	4		YGIPQISTGDMLR	23	13	9	80.77	b2y3y4y5y6y7y8y10y13	1450.73	73.388	25529	2	725.87	-2.10
P0A1V4 KAD_SALTY Adenylate kinase	5		GTQAQFIMEK	13	10	10	66.67	b5°b9y3°y3y5y7y8*y8y9y1 0	1152.59	49.560	15466	2	576.80	13.34
P0A1V4 KAD_SALTY Adenylate kinase	6		NGFLLDGFPR	78	10	6	43.83	b4b5b8y6y9°y9	1135.57	54.259	3725	2	568.29	-21.28
P0A1V4 KAD_SALTY Adenylate kinase	7	Carbamidomethyl+C(6)	IAQEDCRNGFLLDGFPR	71	17	4	20.5	y6y10°y10y12	2007.98	89.533	34747	2	1004.49	4.32
P0A1V4 KAD_SALTY Adenylate kinase	8		DDVTGEDLTTRK	145	12	6	29.86	b4°b4b11y7y8°y8	1349.67	46.004	17813	3	450.56	11.22
P0A1V4 KAD_SALTY Adenylate kinase	9		IILLGAPGAGKGTQAQFIMEK	2	21	3	11.55	b3y3y19	2143.18	73.441	15625	3	715.06	-7.52
P0A1V4 KAD_SALTY Adenylate kinase	10		YAKVDGTQAVADV R	192	14	3	15.39	b10y8y11	1492.76	69.024	4597	2	746.88	-12.43
P0A1V4 KAD_SALTY Adenylate kinase	11		LVEYHQMTAPLIGYYQKEAEGN TK	167	25	6	10.97	b9y5°y5*y5y11°y11	2854.40	54.348	3278	6	476.57	-1.28
P0A1V4 KAD_SALTY Adenylate kinase	12		YGIPQISTGDMLRAAVK	23	17	5	13.09	b8b10°b10*b10y3	1819.95	42.472	1676	2	910.48	-11.67

P0A1V4 KAD_SALTY Adenylate kinase	13		GTQAQFIM	13	8	4	29.11	y3y6*y6y7	895.44	49.585	3519	2	448.23	10.29
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	1		SATPAQAQAVHK	176	12	18	93.89	b2b3°b3b11b12y1y2y3y4y5*y5y6*y6y7*y7y8y9y12	1208.63	19.310	59727	2	604.82	-7.98
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	2	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	7	22.8	b6y4y8y11°y11y18y24	2589.30	83.499	49721	3	863.77	-1.04
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	3		TQGAAAFEGAVIAYEPVWAIGTGK	152	24	18	37.49	b1°b1b2°b2°b2b4b7°b7b11°b11b12b13°b13y1y2y7y12y24	2407.24	94.408	27602	2	1204.12	4.06
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	4	Carbamidomethyl+C(14)	FAVLKEQGLTPVLCIGETEAENEA GK	112	26	5	21.6	y2y3y6y7*y7	2803.41	136.440	4112	2	1402.21	-4.01
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	5		DIGAQYIIHGSERR	84	15	3	22.55	b4b11b12	1727.91	79.585	2591	2	864.46	-3.67
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	6	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	5	19.95	b4°b4b6b7y8	2433.23	98.555	2016	3	811.75	11.74
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	7	Carbamidomethyl+C(9)	EQGLTPVLCIGETEAENEAGK	117	21	5	11.55	b14y2y3y12°y12	2245.09	70.078	1704	3	749.04	11.64
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	8		LNGSR	11	5	2	11.25	y4°y4	546.30	32.016	4374	1	546.30	-5.92
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	9		DIGAQYIIHGSER	84	14	4	23.17	y4y5°y5y10	1571.82	68.962	1684	2	786.41	1.55
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	10	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAENEAGKTEEV CAR	117	28	20	128.06	b5°b5b13y3y4y5°y5y7y10°y10y12y13y14y18y20y21y23*y23y24y26	3090.43	72.966	180080	3	1030.81	-2.45
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	11		HMVNELVANLRK	16	12	3	28.15	b4b6b8	1423.77	62.679	12188	3	475.26	-13.03
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	12	Carbamidomethyl+C(14)	FAVLKEQGLTPVLCIGETEAENEA GK	112	26	3	34.15	y4y5y6	2803.39	115.935	8805	3	935.13	-10.45
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	13	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	6	23.15	b4b5°b5b8b11y3	2589.32	91.497	7208	3	863.78	4.05
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	14		TYHKESDELIAK	99	12	5	27.94	b6y3y6°y6y7	1433.72	45.974	7098	2	717.36	-5.19
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	15		RHPLVMGNWK	1	10	3	29.11	y4y5y7	1237.65	34.534	3525	2	619.33	-7.10
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	16		TPAQAQAVHK	178	10	5	31.16	b6°b6b7b8*b8	1050.56	19.312	24935	2	525.78	-8.37
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	17		PAQAQAVHK	179	9	8	52.87	b3*b3b4b6*b6b7*b7b8	949.51	19.316	24844	2	475.26	-13.95
Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTEPTWFPDSQTLAFTSDQAGRPQVYK	287	29	9	14.4	b1b2*b2b5°b5y14y20y24y29	3285.56	78.328	65764	3	1095.86	4.09
Q8ZQT5 TOLB_SALTY Protein tolB	2		WAGPGAAPEDIGGIVAADLR	43	20	15	64.49	b2b5b7b10b13°b13b14b15y1y2y5y6y9y13y20	1936.00	86.259	55750	2	968.51	6.43
Q8ZQT5 TOLB_SALTY Protein tolB	3		IEITQGVDSARPIGVVPFK	24	19	9	24.92	b2b9b11y1y2y3y15y16y19	2026.11	71.229	51126	3	676.04	-10.72
Q8ZQT5 TOLB_SALTY Protein tolB	4		LPATDGQVK	413	9	10	76.5	b5b8y3y5y6y7°y7y8*y8y9	928.50	28.349	42324	2	464.76	-6.18
Q8ZQT5 TOLB_SALTY Protein tolB	5		SALVIQTLANGAVR	223	14	6	44.43	b3b4y2y9y10y11	1412.82	71.518	26906	2	706.91	-4.23
Q8ZQT5 TOLB_SALTY Protein tolB	6		MNINGGAAQR	316	10	5	32.12	y5y6y7*y7y10	1031.50	28.453	16838	2	516.25	-5.44
Q8ZQT5 TOLB_SALTY Protein tolB	7		HNGAPAFSPDGTK	244	13	7	46.3	b2b3b4b5b11y6y8	1298.60	63.238	12973	3	433.54	-7.33
Q8ZQT5 TOLB_SALTY Protein tolB	8		FMVMVSSNNGQQHIAK	344	16	4	13.71	b9y2y11y14	1790.87	77.243	2360	3	597.63	3.95
Q8ZQT5 TOLB_SALTY Protein tolB	9		IAYVVQTNNGGQFPYELR	166	17	3	20.08	b4y4y5	1955.02	110.850	1667	3	652.34	7.24

Q8ZQT5 TOLB_SALTY Protein tolB	10		VSDYDGYNQFVVHR	183	14	5	20.83	b9y9y10°y10*y10	1698.76	54.634	67216	3	566.93	-15.16
Q8ZQT5 TOLB_SALTY Protein tolB	11		QVASFPR	237	7	3	35.01	y3y4y5	804.42	39.122	19420	2	402.72	-14.26
Q8ZQT5 TOLB_SALTY Protein tolB	12		YAGHTASDEVFEK	142	13	3	25.77	b4b8b10	1453.68	66.908	13246	3	485.23	13.02
Q8ZQT5 TOLB_SALTY Protein tolB	13		QWLRYAGHTASDEVFEK	138	17	5	20.08	b10*b10y6y7°y7	2036.99	95.488	23139	2	1019.00	5.69
Q8ZQT5 TOLB_SALTY Protein tolB	14		ARLPATDGQVK	411	11	5	39.23	b5b7b8y5y8	1155.64	30.208	12877	2	578.32	-8.03
Q8ZQT5 TOLB_SALTY Protein tolB	15		NSGKFNPDDR	63	10	3	22.12	b6b9y6	1147.57	46.736	3843	2	574.29	-14.89
Q8ZQT5 TOLB_SALTY Protein tolB	16		TGSLNLYVMDLASGQIRQITDGR	264	23	4	11.17	b4°b4b6y3	2508.31	74.806	3762	2	1254.66	8.37
Q8ZQT5 TOLB_SALTY Protein tolB	17	Phosphoryl STY(13)	TGSLNLYVMDLASGQIR	264	17	3	20.08	b11b12y7	1917.90	89.261	5923	3	639.97	-3.69
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		GYLSPYFINKPETGAVELESPFILLADKK	197	29	10	29.28	b2b3b4°b4b16y2y4y26y27y29	3239.71	96.754	199253	4	810.68	-4.60
P0A1D3 CH60_SALTY 60 kDa chaperonin	2		ANDAAGDGTTTATVLAQSIITEGLK	80	25	27	162.32	b2*b2b3*b3b4*b4b5b6°b6b13b14b15b18°b18y1y3y4°y4y5y6y7y8y9y10y11y13y25	2418.23	92.692	148971	3	806.75	-2.32
P0A1D3 CH60_SALTY 60 kDa chaperonin	3		QQIEEATSDYDREK	350	14	6	32.87	y3y5y7y8y14*y14	1711.75	34.130	84587	3	571.26	-14.33
P0A1D3 CH60_SALTY 60 kDa chaperonin	4		AVAAAVEELK	122	10	10	63.66	b2b3y3°y3y5°y5y6y7y8y10	1000.56	47.935	72155	2	500.78	-9.03
P0A1D3 CH60_SALTY 60 kDa chaperonin	5	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	10	63.7	b18y5y6y9y12*y12y13y14y15y18	1957.02	62.228	71518	2	979.01	6.74
P0A1D3 CH60_SALTY 60 kDa chaperonin	6		EMLPVLEAVAK	231	11	8	44.46	b2°b2b3y4y6y7y8y11	1199.66	80.660	71032	2	600.34	-6.11
P0A1D3 CH60_SALTY 60 kDa chaperonin	7	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	11	63.66	b2b3°b3y2y4y5y6°y6y7y9y10	1063.50	35.773	70125	2	532.25	-7.35
P0A1D3 CH60_SALTY 60 kDa chaperonin	8		VVINKDTTTIIDGVGEEAAIQGR	322	23	7	43.66	b2b3y4y7y8y9y10	2399.28	68.424	59484	3	800.43	-1.02
P0A1D3 CH60_SALTY 60 kDa chaperonin	9		SFGAPTITK	42	9	10	37.97	b2b3°b3b7°b7y1y2y5°y5y7	921.49	45.514	58700	2	461.25	-14.11
P0A1D3 CH60_SALTY 60 kDa chaperonin	10		AIAQVGTISANSDETVGK	142	18	20	90.43	b1b2b3b4°b4b7b11b15y1y2y8y9y10y12*y12y13°y13y14*y14y18	1760.91	48.868	50406	2	880.96	4.16
P0A1D3 CH60_SALTY 60 kDa chaperonin	11		VEDALHATR	395	9	6	38.49	b2b8y4y6y7y9	1011.51	27.072	46284	2	506.26	-9.65
P0A1D3 CH60_SALTY 60 kDa chaperonin	12		GGDGYNGYNAATEEYGNMIDMGILDPTK	470	28	6	21.96	b2y1y3y4y10y28	2966.30	88.959	30375	3	989.44	5.10
P0A1D3 CH60_SALTY 60 kDa chaperonin	13		AVAAGMNPMDLKR	105	13	12	80.77	b1y2y3y6°y6y7°y7y8y9y10y11y13	1373.70	51.578	25939	2	687.35	-1.78
P0A1D3 CH60_SALTY 60 kDa chaperonin	14		LIAEAMDK	160	8	6	49.9	y2y3y4y6y7y8	890.45	39.794	24759	2	445.73	-13.23
P0A1D3 CH60_SALTY 60 kDa chaperonin	15		AGKPLLIHAEDVEGEALATLVVNTMR	242	26	10	41.75	b3b6b7y1y4y5y6°y6y8*y8	2723.49	136.286	13412	3	908.50	-4.30
P0A1D3 CH60_SALTY 60 kDa chaperonin	16		APGFGDR	277	7	7	35.01	b2b5y2y4°y4y6y7	719.34	28.316	9378	2	360.17	-7.98
P0A1D3 CH60_SALTY 60 kDa chaperonin	17		DTTTIIDGVGEEAAIQGR	327	18	3	12.58	b5b11y12	1845.93	55.879	7170	3	615.98	3.84
P0A1D3 CH60_SALTY 60 kDa chaperonin	18	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDLPK	501	25	11	26.09	b1b5°b5b8°b8b22y1y7°y7y8y11	2670.32	136.414	5079	3	890.78	-1.01
P0A1D3 CH60_SALTY 60 kDa chaperonin	19		ATLEDLGQAK	311	10	9	29.11	b10*b10y5°y5y6y9°y9*y9y10	1045.55	45.997	4549	2	523.28	-0.23
P0A1D3 CH60_SALTY 60 kDa chaperonin	20		GVNVLADAVK	18	10	6	49.4	b8°b8y4y5y6y8	985.55	56.683	110167	2	493.28	-15.73

IP0A1D3 CH60_SALTY 60 kDa chaperonin	21		LAGGVAVIK	371	9	4	38.49	b5b6b7y7	827.52	45.666	70102	2	414.26	-19.62
IP0A1D3 CH60_SALTY 60 kDa chaperonin	22		NVVLDK	36	6	2	26.14	b3b5	687.40	44.572	24915	1	687.40	-6.04
IP0A1D3 CH60_SALTY 60 kDa chaperonin	23		EIELEDK	58	7	7	54.5	b3°b3y3y4°y4y5y6	875.43	42.481	5900	2	438.22	-5.93
IP0A1D3 CH60_SALTY 60 kDa chaperonin	24		AVAAGMNPMDLK	105	12	5	41.41	b11y4y5y8y10	1217.62	64.175	5298	2	609.32	18.45
IP0A1D3 CH60_SALTY 60 kDa chaperonin	25		FGNDAR	7	6	4	34.38	b3y3y4°y4	679.31	41.594	5097	1	679.31	-3.23
IP0A1D3 CH60_SALTY 60 kDa chaperonin	26		VVINK	322	5	1	11.25	y3	572.37	31.380	4817	1	572.37	-5.33
IP0A1D3 CH60_SALTY 60 kDa chaperonin	27		SDAPDLGAAGGMGGMGGMGGM M	526	22	5	25.3	b3b8b9°b9b19	1927.77	81.219	3533	2	964.39	12.22
IP0A1D3 CH60_SALTY 60 kDa chaperonin	28		FENMGAQMVK	65	10	4	32.12	y7y8*y8y9	1154.56	118.842	3162	1	1154.56	20.83
IP0A1D3 CH60_SALTY 60 kDa chaperonin	29		QQIEEATSDYDR	350	12	10	53.33	b4°b4*b4b7°b7b8b11y10y11°y11	1454.67	136.445	2662	1	1454.67	19.39
IP0A1D3 CH60_SALTY 60 kDa chaperonin	30		GYLSPYFINKPETGAVELESPFILL ADK	197	28	4	10.94	b5b8°b8y22	3111.65	99.085	2618	4	778.67	7.69
IP0A1D3 CH60_SALTY 60 kDa chaperonin	31		VGAATEVEMK	380	10	8	62.86	b6°b6b8y3y5y6y9°y9	1034.52	35.877	2117	1	1034.52	-2.48
IP0A1D3 CH60_SALTY 60 kDa chaperonin	32		VTLGPK	28	6	3	23.13	b4°b4y4	614.38	28.922	1782	1	614.38	-9.34
IP0A1D3 CH60_SALTY 60 kDa chaperonin	33		IADLKGQNEQNVGIK	425	16	12	70.05	b3b4b9*b9y3y4y8y9y11°y11*y11y14	1741.89	40.699	137603	3	581.30	-11.00
IP0A1D3 CH60_SALTY 60 kDa chaperonin	34		EIELEDKFENMGAQMVK	58	17	11	33.62	b5b8°b8y6y7°y7y10°y10*y10y13°y13	2010.94	74.199	80661	3	670.99	-4.25
IP0A1D3 CH60_SALTY 60 kDa chaperonin	35		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	7	16.04	b7b13b15y7*y7y9y21	3675.86	123.197	42137	3	1225.96	-2.26
IP0A1D3 CH60_SALTY 60 kDa chaperonin	36		VGKEGVITVEDGTGLQDELDDVVE GMQFDR	168	29	7	18.83	b6b11b15y6y11°y11y17	3135.50	74.153	13186	4	784.63	-3.82
IP0A1D3 CH60_SALTY 60 kDa chaperonin	37		AIAQVGTISANSDETGVGLIAEAM DK	142	26	4	19.63	b3y4y5y20	2632.35	92.487	12949	3	878.12	0.93
IP0A1D3 CH60_SALTY 60 kDa chaperonin	38		AVAAGMNPMDLKR	105	13	5	45.05	b3b4b5y6y7	1373.72	48.887	7619	2	687.36	10.31
IP0A1D3 CH60_SALTY 60 kDa chaperonin	39		EVASKANDAAGDGTTTATVLAQS IITEGLK	75	30	7	34.31	b3b7b9b10°b10b14b17	2932.47	88.265	5469	3	978.16	-14.07
IP0A1D3 CH60_SALTY 60 kDa chaperonin	40		DGVSVAREIELEDK	51	14	8	41.48	b4°b4b5b9y3°y3y7y9	1559.78	49.617	4295	2	780.39	-7.98
IP0A1D3 CH60_SALTY 60 kDa chaperonin	41		DVKFGNDAR	4	9	8	52.75	b4b5°b5b6b8y7°y7*y7	1021.51	38.078	3837	2	511.26	0.42
IP0A1D3 CH60_SALTY 60 kDa chaperonin	42		VGAATEVEMKEK	380	12	4	17.94	b8b11°b11y8	1291.64	59.821	2104	3	431.22	-13.70
IP0A1D3 CH60_SALTY 60 kDa chaperonin	43	Phosphoryl STY(6)	SFGAPTITKDGVSVAR	42	16	3	13.71	b4b9y12_HPO3 y12	1685.80	59.825	3467	3	562.60	-10.28
IP0A1D3 CH60_SALTY 60 kDa chaperonin	44	Phosphoryl STY(8)	SFGAPTITKDGVSVAIELEDK	42	23	3	11.17	b7b13y14	2542.21	87.517	2531	3	848.07	-10.37
IP0A1D3 CH60_SALTY 60 kDa chaperonin	45	Oxidation+M(2)	EMLPVLEAVAK	231	11	5	19.74	b5b10°b10y5°y5	1215.66	68.981	5383	2	608.33	-7.13
IP0A1D3 CH60_SALTY 60 kDa chaperonin	46	Oxidation+M(9)	VGAATEVEMKEK	380	12	3	21.92	b3b4y11	1307.64	74.688	4403	3	436.55	-8.31
IP0A1D3 CH60_SALTY 60 kDa chaperonin	47	Oxidation+M(9)	AVAAGMNPMDLKR	105	13	3	16.52	b8b11y5	1389.70	50.324	1707	2	695.35	1.93
IP0A1D3 CH60_SALTY 60 kDa chaperonin	48	Carbamidomethyl+C(18) ;Oxidation+M(19)	SALQYAASVAGLMITTECMVTDL PK	501	25	4	10.97	b9°b9b15y8	2686.35	94.332	1551	2	1343.68	13.09
IP0A1D3 CH60_SALTY 60 kDa chaperonin	49		AAGMNPMDLKR	107	11	1	7.24	b3	1203.59	51.537	47127	2	602.30	-2.74

P0A1D3 CH60_SALTY 60 kDa chaperonin	50		EDALHATR	396	8	0	2.51		912.44	27.020	32174	2	456.73	-11.77
P0A1D3 CH60_SALTY 60 kDa chaperonin	51		GMNPMDLKR	109	9	1	7.24	b3	1061.53	51.588	6812	2	531.27	10.92
P0A1D3 CH60_SALTY 60 kDa chaperonin	52		AIAQVGTISANS	142	12	0	8.16		1131.60	48.891	4736	3	377.87	1.62
P0A1D3 CH60_SALTY 60 kDa chaperonin	53		TIIDGVGEEAAIQGR	330	15	0	11.3		1528.79	68.354	3523	2	764.90	-4.39
P0A1D3 CH60_SALTY 60 kDa chaperonin	54		AIAQVGTISANSDETV	142	16	2	12.47	y10y14	1575.78	48.840	2743	2	788.40	-1.94
P0A1D3 CH60_SALTY 60 kDa chaperonin	55	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	0	8.16		1938.97	62.232	15039	3	647.00	-9.57
P66313 RL6_SALTY 50S ribosomal protein L6	1		TLNDAVEVK	35	9	12	55.76	b2°b2b3y1y2y3°y3y4y7y8y9*y9	988.52	39.022	114554	2	494.76	-8.64
P66313 RL6_SALTY 50S ribosomal protein L6	2		ALLNSMVIGVTEGFTK	69	16	3	22.09	y8y9y12	1679.91	95.318	71567	2	840.46	0.87
P66313 RL6_SALTY 50S ribosomal protein L6	3		DGYADGWAQAGTAR	55	14	10	50.61	b3y4y6°y6y7°y7*y7y9y11y14	1438.64	50.364	69858	2	719.82	2.72
P66313 RL6_SALTY 50S ribosomal protein L6	4		INGQVITIK	18	9	5	50.53	y3y4y7y8y9	985.60	48.939	51665	2	493.30	-8.79
P66313 RL6_SALTY 50S ribosomal protein L6	5		APVVVPAGVDVK	6	12	12	98.67	b2b3b4b5y2y3y5y7y8y9y10y12	1150.68	53.689	46484	2	575.84	-6.26
P66313 RL6_SALTY 50S ribosomal protein L6	6		ALLNSMVIGVTEGFTKK	69	17	5	20.5	b2b3b6b15y1	1807.97	89.536	43112	3	603.33	-14.79
P66313 RL6_SALTY 50S ribosomal protein L6	7		HADNALTFGPR	44	11	12	49.69	b1b2b3b5b6b11*b11y4y5y9°y9*y9	1198.59	47.779	39039	2	599.80	-6.62
P66313 RL6_SALTY 50S ribosomal protein L6	8		LQLVGVGYYR	86	9	6	33.25	b2y2y5y6y7y9	1004.58	60.549	26783	2	502.79	-7.90
P66313 RL6_SALTY 50S ribosomal protein L6	9		YADEVVR	163	7	7	60.52	b3b6°b6y4y5y6°y6	851.42	30.675	6857	2	426.21	-10.18
P66313 RL6_SALTY 50S ribosomal protein L6	10		NGELTR	29	6	3	23.13	y4y5°y5	689.36	37.160	6211	1	689.36	4.07
P66313 RL6_SALTY 50S ribosomal protein L6	11		GADKQVIGQVAADLR	134	15	10	46	b3b4b5°b5*b5b9°b9*b9b12y8	1540.83	60.607	39332	3	514.28	-12.28
P66313 RL6_SALTY 50S ribosomal protein L6	12	Oxidation+M(6)	ALLNSMVIGVTEGFTK	69	16	3	13.71	b8b10y7	1695.89	52.815	10242	2	848.45	-2.16
P66313 RL6_SALTY 50S ribosomal protein L6	13		SMVIGVTEGFTKK	73	13	2	7.99	b5°b5	1396.77	89.533	5977	2	698.89	11.36
P66313 RL6_SALTY 50S ribosomal protein L6	14		INGQVITIK	18	9	1	7.74	b3	968.57	48.889	15638	2	484.79	1.39
P66313 RL6_SALTY 50S ribosomal protein L6	15		HADNALTFGPR	44	11	0	3.77		1180.58	47.719	8396	3	394.20	0.21
P22107 TRAT_SALTY TraT complement resistance protein	1		ATVTTDNVAALR	177	12	15	72.82	b3°b3b6b8°b8b9°b9*b9y4y8y9°y9y10*y10y12	1231.65	45.994	41193	2	616.33	-8.13
P22107 TRAT_SALTY TraT complement resistance protein	2		IQTSTETGNQHK	196	12	10	68.89	b2y2y3y5y6°y6y8°y8y9y10	1343.64	14.869	16179	3	448.55	-14.90
P22107 TRAT_SALTY TraT complement resistance protein	3		QGTSGAK	189	7	3	32	b4b5y3	648.33	59.833	12413	1	648.33	-9.41
P22107 TRAT_SALTY TraT complement resistance protein	4		GYTVVTSPPDK	79	10	4	45.13	y4y5y6y7	1066.54	36.666	9395	2	533.77	-0.92
P22107 TRAT_SALTY TraT complement resistance protein	5	Carbamidomethyl+C(16)	LMMVTLVSSTLALSGCGAMSTAIK	5	24	8	43.08	b4b5°b5b6b8°b8y10y11	2442.28	136.431	6502	3	814.76	11.60
P22107 TRAT_SALTY TraT complement resistance protein	6		AYYWIQANVLK	89	11	3	22.75	b4b5y8	1368.71	63.997	1703	3	456.91	-14.09
P22107 TRAT_SALTY TraT complement resistance protein	7		ATVTTDNVAALRQGTSGAK	177	19	7	36.96	b3b9b10*b10b11y3y7	1861.00	54.290	88033	3	621.00	10.69
P22107 TRAT_SALTY TraT complement resistance protein	8		YQTRVVSNAK	208	11	6	34.97	b4y4y6°y6y10*y10	1279.67	61.914	10665	3	427.23	-2.19

P22107 TRAT_SALTY TraT complement resistance protein	9		IQTSTETGNQHKYQTR	196	16	7	30.5	b3*b3b6*b6b7b11y8	1891.91	22.269	3029	4	473.73	-7.61
P22107 TRAT_SALTY TraT complement resistance protein	10	Phosphoryl STY(7)	DMSDLQSLIAK	63	11	7	60.02	y4y5°y5y6*y6y8y10	1300.59	38.144	2483	3	434.20	10.89
P22107 TRAT_SALTY TraT complement resistance protein	11	Oxidation+M(7)	NTSDKDMSDLQSLIAK	58	16	3	21.42	b5b13b15	1781.87	77.193	41362	2	891.44	8.29
P22107 TRAT_SALTY TraT complement resistance protein	12		TDNVAALR	181	8	3	7.2	b7°b7*b7	859.46	46.024	4848	2	430.23	-6.04
P22107 TRAT_SALTY TraT complement resistance protein	13		TSTETGNQHK	198	10	1	7.2	b5	1102.52	14.859	1505	2	551.76	2.99
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTDSDAVGNAVK	84	17	17	92.26	b2b3b4b5y2y3y9y11*y11y12°y12y13*y13y14*y14y15y17	1739.96	71.448	57657	2	870.48	0.84
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	2		LAATIAQLPDQIGAK	253	15	10	62.94	b3b5y3y4y6°y6y7y8y10y15	1509.86	66.945	30072	2	755.43	-4.77
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	3		FNVLASQPADFDR	178	13	7	27.99	b7*b7y3°y3y6y8°y12	1479.73	67.136	13144	2	740.37	6.68
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	4		IPVITLDR	107	8	3	30.87	b3y4y7	926.56	62.537	26458	2	463.78	-5.80
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	5		GVEVADK	268	7	6	57.51	b3b4°b4b6y3y4	717.38	47.842	6305	1	717.38	-0.51
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	6		YPVDLK	285	6	4	34.38	b3b4b5°b5	734.42	62.636	5846	1	734.42	10.31
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	7		GLNVMQNLLTAHPDVQAVFAQNDEMALGALR	193	31	4	21.95	b5b6*b6y9	3336.62	111.333	2858	3	1112.88	-19.46
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	8		EADK	50	4	1	10.62	y3	462.22	35.340	2783	1	462.22	-0.13
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	9		MNMK	0	4	1	10.62	b3	523.23	82.245	2006	1	523.23	-11.32
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	10		ERGEGFQQAVALAHK	164	14	4	23.17	b5b7b8*b8	1527.76	74.166	16723	3	509.92	-4.63
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	11		FNVLASQPADFDRTK	178	15	5	26.18	b10b11°b11y8y11	1708.89	87.543	12702	2	854.95	13.57
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	12		QATKGDVVSHIASDNVLGGK	115	20	3	32.03	b15b16b17	1996.03	69.053	3419	3	666.02	-7.28
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	13		ELANVQDLTVRGTK	70	14	3	23.96	b4b6b12	1543.83	89.565	1670	3	515.28	-9.73
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	14		EADKLGYNLVVLDSQNNPAK	50	20	5	11.82	b6y4*y4y7*y7	2188.16	27.751	1601	6	365.53	13.95
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	12	71.69	b2b4y1y2y3y4y6°y6y8y9y10y12	1377.65	79.028	171181	2	689.33	2.22
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AVVESIQR	69	8	8	69.39	b3b6y4y5°y5y6y7y8	901.50	33.346	100296	2	451.25	-11.44
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3		AAVTMPSSK	22	9	15	58.77	b1b2b9y1y2°y2y3y4°y4y5y6°y6y7°y7y9	891.45	31.917	88496	2	446.23	-7.81
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4		GVMTDR	108	6	2	23.13	b4y5	678.32	32.041	3909	1	678.32	-9.18
P0A7X0 RS8_SALTY 30S ribosomal protein S8	5		NGQAANKAAVTMPSSK	15	16	3	13.71	b9b12y6	1574.78	49.595	4082	3	525.60	-11.01
P0A7X0 RS8_SALTY 30S ribosomal protein S8	6		VTMPSSK	24	7	0	2.51		749.38	31.883	18955	1	749.38	-3.10
P0A7X0 RS8_SALTY 30S ribosomal protein S8	7		AVTMPSSK	23	8	0	2.51		820.43	31.923	6442	2	410.72	6.77
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VVGQLGQVLGPR	122	12	11	71.69	b2b4y1y3y4y6y7y8y10*y10y12	1222.72	59.648	149719	2	611.86	-9.48
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VGTVTPNVAEAVK	141	13	4	31	y8y9y10y13	1284.72	48.522	141037	2	642.86	0.19
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VAVFTQGPNAEAAK	74	14	9	70.4	b4b13y4y7y8y9*y9y10y11	1402.73	45.838	90978	2	701.87	-4.44

P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		AAGAELVGMEDLADQIK	88	17	7	33.83	b3b4b7y10*y10y11y17	1730.87	80.469	32941	2	865.94	4.87
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		GATVLPHGTR	60	11	6	30.2	b8y4y6*y6y7y11	1065.57	30.271	27373	2	533.29	-5.04
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		QYDINEAIALLK	19	12	3	17.94	b4y4y6	1390.76	86.041	46782	2	695.88	-0.53
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		GEMNFDVVIASPDAMR	106	16	4	13.71	b12b14*b14y12	1751.79	72.362	10973	3	584.60	-11.71
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		SDQNVR	54	6	1	11.88	b4	718.35	61.886	2973	1	718.35	4.67
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9		VSISTTMGAGVAVDQAGLSASAN	211	23	5	13.64	b6b13y5*y5y9	2107.07	61.895	2359	2	1054.04	16.92
P0A2A3 RL1_SALTY 50S ribosomal protein L1	10		KGEMNFDVVIASPDAMR	105	17	3	20.08	b10b11y5	1879.92	70.833	10478	2	940.46	9.81
P0A2A3 RL1_SALTY 50S ribosomal protein L1	11		KVSISTTMGAGVAVDQAGLSASAN	210	24	3	20.34	b16y13y14	2235.13	87.181	2982	3	745.71	-1.31
P0A2A3 RL1_SALTY 50S ribosomal protein L1	12		VAVFTQGPNAEAAKAAGAELVGMEDLADQIK	74	31	3	11.16	b12b14y4	3114.57	111.794	2411	3	1038.86	-2.74
P0A2A3 RL1_SALTY 50S ribosomal protein L1	13	Oxidation+M(9)	AAGAELVGMEDLADQIK	88	17	6	25.6	b3b6*b6b10y8y14	1746.85	64.122	4646	3	582.96	-4.26
P0A2A3 RL1_SALTY 50S ribosomal protein L1	14		TVLPHGTR	62	9	0	3.77		937.51	30.258	20076	2	469.26	-12.89
P02910 HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTQTETFGNEHWAPK	135	20	18	110.42	b2b3b4y2y3y4y7*y7y8y10y11*y11y12y13y15y17y20	2199.07	64.152	127685	3	733.70	-5.66
P02910 HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	15	127.03	b4b8b11*b11y4y5y6y7y8y9y10y11*y11y12y13	1425.68	55.822	111090	2	713.35	-4.02
P02910 HISJ_SALTY Histidine-binding periplasmic protein	3		NSDIQPTVASLK	120	12	13	83.61	b2*b2b3*b3b4y3y4y7y8*y8y9y10y12	1272.68	48.629	84029	2	636.84	-1.92
P02910 HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	7	34.94	b8b16y4*y4y5y6y20	2273.20	104.442	62315	2	1137.10	5.48
P02910 HISJ_SALTY Histidine-binding periplasmic protein	5		QPVGKDYK	193	8	12	49.9	b2*b2b3b5b7*b7*b7b8*b8y5y8*y8	934.50	54.324	21235	2	467.75	1.96
P02910 HISJ_SALTY Histidine-binding periplasmic protein	6		LFGVGTGMGLR	211	11	4	19.74	b3b9*b9y6	1107.58	74.135	4990	2	554.30	-13.78
P02910 HISJ_SALTY Histidine-binding periplasmic protein	7		GIEIVSYQGQDNIYSDLTAGR	155	21	15	56.41	b3*b3b10b11*b11b12y4*y4y6*y6y7*y7y9y12*y12	2299.15	62.665	4854	4	575.54	14.23
P02910 HISJ_SALTY Histidine-binding periplasmic protein	8		IDAAFQDEVAASEGFLK	176	17	5	28.53	b4b5b8b14*b14	1810.85	55.091	4628	3	604.29	-21.91
P02910 HISJ_SALTY Histidine-binding periplasmic protein	9		NAQGELVGFDIDLAK	42	15	4	14.47	b10b14*b14y7	1589.81	75.378	2241	2	795.41	-1.77
P02910 HISJ_SALTY Histidine-binding periplasmic protein	10		QQEIAFTDK	99	9	8	64	b4*b4b6*b6b7y5y7y8	1079.54	78.114	2240	2	540.27	3.28
P02910 HISJ_SALTY Histidine-binding periplasmic protein	11		IGTDPTYAPFESKNAQGELVGFDIDLAK	29	28	4	19.6	b6y3y4y14	2996.51	96.663	27159	3	999.51	7.17
P02910 HISJ_SALTY Histidine-binding periplasmic protein	12	Carbamidomethyl+C(18)	NAQGELVGFDIDLAKELCK	42	19	3	12.16	b3b12y11	2120.05	87.222	10573	3	707.36	-8.41
P02910 HISJ_SALTY Histidine-binding periplasmic protein	13		ADGTYEKLAK	240	10	4	36.38	b3b4b5y9	1095.57	32.820	8201	2	548.29	5.24
P02910 HISJ_SALTY Histidine-binding periplasmic protein	14		IDAAFQDEVAASEGFLKQPVGK	176	22	3	17.85	b3b10b12	2320.16	64.038	4775	3	774.06	-11.26
P02910 HISJ_SALTY Histidine-binding periplasmic protein	15		EALNKAFEMR	229	11	8	47.47	b9*b9y3y4y7*y7y8*y8	1279.64	59.743	3668	2	640.32	-7.15
P02910 HISJ_SALTY Histidine-binding periplasmic protein	16		IRIGTDPTYAPFESK	27	15	4	22.55	b9*b9b13b14	1694.86	68.971	2883	3	565.63	-7.78
P02910 HISJ_SALTY Histidine-binding periplasmic protein	17	Phosphoryl STY(9)	IDAIMSSLSITEK	85	13	5	23.58	b5b8*b8y3y6	1487.71	38.076	1684	3	496.58	10.58

P0A1H3 EFG_SALTY Elongation factor G	1		VYSGVVNSGDTVLSNVK	337	17	13	67.97	b2b5b11b12b13y2y5y10y11*y11y12y14y17	1737.91	62.771	103981	2	869.46	4.14
P0A1H3 EFG_SALTY Elongation factor G	2		IATDPFVGNLTFFR	323	14	9	48.84	b2b4y2y3y4y7y8y10y14	1597.84	94.010	67111	2	799.43	3.90
P0A1H3 EFG_SALTY Elongation factor G	3		IGEVHDGAATMDWMEQEQR	39	20	10	45.04	b3b11b12y2°y2y3y5y6y7y20	2331.99	63.181	49614	3	778.00	-1.47
P0A1H3 EFG_SALTY Elongation factor G	4		EFNVEANVGKPVAYR	475	16	8	27.39	b3°b3b8y4y6*y6y12y16	1820.91	54.265	43848	3	607.64	-10.19
P0A1H3 EFG_SALTY Elongation factor G	5		SGPLAGYPVVDLGVR	562	15	9	29.49	b2b5b7°b7y2y4y8y10y15	1499.82	77.270	32813	2	750.41	-2.77
P0A1H3 EFG_SALTY Elongation factor G	6		LHFGSYHDVDSSELAFK	577	17	5	13.09	b6y1y12y16y17	1951.91	92.713	30620	3	651.31	-2.88
P0A1H3 EFG_SALTY Elongation factor G	7	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTTGDTLCDPENPIILER	378	30	7	23.68	b3b7b18y4y10y11y30	3138.61	85.841	22379	3	1046.88	4.12
P0A1H3 EFG_SALTY Elongation factor G	8		GQSEVTGVK	643	10	5	29.11	y4y7y8°y8y10	1033.50	25.976	19207	2	517.26	-12.52
P0A1H3 EFG_SALTY Elongation factor G	9		GQYGHVVIDMYPLEPGSNPK	512	20	6	21.52	b4b9b12y2y10y19	2201.07	74.265	15769	3	734.36	-1.11
P0A1H3 EFG_SALTY Elongation factor G	10		YLGGEELTEEEIK	236	13	7	33.29	b5b7b8y5°y5y9y13	1509.74	58.563	11605	2	755.38	7.60
P0A1H3 EFG_SALTY Elongation factor G	11		AINWNDADQGVTFEYEDIPADMDLANEWHQNLIESAEESEELMEK	189	47	14	72	b3b4b11y3y4y6y7y8y9°y9y10°y10y13y29	5380.39	126.572	10778	4	1345.85	0.64
P0A1H3 EFG_SALTY Elongation factor G	12		YDDAPNNVAQAVIEAR	686	16	4	20.25	b12b13y8y16	1745.83	74.026	6473	2	873.42	-10.70
P0A1H3 EFG_SALTY Elongation factor G	13		GVQAMLDIVIDYLPSPVDVPAINGILDDGK	273	30	8	20.5	b8b12°b12b13°b13y2y14y21	3095.59	103.999	4357	4	774.65	-1.10
P0A1H3 EFG_SALTY Elongation factor G	14		VEVETPEENTGDVIGDLSR	618	19	7	35.33	b10b12y12*y12y13*y13y14	2058.97	59.778	2801	4	515.50	-5.45
P0A1H3 EFG_SALTY Elongation factor G	15		LGANPVPLQLAIGAEEGFTGVVDLVK	161	26	8	26.57	b5*b5b6*b6y5y8y14°y14	2607.40	120.455	20833	3	869.80	-15.45
P0A1H3 EFG_SALTY Elongation factor G	16		VVGQIK	153	6	1	11.88	b4	643.41	45.686	14687	1	643.41	-7.21
P0A1H3 EFG_SALTY Elongation factor G	17		HASDDEPFSALAFK	309	14	3	15.39	b6y7y9	1534.72	72.050	8703	2	767.86	-0.64
P0A1H3 EFG_SALTY Elongation factor G	18		ADQEK	425	5	1	11.25	y3	590.27	38.109	7485	1	590.27	-14.79
P0A1H3 EFG_SALTY Elongation factor G	19		GGVIPGEYIPAVDK	541	14	3	23.17	b6b11b12	1414.79	72.687	7065	2	707.90	20.02
P0A1H3 EFG_SALTY Elongation factor G	20		IHAEVPLSEMGYATQLR	653	18	7	16.78	b3b13°b13y10*y10y12°y12	2062.00	74.137	5359	2	1031.50	-20.48
P0A1H3 EFG_SALTY Elongation factor G	21		TTTTTER	23	6	1	11.88	y5	708.36	34.596	4634	2	354.68	10.43
P0A1H3 EFG_SALTY Elongation factor G	22		ASYTMEFLK	677	9	4	25.47	b4°b4b5y6	1089.54	59.738	4111	2	545.27	6.72
P0A1H3 EFG_SALTY Elongation factor G	23	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETVWR	104	24	6	19.8	b4b5°b5b9y6°y6	2621.23	38.026	3586	3	874.42	-20.21
P0A1H3 EFG_SALTY Elongation factor G	24		INIIDTPGHVDFTIEVER	83	18	5	16.78	b4b9*b9y7y11	2068.04	90.567	3487	2	1034.52	-15.46
P0A1H3 EFG_SALTY Elongation factor G	25		VWTDEESNQTHIAGMGELHLDIIVDR	446	26	3	10.93	b10b12y12	2954.40	129.062	2684	3	985.47	-20.74
P0A1H3 EFG_SALTY Elongation factor G	26		EDPSFR	440	6	2	11.88	y5°y5	750.34	49.662	2082	1	750.34	1.46
P0A1H3 EFG_SALTY Elongation factor G	27	Carbamidomethyl+C(11)	VLNNEIILVTCGSAFK	255	16	4	22.09	y4y7y8°y8	1777.96	86.408	2027	3	593.32	4.81
P0A1H3 EFG_SALTY Elongation factor G	28		NIGISAHIDAGK	11	12	4	28.15	y4y6°y6y9	1195.62	95.384	1977	1	1195.62	-17.56

P0A1H3 EFG_SALTY Elongation factor G	29		GITITSAATTAFWSGMAKQYEPHR	59	24	4	21.34	y4y6y7°y7	2624.26	76.867	44481	4	656.82	-11.54
P0A1H3 EFG_SALTY Elongation factor G	30		QYEPHRINIIDTPGHVDFTIEVER	77	24	3	17.36	y4y6y11	2878.45	100.751	24587	3	960.16	1.10
P0A1H3 EFG_SALTY Elongation factor G	31		YLGGEELTEEEIKQALR	236	17	4	21.75	b4b7b8°b8	1977.99	74.970	20085	3	660.00	-11.05
P0A1H3 EFG_SALTY Elongation factor G	32	Carbamidomethyl+C(13)	QRVLNNEILVTCGSAFK	253	18	4	12.58	b3*b3y8y14	2062.09	96.463	18293	3	688.03	-10.89
P0A1H3 EFG_SALTY Elongation factor G	33		SGPLAGYPVVDLGVRLHFGSYHD VDSSELAfk	562	32	7	34.11	b6b7°b7b8y11°y11y13	3432.77	94.435	15939	4	858.95	12.80
P0A1H3 EFG_SALTY Elongation factor G	34		IAFVNKMDR	137	9	6	50.99	b4b7b8°b8y6y8	1093.59	46.783	7831	2	547.30	2.68
P0A1H3 EFG_SALTY Elongation factor G	35	Carbamidomethyl+C(13)	SMRVLDGAVMVYCAVGGVQPQS ETVWR	101	27	4	32.37	b11b12y11y12	2995.47	70.012	6446	3	999.16	2.36
P0A1H3 EFG_SALTY Elongation factor G	36		QSGGRGQYGHVVIMYPLEPGSN PK	507	25	4	15.44	b7b11b14y7	2686.32	109.400	5222	3	896.11	5.91
P0A1H3 EFG_SALTY Elongation factor G	37		GYEFINDIKGGVIPGEYIPAVDK	532	23	4	17.57	b5b8b12°b12	2494.26	84.169	5000	3	832.09	-9.69
P0A1H3 EFG_SALTY Elongation factor G	38	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETV WRQANK	104	28	7	42.99	b4b5b6b7b10y11*y11	3062.49	123.709	3251	3	1021.50	-9.65
P0A1H3 EFG_SALTY Elongation factor G	39		NIGISAHDAGKTTTTER	11	18	4	12.58	b12y10°y10y13	1884.98	92.197	2163	2	942.99	1.55
P0A1H3 EFG_SALTY Elongation factor G	40		INIIDTPGHVDFTIEVERSMR	83	21	4	20.41	b11b12b20y11	2442.27	97.417	2055	4	611.32	9.00
P0A1H3 EFG_SALTY Elongation factor G	41		VYSGVVNSGDTVLSNVKTAR	337	20	3	18.61	b10b13b16	2066.07	104.963	1739	3	689.36	-8.98
P0A1H3 EFG_SALTY Elongation factor G	42		GQESEVTGVKIHAEVPLSEMFY ATQLR	643	28	5	21.74	b10y7y9y12y13	3076.58	120.759	1558	3	1026.20	13.57
P0A1H3 EFG_SALTY Elongation factor G	43	Phosphoryl STY(9)	MEFPEPVISIAVEPK	408	15	5	20.16	b8b12y3°y3y7_HPO3 y7	1765.81	42.459	7232	3	589.28	-14.03
P0A1H3 EFG_SALTY Elongation factor G	44	Phosphoryl STY(8)	VYSGVVNSGDTVLSNVK	337	17	8	33.62	b4°b4b6°b6b12_HPO3 b12b13y8y12	1817.88	48.795	5012	3	606.63	9.07
P0A1H3 EFG_SALTY Elongation factor G	45	Oxidation+M(10)	IHAEVPLSEMFYATQLR	653	18	4	19.85	b4b9b15y9	2078.06	96.453	23209	3	693.36	13.04
P0A1H3 EFG_SALTY Elongation factor G	46	Carbamidomethyl+C(10) ;Oxidation+M(7)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	6	22.8	b4b6b9b14y13*y13	2637.27	95.498	21726	3	879.76	-4.91
P0A1H3 EFG_SALTY Elongation factor G	47	Oxidation+M(10)	GQYGHVVIMYPLEPGSNPK	512	20	4	11.82	b7b12°b12y13	2217.07	74.224	1929	2	1109.04	1.10
P0A1H3 EFG_SALTY Elongation factor G	48		EENTGDVIGDLR	624	13	1	8.58	b8	1404.67	59.787	21302	2	702.84	6.60
P0A1H3 EFG_SALTY Elongation factor G	49		EFNVEANVGKPVAYR	475	16	5	13.71	b6b11*b11y10*y10	1802.93	54.321	2139	3	601.65	8.12
P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	11	66.67	b2*b2b3y1y2y3y5y6y8y9y 10	1129.61	39.533	173518	2	565.31	-6.59
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	11	70.4	b3b13y2y4y6y7y8°y8y9y10 y14	1452.65	58.051	98911	2	726.83	2.10
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3		SFTFVTK	65	7	10	43.25	b1b2b6°b6y1y2y3y4y5y7	829.44	54.377	64415	2	415.22	-8.02
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4		SGSGKPNKDK	87	10	9	34.34	b1b6b7b10°b10y2°y2y3y9	1017.53	32.045	17311	2	509.27	-1.80
P0A7K0 RL11_SALTY 50S ribosomal protein L11	5		SIEGTAR	127	7	10	32	b1b2°b2b4°b4b7y5°y5y6y7	733.38	32.001	9943	1	733.38	-10.82
P0A7K0 RL11_SALTY 50S ribosomal protein L11	6		TPPAAVLLK	72	9	3	25.47	b5y5y7	909.56	54.894	91148	2	455.28	-16.78
P0A7K0 RL11_SALTY 50S ribosomal protein L11	7		AQLQEIAQTKAADMTGADIEAMT R	103	24	3	17.36	y3y10y14	2563.25	72.769	6278	3	855.09	0.38
P0A7K0 RL11_SALTY 50S ribosomal protein L11	8		SIEGTARSMGLVVED	127	15	7	38.82	b5b6b8y7y8y11°y11	1563.78	60.569	4733	2	782.40	9.52

P0A7K0 RL11_SALTY 50S ribosomal protein L11	9		AFNAKTDSIEK	40	11	4	19.74	b8b10*b10y5	1223.62	54.365	1731	2	612.32	-3.19
P0A7K0 RL11_SALTY 50S ribosomal protein L11	10	Oxidation+M(12)	AADMTGADIEAMTR	113	14	3	15.39	b4y6y11	1468.65	41.654	10941	3	490.22	3.08
P0A7K0 RL11_SALTY 50S ribosomal protein L11	11		QLQEIAQTK	104	9	4	17.86	b3*b3b8*b8	1058.57	39.544	16773	2	529.79	-11.65
P0A7K0 RL11_SALTY 50S ribosomal protein L11	12		LQEIAQTK	105	8	0	3.14		930.52	39.517	1920	1	930.52	-9.38
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	1		AESFTTTNR	1	9	5	38.49	b7y4y5y6y9	1026.48	45.985	7916	2	513.75	-2.26
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	2		HGHAFNDLDLGKR	37	13	6	9.46	b2b5y12*y12y13*y13	1479.74	59.703	7370	2	740.38	-0.50
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	3		GEREPVTD AER	65	11	10	42.24	b2b3*b3b4*b4b8y2*y2y6y7	1258.60	23.116	3761	2	629.80	-4.07
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	4		HGDFTIK	23	7	4	35.01	b3b5*b5b6	817.41	31.990	4578	2	409.21	-13.59
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	5		HGHAFNDLDLGK	37	12	13	49.35	b6b11°b11y4°y4y6°y6y8°y8*y8y9°y9*y9	1323.67	46.763	2207	2	662.34	19.64
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	6		EAQLLERHGHAFNDLDLGK	30	19	4	33.38	y8y9y10y12	2163.07	74.842	21529	3	721.70	-9.26
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	7	Carbamidomethyl+C(14)	EPVTEEEKLFVAVCR	50	15	3	14.47	b5b8y4	1805.92	59.718	4217	4	452.24	7.23
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	8		YFDNKHYPR	10	9	5	38.49	b8y6y7y8°y8	1239.60	49.629	3951	2	620.30	6.11
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	9		HYPRGFSR	15	8	7	64.62	b3b4b5b6b7°b7y4	1019.51	46.751	2385	2	510.26	-5.75
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	10		REPVT EEEK	49	9	6	37.97	b3°b3b5y6°y6y7	1116.56	30.761	2038	2	558.78	2.73
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	11		HGHAFNDLDLGK	37	12	6	24.01	y7°y7y8*y8y11*y11	1323.64	59.749	3617	2	662.32	-5.63
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	1		SGAMAGTVLNDANNQAK	269	17	21	78.25	b1b2b3°b3b9°b9b10b11b17y1y2y4*y4y7y8°y8y9y12°y12*y12y13	1661.79	46.789	32433	2	831.40	1.69
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	2		ESGVIQGDLIAK	136	12	6	19.12	b1b2b9b10*b10y2	1229.66	54.288	4571	2	615.33	-12.41
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	3		VLTL SAVMASLLFGAHAHAADTR	4	23	4	24.96	y3y4y8y13	2352.27	88.274	2521	3	784.76	6.95
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	4		GEPGHPDAEAR	170	11	3	22.75	b5y5y6	1135.53	92.042	1742	1	1135.53	10.86
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	5		SSIPVFGVDALPEALALVK	250	19	5	26.64	b7y4y8y13y14	1926.10	108.371	47792	2	963.55	3.93
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	6		SAPDVQLLMNDSQNDQSK	52	18	3	12.58	b7b13y8	1989.95	77.284	31572	2	995.48	16.50
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	7		ALAINLVDPAAGTVIEK	84	18	6	40.52	b3y7y10y11y13y14	1766.01	81.094	24410	2	883.51	2.70
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	8		EPSR	115	4	1	10.62	b3	488.25	38.163	9609	1	488.25	12.81
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	9		MDAWLSGPNANK	214	12	6	41.41	b6y5*y5y7y8y10	1303.61	48.836	7796	3	435.21	-2.81

P23905 DGAL_SALTY D-galactose-binding periplasmic protein	10		AYYVGTD SK	127	9	9	81.27	b3b4b5y4°y4y5y7°y7y8	1003.48	32.023	4158	2	502.24	8.39
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	11		ALDSYDK	120	7	4	32	b3b4°b4y3	811.39	72.590	3475	1	811.39	12.26
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	12		DNLSEFTQK	323	9	6	50.99	b3b4b8y3*y3y7	1081.53	42.471	3428	2	541.27	15.35
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	13		HWQANQG WDLNK	148	12	11	65.37	b3b4b5y5°y5y8y9°y9*y9y10*y10	1496.70	42.483	1573	3	499.57	-4.49
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	14		NLAEGKGAADGTSWK	293	15	4	22.55	y4y12y13°y13	1504.76	56.081	15127	2	752.88	13.63
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	15		DGKSAPDVQLLMNDSQNDQSK	49	21	13	58.34	b3b5b6b9b10°b10*b10b11°b11*b11y4°y4y5	2290.05	59.732	11049	3	764.02	-5.86
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	16		AIEKD GK	45	7	3	32	b5b6y6	760.42	32.911	8634	2	380.71	-2.25
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	17		ALDSYDKAYYVGTD SK	120	16	3	13.71	b8y3y5	1795.84	49.605	5718	3	599.29	2.85
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	18		TTYVVKELNDK	181	11	4	28.77	b3b8y3y6	1309.68	45.437	5615	2	655.34	-14.82
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	19		MDAWLSGPNANKIEVVIANNDAMAMGAVEALK	214	32	3	22.24	b5y10y11	3343.68	103.638	4749	4	836.68	9.20
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	20		ATFDLAKNLAEGK	286	13	6	25.77	b3°b3b6°b6b8°b8	1377.72	74.121	3453	2	689.37	-9.83
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	21		ESGVIQGD LIAKHWQANQG WDLNK	136	24	5	20.34	b7°b7°b7y5y6	2707.35	67.094	3164	3	903.12	-1.80
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	22		HWQANQG WDLNKDGK	148	15	3	22.55	y5y7y8	1796.85	53.421	2995	2	898.93	2.45
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	23		SGAMAGTVLNDANNQAKATFDLAK	269	24	5	34.03	b7b8b9y4y7	2408.22	83.333	2524	3	803.41	11.86
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	24	Oxidation+M(13)	IEVVIANNDAMAMGAVEALK	226	20	6	29.14	b9b12y11y12y15y19	2075.04	67.136	52350	3	692.35	-5.29
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	25	Oxidation+M(4)	SGAMAGTVLNDANNQAK	269	17	3	13.09	b4b12y3	1677.79	45.501	20672	3	559.94	5.09
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	26	Oxidation+M(13)	GIQTEQLALDTAMWDTAQAKDK	192	22	4	11.33	b6°b6b13y11	2450.15	81.387	2604	3	817.39	-13.45
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	27		SGAMAGTVLND	269	11	2	7.99	y6*y6	1035.48	46.754	2669	2	518.24	0.47
P66038 RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLATEALAK	40	29	12	71.67	b9b10°b10b11°b11b12b13b14y3y9y15y29	3110.69	99.080	87702	3	1037.57	4.71
P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	12	82.9	b3b6b13y4y5y8y9y10y12y14y15y19	2109.07	102.178	58304	2	1055.04	4.63
P66038 RISB_SALTY 6	3		GAEAALTALEMINVLK	136	16	5	22.25	b5b8b12y1y4	1643.90	103.854	29676	2	822.45	-1.41

[P66038]RISB_SALTY 6	4		VAITIAIAR	14	7	3	35.01	y3y4y6	743.46	44.755	17029	2	372.23	-20.61
[P66038]RISB_SALTY 6	5		DDNITVVWVPGAYELPLATEALA KSGK	45	27	5	14.83	b8°b8b12b23y3	2857.48	60.623	31144	4	715.12	-7.69
[P66038]RISB_SALTY 6	6	Phosphoryl STY(13)	DDNITVVWVPGAYELPLATEALA K	45	24	5	11.05	b8°b8b12°b12y12	2665.29	93.119	17798	3	889.10	-5.22
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	1		EMLEDLVAAAFNDAARR	66	17	4	13.09	b12°b12b14y6	1891.93	59.869	4515	2	946.47	-1.74
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	2		VEIDPSLLEDDKEMLEDLVAAAFN DAAR	54	28	6	14.59	b2b4°b7y4y6y10	3089.48	128.501	2867	4	773.12	-7.35
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	3	Carbamidomethyl+C(9)	VTINGAHNCR	43	10	9	52.41	b2b6°b6y2y4y5y7*y7y8	1141.55	20.547	2289	2	571.28	-4.81
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	4		EMLEDLVAAAFNDAAR	66	16	4	18.85	b3b9y7y9	1735.86	72.419	8428	2	868.43	16.95
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	5		MASVSSGMQLPPGFK	91	15	6	29.49	b7b10y5y9y10°y10	1536.75	57.562	6233	2	768.88	-4.61
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	6		MQEEIAQLEVTGESGAGLVK	23	20	3	11.82	b9b13y4	2089.07	89.662	3664	3	697.03	10.63
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	7		EKMASVSSGMQLPPGFK	89	17	6	17.73	b5b7y11°y11*y11y15	1793.91	65.671	95057	2	897.46	10.89
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	8		FGKGGLGNLMK	1	11	4	19.74	b6b10°b10y9	1121.62	30.737	3267	2	561.31	2.61
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	9		GGLGNLMKQAQQMQEK	4	16	4	31.96	b10y5y6y7	1760.88	46.021	2189	2	880.94	1.18
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	10		MASVSSGMQLPPGFKMPF	91	18	3	12.58	b6y4y13	1911.93	107.225	1694	2	956.47	9.00
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	11	Phosphoryl STY(11)	MQEEIAQLEVTGESGAGLVK	23	20	4	18.1	b8b10_H3PO4 b10b12y12	2169.03	53.591	3435	3	723.68	12.04
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	12	Oxidation+M(2)	EMLEDLVAAAFNDAARR	66	17	15	66.03	b3b7b8b10°b10b15°b15b1 6y6*y6y7°y7y10°y10*y10	1907.93	74.174	153852	3	636.65	-0.96
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	13	Oxidation+M(8)	MASVSSGMQLPPGFK	91	15	4	23.8	b6y6y8y14	1552.77	100.169	4998	3	518.26	9.98
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB	14		EMLEDLVAAA	66	10	0	7.54		1061.51	59.794	2859	2	531.26	-10.23
[P66593]RS6_SALTY 30S ribosomal protein S6	1		YSAAITGAEGK	24	11	10	63.95	b3°b3b4b7y2y5y6y7y9y11	1067.52	33.950	212315	2	534.27	-11.43
[P66593]RS6_SALTY 30S ribosomal protein S6	2		AHYVLMNVEAPQEVIDELETTFR	56	23	4	11.17	b2b3y4y9	2704.33	112.248	97865	3	902.12	1.63
[P66593]RS6_SALTY 30S ribosomal protein S6	3		HYEIVFMVHPDQSEQVPGMIER	2	22	8	28.38	b2b4b8b9y6y10*y10y20	2641.28	76.768	4619	3	881.10	10.63
[P66593]RS6_SALTY 30S ribosomal protein S6	4		LEDWGRR	38	7	9	60.52	b2b3b5°b5b6y2y3y6y7	931.47	42.423	3672	2	466.24	-2.62
[P66593]RS6_SALTY 30S ribosomal protein S6	5		FNDAVIR	79	7	3	35.01	y3y4y5	834.43	42.841	106401	2	417.72	-15.36
[P66593]RS6_SALTY 30S ribosomal protein S6	6		QLAYPINK	45	8	3	30.87	b3b5y4	946.53	44.021	8761	1	946.53	-7.22
[P66593]RS6_SALTY 30S ribosomal protein S6	7		HAVTEASPMVK	93	11	10	68.72	b4b7°b7b9y5°y5y6y7y10°y 10	1169.58	45.990	3217	2	585.30	-12.42
[P66593]RS6_SALTY 30S ribosomal protein S6	8		RHYEIVFMVHPDQSEQVPGMIER	1	23	5	19.95	b11y4y5y9*y9	2797.34	83.491	13122	3	933.12	-6.37
[P66593]RS6_SALTY 30S ribosomal protein S6	9		TKHAVTEASPMVK	91	13	3	16.52	b6b12y6	1398.75	42.386	2350	2	699.88	6.20
[P66593]RS6_SALTY 30S ribosomal protein S6	10	Oxidation+M(6)	AHYVLMNVEAPQEVIDELETTFR	56	23	7	45.71	b11b12b13b14y10°y10y13	2720.32	112.627	12093	2	1360.67	0.27
[P66593]RS6_SALTY 30S ribosomal protein S6	11	Oxidation+M(9)	HAVTEASPMVK	93	11	3	19.74	b5b7y7	1185.59	48.698	4578	2	593.30	-1.03
[P0A1P6]GLNA_SALTY Glutamine synthetase	1		LVPGYEAPVMLAYSAR	322	16	9	59.59	b12b15°b15y4y5y9y10y11 y14	1736.91	78.231	34862	2	868.96	2.81

P0A1P6 GLNA_SALTY Glutamine synthetase	2		AINALANPTTNSYKR	307	15	6	32.32	b11y5y7y8y10y15	1633.86	43.408	33874	3	545.29	-4.26
P0A1P6 GLNA_SALTY Glutamine synthetase	3		EIPQVAGSLEEALNALDLDR	406	20	7	18.61	b2y5°y5y7*y7y12y20	2153.11	96.570	31587	3	718.37	-1.59
P0A1P6 GLNA_SALTY Glutamine synthetase	4		AGGVFTDEAIDAYIALR	430	17	9	52.28	b5b6b7b11b12b14y2y13y17	1781.92	60.565	28360	2	891.46	6.78
P0A1P6 GLNA_SALTY Glutamine synthetase	5		GGYFPVPPVDSAQDIR	177	16	9	30.5	b2b3y2y5y6y10y12°y12y16	1717.86	70.814	28165	2	859.44	5.40
P0A1P6 GLNA_SALTY Glutamine synthetase	6		MSAEHVLTMLNEHEVK	0	16	4	22.09	y6y7y11y16	1867.89	81.375	26942	3	623.30	-9.61
P0A1P6 GLNA_SALTY Glutamine synthetase	7		YAGLSEQUALYYIGGVIK	287	17	4	21.75	b9b10°b10b13	1844.98	68.908	17191	3	615.66	-1.52
P0A1P6 GLNA_SALTY Glutamine synthetase	8		ADEIQIYK	232	8	9	27.86	b1b2°b2b4b5°b5y7°y7*y7	979.52	48.824	16257	2	490.26	9.10
P0A1P6 GLNA_SALTY Glutamine synthetase	9		ATGIADTVLFGPEPEFFLFDDIR	117	23	6	13.64	b2b6b16y2y3y5	2570.26	117.879	16062	3	857.43	-6.65
P0A1P6 GLNA_SALTY Glutamine synthetase	10		MTPHPVEFELYYSV	455	14	5	15.39	b2°b2b8y5y10	1711.82	52.812	9785	3	571.28	10.84
P0A1P6 GLNA_SALTY Glutamine synthetase	11	Carbamidomethyl+C(1)	CDILEPGTLQGYDRDPR	89	17	4	22.21	b8y3y4y10	2004.97	34.501	5642	3	669.00	13.64
P0A1P6 GLNA_SALTY Glutamine synthetase	12		NGTNLFSGDK	277	10	3	29.11	y5y7y8	1052.51	67.218	4387	1	1052.51	8.70
P0A1P6 GLNA_SALTY Glutamine synthetase	13		AINALANPTTNSYK	307	14	3	15.39	b11y7y11	1477.78	61.525	27644	2	739.40	13.13
P0A1P6 GLNA_SALTY Glutamine synthetase	14		YVVHNVahr	240	9	3	25.47	b5b7y6	1094.56	39.145	19504	2	547.79	-20.63
P0A1P6 GLNA_SALTY Glutamine synthetase	15		IPVVASPK	345	8	3	35.64	y3y4y5	810.50	39.020	19452	2	405.75	-13.40
P0A1P6 GLNA_SALTY Glutamine synthetase	16		NLYDLPPEEAK	395	11	6	31.78	b3b10y4°y4y5°y5	1288.67	59.832	15339	2	644.84	21.60
P0A1P6 GLNA_SALTY Glutamine synthetase	17		SAEHVLTMLNEHEVK	1	15	11	83.07	b6°b6b8b12y4y5y6°y6y7y8y9	1736.84	59.757	10887	3	579.62	-11.03
P0A1P6 GLNA_SALTY Glutamine synthetase	18		FTDTK	21	5	1	11.25	b4	611.31	81.250	3813	1	611.31	4.89
P0A1P6 GLNA_SALTY Glutamine synthetase	19		FNTMTK	225	6	4	34.38	b5y3y4°y4	741.35	32.028	3041	1	741.35	-8.64
P0A1P6 GLNA_SALTY Glutamine synthetase	20	Carbamidomethyl+C(1)	CDILEPGTLQGYDR	89	14	8	36.64	b6°b6b7°b7y4y8°y8y9	1636.78	30.738	1796	3	546.27	10.74
P0A1P6 GLNA_SALTY Glutamine synthetase	21		GINESDMVLPDASTAVIDPFFADSTLIIR	59	30	8	35.58	b3b6b8b10b14y3y4y6	3238.58	114.123	1786	2	1619.79	-7.99
P0A1P6 GLNA_SALTY Glutamine synthetase	22	Carbamidomethyl+C(19)	TATFMPPKPMFGDNGSGMHCHMSLAK	252	25	3	10.97	b9y3y7	2753.17	66.220	1595	5	551.44	-15.43
P0A1P6 GLNA_SALTY Glutamine synthetase	23		EQHVTIPAHQVNAEEFEEGK	28	20	6	18.1	b6b11*b11b14°b14y8	2310.12	82.090	1551	3	770.71	0.00
P0A1P6 GLNA_SALTY Glutamine synthetase	24		FGASISGSHVAIDDIEGAWNSSTKYEGGNK	140	30	4	11.06	b6b9°b9y9	3097.45	52.627	37281	3	1033.15	0.16
P0A1P6 GLNA_SALTY Glutamine synthetase	25		VRMTPHPVEFELYYSV	453	16	5	22.25	b6y3°y3y8y12	1966.94	62.656	27629	3	656.32	-14.34
P0A1P6 GLNA_SALTY Glutamine synthetase	26		LVPGYEAPVMLAYSARNR	322	18	3	12.58	b10b13y7	2007.07	101.961	12010	2	1004.04	11.98
P0A1P6 GLNA_SALTY Glutamine synthetase	27		AEDYLRATGIADTVLFGPEPEFFLFDDIR	111	29	5	10.99	b12y5°y5y10°y10	3317.64	71.183	6372	4	830.17	0.59
P0A1P6 GLNA_SALTY Glutamine synthetase	28		NKIHPEAMDK	384	11	5	30.2	b7b9b10°b10y4	1239.61	59.784	2223	2	620.31	-1.08
P0A1P6 GLNA_SALTY Glutamine synthetase	29	Phosphoryl STY(13)	AGGVFTDEAIDAYIALR	430	17	5	32	b3b7b10b12y6	1861.87	51.465	8048	2	931.44	4.26
P0A1P6 GLNA_SALTY Glutamine synthetase	30	Phosphoryl STY(26)	GINESDMVLPDASTAVIDPFFADSTLIIR	59	30	5	21.33	b9y3y6y8_H3PO4 y8y9	3318.59	46.749	8010	4	830.40	8.53

P0A1P6 GLNA_SALTY Glutamine synthetase	31	Phosphoryl STY(7)	GKEQHVTIPAHQVNAEFFEEGK	26	22	3	20.08	b5b6y7	2575.19	49.677	4281	3	859.07	2.28
P0A1P6 GLNA_SALTY Glutamine synthetase	32		ANPTTNSYKR	312	10	2	7.53	b9°b9	1151.58	43.456	5150	2	576.29	-2.65
P0A1P6 GLNA_SALTY Glutamine synthetase	33		NALANPTTNSYKR	309	13	0	6.28		1449.75	43.423	3486	2	725.38	1.85
P0A1P6 GLNA_SALTY Glutamine synthetase	34		GSLEEALNALDLDR	412	14	2	20.46	b4b5	1515.75	96.494	3024	2	758.38	-7.09
P0A1P6 GLNA_SALTY Glutamine synthetase	35		YAGLSEQALY	287	10	0	7.54		1114.55	68.854	1681	1	1114.55	8.87
P0A1P6 GLNA_SALTY Glutamine synthetase	36		ADEIQIYK	232	8	0	1.88		961.49	48.754	2677	2	481.25	-0.83
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		QLDPLVVGQEHYDTAR	343	16	9	70.89	y4°y4y5y8y9y10°y10y13y14	1840.90	58.519	50920	3	614.31	-9.81
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		FLSQPFFVAEVFTGSPGK	399	18	4	16.78	b3b10y3y7	1958.02	100.545	29041	2	979.51	8.42
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		QIASLGIYPDVDLSTSR	324	19	10	52.85	b9b12y4y7°y7y11y13y14y15y19	2003.06	81.094	26110	2	1002.03	5.42
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4		NIAIEHSGYSVFAGVGER	165	18	3	12.58	b8y5y11	1905.94	58.238	22650	2	953.48	-0.45
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		MPSAVGYQPTLAEEMGVLQER	261	21	12	40.4	b3°b3b11b21y3°y3y4y6y7y9°y9y21	2306.13	82.247	19243	2	1153.57	7.83
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		TVNMMELIR	156	9	10	50.99	b2b3b4y1y3y6y7°y7*y7y9	1106.56	76.752	16891	2	553.78	-8.27
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		IMNVLGEPVDMK	87	12	5	25.14	y2y6°y6y8y9	1345.67	32.965	12169	3	449.23	-11.88
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		TIAMGSSDGLRR	53	12	5	21.92	b11b12y2y6y7	1263.64	54.272	7160	2	632.32	-5.22
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		TREGNDFYHEMTDSNVIDK	183	19	10	47.75	b4°b4b5°b5y8°y8y9y11y12y19	2271.03	68.959	5906	3	757.68	13.98
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		FRDEGRDVLLFVDNIYR	230	17	7	33.83	b3b4y4y5y7°y7y17	2127.08	96.407	4630	2	1064.04	-10.90
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		TIAMGSSDGLR	53	11	3	19.74	b10y8y10	1107.53	112.650	1835	1	1107.53	-14.00
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		VALTGLTMAEK	219	11	8	69.52	b8b10y4y5y6°y6y7y9	1133.61	59.767	65654	2	567.31	-8.29
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		VSLVYGQMNEPPGNR	202	15	3	14.47	b14y4y9	1660.80	54.778	39804	2	830.90	-6.32
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		AAPSYEELSNSQELLETGIK	112	20	4	27.48	y5y12y15y17	2179.09	74.287	34991	2	1090.05	6.72
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15		GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	6	16.28	b5b24y6°y6y11y13	3057.45	93.247	26697	3	1019.82	22.60
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16		VYDALEVQNGNEK	25	13	6	27.99	b6y5y7°y7*y7y10	1478.74	40.619	24596	3	493.59	20.14
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17		YQELK	367	5	1	11.25	b4	680.36	31.483	8288	1	680.36	-5.56
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	6	64.63	b3b5b7b8y4y5	1193.60	38.084	2119	2	597.30	-2.66
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19		GEIGEER	99	8	3	30.87	b3b5y6	918.43	102.154	1557	1	918.43	17.21
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20		DEGRDVLLFVDNIYR	232	15	4	23.8	b8y4y6y7	1823.95	100.243	303507	2	912.48	12.85
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	21		TIAMGSSDGLRR	53	12	3	17.94	b6b10y10	1263.65	38.184	27638	2	632.33	4.54
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	22		YTLAGTEVSALLGRMPSAVGYQP TLAEEMGVLQER	247	35	6	11.73	b9°b9b11°b11y10°y10	3737.86	136.206	15575	3	1246.62	-8.49
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	23		ATLGRIMNVLGEPVDMK	82	17	3	13.09	b5y3y10	1843.96	87.582	6634	2	922.48	-11.85

Q7CPE2 ATPB_SALTY ATP synthase subunit beta	24	Carbamidomethyl+C(6)	VIDLMCPFAKGGK	132	13	6	33.29	b8b9°b9b12y9y11	1435.74	68.954	3798	2	718.37	-1.53
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	25		IMNVLGEPVDMKGEIGEEER	87	20	4	18.1	b7y6y10y12	2245.09	70.711	3538	3	749.04	3.37
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	26		DLEHPIEVPVGKATLGR	70	17	6	20.96	b3°b3b5b9y4°y4	1831.01	32.906	2405	4	458.51	2.80
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	27	Carbamidomethyl+C(6); Oxidation+M(5)	VIDLMCPFAK	132	10	4	36.38	b7y5y6y7	1209.59	60.632	6666	2	605.30	-12.41
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	28	Oxidation+M(4)	TIAMGSSDGLR	53	11	4	26.73	y7y9y10°y10	1123.55	46.773	5619	2	562.28	10.32
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	29	Oxidation+M(2)	IMNVLGEPVDMK	87	12	3	17.94	b4b10y6	1361.67	89.732	1504	2	681.34	-11.03
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	30		PSAVGYQPTLAEEMGVLQER	262	20	4	21.2	b3°b3b4b15	2175.07	82.266	2054	3	725.70	-2.13
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	1		VITDVHEASQAQPVADVVDVIQL PAFLAR	91	29	6	12.01	b8b12*b12y2y6y14	3101.67	105.280	27730	3	1034.56	2.52
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	2		SSIHYSYR	63	7	4	32	b4y3y4y7	849.43	52.651	19906	1	849.43	10.20
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	3		AGMAVGLAGLFLESHDPANAK	226	22	6	27.01	b6b9y5y7y12y13	2166.08	89.046	19161	3	722.70	-9.13
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	4		VANDLPFVLFGGMNVLESR	12	19	15	92.06	b1b8y2°y2y3y4y5y7y8y10°y10y11y13y14y19	2078.08	110.883	16846	2	1039.54	2.47
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	5	Carbamidomethyl+C(17)	VSGNSPVIFDVTHALQCR	189	18	5	12.58	b1b5b13*b13y10	1999.98	80.234	7641	3	667.33	-10.31
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	6	Carbamidomethyl+C(17)	VSGNSPVIFDVTHALQCRDPFGAA SGGRR	189	28	4	10.94	b7*b7y7y13	2915.41	86.422	4649	4	729.61	-4.27
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	7	Carbamidomethyl+C(2)	ICEHYVTVTQK	36	11	6	30.2	b7b9°b9b10y8*y8	1377.70	46.783	27952	3	459.90	9.66
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	8		GQVTELAR	218	8	9	69.39	b3b4°b4*b4b6y3y4°y4y6	873.47	32.868	11489	2	437.24	-14.05
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	9		ASFDK	55	5	1	11.25	b4	567.27	49.657	11259	1	567.27	-11.40
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	10		DLAMR	31	5	2	22.5	b3y3	605.31	47.806	8482	1	605.31	-2.12
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	11		QTDLVEAMAK	120	10	7	49.4	b5b6b7b9°b9y9°y9	1105.58	51.306	6836	2	553.29	18.88
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	12		GANFGYDNLVVDMLGFSVMK	168	20	4	15.24	b5b12y6y13	2177.03	103.085	4798	3	726.35	-3.36
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	13		GPGLEEGMK	70	9	3	25.47	b3b6y5	917.45	53.477	2564	2	459.23	9.18
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	14		DPFGAASGGR	207	10	3	29.11	b4b6b7	934.45	67.024	2377	1	934.45	13.52
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	15		GQVTELARAGMAVGLAGLFLESH PDPANAK	218	30	3	11.06	b7y7y14	3020.57	87.057	75212	3	1007.53	3.31
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	16	Carbamidomethyl+C(23)	AGMAVGLAGLFLESHDPANAKC DGPSALPLAK	226	33	3	23.21	b4b5b9	3275.63	90.441	14366	4	819.66	-6.78
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	17	Carbamidomethyl+C(4)	VILCDRGANFGYDNLVVDMLGFS VMK	162	26	3	10.93	b11y10y16	2933.43	57.577	13250	5	587.49	-3.33
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	18		ANRSSIHYSYR	60	10	8	62.86	b3b4b7*b7b9y5°y5y9	1190.59	41.678	3858	3	397.53	-12.41
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	19	Oxidation+M(8)	GPGLEEGMK	70	9	4	25.47	b4b7y6°y6	933.43	71.305	23226	2	467.22	-4.05
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	20	Oxidation+M(8)	QTDLVEAMAK	120	10	5	49.4	b3y4y5y6y7	1121.56	49.601	5708	2	561.28	7.29
P65215 KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	21	Oxidation+M(3)	AGMAVGLAGLFLESHDPANAK	226	22	4	20.08	b10y9°y9y10	2182.08	73.540	3108	3	728.03	-9.62
Q8ZRP4 DAPD_SALTY 2	1		EAVNQVISLLDSGALR	28	16	8	42.16	b6*b6b7y3y6y9y10y16	1684.93	92.969	60097	2	842.97	5.22

Q8ZRP4 DAPD_SALTY 2	2		INDNQVIDGAESR	68	13	15	74.24	b1b3b8b9y7°y7y8y9°y9*y9y10*y10y11°y11y13	1430.69	41.680	22556	2	715.85	0.68
Q8ZRP4 DAPD_SALTY 2	3		MQQLQNVIETAFER	0	14	4	20.83	b4*b4y7y8	1706.85	31.956	31381	3	569.62	-4.36
Q8ZRP4 DAPD_SALTY 2	4		IDGQWVTHQWLK	48	12	5	41.41	b3b6b9b10y8	1510.75	70.031	3505	3	504.26	-18.10
Q8ZRP4 DAPD_SALTY 2	5		AVLLSFR	61	7	3	35.01	y3y4y5	805.48	67.024	3398	2	403.24	-21.90
Q8ZRP4 DAPD_SALTY 2	6		MQQLQNVIETAFERR	0	15	4	14.47	b4b10°b10y6	1862.93	66.281	7714	3	621.65	-13.11
Q8ZRP4 DAPD_SALTY 2	7		EAVNQVISLLDSGALRVAEK	28	20	8	24.15	b3b7*b7y3°y3y4°y4y11	2112.16	46.039	6349	5	423.24	-1.73
Q8ZRP4 DAPD_SALTY 2	8		IYDRETGEVHYGR	213	13	9	80.72	b3b4b6b11b12y4y5y10y12	1594.77	69.022	3255	3	532.26	8.11
Q8ZRP4 DAPD_SALTY 2	9	Phosphoryl STY(13)	SEVVEGVVIEEGSVISMGVYLGQSTK	187	26	8	23.05	b3b13y5y10*y10y12y14_HPO3y14°y14	2776.35	74.184	16099	4	694.84	7.12
P60446 RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	7	59.4	y3y5y6y7y8y9*y10	1115.63	56.965	122792	2	558.32	-9.96
P60446 RL3_SALTY 50S ribosomal protein L3	2		IFTEDGVSSIPVTVIEVEANR	13	20	10	32.71	b2b7y1y4°y4y5y6°y6y13y20	2188.16	88.819	60015	2	1094.58	5.58
P60446 RL3_SALTY 50S ribosomal protein L3	3		TQDATHGNSLSHR	128	13	14	67.25	b1b4°b4*b4b10b11b12y2y4y5y7°y7*y7y10	1423.69	45.968	16791	3	475.23	14.23
P60446 RL3_SALTY 50S ribosomal protein L3	4		MAGQMGNER	160	9	11	68.26	b2b4b5y1y2y4y5°y5y7y8y9	993.43	21.355	13938	2	497.22	2.95
P60446 RL3_SALTY 50S ribosomal protein L3	5		GLWEFR	77	6	6	45.63	b4°b4b5°b5y4y5	807.42	46.751	36675	2	404.21	8.69
P60446 RL3_SALTY 50S ribosomal protein L3	6	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	3	12.58	b15y4y15	1738.92	54.505	34897	3	580.31	-16.01
P60446 RL3_SALTY 50S ribosomal protein L3	7		NLLLVK	184	6	2	23.13	y3y4	699.48	57.485	16254	1	699.48	-0.61
P60446 RL3_SALTY 50S ribosomal protein L3	8		VTKPEAGHFAK	59	11	8	47.47	b8°b8y4y5y7°y7y10°y10	1184.62	46.765	12082	2	592.81	-20.20
P60446 RL3_SALTY 50S ribosomal protein L3	9		AVQVTTGAK	46	9	7	52.75	b3*b3y4y5y6y7*y7	874.48	22.366	7775	2	437.75	-18.01
P60446 RL3_SALTY 50S ribosomal protein L3	10		VPGSIGQNQTPGK	141	13	5	26.23	b4°b4b6b7y11	1282.65	54.305	3232	3	428.22	-21.13
P60446 RL3_SALTY 50S ribosomal protein L3	11		LAEGEEYTVGQSSISVELFADVK	83	22	4	11.33	b4°b4b11y11	2384.16	89.547	2162	2	1192.59	-9.63
P60446 RL3_SALTY 50S ribosomal protein L3	12		DLANDGYR	38	8	9	83.65	b5b6b7y3y4°y4y6y7°y7	923.43	32.851	1838	1	923.43	8.72
P60446 RL3_SALTY 50S ribosomal protein L3	13	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	9	48.35	b4b5b7°b7y3y5y6y8y12	1809.96	56.748	115765	3	603.99	-13.42
P60446 RL3_SALTY 50S ribosomal protein L3	14		IFTEDGVSSIPVTVIEVEANRVTQVK	13	25	6	17.37	b5b7°b7b11y16y18	2743.49	95.774	69645	3	915.17	0.27
P60446 RL3_SALTY 50S ribosomal protein L3	15		TQDATHGNSLSHRVPGSIGQNQTPGK	128	26	4	21.6	y7y10*y10y11	2687.31	55.132	34366	4	672.58	-4.54
P60446 RL3_SALTY 50S ribosomal protein L3	16		AGVEAGRGLWEFR	70	13	6	33.29	b4b11y4y11y12°y12	1447.73	60.528	20298	2	724.37	-7.00
P60446 RL3_SALTY 50S ribosomal protein L3	17		WNFRTQDATHGNSLSHR	124	17	4	13.09	b4b11y3°y3	2026.95	95.495	4598	2	1013.98	-6.56
P60446 RL3_SALTY 50S ribosomal protein L3	18		KMAGQMGNER	159	10	5	45.59	b4b5y4y5y8	1121.52	18.285	2475	2	561.26	-1.09
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	13	102.35	b2y1y3y5y6y7y9y10y11y14y17y19y21	2215.15	75.650	44968	3	739.06	-8.05
Q56073 DNAK_SALTY Chaperone protein dnaK	2		ASSGLNEEEIQK	502	12	13	41.41	b1b2°b2b11y1y5y6°y7°y7y8y9°y9y12	1304.63	35.208	20426	2	652.82	-4.77
Q56073 DNAK_SALTY Chaperone protein dnaK	3		TAEDYLGEVPTEAVITVPAYFNDAQR	125	26	10	40.24	b3b6b14°b14y3y4y8y9y12y26	2869.40	94.181	19794	3	957.14	4.68
Q56073 DNAK_SALTY Chaperone protein dnaK	4		QAVTNPQNTLFAIKR	56	15	6	31.07	b2b3b5b8°b8b9	1700.96	72.840	16140	2	850.99	11.34
Q56073 DNAK_SALTY Chaperone protein dnaK	5		QVEEAGDK	548	8	3	24.39	y4°y4y7	875.42	38.124	8459	2	438.21	8.44

IQ56073 DNAK_SALTY Chaperone protein dnaK	6		TTPSIIAYTQDGETLVGQPAKR	34	22	7	21.21	b2b3°b3b4b13°b13y2	2346.25	68.994	6260	3	782.75	7.60
IQ56073 DNAK_SALTY Chaperone protein dnaK	7		QATKDAGR	151	8	5	27.86	b5°b5b6°b6y5	846.43	86.319	5900	1	846.43	-11.10
IQ56073 DNAK_SALTY Chaperone protein dnaK	8		MVRDAEANAESDR	514	13	3	16.52	b4b11y9	1463.66	67.056	5475	2	732.33	1.17
IQ56073 DNAK_SALTY Chaperone protein dnaK	9		FQDEEVQR	76	8	6	42.12	b4y3y4°y4y7y8	1050.47	28.985	4825	2	525.74	-9.88
IQ56073 DNAK_SALTY Chaperone protein dnaK	10		VLENAEGDR	25	9	7	25.47	b2b4°b4°b4b6b9y7	1002.49	23.597	3906	2	501.75	8.22
IQ56073 DNAK_SALTY Chaperone protein dnaK	11		LMEIAQQQHAQQAGSADASAN NAK	597	25	4	15.44	b3b9b14y8	2610.26	101.632	2068	4	653.32	10.48
IQ56073 DNAK_SALTY Chaperone protein dnaK	12		TTPSIIAYTQDGETLVGQPAK	34	21	3	20	b12y12y13	2190.12	93.531	1595	2	1095.56	-3.68
IQ56073 DNAK_SALTY Chaperone protein dnaK	13		IIGADNGDAWLDVK	92	14	3	15.39	b8b13y9	1486.76	71.015	12782	2	743.88	3.28
IQ56073 DNAK_SALTY Chaperone protein dnaK	14		GMPQIEVTFDIDADGILHVS AK	467	22	10	42.4	b4b5b7b8°b8b10b13°b13°b13y13	2356.14	95.421	11329	4	589.79	-18.55
IQ56073 DNAK_SALTY Chaperone protein dnaK	15		LPADDK	556	6	3	34.38	b3y3y4	658.34	46.776	11090	1	658.34	-0.19
IQ56073 DNAK_SALTY Chaperone protein dnaK	16		SLGQFNLDGINPAPR	452	15	4	14.47	b5°b5b14y11	1598.83	85.524	10969	2	799.92	-0.92
IQ56073 DNAK_SALTY Chaperone protein dnaK	17		NQGDHLLHSTR	536	11	5	28.77	b4b9y4y8°y8	1277.63	42.502	4971	2	639.32	-4.20
IQ56073 DNAK_SALTY Chaperone protein dnaK	18		TIAVYDLGGGTFDISIIEIDVDGE K	188	26	4	22.39	b9b22y3y4	2769.38	99.360	3784	3	923.80	2.03
IQ56073 DNAK_SALTY Chaperone protein dnaK	19		MQELAQVSQK	587	10	3	22.12	b4b7y9	1161.62	74.894	2822	2	581.31	19.02
IQ56073 DNAK_SALTY Chaperone protein dnaK	20		FEELVQTR	528	8	5	42.12	b4b6b7y7°y7	1021.51	42.450	2643	2	511.26	-17.92
IQ56073 DNAK_SALTY Chaperone protein dnaK	21		MPMVQK	345	6	2	23.13	b4y5	733.37	30.177	2405	1	733.37	-0.33
IQ56073 DNAK_SALTY Chaperone protein dnaK	22		IELSSAQQTVDNLPYITADATGPK	270	24	4	11.05	b9y6°y6y11	2532.34	109.435	1919	3	844.78	20.92
IQ56073 DNAK_SALTY Chaperone protein dnaK	23		KDVNPDEAVAIGA AVQGGVLTG DVK	362	25	3	10.97	b11b15y7	2423.29	78.818	41268	3	808.44	6.35
IQ56073 DNAK_SALTY Chaperone protein dnaK	24		QATKDAGR	151	8	3	27.86	b6y6y7	846.44	45.304	39197	2	423.72	-8.08
IQ56073 DNAK_SALTY Chaperone protein dnaK	25		VLENAEGDR TTPSIIAYTQDGETLVGQPAK	25	30	8	21.33	b6°b6°b6b9b10b14y13°y13	3173.60	71.265	6018	3	1058.54	1.46
IQ56073 DNAK_SALTY Chaperone protein dnaK	26		MQELAQVSQKLMEIAQQQHAQQ QAGSADASANNAK	587	35	4	11.73	b10b12y14°y14	3752.82	118.573	5477	4	938.96	3.32
IQ56073 DNAK_SALTY Chaperone protein dnaK	27		IIGADNGDAWLDVKGQK	92	17	5	32.59	b3b6b13y12y13	1799.93	136.312	2741	2	900.47	1.97
IQ56073 DNAK_SALTY Chaperone protein dnaK	28		ITIKASSGLNEEEIQK	498	16	3	22.09	y6y7y9	1759.92	100.553	2613	2	880.46	-12.14
IQ56073 DNAK_SALTY Chaperone protein dnaK	29		ASDNKSLGQFNLDGINPAPR	447	20	7	32.71	b5°b5b8b9b10°b10y11	2114.05	69.991	2012	3	705.36	-4.85
IQ56073 DNAK_SALTY Chaperone protein dnaK	30	Phosphoryl STY(12)	IINEPTAAALAYGLDK	167	16	3	20.25	b13_H3PO4 b12b13y4	1739.86	68.505	13748	3	580.63	5.61
IQ56073 DNAK_SALTY Chaperone protein dnaK	31	Phosphoryl STY(15)	IELSSAQQTVDNLPYITADATGPK	270	24	12	54.91	b7b8°b8y7°y7y8°y8y11y12°y12y13_HPO3 y13°y13	2612.23	60.548	5811	3	871.42	-3.18
IQ56073 DNAK_SALTY Chaperone protein dnaK	32	Phosphoryl STY(14)	TTPSIIAYTQDGETLVGQPAK	34	21	6	28.93	b3b13b18y8°y8y9	2270.11	74.193	4658	2	1135.56	12.58
IQ56073 DNAK_SALTY Chaperone protein dnaK	33	Phosphoryl STY(7)	MAPPQISAEVLK	109	12	7	41.9	b4b5b6°b6y8y10°y10	1363.66	46.825	2326	2	682.33	-0.45
IQ56073 DNAK_SALTY Chaperone protein dnaK	34	Oxidation+M(2)	GMPQIEVTFDIDADGILHVS AK	467	22	9	39.54	b5b6°b6b9b12b17y5y11y13	2372.21	102.632	4467	3	791.41	11.73

Q56073 DNAK_SALTY Chaperone protein dnaK	35		VLENAEGDR	25	9	0	2.51		985.46	23.523	16080	2	493.24	10.53
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	1		MLQSNEYFSGK	0	11	6	22.75	b9b10°b10y1y4y11	1303.60	50.053	25918	2	652.30	-2.34
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	2		VLLPGTVEWK	53	10	4	23.88	b3y6y7y10	1141.65	71.600	22414	2	571.33	-7.48
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	3	Carbamidomethyl+C(28)	VYTAGEVFNVPGHSEFHLQVAEP ASYLCR	63	29	9	33.87	b3b4b5°b5y2y5°y5y11y29	3277.62	129.603	3101	4	820.16	13.04
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	4		SIGFTSSSTGR	13	11	6	30.2	b9°b9y3y4y7°y7	1099.54	38.059	2659	2	550.27	1.89
Q8ZRE7 YAIE_SALTY UPF0345 protein yaiE	5	Carbamidomethyl+C(28)	VYTAGEVFNVPGHSEFHLQVAEP ASYLCRYL	63	31	4	11.16	b6b11°b11y11	3553.75	117.036	3135	4	889.19	7.28
P69226 IF1_SALTY Translation initiation factor IF-1	1		AKEDNIEMQGTVLETLPNTMFR	1	22	7	40.25	b6b7b8b11y6y9y14	2537.25	85.347	51890	3	846.42	5.00
P69226 IF1_SALTY Translation initiation factor IF-1	2		VELENGHVVTAHISGK	23	16	5	12.88	b6°b6°b6b8°b8	1689.89	102.613	18573	2	845.45	-2.96
P69226 IF1_SALTY Translation initiation factor IF-1	3		EDNIEMQGTVLETLPNTMFR	3	20	4	11.82	b13y3y7°y7	2338.13	89.089	1921	2	1169.57	11.90
P67093 UG_SALTY Universal stress protein G	1		TIIMPVDVFEMELSDK	3	16	10	40.4	b2b3b12°b12y6y12y13°y13y14y16	1866.93	105.276	75629	2	933.97	6.47
P67093 UG_SALTY Universal stress protein G	2		HATLPVLVVR	132	10	7	33.37	b2b3°b3y2y6y8y9	1104.68	62.625	19472	2	552.85	-5.08
P67093 UG_SALTY Universal stress protein G	3		LQTMVGHFSIDPSR	69	14	3	13.68	y7y8°y13	1587.81	86.350	3542	3	529.94	9.92
P67093 UG_SALTY Universal stress protein G	4		NPSITTHLLGSNASSVVR	114	18	3	12.58	b5b10y10	1853.00	62.500	31860	2	927.01	8.96
P67093 UG_SALTY Universal stress protein G	5		FAADVR	50	6	1	11.88	b3	678.35	30.099	7502	1	678.35	-11.25
P67093 UG_SALTY Universal stress protein G	6		FGSVRDVVNEMGEELDADV VVIGSR	89	25	4	10.97	b9°b9y3y18	2692.30	125.697	63154	3	898.11	-7.71
P67093 UG_SALTY Universal stress protein G	7		HAEFLAQQDGVIIHLHLVPGSAS MSLHRFAADVR	22	34	3	17.3	b7b11b14	3722.88	85.857	11200	4	931.48	-13.84
P67093 UG_SALTY Universal stress protein G	8		FEEHLQHEAETRLQTMVGHFSIDPSR	57	26	3	10.93	b6y9y13	3094.48	103.882	7317	3	1032.17	0.79
P67093 UG_SALTY Universal stress protein G	9		RFEHLQHEAETR	56	13	6	28.35	b6b7°b7y5y9°y9	1681.80	45.397	6950	3	561.27	-0.07
P67093 UG_SALTY Universal stress protein G	10	Oxidation+M(4)	LQTMVGHFSIDPSR	69	14	6	31.99	b4°b4b9b13y7y13	1603.81	60.637	17734	2	802.41	12.71
P67093 UG_SALTY Universal stress protein G	11	Oxidation+M(4)	TIIMPVDVFEMELSDK	3	16	5	27.39	b5b11b15y6y8	1882.91	78.200	4559	3	628.31	-2.72
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		VLVLVAAPEGIAALEK	155	16	6	37.27	b3b4b6y9y11y12	1592.96	86.656	43323	2	796.99	1.69
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		AGLGMMEGVLENVPSAR	78	17	9	43.62	b13°b13b14y4y6y12y14°y14y17	1730.87	82.504	30893	2	865.94	7.69
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		ITVVPILR	70	8	4	35.64	y4y5y6y8	910.60	70.700	13600	2	455.80	-11.39
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		ELASEVGSLLTYEATADLETEK	29	22	5	11.33	b1b4y2y7y10	2369.19	66.212	2030	3	790.40	11.95
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		NEETLEPVYPYFQK	103	13	5	16.52	b4°b4b10°b10y8	1593.81	58.364	9759	2	797.41	16.31
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	6	Oxidation+M()	AGLGMMEGVLENVPSAR	78	17	6	28.98	b3b4b6b16°b16y8	1746.86	94.356	1724	2	873.93	3.70
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	7		VGSLLTYEATADLETEK	34	17	2	9.62	b12°b12	1839.94	66.212	2610	3	613.98	8.43
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	5	26.23	b2b3y7y10y11	1365.68	63.718	84059	2	683.35	-0.27
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2		ATFVVDPPQGHQAEIVTAEGIGR	120	23	10	32.7	b2b4b6y2y4y7y8y10y12°y12	2384.27	129.439	55447	3	795.43	-6.25

P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		LGVDVYSVSTDTHFTHK	63	17	6	25.6	b4b11y2y3y9y11	1905.91	58.498	15680	3	635.98	-11.34
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		AWHSSSETIAK	80	11	4	31.78	b9b10y5y9	1216.58	30.658	11275	3	406.20	-13.24
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		NFDNMREDEGLADR	106	14	6	15.39	b2*b2b11y5y9*y9	1681.74	47.914	7875	2	841.38	12.48
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTELGDVA DHYEELQK	32	31	6	20.39	b5b11y2y6y7y11	3757.74	119.509	7377	3	1253.25	4.29
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7		NGEFIEVTEKDTEGR	17	15	6	23.8	b2b6y4*y4y8y10	1723.79	63.268	4781	3	575.27	-14.52
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8		ATFVVDPPQGIIQAIEVTAEGIGRDA SDLLR	120	30	3	11.06	b6y6y8	3154.66	137.227	2132	3	1052.22	-5.49
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9	Carbamidomethyl+C(13)	AAQYVAAHPEVCPAK	153	16	14	117.15	b3b4*b4b5*b5b8b9b10y3y4y8y9y11y12	1668.79	35.855	105482	3	556.93	-16.17
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10		EGEATLAPSLDLVGK	171	15	5	20.16	b6b9y3y11*y11	1499.78	53.595	10061	2	750.39	-8.79
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	11		NGEFIEVTEKDTEGR	17	15	8	59.77	b5b7b8*b8b9y8y9y10	1723.81	60.585	2295	3	575.28	0.85
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	12	Phosphoryl STY(17)	ATFVVDPPQGIIQAIEVTAEGIGR	120	23	8	43.66	b3y5y6*y6y11_H3PO4y10y11*y11y12	2464.24	49.587	2565	6	411.55	-0.79
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	13		NGEFIEVTEK	17	10	3	22.55	y3y5y8	1165.56	63.249	1552	2	583.29	-7.85
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTASPYASYLQYGHIANIDD IIAGKKPATDLGVK	125	38	12	77.9	b3b4b5b6b7b8*b8y3y4y8y31y38	4001.01	83.962	155920	5	801.01	-13.55
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		LVEPEWFK	352	8	5	27.86	b6y2y5y6y8	1047.54	71.905	87655	2	524.27	-10.60
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3		NQGDLPAYSYTPPYTDGAK	333	19	5	12.16	b5y7*y7y11y19	2057.95	62.738	58408	3	686.65	0.47
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4		WSDGTPVTAHDFVYSWQR	107	18	13	49.44	b2*b2y4*y4y5*y5*y5y7*y7y9y10y13y18	2151.99	73.345	49336	3	718.00	3.06
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		AEQQLDKDSAIVPYYYYVNAR	494	21	3	11.55	b11y3y9	2442.22	73.897	48675	3	814.75	-2.30
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		TVINQVTYLPISSEVTDVNR	241	20	8	56.38	y3y4y5y9y11y12y14y20	2248.19	77.778	42313	2	1124.60	4.02
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7		NLGVNVNLENQEWK	410	14	8	34.58	b3y1y3y8y10y11*y11y14	1656.84	67.477	29929	2	828.93	5.38
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		ALDDHTFEVTLSEPVPYFYK	163	20	3	11.82	b14y5y7	2371.15	86.844	24927	3	791.05	-1.54
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	8	14.4	b1b3b8*b8b12y1y3y29	3091.54	88.969	21773	3	1031.18	0.08
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10	Carbamidomethyl+C(6)	VDPYLCTYYEINNQK	291	16	4	20.25	b3b4y2y8	2082.97	71.407	6875	2	1041.99	12.19
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		VWTFHLRENAK	96	11	6	44	b1b5b6b9b10*b10	1400.74	63.096	5668	2	700.87	-5.32
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		DLFEGLLISDVEGHPSPGVAEK	67	22	6	14.1	b5*b5b12y9*y9y13	2309.16	113.781	2139	3	770.39	-2.33

[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	13	Carbamidomethyl+C(4)	AGWCADYNEPTSFLNTMLSDSSNNTAHYK	439	29	4	21.4	b4y12y13*y13	3294.42	90.842	72548	3	1098.81	1.93
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	14		SGEIDMTYNNMPIELFQK	263	18	6	33.08	b3b11b14y3y4y7	2130.00	87.265	68345	2	1065.50	6.30
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	15		EIPNEVR	284	7	5	46.26	b4b5y5y6*y6	856.47	31.417	5971	2	428.74	15.25
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	16		IEGVPESNVSR	56	11	15	95.03	b3b7y3y4°y4*y4y5*y5y6y8y9°y9*y9y10°y10	1186.60	37.241	4787	2	593.80	-3.70
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	17		SNITK	1	5	1	11.25	y4	562.31	27.454	2309	1	562.31	-12.81
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	18		HQGTFDVAR	430	9	3	25.47	b6y4y6	1030.53	31.379	1803	2	515.77	18.01
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	19		WTQPANIVTNGAYK	204	14	4	15.39	b5°b5b7y9	1562.77	38.036	1661	3	521.59	-19.14
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	20		DSAIVPVYYYVNAR	501	14	4	21.71	b3b5y7y10	1629.85	57.625	1607	2	815.43	14.98
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	21		KNLGVNVNLENQEWK	409	15	3	31	y8y9y10	1784.93	54.331	132769	3	595.65	2.05
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	22		FGDKWTQPANIVTNGAYK	200	18	5	19.85	b4b12°b12b14y3	2009.99	80.102	51272	2	1005.50	-8.50
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	23		TVINQVTYLPISSEVTDVNRYS	241	22	7	32.37	y9°y9y10y13*y13y16y19	2567.34	77.833	36264	3	856.45	-2.66
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	24		IVLERNPQYWDNAK	227	14	3	23.96	y4y6y9	1745.89	54.287	22048	3	582.63	-6.85
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	25		VKNQGDLPAYSYTPPYTDGAK	331	21	3	11.55	b6b11y6	2285.09	69.906	18077	4	572.03	-6.09
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	26	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYEINNQK	284	23	6	13.64	b4b6°b6y10°y10y21	2920.39	76.823	13642	3	974.13	1.67
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	27		AEQQLDKDSAIVPVYYYVNAR	494	21	6	46.2	b5b7y5y6y7y8	2442.25	74.040	8245	2	1221.63	6.80
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	28		SELYAKAEQQLDK	488	13	8	42.99	b4b5b7°b7y4y8*y8y9	1522.79	49.635	3019	3	508.27	13.07
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	29		NQGDLPAYSYTPPYTDGAKLVEPEWFK	333	27	5	19.6	b8y4°y4y5y7	3086.47	85.300	2042	3	1029.49	-3.64
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	30		LADPNTASPYASYLQYGHIANIDDII	125	26	1	16.79	y11	2835.37	83.885	3920	3	945.80	-3.96
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	31		ALDDHTFEVTLIS	163	12	1	8.91	y6	1347.63	86.787	1976	3	449.88	-11.59

P0A2A9 RS16_SALTY 30S ribosomal protein S16	1		IAHWVGQGATISDR	56	14	22	155.39	b2b3b4b6b7b10b13y1y2y3y4°y4y5°y5y7y8y9*y9y11°y11y12y14	1510.76	48.836	122587	3	504.26	-10.18
P0A2A9 RS16_SALTY 30S ribosomal protein S16	2		VGFFNPIASEKEEGTR	35	16	5	21.42	y5°y5y8y10°y10	1780.88	67.187	2543	2	890.94	-3.50
P0A2A9 RS16_SALTY 30S ribosomal protein S16	3		RPFYQVVVTDSR	13	12	3	21.92	b6y8y9	1466.75	44.544	6456	3	489.59	-18.06
P0A2A9 RS16_SALTY 30S ribosomal protein S16	4		VAALIK	70	6	2	23.13	b3y5	614.42	37.239	2808	1	614.42	-3.38
P0A2A9 RS16_SALTY 30S ribosomal protein S16	5		NGRFIER	28	7	3	35.01	b3b5b6	891.48	47.858	37710	2	446.25	5.00
P0A2A9 RS16_SALTY 30S ribosomal protein S16	6		EEGTRLDLDR	46	10	5	49.4	b5b7b8b9y4	1203.59	66.270	7558	2	602.30	-8.01
P0A2A9 RS16_SALTY 30S ribosomal protein S16	7		FIERVGFFNPIASEK	31	15	4	14.47	b10y7*y7y10	1753.93	55.233	4501	2	877.47	3.34
P0A2A9 RS16_SALTY 30S ribosomal protein S16	8		VGFFNPIASEKEEGTR	35	16	9	52.62	b3b4b9b10°b10y7y9y10°y10	1780.88	48.865	3409	3	594.30	-1.30
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1		VTLEPLER	25	8	8	53.37	b4y1y3y4°y4y5y6y8	956.53	52.715	67726	2	478.77	-10.40
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2	Carbamidomethyl+C(6)	LLVDACYSPVER	170	12	10	83.15	b2y2y5y6y7y8y9y10y11y12	1421.70	59.816	52157	2	711.36	-3.69
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3		LENWPPASIADE	317	12	15	70.6	b2b3b4°b4b5b7°b7b8°b8°b9°b9y1y8y9y12	1341.64	42.447	16379	2	671.32	5.46
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4		EGVQEDILEILLNLK	71	15	6	14.47	b2°b2b4b11*b11y3	1725.97	123.298	12757	2	863.49	3.68
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5		IHSEEDERPIGR	158	12	4	21.92	b2b3b4y7	1437.72	66.950	12558	2	719.36	5.86
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		LVIEMETNGTIDPEEAIR	200	18	4	16.78	b5b7y7y10	2029.97	89.541	74255	2	1015.49	-18.34
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		LVDIEQVSSTHAK	12	13	17	85.49	b3°b3b5°b5b6°b6°b6b10°b10y3y5°y5y7y8*y8y10°y10	1426.72	46.015	57388	3	476.25	-20.53
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8		MQGSVTEFLKPR	0	12	3	21.92	b10b11y10	1392.71	59.814	22422	3	464.91	-15.08
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9		TDLDK	195	5	2	11.25	b3°b3	591.30	101.757	14664	1	591.30	4.75
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	10	Carbamidomethyl+C(4)	SANCLK	265	6	1	11.88	y3	692.34	91.771	9959	1	692.34	-1.15
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	11		VEQR	191	4	3	21.87	b3y3*y3	531.29	30.728	2640	1	531.29	10.57
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	12		TPNLGK	291	6	1	11.88	y3	629.36	30.266	1646	1	629.36	-6.79
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	13		GYVPASTRIHSEEDERPIGR	150	20	9	47.92	b3b7b8b11°b11b12y3y6y11	2269.13	69.920	36478	3	757.05	-2.47
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	14		QPEVKEEKPEFDPILLRPVDDLELTVR	238	27	6	45.21	b8b9b10°b10b11b13	3204.67	60.613	4319	3	1068.90	-13.41

P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	15	Carbamidomethyl+C(6)	LLVDACYSPVERIAYNVEAAR	170	21	6	32.33	b6b7b8b10y7°y7	2409.19	114.678	2442	3	803.74	-13.38
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	16		GLSLGMRLNWPPASIADE	310	19	7	26.64	b10°b10y5y8°y8y9y12	2056.03	89.620	1808	3	686.01	6.29
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	17	Phosphoryl STY(7)	LVIEMETNGTIDPEEAIIR	200	18	8	36.75	b3y7°y7y8°y8y10y11*y11	2110.00	74.128	1528	2	1055.50	13.31
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	18	Oxidation+M(5)	LVIEMETNGTIDPEEAIIR	200	19	6	30.43	b5b12y4y8y10y11	2202.11	54.329	4757	4	551.28	0.44
P29768 NANH_SALTY Sialidase	1		SDISLYAHNLYSGEVK	309	16	9	39.43	b1b2b3b7b10b12y4y10*y10	1795.90	72.360	39468	2	898.45	5.64
P29768 NANH_SALTY Sialidase	2		HNTASDQSFIDTAAAR	56	16	5	13.71	b2b3°b3b7y6	1704.79	42.504	7462	3	568.93	-4.01
P29768 NANH_SALTY Sialidase	3	Carbamidomethyl+C(6)	VMDPTCIVANIQGR	97	14	8	24.88	b2b10°b10y2y9y11y12°y12	1573.77	68.952	5024	2	787.39	-10.47
P29768 NANH_SALTY Sialidase	4		IAIYNDR	83	7	10	43.25	b2b4b5°b5b6b7°b7y2y6°y6	864.45	30.748	3632	1	864.45	-4.94
P29768 NANH_SALTY Sialidase	5		LVFPVQMVR	188	9	5	25.47	b6°b6b7°b7y8	1088.61	32.008	12288	3	363.54	-18.28
P29768 NANH_SALTY Sialidase	6		APDTDWDLVLYK	134	12	3	17.94	b5b11y9	1435.72	69.968	7389	2	718.37	9.27
P29768 NANH_SALTY Sialidase	7		NGTISAMLGGVGSGLQLNDGK	167	21	4	11.55	b13°b13b15y7	1989.04	74.981	7060	2	995.02	17.92
P29768 NANH_SALTY Sialidase	8		TWGAAYR	126	6	1	11.88	y5	753.36	32.871	4498	2	377.18	-12.80
P29768 NANH_SALTY Sialidase	9		LVAAHSSAQNK	292	11	4	28.77	b6b9y3y5	1125.61	39.155	3949	2	563.31	7.81
P29768 NANH_SALTY Sialidase	10		HNTASDQSFIDTAAARSTDGGK	56	22	3	17.85	y4y10y14	2250.07	55.398	5497	4	563.27	13.24
P29768 NANH_SALTY Sialidase	11		GNTIVGSGSGGTTKYFR	20	17	3	13.09	b6y6y10	1701.85	80.553	3356	2	851.43	-3.44
P29768 NANH_SALTY Sialidase	12	Carbamidomethyl+C(19)	LIDDFYPKVGNASGAGYSCLSYR	325	23	4	17.57	b6b8°b8b10	2553.25	125.750	1966	4	639.07	15.11
P29768 NANH_SALTY Sialidase	13	Carbamidomethyl+C(9)	LSRVMDPTCIVANIQGR	94	17	4	13.09	b7°b7y6y11	1930.00	103.617	1584	3	644.01	2.28
P29768 NANH_SALTY Sialidase	14	Phosphoryl STY(8)	NVDKETLYVVYEANGSIEFQDLSR	349	24	9	42.54	b7b8b13_H3PO4 b13y5°y5y6y7y11°y11	2869.35	80.139	19498	3	957.12	8.93
P29768 NANH_SALTY Sialidase	15	Phosphoryl STY(7)	GNTIVGSGSGGTTK	20	14	5	15.39	b3°b3y7°y7y9	1315.57	42.522	4001	2	658.29	-9.74
P29768 NANH_SALTY Sialidase	16	Phosphoryl STY(5)	NGTISAMLGGVGSGLQLNDGK	167	21	7	23.49	b3°b3b6y5y11°y11y12	2068.98	95.516	1946	3	690.33	6.84
P29768 NANH_SALTY Sialidase	17	Oxidation+M(7)	NGTISAMLGGVGSGLQLNDGK	167	21	14	62.52	b4°b4b8b9°b9b10b11°b11 b13°b13b14y4°y4y13	2005.02	46.013	4165	3	669.01	7.61
P29768 NANH_SALTY Sialidase	18		IDTAAAR	65	7	2	7.74	b5°b5	717.40	42.462	3419	2	359.20	12.34
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		VTDIEPLVGGETESSVR	171	18	11	46.96	b2b3°b3b5b6b7y9y13y14°y14y18	1862.96	69.882	23442	2	931.98	5.24
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		AVLPGMVER	115	9	10	47.52	b1y2°y2y4°y4y5y6°y6y7°y7	971.53	53.500	19727	2	486.27	-9.11
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		AAIEEMMASLPAQWR	58	15	6	32.2	b4b5°b5y4y5*y5	1703.84	91.501	17068	2	852.43	12.04
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4		TYENTTALTPEITEAVWWVATL PAHVNIINTVEMMPVTQSFAGLSV HR	199	48	4	15.07	b13b23°b23y4	5340.60	136.522	13312	4	1335.91	-6.22
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		DELGENVLT AQLDVR	41	15	5	31	b8°b8b9b10b15	1671.85	42.460	4078	2	836.43	-3.29
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		TDLHGTA VR	162	9	4	37.97	b4b6y5y8	969.49	56.805	14708	2	485.25	-19.45

[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		ASVEDWETMIDTNNK	93	15	6	14.47	b4°b4y4°y4y6*y6	1752.81	72.639	6793	2	876.91	17.83
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	8		FVENGHKVIATGR	19	13	4	24.01	b4b7b8*b8	1427.80	59.308	13480	2	714.40	14.11
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	9		NRGHIINIGSTAGSWPYAGGNVYG ATK	124	27	4	12.37	b4b14y5y11	2761.40	125.401	1633	3	921.14	8.84
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	10	Phosphoryl STY(4)	VIATGRR	26	7	3	35.01	b4y3y6	852.43	30.670	9289	2	426.72	-11.89
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	11	Carbamidomethyl+C(14) ;Phosphoryl STY(8)	IVLVTGATAGFGECIARR	1	18	6	24.05	b9b11y6y8y10°y10	1970.99	79.299	3061	2	986.00	4.52
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	12	Carbamidomethyl+C(15) ;Phosphoryl STY(9)	MIVLVTGATAGFGECIARR	0	19	9	43.06	b9°b9b14y4y6y7y9°y9y10	2102.05	70.920	2351	5	421.22	13.94
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	13	Oxidation+M(9)	ASVEDWETMIDTNNK	93	15	7	20.16	b3°b3b10y4*y4y9*y9	1768.75	42.455	23082	4	442.94	-9.32
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	14	Carbamidomethyl+C(15) ;Oxidation+M(1)	MIVLVTGATAGFGECIAR	0	18	4	21.61	b15y7y8y14	1881.95	95.535	4364	2	941.48	-1.62
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	15	Oxidation+M()	AAIEEMMASLPAQWR	58	15	8	23.8	b12y3*y3y11°y11*y11y13° y13	1719.81	72.459	4100	3	573.94	-6.96
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	1		YENLFAQLNDR	3	11	18	87.76	b1b2b4b7°b8°b8b10b11°b1 ly3°y3y5y6°y6y7*y7y10y1 1	1382.68	59.769	51374	2	691.84	6.27
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	2	Carbamidomethyl+C(11)	AFAAGVTPAQCFEMLALIR	70	19	6	28.4	b2b3b6b8b11y12	2066.06	102.191	10780	2	1033.53	2.48
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	3		QVASYGR	164	7	8	35.01	b2b4°b4°b4y2y4y6°y6	780.40	38.040	10098	2	390.70	-5.40
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	4		EGAFVPFVTLGDPGIEQSLK	15	20	6	11.82	b2°b2b7°b7y7y11	2104.10	85.662	7668	3	702.04	3.13
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	5		HPTIPIGLLMYANLVFNNGIDAFY AR	91	26	5	21.36	b20y3y5y8y10	2920.54	42.491	4701	6	487.60	7.44
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	6	Carbamidomethyl+C(1)	CEQVGVDSVLVADVPVEESAPFR	117	23	4	22.67	b10b11y8y13	2502.23	84.125	2294	3	834.75	3.90
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	7		SGVTGAENR	179	9	4	37.97	b4b5y5y6	890.43	45.982	6340	1	890.43	-7.40
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	8		AGAAGAISGSAIVK	225	14	3	23.96	b3b5b9	1172.67	46.798	6234	3	391.56	9.06
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	9		IIDLIDAGADALELGVFSDPLAD GPTIQNANLR	35	35	4	11.67	b12b14y11y15	3605.86	112.454	5604	3	1202.63	-2.17
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	10		EYHAAPALQGFGISSPEQVSAAVR	201	24	4	19.8	b18y12y14y15	2485.19	136.848	1531	2	1243.10	-21.61
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	11		MERYENLFAQLNDR	0	14	9	40.6	b8y3°y3y5°y5y7y11°y11*y 11	1798.83	48.835	10465	3	600.28	-12.21
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	12		ERYENLFAQLNDR	1	13	4	16.52	b8y6*y6y10	1667.82	97.736	2398	3	556.61	2.20
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	13	Carbamidomethyl+C(11) ;Oxidation+M(14)	AFAAGVTPAQCFEMLALIR	70	19	5	31.54	b9b10°b10b11y9	2082.07	78.073	4725	3	694.69	7.15
[P00929]TRPA_SALTY Tryptophan synthase alpha chain	14		FAQLNDR	7	7	1	7.24	b3	863.43	59.833	4607	1	863.43	-9.40
[P67179]YEBC_SALTY UPF0082 protein yebC	1		VRDALEAAGLK	181	11	11	56.5	b9°b9b10°b10y1y2y4y6y7y 8y11	1142.65	32.894	45485	2	571.83	-5.34

[P67179 YEBC_SALTY UPF0082 protein yebC	2		ADMDAETAPK	205	10	5	29.11	b2y5y7y8y10	1048.45	25.921	15227	2	524.73	-7.34
[P67179 YEBC_SALTY UPF0082 protein yebC	3		LGGGDPDANPR	37	11	11	47.47	b1b5y1y2y4*y5y6y8*y8y10y11	1068.50	23.637	14346	2	534.75	-5.03
[P67179 YEBC_SALTY UPF0082 protein yebC	4		ALANNMTR	55	8	4	42.12	b3b5b6y6	890.46	70.990	6333	2	445.74	13.09
[P67179 YEBC_SALTY UPF0082 protein yebC	5		ALANNMTRDTLNR	55	13	9	46.3	b2b4b5b6b11y8*y8y12y13	1489.76	54.266	5005	2	745.39	5.98
[P67179 YEBC_SALTY UPF0082 protein yebC	6		AAQDAK	14	6	5	34.38	b5y3y4*y4*y4	603.30	61.909	16310	1	603.30	-8.90
[P67179 YEBC_SALTY UPF0082 protein yebC	7		DALEAAGLK	183	9	5	37.97	b3b8*b8y4y7	887.50	46.743	5509	2	444.25	13.55
[P67179 YEBC_SALTY UPF0082 protein yebC	8		TVAEVR	108	6	1	11.88	b3	674.39	41.645	3845	1	674.39	6.52
[P67179 YEBC_SALTY UPF0082 protein yebC	9	Carbamidomethyl+C(1)	CGGNLGTGDSVAYLFSK	119	17	3	13.09	b5y12y14	1745.84	75.373	2775	2	873.42	14.26
[P67179 YEBC_SALTY UPF0082 protein yebC	10		ADSAEVSMPSTK	192	13	11	44.75	b4*b4b9*b9b10*b10y4*y4y6y10*y10	1335.66	46.825	2664	2	668.33	8.77
[P67179 YEBC_SALTY UPF0082 protein yebC	11		GDEDTIMEAALEAGAEDVVTYDDGAIDVYTAWEEMGK	144	37	3	17.76	y4y10y12	3979.79	91.663	2149	3	1327.27	15.03
[P67179 YEBC_SALTY UPF0082 protein yebC	12		WANTRHR	6	7	5	35.01	b4*b4b5b6*b6	940.49	31.985	3666	1	940.49	7.01
[P67179 YEBC_SALTY UPF0082 protein yebC	13		AGHSKWANTR	1	10	6	33.37	b3y3*y3*y3y7y8	1127.55	48.782	2684	2	564.28	-14.62
[P67179 YEBC_SALTY UPF0082 protein yebC	14		KAAQDAK	13	7	6	32	b5*b5b6*b6y6*y6	731.40	25.489	2069	2	366.20	-12.43
[P67179 YEBC_SALTY UPF0082 protein yebC	15	Carbamidomethyl+C(6)	HAFSKCGNLTGDSVAYLFSK	114	22	6	32.03	b4b10b11b12*b12y11	2316.12	136.356	2018	2	1158.56	5.17
[P67179 YEBC_SALTY UPF0082 protein yebC	16	Oxidation+M(6)	ALANNMTR	55	8	4	49.9	b3y3y5y7	906.43	90.664	5495	1	906.43	-12.79
[P67179 YEBC_SALTY UPF0082 protein yebC	17	Oxidation+M(6)	ALANNMTRDTLNR	55	13	5	23.58	b9b11y5y10*y10	1505.75	74.141	3871	2	753.38	2.03
[P67179 YEBC_SALTY UPF0082 protein yebC	18		ALEAAGLK	184	8	4	19.28	b4*b4b5*b5	772.45	32.908	19631	2	386.73	-10.67
[P67179 YEBC_SALTY UPF0082 protein yebC	19		RDALEAAGLK	182	10	5	26.73	b3*b3b7b8*b8	1043.58	32.877	9125	2	522.29	-6.32
[P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	1	Carbamidomethyl+C(10)	VAEVIDIPFCVAGGIR	68	16	4	20.25	b1b3b4y9	1715.91	91.484	13785	2	858.46	-3.91
[P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	2		VTQWETLDWVQEVQQR	153	16	7	30.5	b2b11y3y5y6y11y16	2045.03	85.203	12759	2	1023.02	8.00
[P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	3	Carbamidomethyl+C(5)	FGVQCIVVGIDTWFDATGK	119	20	9	41.64	b5b13y6y11*y11y12y13*y13y18	2228.08	113.710	4977	2	1114.54	4.16
[P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	4		DADVDGALAASVFHK	221	15	3	14.47	b4b13y3	1515.71	58.458	4421	2	758.36	-19.41
[P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	5		GAGEIVLNMMNQDGVR	169	16	4	18.85	b4b14y5y8	1703.83	58.600	2716	2	852.42	5.73
[P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	6		NGYDLTQLK	185	9	4	50.53	b3b5b7b8	1051.52	59.762	2708	2	526.26	-19.97
[P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	7		YHVNQYTGDENRTR	139	14	3	15.39	b4b8y13	1752.82	80.453	6812	3	584.95	9.40

P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	8		RYADEGADELVFYDITASSDGR	37	22	9	19.56	b4°b4b6°b6b13°b13y6y9°y9	2450.10	118.812	2251	3	817.37	-5.48
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	9		NHEIIGDIVPLAKR	24	14	3	15.39	b4b6y4	1574.92	31.404	1910	2	787.96	13.02
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	10	Carbamidomethyl+C(3)	DVCRVPLIASGGAGTMEHFLEAFR	197	24	3	11.05	b6y7y10	2633.26	93.439	1766	2	1317.14	-12.70
Q8ZP54 RNB_SALTY Exoribonuclease 2	1		GEAIARPQEDITQQMAER	516	18	4	19.99	b6y5y6y18	2042.98	136.163	21319	2	1022.00	-3.88
Q8ZP54 RNB_SALTY Exoribonuclease 2	2		RELDAQPSGFILDSR	453	14	18	90.38	b2°b2b5°b5b7°b7*b7b9b10b11y5°y5y6y8y9*y9y10y14	1590.78	45.987	20355	2	795.89	-5.83
Q8ZP54 RNB_SALTY Exoribonuclease 2	3		AFTNYLPGFNIPMLPR	248	16	5	21.42	b6b11°b11b14y2	1850.96	68.885	5110	2	925.99	0.26
Q8ZP54 RNB_SALTY Exoribonuclease 2	4		ERESAEPEELIEPFLTR	68	17	6	22.21	b2b3b11°b11b12y10	2045.00	68.567	3800	3	682.34	-6.80
Q8ZP54 RNB_SALTY Exoribonuclease 2	5	Carbamidomethyl+C(23)	AFTNYLPGFNIPMLPRELSDDLCS LR	248	26	3	10.93	b3b6y12	3039.54	110.349	2898	3	1013.85	10.60
Q8ZP54 RNB_SALTY Exoribonuclease 2	6		MIIAADGTIDDDIAFFAATIESK	285	23	4	17.57	b2b3b8b12	2428.20	79.497	2810	3	810.07	3.52
Q8ZP54 RNB_SALTY Exoribonuclease 2	7	Carbamidomethyl+C(12)	IVEESMIAANLCAAR	387	15	5	20.16	b4b14y6y13*y13	1647.83	96.664	2512	3	549.95	3.41
Q8ZP54 RNB_SALTY Exoribonuclease 2	8		HNLEKEAPNGVATEMLDEGLER	167	22	4	11.33	b2b4b9y9	2452.18	45.342	1878	6	409.54	-0.50
Q8ZP54 RNB_SALTY Exoribonuclease 2	9		SYFIPPPQMK	42	10	7	52.41	b3b6°b6b7b9y4*y4	1207.62	32.038	90777	2	604.31	-0.71
Q8ZP54 RNB_SALTY Exoribonuclease 2	10	Carbamidomethyl+C(18)	THGLHVDAAEEVLTLEGFCK	432	19	4	18.91	b10y4y10y12	2155.02	103.143	20484	3	719.01	-11.56
Q8ZP54 RNB_SALTY Exoribonuclease 2	11	Carbamidomethyl+C(2)	ICLSR	342	5	1	11.25	y4	648.35	53.495	11096	1	648.35	-7.25
Q8ZP54 RNB_SALTY Exoribonuclease 2	12		DVGDWLYAR	543	9	3	25.47	b4y6y7	1094.51	50.255	10364	2	547.76	-16.51
Q8ZP54 RNB_SALTY Exoribonuclease 2	13		LGFGIYNVHTGFDPANADALAAL LK	407	25	4	17.2	b4b7°b7b15	2588.30	61.918	6306	3	863.44	-20.66
Q8ZP54 RNB_SALTY Exoribonuclease 2	14		EAPNGVATEMLDEGLER	172	17	5	20.96	b3b9b11°b11y14	1830.81	76.691	5605	3	610.94	-21.87
Q8ZP54 RNB_SALTY Exoribonuclease 2	15	Carbamidomethyl+C(7)	ELSDDLCSLR	264	10	10	71.11	b3°b3b4b9y4y6°y6y7y8°y8	1207.55	37.236	2774	3	403.19	-7.68
Q8ZP54 RNB_SALTY Exoribonuclease 2	16		VMHGDR	53	6	1	11.88	y3	714.34	49.649	2365	1	714.34	12.99
Q8ZP54 RNB_SALTY Exoribonuclease 2	17	Carbamidomethyl+C(10)	ANEVRPALACR	274	11	6	22.75	b5°b5°b5b6°b6y4	1256.68	31.428	1537	3	419.57	22.44
Q8ZP54 RNB_SALTY Exoribonuclease 2	18	Carbamidomethyl+C(2)	ICLSRSEWR	342	9	3	25.47	b4b8y3	1206.61	41.235	20404	3	402.88	5.87
Q8ZP54 RNB_SALTY Exoribonuclease 2	19		LQLTVAIADPTAWIAEGSKLDNTA K	221	25	3	20.51	b3y5y6	2626.37	46.790	8450	6	438.57	-13.57
Q8ZP54 RNB_SALTY Exoribonuclease 2	20	Carbamidomethyl+C(16)	IANRIVEESMIAANLCAAR	383	19	5	26.64	b11y6y8y9y11	2102.06	83.344	7819	3	701.36	-10.80
Q8ZP54 RNB_SALTY Exoribonuclease 2	21		AGTNTRFAAEIIDVSR	557	16	5	31.96	b6b7°b7b8y10	1720.87	59.817	6580	3	574.30	-14.97
Q8ZP54 RNB_SALTY Exoribonuclease 2	22		AVIKGEAIARPQEDITQQMAER	512	22	4	21.21	y3y9°y9y10	2454.29	80.490	5134	3	818.77	4.08
Q8ZP54 RNB_SALTY Exoribonuclease 2	23		KYGDMINHR	500	9	6	58.77	b3b4b6b7°b7b8	1133.54	32.042	4572	2	567.27	-8.62
Q8ZP54 RNB_SALTY Exoribonuclease 2	24		HNLEKEAPNGVATEMLDEGLER	167	22	3	11.33	b10y5y8	2452.21	81.403	3924	3	818.07	12.84

Q8ZP54 RNB_SALTY Exoribonuclease 2	25		LNRMAER	536	7	3	35.01	b6y3y6	889.47	23.201	3300	2	445.24	0.21
Q8ZP54 RNB_SALTY Exoribonuclease 2	26	Carbamidomethyl+C(43)	LGFGIYNVHTGFDPANADALAAL LKTHGLHVDAAEVLTLLEGFCK	407	44	10	44.02	b6b11*b11y3y4y6°y6y7y8° y8	4724.32	136.338	3109	4	1181.84	-12.71
Q8ZP54 RNB_SALTY Exoribonuclease 2	27	Carbamidomethyl+C(12)	IVEESMIAANLCAARVLR	387	18	5	45.85	b5b6b7b8b14	2016.07	76.742	2556	3	672.70	-0.91
Q8ZP54 RNB_SALTY Exoribonuclease 2	28		DVGDWLYARFLNDK	543	14	3	15.39	b8y3y12	1711.84	83.343	2201	2	856.42	-3.07
Q8ZP54 RNB_SALTY Exoribonuclease 2	29		FAAEIIDVSRGGMR	563	14	5	21.71	b7°b7b9y8y11	1521.77	53.535	2086	2	761.39	-10.27
Q8ZP54 RNB_SALTY Exoribonuclease 2	30		GEAIARPQEDITQQMAERR	516	19	3	12.16	b3b12y4	2199.12	86.739	2058	2	1100.07	14.10
Q8ZP54 RNB_SALTY Exoribonuclease 2	31	Carbamidomethyl+C(7); Carbamidomethyl+C(20)	ELSDDLCSLRANEVRPALACR	264	21	3	18.19	b4b9b11	2445.16	74.921	1646	3	815.73	-14.88
Q8ZP54 RNB_SALTY Exoribonuclease 2	32		ATEKGFGFLEVDAQK	27	15	9	29.49	b3°b3b5b8°b8y11°y11y13° y13	1639.82	71.338	1557	2	820.41	-9.08
Q8ZP54 RNB_SALTY Exoribonuclease 2	33	Phosphoryl STY(13)	RELDAQPSGFLDSR	453	14	3	23.17	b4b11b12	1670.73	87.411	4093	3	557.58	-11.11
Q8ZP54 RNB_SALTY Exoribonuclease 2	34	Oxidation+M(15)	HNLEKEAPNGVATEMLDEGLER	167	22	6	31.31	b14y5y7y8y13y20	2468.14	67.872	7153	2	1234.58	-11.87
Q8ZP54 RNB_SALTY Exoribonuclease 2	35	Oxidation+M(15)	GEAIARPQEDITQQMAER	516	18	5	24.18	b6b7y7y10°y10	2059.00	67.465	2662	3	687.00	5.10
Q8ZP54 RNB_SALTY Exoribonuclease 2	36	Oxidation+M(9)	SYFIPPPQMK	42	10	10	78.89	b3°b3b5b7y3y4y5*y5y6*y 6	1223.60	40.543	2265	3	408.54	-7.68
P05989 ILVC_SALTY Ketol-acid reductoisomerase	1		GFGVPTLIAVHPENDPQGEGMAIA K	167	25	11	48.01	b2b3b4y3y7y8y10y14°y14y 21y25	2548.29	78.008	44052	3	850.10	0.29
P05989 ILVC_SALTY Ketol-acid reductoisomerase	2		QGGITLMMDR	266	10	5	41.15	b7°b7y3y5y8	1121.55	61.801	25194	2	561.28	3.48
P05989 ILVC_SALTY Ketol-acid reductoisomerase	3		ANYFNTLNL	1	10	5	22.12	b7b10y3y6y10	1225.63	68.818	24288	2	613.32	0.20
P05989 ILVC_SALTY Ketol-acid reductoisomerase	4		LIQFGWETITEALK	252	14	3	15.39	b3b7y3	1648.89	102.435	21410	2	824.95	-3.18
P05989 ILVC_SALTY Ketol-acid reductoisomerase	5		AYALSEQLK	284	9	8	33.25	b1b2b5b7b8°b8y2y9	1022.54	48.811	8073	2	511.78	-6.63
P05989 ILVC_SALTY Ketol-acid reductoisomerase	6		AYALSEQLKEIMAPLFQK	284	18	7	19.85	b2b8°b8b10b12°b12y7	2080.10	105.587	6014	3	694.04	-8.33
P05989 ILVC_SALTY Ketol-acid reductoisomerase	7		DGAALGYSHGFNIVEVGEQIR	123	21	4	11.55	b3b5y12*y12	2232.10	88.859	2728	3	744.71	-1.75
P05989 ILVC_SALTY Ketol-acid reductoisomerase	8		AWAAATGGHR	192	10	6	51.61	b2b4b6b9y5y8	997.49	101.286	2538	1	997.49	-3.85
P05989 ILVC_SALTY Ketol-acid reductoisomerase	9		TAFETAPQYEGK	336	12	7	38.89	b4b6y2y3y5y8*y8	1341.62	28.370	2158	3	447.88	-11.92
P05989 ILVC_SALTY Ketol-acid reductoisomerase	10	Carbamidomethyl+C(6)	VVIVGCGAQGLNQLNMR	39	18	3	19.74	y9y12y17	1885.98	72.845	1810	2	943.49	0.78
P05989 ILVC_SALTY Ketol-acid reductoisomerase	11		AGVLESSFVAEVK	202	13	4	16.52	b9°b9b11y3	1335.70	37.159	1612	2	668.35	-12.34
P05989 ILVC_SALTY Ketol-acid reductoisomerase	12		LSNPAK	276	6	2	11.88	y5*y5	629.37	38.015	20314	1	629.37	14.93
P05989 ILVC_SALTY Ketol-acid reductoisomerase	13		SVQPLMK	116	7	6	46.26	b3°b3°b3b4y4y5	802.43	37.160	8008	2	401.72	-20.76
P05989 ILVC_SALTY Ketol-acid reductoisomerase	14		LLTWR	326	5	1	11.25	y4	688.42	55.130	4161	2	344.72	14.98
P05989 ILVC_SALTY Ketol-acid reductoisomerase	15		DSGLDISYALR	57	11	7	60.48	b4b7b8b9°b9b10y9	1209.62	46.808	3152	2	605.31	6.46
P05989 ILVC_SALTY Ketol-acid reductoisomerase	16		LVAEGTDPAYAEK	239	13	6	49.31	b8b11y6y7y11y12	1363.66	47.910	2696	2	682.33	-12.98

[P05989]ILVC_SALTY Ketol-acid reductoisomerase	17		VGTYEELIPQADLVVNLTDPDKQHS DVVR	88	28	8	36.94	b11y5y6y10y12*y12y13y20	3135.61	82.449	32187	4	784.66	-6.77
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	18	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21))	SDLMGEQTILCGMLQAGSLLCFD KLVAEGTDPAYAEK	215	37	6	20.28	b3b5y6*y6y7y9	4031.92	118.517	15225	3	1344.64	1.57
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	19		ANYFNTLNLRQQLAQLGK	1	18	4	19.85	b9b12b15y3	2092.13	90.552	9512	2	1046.57	-2.10
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	20	Carbamidomethyl+C(7)	KVVIVGCGAQGLNQGLNMR	38	19	3	21.34	y3y9y10	2014.09	59.808	4660	2	1007.55	9.09
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	21		AWAAATGGHRAGVLESSFVAEV K	192	23	7	13.64	b7°b7b10y4°y4y8°y8	2314.21	46.009	1538	6	386.54	7.17
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	22	Phosphoryl STY(5)	AYALSEQLK	284	9	3	25.47	b3b7y4	1102.52	29.651	2772	2	551.77	13.73
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	23	Phosphoryl STY(10)	LIQFGWETITEALK	252	14	3	15.39	b10y3y10_HPO3 y10	1728.85	69.880	2324	2	864.93	-0.14
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	24	Oxidation+M()	GVLMIAMVK	357	9	3	25.47	b3b7y6	977.56	62.621	25821	2	489.28	7.87
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	25	Oxidation+M(6)	SVQPLMKDGAALGYSHGFNIVEV GEQIR	116	28	8	21.74	b3*b3b8°b8b9b11y7°y7	3031.56	136.347	5107	3	1011.19	10.23
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	26		PTLIAVHPENDPQGEGMAIAK	171	21	2	12.73	b11b14	2188.10	78.058	3319	2	1094.55	-4.46
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	1	Carbamidomethyl+C(1)	CTWVASDFDALIPSLK	66	16	3	13.71	b11b14y4	1822.92	99.119	22161	2	911.96	9.78
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	2		QQEIAFSDK	99	9	4	33.25	y4y5y8*y8	1065.52	63.288	16106	2	533.27	2.41
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	3		IGTDTTYAPFSSK	29	13	12	59.77	b2b5b9y3y4°y4y5°y5y11°y11y12y13	1387.68	53.538	15015	2	694.34	1.23
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	4		EYAFAGPSVKDK	198	12	7	25.14	b2b3b10b11b12°b12y12	1311.64	59.812	7561	2	656.32	-14.33
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	5		QPAGKEYAFAGPSVK	193	15	3	22.55	b9b11b13	1549.82	75.533	6994	2	775.41	11.74
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	6		IGTDTTYAPFSSKDAK	29	16	3	13.71	b6y3y6	1701.85	56.815	2425	2	851.43	7.96
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	7		ALTELK	234	6	1	11.88	b4	702.41	42.385	7051	1	702.41	-7.65
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	8		YFGDGTGVGLR	211	11	5	44	y3y7°y7y8y10	1141.55	49.585	4593	2	571.28	-10.69
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	9		HVGVLQGSTQEAYANDNWR	134	19	8	39.48	b4b10b12°b12*b12b13°b13b14	2145.05	70.770	2310	2	1073.03	19.35
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	10		DDTELK	223	6	2	23.13	y4y5	720.35	33.872	1685	1	720.35	10.85
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	11		LDAALQDEVAASEGFLKQPAGK	176	22	4	16.79	b3b7b21y5	2258.19	85.859	8106	3	753.40	12.22
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	12		RQQEIAFSDK	98	10	8	43.83	b4*b4b8°b8b9°b9y4y7	1221.62	69.944	6039	2	611.31	-0.90

P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	13		HVGVLQGSTQEAYANDNWRTK	134	21	4	17.4	b4y9y12y14	2374.13	86.982	3425	2	1187.57	-8.95
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	14		IGTDTTYAPFSSKDAK	29	16	3	21.42	b3b5b10	1701.83	103.516	1673	2	851.42	-3.87
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	15		QQEIAFSDKLYAADSR	99	16	4	20.25	b13*b13b14y10	1841.90	48.832	1654	2	921.45	-2.78
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	16		ALTELQRQDGYDK	234	13	6	26.23	b9°b9*b9y3y6y7	1509.73	42.417	1606	2	755.37	-13.91
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	17	Phosphoryl STY()	IGTDTTYAPFSSKDAK	29	16	9	40.4	b6°b6b8b9°b9b10_H3PO4 b10°b10y3y10	1781.81	42.446	1670	3	594.61	10.35
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	1		GSQVYIEGQLR	74	11	7	31.78	b3b8y1y2y5*y5y6	1249.66	31.952	36186	3	417.23	6.84
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	2		YTTEINVPQIGGVMMQLGGR	97	20	7	21.52	b7°b7b10b14y4y10y20	2164.11	97.268	27285	2	1082.56	9.70
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	3		VILVGNLQDPEVR	8	14	11	64.07	b3y2y4y7y8y9°y9y10*y10y11*y11	1508.84	66.351	13272	2	754.92	-1.70
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	4		YMPSGGAVANLTLATSESWR	22	20	3	11.82	b4y4y17	2111.01	72.774	9043	3	704.34	-7.98
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	5		WTDQSGQER	88	9	5	25.47	b3y2y4°y4y7	1106.47	21.411	3421	2	553.74	-11.03
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	6		YMPSGGAVANLTLATSESWRDK	22	22	15	71.6	b3b4b11b12b13°b13b14°b14°b14y4y6°y6y8y9°y9	2354.16	60.595	12862	3	785.39	8.61
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	7		EQTEWHRVVMFGK	50	13	3	21.29	b10b11y12	1646.81	136.730	3974	1	1646.81	-0.30
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	8		VILVGNLQDPEVRYMPSGGAVANLTLATSESWR	8	34	3	17.3	y5y8y11	3600.80	119.547	2994	4	900.96	-13.36
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	9	Phosphoryl STY(8)	LAEVAGEYLRK	63	11	3	19.74	b6y5_H3PO4 y5y7_H3PO4 y7	1328.66	67.900	9635	2	664.83	2.66
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1	Carbamidomethyl+C(7)	LWVNPDCLGK	719	10	6	49.4	b6y4y6y7y8y10	1201.60	61.312	75009	2	601.31	-0.61
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	6	13.71	b6y1y5°y7y10y16	1834.94	100.251	38382	2	917.98	4.92
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	3		QAGIDLLPVGDFAWYDHVLTTSLLGNVPAR	52	31	15	53.9	b5°b5°b5b6°b6b7°b7b14y3y5y6y7*y7y24y31	3351.78	119.961	37151	3	1117.93	1.24
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	4		LAAITAQDSQRENPYEVR	395	18	12	48.97	b3b5b8°b8b9°b9b11y2y5°y5y14y16	2061.02	47.957	21871	3	687.68	-9.36
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	5		APTGEPA AAAAEMTK	103	14	10	83.69	b6b7b8b11°b11b12b13y7y9y12	1344.64	39.745	16464	2	672.83	-1.45
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	6		LAAITAQDSQR	395	11	7	30.2	b2b3y2y3y7y8y11	1173.62	34.549	13899	2	587.31	-0.73
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	7		GNLDANHYR	449	9	3	25.47	b4b7y6	1059.49	26.601	1948	2	530.25	-5.07
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8		AQESYWAGNTTREALAVGR	21	20	5	21.24	b3°b3b4b12y20	2193.09	51.326	1806	3	731.70	-7.68

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	9	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETR	315	22	3	20.08	b10b11y8	2441.24	104.722	39159	4	611.07	-2.50
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	10		YAQSLTDKPKVK	538	11	3	26.73	b7b9b10	1249.70	61.268	34848	2	625.35	18.85
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	11		GQQFR	132	5	1	11.25	y4	635.33	42.554	19897	1	635.33	1.92
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	12		WFNTNYHYIYPEFSK	117	15	4	14.47	b9y6y9°y9	1944.89	52.794	17999	2	972.95	-19.39
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	13		AQESYWAGNTTR	21	12	9	55.67	b4°b4y6y7*y7y8y9°y9y11	1383.63	41.594	13771	2	692.32	0.53
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	14		ADLTEK	298	6	3	34.38	b3y4y5	676.35	32.955	5330	1	676.35	-1.62
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	15		SDWDAYLEWGVAEFR	611	15	6	36.3	b14y4y8y9°y9y10	1843.85	60.589	4375	3	615.29	13.04
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	16		GWPETR	731	6	3	23.13	b5y5°y5	745.36	59.792	2409	1	745.36	-8.19
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	17		DEVADLEAAGIGIIQIDEPALR	582	22	7	27.39	b7b9°b9b12b20y6y9	2308.16	46.736	2392	6	385.53	-18.19
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	18		LDTEVK	337	6	1	11.88	b4	704.39	22.398	2229	1	704.39	10.74
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	19		VHNAAVEK	386	8	3	30.87	b5b7y4	867.48	62.580	2181	2	434.24	16.53
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	20		DALNSGETAALEEWSAPIQAR	360	21	4	11.55	b6°b6b10y13	2229.09	80.709	2039	3	743.70	4.93
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	21		FKLPAPWPTTTIGSFQPTTEIR	420	21	6	25.72	b14y3y5y7*y7y13	2391.26	89.509	22732	3	797.76	-6.53
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	22		KGNLDANHYR	448	10	4	33.37	b5b6b9y4	1187.60	41.645	4831	2	594.30	4.63
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	23		TRGWPETR	729	8	5	43.88	b6b7y5°y5y7	1002.50	69.044	4343	1	1002.50	-9.19
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	24		ARHWEQQK	44	8	4	30.87	b3b7y3*y3	1082.55	26.528	3890	3	361.52	1.69
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	25		GRAPTGEPAAAAEMTK	101	16	6	18.85	b11°b11b13°b13y4y9	1557.79	40.621	2131	2	779.40	11.13
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	26	Phosphoryl STY(8)	DALNSGETAALEEWSAPIQARR	360	22	3	20.08	b6b7y11	2465.17	95.475	24357	2	1233.09	14.56
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	27	Carbamidomethyl+C(11) ;Phosphoryl STY(8)	GMLTGPVTILCWSFPR	549	16	4	22.25	b4b7b10_H3PO4 b10y7	1914.91	54.301	1541	2	957.96	12.18

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	28	Phosphoryl STY(11)	LPAPWPTTTIGSFPQTTEIR	422	19	3	19.94	b12b13y7	2196.07	81.725	1530	2	1098.54	1.22
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	29	Oxidation+M(12)	APTGEPA AAAEMTK	103	14	4	15.39	b5y7°y7y9	1360.64	26.624	40399	2	680.83	1.88
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	30	Carbamidomethyl+C(11);Oxidation+M(2)	GMLTGPVTILCWSFPR	549	16	4	13.71	b11°b11y5y13	1850.93	64.199	3983	3	617.65	-1.65
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	31		LAAITAQDSQ	395	10	1	7.24	y5	1017.52	34.539	4586	2	509.26	-1.62
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1		GGDNYSDKPAPLGGGGAR	151	18	11	86.41	b2y5y6y7y8y10y11y12y13°y13y18	1688.77	33.854	84722	3	563.60	-14.31
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2	Carbamidomethyl+C(3)	FACGVIEK	169	8	11	58.14	b2y1y2°y2y3y4y5y6°y6y7y8	923.46	41.646	70555	2	462.23	-10.51
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3		EVPALMAGGHLDPEK	84	15	5	14.47	b6y7y11°y13y15	1563.78	57.986	16441	2	782.39	-0.62
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	4		HLGPYNDK	102	8	5	27.86	b2b5b6°b6y6	943.46	69.945	4241	1	943.46	-0.97
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	5		GHLGDLPLGVVNADGTATYPLLA PR	110	25	8	45.7	b3b4b5b10b15°b15b16°b16	2517.30	86.309	11893	4	630.08	-17.17
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	6		GHSLMIHKG GDNYS DKPAPLGGG GAR	143	26	3	10.93	b13y6y20	2592.26	76.753	3487	4	648.82	-6.50
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	7		TGKHLGPYNDK	99	11	7	47.01	b9b10°b10y5y7°y7y10	1229.65	45.979	2968	2	615.33	14.89
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	8	Oxidation+M(6)	EVPALMAGGHLDPEK	84	15	7	29.49	b3°b3b6b8y9y11°y11	1579.79	67.048	6113	2	790.40	10.28
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	9	Oxidation+M(9)	DGKEVPALMAGGHLDPEK	81	18	3	12.58	b11y4y12	1879.92	79.205	2155	3	627.31	-0.84
P26983 RP5M_SALTY Probable sigma(54) modulation protein	1		LEQYFER	26	7	13	46.26	b2b3°b4°b4b5°b5b7y2°y2y3°y3y4y7	984.47	46.765	21265	2	492.74	-6.70
P26983 RP5M_SALTY Probable sigma(54) modulation protein	2		MQLNITGHNVEITEALREFVTTK	0	23	8	31.78	b2b6°b6b7°b7b8b13y6	2644.40	88.339	9355	3	882.14	7.57
P26983 RP5M_SALTY Probable sigma(54) modulation protein	3		FAKLEQYFER	23	10	7	32.58	b7°b7°b7b9y3y7°y7	1330.66	48.837	4601	3	444.23	-11.38
P26983 RP5M_SALTY Probable sigma(54) modulation protein	4		VTHISDATLHVNGGEIHASAEQD MYAAIDGLIDKLAR	45	38	4	24.79	b6°b6b7b13	3988.95	96.624	3756	3	1330.32	-8.14
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	1	Carbamidomethyl+C(10);Carbamidomethyl+C(13);Carbamidomethyl+C(17)	LIAGPSVYICDECVDLCNDIREEIK	27	26	3	10.93	b3b8y10	3094.52	61.893	12532	4	774.38	8.44
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	2		EEIKEVAPHRER	49	12	8	30.95	b1b4b6°b6b11y2°y2y7	1492.78	46.818	11891	3	498.26	-7.11
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	3		SNILLIGPTGSGK	112	13	11	33.29	b1b3°b3°b3b12y2y4y7°y7y8°y8	1256.71	62.671	9059	2	628.86	-8.64
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	4		THLDDYVIGQEQA K	71	14	4	15.39	b2b4b10y4	1616.81	58.161	4966	3	539.61	9.14
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	5		LLDVPFTMADATTLTEAGYVGED VENIIQK	134	30	7	19.33	b10°b10y1y3y6y10y25	3253.59	110.596	4747	3	1085.20	-8.48
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	6	Carbamidomethyl+C(4);Carbamidomethyl+C(7)	LLYCSFCGK	11	9	3	25.47	b4b7y4	1147.51	97.402	1562	1	1147.51	-12.55

Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	7		HPQQEFLQVDTSK	229	13	10	33.29	b5°b5b8y7y8°y8*y8y10°y10*y10	1556.79	69.015	78468	3	519.60	12.62
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	8		VVIDESVIAGQSKPLLIYGKPEAQA SGE	395	28	3	10.94	b7b12y8	2898.52	105.902	27351	4	725.38	-10.53
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	9		QYQALFNLEGVDLEFR	335	16	3	20.25	b7b8y6	1942.00	60.663	4199	2	971.50	16.53
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	10		ASEGELLSQVEPEDLIK	280	17	4	13.09	b3b6°b6y11	1856.93	60.643	2930	2	928.97	-10.72
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	11		VLAVAVYNHYK	86	11	4	26.73	y4y5y7*y7	1276.70	63.207	2042	3	426.24	-6.50
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	12		SIVEAALLDTMYDLPSMEDVEK	373	22	8	37.55	b6b13y4y7y9y11y13°y13	2469.14	118.783	1603	2	1235.07	-16.41
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	13		SALPTPHEIRTHLDDYVIGQEQAk	61	24	7	21.99	b3°b3b7y7y10y11°y11	2718.35	94.379	92813	3	906.79	-13.29
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	14	Carbamidomethyl+C(9); Carbamidomethyl+C(12)	DGSGKLLYCSFCGK	6	14	3	20.83	b10b11y10	1591.72	90.626	17381	2	796.36	-2.84
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	15		TGARGLR	366	7	5	49.27	b3°b3b6y4y5	730.43	30.709	5132	1	730.43	-4.93
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	16	Carbamidomethyl+C(4); Carbamidomethyl+C(7)	LLYCSFCGKSQHEVR	11	15	12	41.99	b5°b5b9y6°y6*y6y9°y9y10°y10*y10y11	1883.91	60.605	3779	3	628.64	8.88
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	17		SDNPSITRDVSGEGVQQALLK	192	21	5	43.12	b9b10b11b12y20	2214.11	70.820	3614	3	738.71	-11.25
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	18		LRNGDTSNGVELGK	98	14	6	27.15	b6b11y12y13°y13*y13	1459.76	60.648	2503	2	730.38	5.52
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	19	Carbamidomethyl+C(5)	LLQKCDYDVQK	164	11	4	31.5	y4y7y9°y9	1409.70	45.991	1674	2	705.35	-5.28
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	20	Phosphoryl STY(6)	TLLAETLAR	125	9	5	37.97	b5b8°b8y4_H3PO4 y4y7	1067.56	46.779	3509	2	534.28	14.98
Q8ZRC0 CLPX_SALTY ATP-dependent Clp protease ATP-binding subunit clpX	21		EEIKEVAPHR	49	10	0	4.4		1207.64	46.786	3359	3	403.22	-1.82
P26982 DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	9	45.51	b3b4y1y4y6y7y9y15y20	2017.08	75.564	47053	3	673.03	-13.50
P26982 DEGP_SALTY Protease do	2		SDIALIQQNPK	160	12	5	29.86	b3b4y3y6y12	1339.76	64.683	31896	2	670.38	-0.82
P26982 DEGP_SALTY Protease do	3		AQVGTMPIVGSK	352	11	11	47.47	b1b2*b2b10y1y3°y3y5y8y9y11	1074.56	35.235	27648	2	537.78	-5.23
P26982 DEGP_SALTY Protease do	4		VGDYTVIAIGNPFLGETVTSGIVS ALGR	186	28	15	54.71	b2b3b4b6°b6b7b8b11°b11y2y3y5y6y8y28	2750.42	117.082	25603	3	917.48	-5.06
P26982 DEGP_SALTY Protease do	5		ILDSKPSVLALNIQR	450	15	4	14.47	b2b3y5y10	1666.96	66.097	21673	3	556.33	-14.72
P26982 DEGP_SALTY Protease do	6		GAFVSQVMPNSSAAK	313	15	10	47.27	b8°b8b10°b10b12y2y8y9y10y15	1493.75	53.618	12107	2	747.38	3.92
P26982 DEGP_SALTY Protease do	7	Carbamidomethyl+C(13); Carbamidomethyl+C(25))	NFQQFFGDDSPFCQDGSPFQNSPF CQGGGNGGNGGQQQK	71	39	7	28.84	b3b4b6y3y5y14y15	4240.75	91.503	3800	3	1414.25	-1.27
P26982 DEGP_SALTY Protease do	8		GYVVTTNNHVVDNASVIK	124	17	3	13.09	b3y10y14	1828.92	50.754	57452	3	610.31	-16.62

P26982 DEGP_SALTY Protease do	9		NLTSQMVEYGVQVK	275	13	4	27.99	b12y5y8y11	1496.75	58.448	51993	2	748.88	5.71
P26982 DEGP_SALTY Protease do	10		LADSDALR	178	8	6	42.12	b6y3y6°y6y7°y7	860.43	32.933	23054	2	430.72	-17.10
P26982 DEGP_SALTY Protease do	11		GELGIMGTELNSELAK	289	16	12	44.17	b3°b3b4b10b14°b14y6°y6y9°y9*y9y13	1661.86	59.726	17392	3	554.63	14.03
P26982 DEGP_SALTY Protease do	12		ANSPPAQIGLK	418	11	9	39.23	b3*b3b4°b4b7°b7*b7y3y9	1069.59	46.046	5888	2	535.30	-11.53
P26982 DEGP_SALTY Protease do	13		GDSSIYLLMQ	465	10	4	22.12	b7y3*y3y7	1126.54	46.738	4381	2	563.77	-4.33
P26982 DEGP_SALTY Protease do	14		NIAELR	443	6	1	11.88	y4	715.41	32.023	2643	2	358.21	4.44
P26982 DEGP_SALTY Protease do	15		VQLSDGR	141	7	6	52.28	b4*b4b6°b6y3y5	774.41	37.150	2404	1	774.41	3.55
P26982 DEGP_SALTY Protease do	16		SGLNVENYENFIQTDAAINR	214	20	5	20.73	b6y7y8y12°y12	2268.11	136.390	1569	2	1134.56	7.75
P26982 DEGP_SALTY Protease do	17		GELGIMGTELNSELAKAMK	289	19	3	19.12	b3b6b14	1991.99	63.970	21507	3	664.67	-13.24
P26982 DEGP_SALTY Protease do	18		VDAQRGAFVSQVMPNSSAAK	308	20	4	31.5	b3b4y9y10	2063.01	66.176	13268	3	688.34	-12.19
P26982 DEGP_SALTY Protease do	19		GAFVSQVMPNSSAAKAGIK	313	19	6	26.64	b8b9b11*b11b13y12	1863.00	54.902	11208	3	621.67	8.52
P26982 DEGP_SALTY Protease do	20		GYVVTNNHVVDNASVIKVLSDGR	124	24	3	11.05	b4b10y4	2584.37	89.711	3845	4	646.85	8.50
P26982 DEGP_SALTY Protease do	21	Phosphoryl STY(7)	AGDVITSLNGKPISSFALR	332	20	4	11.82	b6°b6b12y14	2097.06	72.734	11129	3	699.69	-3.96
P26982 DEGP_SALTY Protease do	22	Phosphoryl STY(6)	GVVVSSVK	410	8	4	49.9	b3b5b7y7	854.42	39.045	9752	2	427.71	-11.93
P26982 DEGP_SALTY Protease do	23	Oxidation+M(30)	AITVNLELQQSSQSQVDSSTIFSGIEGAEMSNK	373	33	3	11.41	b14b17y14	3514.64	73.255	9977	3	1172.22	-12.02
P26982 DEGP_SALTY Protease do	24	Oxidation+M(6)	AQVGTMPVGSK	352	11	8	28.77	b3b8°b8y6°y6y10°y10*y10	1090.57	45.986	6212	2	545.79	13.32
P26982 DEGP_SALTY Protease do	25	Oxidation+M(2)	FMALGSGVVIDAAK	110	14	7	46.93	b3b5b7b9y3y5°y5	1408.74	68.949	4371	2	704.88	-4.33
P66955 TALB_SALTY Transaldolase B	1		LIDDAVAWAK	50	10	7	34.34	b2b4°b4b5y2y6y8	1101.60	45.945	10979	2	551.30	3.88
P66955 TALB_SALTY Transaldolase B	2		LYQPQDATTNPSLILNAAQIPEYR	25	24	8	27.31	b7b8y2y4°y4y7y9y24	2716.39	82.184	10797	3	906.14	-0.09
P66955 TALB_SALTY Transaldolase B	3		LYQPQDATTNPSLILNAAQIPEYRK	25	25	4	10.97	b3y5y22y25	2844.46	76.237	10120	3	948.83	-8.58
P66955 TALB_SALTY Transaldolase B	4		ISTEVDAR	92	8	6	42.12	b7y2y5y6°y6y7	890.45	28.356	10046	2	445.73	-11.10
P66955 TALB_SALTY Transaldolase B	5	Carbamidomethyl+C(11)	NVGEILELAGCDR	228	13	7	26.23	b1b2b7°b7y8y9y11	1445.71	74.939	9603	2	723.36	4.73
P66955 TALB_SALTY Transaldolase B	6	Carbamidomethyl+C(5)	EGINCNLTLIFSFAQAR	148	17	5	13.09	b2°b2b12y3y14	1953.96	108.135	8002	2	977.48	-13.18
P66955 TALB_SALTY Transaldolase B	7		ELAESEGAIER	250	11	6	59.51	b6b7y6y7y9y10	1203.59	129.426	2262	2	602.30	6.39
P66955 TALB_SALTY Transaldolase B	8		ILDWYK	181	6	1	11.88	b5	837.46	30.263	10135	2	419.23	11.01
P66955 TALB_SALTY Transaldolase B	9		LSFSGEVK	262	8	6	42.12	b7y5y6°y6y7°y7	866.47	42.497	9781	2	433.74	10.99
P66955 TALB_SALTY Transaldolase B	10		QHGYETVVMGASFR	214	14	3	15.39	b3b12y5	1581.72	45.493	9727	3	527.91	-15.74
P66955 TALB_SALTY Transaldolase B	11		DYAPAEDPGVVSVTEIYEYYK	193	21	4	14.63	b5b13y3y5	2408.12	93.355	8104	3	803.38	2.13
P66955 TALB_SALTY Transaldolase B	12		LYNDAGISNDR	117	11	11	56.5	b3°b3b4b7°b7°b7b10°b10y4y8°y8	1237.60	46.794	5406	2	619.30	11.84
P66955 TALB_SALTY Transaldolase B	13		AQQVVDATDK	66	10	3	22.12	b3b7y7	1074.55	42.390	4702	2	537.78	7.95
P66955 TALB_SALTY Transaldolase B	14		LSYDTEASIAK	100	11	5	22.75	b9b10°b10y10°y10	1197.59	60.597	1698	2	599.30	-11.82
P66955 TALB_SALTY Transaldolase B	15		MIGDLL	311	6	1	11.88	y4	661.37	30.762	1598	1	661.37	9.78
P66955 TALB_SALTY Transaldolase B	16		AQQVVDATDKLAVNIGLEILK	66	21	4	18.19	b6b10°b10b14	2238.25	78.088	256230	3	746.75	-9.93
P66955 TALB_SALTY Transaldolase B	17		ISTEVDARLSYDTEASIAK	92	19	5	32.7	b7b8y8y9y11	2069.04	69.005	11886	3	690.35	-1.30
P66955 TALB_SALTY Transaldolase B	18		ELAESEGAIERK	250	12	5	25.88	b4b9y4y9°y9	1331.69	49.594	4078	2	666.35	6.97

P66955 TALB_SALTY Transaldolase B	19		LYQPQDATTNPSSLILNAAQIPEYR K	25	25	3	17.2	b5b11b13	2844.45	115.015	2350	3	948.82	-13.05
P66955 TALB_SALTY Transaldolase B	20	Phosphoryl STY(9)	QFTTVVADTGDIAMK	9	16	6	34.59	b4b5b13y6°y6y7	1747.80	45.997	10552	3	583.27	5.66
P66955 TALB_SALTY Transaldolase B	21		QPQDATTNPSSLILNAAQIPEYR	27	22	4	12.59	b12b14°b14*b14	2440.21	82.186	2092	3	814.07	-15.11
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	1		FLPNPHWDPK	184	10	7	49.4	b3b7b8b9*b9y6y10	1250.63	44.076	83144	2	625.82	-4.39
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	2		ERELTMVFESFGFK	156	14	9	40.91	b4b12°b12y3y6°y6y7°y7y9	1719.83	94.449	14734	2	860.42	-3.90
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	3		ELTMVFESFGFK	158	12	4	21.92	b2b10b11y11	1434.71	75.484	2065	3	478.91	10.98
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	4		ADLIVDTSEMSVHELAEMLR	129	20	7	24.15	b9°b9b10b13y5°y5y10	2259.11	107.618	90179	2	1130.06	6.27
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	5		TLEK	277	4	2	10.62	b3°b3	490.28	33.850	26625	1	490.28	-10.71
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	6	Carbamidomethyl+C(9)	SYLTVAGCTGGK	238	13	5	16.52	b4°b4b8°b8y8	1326.67	22.306	8031	3	442.90	1.29
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	7		HTEVHNFIYQTR	211	12	3	17.94	b5y3y6	1544.76	35.675	6420	3	515.59	0.95
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	8		NLSLESAIDK	108	10	4	22.12	b7°b7y3y6	1089.58	61.954	4221	2	545.30	4.59
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	9		HGIPIDADYVFDVR	170	14	4	23.96	b7°b7b10b13	1616.82	59.783	3054	3	539.61	8.53
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	10		SYLELWLPLETNNR	223	15	4	20.16	b9b11y3y11	1878.90	113.840	2073	2	939.95	-21.89
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	11	Carbamidomethyl+C(9)	SYLTVAGCTGGKHR	238	15	3	14.47	b11b13y6	1619.83	85.515	8831	3	540.62	0.60
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	12		ELTMVFESFGFKHGIPIDADYVFD VR	158	26	3	10.93	b10y6y12	3032.46	101.253	6218	3	1011.49	-7.41
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	13		SVYIAEQLADYFRSR	253	15	7	23.8	b6°b6b8*b8b14y11°y11	1817.94	70.038	2489	3	606.65	10.88
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	14		ERELTMVFESFGFK	156	14	6	34.58	b4b6b10b11y11°y11	1719.82	67.861	2030	2	860.42	-10.01
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	15		NLSLESAIDKESDLLEPLR	108	19	4	31.54	b9b10b11y9	2142.13	88.279	1570	3	714.71	-0.34
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	16	Oxidation+M(4)	ELTMVFESFGFK	158	12	7	41.9	b6°b6b9y6y7°y7y8	1450.70	54.397	7186	3	484.24	4.21
Q8ZLR8 YHBJ_SALTY UPF0042 protein yhbJ	17	Oxidation+M(9)	SYLELWLPLETNNR	223	15	4	20.16	b4b6y4y6	1894.92	90.444	1890	3	632.31	-8.18
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	1		QTFNTAIAAIMELMNK	719	16	14	44.84	b2°b2*b2b6b7b9y1y5°y5y6 y8*y8y10y16	1795.92	90.583	79906	3	599.31	8.70
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	2	Carbamidomethyl+C(7); Carbamidomethyl+C(23) ;Carbamidomethyl+C(24))	TSAVNWC PN DQTVLANEQVIDGC CWR	152	26	5	12.62	b5b9y9°y9y12	3093.38	67.388	17730	3	1031.80	7.34
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	3		GVLFNSGEFDGLAFEAAFNAIADK	378	24	4	11.05	b3b9y7°y7	2503.21	69.820	17497	4	626.56	-1.07
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	4	Carbamidomethyl+C(15)	TLGFGYDWSREIATCTPEYYR	113	21	8	11.55	b1°b1b8b11°b11y1y8°y8	2585.21	125.550	15901	4	647.06	11.80
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	5	Carbamidomethyl+C(4)	QLLCQGMVLADAFYVVGENDER	561	22	6	22.92	b4b7y6°y6y7y12	2533.22	77.309	15805	3	845.08	14.26
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	6		QEQRPEEIESK	1	12	4	17.94	b5b8y8°y8	1535.74	38.204	14999	3	512.59	6.04
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	7		TFEVTEDESKEK	22	12	11	41.41	b1b4y2°y2y5°y5y6°y6y8y1 0y12	1441.67	45.933	14354	3	481.23	1.95
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	8		ITVPVDATEEQVRER	813	15	5	26.18	b10b11y6y12y15	1741.91	54.261	12266	2	871.46	0.21

Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	9		AGQEHLVAK	828	9	7	50.99	b1b6b7b8y4y7y9	952.51	30.106	12173	2	476.76	-7.50
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	10		NNTAPAPWTYDNIAYMK	92	17	10	33.62	b1b2b3b4°b4b7b9°b9y4y9	1969.94	38.064	7448	3	657.32	12.39
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	11		NWVSPVDAIVERDEK	583	15	4	20.49	b6y8°y8y9	1756.91	96.643	6168	2	878.96	12.51
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	12		ITVPVDATEEQVR	813	13	6	27.99	b2b10y6°y6y8y12	1456.77	95.441	5385	2	728.89	5.11
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	13		NYTIGDVVAR	54	10	5	19.62	b1b8b9°b9y10	1107.59	42.442	4532	2	554.30	8.05
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	14		LMRDAGMVTSDPEAK	546	15	3	14.47	b9b12y12	1620.78	50.211	4513	2	810.89	3.62
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	15		NWVSPVDAIVER	583	12	9	28.15	b1b2b5°b5b7°b7b9y2°y2	1384.74	37.158	3928	3	462.25	12.52
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	16		AKDAAGHELVYTGMASK	603	16	3	13.71	b7y5y14	1677.83	87.508	2986	3	559.95	2.47
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	17		EIPQWFIK	186	8	6	42.12	b4°b4b6b7y6°y6	1060.57	32.019	35212	2	530.79	-12.55
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	18		AANYWLPVDIYIGGIEHAIMHLLYFR	516	26	6	19.63	b7b8°b8b10y11°y11	3075.54	133.438	9584	3	1025.85	-17.23
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	19		NNGIDPQVMVER	624	12	3	25.14	y4y5y7	1371.69	26.689	7355	3	457.90	16.82
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	20		MQEQRPEEIESK	0	13	4	16.52	b8°b8y3y5	1666.80	76.689	5748	3	556.27	15.16
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	21		LVYEHTAK	675	8	5	30.87	b5b7°b7y6°y6	960.50	37.185	4723	2	480.75	-13.53
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	22		TTVNGMPALR	475	10	7	49.4	b7y6y7y8°y8y9°y9	1059.54	42.448	4576	2	530.27	-21.43
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	23		GVDGTGYK	301	7	3	35.01	b3y3y5	739.36	31.437	2958	2	370.19	0.74
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	24		TLGFGYDWSR	113	10	7	43.83	b7b9°b9y4y8°y8y9	1201.54	37.141	1840	2	601.27	-18.19
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	25		VTDDIGR	711	7	3	32	b3b4y6	775.40	38.033	1631	1	775.40	8.82
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	26		NNGIDPQVMVERYGADTVR	624	19	3	12.16	b6y7y10	2134.01	84.115	63289	3	712.01	-12.58
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	27		YGADTVRLFMFMFASPADMTLEWQESGVEGANR	636	32	3	11.27	b8y7y12	3579.65	117.850	18423	3	1193.89	4.16
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	28		LAEKGVGER	402	9	7	52.75	b8y3y4°y4y5°y5y7	958.54	62.614	17879	2	479.77	8.21
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	29		LAKAPQEGEQDR	735	12	6	30.95	b11y3°y3y5y11°y11	1341.68	59.731	10757	3	447.90	3.09
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	30		NTKVAEAEEMATMEK	286	14	3	15.39	b9y3y5	1552.73	71.436	5850	2	776.87	-4.01
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	31	Carbamidomethyl+C(5)	EKYYCLSMPLPYPSGR	32	15	5	26.18	b11°b11b13y12y13	1863.88	74.139	5453	2	932.45	3.60
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	32		NQLKTLGFGYDWSR	109	14	3	15.39	b3y5y11	1684.84	60.614	4846	3	562.29	-0.72
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	33		ADPEWAKTTVNGMPALR	468	17	8	62.28	b7°b7b8b9b11b12b13y8	1856.95	59.784	3459	2	928.98	9.99
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	34		WEQKFFTELYK	134	11	5	34.97	b6b7°b7b8y10	1518.75	70.016	2297	2	759.88	-6.19
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	35		AKDAAGHELVYTGMASK	603	16	3	20.25	b12y7y8	1677.83	92.208	1822	2	839.42	4.95
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	36		KGVDGTGYK	300	8	5	35.64	b4°b4b5°b5b7	867.45	22.294	1670	2	434.23	-10.98
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	37		NWVSPVDAIVERDEK	583	15	7	31.07	b3b5°b5b6°b6b13°b13	1756.90	90.603	1586	3	586.30	6.25

Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	38		ITVPVDATEEQVRER	813	15	4	22.55	b6b9b11°b11	1741.89	82.255	1555	2	871.45	-10.23
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	39	Oxidation+M()	VAEAEMATMEKK	289	12	6	25.88	b4°b4b11°b11y4y10	1353.64	50.237	26702	2	677.32	0.63
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	40	Oxidation+M(2)	LMRDAGMVTSDPEAK	546	15	6	23.8	b5°b5b6°b6b11y6	1636.79	72.567	19810	2	818.90	15.07
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	41	Oxidation+M(28)	AIHPLTGEEIPVWAANFVLMHEYGT GAVMAVPGHDQR	308	36	4	11.92	b13y8y11*y11	3892.86	121.918	9107	4	973.97	-14.74
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	42	Carbamidomethyl+C(4); Oxidation+M(7)	QLLCQGMVLADAFYYVGENDER	561	22	3	20.08	b13y4y5	2549.20	69.072	7524	2	1275.10	6.42
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	43	Oxidation+M(14)	AKDAAGHELVYTGMSK	603	16	3	13.71	b4b9y3	1693.83	75.457	4361	2	847.42	2.38
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	44	Oxidation+M(6)	VAEAEMATMEK	289	11	5	30.2	b5y4°y4y5y7	1225.54	41.621	3899	2	613.27	-6.28
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	45	Oxidation+M(19)	TTVNGMPALRETDTFDTFMESW YYAR	475	27	3	20.92	b9b10y5	3205.41	81.305	3753	3	1069.14	-3.88
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	46		VDATEEQVRER	817	11	2	7.53	b10°b10	1331.66	54.255	3705	2	666.33	3.85
Q8ZQZ6 SYL_SALTY Leucyl-tRNA synthetase	47		ATEEQVRER	819	9	0	6.28		1117.55	54.273	3351	2	559.28	-9.18