

LC-MS run 2: 6926_220709_1a2_02

Protein name	Peptide Rank	Peptide Modification	Peptide Sequence	Peptide sequence start	Peptide sequence Length	Peptide Matched Products	Score	By Matches	Precursor MH+ (Da)	Retention time (min)	Intensity	z	Precursor m/z	MH+ Error (ppm)
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	1		IAAANVPAFVSGK	70	13	26	228.16	b2b3b4b5*b5b6*b6b7b9b12y2y3y4y5y6y7*y7y8y9*y9*y9y10*y10y11y12y13	1244.70	60.158	623228	2	622.85	-2.35
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVGFGTFK	22	29	53	425.17	b2b3b4b5*b5b6*b6b7*b7b8*b8b9*b9b11b12b14b17b20b23b24b25b26b29y1y2y3y4y5*y5y6*y6y7y8y10y13*y13*y13y14y15*y15*y15y18y19y20*y20y21y22y23y24y25y26y27y29	2966.56	115.107	587334	3	989.53	-3.05
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	3		AALESTLAAITESLK	22	15	11	89.89	b3b4b6b8b13y1y2y3y5y8y12	1517.85	97.542	48286	2	759.43	2.90
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	4		TQLIDVIADK	3	10	5	47.95	b2b5y3y6y8	1115.63	66.642	21057	2	558.32	-2.52
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	5		ALKDAVK	83	7	3	37.49	b3b4y4	744.45	45.424	28898	2	372.73	-14.84
P0A1H5 EFTU_SALTY Elongation factor Tu	1		AIDKPFLLPIDVFSISGR	205	19	33	275.94	b2b3b4*b4b6*b6b7b8b9b10b12b13y1y2y3y4y5*y5y6*y6y7*y7y8y9*y9y10y11*y11y12y13y15y16y19	2117.14	104.745	777486	3	706.39	-9.46
P0A1H5 EFTU_SALTY Elongation factor Tu	2		GITINTSHVEYDTPTR	59	16	27	195.92	b2b3*b3b9b10b12b13b16y2y3y4y5y6y7*y7y8y9*y9y10*y10y11y12*y12*y12y14*y14y16	1803.86	50.071	412246	3	601.96	-14.08
P0A1H5 EFTU_SALTY Elongation factor Tu	3		ELLSQYDFPGDDTPIVR	155	17	17	156.43	b2b9b13y1y3y4y5y6y8y9*y9y10y11y12y13y14y17	1964.97	77.559	401974	2	982.99	4.78
P0A1H5 EFTU_SALTY Elongation factor Tu	4		TTLTAAITTVLAK	25	13	24	182.44	b2*b2b3*b3b4*b4b5*b5b6*b6b7*b7b13y2y3y4y5y6y7y8y9y10y11y13	1303.78	85.126	370610	2	652.39	-6.09
P0A1H5 EFTU_SALTY Elongation factor Tu	5		IIELAGFLDSYIPEPER	188	17	31	282.12	b2b3b4b5b6b7b8b11*b11b12*b12b14y1y2*y2y3*y3y4y5*y5y6y7y8y9y10y11y12y13y14y15y17	1962.04	102.514	357836	2	981.52	7.96
P0A1H5 EFTU_SALTY Elongation factor Tu	6		QVGVPYIIVFLNK	124	13	16	83.51	b2*b2b3*b3b4*b4b6*b6b13y1y4y5y6y9y11y13	1489.87	99.594	346394	2	745.44	-1.97
P0A1H5 EFTU_SALTY Elongation factor Tu	7		ALEGDAEWEAK	177	11	6	47.56	b2y5y7y8y9*y9	1218.56	46.966	233877	2	609.78	-2.00
P0A1H5 EFTU_SALTY Elongation factor Tu	8		TTDVTGTIELPEGVEMVMPGDNIK	334	24	38	223.09	b1b2*b2b3*b3b4b5b8*b8b9*b9b10*b10b16*b16b17b18y1y2y3y5y6*y6*y6y7*y7*y7y8y9y10*y10y13*y13y14*y14y15y16y24	2546.26	87.460	222597	2	1273.63	9.59
P0A1H5 EFTU_SALTY Elongation factor Tu	9		VGEEVEIVGIK	238	11	9	81.81	b2y3y4y5y7y8y10*y10y11	1171.65	60.838	180865	2	586.33	-3.02

P0A1H5 EFTU_SALTY Elongation factor Tu	10	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	7	51.93	b2y2y4y6y7y8y10	1187.52	53.380	135172	2	594.26	-2.36
P0A1H5 EFTU_SALTY Elongation factor Tu	11	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEV	137	18	23	176.61	b2b3b4b6b8b9b10b11b13y1y2y3*y3y4y5*y5y6y7y8y12*y12y14y18	2224.00	106.641	108704	2	1112.50	8.67
P0A1H5 EFTU_SALTY Elongation factor Tu	12		FESEVYILSKDEGGR	304	15	3	18.16	b3b7y7	1728.85	65.947	7804	2	864.93	1.84
P0A1H5 EFTU_SALTY Elongation factor Tu	13	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	4	18.16	b6y4y7*y7	1768.78	34.921	4739	3	590.27	-1.45
P0A1H5 EFTU_SALTY Elongation factor Tu	14		NMITGAAQMDGAILVVAATDGPMPQTR	90	27	6	11.92	b8°b8y7*y7*y7y11	2729.34	127.164	2586	3	910.45	0.63
P0A1H5 EFTU_SALTY Elongation factor Tu	15		MVVTLIHPIAMDDGLR	358	16	22	195.92	b3b4°b4b5°b5b7°b7b13y3y4y5°y5y6y7y8y9°y9y10°y10y11y12y13	1780.92	79.459	736193	3	594.31	-15.90
P0A1H5 EFTU_SALTY Elongation factor Tu	16		AGENVGVLLR	270	10	14	129.56	b3b4*b4b5°b5*b5y3y4y5y6y7*y7y8y9	1027.57	56.847	387741	2	514.29	-15.21
P0A1H5 EFTU_SALTY Elongation factor Tu	17		TVGAGVVAK	382	9	6	74.98	b3y3y5y6y7y8	801.47	29.020	174840	2	401.24	-22.24
P0A1H5 EFTU_SALTY Elongation factor Tu	18		GYRPQFYFR	325	9	5	45	b3b4y4y5*y5	1233.59	59.194	103174	3	411.87	-21.47
P0A1H5 EFTU_SALTY Elongation factor Tu	19		LLDEGR	264	6	2	26.87	y4y5	702.38	27.521	16288	1	702.38	-3.91
P0A1H5 EFTU_SALTY Elongation factor Tu	20		EEIER	284	5	2	13.23	b3°b3	675.33	112.564	4508	1	675.33	6.06
P0A1H5 EFTU_SALTY Elongation factor Tu	21		TKPHVNVGTIGHVDHGK	8	17	3	16.34	b12y3y8	1795.93	34.314	2816	4	449.74	-16.58
P0A1H5 EFTU_SALTY Elongation factor Tu	22		HTPFFK	319	6	1	13.63	y4	776.40	53.419	2127	2	388.70	-8.65
P0A1H5 EFTU_SALTY Elongation factor Tu	23		GTVVTGRVER	224	10	6	58.17	b4b5b6b9°b9y3	1073.60	26.267	23698	2	537.30	-10.35
P0A1H5 EFTU_SALTY Elongation factor Tu	24	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLELVEMEV	124	31	6	49.99	y3y5°y5y6y7y8	3694.86	128.113	21536	3	1232.29	5.68
P0A1H5 EFTU_SALTY Elongation factor Tu	25		GSALKALEGDAEWEAK	172	16	3	17.18	b11b14y8	1674.82	88.649	4593	2	837.91	-7.94
P0A1H5 EFTU_SALTY Elongation factor Tu	26		FESEVYILSKDEGGR	304	15	3	18.16	b6b8y12	1728.86	97.051	3667	2	864.94	11.16
P0A1H5 EFTU_SALTY Elongation factor Tu	27		ARGITINTSHVEYDTPTR	57	18	3	23	b3b4y5	2031.02	94.725	2849	3	677.68	-3.43
P0A1H5 EFTU_SALTY Elongation factor Tu	28	Carbamidomethyl+C(3)	STCTGVEMFRK	253	11	4	24.33	b6b10y5°y5	1315.62	136.465	1540	1	1315.62	7.89
P0A1H5 EFTU_SALTY Elongation factor Tu	29	Oxidation+M(1)	MVVTLIHPIAMDDGLR	358	16	7	56.34	b3b4y4y8y9y10°y10	1796.92	74.234	56759	3	599.64	-11.55
P0A1H5 EFTU_SALTY Elongation factor Tu	30	Carbamidomethyl+C(3); Oxidation+M(8)	STCTGVEMFRK	253	11	4	24.33	b3°b3y3y9	1331.59	43.811	4661	3	444.54	-12.19
P0A1H5 EFTU_SALTY Elongation factor Tu	31	Oxidation+M(16)	TTDVTGTIELPEGVEMVMPGDNIK	334	24	4	12.72	b4y8*y8y13	2562.27	80.208	2169	2	1281.64	14.77
P0A1H5 EFTU_SALTY Elongation factor Tu	32		TINTSHVEYDTPTR	61	14	9	42.89	b3°b3b4°b4*b4b9°b9*b9b10	1633.79	50.064	16706	2	817.40	4.18
P0A1H5 EFTU_SALTY Elongation factor Tu	33		NTSHVEYDTPTR	63	12	6	24.89	b4°b4*b4b6b8°b8	1419.65	50.075	3873	2	710.33	3.27
P0A1H5 EFTU_SALTY Elongation factor Tu	34		INTSHVEYDTPTR	62	13	5	25.56	b3°b3b9b10°b10	1532.74	50.094	3267	2	766.87	4.86
P0A1H5 EFTU_SALTY Elongation factor Tu	35		GHADYVK	83	7	1	7.26	b3	789.39	34.952	1518	1	789.39	4.48
P0A1H5 EFTU_SALTY Elongation factor Tu	36		GITINTSHVEYDTPTR	59	16	0	4.44		1785.86	50.061	19335	3	595.96	-3.96

[P0A1S2]HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	38	280.73	b2b3°b3b4°b4b5°b5b6°b6b7°b7b8b9b12°b12b14°b14°b14b21y1y2y3y4y5y6y7°y7°y7y8y9y10y13y14y15y16y17y18y21	2216.12	97.598	432108	2	1108.56	11.35
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	2		REEESAAAAEVEER	40	14	23	178.07	b2b3b4b6°b6b7°b7b8b10b11b13b14y1y2y4y5°y5y6y7y9°y9y12y14	1575.73	32.518	118376	2	788.37	6.04
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	3		YSYVDENGETK	96	11	9	87.26	b4y2y4y5y7y8y9y10y11	1304.57	33.701	92824	2	652.79	1.22
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	4		TPAVIKK	114	7	8	53.73	b2y1y2y3y4y5y6y7	756.49	20.275	10758	2	378.75	-12.02
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	5		LQQYREMLIADGIDPNELLNSMAAAK	57	26	4	12.15	b8y10°y10y14	2904.50	137.117	7986	3	968.84	14.46
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	6	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEVVVNER	19	21	25	241.74	b3°b3b4°b4b6b14°b14y3°y3y4°y4y5y6y7y8y9y10y11y12y13y14y15y16y17y19	2563.25	124.214	206669	3	855.09	-4.57
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	7		YSYVDENGETKKTWTGQGR	96	18	12	95.4	b3°b3y4y5y6°y6y11°y11y12y13y15y16	2090.93	47.419	99752	3	697.65	-3.85
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	8		AARPAKYSYVDENGETK	90	17	3	16.34	b9y5y10	1898.94	53.175	11781	4	475.49	7.65
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	9		EEESAAAAEVEERTR	41	15	4	18.16	b3b13y10°y10	1676.76	67.706	5037	4	419.95	-7.64
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	10	Carbamidomethyl+C(6); Oxidation+M(14)	AQARECTLETLEEMLEK	15	17	4	16.34	b12y9y12°y12	2066.97	85.294	3493	3	689.66	-2.72
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	11		MLIADGIDPNELLNSMAAAK	63	20	2	12.7	b6b11	2087.02	97.647	9574	3	696.35	-13.10
[P25077]MDH_SALTY Malate dehydrogenase	1		VAVLGAAGGIGQALALLK	2	19	31	343.63	b2b3b4b5b6b7b8b9b10b11b15b16b17b18b19y1y2y3y4y5y6y7y9y10y11y12y13y14y15y16y19	1735.08	120.358	234676	2	868.05	-0.35
[P25077]MDH_SALTY Malate dehydrogenase	2		NQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVK	21	33	33	128.14	b1°b1b2°b2b3°b3b5°b5b8b9°b9°b9b10b12b13°b13b15°b15b23y1y2y3y5°y5y6y7y12y15°y15y18y19y30y33	3388.82	94.545	202275	3	1130.28	5.19
[P25077]MDH_SALTY Malate dehydrogenase	3	Carbamidomethyl+C(2)	ACVGIIITNPVNTTVAIAAEVLKK	111	23	15	104.4	b2b3b4b5b10y1y3y8y12y15y16y18y20y21y23	2382.33	105.156	156953	3	794.78	-3.79
[P25077]MDH_SALTY Malate dehydrogenase	4		FFSQPLLLGK	262	10	10	74.41	b2b3°b3y2y3y4y5y6y8y10	1149.66	76.442	143141	2	575.33	-7.11
[P25077]MDH_SALTY Malate dehydrogenase	5		IQNAGTEVVEAK	205	12	22	138.37	b2°b2b3°b3b4b6y1y2y3°y3y4y5y6y8y9y10°y10°y10y11°y11°y11y12	1258.65	35.311	111121	2	629.83	-7.27
[P25077]MDH_SALTY Malate dehydrogenase	6		SIGTLSAFEQHSLDAMLDTLKK	279	22	12	57.19	b1b2b10b13y2y5y6y12y16y17y21y22	2405.23	95.441	105262	3	802.42	-2.03
[P25077]MDH_SALTY Malate dehydrogenase	7		DIQLGEDFINK	301	11	16	76.46	b2°b2b3°b3b4b10y1y2y4y7y8y9°y9°y9y11°y11	1291.65	68.614	96148	2	646.33	-2.93
[P25077]MDH_SALTY Malate dehydrogenase	8		LFGVTTLDIIR	142	11	7	69.77	b3b4b5y3y6y9y11	1247.73	89.602	81571	2	624.37	-6.16
[P25077]MDH_SALTY Malate dehydrogenase	9		AGGGSATLSMGQAAAR	217	16	17	111.18	b8b12°b12b13b16y6y7y8y9°y9y10°y10°y10y11°y11y12y16	1405.69	40.693	80924	2	703.35	-0.09

P25077 MDH_SALTY Malate dehydrogenase	10		SNTFVAELK	153	9	9	59.99	b2*b2b4b6b7y2y4y7y9	1008.53	54.805	69446	2	504.77	-6.17
P25077 MDH_SALTY Malate dehydrogenase	11		SDLFNVNAGIVK	87	12	13	79.88	b1°b1b2b3b4y2y4y6*y6y7y8y9y12	1276.68	70.311	59952	2	638.85	-4.40
P25077 MDH_SALTY Malate dehydrogenase	12		FGLSLVR	233	7	3	40.5	y4y5y6	791.46	67.205	77123	2	396.23	-20.36
P25077 MDH_SALTY Malate dehydrogenase	13		NLVQQIAK	99	8	5	49.36	b3b4b6*b6y6	913.53	49.572	62767	2	457.27	-14.30
P25077 MDH_SALTY Malate dehydrogenase	14		SIGTLSAFEQHSLDAMLDTLK	279	21	3	13.89	b9b11y8	2277.13	101.382	5603	3	759.71	-6.00
P25077 MDH_SALTY Malate dehydrogenase	15		NGVEER	272	6	1	13.63	y5	703.34	32.351	4261	1	703.34	0.26
P25077 MDH_SALTY Malate dehydrogenase	16		IKGFSGEDATPALEGADVVLISAGVAR	54	27	3	22.77	y4y6y7	2643.40	87.787	30308	3	881.81	1.57
P25077 MDH_SALTY Malate dehydrogenase	17		GKLPTVEVVPVIGGHSGVTILPLLSQIPGVSFTEQEAAELTK	162	42	5	21.41	b21y11°y11y12y15	4341.36	113.302	25744	4	1086.10	-0.11
P25077 MDH_SALTY Malate dehydrogenase	18		RIQNAGTEVVEAK	204	13	4	20.67	b4y3y7°y7	1414.77	32.950	13022	2	707.89	2.24
P25077 MDH_SALTY Malate dehydrogenase	19		SIGTLSAFEQHSLDAMLDTLKK	279	22	5	13.45	b3°b3b12*b12y13	2405.24	81.924	4269	3	802.42	2.64
P25077 MDH_SALTY Malate dehydrogenase	20	Oxidation+M(16)	SIGTLSAFEQHSLDAMLDTLKK	279	22	3	23.33	b8b9b13	2421.26	68.116	18345	3	807.76	9.68
P25077 MDH_SALTY Malate dehydrogenase	21	Oxidation+M(10)	AGGGSATLSMGQAAAR	217	16	5	17.18	b7°b7y8y10°y10	1421.68	40.716	2771	2	711.34	0.94
P25077 MDH_SALTY Malate dehydrogenase	22		IGTLSAFEQHSLDAMLDTLKK	280	21	4	12.53	b10°b10*b10b13	2318.22	95.436	42023	3	773.41	8.00
P25077 MDH_SALTY Malate dehydrogenase	23		LSMGQAAAR	224	9	0	4.44		904.46	40.743	4182	2	452.74	-3.58
P0A1D5 CH10_SALTY 10 kDa chaperonin	1		VGDIVIFNDGYGVK	60	14	27	241.79	b2b3b4°b4b5°b5b6b8b11°b11b13°b13y1y3y4y5y6°y6y7y8°y8y9y10y11y12y13y14	1495.79	74.152	288608	2	748.40	4.16
P0A1D5 CH10_SALTY 10 kDa chaperonin	2		ILDNGTVQPLDVK	47	13	34	225.15	b1b2b5*b5b6*b6b7°b7b8°b8°b8b9°b9b10b12y1y2y3y4y5y6°y6°y6y7y8y9*y9y10y11°y11*y11y12y13*y13	1411.78	58.048	270505	2	706.39	-0.95
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	11	109.48	y2y3y4y6y7y8°y8y9y11y12y14	1188.65	44.349	116070	2	594.83	-7.09
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIAVGK	37	8	5	54.13	y3y4y5y6y8	786.46	42.164	43707	2	393.74	-10.17
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		IDNEEVLIMSESDILAIVEA	77	20	6	32.25	b5°b5b7b8b12y10	2203.11	69.839	1862	3	735.04	3.21
P0A1D5 CH10_SALTY 10 kDa chaperonin	6	Phosphoryl STY(8)	SAGGIVLTGSAAGK	20	14	5	38.77	b7b9_H3PO4b9b11°b11b12	1268.62	51.354	2462	3	423.55	6.45
P64076 ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	31	281.89	b2*b2b3*b3b4*b4b5b6b7°b7b8b9b10b11b13b14b15y1y2y3y4y6y7y8y9y10y11°y11y12y13y15	1605.89	86.391	252153	2	803.45	1.22
P64076 ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	33	253.93	b2b3°b3b5°b5b7b8°b8b11b12°b12b13°b13b14b16b18b22y1y2y4y5y6y7y8y9y10y11y12*y12y13y14y16y22	2118.07	76.200	236501	2	1059.54	7.15
P64076 ENO_SALTY Enolase	3		AVGAVNGPIAQAILGK	66	16	7	42.7	b5y2y6y10y11y12y16	1478.87	75.902	154073	2	739.94	-0.83
P64076 ENO_SALTY Enolase	4		YSMPVPMMNIIINGGEHADNNVDIQEFMIQPVGAK	143	34	17	98.3	b2°b2b3°b3b4b5y3y5y6*y6y8y9y10y12y13y29y34	3759.80	99.048	131986	3	1253.94	9.87

P64076 ENO_SALTY Enolase	5		GMNTAVGDEGGYAPNLGSNAEA LAVIAEAVK	200	31	23	117.08	b2b4b5°b5b6°b6°b6b8b12 b13b23y1y2y3y4y6y7y8y1 0y13y15y18y31	2989.46	95.725	125235	3	997.16	0.74
P64076 ENO_SALTY Enolase	6	Carbamidomethyl+C(16)	AAGYELGKDITLAMDCAASEFYK DGK	231	26	25	165.88	b2b3b4b6b8b9°b9b11°b11 b15y2y3°y3y5y6y8°y8y9y1 0y11y12y13y14y24y26	2824.28	98.442	121651	4	706.83	-12.10
P64076 ENO_SALTY Enolase	7		AFTSEEFTHFLEELTK	266	16	23	183.66	b2b3b4°b4b12b13°b13b14 b16y1y3y4°y4y5y6y9y10°y 10y11y12y13y14y16	1928.90	103.610	107947	3	643.64	-11.96
P64076 ENO_SALTY Enolase	8		DAGYTAVISHR	360	11	11	87.26	b2b3y1y2y3y4y5y6y7y9y1 1	1189.59	42.039	90012	2	595.30	-4.62
P64076 ENO_SALTY Enolase	9		GIANSILIK	333	9	8	57.55	b2y1y2y3y4y6y7y9	928.57	60.949	89739	2	464.79	-13.34
P64076 ENO_SALTY Enolase	10		IQLVGDDLFTVNTK	311	14	14	105.9	b2°b2b3b4y1y2y4y5y6y9y 10y11y12y14	1562.85	78.314	80316	2	781.93	1.95
P64076 ENO_SALTY Enolase	11		IEEALGEK	411	8	5	40.9	y1y3y6y7y8	888.46	31.764	41103	2	444.73	-9.21
P64076 ENO_SALTY Enolase	12		ILKEGIEK	325	8	8	40.9	y1y2°y2y4y5°y5y6y8	929.56	29.679	38608	2	465.28	-8.60
P64076 ENO_SALTY Enolase	13		GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	7	29.95	b7b12°b12b14y7y8y30	2856.38	92.808	30898	3	952.80	8.03
P64076 ENO_SALTY Enolase	14		IMIDLDGTENK	92	11	6	41.54	b10y2y7y8y9°y9	1248.61	59.723	20333	2	624.81	-2.44
P64076 ENO_SALTY Enolase	15		YVLAGEGNK	257	9	7	54.54	b9y2y3y5°y5y6y7	950.49	33.974	11130	1	950.49	-1.80
P64076 ENO_SALTY Enolase	16		SNFGANAILAVSLANAK	103	17	8	23.74	b1b2°b2°b2b4b6b12y2	1660.89	79.189	2983	2	830.95	-7.72
P64076 ENO_SALTY Enolase	17	Carbamidomethyl+C(8)	DITLAMDCAASEFYKDGK	239	18	5	15.6	b2b3°b3b7y11	2034.92	94.528	2281	4	509.48	1.26
P64076 ENO_SALTY Enolase	18		GMPLYEHIAELNGTPGK	126	17	11	79.91	b3b6b10y3y4y6y10y12°y1 2y13°y13	1826.88	67.693	110589	3	609.63	-19.24
P64076 ENO_SALTY Enolase	19		YNQLIR	405	6	2	26.87	y3y4	806.44	38.875	72449	2	403.72	-13.40
P64076 ENO_SALTY Enolase	20		EIIDSR	10	6	1	13.63	b4	732.38	29.032	17599	1	732.38	-8.42
P64076 ENO_SALTY Enolase	21		MGSEVFHHLAK	184	11	3	27.34	b3b4y7	1255.61	43.669	12265	3	419.21	-12.44
P64076 ENO_SALTY Enolase	22		EALELR	46	6	3	40.1	b4b5y3	730.41	41.064	12173	1	730.41	-5.26
P64076 ENO_SALTY Enolase	23	Carbamidomethyl+C(8)	DITLAMDCAASEFYK	239	15	5	31.85	b3°b3b4y3y7	1734.74	72.339	5715	4	434.44	-19.91
P64076 ENO_SALTY Enolase	24		VLGDKIQLVGDDLFTVNTK	306	19	10	53.78	b4b7°b7y4°y4y5y6y10°y1 0y17	2075.12	80.231	66430	3	692.38	-6.71
P64076 ENO_SALTY Enolase	25		DGKYVLAGEGNK	254	12	4	26.28	b11y8y9°y9	1250.63	44.318	59886	2	625.82	-7.22
P64076 ENO_SALTY Enolase	26		GKGMMNTAVGDEGGYAPNLGSNA EALAVIAEAVK	198	33	7	42.18	b6b7b10b12b14b15y5	3174.59	90.563	29253	3	1058.87	6.08
P64076 ENO_SALTY Enolase	27		EIIDSRGNPTVEAEVHLEGGFVG MAAPSGASTGSR	10	36	7	16.64	b5b12y5°y5y11y14°y14	3569.73	93.893	18234	4	893.19	1.50
P64076 ENO_SALTY Enolase	28		IEEALGEKAPYNGR	411	14	7	60.46	b7y4y5°y5y6y7y9	1546.77	40.208	15536	3	516.26	-13.57
P64076 ENO_SALTY Enolase	29		AAAAAKGMPLYEHIAELNGTPGK	120	23	3	13.06	b4b8y8	2310.20	51.763	12939	3	770.74	4.12
P64076 ENO_SALTY Enolase	30		SNFGANAILAVSLANAKAAAAAK	103	23	3	23.15	b3b4b9	2144.18	100.721	7758	3	715.40	-0.80
P64076 ENO_SALTY Enolase	31		SGETEDATIADLAVGTAAGQIKTG SMSR	371	28	3	11.71	b9b13y6	2737.37	101.674	2496	3	913.13	14.54
P64076 ENO_SALTY Enolase	32		DAGYTAVISHRSGETEDATIADLA VGTAAGQIK	360	33	3	16.83	b5b7b11	3288.59	68.573	2206	3	1096.87	-12.69
P64076 ENO_SALTY Enolase	33		GYTAVISHR	362	9	1	7.87	b3	1003.53	42.079	44804	2	502.27	-4.87
P64076 ENO_SALTY Enolase	34		LKEGIEK	326	7	0	1.21		816.47	29.685	30191	2	408.74	-14.35
P64076 ENO_SALTY Enolase	35		ANSILIK	335	7	8	38.3	b3°b3°b3b4°b4°b4b5°b5	758.47	60.950	15949	1	758.47	-6.28
P64076 ENO_SALTY Enolase	36		LAGEGNK	259	7	0	1.61		688.36	33.983	6978	1	688.36	-1.60
P64076 ENO_SALTY Enolase	37		AASEFYKDGK	247	10	0	8.47		1115.55	98.465	6234	1	1115.55	11.93
P64076 ENO_SALTY Enolase	38		TSEEFTHFLEELTK	268	14	3	25.56	b3b10b11	1710.84	103.649	2432	2	855.92	7.85
P64076 ENO_SALTY Enolase	39		AFTSEEFTHFLEELTK	266	16	0	4.44		1910.89	103.614	3742	3	637.64	-11.50
P64076 ENO_SALTY Enolase	40		DAGYTAVISHR	360	11	3	27.34	b7b8y8	1171.57	41.986	1714	3	391.19	-11.77

[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	41	298.51	b2b3b4*b4b5°b5*b5b6°b6*b6b7*b7b8*b8b17y1y3y4y6y7*y7y8*y8y9y10y11y12y14y15°y15y16°y16y17y18*y18y19y20y22°y22y24*y24	2574.32	98.608	481927	3	858.78	0.38
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	2		LVSWYDNETGYSNK	307	14	17	146.17	b2b6b7b12y2y3°y3y5y6°y6y7y8y9y10y11y12y14	1675.77	58.880	269851	2	838.39	5.39
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	3		AGIALNDNFVK	296	11	18	123.94	b3b4b10b11y1y2y3y4*y4y5°y5*y5y6y7y8*y8y10y11	1161.62	62.038	243338	2	581.31	-4.62
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		GASQNIIPSSTGAAK	198	15	25	186.94	b3°b3b5*b5b6*b6b7°b7*b7b10b11b13y1y2y4y5°y5y6y7y8°y8y9y10y11y15	1401.73	41.592	216638	2	701.37	-3.48
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		AATYEQIK	249	8	7	49.36	b6b8y5y6°y6y7y8	923.47	31.566	158085	2	462.24	-12.95
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		VLDLIAHISK	321	10	9	87.64	b3y2y3y4y5y6y7y8y10	1108.66	65.497	141633	2	554.84	-8.70
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		VPTPNVSVVDLTVR	232	14	13	126.4	b3y2y3y4y5y6y7y9y10y11y12°y12y14	1495.85	71.649	138465	2	748.43	1.88
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		SDIEIVAINDLLAEYMayMLK	24	22	22	146.12	b1b2b3b4°b4b5b6b7b10*b10b14b21y1y2y3y4y5y6y9y10y14y22	2530.24	126.444	67503	3	844.08	-2.51
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		VLPELNGK	217	8	9	57.14	b2y2y3y4y6°y6*y6y7y8	869.50	45.384	62218	2	435.25	-12.42
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		VVLTGPSKDNTPMFVK	116	16	10	49.13	y1y2y3y5y10*y10y13y14y16*y16	1732.91	58.095	49654	3	578.31	-14.51
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11		WDEVGVDVVAEATGIFLTDETAR K	84	24	6	16.89	b4b9°b9y6y9y24	2621.29	86.765	24014	3	874.44	-5.77
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12	Carbamidomethyl+C(20)	GVLGYTEDDVVSTDFNGEVCTSV FDAK	269	27	9	46.59	b4b5b7b11b14b18y4°y4y12	2924.27	94.537	4385	3	975.43	-14.69
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13		AAAEGEMK	261	8	3	36.13	b3b6y7	806.38	89.128	3124	1	806.38	9.46
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14		WDEVGVDVVAEATGIFLTDETAR	84	23	3	22.09	b10y11y12	2493.18	74.739	1618	3	831.73	-14.59
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEGQDIVSNASCTTNCL APLAK	132	28	36	335.54	b3b4b5b6b7°b7*b7b8b10°b10b11*b11b12°b12b13b15b16b21b24*b24b26b27y3y4y5y6y8y9y10y11y12°y12y13y14y15y16	3044.42	67.252	274471	3	1015.48	3.05
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		TVDGPSHKDWR	184	11	3	24.33	b10y8y10	1297.63	72.216	14219	2	649.32	3.10
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		DNTPMFVKGANFDK	124	14	3	27.09	y5y7y8	1583.77	75.357	7596	2	792.39	13.72

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		KHITAGAK	107	8	5	67.37	y3y4y5y6y7	825.48	12.751	6369	2	413.25	-13.38
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19		GGRGASQNIPSSSTGAAK	195	18	3	15.6	b6b15y8	1671.90	51.271	4141	3	557.97	12.78
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20	Oxidation+M(13)	VINDNFGIIIEGLMTTVHATTATQK	160	24	3	22.02	b14y11y12	2590.30	77.761	2521	3	864.10	-7.63
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	21		DLIAHISK	323	8	3	33.93	b3b5b6	896.51	65.483	45135	2	448.76	-12.59
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	22		LDLIAHISK	322	9	2	20.7	b3b6	1009.60	65.482	44995	2	505.30	-6.59
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	23		LIAHISK	324	7	0	2.02		781.48	65.466	2674	2	391.25	-13.20
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	24		LPELNGK	218	7	0	1.21		770.43	45.386	1771	2	385.72	-14.34
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	25		AATYEQIK	249	8	0	1.21		906.46	31.564	32441	2	453.73	3.03
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	26		VVLTGPSKDNTPMFVK	116	16	0	4.44		1715.91	58.052	29834	2	858.46	4.06
P66593 RS6_SALTY 30S ribosomal protein S6	1		AHYVLMNVEAPQEVIDELETTFR	56	23	24	200.99	b2b3b4b5b6b7b8*b8b9b10b13b15y2y4y5y6y7y8*y8y9y10*y10y13y23	2704.33	110.806	169805	3	902.11	-1.08
P66593 RS6_SALTY 30S ribosomal protein S6	2		YSAAITGAEGK	24	11	12	110.71	b4b7b8y2y3*y3y4y5y6y7y9y11	1067.53	34.156	91235	2	534.27	-5.37
P66593 RS6_SALTY 30S ribosomal protein S6	3		HAVTEASPMVK	93	11	15	113.72	b2b4°b4b5°b5b6b7°b7y1y4y5y8y9y10y11	1169.59	30.982	63227	2	585.30	-3.97
P66593 RS6_SALTY 30S ribosomal protein S6	4		HYEIVFMVHPDQSEQVPGMIER	2	22	3	23.33	b3b5b6	2641.26	124.869	1796	3	881.09	1.29
P66593 RS6_SALTY 30S ribosomal protein S6	5		QLAYPINK	45	8	4	36.13	b3b6y5*y5	946.53	38.002	28688	2	473.77	-10.90
P66593 RS6_SALTY 30S ribosomal protein S6	6		FNDAVIR	79	7	6	63.95	b4y3y4y5y6*y6	834.45	42.612	10006	1	834.45	-1.39
P66593 RS6_SALTY 30S ribosomal protein S6	7		SMVMR	86	5	1	13.23	b3	623.31	71.795	1848	1	623.31	12.63
P66593 RS6_SALTY 30S ribosomal protein S6	8		HYEIVFMVHPDQSEQVPGMIERYSAITGAEGK	2	33	3	11.06	b8y3y12	3689.79	120.405	2006	5	738.76	4.50
P66593 RS6_SALTY 30S ribosomal protein S6	9		MRHYEIVFMVHPDQSEQVPGMIER	0	24	6	19.47	b4b6°b6b9°b9y11	2928.36	74.135	1802	4	732.85	-11.92
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	23	188.37	b1b2b3b4b6b9y1y2y3y4y5°y5y6y7y8y10y11y12y13*y13y14y16y18	1970.00	63.980	193988	3	657.34	-9.73
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		ESSVPFSYYDNQQK	47	14	9	67	b3b11y4y6y8y9*y9y10y14	1691.76	56.265	192994	2	846.38	1.37

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		VVGYSQDYSNAIVEAVK	61	17	35	274.91	b2b3b4b6b7b9b10b11°b11b12°b12*b12b13b14*b14b16°b16y1y2y3y4°y4y5y9y10*y10y11y12°y12*y12y13y14*y14y15y17	1841.94	68.544	151441	2	921.47	5.37
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		NGVIVVGHR	38	9	12	89.46	b2b3*b3b4y1y2y3y4y5y6y7y9	950.54	32.982	120405	2	475.78	-9.82
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5		AVAFMMDDALLAGER	198	15	14	137.24	b3b4b5b11b12y3y4y9y10°y10y11y12y13y15	1609.78	85.367	97229	2	805.39	2.96
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(19)	KPDNWEIVGKPQSQEAYGCMLRK	217	23	5	24.6	b7b9y6y9y13	2734.32	57.133	84757	4	684.33	-10.27
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7		LIPITSQNR	89	9	6	38.3	b2y5y6°y6y7y9	1041.60	43.523	66303	2	521.30	-9.02
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8		QAAFSDTIFVVGTR	122	14	7	39.87	b3b5b10y1y6y12y14	1511.79	77.539	29364	2	756.40	3.71
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9	Carbamidomethyl+C(21)	AKKPDNWEIVGKPQSQEAYGCMLR	215	24	4	23.45	b19y7y8y12	2805.36	58.943	18703	4	702.10	-6.61
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		LMDDTIAQAQTSGEAEK	247	17	6	34.05	b5°b5b7y3y8y9	1807.86	46.914	12808	2	904.43	9.93
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11		LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	3	11.39	b27y10y14	2869.39	94.334	28140	3	957.14	-17.19
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12	Carbamidomethyl+C(19)	KPDNWEIVGKPQSQEAYGCMLR	217	22	4	24.25	b6b7b9y5	2606.21	62.363	24696	4	652.31	-14.80
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	13	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTT NNLER	89	31	9	60.23	y4*y4y6y8°y8y9y10y11y21	3548.80	87.633	261385	3	1183.61	6.67
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	14		IISAKDHGDSFR	180	12	3	26.28	b11y10y11	1345.69	58.000	15130	2	673.35	-0.64
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	15		LMDDTIAQAQTSGEAEKWFDK	247	21	3	23.54	y5y6y19	2384.09	70.384	11700	3	795.37	-7.37
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	16		KLMDDTIAQAQTSGEAEK	246	18	6	26.61	b4y7°y7y8°y8y10	1935.94	44.719	5387	3	645.98	3.41
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	17	Phosphoryl STY(5)	AVVVTSGTTSEILLHK	154	16	4	27.7	b3b6_H3PO4 b6b12y13	1734.92	81.457	20967	3	578.98	12.59
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	18	Phosphoryl STY(18)	NGVIVVGHRESSVPFSYYDNQQK	38	23	3	13.06	b3b19y4	2703.25	93.269	3635	3	901.76	2.17
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	19	Carbamidomethyl+C(21);Oxidation+M(22)	AKKPDNWEIVGKPQSQEAYGCMLR	215	24	3	12.72	b9b11y7	2821.38	114.178	8505	3	941.13	1.21
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	20	Oxidation+M(2)	LMDDTIAQAQTSGEAEK	247	17	4	16.34	b6b8°b8y6	1823.83	57.278	4764	3	608.62	-0.27

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	21	Carbamidomethyl+C(13)	IVGK PQS QEAYGCMLRK	223	17	0	7.26		1964.99	57.153	3652	3	655.67	-8.01
P67091 UF_SALTY Universal stress protein F	1		TILVPIDISDSELTQR	3	16	23	150.2	b2°b2b3°b3b4°b4y2*y2y3y4y6*y6y7y8y9*y9y10y12°y12*y12y13y14y16	1799.98	82.833	99040	2	900.49	4.00
P67091 UF_SALTY Universal stress protein F	2	Carbamidomethyl+C(4)	HAECSVLVVR	134	10	8	28.7	b1b2b3°b3b10y8y9°y9	1169.60	41.948	49449	2	585.31	-5.53
P67091 UF_SALTY Universal stress protein F	3		SQLEAIKK	69	9	8	45	b2b6°b6b8y2y3y7y9	1029.63	45.113	26453	2	515.32	0.59
P67091 UF_SALTY Universal stress protein F	4		VQAHVAEGSPK	85	11	13	87.26	b1b2b5y1y2y3y5y6y7°y7y8y9y11	1122.59	19.161	15702	2	561.80	-3.26
P67091 UF_SALTY Universal stress protein F	5		VQAHVAEGSPKDK	85	13	8	43.14	b2*b2y2y4y6y7y8y13	1365.69	16.393	14895	3	455.90	-13.05
P67091 UF_SALTY Universal stress protein F	6		LPADMVIIASHRPDITTYLLGSNAAVVR	105	29	3	22.73	b5b6b10	3064.62	89.694	5808	4	766.91	-12.43
P67091 UF_SALTY Universal stress protein F	7		LEAIKK	71	7	0	1.61		814.53	45.121	4428	2	407.77	-11.39
P67091 UF_SALTY Universal stress protein F	8		QAHVAEGSPK	86	10	4	36.09	b3*b3b5b7	1023.52	19.170	3780	2	512.26	-6.26
P67091 UF_SALTY Universal stress protein F	9		AHVAEGSPK	87	9	1	7.87	b3	895.46	19.179	2106	2	448.23	-5.04
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	1		MITGIQITK	0	9	6	38.3	b2y2y3y6y7y9	1004.57	55.541	125064	2	502.79	-9.11
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	2		SGFAEDEVVAVSK	35	13	11	56.38	b2b3b9b13y2°y2y4y8y9y10y13	1337.66	55.123	85262	2	669.33	1.28
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	3		LGEIEYR	48	7	6	40.5	b3y2y4y6°y6y7	879.45	42.761	84856	2	440.23	-10.97
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	4		FNSLTPEQQR	106	10	17	113.32	b2*b2b3°b3b5b6b10y1y3y4°y4y5y6y7y8°y8y10	1219.60	38.672	60479	2	610.31	-1.60
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	5		EIPMEVKPEVR	55	11	7	65.56	y2y4y6y7y8y9y11	1326.71	48.968	60249	2	663.86	0.74
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	6		AANDDLLNSFWLLDSEK	9	17	5	26.18	b3b6b10y4y17	1950.96	88.670	50559	2	975.98	8.57
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	7		FNSLTPEQQRDIAR	106	15	4	18.16	b6°b6b12y3	1773.90	74.139	2423	2	887.46	-10.87
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	8		VEGGQHNLNVNVL	66	13	13	135.76	b3b6b12y3y4*y4y5y6y7y8y11y12°y12	1434.76	50.538	86134	3	478.92	-17.61
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	9		TFTESL	121	6	2	26.87	b4b5	697.33	56.085	37324	1	697.33	-8.31
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	10		AANDDLLNSFWLLDSEKGEAR	9	21	30	260.88	b3b4b5°b5*b5b6°b6*b6b7°b7b10y4y5y7°y7y8°y8y9°y9y10y11y12y13y14y15y16y17y18y19°y19	2364.14	93.258	177017	3	788.72	-3.92
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	11		VSGYAVRFNSLTPEQQR	99	17	4	26.18	b5b10b12y5	1951.97	82.676	6260	2	976.49	-12.07
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	12		SGFAEDEVVAVSKLGEIEYR	35	20	3	14.39	b3b10y19	2198.10	117.054	2530	3	733.37	-0.89
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	13		PMEVKPEVR	57	9	3	18.88	b3b5°b5	1084.57	48.979	56907	2	542.79	-6.98
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	14		TGIQITK	2	7	3	23.3	b4b5°b5	760.45	55.540	6198	1	760.45	-8.67
Q7CQ05 GRCA_SALTY Autonomous glycy1 radical cofactor	15		EIPMEVKPEVR	55	11	0	2.42		1308.68	48.978	18953	3	436.90	-9.33

P66038 RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	16	94.35	b3b9b10°b10b11°b11b12b 13°b13b14°b14y4y12y15y 16y29	3110.70	99.046	74867	3	1037.57	6.99
P66038 RISB_SALTY 6	2		GAEAAALTALEMINVLK	136	16	21	199.9	b3b4b5°b5b6b7b8°b8b9°b9 b12b13b14b15y1y3y4y5y6 y8y16	1643.91	103.585	53793	2	822.46	2.75
P66038 RISB_SALTY 6	3		FNQFINDSLLDGAVDALTR	21	19	20	152.31	b2b3b4°b4b8b11b12y2y4y 5y6y8y9°y9y10y13°y13y14 y15y19	2109.08	101.939	53155	2	1055.05	11.11
P66038 RISB_SALTY 6	4		ANVAAPDAR	5	9	7	38.3	b2°b2y2y2y5y6y7y9	884.45	23.530	13125	2	442.73	-5.93
P66038 RISB_SALTY 6	5		VAITTIAR	14	7	3	40.5	y4y5y6	743.47	44.807	7088	2	372.24	-15.52
P66038 RISB_SALTY 6	6		MNIK	0	5	1	13.23	b3	618.36	72.101	3510	1	618.36	-12.34
P66038 RISB_SALTY 6	7	Oxidation+M(11)	GAEAAALTALEMINVLK	136	16	4	25.56	b6°b6b7b10	1659.90	72.284	1518	2	830.45	1.54
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		LADVLAANAR	57	11	18	114.51	b1b2b3b4°b4y1y2y4y5°y5 y6°y6y7°y7y8y9y10y11	1084.60	53.921	123822	2	542.81	-6.08
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGSLGDQVNVK	8	14	24	179.83	b2b3b4°b4b9b10°b10b12° b12b13b14y1y3y6y7y8y9y 10°y10y11°y11y12°y12y14	1413.76	57.403	93511	2	707.39	-4.40
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		MQVILLDK	0	8	7	54.13	b2°b2y3y4y5y6y8	959.55	64.820	78554	2	480.28	-11.96
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		DIADAVTAAGVDVAK	97	15	10	71.88	b2b6y6y7°y7y8y9°y9y11y1 3	1415.74	67.016	73920	2	708.37	-0.52
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		INALETVTIASK	71	12	7	34.29	b2°b2b3°b3y7y10y11	1259.72	61.767	58315	2	630.36	-3.20
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		LFGSIGTR	89	8	4	33.12	b4y6°y6y7	850.47	52.459	31006	2	425.74	-5.24
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		LPNGVLR	116	7	4	40.5	y4y5°y5y6	768.46	43.575	32694	2	384.73	-15.81
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		NFLVPK	27	6	1	13.63	y3	717.42	51.290	19508	1	717.42	-13.10
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	9		TTGEHEVNFQVHSEVFAK	123	18	3	15.6	b10y7y11	2059.03	65.732	2509	3	687.02	21.70
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	10		DIADAVTAAGVDVAKSEVR	97	19	3	14.96	b11b14y6	1886.96	76.242	58023	3	629.66	-14.23
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	11		AGDEGKLFGSIGTR	83	14	5	30.78	b10y3y6°y6y7	1407.71	55.047	46392	3	469.91	-12.40
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	12	Phosphoryl STY(6)	VANLGSLGDQVNVK	8	14	5	19.31	b4°b4y7y9°y9	1493.72	58.013	1757	2	747.36	-5.39
P06179 FLIC_SALTY Flagellin	1		AQILQQAGTSVLAQANQVPQNVL SLLR	468	27	33	190.55	b2°b2b3°b3b4°b4b5°b5b6° b6b7b10°b10b11°b11b15° b15b16b18°b18y1y2y4y5y 6y7°y7y9y10y11y12y14y2 7	2860.60	105.978	105579	3	954.21	0.85
P06179 FLIC_SALTY Flagellin	2		SQSALGTAIER	20	11	13	82.03	b2°b2°b2b3b5y4y5y6y7°y7 y9°y9y11	1132.59	42.657	64826	2	566.80	-3.02
P06179 FLIC_SALTY Flagellin	3		FNSAITNLGNTVNNLTSAR	432	19	15	102.69	b2b11b12°b12b13y3y4y6y 7°y7y11y13y14°y14y19	2007.04	79.113	62691	2	1004.02	8.15
P06179 FLIC_SALTY Flagellin	4		IDAALAQVDTLR	411	12	12	114.12	b2b3b4y3y4y6y7y8y9y11°y 11y12	1285.71	61.876	51166	2	643.36	-0.57
P06179 FLIC_SALTY Flagellin	5		INSAKDDAAGQAIANR	37	16	18	120.61	b2°b2b6°b6°b6b10b11y1y 3°y3y4y5y7y8y9y10y11y1 6	1614.80	30.836	45939	3	538.94	-12.62
P06179 FLIC_SALTY Flagellin	6		QINSQTLGLDTLNVQQK	161	17	8	41.63	b9b10°b17y5y10y11y12y1 7	1900.03	66.081	43384	2	950.52	7.20
P06179 FLIC_SALTY Flagellin	7		NANDGISIAQTTEGALNEINNNLQ R	66	25	11	22.77	b2b13b16°b16y2y3y6°y6y 9°y9y25	2670.34	87.465	39100	2	1335.67	10.61

P06179 FLIC_SALTY Flagellin	8		AQVINTNSLSLLTQNNLNK	1	19	7	14.96	b7°b7b9y7°y7*y7y19	2085.15	63.253	23058	3	695.72	8.31
P06179 FLIC_SALTY Flagellin	9		ELAVQSANSTNSQSDLDLSIAEIT QR	93	26	8	21.97	b8°b8b10y3*y3y7y9y26	2805.35	71.327	19384	3	935.79	-0.17
P06179 FLIC_SALTY Flagellin	10		DDAAGQAIANR	42	11	6	38.35	b2b4b9y7y8y11	1101.52	28.900	13864	2	551.27	-4.10
P06179 FLIC_SALTY Flagellin	11		IEDSDYATEVSNMSR	453	15	4	36.75	y5y6y10y13	1716.76	54.035	12003	2	858.88	13.79
P06179 FLIC_SALTY Flagellin	12		ASATGLGGTDQK	204	12	5	40.18	b3°b3b4y3y4	1105.56	28.230	4271	2	553.28	10.60
P06179 FLIC_SALTY Flagellin	13		YYAK	229	4	1	12.83	y3	544.27	90.533	2490	1	544.27	-6.73
P06179 FLIC_SALTY Flagellin	14		LGGADGKTEVVSIGGK	363	16	3	17.18	b10b12y13	1487.80	58.570	10687	3	496.60	-6.89
P06179 FLIC_SALTY Flagellin	15		ASATGLGGTDQKIDGDLK	204	18	5	15.6	b12°b12y10y12*y12	1746.86	63.808	7878	3	582.96	-13.98
P06179 FLIC_SALTY Flagellin	16		AEGHNFKAQPDLAEEAAATTTENP LQK	385	26	6	18.31	b7b9°b9b13°b13y3	2752.32	95.459	2682	3	918.11	-13.22
P06179 FLIC_SALTY Flagellin	17		SDLGAVQNRFNSAITNLGNTVNN LTSAR	423	28	4	17.73	b7°b7b12b14	2947.54	72.991	2499	3	983.18	13.00
P06179 FLIC_SALTY Flagellin	18		AQPDLEAAATTTENPLQKIDAAL AQVDTLR	392	31	4	26.16	b3b8b11b12	3235.69	95.340	1975	3	1079.24	3.24
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	1		AAADLQLQGVPMFVNGK	158	18	28	207.05	b2b4b5b6°b6b7b9b10°b10° *b10b13b17y2y3*y3y4y5y 6y7*y7y8y10y11*y11y12y 14y18*y18	1829.96	81.583	150942	2	915.49	3.80
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	2		YQINPQGMDTSSMDVFVQQYAD TVK	176	25	14	42.73	b2°b2b3b4°b4b14b17y2y4 y5y12°y12°y12y25	2865.34	87.310	109017	2	1433.17	12.27
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	3		TQTVQSAADIR	116	11	18	94.47	b2°b2b3°b6b8b9b11y2y5°y 5y6y7°y7*y7y8y9°y9y11	1189.62	35.944	50341	2	595.31	1.64
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		YHVEFLGPLGK	77	11	4	35.34	b3b5y3y8	1259.66	70.148	13444	3	420.56	-16.67
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	5		VFVDAGVK	128	8	4	36.13	b3b5°b5y5	834.47	84.482	10307	1	834.47	0.00
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	6		ELTQAWAVAMALGVEDK	88	17	4	22.96	b3b8y5y11	1831.89	34.923	1727	2	916.45	-18.12
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	7	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	4	23.33	b5b6°b6y10	1847.91	94.095	10997	2	924.46	-5.55
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	1		TQFMGPEGVANVSLSNIAGESAE GLLVTKPK	240	31	32	227.25	b1°b1b2°b2b3°b3b4b5°b5° b5b6b9b11b12y2y3y4y5y6 y8y9y13y14y17y18y19y22 y26y27y28y29y31	3144.64	89.134	309250	3	1048.88	3.34
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	2		NYDQVPANKPIVDAIK	271	16	14	93.75	b2°b2b3b5y1y2y3y5y7y9y 11y14*y14y16	1784.93	54.302	241722	3	595.65	-14.91
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	3	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILM ITPAATAPELTAR	92	38	23	131.25	b2b5b7b9b10b11°b11b12° b12°b12b25b26b27°b27y4 y6y8y10y11y12y13y15y38	4078.02	90.046	146440	3	1360.01	10.18
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	4		TTGLDSQDGPTAAK	137	14	26	172.05	b2°b2b3°b3b4b5°b5b8b10° b10b11°b11y2y3y5y6y8°y8 y9y10°y10*y10y11y12°y12 y14	1361.65	30.212	138921	2	681.33	0.00
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	5		ENIDFVYYGGYHPEMGQILR	212	20	11	66.87	b2°b2y2y3y8y9y12y13y14y 16y20	2401.13	80.792	114420	3	801.05	-0.71
P17215 LIVJ_SALTY Leu/Ile/Val/Thr- binding protein	6		VAVVGAMSGPVAQYGDQEFTGA EQAIADINAK	25	32	23	131.64	b2b3b6b7b8b12b15°b15b2 6y2y3*y3y5°y5y6y7y8y11y 12y14y25y26y32	3207.58	90.703	109534	3	1069.86	4.72

P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	7		GGVNVVFFDGITAGEKDFSTLVAR	185	24	17	112.71	b4b5*b5b6*b6y1y2y3y6y7y12y13y17y18y19y21y24	2499.29	102.533	96743	3	833.77	1.47
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	8		GATVDTVMGPLSWDEK	326	16	10	63.34	b7b8b10*b10b11y3°y3y7y9y16	1705.83	62.754	32650	2	853.42	10.66
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	9		QDPSGAFVWTTYAALQSLQAGLNHSDDPAEIAK	290	33	8	22.38	b4b8b11y2y6y8y11y33	3501.71	110.016	11805	3	1167.91	5.16
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	10		GFEFGVFDWHANGTATDAK	346	19	6	23.68	b2b5y5y7y11y19	2069.94	84.238	10109	3	690.65	1.65
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	11		QQYGEGLAR	168	9	3	30.51	b6y5y8	1021.50	33.608	3679	1	1021.50	-1.25
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	12	Carbamidomethyl+C(6)	TLLAGCIALSLSHMAFADDIK	4	21	4	37.45	y5y6y7y12	2247.11	105.443	1904	2	1124.06	-18.14
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	13		GGVNVVFFDGITAGEK	185	16	4	24.3	b7b10y5y8	1609.80	56.664	1679	2	805.41	-10.92
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	14		KQDPSGAFVWTTYAALQSLQAGLNHSDDPAEIAK	289	34	39	299.62	b3°b3*b3b4b5b7°b7b8b9°b9b11b12*b12b13°b13b14b15b18y3y6y7y9°y9y11y13y14°y14y15*y15y16y17y18*y18y19y20y21y22y24y25	3629.77	103.050	384857	4	908.20	-3.70
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	15		ENIDFVYYGGYHPEMGQILRQSR	212	23	3	13.06	b3b8y12	2772.33	111.870	3880	3	924.78	4.14
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	16	Carbamidomethyl+C(7); Phosphoryl STY(31)	YVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTAR	92	38	7	41.1	b11b12y6y9y10y12y15	4157.91	110.890	7843	5	832.39	-5.40
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	17	Oxidation+M(15)	ENIDFVYYGGYHPEMGQILR	212	20	3	14.39	b3b10y9	2417.14	65.302	31597	4	605.04	7.88
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	18	Oxidation+M(16)	KENIDFVYYGGYHPEMGQILR	211	21	4	13.89	b3b11°b11y11	2545.20	70.640	14252	3	849.07	-8.44
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	19	Oxidation+M(8)	GATVDTVMGPLSWDEK	326	16	5	28.37	b9y5y6y13°y13	1721.82	91.544	13314	3	574.61	7.02
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	20	Carbamidomethyl+C(6); Oxidation+M(14)	TLLAGCIALSLSHMAFADDIK	4	21	3	13.89	b6b14y5	2263.13	110.320	1807	3	755.05	-5.07
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	21	Carbamidomethyl+C(7)	YVIGHLCS	92	8	0	13.31		948.46	90.070	1735	1	948.46	3.86
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	22		TYAALQSLQAGLNHSDDPAEIAK	300	23	0	11.29		2413.22	110.003	1529	3	805.08	6.78
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	23		QQYGEGLAR	168	9	3	38.3	y4y6y7	1003.49	33.638	6360	2	502.25	-1.22
P02910 HISJ_SALTY Histidine-binding periplasmic protein	1		NSDIQPTVASLK	120	12	25	137.57	b1*b1b2°b2*b2b3*b3b4*b4b5*b5b7°b7y3y4°y4y5y7y8°y8*y8y9y10*y10y12	1272.67	48.839	134847	2	636.84	-6.43
P02910 HISJ_SALTY Histidine-binding periplasmic protein	2		VGVLQGTQTETFGNEHWAPK	135	20	14	119.92	b2b4b5y2y4y8y9y10y11y12y15y17y19y20	2199.07	64.043	130600	3	733.70	-4.55
P02910 HISJ_SALTY Histidine-binding periplasmic protein	3		IGTDPTYAPFESK	29	13	22	165.23	b2b3b4b7b8b13y3°y3y4°y4y5°y5y6°y6y7y9°y9y10°y10y11y12y13	1425.69	56.167	125302	2	713.35	0.94
P02910 HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	16	84.77	b2b3°b3b6b8b12b16*b16y2y3y4°y4y5y10y14y20	2273.22	104.465	87912	2	1137.11	13.53
P02910 HISJ_SALTY Histidine-binding periplasmic protein	5		FGGPAVKDEK	201	10	14	101.84	b2b8°b8b9y2°y2y3y4°y4y5y6y7y8y10	1047.54	27.178	50582	2	524.27	-4.89
P02910 HISJ_SALTY Histidine-binding periplasmic protein	6		NAQGELVGFDIDLAK	42	15	7	29.48	b1b6*b6b7b13y12y15	1589.83	80.125	38235	2	795.42	5.30

[P02910]HISJ_SALTY Histidine-binding periplasmic protein	7	Carbamidomethyl+C(18)	NAQGELVGFDIDLAKELCK	42	19	4	23.68	b3b5b12y3	2120.06	87.054	13948	3	707.36	-4.72
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	8		LFGVGTGMGLR	211	11	6	52.55	b3b10°b10y5y7y9	1107.59	72.944	57733	2	554.30	-2.87
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	9		AFAEMR	234	6	2	13.63	y5°y5	724.34	36.757	6254	1	724.34	-2.95
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	10		GIEIVSYQGQDNISDLTAGR	155	21	3	13.89	b13y3y9	2299.15	80.491	3353	2	1150.08	11.47
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	11		IDAAFQDEVAASEGFLKQPVGK	176	22	6	25.64	b4°b4b13y4y18y20	2320.18	78.875	46461	3	774.06	-2.10
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	12		RVGVLQGTQTETFGNEHWAPK	134	21	3	13.89	b4y4y8	2355.18	59.165	17627	3	785.73	0.00
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	13		EALNKAF AEMR	229	11	3	24.33	b4y8y10	1279.65	57.144	3943	2	640.33	4.01
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	14	Phosphoryl STY(7)	IDAIMSSLSITEKR	85	14	5	30.78	b5b6b10y10°y10	1643.82	55.580	2579	2	822.41	10.77
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	15	Oxidation+M(5)	IDAIMSSLSITEK	85	13	3	25.44	b4b5y10	1423.72	48.716	4599	3	475.25	-8.32
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	16	Oxidation+M(8)	LFGVGTGMGLR	211	11	4	35.34	b5b8y7y9	1123.58	39.686	1962	2	562.29	-11.08
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	17		GGPAVKDEK	202	9	3	33.93	b3b4b7	900.47	27.178	15362	2	450.74	-8.54
[P0A1E3]CYSK_SALTY Cysteine synthase A	1		LTLTMPETMSIER	87	13	18	135.76	b2°b2b5°b5b9°b9b12°b12y1y4y5y6y8y9y10y11y12y13	1521.77	74.732	131100	2	761.39	2.41
[P0A1E3]CYSK_SALTY Cysteine synthase A	2		YLLQQFSNPANPEIHEK	137	18	25	203.15	b2b3b4b9b12b15y2°y2y3y4y6y7y8y9°y9y10°y10y11y12°y12y13°y13y15y17y18	2141.09	74.686	124219	3	714.37	-5.82
[P0A1E3]CYSK_SALTY Cysteine synthase A	3		IQGIGAGFIPGNLDLK	226	16	13	70.25	b2°b2b3b4b8y2y7°y7y8y10y12y14y16	1612.90	84.118	113614	2	806.95	-1.97
[P0A1E3]CYSK_SALTY Cysteine synthase A	4		YLSTALFADLFTEKELQQ	305	18	20	120.76	b2b4°b4b11b13b14°b14b16y2°y2y5y6y7°y7y8y10y11y12°y12y18	2117.10	103.005	102853	2	1059.05	9.34
[P0A1E3]CYSK_SALTY Cysteine synthase A	5		IYEDNSLTIGHTPLVR	3	16	6	39.88	b2y2y7y8y9y15	1827.94	62.291	83092	3	609.99	-10.55
[P0A1E3]CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	12	111.11	b2b3b4b5b6y1y3y6y7y9y10y12	1283.73	64.658	68701	2	642.37	-3.52
[P0A1E3]CYSK_SALTY Cysteine synthase A	7		GVLKPGVELVEPTSGNTGIALAYVAAAR	56	28	12	95.18	b11y3y4y5y6y7y9y11y14y16y17y28	2753.53	82.107	67602	3	918.51	3.37
[P0A1E3]CYSK_SALTY Cysteine synthase A	8		LQEDESFTNK	283	10	7	57.38	b3b4y6°y6y7y8y10	1210.56	35.890	52781	2	605.79	3.63
[P0A1E3]CYSK_SALTY Cysteine synthase A	9		ALGANLVLTEGAK	105	13	6	20.67	b2b5y5°y5y7y13	1256.72	61.922	28832	2	628.86	-2.23
[P0A1E3]CYSK_SALTY Cysteine synthase A	10		VVGITNEEAISTAR	246	14	6	39.08	b3b10y9y10°y10y12	1459.77	50.187	25141	2	730.39	-3.43
[P0A1E3]CYSK_SALTY Cysteine synthase A	11		YLSTALFADLFTEK	305	14	7	45.47	b11y4°y4y8y9y10y14	1618.84	103.935	18576	2	809.92	1.89
[P0A1E3]CYSK_SALTY Cysteine synthase A	12		IGANMIWDAEK	44	11	13	94.47	b5°b5b6b8b9b10y1y3°y3y9y10y11°y11	1247.61	66.208	17104	2	624.31	2.64
[P0A1E3]CYSK_SALTY Cysteine synthase A	13		IGANMIWDAEKR	44	12	6	22.3	b2b7y7y11y12°y12	1403.70	63.946	15244	2	702.35	-9.13
[P0A1E3]CYSK_SALTY Cysteine synthase A	14		AEEIVASDPQK	126	11	4	27.34	b4b5y2y6	1186.60	29.708	1841	2	593.80	2.67
[P0A1E3]CYSK_SALTY Cysteine synthase A	15		GKTDLITVAVEPTDSPVIAQALAGEEIKPGPHK	193	33	4	25.83	y5y10y11y22	3381.80	80.287	92583	4	846.21	-6.86
[P0A1E3]CYSK_SALTY Cysteine synthase A	16		LIDKVVGITNEEAISTAR	242	18	4	24.85	b8y5y7y12	1929.08	60.316	34740	2	965.04	5.38

[P0A1E3]CYSK_SALTY Cysteine synthase A	17		VESRNPSFSVK	31	11	3	24.33	b3b7y9	1249.66	31.747	30869	3	417.22	4.49
[P0A1E3]CYSK_SALTY Cysteine synthase A	18		AEEIVASDPQKYLLQQFSNPANPEIHEK	126	29	5	14.54	b3b5°b5y6y9	3308.67	77.846	25929	4	827.92	-3.98
[P0A1E3]CYSK_SALTY Cysteine synthase A	19		LQEDESFTNKNIVILPSSGER	283	22	3	13.45	b4b10y6	2475.28	70.247	8961	3	825.76	1.87
[P0A1E3]CYSK_SALTY Cysteine synthase A	20		LLQQFSNPANPEIHEK	138	17	1	7.33	b11	1978.03	74.682	8576	2	989.52	-3.21
[P0A1E3]CYSK_SALTY Cysteine synthase A	21		IVASDPQK	129	8	1	7.87	b7	857.48	29.656	3133	2	429.24	9.18
[P0A1E3]CYSK_SALTY Cysteine synthase A	22		GITNEEAISTAR	248	12	0	3.63		1261.63	50.193	2066	2	631.32	-6.19
[P41031]CY_SALTY Thiosulfate-binding protein	1		AYLNWLYSPQAQTIIHYYR	265	21	31	237.73	b2b3b4*b4b5*b5b6*b6b8b9b10y2y3y4y6°y6y7y8°y8y9y10°y10*y10y11y13y14y15y16y17y21*y21	2664.33	93.825	129277	3	888.78	0.55
[P41031]CY_SALTY Thiosulfate-binding protein	2		TEQFMTQFLK	179	10	11	87.64	b2b3y2y3y4*y4y5y6y7y8y10	1272.62	76.176	122516	2	636.82	-4.51
[P41031]CY_SALTY Thiosulfate-binding protein	3		ELFAALNPPFEQQWAK	37	16	16	86.49	b2°b2b5b7*b7b13y1y4*y4y6*y6y8y9y10°y10y12	1888.97	90.590	118976	2	944.99	4.72
[P41031]CY_SALTY Thiosulfate-binding protein	4		GLGDVLISFESEVNNIRK	208	18	19	133.9	b2b4b5°b5b12b16y2y5y6y8y9y10*y10y11y12*y12y13y16y18	1990.04	101.834	106937	3	664.02	-10.80
[P41031]CY_SALTY Thiosulfate-binding protein	5		FGSWPEVMK	311	9	8	64.76	b2b3y2y3y5y6y8y9	1080.51	69.350	97798	2	540.76	-7.91
[P41031]CY_SALTY Thiosulfate-binding protein	6		LPNNSSPFYSTMGFLVR	110	17	22	153.5	b2b4b5°b5*b5b6°b6*b6b7b17y1y2y3y4y5y8y9y11y12y13y14y17	1929.96	92.701	95305	2	965.49	5.88
[P41031]CY_SALTY Thiosulfate-binding protein	7		VNNPEIMGK	286	9	16	89.46	b1b2*b2b4b7y2y3y5y6°y6y7°y7*y7y8*y8y9	1001.50	36.870	74959	2	501.25	-6.40
[P41031]CY_SALTY Thiosulfate-binding protein	8		QYEAQGFEVVIPK	226	13	14	76.6	b2*b2b3°b3*b3b7b13y2y3y5y8y9y11y13	1507.78	70.597	71974	2	754.39	-0.65
[P41031]CY_SALTY Thiosulfate-binding protein	9		NVEVFDTGGR	189	10	16	86.85	b1*b1b2*b2b4*b4b8y1y4y5y6y7°y7y8°y8y10	1093.52	47.813	65617	2	547.26	-5.92
[P41031]CY_SALTY Thiosulfate-binding protein	10		QALAILQLK	71	10	7	58.17	b3*b3b10y3y5y6y7	1054.65	75.640	64960	2	527.83	-9.72
[P41031]CY_SALTY Thiosulfate-binding protein	11		NIHDWSDLVR	132	10	6	54.94	y2y3y4y6y8y10	1254.62	63.508	52057	2	627.81	-3.31
[P41031]CY_SALTY Thiosulfate-binding protein	12		GLGDVLISFESEVNNIR	208	17	6	27.43	b10y2y9y10y12y17	1861.97	107.866	29618	2	931.49	3.67
[P41031]CY_SALTY Thiosulfate-binding protein	13		ADVVTYNQVTDVQILHDK	81	18	9	32.79	b1b2b3b10*b10y3y4y14y18	2058.03	64.540	13489	3	686.68	-7.47
[P41031]CY_SALTY Thiosulfate-binding protein	14		LPNNSSPFYSTMGFLVRK	110	18	7	26.61	b7°b7b12b13*b13y11y18	2058.03	83.907	3208	3	686.68	-8.42
[P41031]CY_SALTY Thiosulfate-binding protein	15		TNLAEFPAWVDK	239	14	3	24.75	b7y4y5	1602.84	70.224	1755	2	801.92	-7.39
[P41031]CY_SALTY Thiosulfate-binding protein	16		LIFPNPK	146	7	4	40.5	y3*y3y5y6	828.48	56.461	61073	2	414.75	-15.69
[P41031]CY_SALTY Thiosulfate-binding protein	17		TNLAEFPAWVDKNVQANGTEK	239	23	13	104.11	b3°b3b4b5y6y7*y7y9y13y16y17y19y20	2544.30	91.216	139285	3	848.77	-2.78
[P41031]CY_SALTY Thiosulfate-binding protein	18		YTYLAAWGAADNADGGDKAK	159	20	5	32.03	y3y6y9y18°y18	2057.95	62.861	67143	3	686.65	-5.22
[P41031]CY_SALTY Thiosulfate-binding protein	19		TSGNARYTYLAAWGAADNADGGDK	153	24	5	19.47	b7b13*b13b15y6	2445.13	94.437	9092	4	612.04	10.48

P41031 CY_SALTY Thiosulfate-binding protein	20		NVEVFDTGGRGATTTFAER	189	19	5	39.46	b5b6y3y4y9	2027.97	57.233	6485	3	676.66	-5.24
P41031 CY_SALTY Thiosulfate-binding protein	21		AYLNWLYSPQAQTIIHHYYRVN NPEIMGK	265	30	6	35.39	b5b6y7y8°y8y11	3646.81	85.195	4984	5	730.17	-2.01
P41031 CY_SALTY Thiosulfate-binding protein	22		VEEKFGSWPEVMK	307	13	4	34.11	b4b6b10y7	1565.75	51.792	4696	2	783.38	-9.36
P41031 CY_SALTY Thiosulfate-binding protein	23		TEQFMTQFLKNVEVFDTGGR	179	20	4	36.07	b10y7y8y9	2347.11	112.464	2982	3	783.04	-13.00
P41031 CY_SALTY Thiosulfate-binding protein	24	Phosphoryl STY(13)	AYLNWLYSPQAQTIIHHYYR	265	21	5	29.8	b3b7y4y8y9	2744.29	81.973	5444	2	1372.65	4.80
P41031 CY_SALTY Thiosulfate-binding protein	25	Oxidation+M(12)	LPNNSSPFYSTMGFLVR	110	17	6	29.95	b3b8y10°y10y11°y11	1945.95	115.109	3852	2	973.48	3.45
P41031 CY_SALTY Thiosulfate-binding protein	26		EVFDTGGR	191	8	0	2.02		880.42	47.811	1935	1	880.42	-0.42
P41031 CY_SALTY Thiosulfate-binding protein	27		QALAILQLK	71	10	0	2.02		1037.63	75.632	2652	2	519.32	1.06
P52616 FLJB_SALTY Phase 2 flagellin	1		AQILQQAGTSVLAQANQPQNVLSLLR	479	27	33	190.55	b2°b2b3°b3b4°b4b5°b5b6°b6b7b10°b10b11°b11b15°b15b16b18°b18y1y2y4y5y6y7°y7y9y10y11y12y14y27	2860.60	105.978	105579	3	954.21	0.85
P52616 FLJB_SALTY Phase 2 flagellin	2		SQSALGTAIER	20	11	13	82.03	b2°b2°b2b3b5y4y5y6y7°y7y9°y9y11	1132.59	42.657	64826	2	566.80	-3.02
P52616 FLJB_SALTY Phase 2 flagellin	3		YFVTIGGFTGADAAK	234	15	7	37.87	b8b9°b9y1y6y7y15	1517.77	74.150	51085	2	759.39	2.33
P52616 FLJB_SALTY Phase 2 flagellin	4		INSAKDDAAGQAIANR	37	16	18	120.61	b2°b2b6°b6°b6b10b11y1y3°y3y4y5y7y8y9y10y11y16	1614.80	30.836	45939	3	538.94	-12.62
P52616 FLJB_SALTY Phase 2 flagellin	5		NANDGISIAQTTEGALNEINNLR	66	25	11	22.77	b2b13b16°b16y2y3y6°y6y9°y9y25	2670.34	87.465	39100	2	1335.67	10.61
P52616 FLJB_SALTY Phase 2 flagellin	6		AQVINTNSLSLLTQNNLNK	1	19	7	14.96	b7°b7b9y7°y7°y7y19	2085.15	63.253	23058	3	695.72	8.31
P52616 FLJB_SALTY Phase 2 flagellin	7		ELAVQSANSTNSQSDLSIQAEITQR	93	26	8	21.97	b8°b8b10y3°y3y7y9y26	2805.35	71.327	19384	3	935.79	-0.17
P52616 FLJB_SALTY Phase 2 flagellin	8		AYANNGTTLDVSLDDAAIK	189	20	6	21.18	b2y6y12°y12y14y20	2008.95	74.192	19365	3	670.32	-14.40
P52616 FLJB_SALTY Phase 2 flagellin	9		DDAAGQAIANR	42	11	6	38.35	b2b4b9y7y8y11	1101.52	28.900	13864	2	551.27	-4.10
P52616 FLJB_SALTY Phase 2 flagellin	10		IEDSDYATEVSNMSR	464	15	4	36.75	y5y6y10y13	1716.76	54.035	12003	2	858.88	13.79
P52616 FLJB_SALTY Phase 2 flagellin	11		FTANIK	53	6	2	26.87	b4y5	693.38	34.642	15603	2	347.20	-11.80
P52616 FLJB_SALTY Phase 2 flagellin	12		NALIAGGVDATDANGAELVK	299	20	5	25.28	b13°b13y9y10y13	1898.94	86.707	5579	2	949.98	-20.44
P52616 FLJB_SALTY Phase 2 flagellin	13		TAANQLGGVDGK	369	12	3	22.3	b5y5y9	1130.57	60.955	5085	1	1130.57	-6.91
P52616 FLJB_SALTY Phase 2 flagellin	14		AQPELAEEAAK	403	11	3	27.34	b8y9y10	1098.56	88.477	4704	2	549.78	-18.78
P52616 FLJB_SALTY Phase 2 flagellin	15		TYNASK	390	6	3	40.1	b3b4y5	683.33	72.231	3268	1	683.33	-9.20
P52616 FLJB_SALTY Phase 2 flagellin	16		FNSAITNLGNTVNNLSEAR	443	19	4	14.96	b3b12°b12y9	2035.03	75.499	1986	2	1018.02	2.76
P52616 FLJB_SALTY Phase 2 flagellin	17		LNEIDR	119	6	2	26.87	b4y4	759.39	28.852	1958	2	380.20	-6.11
P52616 FLJB_SALTY Phase 2 flagellin	18		YYAADYDEATGAIK	341	14	3	19.31	b4b10y9	1550.71	51.272	1628	3	517.57	3.46
P52616 FLJB_SALTY Phase 2 flagellin	19		SRIEDSDYATEVSNMSR	462	17	8	68.89	b8b11b12y3y4y7y8y10	1959.89	51.452	22657	2	980.45	10.71

P52616 FLJB_SALTY Phase 2 flagellin	20		NALIAGGVDATDANGAELVKMSY TDK	299	26	6	25.6	b13b14y4°y4y12°y12	2624.31	77.043	20006	3	875.44	8.37
P52616 FLJB_SALTY Phase 2 flagellin	21		TEVVTIDGKTYNASK	381	15	3	18.16	b3b11y9	1625.84	58.566	14399	3	542.62	-1.28
P52616 FLJB_SALTY Phase 2 flagellin	22		TYNASKAAGHDFK	390	13	6	54.62	b4b9b10b12y6y9	1409.66	47.373	12821	2	705.34	-12.30
P52616 FLJB_SALTY Phase 2 flagellin	23		TAANQLGGVDGKTEVVTIDGK	369	21	6	20.53	b11b14°b14*b14b17*b17	2073.10	90.739	4261	3	691.70	8.24
P52616 FLJB_SALTY Phase 2 flagellin	24		TEVQELKDTPAVVSADAK	281	18	4	21.78	b8b10y3y6	1900.99	94.509	3584	2	951.00	2.44
P52616 FLJB_SALTY Phase 2 flagellin	25		LNEIDRVSGQTQFNGVK	119	17	5	16.34	b6*b6b9y10*y10	1904.97	86.276	2376	2	952.99	-4.87
P52616 FLJB_SALTY Phase 2 flagellin	26		TTSYTAADGTTKTAANQLGGVD GK	357	24	8	36.89	b7b10b13b14b16°b16*b16 y5	2328.15	80.034	2137	3	776.72	6.08
P52616 FLJB_SALTY Phase 2 flagellin	27		AKTTSYTAADGTTK	355	14	3	19.31	b8b13y8	1415.69	88.209	2049	2	708.35	-7.67
P52616 FLJB_SALTY Phase 2 flagellin	28		AQPELAEAAAKTENPLQK	403	19	4	36.32	b12y7y8y9	2010.03	64.535	1693	2	1005.52	-9.96
P52616 FLJB_SALTY Phase 2 flagellin	29		DTPAVVSADAKNALIAGGVDATD ANGAELVK	288	31	3	11.26	b8y7y12	2953.55	86.916	1633	3	985.19	13.23
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	1		SGAMAGTVLNDANNQAK	269	17	20	118.81	b2b3b4b8°b8b9b16b17y1y 3y5y8y9°y9*y9y10y12°y12 y13y17	1661.80	46.928	85794	2	831.40	4.55
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	2		SSIPVFGVDALPEALALVK	250	19	17	141.67	b6°b6b7b10°b10y2y3y4y5y 6y8y9y11y13y14y16y19	1926.10	108.448	84397	2	963.55	2.73
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	3		VPYVGVDKDNLSEFTQK	315	17	12	88.73	b3b13y2y5y6y8y9*y9y10y 13y14y17	1938.97	62.230	69794	3	646.99	-7.81
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	4		ALAINLVDPAAGTVIEK	84	18	12	67.45	b2b3b4b5*b5b6y2°y2y10y 11y14y18	1766.01	81.284	65877	2	883.51	3.39
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	5		GQNVPPVFFNKEPSR	104	15	6	25.83	b4b13y1y6y11*y11	1717.88	57.987	16040	3	573.30	-12.93
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	6		HWQANQGWDLNKDGK	148	15	5	25.83	b2b4b7y7y10	1796.83	47.428	7823	3	599.61	-10.87
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	7		SAPDVQLLMNDSQNDQSK	52	18	5	36.58	b5b6°b6y6y7	1989.94	62.091	2763	2	995.48	12.94
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	8		GIQTEQLALDTAMWDTAQAK	192	20	5	32.25	b3b4b10b13y8	2191.04	82.953	2093	3	731.02	-13.48
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	9		QNDQIDVLLAK	70	11	3	24.33	b7y6y10	1256.71	54.484	4235	2	628.86	20.30
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	10		AYYVGTDISK	127	9	5	45.51	b5b6°b6b7y5	1003.49	100.701	1773	1	1003.49	13.75
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	11		SAPDVQLLMNDSQNDQSKQNDQI DVLLAK	52	29	4	16.93	b3y5y21y27	3227.61	78.877	29284	3	1076.54	7.94
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	12		GQNVPPVFFNKEPSR	104	15	6	37.14	b4*b4b9y6y8y11	1717.88	62.069	9185	3	573.30	-10.87
P23905 DGAL_SALTY D-galactose- binding periplasmic protein	13		ELNDKGIQTEQLALDTAMWDTAQ AK	187	25	7	56.32	b12y3y6y8y9y10y11	2790.35	80.785	9179	3	930.79	-2.80

P23905 DGAL_SALTY D-galactose-binding periplasmic protein	14		DGKSAPDVQLLMNDSQNDQSK	49	21	3	13.89	b9b13y12	2290.09	75.226	5713	3	764.03	10.77
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	15		ESGVIQGDLIAKHWQANQGWDL NK	136	24	5	26.19	b8b9y9y11°y11	2707.35	93.389	2936	3	903.12	-2.80
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	16		DKMDAWLSGPNANK	212	14	3	19.31	b10y6y9	1546.73	136.593	1981	1	1546.73	-2.68
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	17	Phosphoryl STY(7)	SGAMAGTVLNDANNQAK	269	17	4	16.34	b6y9°y9y15	1741.77	91.395	2048	3	581.26	13.60
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTASPYASYLQYGHIANIDD IIAGKKPATDLGVK	125	38	34	170.49	b2b3b5*b5b6°b6*b6b7°b7 *b7b8°b8*b8b9°b9b10°b10 b11b13b20y1y2y3y4y8y9y 12y19y23y27y30y31y35y3 8	4001.02	83.834	218116	5	801.01	-12.08
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		AEQQLDKDSAIVPVYYYVNAR	494	21	18	122.94	b4b5b7°b7b8b11b12b13y3 *y3y4y5*y5y7y9*y9y10y2 1	2442.23	73.686	123540	3	814.75	0.30
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3	Carbamidomethyl+C(4)	AGWCADYNEPTSFLNTMLSDSSN NTAHYK	439	29	7	33.93	y2y3y15y20y22y4y29	3294.43	90.849	107802	3	1098.82	6.37
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4		WSDGTPVTAHDFVYSWQR	107	18	19	168.79	b2y1y3y4y5y6y7y8°y8y9*y 9y10y11y13°y13y15y17y18 *y18	2151.98	72.932	98454	3	718.00	-2.72
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		ALDDHTFEVTLSEPVPYFYK	163	20	11	71.99	b5b11b13y2y4y5y7y9°y9y1 0y11	2371.16	86.734	85805	3	791.06	3.09
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		LVEPEWFK	352	8	9	62.59	b1b5y2y3y5y6°y6y7y8	1047.54	71.759	84747	2	524.27	-8.39
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7		TVINQVTYLPISSEVTDVNR	241	20	20	163.31	b2b5b8°b8b9b12y3y4y5y6 y7y8°y8y9y11y12°y12y13y 14y20	2248.20	77.891	83767	2	1124.60	8.14
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		NLGVNVNLENQEWK	410	14	7	44.79	b1y7°y7y8y11y12y14	1656.84	67.489	63838	2	828.92	4.49
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9		SGEIDMTYNNMPIELFQK	263	18	10	31.03	b2b3b13y1y2y3y5y11°y11y 18	2130.01	87.366	56816	2	1065.51	11.23
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		NQGDLPAYSYTPPYTDGAK	333	19	12	57.6	b5b7°b7b10b11y2y8°y8y9y 11y14y19	2057.97	59.983	56290	2	1029.49	11.03
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	9	25.31	b1b2b3b6b9y4y10y14y29	3091.56	89.032	38958	3	1031.19	7.11
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		NPQYWDNAK	232	9	8	45.51	b2b3y1y3*y3y6y7y9	1135.52	40.198	37537	2	568.26	-0.32
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	13		DLFEGLLISDVEGHPSPGVAEK	67	22	4	29.78	y6y8y12y14	2309.16	89.923	21906	3	770.39	-4.55
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	14		LIADTLK	474	7	5	40.5	b5y3y5°y5y7	773.47	44.045	19933	2	387.24	-13.10
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	15		TFLDTR	424	6	1	13.63	y4	752.38	44.283	13052	1	752.38	-13.47

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	16		DPLDNIYVK	527	9	3	30.51	b4b8y3	1076.57	70.717	9593	2	538.79	2.61
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	17		VWTFHLR	96	7	4	40.5	y4y5y6°y6	958.52	66.162	9152	2	479.76	-6.24
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	18	Carbamidomethyl+C(6)	VDPYLCTYYYEINNQK	291	16	3	25.56	y6y8y9	2082.98	71.613	7551	2	1042.00	17.58
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	19		FGDK	200	4	1	12.83	b3	466.23	34.084	4313	1	466.23	7.92
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	20		IEGVPESNVSR	56	11	4	24.33	b4°b4b7y4	1186.63	73.437	2012	1	1186.63	18.72
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	21		NNGSEVQSLDPHKIEGVPESNVSR	43	24	13	105.43	b5°b5*b5y3y5y6y7y10y11y12y14y18y22	2592.24	51.818	78654	4	648.81	-11.40
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	22	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYEINNQK	284	23	7	42.52	b4b15y4y7y8y11y21	2920.40	76.936	40830	3	974.14	5.10
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	23		SPAFDKLIADTLK	468	13	3	28.15	b4b5b11	1418.79	78.374	38470	2	709.90	-2.15
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	24		TVINQVTYLPISSEVTDVNRYS	241	22	4	29.4	y10y13y19y20	2567.35	77.741	16845	3	856.45	-0.48
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	25		NQGDLPAYSYTPPYTDGAKLVEP EWFK	333	27	5	15.35	b7*b7b9y4y6	3086.50	92.212	7371	3	1029.51	8.54
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	26		DLFEGLLISDVEGHPSPGVAEKWE NK	67	26	4	18.31	b3b5b13y6	2866.45	100.343	5620	3	956.15	7.75
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	27		VKNQGDLPAYSYPYTDGAK	331	21	3	22.34	b6y7y8	2285.09	97.694	3377	2	1143.05	-9.08
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	28		LVEPEWFKWSQQK	352	13	5	34.11	b6°b6y5y8y10	1704.85	67.687	3117	3	568.95	-14.32
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	29		FGDKWTQPANIVTNGAYK	200	18	5	23	b5y5*y5y6°y6	2010.00	67.619	2674	2	1005.50	-3.16
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	30		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	2	12.81	y4y7	3091.57	83.861	2983	4	773.65	9.16
O54297 RS4_SALTY 30S ribosomal protein S4	1		VVNIASYQVSPNDVVSIR	128	18	25	209.39	b2b3b8b9b10b14b15°b15b17b18y1y2y3y4y5y7y8y9y10y11y12y13y14°y14y18	1960.07	72.942	66507	2	980.54	9.09
O54297 RS4_SALTY 30S ribosomal protein S4	2		AALELAEQR	156	9	11	74.98	b3y2y3y4y5*y5y6°y6*y6y7y9	1000.53	43.937	56710	2	500.77	-8.85
O54297 RS4_SALTY 30S ribosomal protein S4	3		SDLSADINEHLVLYSK	188	18	3	22.76	b4b7b15	2046.05	99.484	3988	2	1023.53	6.56
O54297 RS4_SALTY 30S ribosomal protein S4	4		IEQAPGQHGAR	33	11	3	27.34	b6y6y7	1163.57	16.474	2246	3	388.53	-21.40
O54297 RS4_SALTY 30S ribosomal protein S4	5		LDNVVYRMGFGATR	97	14	5	19.31	b6°b6*b6y6y13	1598.83	75.579	35415	3	533.61	11.76
O54297 RS4_SALTY 30S ribosomal protein S4	6		EKPTWLEVDAGKMEGTYK	165	18	4	23	b9y9y10°y10	2082.01	64.613	27865	3	694.67	-6.57

I054297 RS4_SALTY 30S ribosomal protein S4	7		KPERSDLSADINEHLIVELYSK	184	22	3	13.45	b7b13y11	2556.33	112.240	5701	3	852.78	-0.29
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	1		DLVESAPAALK	85	11	8	81.81	b2y4y5y6y7y8y9y11	1113.61	54.131	73449	2	557.31	-5.81
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		DQIIEAVSAMSVM DVVELISAMEE K	5	25	24	168.5	b2*b2b3*b3b4b5b6b7b8b10b20y2*y2y3y4y5*y5y6y7y9y10*y10y11y25	2737.34	137.101	26598	3	913.12	3.57
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	3		SITKDQIIEAVSAMSVM DVVELISA MEEK	1	29	9	45.4	y2*y2y3y6y7y9*y9y10y15	3166.61	136.497	5447	3	1056.21	6.71
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	4		SLEEAGAEVEVK	109	12	5	26.28	b5y2y9y10y12	1260.63	45.988	2786	2	630.82	1.84
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	5		EAKDLVESAPAALK	82	14	6	31.57	b4*b4b11b13*b13y8	1441.79	60.934	7674	2	721.40	2.37
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	6		DDAEALKK	101	8	6	62.59	b3y3y4y5*y5y6	889.45	26.583	1958	2	445.23	-10.57
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	7	Oxidation+M(13)	DQIIEAVSAMSVM DVVELISAMEE K	5	25	4	23.12	b17y12y14y15	2753.34	136.669	5108	3	918.45	4.08
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	8	Oxidation+M()	SITKDQIIEAVSAMSVM DVVELISA MEEK	1	29	6	25.31	b6b12b24y4y7y12	3182.58	96.926	3092	4	796.40	-1.07
I0A299 RL7_SALTY 50S ribosomal protein L7/L12	9		VESAPAALK	87	9	0	2.42		885.49	54.093	1748	2	443.25	-14.06
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	1		LVGVGFFTSGGNGAQEAGK	35	19	11	39.17	b1b2b12b16*b16y1y3y4y12y15y19	1795.92	90.539	109756	3	599.31	12.64
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	2		AYPDLDAIIPDANALPAAQAEE NLKR	209	28	21	165.63	b2b5b6b7b8b9b10b11b13y1y4y5*y5y6y9y12y18y19y20y23y28	2863.50	88.330	82219	3	955.17	1.36
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	3		NNLAIVGFSTPNVMRPYVQR	237	20	16	76.98	b2*b2b3*b3b4*b4b5*b5b13y5y12*y12y15y16y17y20	2276.20	78.745	79937	3	759.40	-0.64
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	4	Carbamidomethyl+C(12)	ILTWSDSTKPECR	111	13	12	97.03	b1b2b5y2y4y5y6y7y8y9y11y13	1620.75	50.802	67821	3	540.92	-11.07
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	5		SLQTAEGIIK	199	10	5	33.93	y2y4y5y7y10	1059.60	51.694	57293	2	530.30	-7.83
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	6		VAFFYSSPTVTDQNQWVK	154	18	9	60.91	b6b9b10y7y8*y8y12y13y18	2117.06	78.501	50182	2	1059.03	11.99
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	7		VTVSPNSEQGYHYEAK	301	16	12	99.3	b6*b6y2y4y7y8y10y11y12y13y14y16	1808.83	37.133	49888	3	603.61	-9.65
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	8		EFGLDV VVQQGK	261	12	7	36.2	b6b10y1y4y5*y5y12	1405.71	83.349	42651	2	703.36	-0.61
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	9		ISVYVANALLK	273	11	6	56.02	b4y4y6y7y10y11	1190.71	74.328	36636	2	595.86	-3.28
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	10		SYIINQGTPK	124	10	7	26.94	b2b6y6y8*y8*y8y10	1170.58	39.068	32247	2	585.79	0.31
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	11		GNGIVLLPER	317	10	6	33.93	b2*b2y3y5y6y10	1067.61	62.121	21709	2	534.31	-7.78
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	12		GTVKEFGLDV VVQQGK	257	16	4	17.18	b10*b10b12y8	1790.92	76.931	11805	3	597.65	-11.18
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	13		ISQHEPGWEIVTTQFGYNDATK	177	22	7	29	b3b8*b8y6y7y12*y12	2521.21	127.521	3837	3	841.07	2.52
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	14		IAFIPK	29	6	2	26.87	y4y5	688.43	54.567	17546	2	344.72	-12.23
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	15		QLGSMLEVMAAHQVDK	134	16	4	23.72	b8*b8y5y6	1756.91	90.545	1609	3	586.31	19.52
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	16		SYIINQGTPKQLGSMLEVMAAHQ VDK	124	26	4	15.82	b9b17y9y12	2908.41	110.760	5902	4	727.86	-9.49
I8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	17		EFGLDV VVQQGKISVYVANALLK	261	23	5	43.03	b8b10b11b12b18	2577.39	103.600	5495	3	859.80	-8.53

Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	18		AKISQEHPGWEIVTTQFGYNDATK	175	24	6	22.02	b10°b10y11°y11y12°y12	2720.31	112.879	4465	3	907.44	-9.06
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	19		SSPTVTDQNQWVK	159	13	0	5.24		1489.71	78.533	2956	3	497.24	-13.93
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	20	Carbamidomethyl+C(10)	TWDSDTKPECR	113	11	0	3.23		1394.61	50.807	2228	2	697.81	4.90
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	1		SATPAQAQAVHK	176	12	22	123.37	b2°b2b3°b3b7°b7b12y1y2y3y4y5°y5y6°y6y7°y7y8y9y10°y10y12	1208.63	19.767	40350	2	604.82	-3.53
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	2		TQGAAAFEGAVIAYEPVWAIGTGK	152	24	15	50.36	b1b2°b2°b2b3b7°b7b11b12b15°b15y11°y11y12y24	2407.26	94.471	32900	2	1204.13	13.39
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	3	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	6	12.72	b2b13°b13y1y4y11	2589.31	83.531	30360	3	863.77	0.94
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	4		HPLVMGNWK	2	9	5	53.29	b3y3y5y8y9	1081.56	51.716	10970	2	541.29	2.48
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	5		DIGAQYIIIGHSER	84	14	6	15.62	b2y2y6°y6y12y14	1571.83	65.411	8412	2	786.42	8.70
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	6		ESDELIACK	103	9	4	30.51	b3b7y8y9	1032.56	27.738	6715	2	516.78	-1.66
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	7	Carbamidomethyl+C(9)	EQGLTPVLCIGETEAEENEAGK	117	21	5	22.34	b5°b5b6°b6y9	2245.06	66.224	4033	3	749.02	-2.83
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	8	Carbamidomethyl+C(9)	KELTGVAGCDVAIAPPEMYIDLAK	27	24	4	19.03	b10b13b16y2	2561.31	95.475	2363	3	854.44	2.67
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	9	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	5	23.83	b12y4°y4y9y10	2433.24	89.045	9746	2	1217.12	14.65
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	10	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAEENEAGKTEEV CAR	117	28	20	165.56	b5°b5y3y4y5°y5y7y12°y12y13y14y15y18y20y21y23°y23y24y25y26	3090.45	73.070	181004	3	1030.82	3.79
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	11	Carbamidomethyl+C(5)	TEEV CARQIDAVLK	138	14	3	27.09	b3b4b8	1631.83	45.095	2460	3	544.62	-6.06
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	12	Oxidation+M()	AAAGSHIMLGAQNVLDNLSGAFTGETSAEMLK	52	32	4	22.8	b3b4b9°b9	3220.60	114.415	3913	4	805.91	12.13
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	13		TPAQAQAVHK	178	10	8	44.96	b3°b3b4°b4°b4b5b8°b8	1050.57	19.767	17119	2	525.79	-3.60
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	14		PAQAQAVHK	179	9	10	79.2	b3°b3b4°b4b5°b5b6°b6b7b8	949.52	19.768	14461	2	475.26	-6.69
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	15		PLVMGNWK	3	8	1	8.82	b6	944.51	51.678	6741	1	944.51	6.85
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	16		ATPAQAQAVHK	177	11	3	17.52	b3°b3b5	1121.60	19.778	1942	2	561.30	-8.92
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	17		SATPAQAQAVHK	176	12	0	2.82		1190.61	19.771	13158	3	397.54	-11.59
P0A1Z2 SKP_SALTY Chaperone protein skp	1		IAIVNMGNLFQQVAQK	23	16	27	178.43	b1b2b3b4b6°b6b8b15y1y2°y2y3°y3y4y5°y5y6°y6y7y8y9y11y12y13°y13y16°y16	1773.97	90.543	247937	2	887.49	0.07
P0A1Z2 SKP_SALTY Chaperone protein skp	2		TGVSNTLENEFK	39	12	19	135.36	b2°b2b3b9°b9b10y2y4y5y6y7y8°y8°y8y9°y9y10y11y12	1338.65	58.395	200556	2	669.83	-3.01
P0A1Z2 SKP_SALTY Chaperone protein skp	3		VANDQSIDLVDANTVAYNSSDV K DITADVLK	126	32	13	77.3	b3b4b5°b5b10b11b12°b12°b12b13b15y1y25	3392.72	90.599	94062	3	1131.58	3.60
P0A1Z2 SKP_SALTY Chaperone protein skp	4		IAIVNMGNLFQQVAQKGTGSNTLENEFK	23	28	8	37.6	b8b12y5y8y10°y10y12y23	3093.56	103.478	3165	4	774.15	-14.13
P0A1Z2 SKP_SALTY Chaperone protein skp	5		AAELQKMETDLQSK	53	14	3	19.31	b5y3y6	1591.80	66.217	2200	3	531.27	-0.15
P0A1Z2 SKP_SALTY Chaperone protein skp	6	Oxidation+M(6)	LEKDVMSQR	82	9	4	45	b5b7y3y4	1121.57	75.301	3223	1	1121.57	9.03

P65702 PGK_SALTY Phohoglycerate kinase	1	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	18	133.47	b2b3b4b7b8b9b15°b15y2y3y4y6y8y9y13y14y15y20	2002.04	99.683	200943	2	1001.53	5.73
P65702 PGK_SALTY Phohoglycerate kinase	2		SVNDVKEDEQILDIGDASAQQLAEILK	272	27	24	136.38	b2b4°b4b5°b5°b5b11b12b13°b13b14b17b25b26y1y2y3y4y5y7y10y12y13y27	2941.51	100.727	192931	3	981.18	3.73
P65702 PGK_SALTY Phohoglycerate kinase	3		VLPAVAMLEER	373	11	8	87.26	b3y3y4y6y7y8°y8y9	1227.67	80.820	155107	2	614.34	-4.77
P65702 PGK_SALTY Phohoglycerate kinase	4		VMVTSHLGRPTGEYNEEFSLLPV VNYLK	53	29	9	26.02	b1b2b5b18b21°b21b22y7y29	3321.66	92.801	132120	4	831.17	-7.13
P65702 PGK_SALTY Phohoglycerate kinase	5	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	18	139.85	b2b5°b5b6b7°b7b9b12y2y5°y5y7y8y9y10y11y12y14	1599.84	69.382	113686	2	800.42	0.53
P65702 PGK_SALTY Phohoglycerate kinase	6		VATEFSETAPATLK	258	14	20	163.87	b2b3°b3b4b8b9b14y1y3y5y6y7y9°y9y10y11y12°y12y13y14	1464.76	53.201	109511	2	732.88	1.00
P65702 PGK_SALTY Phohoglycerate kinase	7		SLYEADLVDEAKR	231	13	9	92.83	y2y3y5y6y8y9y10y11y13	1508.74	54.763	97811	3	503.58	-13.59
P65702 PGK_SALTY Phohoglycerate kinase	8		TILWNGPVGVFEPNFR	302	17	20	130.38	b2b11b12b13°b13y2y4*y4y5y6°y6y7*y7y11*y11y12y13°y13y14y17	1993.04	106.996	83182	2	997.03	5.21
P65702 PGK_SALTY Phohoglycerate kinase	9		ADLNVPVKEGK	19	11	12	82.03	b5°b5b9y1y2y3y4°y4y6y7y8y11	1169.66	37.444	68141	2	585.33	3.13
P65702 PGK_SALTY Phohoglycerate kinase	10		ASLPTIELALK	38	11	7	65.56	y1y3y4y6y7y8y11	1155.69	77.954	67861	2	578.35	-6.65
P65702 PGK_SALTY Phohoglycerate kinase	11		LTVLDSLSK	197	9	5	38.3	y2y3y4y6y9	975.56	62.514	64727	2	488.29	-8.70
P65702 PGK_SALTY Phohoglycerate kinase	12		LVKDYLDGVDV AEGELVVLENV R	90	23	7	50.8	b7b8b13y4y5y6y23	2544.36	97.652	58508	3	848.79	1.82
P65702 PGK_SALTY Phohoglycerate kinase	13		TILWNGPVGVFEPNFRK	302	18	8	46.47	b2b12y5y10y13y14y16y18	2121.11	97.398	33326	3	707.71	-6.45
P65702 PGK_SALTY Phohoglycerate kinase	14		MTDLDLAGKR	5	10	6	36.94	b2y1y3y4y5y10	1119.58	43.176	31180	2	560.29	-3.38
P65702 PGK_SALTY Phohoglycerate kinase	15		IADQLIVGGGIANTFVAAQGHSVG K	206	25	7	35.43	b1b2b3b4b5y2y3	2423.29	78.906	30890	3	808.44	-4.43
P65702 PGK_SALTY Phohoglycerate kinase	16	Carbamidomethyl+C(5)	YAALCDVFMDAFGTAHR	128	18	9	60.04	b2b3b4y3y4y6y8y13°y13	2043.94	90.659	18706	3	681.98	-1.91
P65702 PGK_SALTY Phohoglycerate kinase	17		ISYISTGGGAFLEFVEGK	355	18	3	15.6	b9y3y12	1874.93	81.544	1696	2	937.97	-12.11
P65702 PGK_SALTY Phohoglycerate kinase	18		DYLDGVDV AEGELVVLENVR	93	20	3	14.39	b5b8y7	2204.12	116.162	12638	3	735.38	3.88
P65702 PGK_SALTY Phohoglycerate kinase	19		AQASTHGIGK	146	10	4	51.93	y4y6y7y8	969.51	16.588	5128	2	485.26	-5.48
P65702 PGK_SALTY Phohoglycerate kinase	20	Carbamidomethyl+C(6)	RLLTTCDIPVPTDVR	243	15	3	18.16	b8y7y10	1755.93	65.050	7465	3	585.98	-9.80
P65702 PGK_SALTY Phohoglycerate kinase	21		SLYEADLVDEAKR	231	13	4	41.38	b5b6b8b11	1508.75	82.382	6965	3	503.59	-3.16
P65702 PGK_SALTY Phohoglycerate kinase	22		TDLDLAGKR	6	9	2	20.7	b4b7	988.54	43.210	16506	2	494.77	-5.12
P65702 PGK_SALTY Phohoglycerate kinase	23		YEADLVDEAKR	233	11	0	3.23		1308.64	54.770	13546	2	654.83	0.65
P65702 PGK_SALTY Phohoglycerate kinase	24		DLNVPVKEGK	20	10	2	21.89	b3b4	1098.61	37.450	7929	2	549.81	-8.89
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		GYLSPYFINKPETGAVELESPFILLADKK	197	29	25	209.28	b2b3b4°b4b5b12y1y2y3y4y5y6y7y9y10y11y12y13y14y19y22y25y26y27y29	3239.71	96.271	229882	4	810.68	-5.12

IP0A1D3 CH60_SALTY 60 kDa chaperonin	2		EMLPVL EAVAK	231	11	8	68.58	b2y2y3y4y6y8y9y11	1199.66	80.757	143928	2	600.34	-4.58
IP0A1D3 CH60_SALTY 60 kDa chaperonin	3		ANDAAGDGT TATVLAQSIITEGLK	80	25	23	184.08	b2b3*b3b4*b4*b4b5b6b7b25y1y2y3y4y5y6y7y8y9y10y11y12y25	2418.23	92.871	139760	3	806.75	-3.33
IP0A1D3 CH60_SALTY 60 kDa chaperonin	4	Carbamidomethyl+C(18)	SALQYAASVAGL MITTECMVTDLPK	501	25	33	211.31	b2b3*b3b4*b4b5*b5*b5b6*b6b7*b7b8b9*b9b10b11*b11b12*b12y1y2y3y4y5y6y7y10*y10y11y13y15y25	2670.31	124.951	125939	3	890.78	-2.19
IP0A1D3 CH60_SALTY 60 kDa chaperonin	5		AVAAAVEELK	122	10	13	100.08	b2b3b5y1y2y3y4*y4y5y6y7y8y10	1000.56	47.936	105757	2	500.78	-9.94
IP0A1D3 CH60_SALTY 60 kDa chaperonin	6	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	16	89.89	b2*b2b3*b3b5y2y4y5y12*y12y13*y13y14y15y16y18	1957.02	62.476	94439	2	979.01	6.80
IP0A1D3 CH60_SALTY 60 kDa chaperonin	7		QQIEEATSDYDREK	350	14	14	109.48	b14y2y3y5y6y7y8*y8y9y10*y10y12y14*y14	1711.75	34.202	89469	3	571.26	-12.98
IP0A1D3 CH60_SALTY 60 kDa chaperonin	8	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	12	74.41	b2b3*b3y1y2y3*y3y4y6y7y8y10	1063.51	35.991	72146	2	532.26	-1.38
IP0A1D3 CH60_SALTY 60 kDa chaperonin	9		GVNVLADAVK	18	10	7	54.94	y1y3y5y6y8*y8y10	985.56	56.581	65199	2	493.28	-9.04
IP0A1D3 CH60_SALTY 60 kDa chaperonin	10		SFGAPTITK	42	9	14	82.76	b1b2b3b4*b4b8y1y2*y2y3y5*y5y7y9	921.49	45.569	64817	2	461.25	-12.32
IP0A1D3 CH60_SALTY 60 kDa chaperonin	11		VVINKDTTTHIDGVGEEAAIQGR	322	23	21	129.72	b1b2b9b10b11b12b21y2y3*y3y4y5*y5y6y8y9*y9y12y13*y13y23	2399.27	68.105	62933	3	800.43	-2.75
IP0A1D3 CH60_SALTY 60 kDa chaperonin	12		GGDGNYGYNAAETEEYGNMIDMGILDPTK	470	28	9	40.8	y2y3y4y5y8y13*y13*y13y28	2966.32	89.128	58106	2	1483.67	13.99
IP0A1D3 CH60_SALTY 60 kDa chaperonin	13		VEDALHATR	395	9	12	117.68	b2b4b5b6y3y4*y4y5y6y7y8y9	1011.51	26.797	51484	2	506.26	-7.00
IP0A1D3 CH60_SALTY 60 kDa chaperonin	14		AVAAGMNPMDLK	105	12	15	113.45	b2b3y2y4y5y6*y6y7y8y9y10*y10y11*y11y12	1217.60	59.044	42307	2	609.30	-1.10
IP0A1D3 CH60_SALTY 60 kDa chaperonin	15		AIAQVGTISANSDET VGK	142	18	11	89.41	y1y2y8y9y10y11y12y13*y13y14y18	1760.91	49.119	37843	2	880.96	4.99
IP0A1D3 CH60_SALTY 60 kDa chaperonin	16		LIAEAMDK	160	8	8	49.36	b2b6y1y2y3y4y6y8	890.46	39.807	37391	2	445.73	-9.12
IP0A1D3 CH60_SALTY 60 kDa chaperonin	17		ATLEDLGQAK	311	10	4	36.94	y5y6y7y10	1045.55	44.824	36332	2	523.28	-1.05
IP0A1D3 CH60_SALTY 60 kDa chaperonin	18		AMEAPLR	445	7	5	40.5	y2y4y5y6y7	787.40	37.460	23943	2	394.21	-12.71
IP0A1D3 CH60_SALTY 60 kDa chaperonin	19		DTTTHIDGVGEEAAIQGR	327	18	4	22.76	b9b13*b13b15	1845.91	80.031	7975	2	923.46	-7.47
IP0A1D3 CH60_SALTY 60 kDa chaperonin	20		LAGGVAVIK	371	9	6	79.24	b6b7y3y4y7y8	827.52	45.621	70734	2	414.26	-15.93
IP0A1D3 CH60_SALTY 60 kDa chaperonin	21		GQNEQNVGIK	430	11	4	27.34	b5y6y7*y7	1201.58	27.761	35576	2	601.29	0.51
IP0A1D3 CH60_SALTY 60 kDa chaperonin	22		VGAATEVEMK	380	10	3	26.94	b3y3y7	1034.52	36.032	32638	2	517.76	-0.94
IP0A1D3 CH60_SALTY 60 kDa chaperonin	23		VAAVK	272	5	1	13.23	y3	487.32	45.376	14048	1	487.32	-12.02
IP0A1D3 CH60_SALTY 60 kDa chaperonin	24		GYLSPYFINKPETGAVELESPFILLADK	197	28	6	39.03	b3b4b10*b10b11y12	3111.66	102.855	7777	3	1037.89	10.98
IP0A1D3 CH60_SALTY 60 kDa chaperonin	25		FGNDAR	7	6	2	13.63	y4*y4	679.32	77.686	2394	1	679.32	3.68
IP0A1D3 CH60_SALTY 60 kDa chaperonin	26		AAVEEGVVAGGGVALIR	404	17	4	36.76	b3b5b7b14	1567.91	67.141	2349	3	523.31	21.64

P0A1D3 CH60_SALTY 60 kDa chaperonin	27		EGVITVEDGTGLQDELDVVEGMQ FDR	171	26	4	25.6	b7b9y4y5	2851.37	112.528	2032	3	951.13	12.93
P0A1D3 CH60_SALTY 60 kDa chaperonin	28		EIELEDKFENMGAMQMK	58	17	12	81.15	b5°b5b9b10°b10y5y7y8y10*y10y12y13	2010.94	74.085	148814	3	670.98	-6.13
P0A1D3 CH60_SALTY 60 kDa chaperonin	29		IADLKGQNEQNNGIK	425	16	16	159.91	b3b9y3y4y6*y6y7y8y9y10*y10y11*y11y13y14y15	1741.89	40.589	82238	3	581.30	-12.75
P0A1D3 CH60_SALTY 60 kDa chaperonin	30		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	22	128.75	b3b4b5b6b7°b7°b7b10°b10b13y5y6y7°y7*y7y8*y8y10y20y21y26y29	3675.90	122.787	30458	3	1225.97	7.77
P0A1D3 CH60_SALTY 60 kDa chaperonin	31		VAQIRQQIEEATSDYDR	345	17	4	16.34	b3°b3y10y12	2022.01	55.603	4807	3	674.67	9.54
P0A1D3 CH60_SALTY 60 kDa chaperonin	32		AVAAGMNPMDLKR	105	13	4	20.67	b6b8y10°y10	1373.69	56.095	1665	2	687.35	-9.77
P0A1D3 CH60_SALTY 60 kDa chaperonin	33		DGVSVAREIELEDK	51	14	5	39.08	b3b13y7y9y10	1559.77	63.803	1591	2	780.39	-14.48
P0A1D3 CH60_SALTY 60 kDa chaperonin	34	Oxidation+M(2)	AMLQDIATLTGGTVISEEIGMELE K	286	25	7	32.03	b4b5b7b9y5°y5y21	2665.31	93.240	16022	3	889.11	-9.16
P0A1D3 CH60_SALTY 60 kDa chaperonin	35	Carbamidomethyl+C(18) ;Oxidation+M(13)	SALQYAASVAGLMITTECMVTDL PK	501	25	6	12.42	b6°b6°b6y8°y8y10	2686.34	119.902	6219	3	896.12	10.63
P0A1D3 CH60_SALTY 60 kDa chaperonin	36	Oxidation+M(9)	VGAATEVEMKEK	380	12	6	48.19	b3b4b6y10°y10y11	1307.65	74.670	6092	3	436.55	-4.48
P0A1D3 CH60_SALTY 60 kDa chaperonin	37	Oxidation+M(6)	LIAEAMDK	160	8	4	51.12	b5b7y4y5	906.45	97.612	3994	1	906.45	-6.13
P0A1D3 CH60_SALTY 60 kDa chaperonin	38		EDALHATR	396	8	0	1.61		912.45	26.783	42718	2	456.73	-5.55
P0A1D3 CH60_SALTY 60 kDa chaperonin	39		GAPTITK	44	7	2	8.82	b5°b5	687.40	45.571	17606	1	687.40	-8.79
P0A1D3 CH60_SALTY 60 kDa chaperonin	40		NVLADAVK	20	8	0	2.02		829.48	56.544	11587	1	829.48	-2.72
P0A1D3 CH60_SALTY 60 kDa chaperonin	41	Carbamidomethyl+C(4)	SVPCSDSK	134	8	0	2.02		879.39	35.990	3233	1	879.39	5.48
P0A1D3 CH60_SALTY 60 kDa chaperonin	42		EMLPVLEAVAK	231	11	0	2.42		1181.65	80.772	6654	2	591.33	-5.37
P0A1D3 CH60_SALTY 60 kDa chaperonin	43		QQIEEATSDYDREK	350	14	0	3.63		1694.74	34.203	3104	3	565.58	-5.55
P0A1D3 CH60_SALTY 60 kDa chaperonin	44		SFGAPTITK	42	9	0	1.61		903.50	45.528	1534	2	452.25	13.04
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	12	128.14	b2b3b4b5y3y5y6y7y8y9y10y12	1150.68	53.961	83026	2	575.84	-6.05
P66313 RL6_SALTY 50S ribosomal protein L6	2		TLNDAVEVK	35	9	6	38.3	y1y3°y3y7y8y9	988.52	39.157	54773	2	494.76	-9.57
P66313 RL6_SALTY 50S ribosomal protein L6	3		ALLNSMVIGVTEGFTK	69	16	11	84.51	b2b5b6b7y2y5y6y7y8y12y16	1679.90	95.010	51373	2	840.45	-3.49
P66313 RL6_SALTY 50S ribosomal protein L6	4		INGQVITIK	18	9	6	64.76	b3y3y4y7y8y9	985.59	49.033	50665	2	493.30	-9.41
P66313 RL6_SALTY 50S ribosomal protein L6	5		QVIGQVAADLR	138	11	7	68.58	y1y2y3y5y6y8y9	1169.65	57.984	24760	2	585.33	-7.72
P66313 RL6_SALTY 50S ribosomal protein L6	6		HADNALTFGPR	44	11	10	71.01	b2b5y3y4y5y9*y9y10*y10y11	1198.59	46.050	14791	2	599.80	-3.06
P66313 RL6_SALTY 50S ribosomal protein L6	7		YADEVVR	163	7	4	40.5	y3y4y5°y5	851.42	31.060	53301	2	426.21	-8.67
P66313 RL6_SALTY 50S ribosomal protein L6	8	Carbamidomethyl+C(26)	GNVVNLSLGFSPVDHQLPAGIT AECTPTQTEIVLK	99	35	3	10.93	b4y11y22	3741.87	80.474	30561	4	936.22	-15.14
P66313 RL6_SALTY 50S ribosomal protein L6	9		LQLVGVGYYR	86	9	3	38.3	y3y5y6	1004.58	60.199	27236	2	502.79	-6.80

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTpVVISNMDEIKELIK	133	19	19	117.5	b2°b2b3°b3b4°b4b19y3y4°y4y5y6y11°y11y12y13y15y17y19	2130.15	93.160	259376	3	710.72	-8.94
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		MVAPVDGTIGK	59	11	16	111.5	b2b3b8y1y2y3y5°y5y6y7y8°y8y9°y9y10y11	1087.58	46.846	152858	2	544.29	-6.17
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		VGDPVIEFDLPLLEEK	115	16	15	109.94	b1b3b5b6b8°b8y3°y3y6y7y9y10y11y13y16	1812.97	100.295	121242	2	906.99	3.50
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		DTGTIEIVAPLSGEIVNIEDVPDVVFAEK	16	29	5	11.54	b2b5y10y14*y14	3069.57	102.883	2186	3	1023.86	-6.12
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		IVGDGIAIKPTGNK	45	14	19	180.41	b3b4b5°b5y3y4y5°y5*y5y6*y6y7y8y9y10y11y12*y12y13	1382.77	44.166	168702	3	461.60	-20.39
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		VKVGDpVIEFDLPLLEEK	113	18	13	93.54	b5b6b7b9y3°y3y4y6°y6y8°y8y10y13	2040.11	95.812	116164	3	680.71	-9.75
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		IAEEGQRVK	106	9	6	45.51	b3b7b8°b8y8*y8	1029.55	39.716	12552	2	515.28	-13.87
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		PVDGTIGK	62	8	8	65.56	b3b4°b4b5°b5b6°b6b7	786.43	46.828	3755	1	786.43	-10.32
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9		LTPVVISNMDEIKELIK	135	17	1	7.42	b12	1942.07	93.161	1767	2	971.54	-13.51
P00924 ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	21	156.83	b1b2*b2b4*b4b5b6*b6b7*b7b8y2y3y5y6y7y8y9y10*y10y12	1286.71	66.832	102203	2	643.86	-1.71
P00924 ENO1_YEAST Enolase 1	2		VNQIGTLSESIK	346	12	8	68.99	b2b5y5y6y7y8y9y12	1288.71	55.036	88146	2	644.86	-0.19
P00924 ENO1_YEAST Enolase 1	3		SIVPSGASTGVHEALEMR	32	18	12	106.54	b2y1y2y6y7y9y10y11y13y14y15y16	1840.91	62.009	79920	3	614.31	-6.90
P00924 ENO1_YEAST Enolase 1	4		TAGIQIVADDLTVTNPK	312	17	10	77.05	b3b5y3y4y10y11y12y13*y13y17	1755.96	73.258	54977	2	878.48	6.40
P00924 ENO1_YEAST Enolase 1	5		AVDDFLISLDGTANK	88	15	4	18.16	b5y5y8y15	1578.80	83.005	29908	2	789.91	1.24
P00924 ENO1_YEAST Enolase 1	6		WLTGPQLADLYHSLMK	272	16	7	37.92	b1b13y8y9y11y14°y14	1872.94	96.710	22887	3	624.99	-12.58
P00924 ENO1_YEAST Enolase 1	7		AAQDSFAAGWGMVSHR	358	17	5	23.74	y7y10°y10y12y17	1789.85	61.834	3940	2	895.43	3.14
P00924 ENO1_YEAST Enolase 1	8		IEEELGDNAVFAGENFHHGDK	415	21	4	13.89	b7y9y11y21	2328.02	78.365	2413	3	776.68	-13.32
P00924 ENO1_YEAST Enolase 1	9		AADALLK	338	8	6	75.83	b6y3y4y5y6y7	814.49	54.287	79262	2	407.75	-16.19
P00924 ENO1_YEAST Enolase 1	10		TFAEALR	178	7	5	66.96	b3b4y3y5y6	807.42	46.139	60791	2	404.22	-15.50
P00924 ENO1_YEAST Enolase 1	11		YDLDFK	258	6	2	26.87	y3y4	800.37	55.622	60430	2	400.69	-14.26
P00924 ENO1_YEAST Enolase 1	12		LNQLLR	409	6	4	26.87	y4*y4y5*y5	756.46	43.114	40617	2	378.74	-11.70
P00924 ENO1_YEAST Enolase 1	13		IATAIEK	330	7	5	50.72	b6y3y5y6°y6	745.43	28.963	28546	2	373.22	-17.52
P00924 ENO1_YEAST Enolase 1	14		NVPLYK	126	6	2	26.87	b3y4	733.42	37.476	15142	1	733.42	-4.24
P00924 ENO1_YEAST Enolase 1	15		IGSEVYHNLK	185	10	6	40.17	b5b6°b6b8°b8y6	1159.59	94.497	3442	1	1159.59	-17.16
P00924 ENO1_YEAST Enolase 1	16		HLADLSK	132	7	4	50.72	b5y3y4y5	783.43	28.983	1863	2	392.22	-6.15
P00924 ENO1_YEAST Enolase 1	17	Carbamidomethyl+C(5)	IGLDCASSEFFK	243	12	3	22.3	b4y3y6	1373.66	63.886	1655	2	687.33	12.44
P00924 ENO1_YEAST Enolase 1	18		VNQIGTLSESIKAAQDSFAAGWGVMVSHR	346	29	3	11.54	b11y5y12	3059.51	87.148	3659	4	765.63	-7.98
P00924 ENO1_YEAST Enolase 1	19		TFAEALRIGSEVYHNLK	178	17	4	16.34	b5b16y9°y9	1948.05	89.159	2630	3	650.02	8.84
P00924 ENO1_YEAST Enolase 1	20	Phosphoryl STY(12)	AVDDFLISLDGTANK	88	15	3	24.18	b10b11y12	1658.76	72.690	1760	3	553.59	3.09
P00924 ENO1_YEAST Enolase 1	21	Oxidation+M(17)	SIVPSGASTGVHEALEMR	32	18	5	32.79	b6b7b13y8y10	1856.89	60.183	24481	3	619.64	-13.28
P00924 ENO1_YEAST Enolase 1	22	Oxidation+M(17)	SIVPSGASTGVHEALEMRDGDGK	32	22	4	34.79	y3y4y5°y5	2272.09	66.747	2007	3	758.03	-1.07
P00924 ENO1_YEAST Enolase 1	23		PSGASTGVHEALEMR	35	15	4	24.52	b8°b8b9b13	1541.75	61.998	5208	2	771.38	7.21

P0AA28 THIO_SALTY Thioredoxin-1	1		MIAPILDEIADEYQGK	37	16	17	120.61	b2b3b4b11y2y3*y3y4*y4y5y6y10y11°y11y13y14y16	1805.91	94.397	225282	2	903.46	6.89
P0AA28 THIO_SALTY Thioredoxin-1	2		LNIDQNPGTAPK	58	12	25	150.8	b2*b2b4*b4b5°b5*b5b6b10y2y3y5°y5y6°y6y7y8°y8y9°y9*y9y10*y10y11y12	1267.66	39.247	155934	2	634.33	-3.95
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	10	74.98	b2b3y1y2y3y4y5y6y7y9	1001.63	91.220	64493	2	501.32	-12.80
P0AA28 THIO_SALTY Thioredoxin-1	4		IIHLTDDSFDTDVLK	4	15	5	43.96	b3y5y6y7y12	1731.86	72.198	20991	3	577.96	-10.93
P0AA28 THIO_SALTY Thioredoxin-1	5		GQLKEFLDANLA	97	12	3	22.3	b8b10y4	1318.68	46.905	5237	2	659.84	-14.72
P0AA28 THIO_SALTY Thioredoxin-1	6	Oxidation+M(1)	MIAPILDEIADEYQGK	37	16	3	17.18	b13y11y13	1821.91	88.257	7031	2	911.46	9.05
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VAVFTQGPNAEAAK	74	14	15	107.37	b3b4b6b11y3y7y8*y8y9°y9*y9y10*y10y11y14	1402.74	45.958	114822	2	701.87	2.26
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VVGQLGQVLGPR	122	12	14	100.22	b1b2b4y1y2y3y4y5y6y7y8y10*y10y12	1222.72	59.751	87325	2	611.86	-6.89
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VGTVTPNVAEAVK	141	13	17	119.52	b2b3°b3b5°b5b7°b7b13y3y4y7y8y9y10y12°y12y13	1284.71	48.760	85470	2	642.86	-2.85
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		AAGAELVGMEDLADQIK	88	17	7	32.8	b3b6b12°b12y10y12°y12	1730.87	80.502	34773	2	865.94	6.42
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		GATVLPHGTR	60	11	10	70.05	b3°b3b4y2y4y5°y5y6y7y11	1065.57	30.210	17093	2	533.29	-6.07
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		FNESVDVAVNLGIDAR	37	16	5	28.37	b9b13b14y5y16	1718.87	77.743	3628	3	573.63	1.92
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		ELATAK	31	6	2	13.63	b5°b5	632.36	28.951	9824	1	632.36	-4.44
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		VSISTTMGAGVAVDQAGLSASAN	211	23	4	13.06	b7b15y15°y15	2107.08	88.265	2571	2	1054.04	22.36
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9		KGEMNFDVVIASPDAMR	105	17	3	16.34	b5b8y7	1879.88	41.161	30980	3	627.30	-12.66
P0A2A3 RL1_SALTY 50S ribosomal protein L1	10		TVLPHGTR	62	9	0	2.42		937.51	30.207	16621	2	469.26	-8.92
P69226 IF1_SALTY Translation initiation factor IF-1	1		VELENGHVVTAHISGK	23	16	7	17.18	b2°b2b9°b9y1y3y14	1689.87	42.425	40572	3	563.96	-14.66
P69226 IF1_SALTY Translation initiation factor IF-1	2		AKEDNIEMQGTVLETLPNTMFR	1	22	17	85.37	b3b6°b6b11b12°b12y3y4y6°y6y7*y7y9*y9y13y15y22	2537.24	85.129	29444	3	846.42	0.48
P69226 IF1_SALTY Translation initiation factor IF-1	3		VELENGHVVTAHISGKMR	23	18	4	24.85	b6b8b14y9	1977.05	82.428	1560	3	659.69	7.16
P69226 IF1_SALTY Translation initiation factor IF-1	4	Phosphoryl STY()	VELENGHVVTAHISGK	23	16	5	27.7	b7b9°b9b12y4	1769.84	72.198	2206	3	590.62	-5.24
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTSDAVGNAVK	84	17	17	97.42	b2b3b4b5b10b13y2y9y12°y12*y12y13*y13y14*y14y15y17	1739.96	71.549	88773	2	870.48	3.72
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	2		LAATIAQLPDQIGAK	253	15	17	147.24	b1b2b3b5°b5y3y4y5y6y7y8y9*y9y10y11y13y15	1509.86	67.140	55834	2	755.44	-0.49
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	3		IPVITLDR	107	8	5	49.36	b3y4y5y6y8	926.56	62.549	50202	2	463.78	-12.25
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	4		ELANVQDLTVR	70	11	5	41.54	b7y3y6y8y11	1257.68	58.403	29582	2	629.34	-3.69
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	5		VIELQGIAGTSAAR	150	14	14	92.15	b1b2b3y1y5y6y7y9y10y11*y11y12°y12y14	1385.77	59.703	28681	2	693.39	-1.76

P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	6		ADVMVVGFDPDGEK	231	16	5	37.92	b11y4y7y10y11	1636.76	64.414	25540	2	818.89	6.64
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	7		FNVLASQPADFDR	178	13	14	82.04	b2*b2b3*b3y1y2y4y6*y6y8y9y10y11y13	1479.73	67.149	25037	2	740.37	3.13
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	8		GLNVMQNLLTAHPDVQAVFAQN DEMALGALR	193	31	10	18.81	b2b4b13y1y2y4y9*y9y13y31	3336.70	103.375	16102	3	1112.90	4.68
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	9		GVEVADK	268	7	3	40.5	y3y4y5	717.38	38.754	4439	1	717.38	5.53
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	10		IAGDYIAK	135	8	6	49.36	b4*b4b6b7*b7y6	850.46	39.757	3614	2	425.73	-9.76
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	11		ELANVQDLTVRGTK	70	14	3	27.88	b5b8b12	1543.86	89.730	19771	2	772.43	9.17
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	12		ADVMVVGFDPDGEKAVK	231	19	5	49.93	b3b4b5b6y12	1934.95	60.923	8607	3	645.65	-2.84
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	13		GTKILLINPTSDAVGNAVK	81	20	4	22.52	b4y9y10*y10	2026.12	58.357	1965	3	676.04	0.60
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	14	Phosphoryl STY(6)	FNVLASQPADFDR	178	13	4	32.35	b10_H3PO4 b10y3y6y7	1559.70	74.734	13168	3	520.57	11.27
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	15	Phosphoryl STY(25)	LGYNLVVLD SQNNPAKELANVQ DLTVR	54	27	5	22.57	b24y4*y4y11y12	3063.53	86.308	3602	5	613.51	-5.18
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	16	Oxidation+M(4)	ADVMVVGFDPDGEK	231	16	3	17.18	b6b10y4	1652.77	85.098	1605	3	551.60	14.25
P0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	16	83.51	b2b3*b3b4*b4b12b13y1y2y5y8*y8y9y10y11y13	1447.78	65.935	95791	2	724.39	-0.51
P0A297 RL10_SALTY 50S ribosomal protein L10	2		AAAFEGELIPASQIDR	109	16	11	72.96	b7b9y1y5y7y8y9y11y12*y12y16	1687.87	69.449	91877	2	844.44	3.69
P0A297 RL10_SALTY 50S ribosomal protein L10	3	Carbamidomethyl+C(9)	VVEGTQFECLKDTFVGPTLIAYSM EHPGAAAR	62	32	5	18.31	b8b11y6y8y13	3494.69	92.969	67723	4	874.43	-4.19
P0A297 RL10_SALTY 50S ribosomal protein L10	4		DTFVGPTLIAYSM EHPGAAAR	73	21	6	13.89	b2*b2b5y1y9y11	2204.11	62.761	59091	4	551.78	12.85
P0A297 RL10_SALTY 50S ribosomal protein L10	5		GALSAVVADSR	20	11	11	71.01	b3y1y2y4y5y6*y6y7y8*y8y11	1045.56	48.856	55514	2	523.29	0.82
P0A297 RL10_SALTY 50S ribosomal protein L10	6		QAIVAEVSEVAK	8	12	11	49.74	b2b3*b3b12*b12y2y3y8y9y10y12	1243.68	57.938	28924	2	622.34	-6.09
P0A297 RL10_SALTY 50S ribosomal protein L10	7		AGREAGVYMR	43	10	6	52.61	b6b8y3y7y8y10	1109.56	46.844	11542	2	555.28	6.27
P0A297 RL10_SALTY 50S ribosomal protein L10	8		EAGVYMR	46	7	6	50.72	b5*b5y3y4y5y7	825.39	32.558	6720	2	413.20	-8.43
P0A297 RL10_SALTY 50S ribosomal protein L10	9		LMATMK	138	6	1	13.63	y5	694.36	42.570	2561	1	694.36	1.58
P0A297 RL10_SALTY 50S ribosomal protein L10	10		LATLPTYEEAIARLMATMK	125	19	4	14.96	b10y6y18*y18	2123.09	58.492	127734	3	708.37	-14.14
P0A297 RL10_SALTY 50S ribosomal protein L10	11		ALNLQDKQAIVA EVSEVAK	1	19	4	25.9	b9y3y8y9	2026.10	72.143	19576	3	676.04	-7.23
P0A297 RL10_SALTY 50S ribosomal protein L10	12	Carbamidomethyl+C(9)	VVEGTQFECLKDTFVGPTLIAYSM EHPGAAAR	62	32	4	11.15	b6b10*b10y9	3494.68	64.444	8272	4	874.43	-8.45
P0A297 RL10_SALTY 50S ribosomal protein L10	13		GVTVDKMTCLR	31	11	5	35.34	b7b9y4y7*y7	1248.64	68.599	5152	2	624.83	-14.76
P0A297 RL10_SALTY 50S ribosomal protein L10	14		AGREAGVYMR	43	10	6	54.37	b5*b5b6b8y7y8	1109.54	47.385	1666	1	1109.54	-12.10
P0A297 RL10_SALTY 50S ribosomal protein L10	15	Phosphoryl STY(3)	LATLPTYEEAIAR	125	13	3	29.91	y6y9y11_H3PO4 y11	1527.73	77.631	6206	3	509.91	-4.79
P0A297 RL10_SALTY 50S ribosomal protein L10	16	Oxidation+M(2)	LMATMK EASAGK	138	12	3	26.28	b11y10y11	1253.61	31.644	6750	2	627.31	-7.50
P0A297 RL10_SALTY 50S ribosomal protein L10	17	Oxidation+M(9)	AGREAGVYMR	43	10	4	26.94	b4b6y9*y9	1125.56	110.157	2443	1	1125.56	7.70
P0A1V4 KAD_SALTY Adenylate kinase	1		VDGTQAVADV R	195	11	8	36.77	b10*b10y1y2y3y4y9y11	1130.58	37.361	56729	2	565.79	-2.70

P0A1V4 KAD_SALTY Adenylate kinase	2		LVEYHQMTAPLIGYYQK	167	17	15	75.43	b7b9°b9*b9b11b12*b12y1y2y3y5y6y10y12*y12	2054.02	69.882	51857	3	685.35	-8.08
P0A1V4 KAD_SALTY Adenylate kinase	3		IILLGAPGAGK	2	11	11	100.49	b2b3y2y3y4y5y6y7y8y9y11	1009.63	61.799	44576	2	505.32	-7.07
P0A1V4 KAD_SALTY Adenylate kinase	4		YGIPQISTGDMLR	23	13	15	120.77	b2b6b11b12y1y3y6y7y8y9°y9y10y12°y12y13	1450.74	73.422	36909	2	725.87	2.52
P0A1V4 KAD_SALTY Adenylate kinase	5		NGFLLDGFPR	78	10	7	55.62	b1b2b3b7y4y5y6	1135.58	81.385	23242	2	568.29	-8.49
P0A1V4 KAD_SALTY Adenylate kinase	6		LVEYHQMTAPLIGYYQKEAEGN TK	167	25	4	21.96	b8b9°b9y6	2854.38	98.040	9043	3	952.13	-10.61
P0A1V4 KAD_SALTY Adenylate kinase	7		FNPPK	136	5	2	26.46	b3y4	602.32	56.441	28997	1	602.32	-9.73
P0A1V4 KAD_SALTY Adenylate kinase	8		TIPQADAMK	88	9	5	45	b5b7°b7y4y5	974.49	68.079	6274	2	487.75	-12.15
P0A1V4 KAD_SALTY Adenylate kinase	9		GTQAQFIMEK	13	10	6	39.38	b3*b3b6y3y7*y7	1152.55	35.989	2607	2	576.78	-20.23
P0A1V4 KAD_SALTY Adenylate kinase	10		IILLGAPGAGKGTQAQFIMEK	2	21	4	21.72	b3y12y14y17	2143.18	73.355	13189	3	715.07	-5.24
P0A1V4 KAD_SALTY Adenylate kinase	11		GTQAQFIMEKYGIPQISTGDMLR	13	23	5	29.51	b3b4b10b15y9	2584.26	76.311	11913	3	862.09	-10.30
P0A1V4 KAD_SALTY Adenylate kinase	12		LVEYHQMTAPLIGYYQKEAEGN TK	167	25	12	61	b3b6°b6b9°b9*y9y5y6y7*y7y10y11	2854.38	136.493	3271	2	1427.69	-9.84
P0A1V4 KAD_SALTY Adenylate kinase	13		VYHVKFNPPK	131	10	3	33.93	b6b8b9	1228.69	47.683	2549	2	614.85	4.77
P0A1V4 KAD_SALTY Adenylate kinase	14	Carbamidomethyl+C(6)	IAQEDCRNGFLLDGFPR	71	17	3	16.34	b3y5y12	2007.98	94.524	2211	3	670.00	6.08
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	1		VLSESDFQVNQLLDILR	49	17	5	23.74	b2y3y5y13y17	1989.08	105.440	32052	2	995.05	9.57
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	2		GIEGASLDVPDEFVHSGK	72	18	19	85.76	b2b4b5°b5b7°b7b9°b9b11b12y2y6y9°y9y10y11°y12°y12y18	1856.89	67.685	30377	3	619.63	-6.84
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	3		GGDLGQPFQFK	148	11	6	38.35	b2b3b4y5y7y11	1193.59	64.334	18517	2	597.30	-0.20
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	4		GVEATIELNDANK	33	13	4	20.67	b3b5°b5y9	1373.68	51.395	66435	3	458.57	-7.38
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	5		PSFDIVSEVDLQEAR	1	15	9	53.67	b12°b12b13y3°y3y7°y7y8y10	1704.87	85.120	6219	2	852.94	17.76
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	6		GIEGASLDVPDEFVHSGKTWYVE AK	72	25	6	35.6	b4b8b10°b10b11b14	2734.35	136.486	2158	2	1367.68	3.30
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	7	Phosphoryl STY(5)	QGIESAVQKK	99	10	4	26.94	b7y4y7°y7	1167.55	39.706	4227	3	389.86	-14.01
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	8	Oxidation+M(1)	MPSFDIVSEVDLQEAR	0	16	3	17.18	b10y4y9	1851.90	81.582	5727	4	463.73	9.56
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	9		EGASLDVPDEFVHSGK	74	16	1	7.33	b7	1686.81	67.679	2811	2	843.91	5.72
P0A1H3 EFG_SALTY Elongation factor G	1		IATDPFVGNLTFFR	323	14	13	72.9	b2b4b14y4y6*y6y7*y7y10y11°y11y12y14	1597.84	93.982	102765	2	799.42	1.60
P0A1H3 EFG_SALTY Elongation factor G	2		VYSGVVNSGDTVLSVK	337	17	21	135.84	b2b5b6b7b12°b12b13b15°b15b17y4y5y10*y10y11y12*y12y14y15*y15y17	1737.91	62.861	80918	2	869.46	2.32
P0A1H3 EFG_SALTY Elongation factor G	3		SGPLAGYPVVDLGV	562	15	16	124.31	b2b3°b3b5°b5b7°b7y3y4y5y8y9y10y11y12y15	1499.82	77.338	62675	2	750.41	0.49
P0A1H3 EFG_SALTY Elongation factor G	4		IGEVHDDAATMDWMEQEQR	39	20	13	77.77	b5°b5b8b10b12y4y5°y5y6*y6y7y9y20	2332.00	62.837	58967	3	778.00	-0.73

P0A1H3 EFG_SALTY Elongation factor G	5		HASDDEPFSSALAFK	309	14	6	45.47	b2b4b5b6b12y3	1534.73	70.919	53847	2	767.87	5.17
P0A1H3 EFG_SALTY Elongation factor G	6		IHAEVPLSEMGYATQLR	653	18	13	86.21	b2b3b4b5b9°b9y2y3y5y6y7y8°y8	2062.03	90.199	53146	3	688.01	-6.51
P0A1H3 EFG_SALTY Elongation factor G	7		GQYGHVVIDMYPLEGNSPK	512	20	11	45.91	b2°b2b5b8b11b12y6*y6y9°y9y12	2201.06	70.860	48971	3	734.36	-5.32
P0A1H3 EFG_SALTY Elongation factor G	8		GQESEVTGVK	643	10	6	33.93	b2y1y3y4y8y10	1033.51	26.279	47596	2	517.26	-8.74
P0A1H3 EFG_SALTY Elongation factor G	9		EFNVEANVGKPVAYR	475	16	8	84.04	y3y4y5y6y8y10y12y16	1820.91	54.056	43127	3	607.64	-9.12
P0A1H3 EFG_SALTY Elongation factor G	10		VEVETPEENTGDVIGDLSR	618	19	13	61.05	b1b2b5°b5b8b9y3y5y6y11*y11y14y19	2059.00	67.647	26934	2	1030.01	10.08
P0A1H3 EFG_SALTY Elongation factor G	11		AKPVLLEPIMK	607	11	4	36.09	b2y4y6y9	1238.75	63.716	21924	2	619.88	-0.89
P0A1H3 EFG_SALTY Elongation factor G	12		YDDAPNNVAQVIEAR	686	16	6	27.7	b1b3y8y10y12y16	1745.85	66.005	21685	2	873.43	4.75
P0A1H3 EFG_SALTY Elongation factor G	13	Carbamidomethyl+C(9)	DVTTGDTLCDPENPIILER	389	19	4	25.9	b3y3y10y11	2158.06	71.386	21394	2	1079.53	11.43
P0A1H3 EFG_SALTY Elongation factor G	14	Carbamidomethyl+C(11)	VLNNEILVTCGSAFK	255	16	6	37.36	b5*b5b6*b6y7y8	1777.96	79.963	20302	2	889.48	2.61
P0A1H3 EFG_SALTY Elongation factor G	15	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTTGDTLCDPENPIILER	378	30	12	63.3	b7b9b17b19b27y1y3y9y10y11°y11y13	3138.61	85.866	18213	3	1046.88	4.28
P0A1H3 EFG_SALTY Elongation factor G	16		LGANPVPLQLAIGAEEGFTGVVDLVK	161	26	4	21.93	b4y11y12y26	2607.43	120.742	14673	3	869.81	-5.34
P0A1H3 EFG_SALTY Elongation factor G	17		GVQAMLDIVIDYLPSPVDVPAINGILDDGDKDTPAER	273	36	14	56.31	b2b3b4b7b12°b12b13y5y7°y7y10y17°y17y23	3764.93	122.918	12862	3	1255.65	6.16
P0A1H3 EFG_SALTY Elongation factor G	18		GGVIPGEYIPAVDK	541	14	9	72.23	b2b3b4b5b6y7y9y10y14	1414.76	66.192	9112	2	707.89	4.92
P0A1H3 EFG_SALTY Elongation factor G	19		YLGGEELTEEEIK	236	13	4	34.48	b7b8y6y11	1509.73	58.462	5477	2	755.37	0.40
P0A1H3 EFG_SALTY Elongation factor G	20		GITITSAATTAFWSGMAK	59	18	3	34.52	y8y9y10	1813.92	70.494	2602	3	605.31	4.11
P0A1H3 EFG_SALTY Elongation factor G	21		VVGQIK	153	6	1	13.63	b4	643.41	45.616	12775	1	643.41	-4.55
P0A1H3 EFG_SALTY Elongation factor G	22		IAFVNK	137	6	3	29.88	y3*y3y5	691.41	40.727	8046	2	346.21	-1.85
P0A1H3 EFG_SALTY Elongation factor G	23		INIIDTPGHVDFTIEVER	83	18	3	15.6	b3b11y10	2068.06	67.059	4021	4	517.77	-3.31
P0A1H3 EFG_SALTY Elongation factor G	24		LHFGSYHDVDSSELAFK	577	17	4	16.34	b3y6°y6y8	1951.93	50.586	2522	3	651.32	8.13
P0A1H3 EFG_SALTY Elongation factor G	25	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETVWR	104	24	4	16.89	b6b17y14y21	2621.27	76.322	2000	3	874.43	-6.43
P0A1H3 EFG_SALTY Elongation factor G	26		QYEPHR	77	6	1	13.63	b3	829.39	68.687	1689	1	829.39	-11.11
P0A1H3 EFG_SALTY Elongation factor G	27		YLGGEELTEEEIKQALR	236	17	5	34.05	b3b4b13y11y15	1977.99	74.160	77801	3	660.00	-9.07
P0A1H3 EFG_SALTY Elongation factor G	28		ASYTMEFLKYDDAPNNVAQVIEAR	677	25	9	65.25	b8b9b13y5y6y7y8*y8y12	2816.36	85.041	53205	3	939.46	2.34
P0A1H3 EFG_SALTY Elongation factor G	29		HASDDEPFSSALAFKIATDPFVGNLTFFR	309	28	3	11.71	b4b14y11	3113.58	88.996	16846	4	779.15	13.49
P0A1H3 EFG_SALTY Elongation factor G	30		MEFPEPVISIAVEPKTK	408	17	3	23.74	b4b12b14	1915.03	69.809	3523	2	958.02	1.59
P0A1H3 EFG_SALTY Elongation factor G	31	Phosphoryl STY(16)	REFNVEANVGKPVAYREAIR	474	21	5	23.54	b6°b6b14b15°b15	2526.23	82.493	44319	2	1263.62	-7.92
P0A1H3 EFG_SALTY Elongation factor G	32	Carbamidomethyl+C(10);Oxidation+M(7)	VLDGAVMVYCAVGGVQPQSETVWR	104	24	5	28.43	b5b7b13b16y11	2637.27	95.450	12672	3	879.76	-2.41

O33921 AGP_SALTY Glucose-1-phohatase	1		TPIGGQLVFQR	335	11	11	67.04	b2°b2b4b7y3*y3y4y8*y8y9y11	1215.68	62.112	110276	2	608.34	-3.21
O33921 AGP_SALTY Glucose-1-phohatase	2		MGTMDPTFNPVITDDSAAFR	141	20	13	78.51	b2b3b5°b5y2y3y5y6y7y8y12y15y20	2186.01	79.269	73484	2	1093.51	11.62
O33921 AGP_SALTY Glucose-1-phohatase	3		IEYVYQSAR	358	9	11	104.45	b2b3b6b7y3y5y6y7y8°y8y9	1128.57	43.248	54961	2	564.79	-1.73
O33921 AGP_SALTY Glucose-1-phohatase	4	Carbamidomethyl+C(14)	EWLVAQGLIPSGECPADTVYAY ANSLQR	87	29	12	40.78	b3°b3b5°b5b9y2y5°y5y6y9y13y20	3205.59	94.617	46737	3	1069.20	7.08
O33921 AGP_SALTY Glucose-1-phohatase	5	Carbamidomethyl+C(3)	HQCSLIDAK	199	9	7	45	b6*b6b7y2y7y8y9	1071.52	32.037	44105	2	536.27	-2.05
O33921 AGP_SALTY Glucose-1-phohatase	6		DTFSANYQQEPGVQGPLK	208	18	7	40.28	b4b10b13y5y8y13y18	1978.97	57.309	43268	2	989.99	7.34
O33921 AGP_SALTY Glucose-1-phohatase	7	Carbamidomethyl+C(14)	LLEQITHYQDSPCK	182	15	5	43.73	y3y4y9y10y15	1818.85	52.138	38654	3	606.95	-13.02
O33921 AGP_SALTY Glucose-1-phohatase	8		NGYQDSLFTSPTVAR	266	15	7	29.48	b3y1y5y11°y11y13y15	1655.81	63.727	37983	2	828.41	2.95
O33921 AGP_SALTY Glucose-1-phohatase	9		VGNSLVDAFTLQYYEGFPMDDQVA WGGIHTDR	226	31	6	21.84	b7y4y6°y6y7°y7	3486.67	105.194	32072	3	1162.90	8.33
O33921 AGP_SALTY Glucose-1-phohatase	10		APLANNGSVLAQSTPNAWPAWD VPGGQLTTK	43	31	15	71.13	b2b3b4b8b9°b9b10*b10b14b18y3y8y9y13y31	3161.61	84.422	26489	3	1054.54	3.24
O33921 AGP_SALTY Glucose-1-phohatase	11		SQLHLDSEYK	172	10	9	52.61	b1b2b3*b3b7b8y6y8y10	1219.59	40.935	25182	2	610.30	-1.00
O33921 AGP_SALTY Glucose-1-phohatase	12		GGVLEVYMGHYTR	74	13	5	34.11	b3y5y7y10y13	1481.70	64.245	22001	3	494.57	-12.77
O33921 AGP_SALTY Glucose-1-phohatase	13	Carbamidomethyl+C(14)	LLEQITHYQDSPCKEK	182	17	4	34.53	b2y5y6y7	2075.99	48.410	18243	3	692.67	-7.53
O33921 AGP_SALTY Glucose-1-phohatase	14		VTVLVGHDNSIASLLTALDFKPYQ LHDQYER	304	31	24	176.99	b4b9b10*b10b11*b11b12b13°b13b15y4°y4*y4y5y6y7y9y10y12y14y15y16y17y20	3542.77	96.707	165478	5	709.36	-16.19
O33921 AGP_SALTY Glucose-1-phohatase	15		NAEALTLK	370	8	4	33.12	b6*b6y6y7	859.48	41.721	44437	2	430.24	-11.01
O33921 AGP_SALTY Glucose-1-phohatase	16	Carbamidomethyl+C(16)	TVATAQFFITGAFPGCDIPVHHQE K	116	25	3	12.42	b7y9y13	2771.42	101.294	10358	3	924.48	19.56
O33921 AGP_SALTY Glucose-1-phohatase	17		NVAAPLVK	281	8	3	40.9	y3y4y5	811.50	40.698	4060	1	811.50	-6.39
O33921 AGP_SALTY Glucose-1-phohatase	18	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	GCPVDANGFCPLDKFDNMNTA AK	389	24	8	39.49	b4y3y8°y8y18y20y22°y22	2641.19	79.266	92406	3	881.07	1.76
O33921 AGP_SALTY Glucose-1-phohatase	19	Carbamidomethyl+C(8); Carbamidomethyl+C(16)	VTLELKGPCVDANGFCPLDK	383	20	5	23.81	y6°y6y8y9°y9	2233.08	68.586	84649	3	745.03	-7.33
O33921 AGP_SALTY Glucose-1-phohatase	20		LKNGYQDSLFTSPTVAR	264	17	13	104.69	b7b9b10*b10b14y3y4y5y6y7°y7y8°y8	1896.96	59.313	42311	3	632.99	-10.94
O33921 AGP_SALTY Glucose-1-phohatase	21		WHDGNANRDLMK	346	12	7	49.74	b10y6y9y10y11°y11*y11	1456.68	83.009	2653	2	728.84	4.44
O33921 AGP_SALTY Glucose-1-phohatase	22	Phosphoryl STY(29)	APLANNGSVLAQSTPNAWPAWD VPGGQLTTK	43	31	6	24.45	b7*b7b28y4y8y9	3241.59	109.328	1816	4	811.15	10.47
O33921 AGP_SALTY Glucose-1-phohatase	23	Oxidation+M(8)	GGVLEVYMGHYTR	74	13	3	20.67	b6y4y11	1497.71	136.574	4322	1	1497.71	-3.91
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		VLVLVAAPEGIAALEK	155	16	11	119.85	b2b3b4b5b6b7y8y9y10y11y12	1592.97	86.794	26301	2	796.99	4.90
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		AGLGMMEGVLENVPSAR	78	17	11	81.67	b4b13b16y2y3y4y5y7y10y12y17	1730.87	82.563	26062	2	865.94	7.41
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		ITVVPILR	70	8	5	54.13	y4y5y6y7y8	910.60	70.429	15706	2	455.80	-14.75
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		VTIEGWNGPVEIDQIK	51	16	4	23.72	b1b6y11y12	1797.93	75.161	1872	3	599.98	-5.64

P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		LVSNI DER	116	8	3	33.12	b6y6y7	945.49	33.411	27575	2	473.25	-9.30
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	6		ELASEVGSLLTYEATADLETEK	29	22	3	13.45	b4b6y6	2369.21	109.967	2986	2	1185.11	19.06
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	7		AHPDVELY TASIDQGLNEHG YIIP GLGDAGDKIFGTK	171	37	4	10.87	b5b12y14°y14	3911.94	89.499	32015	4	978.74	-0.31
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	8	Phosphoryl STY(14)	FRELASEVGSLLTYEATADLETEK	27	24	3	22.02	b7y9y10	2752.32	98.840	2697	3	918.11	12.06
P67093 UG_SALTY Universal stress protein G	1		HATLPVLVVR	132	10	6	43.18	b2b3y1y7y8y9	1104.68	60.839	98398	2	552.85	-4.97
P67093 UG_SALTY Universal stress protein G	2		NPSITTHLLGSNASSVVR	114	18	12	52.82	b2*b2y2y4y5y9y10*y10y11°y11y18*y18	1852.97	59.200	70783	3	618.33	-11.59
P67093 UG_SALTY Universal stress protein G	3		TIIMPVDVFEMELSDK	3	16	11	84.15	b2b3b4b7y3y4y6y12y13y14y16	1866.93	105.035	68758	2	933.97	6.21
P67093 UG_SALTY Universal stress protein G	4		LQTMVGHF SIDPSR	69	14	8	58.7	b4*b4y3y4y6y11°y11y12	1587.77	64.204	106562	3	529.93	-15.91
P67093 UG_SALTY Universal stress protein G	5		FAADVR	50	6	1	13.63	b3	678.35	75.997	5748	1	678.35	-3.33
P67093 UG_SALTY Universal stress protein G	6		HAEFLAQDGV IHLHLVLP GSAS MSLHRFAADVR	22	34	4	10.99	b18y6y11°y11	3722.90	85.994	12823	4	931.48	-8.46
P67093 UG_SALTY Universal stress protein G	7		MYKTIIMPVDVFEMELSDK	0	19	3	14.96	b3y7y11	2289.11	99.464	2655	3	763.71	-5.01
P67093 UG_SALTY Universal stress protein G	8		FEHLQHEAETRLQTMVGHF SIDP SR	57	26	4	22.83	b7y9y10y12	3094.52	78.524	1801	3	1032.18	14.28
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	1		QGNANIVFFDGITAGEKDFSALIA R	186	25	14	50.44	b2*b2b3*b3b4*b4b11b25y6y13y15y17y18y25	2654.36	105.211	52505	3	885.46	1.10
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	2		TAGLDSSQGPTAAK	139	14	17	115.15	b3°b3b4°b4b5°b5b12y1y4y6y8°y8y10*y10y11y12y14	1303.65	29.602	51391	2	652.33	-0.28
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	3		VAIVGAMSGPVAQWGDMEFNGA R	27	23	6	17.51	b1b2b3b9y5y9	2363.15	88.250	37544	3	788.39	10.85
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	4		LQKENIDFVYYGGYYPEMGQLMR	211	23	5	23.83	b9y6y12y13y23	2814.34	85.727	36893	3	938.78	3.56
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	5		TQFMGPEGVGNASLSNIAGGAAE GMLVTMPK	242	31	11	36.42	b2*b2b3b4y2y4y8y13°y13y17y31	3035.47	93.432	35878	3	1012.50	3.78
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	6	Carbamidomethyl+C(10)	LVGVEYDDACDPK	66	13	6	34.48	b2b3b11y8y9y13	1480.67	47.729	21148	2	740.84	2.06
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	7		QQYGEGLAR	170	9	3	30.51	b6y5y8	1021.50	33.608	3679	1	1021.50	-1.25
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	8		YILETVKPQR	153	10	4	54.94	y3y4y6y8	1246.69	45.878	43604	3	416.24	-18.80
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	9		IAIIHDK	163	7	3	40.5	y3y5y6	809.48	33.558	27954	2	405.24	-13.42
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	10		DPSGPYVWITYAAVQSLATAMTR	293	23	3	13.06	b14y4y10	2498.29	91.992	11645	3	833.44	21.40
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	11	Carbamidomethyl+C(14)	IVNDGIQYVIGHLCSSSTQPASDIY EDEGILMISPGATNPELTQR	87	45	5	37.79	b3b12y12y13y14	4889.42	97.943	11521	3	1630.48	11.98
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	12		QGNANIVFFDGITAGEK	186	17	3	24.99	y3y4y11	1780.87	65.222	8709	3	594.30	-6.92
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	13		RYDQDPANK	273	9	5	59.99	b3b5y3y4y5	1106.52	16.113	3740	2	553.76	-4.96
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	14		GYQYIMRTAGLDSSQGPTAAK	132	21	8	36.29	b3b8b9b12y12*y12y15°y15	2215.08	83.248	2093	3	739.03	0.99
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	15	Oxidation+M(21)	DPSGPYVWITYAAVQSLATAMTR	293	23	5	49.1	b4y7y8y9y10	2514.20	55.135	4011	4	629.31	-11.94
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	16	Oxidation+M(22)	KDPSGPYVWITYAAVQSLATAMT R	292	24	3	12.72	b12y10y15	2642.36	101.638	2166	3	881.46	10.35

Q7CR87 SURA_SALTY Chaperone surA	1		ITVLPQEVDALAK	149	13	11	92.84	b3°b3b4y2y5y8y9y10*y10y11y12	1396.80	71.365	51750	2	698.91	-0.52
Q7CR87 SURA_SALTY Chaperone surA	2		IQELPGIFAQALSTAK	235	16	14	59.36	b2b3°b3*b3b4*b6b11b15y2y4°y4y12y14y16	1686.94	90.649	50698	2	843.98	1.16
Q7CR87 SURA_SALTY Chaperone surA	3		ITDEQLDQAIAANIAK	90	15	6	43.16	b5b9b10y4y5y15	1642.87	81.227	40567	2	821.94	2.75
Q7CR87 SURA_SALTY Chaperone surA	4		LAYDGLNYSTYR	117	12	5	68.98	y3y6y8y10y11	1435.69	59.242	35907	2	718.35	3.83
Q7CR87 SURA_SALTY Chaperone surA	5		LNAGQAGQQLPDDATLR	50	17	11	51.18	b9*b9y1y4y7y8y9y11°y11*y11y17	1767.91	51.604	34290	2	884.46	6.15
Q7CR87 SURA_SALTY Chaperone surA	6		QIGTQNDASTELNLSHILIALPENP TSEQVNDAQR	162	35	4	10.93	b6y3y14y35	3816.93	89.472	26817	3	1272.98	8.12
Q7CR87 SURA_SALTY Chaperone surA	7		QAESIVEEAR	197	10	5	26.94	b6b10y4y8y10	1131.57	38.891	23904	2	566.29	3.34
Q7CR87 SURA_SALTY Chaperone surA	8		VAAVVNNGVVLESVDVGLMQSV K	27	23	13	42.52	b2b3b14y5°y5y8*y8y10y11*y11y13*y13y23	2343.21	91.817	19998	3	781.74	-6.98
Q7CR87 SURA_SALTY Chaperone surA	9		GQSQISIVTEVHAR	274	14	5	45.47	b6y6y8y9y10	1498.74	37.589	18926	3	500.25	-11.40
Q7CR87 SURA_SALTY Chaperone surA	10		LIMDQIILQMGQK	73	13	4	32.35	b6y4y6y7	1530.84	88.808	24493	2	765.92	-0.16
Q7CR87 SURA_SALTY Chaperone surA	11		HILLKPSMINDQQAR	288	16	3	25.56	y7y8y10	1860.99	49.832	7842	3	621.00	-10.04
Q7CR87 SURA_SALTY Chaperone surA	12		EYSQDPGSANQGGLGWATPDIF DPAFR	326	28	5	26.86	y4y7y8y11°y11	3011.38	94.493	3897	2	1506.19	12.73
Q7CR87 SURA_SALTY Chaperone surA	13		QNNMTMDQMR	105	10	3	28.7	b3y5y6	1268.52	53.958	2145	1	1268.52	3.75
Q7CR87 SURA_SALTY Chaperone surA	14		GQISAPVHSSFGWHLIELLDTR	362	22	4	13.45	b6b9*b9y3	2463.29	117.080	1527	3	821.77	3.96
Q7CR87 SURA_SALTY Chaperone surA	15		LAITYSADQALKGGQMGWGR	214	21	7	58.89	y4y8*y8y16y17y18y19	2251.12	65.880	26417	3	751.05	-2.28
Q7CR87 SURA_SALTY Chaperone surA	16		KGDIVGPIR	251	9	3	38.3	y4y7y8	954.56	38.590	21233	2	477.78	-12.08
Q7CR87 SURA_SALTY Chaperone surA	17		TDAAQKDR	388	8	3	36.13	b4y5y7	904.45	41.675	4243	1	904.45	1.08
Q7CR87 SURA_SALTY Chaperone surA	18		GQSQISIVTEVHARHILLKPSIMN DQQAR	274	30	6	40.23	y6y9°y9y10y11y13	3340.74	90.622	3842	4	835.94	-4.17
Q7CR87 SURA_SALTY Chaperone surA	19		RITVLPQEVDALAK	148	14	3	24.75	b4b5y3	1552.89	66.267	2732	2	776.95	-7.86
Q7CR87 SURA_SALTY Chaperone surA	20		KFSEEAATWMQEQR	404	14	4	19.31	b8y4*y4y11	1740.81	57.057	2618	3	580.94	2.45
Q7CR87 SURA_SALTY Chaperone surA	21		LNAGQAGQQLPDDATLRHQILER	50	23	4	13.06	b6*b6b10y3	2544.29	76.000	1562	3	848.77	-13.72
Q7CR87 SURA_SALTY Chaperone surA	22		LNAGQAGQQLPDDATL	50	16	0	4.84		1611.81	51.645	5008	2	806.41	5.76
Q7CR87 SURA_SALTY Chaperone surA	23		GQSQISIVTEVHAR	274	14	0	3.63		1481.74	37.589	1782	3	494.58	4.45
Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTEPTWFPDSQTLAFTSDQAG RPQVYK	287	29	16	80.66	b2b4°b4b5°b5b8y9y11°y11y13y14y21y22y24y25y29	3285.57	78.462	77957	3	1095.86	8.62
Q8ZQT5 TOLB_SALTY Protein tolB	2		WAGPGAAPEDIGGIVAADLR	43	20	11	84.75	b6b7b8y2y4y5y6y9y13y15y20	1936.00	86.308	70097	2	968.51	5.42
Q8ZQT5 TOLB_SALTY Protein tolB	3		VSDYDGYNQFVVHR	183	14	9	68.77	b4b10y2y4y7y9y10y12y14	1698.77	54.525	69442	3	566.93	-10.99
Q8ZQT5 TOLB_SALTY Protein tolB	4		IEITQGVDSARPIGVVPEFK	24	19	13	81.78	b2°b2b11b12*b12y2y3y14y15y16y17y18y19	2026.12	71.179	62378	3	676.04	-7.59
Q8ZQT5 TOLB_SALTY Protein tolB	5		LAYVTFESGR	213	10	5	26.94	b2b3y5y7y10	1142.58	58.279	38981	2	571.80	-0.32

Q8ZQT5 TOLB_SALTY Protein tolB	6		IAYVVQTNGGQFPYELR	166	17	9	34.05	b1b2b3b12y2y5°y5y6y12	1955.02	74.115	31847	2	978.01	10.12
Q8ZQT5 TOLB_SALTY Protein tolB	7		MNINGGAAQR	316	10	12	81.4	b2*b2y1y3y5y6y7*y7y8y9y10*y10	1031.50	28.724	30973	2	516.26	-0.47
Q8ZQT5 TOLB_SALTY Protein tolB	8		TGSLNLYVMDLASGQIR	264	17	4	16.34	b12y9y11y17	1837.95	90.178	28852	2	919.48	0.93
Q8ZQT5 TOLB_SALTY Protein tolB	9		SALVIQTLANGAVR	223	14	7	59.21	b3b4y6y9y10y11y14	1412.82	71.573	25630	2	706.91	-0.09
Q8ZQT5 TOLB_SALTY Protein tolB	10		SPQPLMSPAWSPDGSK	197	16	6	41.35	b1b4b7b9y6y7	1684.81	60.176	11128	3	562.28	8.26
Q8ZQT5 TOLB_SALTY Protein tolB	11		YAGHTASDEVFEK	142	13	3	28.15	b6b9b10	1453.64	37.952	37865	3	485.22	-10.58
Q8ZQT5 TOLB_SALTY Protein tolB	12		HNGAPAFSPDGTK	244	13	4	32.35	b8y9y11y12	1298.63	33.266	13746	2	649.82	15.98
Q8ZQT5 TOLB_SALTY Protein tolB	13		FNPLDR	67	6	1	13.63	y4	761.39	46.076	5568	2	381.20	-2.65
Q8ZQT5 TOLB_SALTY Protein tolB	14		LPATDGQVK	413	9	4	57.55	y4y5y7y8	928.53	28.634	1668	1	928.53	18.47
Q8ZQT5 TOLB_SALTY Protein tolB	15		LPATDGQVKSPAWSPYL	413	17	3	16.34	b9y6y12	1829.95	88.740	156140	3	610.65	3.67
Q8ZQT5 TOLB_SALTY Protein tolB	16		ARLPATDGQVK	411	11	4	41.54	b5b7b9y6	1155.64	29.994	10516	2	578.32	-5.60
Q8ZQT5 TOLB_SALTY Protein tolB	17		SPQPLMSPAWSPDGSKLAYVTFESGR	197	26	9	36.37	b8b10°b10*b10b13y6y8y10y13	2808.38	136.530	2317	2	1404.69	4.17
Q8ZQT5 TOLB_SALTY Protein tolB	18		WAGPGAAPEDIGGIVAADLRNSGK	43	24	3	12.72	b5b7y4	2322.20	103.077	1973	2	1161.60	5.36
Q8ZQT5 TOLB_SALTY Protein tolB	19	Oxidation+M(9)	TGSLNLYVMDLASGQIR	264	17	6	36.76	b7b9°b9b13b15*b15	1853.92	103.053	3084	2	927.46	-11.52
Q8ZQT5 TOLB_SALTY Protein tolB	20		VIQTLANGAVR	226	11	1	7.32	b3	1141.65	71.592	18133	2	571.33	-13.47
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	1		TGEDIPITAR	66	10	11	106.1	b3b4°b4b5°b5y3y5y6y7y9y10	1072.56	43.609	61066	2	536.78	-4.67
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	2		LSGFGNFDLR	45	10	12	52.61	b3b7*b7b10y1y2y4y8y9°y9*y9y10	1125.57	72.875	36749	2	563.29	-2.28
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	3		ALENGEQVK	36	9	9	45	b4*b4b5b9y6°y6y8*y8y9	987.50	29.647	2066	2	494.26	-7.97
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	4		NQRPGR	57	6	1	13.63	b3	727.40	50.523	6164	2	364.20	3.86
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	5		ELVELFFEEIR	24	11	3	24.33	b8y7y9	1423.73	102.622	1923	2	712.37	-10.29
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	6		NPKTGEDIPITAR	63	13	4	32.35	b6b10b11y8	1411.77	56.832	30379	3	471.26	8.99
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	7		DAKELVELFFEEIR	21	14	5	33.05	b3b7y7y8°y8	1737.92	33.503	12596	4	435.24	8.29
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	8		ALENGEQVKLSGFGNFDLR	36	19	4	22.74	b4y6°y6y7	2094.08	57.991	11761	4	524.28	10.84
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	9		SRVENASPK	88	9	3	30.51	b7b8y7	987.52	26.580	2460	2	494.26	-5.44
P66764 METK_SALTY S-adenosylmethionine synthetase	1		SLQEAVMEEIIPILPSEWLNSTSK	197	25	20	98.13	b2°b2b5°b5b6°b6b9b11*b11b12y1y6y7y10y11°y11y12*y12y13y25	2856.51	111.823	54479	3	952.84	2.05
P66764 METK_SALTY S-adenosylmethionine synthetase	2	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGRK	230	16	7	59.35	b13b14y9y10°y10y12y13	1664.81	62.678	27956	3	555.61	-7.92
P66764 METK_SALTY S-adenosylmethionine synthetase	3		ADPLEQQAGDQGLMFGYATNETDVLMPAPITYAHR	109	35	5	21.47	b3y5y9y10y35	3749.79	91.693	6167	3	1250.60	8.66
P66764 METK_SALTY S-adenosylmethionine synthetase	4	Carbamidomethyl+C(3)	VACETYVK	39	8	4	33.12	b4y6°y6y7	969.47	30.113	26075	2	485.24	-5.29
P66764 METK_SALTY S-adenosylmethionine synthetase	5		IIVDTYGGMAR	246	11	3	31.32	y5y7y8	1195.61	53.155	14551	2	598.31	-4.59

[P66764]METK_SALTY S-adenosylmethionine synthetase	6		ETAAYGHFGR	353	10	3	28.7	b7b8y7	1108.52	109.991	2702	1	1108.52	6.28
[P66764]METK_SALTY S-adenosylmethionine synthetase	7		HLFTSESVSEGHDPK	3	15	3	24.18	b12y6y7	1669.81	54.033	2539	2	835.41	16.30
[P66764]METK_SALTY S-adenosylmethionine synthetase	8		TGMVLVGGEITTSAWVDIEEITR	47	23	3	22.09	b12b13y9	2477.22	57.969	1687	3	826.41	-16.16
[P66764]METK_SALTY S-adenosylmethionine synthetase	9		ENFPWEKTDK	363	10	3	26.94	b3b7y8	1293.60	64.403	72496	2	647.30	-11.32
[P66764]METK_SALTY S-adenosylmethionine synthetase	10		QSPDINQGVDRADPLEQGAGDQG LMFGYATNETDVLMPAPITYAHR	98	46	3	11.18	b11y5y9	4959.37	88.973	18405	4	1240.60	8.27
[P66764]METK_SALTY S-adenosylmethionine synthetase	11		SQVTFQYDDGKIVGIDAVVLSTQ HAEDIDQK	166	31	3	11.26	b16y7y27	3419.65	111.248	2580	4	855.67	-14.78
[P66764]METK_SALTY S-adenosylmethionine synthetase	12	Carbamidomethyl+C(10); Oxidation+M(7)	FVIGGPMGDCGLTGRK	230	16	4	24.3	b4b8y8y11	1680.84	69.255	11298	3	560.95	13.65
[P66764]METK_SALTY S-adenosylmethionine synthetase	13	Carbamidomethyl+C(1); Oxidation+M(18)	CEIQVSYAIGVAEPTSIMVETFGTE K	294	26	5	26.5	b6b13y7y10y11	2875.35	76.961	4031	3	959.12	-7.98
[P66764]METK_SALTY S-adenosylmethionine synthetase	14		SLQEAVMEEIIPLPSE	197	18	0	8.07		2026.05	111.786	4255	3	676.02	-11.93
[Q8ZQD4]LOLA_SALTY Outer-membrane lipoprotein carrier protein	1		TLWFYNPFVEQATATWLK	85	18	16	104	b2b3b4b5*b5b6*b6b7y1y2 y3y9y12y13y14y18	2215.15	116.633	34580	2	1108.08	10.58
[Q8ZQD4]LOLA_SALTY Outer-membrane lipoprotein carrier protein	2		DATGNTPFMLIAR	103	13	6	25.44	b2b5*b5b6y7y13	1406.71	79.185	30142	2	703.86	-0.69
[Q8ZQD4]LOLA_SALTY Outer-membrane lipoprotein carrier protein	3		VTDGSGAAVQEGQGDLWVK	44	19	10	50.1	b1b3*b3b5b6b10b13y9y12 y19	1916.94	57.947	17950	2	958.98	5.03
[Q8ZQD4]LOLA_SALTY Outer-membrane lipoprotein carrier protein	4		VSSFHATFTQK	33	11	3	24.33	b5b10y6	1252.61	41.509	9875	3	418.21	-16.76
[Q8ZQD4]LOLA_SALTY Outer-membrane lipoprotein carrier protein	5		QDGDNFVLTPK	128	11	3	27.34	b10y3y4	1233.62	53.834	7846	2	617.31	3.56
[Q8ZQD4]LOLA_SALTY Outer-membrane lipoprotein carrier protein	6		SAYQLKSQQNGAVDPSK	170	17	4	27.43	b8b9b13y12	1820.90	60.856	4684	2	910.96	-5.97
[Q8ZQD4]LOLA_SALTY Outer-membrane lipoprotein carrier protein	7		QDGDNFVLTPKASGNLK	128	18	4	15.6	b8b11*b11y6	1917.96	89.309	3903	2	959.48	-3.12
[Q8ZQD4]LOLA_SALTY Outer-membrane lipoprotein carrier protein	8	Oxidation+M(9)	RPNLFNWHMTQPDESILVSDGK	63	22	4	24.25	b11y5y6y11	2600.25	38.209	6725	3	867.42	-1.22
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	1		TALTDHLDTMAER	70	13	4	28.15	y5y7y8y13	1473.68	52.942	49605	3	491.90	-13.92
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	2		AVQLGGVALGTTQVINSK	83	18	7	31.03	b2b4b15y2y9y11y13	1756.00	68.178	25320	2	878.51	4.10
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	3		AIGEAKDEDTADIFTAASR	134	19	9	81.78	b12*b12b13y4y5y6y7y8y1 3	1980.94	59.032	25121	3	660.99	-4.25
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	4		ASNLLYTR	10	8	4	40.9	y1y4y5y6	937.50	44.785	22233	2	469.25	-11.00
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	5		GANFIADVHEMLDGFR	55	15	4	40.72	y6y8y9y10	1676.85	65.217	2160	2	838.93	14.92
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	6		SYPLDIHNVQDHLKELADR	105	19	5	22.74	b9*b9b10*b10y12	2263.15	83.908	1806	2	1132.08	0.43
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	7		SYPLDIHNVQDHLK	105	14	4	19.31	b10y8*y8y12	1678.85	91.061	2030	2	839.93	-4.22

[Q7CQV9]DPS_SALTY DNA protection during starvation protein	8		SYPLDIHNVQDHLKELADR	105	19	3	21.91	b4b6b8	2263.16	66.634	6178	4	566.55	8.09
[P64052]EFTS_SALTY Elongation factor Ts	1		ITDVEVLK	104	8	4	40.9	y4y6y7y8	916.52	49.222	124491	2	458.77	-12.72
[P64052]EFTS_SALTY Elongation factor Ts	2		VASLEGDVLGSYQHGAR	134	17	15	131.81	b3y4y5*y5y7y8°y8y9y10°y10y11y12y13y15y17	1758.85	59.598	119678	3	586.96	-13.95
[P64052]EFTS_SALTY Elongation factor Ts	3		AEITASLVK	1	9	5	54.54	y3y5y6y7y9	931.54	49.269	102987	2	466.27	-8.91
[P64052]EFTS_SALTY Elongation factor Ts	4		FTGEVSLTGQPFVMEPSK	222	18	7	40.28	b5b11b15y1y3y6y13	1953.98	75.535	75548	2	977.49	9.06
[P64052]EFTS_SALTY Elongation factor Ts	5		GADEELVK	159	8	7	51.12	b3b5°b5b8y5y6y8	860.43	32.032	64083	2	430.72	-6.95
[P64052]EFTS_SALTY Elongation factor Ts	6		IGENINIR	125	8	8	54.13	y2y3*y3y5y6y7°y7y8	928.51	45.149	63474	2	464.76	-10.39
[P64052]EFTS_SALTY Elongation factor Ts	7		VLDAAVAGK	95	9	7	67.77	b2y3y4y6y7y8y9	843.48	34.343	36400	2	422.25	-11.36
[P64052]EFTS_SALTY Elongation factor Ts	8		ALTEANGDIELAIENMRK	25	18	6	32.79	b6°b6b10b11y14y16	1988.00	75.127	33555	3	663.34	-7.80
[P64052]EFTS_SALTY Elongation factor Ts	9		AGNVAADGVK	52	11	7	50.57	y1y2y4y5y6y7y11	1014.55	37.432	21728	2	507.78	-9.51
[P64052]EFTS_SALTY Elongation factor Ts	10	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	7	68.17	b2y3y4°y4y5y6y7	1098.47	21.788	16969	2	549.74	-2.44
[P64052]EFTS_SALTY Elongation factor Ts	11		EHNADVTGFIR	247	11	5	35.34	b3°b3b6y5y9	1258.62	49.947	13672	2	629.82	4.66
[P64052]EFTS_SALTY Elongation factor Ts	12		EYQVQLDIAMQSGKPKEIAEK	193	21	5	30.04	b4°b4b9b10b19	2405.21	73.392	2904	3	802.41	-12.79
[P64052]EFTS_SALTY Elongation factor Ts	13		IGVLVAAK	151	8	4	54.13	y3y5y6y7	770.50	47.734	52019	2	385.75	-19.09
[P64052]EFTS_SALTY Elongation factor Ts	14		EYQVQLDIAMQSGKPK	193	16	8	56.23	b3b9°b9b10b14y10y11y13	1834.95	100.297	28289	2	917.98	8.58
[P64052]EFTS_SALTY Elongation factor Ts	15		ALTEANGDIELAIENMR	25	17	3	16.34	b14y4y6	1859.91	86.839	18901	3	620.64	-1.05
[P64052]EFTS_SALTY Elongation factor Ts	16		VALVAK	119	6	1	13.63	y4	600.41	47.721	3018	1	600.41	0.00
[P64052]EFTS_SALTY Elongation factor Ts	17		DAGFQAFADK	85	10	3	28.7	b4b5y9	1069.47	28.776	2537	2	535.24	-18.95
[P64052]EFTS_SALTY Elongation factor Ts	18		FEVGEGIEKVETDFAAEVAAMSK	258	23	4	28.83	y4y6y7y11	2457.17	106.689	96234	3	819.73	-4.37
[P64052]EFTS_SALTY Elongation factor Ts	19		KAGNVAADGVK	51	12	5	44.21	b3b5y3y4y11	1142.65	32.144	37943	2	571.83	-6.52
[P64052]EFTS_SALTY Elongation factor Ts	20		KALTEANGDIELAIENMR	24	18	4	32.6	y5y6y12y16	1988.02	67.609	11294	2	994.52	6.63
[P64052]EFTS_SALTY Elongation factor Ts	21		RVASLEGDVLGSYQHGAR	133	18	6	47.38	y3y8*y8y9y12y13	1914.97	81.530	1879	2	957.99	-2.42
[P64052]EFTS_SALTY Elongation factor Ts	22	Phosphoryl STY(6)	FTGEVSLTGQPFVMEPSK	222	18	4	26.61	b5y5y6y11	2033.94	77.774	5840	2	1017.47	10.98
[P64052]EFTS_SALTY Elongation factor Ts	23	Oxidation+M(16)	ALTEANGDIELAIENMR	25	17	3	16.34	b4b7y5	1875.91	49.596	1865	3	625.97	-1.30
[P64052]EFTS_SALTY Elongation factor Ts	24		TDVEVLK	105	7	4	40.9	b3b4°b4b5	803.44	49.199	5727	1	803.44	-14.51
[P64052]EFTS_SALTY Elongation factor Ts	25	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	0	2.02		997.42	21.795	4205	2	499.22	-2.02
[P64052]EFTS_SALTY Elongation factor Ts	26		LDAAVAGK	96	8	0	1.61		744.42	34.309	2689	1	744.42	-6.89
[P64052]EFTS_SALTY Elongation factor Ts	27		VLDAAVAG	95	8	1	8.82	y7	715.40	34.289	2288	2	358.20	-3.67
[P64052]EFTS_SALTY Elongation factor Ts	28		EHNADVTGFIR	247	11	1	7.87	y4	1240.59	49.969	1510	3	414.20	-9.35

Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	1		TMNTPHGDAITVFDLR	23	16	12	86.86	b2b10y1y2y3y4y5y6y10y11y12y16	1787.85	71.895	50587	3	596.62	-10.99
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	2		TGFYMSLIGTPDEQR	84	15	7	39.98	b12y3*y3y7y8y12y15	1714.82	79.275	20509	2	857.92	7.05
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	3	Carbamidomethyl+C(15)	VQDQNQIPELNVYQCGTYQMHSLSAQDIAR	113	31	11	52.54	b2*b2b8b10y3y4y9y10y11y24y31	3635.71	75.955	19971	3	1212.57	6.85
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	4		MQAPAVR	13	7	5	37.49	b2b3y3y4y7	772.40	31.203	17693	2	386.71	-11.22
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	5	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCR	65	19	5	28.51	b9b11y5y6y19	2096.97	72.307	5713	3	699.66	-8.73
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	6		MPLLDSFAVDHTR	0	13	3	20.67	b8y3y11	1501.76	61.857	1650	2	751.38	7.48
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	7		PLLDSFAVDHTR	1	12	7	74.65	b5b7b10y3y5y7y8	1370.68	63.864	2296	2	685.84	-20.75
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	8	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCRTGFYMSLIGTPDEQR	65	34	4	13.07	b6b9y7y13	3792.78	107.706	11205	4	948.95	0.97
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	9		TGFYMSLIGTPDEQRVADAWK	84	21	4	13.89	b9y4*y4y12	2385.17	109.980	2700	3	795.73	7.17
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	10	Carbamidomethyl+C(18)	TMNTPHGDAITVFDLRFCIPNK	23	22	3	22.2	b11b12y7	2547.28	136.474	2012	2	1274.14	12.65
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	11	Carbamidomethyl+C(15);Oxidation+M(20)	VQDQNQIPELNVYQCGTYQMHSLSAQDIAR	113	31	3	11.26	b3b7y11	3651.68	105.236	2761	3	1217.90	-1.07
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	12	Carbamidomethyl+C(18);Oxidation+M(16)	DHLNGNGVEIIDISPMGCR	65	19	4	20.73	b3b5y3y9	2112.96	47.397	2660	2	1056.98	-9.71
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	13	Oxidation+M(1)	MPLLDSFAVDHTR	0	13	3	20.67	b6y6y10	1517.76	76.084	2491	2	759.38	9.25
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	14	Oxidation+M(13)	GIHTLEHLFAGFMR	51	14	7	59.12	b7*b7b9b11y3y4y5	1644.84	63.278	2008	2	822.92	4.45
Q8ZP20 TREA_SALTY Periplasmic trehalase	1		VAAAAQAHLQLPGGLATTSVK	428	21	12	58.45	b1b2b9b11y4y7y9*y9y10y13y19y21	2004.11	58.361	31813	3	668.71	-8.04
Q8ZP20 TREA_SALTY Periplasmic trehalase	2		TFADAIPNSDPLMILADYR	68	19	15	61.56	b1b2*b2b5*b5b6y2y4*y4y5*y5y6y9y13y19	2123.07	102.225	29448	2	1062.04	8.62
Q8ZP20 TREA_SALTY Periplasmic trehalase	3		TTTIAPVDLNALLYQLEK	335	18	14	51.88	b3*b3b4*b4b8y1y2*y2y3y5*y5y13y14y18	2003.12	104.358	24799	2	1002.07	8.84
Q8ZP20 TREA_SALTY Periplasmic trehalase	4	Carbamidomethyl+C(6);Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLSATPTK	534	29	5	24.95	b2b3b9y23y24	3199.57	64.719	20341	4	800.65	-3.59
Q8ZP20 TREA_SALTY Periplasmic trehalase	5		DQLTAAALFPLYVNAAAK	405	18	4	24.52	b4b5b7*b7	1877.01	97.867	10266	2	939.01	-4.49
Q8ZP20 TREA_SALTY Periplasmic trehalase	6		EYAYWMEGVETLQPGQQNQNR	243	20	5	14.39	b2b3y5y13y20	2427.11	98.447	9243	4	607.53	1.21
Q8ZP20 TREA_SALTY Periplasmic trehalase	7		WDSLLPLPESYVVPGGR	142	17	5	22.96	b6b11y4y12y17	1884.99	92.247	8049	2	943.00	3.56
Q8ZP20 TREA_SALTY Periplasmic trehalase	8		VADMVANFGYEIDAWGHIPNGNR	183	23	5	29.51	b3b5b8b10y12	2546.18	102.557	3178	3	849.40	-3.07
Q8ZP20 TREA_SALTY Periplasmic trehalase	9		WMDNPQQLSTIR	323	12	3	35.53	y8y9y10	1488.73	63.206	38104	2	744.87	0.74
Q8ZP20 TREA_SALTY Periplasmic trehalase	10		SQPPFFAFMVELLAQHEGDDALK	212	23	6	20.15	b5*b5b9*b9b13y8	2590.21	87.466	35663	3	864.08	-20.64
Q8ZP20 TREA_SALTY Periplasmic trehalase	11		AIEMHLWNNK	380	10	4	26.94	b6*b6y3y7	1255.61	43.162	20609	3	419.21	-11.86
Q8ZP20 TREA_SALTY Periplasmic trehalase	12		FLTNVQHTYDR	486	11	4	24.33	b8y3*y3y7	1393.68	69.883	14627	3	465.23	-1.66
Q8ZP20 TREA_SALTY Periplasmic trehalase	13		LFPDQK	62	6	1	13.63	y3	747.41	51.335	12900	1	747.41	12.33
Q8ZP20 TREA_SALTY Periplasmic trehalase	14		SNPNRPATEIYR	296	12	4	32.23	b7b9y5y8	1417.75	45.118	2564	3	473.25	19.46

Q8ZP20 TREA_SALTY Periplasmic trehalase	15		DTPRPESWVEDIATAK	280	16	3	23.72	b5b6y7	1814.90	56.853	2393	2	907.95	2.42
Q8ZP20 TREA_SALTY Periplasmic trehalase	16		YVPPAGQSLR	113	10	3	26.94	b5b9y5	1087.57	45.519	2026	2	544.29	-14.25
Q8ZP20 TREA_SALTY Periplasmic trehalase	17		NVEKWDSLLPLPESYVVPGR	138	21	5	24.73	b11*b11y3y4y10	2355.24	88.689	30946	3	785.75	1.24
Q8ZP20 TREA_SALTY Periplasmic trehalase	18		QKAIEMHLWNNK	378	12	4	34.29	b6b10b11y7	1511.78	74.082	2732	2	756.39	1.37
Q8ZP20 TREA_SALTY Periplasmic trehalase	19	Phosphoryl STY(8)	HFVDVNFTLPK	98	11	8	52.55	b4b7y5°y5y7y9°y9*y9	1396.67	69.793	14484	2	698.84	10.93
Q8ZP20 TREA_SALTY Periplasmic trehalase	20	Oxidation+M(13)	TFADAIPNSDPLMILADYR	68	19	9	29.46	b6°b6b8°b8b14°b14*b14y7y11	2139.05	103.019	17367	3	713.69	3.08
Q8ZP20 TREA_SALTY Periplasmic trehalase	21	Oxidation+M(9)	SQPPFFAFMVELLAQHEGDDALK	212	23	10	55.94	b9°b9b11y6y7y8y10*y10y11*y11	2606.27	136.433	7956	3	869.43	3.47
P05989 ILVC_SALTY Ketol-acid reductoisomerase	1		GFGVPTLIAVHPENDPQGEGMAIAK	167	25	8	32.32	b2b3b4y2y8y14y21y25	2548.29	77.977	55742	3	850.10	1.34
P05989 ILVC_SALTY Ketol-acid reductoisomerase	2		DGAALGYSHGFNIVEVGEQIRK	123	22	8	29	b3b5°b5b6°b6y6y17y22	2360.20	73.132	52955	3	787.40	0.00
P05989 ILVC_SALTY Ketol-acid reductoisomerase	3		LIQFGWETITEALK	252	14	7	38.56	b3y1y2y9y10y11y14	1648.90	102.187	38951	2	824.95	1.04
P05989 ILVC_SALTY Ketol-acid reductoisomerase	4		AYALSEQLKEIMAPLFQK	284	18	6	21.78	b2b3b8y5y9y18	2080.10	103.967	32714	3	694.04	-6.10
P05989 ILVC_SALTY Ketol-acid reductoisomerase	5		ANYFNTLNL	1	10	15	121.1	b2*b2b3*b3b6b7b9*b9y3y4y6y7*y7y8y10	1225.63	68.620	28887	2	613.32	-5.08
P05989 ILVC_SALTY Ketol-acid reductoisomerase	6		TAFETAPQYEGK	336	12	11	78.91	b4°b4b6y6y7y8°y8y9°y9y10y12	1341.64	42.679	18456	2	671.32	4.19
P05989 ILVC_SALTY Ketol-acid reductoisomerase	7	Carbamidomethyl+C(6)	VVIVGCGAQGLNQLNMR	39	18	3	15.6	b7y6y8	1885.97	65.255	6958	2	943.49	0.06
P05989 ILVC_SALTY Ketol-acid reductoisomerase	8	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21))	SDLMGEQTILCGMLQAGSLLCFDK	215	24	5	19.47	b5°b5b8b12y4	2687.29	93.295	17347	3	896.44	13.45
P05989 ILVC_SALTY Ketol-acid reductoisomerase	9		DGAALGYSHGFNIVEVGEQIR	123	21	7	40.93	b5°b5b14°b14y5y6y7	2232.11	92.204	15716	2	1116.56	3.94
P05989 ILVC_SALTY Ketol-acid reductoisomerase	10		AYALSEQLK	284	9	3	30.51	b4b6y7	1022.55	48.812	5754	2	511.78	-3.70
P05989 ILVC_SALTY Ketol-acid reductoisomerase	11		LVAEGTDPAYAEK	239	13	3	20.67	b10y6y8	1363.65	47.989	5671	3	455.22	-14.59
P05989 ILVC_SALTY Ketol-acid reductoisomerase	12		DEFADGASYLQGK	25	13	4	20.67	b4°b4y9y11	1400.64	94.524	2307	2	700.82	2.70
P05989 ILVC_SALTY Ketol-acid reductoisomerase	13		AWAAATGGHR	192	10	4	28.7	b5y6°y6y7	997.50	107.706	2085	1	997.50	8.51
P05989 ILVC_SALTY Ketol-acid reductoisomerase	14		QGGITLMMDR	266	10	7	54.37	b4b5°b5*b5y3y7y8	1121.56	64.411	1699	2	561.28	14.48
P05989 ILVC_SALTY Ketol-acid reductoisomerase	15		VGTYEELIPQADLVVNLTDPKQHS DVVR	88	28	10	42.93	b6b11b13°b13b16y10y11y13*y13y20	3135.62	82.431	47446	4	784.66	-4.28
P05989 ILVC_SALTY Ketol-acid reductoisomerase	16	Carbamidomethyl+C(11)	DITVVMVAPKCPGTEVR	145	17	3	16.34	b3y7y10	1871.97	58.567	27276	2	936.49	0.13
P05989 ILVC_SALTY Ketol-acid reductoisomerase	17	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21))	SDLMGEQTILCGMLQAGSLLCFDKLVAEGTDPAYAEK	215	37	9	39.43	b3b4b10y4y6°y6y9y11y17	4031.95	118.686	13869	3	1344.66	10.05
P05989 ILVC_SALTY Ketol-acid reductoisomerase	18		LIQFGWETITEALKQGGITLMMDR	252	24	3	22.02	b11y11y12	2751.41	75.055	5944	3	917.81	-2.57
P05989 ILVC_SALTY Ketol-acid reductoisomerase	19	Phosphoryl STY(10)	LVAEGTDPAYAEK	239	13	5	20.67	b7°b7b9y3°y3	1443.64	83.341	3240	3	481.89	7.69
P05989 ILVC_SALTY Ketol-acid reductoisomerase	20	Phosphoryl STY(8)	DSGLDISYALRK	57	12	4	36.2	b4b7y6_H3PO4 y5y6	1417.68	136.520	1800	1	1417.68	11.45
P05989 ILVC_SALTY Ketol-acid reductoisomerase	21	Phosphoryl STY(3)	LLTWREETGK	326	10	3	26.94	b3b6y6	1312.61	136.469	1575	1	1312.61	-9.95

P05989 ILVC_SALTY Ketol-acid reductoisomerase	22	Oxidation+M(6)	DITVVMVAPK	145	10	3	26.94	b3b6y3	1088.60	29.655	19675	2	544.80	-1.57
P0A1P6 GLNA_SALTY Glutamine synthetase	1		AGGVFTDEAIDAYIALR	430	17	5	16.34	b5b14y2y12y17	1781.88	77.247	61826	2	891.44	-13.77
P0A1P6 GLNA_SALTY Glutamine synthetase	2		LVPGYEAPVMLAYSAR	322	16	8	53.2	b15y1y2y9y11y13y14y15	1736.91	78.365	38069	2	868.96	4.99
P0A1P6 GLNA_SALTY Glutamine synthetase	3		GGYFPVPPVDSAQDIR	177	16	11	74.35	b3b6b12b14y2y4°y4y10y11y12y16	1717.86	70.768	31802	2	859.43	4.55
P0A1P6 GLNA_SALTY Glutamine synthetase	4		AINALANPTTNSYKR	307	15	13	89.09	b2b3y4y6y7*y7y8*y8y9*y9y10y13y15	1633.85	43.350	29927	3	545.29	-8.74
P0A1P6 GLNA_SALTY Glutamine synthetase	5		ATGIADTVLFGPEPEFFLFDDIR	117	23	13	56.48	b2°b2b4b6°b6b13b21y1y2y4y5°y5y6	2570.28	117.946	22352	3	857.43	-1.61
P0A1P6 GLNA_SALTY Glutamine synthetase	6		NLYDLPPEEAK	395	11	6	47.78	b4b6b7y4°y4y6	1288.65	45.021	19494	3	430.22	6.44
P0A1P6 GLNA_SALTY Glutamine synthetase	7		GINESDMVLPMDASTAVIDPFFADSTLIIR	59	30	13	95.24	b9*b9y3y4y6y7y8y9y11y12y13y20y30	3238.62	114.200	14208	3	1080.21	5.43
P0A1P6 GLNA_SALTY Glutamine synthetase	8		AINALANPTTNSYK	307	14	4	38.77	y7y9y10y12	1477.76	48.612	12989	2	739.39	-0.99
P0A1P6 GLNA_SALTY Glutamine synthetase	9		SAEHVLTMLNEHEVK	1	15	6	24.18	b2b6°b6b7y9*y9	1736.84	55.669	7484	3	579.62	-10.89
P0A1P6 GLNA_SALTY Glutamine synthetase	10	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	8	27.62	b7b15°b15y2y5y7y8y24	2565.28	136.702	7400	3	855.77	-2.57
P0A1P6 GLNA_SALTY Glutamine synthetase	11		EIPQVAGSLEEALNALDLDR	406	20	5	19.79	b8b10°b10y12y15	2153.12	102.913	3510	2	1077.06	5.44
P0A1P6 GLNA_SALTY Glutamine synthetase	12		MSAEHVLTMLNEHEVK	0	16	4	17.18	b3b7y10°y10	1867.90	68.661	3648	2	934.45	-3.40
P0A1P6 GLNA_SALTY Glutamine synthetase	13		FNTMTK	225	6	2	13.63	b5*b5	741.35	31.896	3231	1	741.35	-9.96
P0A1P6 GLNA_SALTY Glutamine synthetase	14		FGASISGSHVAIDDIEGAWNSSTK	140	24	4	22.02	b11y4y5*y5	2449.17	86.569	3123	3	817.06	3.49
P0A1P6 GLNA_SALTY Glutamine synthetase	15	Carbamidomethyl+C(1)	CDILEPGTLQGYDR	89	14	5	27.61	b7°b7b11y5y9	1636.77	75.543	1603	3	546.26	5.74
P0A1P6 GLNA_SALTY Glutamine synthetase	16		NGTNLFSGDKYAGLSEQALYYIGGVIK	277	27	3	11.92	b3b10y13	2878.45	111.814	23105	4	720.37	-4.41
P0A1P6 GLNA_SALTY Glutamine synthetase	17		GKEQHV TIPAHQVNAEFFEEGK	26	22	3	13.45	b3b5y11	2495.25	113.409	11489	3	832.42	7.34
P0A1P6 GLNA_SALTY Glutamine synthetase	18		EIPQVAGSLEEALNALDLDFLFLK	406	24	3	23.01	y19y21y22	2670.40	112.777	9532	3	890.80	-0.55
P0A1P6 GLNA_SALTY Glutamine synthetase	19		FGASISGSHVAIDDIEGAWNSSTKYEGGNK	140	30	4	14.19	b9b12y5y13	3097.49	77.172	6296	4	775.13	12.61
P0A1P6 GLNA_SALTY Glutamine synthetase	20		ATGIADTVLFGPEPEFFLFDDIRFGASISGSHVAIDDIEGAWNSSTK	117	47	6	22.02	b8b14b15y6y11*y11	5000.37	69.825	5974	5	1000.88	-10.45
P0A1P6 GLNA_SALTY Glutamine synthetase	21		IHPGEAMDKNLYDLPPEEAK	386	20	6	38.9	b7b11b13b16y8y15	2267.07	68.510	4512	3	756.36	-14.11
P0A1P6 GLNA_SALTY Glutamine synthetase	22		HAKAINALANPTTNSYK	304	17	6	39.19	y3°y3y4y5*y5y12	1813.94	86.284	1799	3	605.32	-7.27
P0A1P6 GLNA_SALTY Glutamine synthetase	23	Carbamidomethyl+C(11);Oxidation+M(17)	FPDPAANPYLCFAALLMAGLDGIK	360	24	3	23.01	b4b8b9	2581.29	87.033	4531	3	861.10	3.59
P0A1P6 GLNA_SALTY Glutamine synthetase	24	Carbamidomethyl+C(4);Oxidation+M()	SEMCLVMEQMGLVVEAHHHEVA TAGQNEVATR	193	32	5	36.6	y8°y8*y8y9y10	3579.66	96.177	3123	3	1193.89	4.84
P0A1P6 GLNA_SALTY Glutamine synthetase	25		NALANPTTNSYKR	309	13	0	4.03		1449.74	43.366	2517	2	725.38	0.17
P66932 TIG_SALTY Trigger factor	1		NVALEEQAVEAVLAK	399	15	14	89.1	b2b3b4b5b9y1y3y5y11*y11y12y13°y13y15	1583.86	80.916	72572	2	792.44	0.46
P66932 TIG_SALTY Trigger factor	2		FGVEDGSVAGLR	255	12	11	59.2	b2b3b8b10°b10y1y2y8y9y11y12	1206.60	57.972	38418	2	603.81	-6.27

P66932 TIG_SALTY Trigger factor	3		GLIEEMASAYEDPKEVIEFYSK	368	22	8	36.44	b2b5°b5b6b14y5y10y19	2548.23	98.875	37194	3	850.08	7.28
P66932 TIG_SALTY Trigger factor	4		ANDIDVPSALIDSEIDVLRR	296	20	9	28.05	b2*b2b3b5*b5y1y4y14y16	2211.15	91.269	35074	3	737.72	-6.29
P66932 TIG_SALTY Trigger factor	5		ELPELTEEFIKR	243	12	4	32.52	y4y7y10y12	1503.79	72.080	28780	3	501.93	-11.61
P66932 TIG_SALTY Trigger factor	6		VEERELPELTEEFIK	239	15	5	18.16	b4°b4b10°b10y11	1860.94	96.737	20875	2	930.97	-10.76
P66932 TIG_SALTY Trigger factor	7		INPAGAPNYVPGEYK	83	15	8	52.42	b7b10b12b14y1y6y8y15	1589.79	62.098	17123	2	795.40	-3.92
P66932 TIG_SALTY Trigger factor	8		ANDIDVPSALIDSEIDVLR	296	19	7	31.67	b4°b4b6y3y13y14y19	2055.08	95.373	16384	2	1028.04	10.69
P66932 TIG_SALTY Trigger factor	9		MIPGFEDGVK	193	10	6	40.17	b5b10y6y7y9y10	1092.53	59.065	15315	2	546.77	-8.94
P66932 TIG_SALTY Trigger factor	10		NKELMDNMR	390	9	11	59.99	b1b2*b2b3b7b8y2y3*y3y4°y4	1150.54	35.965	7173	2	575.77	5.20
P66932 TIG_SALTY Trigger factor	11		QDVLGDLMSR	63	10	3	26.94	b3b5y3	1133.55	34.909	13031	2	567.28	-11.95
P66932 TIG_SALTY Trigger factor	12		YGASVR	57	6	1	13.63	b4	652.34	27.574	9051	1	652.34	-2.15
P66932 TIG_SALTY Trigger factor	13		GLIEEMASAYEDPK	368	14	3	27.88	b6b8b12	1552.72	71.468	7995	2	776.86	0.71
P66932 TIG_SALTY Trigger factor	14		ATSFNELMNQQA	420	12	3	22.3	b4y3y7	1353.63	64.983	4395	2	677.32	13.08
P66932 TIG_SALTY Trigger factor	15		MQVSVETTQGLGR	0	13	3	20.67	b3b6y11	1405.74	57.154	4316	2	703.37	19.10
P66932 TIG_SALTY Trigger factor	16		ATDFVLAMGQGR	181	12	3	22.3	b3b10y6	1265.64	58.592	3509	3	422.55	5.98
P66932 TIG_SALTY Trigger factor	17		ELPELTEEFIK	243	11	5	31.32	b3°b3b4b7°b7	1347.73	85.115	1925	2	674.37	19.75
P66932 TIG_SALTY Trigger factor	18		GLIEEMASAYEDPKEVIEFYSK	368	22	5	49.21	b6b7b8y4y5	2548.18	82.498	38593	3	850.07	-13.41
P66932 TIG_SALTY Trigger factor	19		EKINPAGAPNYVPGEYK	81	17	4	16.34	b14y10°y10y13	1846.94	76.797	32004	3	616.32	2.97
P66932 TIG_SALTY Trigger factor	20		RFGVEDGSVAGLR	254	13	5	41.39	b6b9b10y7y10	1362.70	49.763	13952	3	454.91	-8.78
P66932 TIG_SALTY Trigger factor	21		MIPGFEDGVKGHK	193	13	3	25.44	b3b4y3	1414.71	38.728	5470	3	472.24	-3.37
P66932 TIG_SALTY Trigger factor	22		QVSVETTQGLGRR	1	13	3	20.67	b10y6y11	1430.76	57.813	2256	3	477.59	-6.14
P66932 TIG_SALTY Trigger factor	23		VKGLIEEMASAYEDPK	366	16	4	24.89	y4y8°y8y12	1779.87	90.565	1960	2	890.44	-7.34
P66932 TIG_SALTY Trigger factor	24		FGGNEKQALELPR	321	13	4	28.15	b4b8°b8b9	1458.75	57.317	1785	2	729.88	-14.64
P66932 TIG_SALTY Trigger factor	25	Oxidation+M(1)	MQVSVETTQGLGR	0	13	3	20.67	b4y3y9	1421.69	73.411	1711	2	711.35	-9.62
P66932 TIG_SALTY Trigger factor	26		ELPELTEEFIKR	243	12	0	2.82		1485.77	72.080	10682	3	495.93	-12.98
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	18	169.31	b2b3b4b7y3y5y6y7y9y10y11°y11y12y14y15y17y19y21	2215.16	75.837	49416	3	739.06	-7.05
Q56073 DNAK_SALTY Chaperone protein dnaK	2		MQELAQVSQK	587	10	7	47.95	b2*b2b3y3y5y8y10	1161.59	37.903	34386	2	581.30	-0.53
Q56073 DNAK_SALTY Chaperone protein dnaK	3		QAVTNPQNTLFAIKR	56	15	4	26.24	b15y3y5y8	1700.92	59.363	33792	3	567.64	-14.43
Q56073 DNAK_SALTY Chaperone protein dnaK	4		ASSGLNEEEIQK	502	12	5	44.96	y4y7y9y10y12	1304.63	35.472	20761	2	652.82	-0.66
Q56073 DNAK_SALTY Chaperone protein dnaK	5		IELSSAQQTVDNLPYITADATGPK	270	24	5	12.72	b1b2b3b9y5	2532.29	88.391	19483	4	633.83	2.60

[Q56073]DNAK_SALTY Chaperone protein dnaK	6		LESLVEDLVNR	304	11	6	27.34	b2b3b4y1y2y6	1286.70	78.439	12825	2	643.86	5.88
[Q56073]DNAK_SALTY Chaperone protein dnaK	7		TTPSIIAYTQDGETLVGQPAKR	34	22	3	13.45	b11y6y20	2346.22	69.083	12211	3	782.74	-4.99
[Q56073]DNAK_SALTY Chaperone protein dnaK	8		QAVTNPQNTLFAIK	56	14	5	24.75	b3y2y11y12y14	1544.84	68.141	10785	2	772.93	-0.32
[Q56073]DNAK_SALTY Chaperone protein dnaK	9		VLENAEGDR	25	9	4	38.3	b9y3y4y7	1002.49	23.899	4752	2	501.75	8.22
[Q56073]DNAK_SALTY Chaperone protein dnaK	10		IIGADNGDAWLDDVK	92	14	4	19.31	b6*b6b8y7	1486.74	53.203	17942	2	743.87	-8.79
[Q56073]DNAK_SALTY Chaperone protein dnaK	11		SLGQFNLDGINPAPR	452	15	5	24.18	b3*b3b4*b4y12	1598.81	35.971	10395	3	533.61	-12.06
[Q56073]DNAK_SALTY Chaperone protein dnaK	12		TTPSIIAYTQDGETLVGQPAK	34	21	3	13.89	b8b12y11	2190.08	93.144	2927	3	730.70	-21.96
[Q56073]DNAK_SALTY Chaperone protein dnaK	13		TFEVLATNGDTHLGGEDFDTR	214	21	4	20.53	b11*b11b15b20	2295.02	73.347	2645	4	574.51	-13.94
[Q56073]DNAK_SALTY Chaperone protein dnaK	14		DVNPDEAVAIGAAYVGGVLTGDVK	363	24	3	22.02	b13b14y5	2295.19	76.296	2548	2	1148.10	1.70
[Q56073]DNAK_SALTY Chaperone protein dnaK	15		TIAVYDLGGGTFDISIIEIDEVDGEK	188	26	3	12.15	b6b10y11	2769.42	87.039	1609	3	923.81	18.51
[Q56073]DNAK_SALTY Chaperone protein dnaK	16		FEELVQTRNQGDHLLHSTR	528	19	4	14.96	b5*b5b12y13	2280.17	85.096	8884	3	760.73	10.49
[Q56073]DNAK_SALTY Chaperone protein dnaK	17		KTAEDYLGEPTVEAVITVPAYFND AQR	124	27	6	39.7	b3b7y7y8y9y12	2997.51	89.692	8081	3	999.84	9.20
[Q56073]DNAK_SALTY Chaperone protein dnaK	18		KVAEFFGK	351	8	4	33.12	b7y4y5*y5	925.50	77.853	6801	2	463.25	-14.11
[Q56073]DNAK_SALTY Chaperone protein dnaK	19	Carbamidomethyl+C(14)	GKIIGIDLGTNSCVAIMDGTQAR	1	24	3	12.72	b17y6y12	2491.23	71.094	6125	3	831.08	-13.33
[Q56073]DNAK_SALTY Chaperone protein dnaK	20		ITIKASSGLNEEEIQK	498	16	4	37.36	b12b13y5y6	1759.94	100.663	2768	2	880.47	-4.58
[Q56073]DNAK_SALTY Chaperone protein dnaK	21		IIGADNGDAWLDDVKGQK	92	17	3	16.34	b8b11y10	1799.94	106.730	1640	3	600.65	5.83
[Q56073]DNAK_SALTY Chaperone protein dnaK	22	Phosphoryl STY(9)	IELSSAQQTVDNLPYTADATGPK	270	24	3	12.72	b7y7y15	2612.24	98.603	54567	4	653.81	-1.31
[Q56073]DNAK_SALTY Chaperone protein dnaK	23	Phosphoryl STY(9)	QAVTNPQNTLFAIK	56	14	4	33.05	b5b8y7y8	1624.80	97.929	1985	3	542.27	-2.70
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	1		AGMAVGLAGLFLESHDPANAK	226	22	9	68.12	b3b4b5y3y4y6*y6y7y22	2166.08	88.958	20687	3	722.70	-9.47
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	2	Carbamidomethyl+C(17)	VSGNSPVIFDVTHALQCR	189	18	10	43.8	b6*b6b12*b12b13y2y4*y4y9y10	1999.98	80.154	10641	3	667.33	-11.72
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	3		VANDLPFVFLFGGMNVLESR	12	19	11	62.51	b2b3b5b11y2y3y4y9y10y14y19	2078.05	110.960	9957	3	693.35	-13.51
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	4	Carbamidomethyl+C(4)	VILCDR	162	6	1	13.63	b4	775.42	28.963	6315	2	388.22	12.36
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	5		GANFGYDNLVVDMLGFSVMK	168	20	3	14.39	b4y6y9	2177.08	75.966	3362	2	1089.05	19.96
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	6		IFQELK	79	6	1	13.63	y3	777.45	32.410	2967	2	389.23	0.39
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	7		GANFGYDNLVVDMLGFSVMKK	168	21	3	20.53	b6b10b19	2305.15	79.118	25692	3	769.06	7.10
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	8	Carbamidomethyl+C(23)	AGMAVGLAGLFLESHDPANAKC DGPSALPLAK	226	33	3	16.83	b3b5b15	3275.69	89.642	5770	4	819.68	11.11
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	9		ASFDKANR	55	8	3	40.9	b3b4b7	908.46	79.833	4749	1	908.46	-1.34
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	10		KPQFVSPGQMGNIVDKFHEGGNDK	138	24	3	22.02	b10b11y12	2629.29	109.906	4362	3	877.10	4.09
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	11	Oxidation+M(3)	AGMAVGLAGLFLESHDPANAK	226	22	5	18.2	b7b14y5*y5y11	2182.07	95.746	17623	3	728.03	-9.85

P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	12	Oxidation+M(8)	QTDLVEAMAK	120	10	10	60.39	b3°b3b7°b7°b7b9°b9y3y9°y9	1121.54	68.532	6213	2	561.28	-6.42
P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	13	Oxidation+M(13)	VANDLPFVLFGGMNVLESR	12	19	4	24.13	y3°y3y8y9	2094.07	67.207	6100	3	698.69	-0.58
P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	14	Oxidation+M(8)	GPGLLEEGRMK	70	9	4	45	b5b7y4y8	933.45	69.250	5087	1	933.45	13.01
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	24	130.76	b2°b2b3b5°b5°b5b8b9°b9b11°b11b12°b12b16y4y5y6y7y9y10°y10y12y17y23	2379.24	65.299	117692	3	793.75	-0.82
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2		AQAFTLVAK	24	9	6	38.3	b2°b2y3y4y7y9	948.54	53.880	75184	2	474.78	-8.43
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	8	32.79	b2b3b5y2y6y13y14y18	1919.02	86.002	59313	2	960.01	6.23
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	13	101.38	b2b3b4b10b11°b11y3y4y5y6y12y15y17	1837.96	86.831	48395	2	919.49	8.90
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		DLSDVLSQYAGK	33	13	9	71.83	b3b5y2y4y6y9y10y11y13	1382.68	60.182	41069	2	691.85	2.12
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		NYGVEIVDGPLK	116	12	5	32.52	b2y4y8y10y12	1303.69	65.536	38283	2	652.35	2.62
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		DLSDVLSQYAGKR	33	14	5	19.31	b4y9°y9y11y14	1538.78	55.590	8995	2	769.90	1.35
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8		AVIVLDENDNVIFSQLVDEITHEPDYDAALNVLK	133	34	6	22.92	b2b3b4b10°b10y34	3811.95	119.037	7859	3	1271.32	6.85
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVRK	48	19	6	42.94	b3y10°y10y11y13y14	2047.08	78.399	5685	3	683.03	-10.02
Q8ZP65 TPX_SALTY Probable thiol peroxidase	10		AVIVLDENDNVIFSQLVDEITHEPDYDAALNVLKA	133	35	20	153.33	b3b4b5b7b8b11°b11b32y3y4y5y6y7y8y12y13y20y24y27y31	3882.98	120.861	74152	3	1295.00	4.78
Q8ZP65 TPX_SALTY Probable thiol peroxidase	11		NNEFLKNYGVEIVDGPLK	110	18	4	26.61	b7b9b10y5	2049.06	77.087	15586	3	683.69	-1.91
Q8ZP65 TPX_SALTY Probable thiol peroxidase	12	Phosphoryl STY(13)	MSQTVHFQGNPVTVANVIPQAGSK	0	24	4	23.01	b5b12°b12b13	2590.21	98.673	3326	4	648.31	-11.12
P26982 DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	7	59.33	b3b4b5y3y4y9y16	2017.08	75.641	71472	3	673.03	-11.68
P26982 DEGP_SALTY Protease do	2		GYVVTNNHVVDNASVIK	124	17	14	106.74	b2b3b6y1y2y3y6y7y8y9y10y14y16y17	1828.94	50.715	59875	3	610.32	-11.01
P26982 DEGP_SALTY Protease do	3		SDIALIQINPK	160	12	10	64.43	b3°b3b10y2y4°y4y5y6y7y12	1339.75	64.721	42176	2	670.38	-5.10
P26982 DEGP_SALTY Protease do	4		NLTSMVEYGQVK	275	13	5	25.44	b12y4y5°y5y13	1496.75	58.328	37938	2	748.88	3.43
P26982 DEGP_SALTY Protease do	5		GAFVSQVMPNSSAAK	313	15	11	71.39	b3b4b5y2y8y10y11°y11°y11y12y15	1493.75	53.937	34842	2	747.38	3.43
P26982 DEGP_SALTY Protease do	6		VGDYTVAINPFGLETVTSGIVSALGR	186	28	19	134.06	b2b3b5°b5b6°b6b7b8b11b12y2y3y4y5y6y9y10y11y28	2750.44	117.252	30557	3	917.48	1.15
P26982 DEGP_SALTY Protease do	7		AQVGTMPVGSK	352	11	9	53.01	b2°b2b6y5°y5y8y9y10y11	1074.56	35.534	30210	2	537.78	-4.32
P26982 DEGP_SALTY Protease do	8		SGLNVENYENFIQTDAAINR	214	20	10	42.47	b11y1y2y3y5y6y8°y8y12y20	2268.11	78.402	26701	2	1134.56	11.19
P26982 DEGP_SALTY Protease do	9	Carbamidomethyl+C(13);Carbamidomethyl+C(25)	NFQQFFGDDSPFCQDGSPPFNPFQGGGNGGNGGQQQK	71	39	5	24.22	b2b4b5y6y13	4240.79	91.648	3810	3	1414.27	8.75
P26982 DEGP_SALTY Protease do	10		GELGIMGTELNSELAK	289	16	5	17.18	b2°b2b3b15y11	1661.85	102.199	1582	3	554.62	7.13
P26982 DEGP_SALTY Protease do	11		LADSDALR	178	8	3	33.12	b3b4y5	860.44	32.972	19827	2	430.72	-7.09
P26982 DEGP_SALTY Protease do	12		ISLGLLR	363	7	4	53.73	y3y4y5y6	771.50	69.116	17213	2	386.25	-15.82
P26982 DEGP_SALTY Protease do	13		NIAELR	443	6	1	13.63	y4	715.40	52.539	8140	1	715.40	-9.81
P26982 DEGP_SALTY Protease do	14		ANSPAAQIGLK	418	11	6	31.32	b4°b4b6°b6b7°b7	1069.62	32.588	6307	3	357.21	16.21
P26982 DEGP_SALTY Protease do	15		VMPSVVVSINVEGSTTVNTPR	48	20	5	14.39	b11b15°b15y11°y11	2087.07	103.354	3188	2	1044.04	-3.51
P26982 DEGP_SALTY Protease do	16		KGDVVIIGANQQPVK	429	14	8	50.76	b5b7y5y6°y6y8°y8y10	1466.83	39.259	16049	2	733.92	1.58

P26982 DEGP_SALTY Protease do	17		RGELGIMGTELNSELAK	288	17	3	23.33	b5b6y8	1817.95	69.431	13407	2	909.48	2.55
P26982 DEGP_SALTY Protease do	18		FDAKVVVGK	149	8	4	36.13	b4°b4b7y3	863.49	35.937	13203	2	432.25	-4.31
P26982 DEGP_SALTY Protease do	19		GDVIIGANQQPVKNIAELR	430	19	3	14.96	b11b13y3	2035.11	65.920	9289	3	679.04	-8.88
P26982 DEGP_SALTY Protease do	20		GELGIMGTELNSELAKAMK	289	19	9	39.17	b8b13b14°b14b17°b17°b17y3y14	1992.01	94.510	3243	3	664.68	-0.49
P26982 DEGP_SALTY Protease do	21		VTNNHVVDNASVIK	127	14	2	7.28	b6°b6	1509.79	50.728	1612	2	755.40	-6.06
P67904 RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAKR	16	15	14	123.33	b2b3y1y4y5y6y7y8y9y10y11°y11y13y15	1673.88	52.777	102657	3	558.63	-14.22
P67904 RS10_SALTY 30S ribosomal protein S10	2		LIDQSTAEIVETAK	16	14	13	98.7	b2b7b9b10y3y4°y4y5y9y10y11*y11y14	1517.81	56.215	71683	2	759.41	1.93
P67904 RS10_SALTY 30S ribosomal protein S10	3		LVDIVEPTEK	72	10	11	74.41	b2b3y2°y2y3y4y5°y5y6y8y10	1142.63	52.478	44088	2	571.82	-3.21
P67904 RS10_SALTY 30S ribosomal protein S10	4		FTVLISPHVNK	48	11	5	56.02	b7y4y5y6y7	1254.69	58.859	56945	3	418.90	-20.72
P67904 RS10_SALTY 30S ribosomal protein S10	5		RLVDIVEPTEK	71	11	12	131.72	b3b4b5b7b10y4°y4y5°y5y6y7y8	1298.73	51.311	53662	2	649.87	0.38
P67904 RS10_SALTY 30S ribosomal protein S10	6		GPIPLPTRK	37	9	3	38.3	y4y5y6	978.60	43.619	30928	2	489.80	-7.55
P67904 RS10_SALTY 30S ribosomal protein S10	7		DQSTAEIVETAKR	18	13	1	7.26	b3	1447.74	52.807	4802	2	724.37	0.34
P0A1P8 GLRX1_SALTY Glutaredoxin-1	1		TVGKPVETVPQIFVDQK	50	17	8	48.96	b9y2y3y5y6y8y13y17	1885.03	65.632	50605	3	629.02	-6.67
P0A1P8 GLRX1_SALTY Glutaredoxin-1	2	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	MFTVIFGRPGCPYCVR	0	16	7	30.83	b2b3°b3b4y12y14y16	1959.93	77.195	35581	3	653.98	-3.74
P0A1P8 GLRX1_SALTY Glutaredoxin-1	3		YIDIHAEGITK	34	11	5	50.57	b3b7b8b10°b10	1259.66	64.399	246866	2	630.33	-3.88
P0A1P8 GLRX1_SALTY Glutaredoxin-1	4	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	MFTVIFGRPGCPYCVRAK	0	18	3	15.6	b7y6y13	2159.08	85.819	2137	3	720.37	5.99
P0A1P8 GLRX1_SALTY Glutaredoxin-1	5	Carbamidomethyl+C(10) ;Carbamidomethyl+C(13))	FTVIFGRPGCPYCVRAK	1	17	3	16.34	b11y8y10	2028.00	73.649	1966	3	676.67	-14.57
P0A1P8 GLRX1_SALTY Glutaredoxin-1	6	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	MFTVIFGRPGCPYCV	0	15	1	7.25	y11	1803.83	77.244	19551	3	601.95	-2.64
P0A1P8 GLRX1_SALTY Glutaredoxin-1	7		PQIFVDQK	59	8	1	7.28	b3	974.54	65.600	9502	1	974.54	7.95
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		QLDPLVVQGEHYDTAR	343	16	16	133.74	b2°b2y3°y3y4y5y7y9y10y11y12y13y14°y14y16°y16	1840.90	58.444	70162	3	614.30	-11.67
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		AAPSYEELSNSQELLETK	112	20	11	63.73	b8b12y1y2y3y4y12y13y14y18y20	2179.10	74.582	63413	2	1090.05	11.88
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		VALTGLTMAEK	219	11	9	84.82	b2y3y5y7y8y9°y9y10y11	1133.62	59.923	56255	2	567.31	-6.68
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4		GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	7	25.72	b5y3y6°y6y9y12y27	3057.41	100.548	55539	3	1019.81	9.42
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	7	70.61	b2b3b6y4y5y6y8	1193.60	81.536	43462	2	597.30	-3.99
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		NIAIEHSGYSVFAGVGER	165	18	5	34.94	b2b6b9b12b14	1905.92	58.083	41760	3	635.98	-14.54
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		MPSAVGYQPTLAEEMGVLQER	261	21	15	44.92	b5°b5b10b12°b12°b12b21y3°y3y6y11*y11y13*y13y21	2306.14	82.414	38571	2	1153.58	12.70
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		YTLAGTEVSALLGR	247	14	9	42.46	b2°b2b10y2y3y6y7y10y14	1450.79	80.780	38278	2	725.90	-2.10
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		VGLFGGAGVGK	145	11	5	31.32	y2y4y7y8y11	961.54	59.633	37063	2	481.27	-9.97

Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		GLDVKDLEHPIEVPVGK	65	17	7	39.2	b3b6b9b12y2y4y17	1844.99	68.022	32686	3	615.67	-12.11
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		QIASLGIYPAVDPLDSTSR	324	19	7	46.24	y4y11y12y14°y14y15y19	2003.06	81.322	30562	2	1002.03	5.85
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		VYDALEVQNGNEK	25	13	4	20.67	b3y8y11y13	1478.72	45.183	16830	2	739.87	7.84
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		TVNMMELIR	156	9	4	53.29	b4y3y5y7	1106.56	76.652	53887	2	553.79	-6.07
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		FLSQPFFVAEVFTGSPGK	399	18	9	62.31	b3b4b6b8y3y5y11y13°y13	1958.03	100.427	33116	2	979.52	10.41
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15		VSLVYQGMNEPPGNR	202	15	4	31.85	b11b14y9y10	1660.81	55.172	30462	2	830.91	-2.28
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16		TIAMGSSDGLR	53	11	3	24.33	b3b10y10	1107.53	43.863	19976	2	554.27	-18.52
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17		DVLLFVDNIYR	236	11	3	27.34	b10y4y5	1366.72	91.862	7490	2	683.86	-15.09
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18		IMNVLGEPVDMK	87	12	3	22.3	b3y6y10	1345.68	69.892	4859	2	673.35	-2.00
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19		IMNVLGEPVDMKGEIGEEER	87	20	3	23.81	y5y8y9	2245.07	70.252	13539	3	749.03	-6.85
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20		EGNDFYHEMTDSNVIDKVSLSVYG QMNEPPGNR	185	32	3	16.96	y5y11y15	3655.64	85.409	10740	4	914.66	-1.74
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	21	Carbamidomethyl+C(26)	AAPSYEELSNSQELLETGIKVIDLM CPFAK	112	30	7	56.79	b3b7b10y4y5y6y7	3353.67	121.395	9220	3	1118.56	2.33
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	22		IVQVIGAVVDVEFPQDAVPRVYD ALEVQNGNEK	5	33	3	22.86	y5y6y26	3610.82	115.732	2066	3	1204.28	-14.60
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	23	Phosphoryl STY(4)	VALTGLTMAEK	219	11	4	35.34	b7b10y7y9	1213.59	73.254	8643	2	607.30	5.93
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	24	Oxidation+M(4)	TIAMGSSDGLR	53	11	3	27.34	b5b6y6	1123.56	98.445	1800	1	1123.56	13.69
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	25		PSAVGYQPTLAEEMGVLQER	262	20	4	30.04	b3b6b7b13	2175.10	82.458	6502	3	725.70	9.54
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	26		NIAIEHSGYSVF	165	12	0	5.24		1336.64	58.037	5776	3	446.22	-9.04
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	27		DVKDLEHPIEVPVGK	67	15	6	61.96	b6b7b8°b8b9b10	1674.89	68.021	3025	3	558.97	-8.02
P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	16	100.08	b2*b2b3b6y1y2y3*y3y5y6 y7*y7y8*y8y9y10	1129.62	39.699	84180	2	565.31	-5.30
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	7	56.77	b2y4y6y7y8y9y14	1452.65	58.127	56944	2	726.83	3.61
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3		GLPIPVVITVYADR	51	14	3	19.31	b4y3y10	1512.88	92.002	51385	2	756.94	1.53
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4		TPPAAVLLK	72	9	5	46.08	b2y3y5y7y9	909.57	54.902	47072	2	455.29	-10.67
P0A7K0 RL11_SALTY 50S ribosomal protein L11	5	Carbamidomethyl+C(29)	LQVAAGMANPSPPVGPALGQQG VNIMEFCK	10	30	6	19.35	b3b7b15y6°y6y14	3081.58	111.276	9757	4	771.15	16.56
P0A7K0 RL11_SALTY 50S ribosomal protein L11	6		SGSGKPNK	87	8	3	36.13	b4b6y7	774.41	40.177	2585	1	774.41	-5.91
P65882 PURA_SALTY Adenylosuccinate synthetase	1	Carbamidomethyl+C(7)	LLLSEACPLILDYHVALDNAR	97	21	14	69.26	b2b7y3y6°y6y9y10°y10*y10y11*y11y15y17y21	2396.25	92.358	28852	3	799.42	-5.09
P65882 PURA_SALTY Adenylosuccinate synthetase	2		EVTTTPLAADDWK	354	13	8	34.11	b5°b5y1y5y7°y7y11y13	1446.71	77.071	22967	2	723.86	1.77
P65882 PURA_SALTY Adenylosuccinate synthetase	3		IEELTGVPIDIISTGPDR	402	18	7	15.6	b2b4°b4y3°y3y5°y5	1925.05	103.574	20596	2	963.03	12.11
P65882 PURA_SALTY Adenylosuccinate synthetase	4	Carbamidomethyl+C(19)	VGAGPFPTELFDETGEFLCK	273	20	7	44.64	b6b9y4y6y7y8y20	2214.08	100.775	19083	2	1107.54	14.89

[P65882]PURA_SALTY Adenylosuccinate synthetase	5		VLDDTMAVADILTSMVVDVSDLLDQAR	186	27	14	93.81	b2b7b8b9b13y3y4y5y6y8°y8y10y11°y11	2905.45	138.252	7721	3	969.16	-0.67
[P65882]PURA_SALTY Adenylosuccinate synthetase	6		GVEPIYETMPGWSESTFGVK	367	20	7	28.05	b2b7b10b12y3y11°y11	2214.05	86.650	4818	3	738.69	5.51
[P65882]PURA_SALTY Adenylosuccinate synthetase	7		LKEVMEYHNFQLVNYK	161	17	5	16.34	b6b10*b10y4y17	2218.09	113.643	4534	2	1109.55	-2.97
[P65882]PURA_SALTY Adenylosuccinate synthetase	8		ENVTSIINGNVVLSPSALMKEMKELEDR	62	28	4	14.93	b3b9y4y16	3059.58	105.848	2272	3	1020.53	1.60
[P65882]PURA_SALTY Adenylosuccinate synthetase	9		AEAVDYQK	178	8	5	36.13	b4b6y7°y7*y7	923.45	62.751	25450	2	462.23	6.61
[P65882]PURA_SALTY Adenylosuccinate synthetase	10		GNNVVVLGTQWGDEGK	1	16	7	34.82	b10°b10b13*b13y6y9y13	1672.82	82.758	12899	3	558.28	-4.38
[P65882]PURA_SALTY Adenylosuccinate synthetase	11		YQGGHNAGHTLVINGEK	33	17	4	23.33	b12y13y14*y14	1794.90	86.543	3580	2	897.95	7.69
[P65882]PURA_SALTY Adenylosuccinate synthetase	12		EVMEYHNFQLVNYK	163	15	4	18.16	b11y6*y6y9	1976.90	85.175	1893	3	659.64	-8.64
[P65882]PURA_SALTY Adenylosuccinate synthetase	13		VLDDTMAVADILTSMVVDVSDLLDQARQR	186	29	5	36.37	b4b5b6b9°b9	3189.61	110.048	11223	3	1063.88	-0.77
[P65882]PURA_SALTY Adenylosuccinate synthetase	14		GNNVVVLGTQWGDEGKGK	1	18	4	24.52	y11y12*y12y14	1857.93	59.413	8510	3	619.98	-8.61
[P65882]PURA_SALTY Adenylosuccinate synthetase	15		EVTTPLAADDWKGVVEPIYETMPGWSESTFGVK	354	33	5	13.31	b4°b4b15y6y10	3641.78	93.948	7728	3	1214.60	11.06
[P65882]PURA_SALTY Adenylosuccinate synthetase	16		MGNNVVVLGTQWGDEGKGK	0	19	4	41.17	b3b4b7b8	1988.99	73.405	3990	3	663.67	3.93
[P65882]PURA_SALTY Adenylosuccinate synthetase	17		AIGTTGRGIGPAYEDK	125	16	7	66.04	y5y6y7y8y11y13°y13	1605.83	69.793	2708	3	535.95	1.44
[P65882]PURA_SALTY Adenylosuccinate synthetase	18	Phosphoryl STY()	ENVTSIINGNVVLSPSALMKEMK	62	23	3	13.06	b3y5y18	2497.20	60.921	215377	3	833.07	-12.22
[P65882]PURA_SALTY Adenylosuccinate synthetase	19	Oxidation+M(19)	ENVTSIINGNVVLSPSALMKEMKELEDR	62	28	3	21.93	b10y7y8	3075.53	133.506	5601	3	1025.85	-12.15
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	1	Carbamidomethyl+C(11)	IAAVAEDGEPCTYIGADGAGHYVK	158	25	6	32.32	b2b3b4y10y13y21	2563.21	61.168	30722	3	855.08	-0.19
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	2		AAVLPANLIQAQR	432	13	5	32.35	b3y4y5y9y13	1364.80	65.279	16364	2	682.90	-2.15
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	3		IVSYAQGFSQLR	329	12	8	68.99	b2b10y6y7y8y9y10y12	1368.73	63.298	15319	2	684.87	1.34
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	4		WTSQSALDLGEPLSLITESVFAR	264	23	10	37.64	b11°b11y1y3y5y6°y6y7°y7y23	2520.30	117.943	13573	3	840.77	0.97
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	5		ITDAYAENADIANLLLAPYFKK	373	22	4	19.97	b2b5b12b14	2454.30	98.541	8749	3	818.77	3.98
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	6		ELSAEGFNFIGTGVSGGEEGALK	113	23	7	28.28	b2b6b7b11*b11y9y11	2269.12	78.403	5944	3	757.04	7.42
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	7		LVPYYTVK	50	8	5	33.12	b2b5y5y6y8	982.56	52.517	5235	2	491.78	-2.42
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	8		ITDAYAENADIANLLLAPYFK	373	21	4	13.89	b7b11*b11y3	2326.23	126.227	2068	3	776.08	13.01
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	9		GDIIDGGNTFFQDTIRR	93	18	4	22.76	b3b9b13°b13	2038.02	107.107	1827	3	680.01	-8.98
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	10		DVVAYAVQNGIPVPTFSAAVAYYDSYR	405	27	7	39.7	b4b7b8b9°b9y3y10	2936.47	134.560	1685	3	979.50	8.65
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	11		MVHNGIEYGDMQLIAEAYSLLK	183	22	3	13.45	b5b7y8	2495.23	107.474	14608	3	832.41	-0.29
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	12		DEDGNYLVDVILDEAANK	242	18	6	34.94	y3y5y8°y8y15°y15	1992.93	55.618	8631	3	664.98	-6.13
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	13		DAYELVAPILTK	146	12	3	32.52	b3b5b9	1332.74	81.020	8184	2	666.87	-2.11
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	14		IADEYQQALR	395	10	6	72.37	b4b5b6b7y7y8	1206.59	43.818	2683	2	603.80	-15.38

[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	15		QQIGVVGMAVMGR	3	13	4	39.34	b4y7y8y9	1345.69	63.289	2620	2	673.35	-15.42
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	16		TEEVIAENPGK	38	11	3	31.32	b3b8b9	1186.59	91.052	2412	2	593.80	-5.14
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	17		GYTVSVFNR	25	9	5	54.54	b3b4b5b8°b8	1042.54	28.897	1717	2	521.77	6.67
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	18	Phosphoryl STY(3)	GPSIMPGGQK	136	10	3	28.7	b7y7y8	1051.46	30.226	3237	2	526.23	0.70
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	19	Phosphoryl STY(5)	EFVESLETPRR	58	11	3	24.33	b4b10_H3PO4 b10y7	1442.67	92.785	1632	2	721.84	4.91
[P14062]6PGD_SALTY 6-phohogluconate dehydrogenase	20	Oxidation+M()	QQIGVVGMAVMGR	3	13	4	28.15	b3*b3b4b8	1361.69	98.397	2446	2	681.35	-12.46
[P63411]ACKA_SALTY Acetate kinase	1	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPEAR	17	26	14	84.6	b2b3b5y1y2y3y4y10y11y12y13y14y19y26	2907.40	105.307	37172	3	969.81	1.68
[P63411]ACKA_SALTY Acetate kinase	2		EGTRPAVVIPTNEELVIAQDASR	374	23	15	112.85	b8°b8b9b14b15y3y5y6y7y11*y11y13y14y15y23	2465.29	69.748	31194	3	822.44	-2.38
[P63411]ACKA_SALTY Acetate kinase	3	Carbamidomethyl+C(7)	LVLVLNCGSSSLK	4	13	8	39.25	b2b3b4y2y8°y8y9y13	1389.77	67.735	26214	2	695.39	-5.71
[P63411]ACKA_SALTY Acetate kinase	4	Carbamidomethyl+C(14)	ESGLGLTEVTSDCR	272	15	7	51.74	b12y2y8y9y10y11y15	1636.80	72.678	15974	2	818.90	6.56
[P63411]ACKA_SALTY Acetate kinase	5		NVAVFDTAHQTMPEESYLYALPYSLYK	144	28	3	11.71	b11y6y17	3297.61	99.460	11542	3	1099.88	9.55
[P63411]ACKA_SALTY Acetate kinase	6		LDAVVFTGGIGENAAMVR	324	18	7	22.76	b2°b2y6*y6y12y14*y14	1819.92	81.934	2645	3	607.31	-11.81
[P63411]ACKA_SALTY Acetate kinase	7	Carbamidomethyl+C(1)	CVDTSMGLTPLEGLVMGTR	224	19	9	62.51	b3b11b13y4y5y10°y10y11y13	2037.02	95.559	27710	2	1019.01	20.08
[P63411]ACKA_SALTY Acetate kinase	8		YGAHGTSHFYVTQEAAK	178	17	5	26.18	b3b7b9y6°y6	1866.92	89.593	4466	2	933.96	21.64
[P63411]ACKA_SALTY Acetate kinase	9	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPEARIK	17	28	3	17.73	b8b13b15	3148.60	99.045	28026	4	787.90	6.44
[P63411]ACKA_SALTY Acetate kinase	10		RYGAHGTSHFYVTQEAAK	177	18	5	23	b8b9°b9y9*y9	2022.98	96.940	8207	2	1011.99	-1.27
[P63411]ACKA_SALTY Acetate kinase	11		DKNVAVFDTAHQTMPEESYLYALPYSLYK	142	30	4	17.29	b8*b8b10b12	3540.67	96.054	7884	4	885.92	-9.38
[P63411]ACKA_SALTY Acetate kinase	12		YIGSYTALMDGRDLDAVVFTGGIGENAAMVR	312	30	3	11.39	b17y4y10	3147.61	78.929	7059	4	787.66	14.35
[P63411]ACKA_SALTY Acetate kinase	13		LGVLGFEVDHERNLAAR	348	17	4	23.33	b10b11°b11y13	1896.00	67.666	6768	2	948.50	-6.76
[P63411]ACKA_SALTY Acetate kinase	14		ELSLGKLGVLGFEVDHER	342	18	4	15.6	b3°b3b16y7	1998.04	111.852	2916	3	666.69	-12.40
[P63411]ACKA_SALTY Acetate kinase	15	Carbamidomethyl+C(18) ;Oxidation+M(1)	MLTKESGLLGLTEVTSDCR	268	19	3	14.96	b3b6y11	2126.03	85.387	42722	4	532.26	-6.89
[P63411]ACKA_SALTY Acetate kinase	16	Oxidation+M(16)	LDAVVFTGGIGENAAMVR	324	18	4	24.85	b4y6y11y16	1835.95	71.202	9223	2	918.48	10.70
[P0A1S4]STPA_SALTY DNA-binding protein stpA	1		ADGINPEELFAMDSAMPR	66	18	17	89.89	b2°b2b5°b5*b5b10*b10y1y2y4y5y6y7y8y9y13y18	1963.91	89.702	15610	2	982.46	10.75
[P0A1S4]STPA_SALTY DNA-binding protein stpA	2		MNLMLQNLNNIR	0	12	8	62.21	b2b3b6b11y4y6y10y12	1473.77	77.056	14982	2	737.39	2.07
[P0A1S4]STPA_SALTY DNA-binding protein stpA	3		AMAREFSIDVLEEMLEK	15	17	5	44.64	b3b4b7b8y3	2011.00	72.960	8146	3	671.01	7.22
[P0A1S4]STPA_SALTY DNA-binding protein stpA	4	Oxidation+M(2)	AMAREFSIDVLEEMLEK	15	17	3	16.34	b8b10y7	2027.01	105.449	20462	3	676.34	11.56
[P0A1S4]STPA_SALTY DNA-binding protein stpA	5	Oxidation+M(1)	MNLMLQNLNNIR	0	12	3	22.3	b3b8y3	1489.75	55.583	10792	2	745.38	-5.08
[P0A1S4]STPA_SALTY DNA-binding protein stpA	6		AMAREFSI	15	8	0	4.84		924.46	72.927	1616	1	924.46	-3.17

[P66541]RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAE LNK	45	14	11	60.46	b5°b5y1y3y5*y5y9y12y13*y13y14	1576.81	85.304	101314	2	788.91	4.41
[P66541]RS2_SALTY 30S ribosomal protein S2	2		EANNLGIPVFAIVDTSNDPDGVDF VIPGNDDAIR	174	34	11	31.5	b5b7°b7°b7y1y4y7y8y14y16y34	3569.77	105.245	22807	3	1190.59	8.00
[P66541]RS2_SALTY 30S ribosomal protein S2	3		LKDLETQSQDGTFEK	113	15	8	29.48	b7°b7°b7b8°b8b10y7y15	1738.85	39.723	8851	3	580.29	-2.32
[P66541]RS2_SALTY 30S ribosomal protein S2	4	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	4	38.77	y3y4y7y9	1694.75	47.938	7586	2	847.88	9.58
[P66541]RS2_SALTY 30S ribosomal protein S2	5		MATVSMRMDLK	0	11	4	38.35	b4b7y6y7	1282.63	49.651	1830	3	428.22	0.48
[P66541]RS2_SALTY 30S ribosomal protein S2	6		MKPFIFGAR	26	9	3	30.51	b4y4y7	1066.57	63.936	4680	2	533.79	-19.34
[P66541]RS2_SALTY 30S ribosomal protein S2	7		DMGGLPDALFVIDADHEHIAIK	152	22	4	13.45	b9°b9y8y13	2377.19	84.407	2526	2	1189.10	0.21
[P66541]RS2_SALTY 30S ribosomal protein S2	8		YWNPKMKPFIFGAR	21	14	3	27.09	b7b8b10	1754.92	63.229	19803	3	585.65	0.97
[P66541]RS2_SALTY 30S ribosomal protein S2	9		TVPMFNEALAE LNKISAR	45	18	3	15.6	b6b9y3	2004.03	52.559	2377	2	1002.52	-14.62
[P66541]RS2_SALTY 30S ribosomal protein S2	10	Oxidation+M(1)	MATVSMRMDLK	0	11	3	24.33	b7y6y10	1298.61	68.040	20407	2	649.81	-10.72
[P66541]RS2_SALTY 30S ribosomal protein S2	11	Oxidation+M(4)	TVPMFNEALAE LNK	45	14	4	34.87	y10y11°y11y12	1592.81	85.212	3187	2	796.91	5.06
[P66541]RS2_SALTY 30S ribosomal protein S2	12	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	0	3.63		1676.70	47.921	3780	3	559.57	-8.81
[P58683]APHA_SALTY Class B acid phohatase	1		TLADNFHIPAANMNPVIFAGDKPE QNTK	149	28	14	74.36	b5y6°y6y7y8°y8y10*y10y11y12*y12y14y20y28	3053.50	79.981	53575	4	764.13	-6.24
[P58683]APHA_SALTY Class B acid phohatase	2		IFYGDSNDNITAAR	187	14	6	19.31	b5y4°y4y8°y8*y8	1557.73	53.195	20632	2	779.37	9.95
[P58683]APHA_SALTY Class B acid phohatase	3		AANSTYKPLPQAGAFGEEVIVNSE Y	212	25	4	12.42	b5°b5y7y9	2655.31	77.203	3297	3	885.77	5.70
[P58683]APHA_SALTY Class B acid phohatase	4		VQWLQEKNMR	177	10	3	26.94	b9y3y9	1331.71	73.631	2979	2	666.36	14.02
[P58683]APHA_SALTY Class B acid phohatase	5	Oxidation+M(13)	TLADNFHIPAANMNPVIFAGDKPE QNTK	149	28	3	11.71	b13y6y9	3069.47	102.876	2162	5	614.70	-13.12
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	9	59.39	b2b3b4y1y7y8y10y12y13	1365.68	63.716	89579	2	683.35	-0.18
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2	Carbamidomethyl+C(13)	AAQYVAAHPEVCPAK	153	16	17	117.73	b2b3b4b5b8°b8y1y2y3y4y5y8°y8y9y11y12y16	1668.80	35.982	76625	3	556.94	-11.56
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		ATFVVDPQGIIQAEIVTAEGIGR	120	23	21	122.23	b2°b2b3°b3b4°b4b5b6b8°b8y1y2y4y5°y5y6y7y8y9y17y23	2384.27	129.255	43169	3	795.43	-5.22
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		NFDNMREDEGLADR	106	14	6	27.88	b1°b1y1y3y5y9	1681.71	47.780	40982	3	561.24	-7.62
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		AWHSSSETIAK	80	11	6	47.78	b3b6b7°b7y4y8	1216.57	30.258	46154	3	406.20	-17.66
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6		NGEFIEVTEK	17	10	3	26.94	b3y4y7	1165.58	33.325	5840	2	583.30	9.22
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7		LGVDVYSVSTDTHFTHK	63	17	3	16.34	b8y9y11	1905.93	56.099	3104	2	953.47	-2.63
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTELGDVA DHYEELQK	32	31	6	25.24	b11y5*y5y7y11y12	3757.78	96.572	2869	4	940.20	16.05
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9		NGEFIEVTEKDTEGR	17	15	3	18.16	b5y5y11	1723.83	119.788	4468	3	575.28	10.27
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10	Carbamidomethyl+C(10)	YVAAHPEVCPAK	156	13	3	25.56	b4b5b10	1398.69	35.985	1844	2	699.85	1.13
[P0A1G5]DKSA_SALTY DnaK suppressor protein	1		TVTHMQDEAANFPDPVDR	57	18	11	86.21	b5b6b7b9b10y4°y4y6y7y8y18	2042.91	56.349	33337	3	681.64	-6.45

P0A1G5 DKSA_SALTY DnaK suppressor protein	2	Carbamidomethyl+C(10);Carbamidomethyl+C(13)	LEARPTADLCIDCK	125	14	5	19.31	b4°b4y2y4y12	1661.81	45.455	23630	3	554.61	7.79
P0A1G5 DKSA_SALTY DnaK suppressor protein	3		ILEAWR	42	6	1	13.63	b4	787.45	40.228	6911	2	394.23	3.02
P0A1G5 DKSA_SALTY DnaK suppressor protein	4	Carbamidomethyl+C(9);Carbamidomethyl+C(12)	VEDEDFGYCESCGVEIGIR	105	19	3	24.13	y9y11y12	2233.97	111.744	4235	3	745.33	16.28
P0A1G5 DKSA_SALTY DnaK suppressor protein	5		TLAEIR	139	6	1	13.63	y4	702.41	35.487	1972	2	351.71	-2.00
P0A1G5 DKSA_SALTY DnaK suppressor protein	6		TSSLSILAIGVEPYQEKPGEIYM NEAQLSHFKR	8	34	3	10.99	b5b14y12	3822.87	99.670	81569	3	1274.96	-7.28
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	1	Carbamidomethyl+C(1)	CTWVASDFDALIPSLK	66	16	10	55.56	b3°b3b5b12y2y3y4y11y14 y16	1822.92	98.933	34417	2	911.96	8.10
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	2		YFGDGTGVGLR	211	11	4	36.09	y3y7y9y11	1141.56	56.597	26342	2	571.28	-1.18
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	3		IGTDTTYAPFSSKDAK	29	16	4	17.18	b6b12y12°y12	1701.85	60.866	16099	3	567.96	12.05
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	4		GVDVVAYANQDLIYSDLTAGR	155	21	3	13.89	b8b13y6	2240.12	92.117	11280	3	747.38	0.00
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	5		IGTDTTYAPFSSK	29	13	4	25.44	b9°b9y8y9	1387.69	64.536	2999	2	694.35	13.28
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	6	Carbamidomethyl+C(15)	GEFIGFDIDLGNECK	45	16	4	17.18	b9y12*y12y14	1844.85	80.060	24233	3	615.62	15.75
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	7		QPAGK	193	5	1	13.23	b3	500.28	46.088	7578	1	500.28	-4.45
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	8		TKGVDVVAYANQDLIYSDLTAGR	153	23	5	22.09	b13b14°b14y4°y4	2469.29	92.739	66263	4	618.08	12.56
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	9		HVGVLQGSTQEAYANDNWRTK	134	21	4	34.68	y6y7°y7y8	2374.18	112.572	2919	3	792.07	12.75
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	10		ALTELQDGTYDK	234	13	6	20.67	b8°b8y8y11°y11*y11	1509.77	99.633	2473	4	378.20	12.69
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	11		IGTDTTYAPFSSKDAK	29	16	4	24.3	b4b6y7y12	1701.81	71.701	2082	2	851.41	-10.76
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	12		QQEIAFSKLYAADSR	99	16	3	25.56	y6y7y10	1841.92	69.722	1608	3	614.64	9.08
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	13	Carbamidomethyl+C(15);Oxidation+M(14)	GEFIGFDIDLGNECK	45	16	4	17.18	b3b11y9°y9	1860.82	27.730	6276	3	620.95	4.92
P02906 SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQEIAAK	263	13	16	92.84	b2b4b5y1y4y5y8*y8y9*y9 y10°y10*y10y11y13*y13	1468.73	51.388	59177	2	734.87	1.91
P02906 SUBI_SALTY Sulfate-binding protein	2		LFTIDEVFGGWAK	298	13	7	32.35	b2b3°b3y5y7y8y13	1482.77	102.615	58203	2	741.89	3.13
P02906 SUBI_SALTY Sulfate-binding protein	3		NVEVLDSGAR	183	10	6	40.17	b2b9y4y5y8y10	1059.53	40.697	47550	2	530.27	-7.95

P02906 SUBI_SALTY Sulfate-binding protein	4		AVAEAYLK	255	8	6	36.13	b2b6y1y3y6y8	864.48	41.532	24193	2	432.74	-8.26
P02906 SUBI_SALTY Sulfate-binding protein	5		QETGDNV VIR	48	10	5	51.93	y3y6y7y8y10	1130.58	36.048	21063	2	565.79	0.86
P02906 SUBI_SALTY Sulfate-binding protein	6		QATSVINGIEADV VTLALAYDVD AIAER	66	28	7	54.39	b11y3y5y9y10y11y12	2917.51	128.751	8546	3	973.18	-0.17
P02906 SUBI_SALTY Sulfate-binding protein	7		LPDNSAPYTSTIVFLVR	104	17	3	23.74	b4b6b13	1892.99	89.572	5435	2	947.00	-12.83
P02906 SUBI_SALTY Sulfate-binding protein	8		QIHDWNDLIKPGSVITPNPK	126	21	5	24.73	b5y4y5*y5y11	2371.24	73.462	37955	4	593.56	-17.30
P02906 SUBI_SALTY Sulfate-binding protein	9		WNYLAAWGYALHHNNNDQAK	153	20	9	63.73	b4b6*b6y7y8y9y11y13y14	2386.07	79.197	26422	4	597.27	-18.31
P02906 SUBI_SALTY Sulfate-binding protein	10		DIQLLNVSYPTR	20	13	3	29.91	y6y9y12	1533.78	71.646	24945	3	511.93	-9.95
P02906 SUBI_SALTY Sulfate-binding protein	11		GSTNTFVER	193	9	4	38.3	y5y7y8*y8	1010.48	41.161	5235	2	505.74	-14.50
P02906 SUBI_SALTY Sulfate-binding protein	12		GIGDVLIAWENEALLATNELGK	202	22	4	13.45	b4b6y6*y6	2326.18	114.128	2676	3	776.07	-19.00
P02906 SUBI_SALTY Sulfate-binding protein	13		AFSAHWKQETGDNV VIR	41	17	3	24.99	b4b5b7	1957.97	86.296	36387	3	653.33	-11.10
P02906 SUBI_SALTY Sulfate-binding protein	14		RLPDNSAPYTSTIVFLVR	103	18	5	31.03	b4b7b9y3y5	2049.10	83.384	31152	3	683.71	-5.36
P02906 SUBI_SALTY Sulfate-binding protein	15		NVEVLDSGARGSTNTFVER	183	19	3	22.74	b3b4y12	2051.01	89.691	6909	3	684.34	-3.57
P02906 SUBI_SALTY Sulfate-binding protein	16		AQKDHFGANGTFDQISK	311	17	6	27.43	b8b9*b9b11y11*y11	1863.88	74.111	3004	2	932.45	-7.99
P02906 SUBI_SALTY Sulfate-binding protein	17		NFYRPRDADVAK	276	12	4	22.3	b4b8*b8y11	1451.76	85.243	2633	3	484.59	14.46
P02906 SUBI_SALTY Sulfate-binding protein	18	Phosphoryl STY(9)	FEIVTPSESILAEP TVSVVDK	226	21	3	13.89	b7b12y13	2340.15	86.557	2322	3	780.72	-1.15
P0A7V6 RS3_SALTY 30S ribosomal protein S3	1		LVADSITSQLER	114	12	11	79.2	b2y1y6y7y8y9*y9y10y11*y11y12	1331.71	61.321	48467	2	666.36	-1.56
P0A7V6 RS3_SALTY 30S ribosomal protein S3	2		ADIDYNTSEAH TTYGVIGVK	179	20	7	41	y4y6y10y11y18*y18y20	2154.03	57.055	32961	3	718.68	-4.19
P0A7V6 RS3_SALTY 30S ribosomal protein S3	3		VVADIAGVPAQINIAEVR	89	18	7	32.6	y1y2y4y5y10y13y18	1835.03	77.528	24025	2	918.02	-5.65
P0A7V6 RS3_SALTY 30S ribosomal protein S3	4		VVADIAGVPAQINIAEVRKPELDA K	89	25	7	25.87	b1b3b4y2y3*y3y17	2616.44	71.436	17625	4	654.87	-11.01
P0A7V6 RS3_SALTY 30S ribosomal protein S3	5		IVIERPAK	54	8	3	40.9	y4y5y6	925.57	31.827	18791	2	463.29	-13.98
P0A7V6 RS3_SALTY 30S ribosomal protein S3	6		GEILGGMAAVEQPEKPAAQPK	204	21	3	13.89	b5y6y17	2121.14	57.591	3823	2	1061.07	17.15
P0A7V6 RS3_SALTY 30S ribosomal protein S3	7		VMFR	127	4	1	12.83	y3	552.30	31.619	2009	1	552.30	13.15
P0A7V6 RS3_SALTY 30S ribosomal protein S3	8		RAVQNAMR	135	8	4	40.9	y3y4y7*y7	945.51	55.585	91595	2	473.26	0.32
P0A7V6 RS3_SALTY 30S ribosomal protein S3	9		LGGAEIARTEWYR	156	13	3	29.91	b6b9b11	1521.76	53.925	2355	2	761.39	-10.59
P0A7V6 RS3_SALTY 30S ribosomal protein S3	10	Phosphoryl STY(5)	LVADSITSQLER	114	12	3	22.3	b4y4y8	1411.69	61.108	6147	3	471.24	14.18
P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	15	113.45	b2b3y2y3*y3y4y5y6*y6y7*y7y8y9y10y12	1196.59	65.049	416506	2	598.80	-2.35
P0A9Y9 CC_SALTY Cold shock-like protein cC	2		DVVFHFSAIQNGGFK	27	15	7	29.48	b8y5y9*y9*y9y11y15	1665.82	74.257	120321	3	555.94	-11.80
P0A9Y9 CC_SALTY Cold shock-like protein cC	3		TLAEGQNVEFEIQDGQK	42	17	5	23.33	b6y3y4*y4y17	1905.91	83.348	11762	2	953.46	-6.85
P0A9Y9 CC_SALTY Cold shock-like protein cC	4		GFGFITPADGSKDVFVHFSAIQGN GFK	15	27	8	26.01	b10*b10b11b15y9*y9*y9y12	2843.42	100.381	7568	3	948.48	3.01

P0A9Y9 CC_SALTY Cold shock-like protein cC	5		TLAEGQNVEFEIQDGQKGPAAVN VTAI	42	27	4	27.16	y8y14y15y20	2799.40	101.680	6679	3	933.80	-6.19
P0A9Y9 CC_SALTY Cold shock-like protein cC	6		GFGFITPADGSKDVFVHFSAIQGN GFK	15	27	4	11.92	b11y3y5*y5	2843.41	88.007	3513	3	948.48	-0.09
P0A9Y9 CC_SALTY Cold shock-like protein cC	7		FVHFSAIQNGNGFK	29	13	0	4.03		1451.73	74.243	5456	2	726.37	-6.81
P0A9Y9 CC_SALTY Cold shock-like protein cC	8		SKDVFVHFSAIQNGNGFK	25	17	2	12.11	b10b13	1880.94	100.345	2451	2	940.97	-14.93
O68883 CISY_SALTY Citrate synthase	1	Carbamidomethyl+C(12)	TAGSSGANPFACIAAGIASLWGPA HGGANEAAALK	240	34	20	91.57	b2°b2b3°b3b4b14y1y2y3y9y13y14y16y17y25y26y27y29y34*y34	3195.58	117.015	53510	3	1065.87	5.81
O68883 CISY_SALTY Citrate synthase	2	Carbamidomethyl+C(9)	DSHPMAVMCGITGALAAFYHDSL DVNNPR	127	29	10	29.02	b7b10y1y2y6y9*y9y10*y10y15	3159.43	109.375	22345	4	790.61	-5.49
O68883 CISY_SALTY Citrate synthase	3	Carbamidomethyl+C(15)	GVFTFDPGFTSTASCESK	38	18	5	48.17	y11y12y13y14y18	1937.88	76.599	21445	2	969.44	11.02
O68883 CISY_SALTY Citrate synthase	4	Carbamidomethyl+C(18)	NDLSYAGNFLNMMFSTPCETYEV NPVLER	189	29	6	26.02	b2b4y5y9y13y14	3411.57	112.178	17458	3	1137.86	10.38
O68883 CISY_SALTY Citrate synthase	5		GTLGQDVIDIR	22	11	4	24.33	b3b6y2y9	1186.64	69.235	11174	2	593.83	1.34
O68883 CISY_SALTY Citrate synthase	6		QLYTGyDK	410	8	7	64.36	b5b6y2°y2y5y6y7	987.49	32.556	2645	2	494.25	10.14
O68883 CISY_SALTY Citrate synthase	7		YSIGQPFVYPR	178	11	5	31.32	b5°b5b6°b6b10	1326.71	72.365	105660	2	663.86	16.10
O68883 CISY_SALTY Citrate synthase	8		ILILHADHEQNASTSTVR	222	18	3	15.6	b9y4y11	2005.03	44.759	19707	3	669.01	-10.17
O68883 CISY_SALTY Citrate synthase	9		LLSK	164	4	1	12.83	y3	460.31	53.632	7911	1	460.31	-7.29
O68883 CISY_SALTY Citrate synthase	10		LFHAFR	120	6	1	13.63	y5	790.44	32.832	5370	2	395.72	-0.85
O68883 CISY_SALTY Citrate synthase	11		AMGIPSSMFTVIFAMAR	371	17	4	27.43	b4b5b8y12	1829.93	74.746	1640	3	610.65	8.21
O68883 CISY_SALTY Citrate synthase	12		TTVTRHTMIHEQITR	105	15	3	26.24	b11b12b14	1823.96	100.278	293243	2	912.48	2.01
O68883 CISY_SALTY Citrate synthase	13		NYDPRATVMR	310	10	3	33.93	b3b4b9	1222.61	76.217	4874	2	611.81	11.38
O68883 CISY_SALTY Citrate synthase	14		MLEISSVKHIPEFVR	274	16	3	17.18	b8b10y13	1914.00	80.024	2412	2	957.50	-9.12
O68883 CISY_SALTY Citrate synthase	15	Phosphoryl STY(9)	LYPNVDFYSGIILK	357	14	3	24.75	b7y6y7	1721.86	64.624	20602	3	574.63	10.42
O68883 CISY_SALTY Citrate synthase	16	Oxidation+M(15)	AMGIPSSMFTVIFAMAR	371	17	3	16.34	b4y6y9	1845.91	100.272	63748	3	615.97	0.99
O68883 CISY_SALTY Citrate synthase	17		LGQDVIDIR	24	9	0	2.42		1028.57	69.259	38362	2	514.79	-6.05
P66170 RL29_SALTY 50S ribosomal protein L29	1		MQAASGQLQQSHLLK	29	15	26	159.81	b1b2°b2b3°b3b4°b4b8b9y1y2y4y6°y6y7°y7*y7y9*y9y10y11y12y13*y13y14y15	1639.84	45.496	230056	3	547.28	-13.99
P66170 RL29_SALTY 50S ribosomal protein L29	2		SVEELNTELLNLLR	9	14	10	88.47	b2y1y3y4y5y6y8y9y10y14	1642.91	101.538	117172	2	821.96	3.79
P66170 RL29_SALTY 50S ribosomal protein L29	3		EQFNLR	23	6	3	26.87	b3y4*y4	806.41	42.577	71735	2	403.71	-12.34
P66170 RL29_SALTY 50S ribosomal protein L29	4		AASGQLQQSHLLK	31	13	12	85.86	b3°b3b4°b4b5°b5°b5b7b10°b10b11b12	1380.75	45.507	3105	2	690.88	-6.72
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	16	149.3	b3b4y2y3y5y7y9y10y11°y11*y11y13y14y15y17y19	2032.90	38.318	94893	3	678.31	-6.49
P02936 OMPA_SALTY Outer membrane protein A	2		SDVLFNFNFK	222	9	6	45.51	b2b3y4y5y6y9	1083.53	69.452	55924	2	542.27	-11.94

P02936 OMPA_SALTY Outer membrane protein A	3		STLKPEGQQALDQLYSQLSNLDPK	231	24	6	16.89	b2b8b22y2y6y9	2673.38	90.265	53390	3	891.80	0.82
P02936 OMPA_SALTY Outer membrane protein A	4		IGSDAYNQGLSEKR	267	14	7	66.48	b3y4y5y6y7y8y14	1537.74	35.072	26449	3	513.25	-11.27
P02936 OMPA_SALTY Outer membrane protein A	5	Carbamidomethyl+C(6)	AALIDCLAPDR	321	11	6	27.34	b8°b8y3y4°y4y11	1214.62	62.670	23499	2	607.81	-0.60
P02936 OMPA_SALTY Outer membrane protein A	6		LGYPITDDLDVYTR	103	14	4	19.31	b2b11y4y9	1640.82	76.915	12368	2	820.91	2.01
P02936 OMPA_SALTY Outer membrane protein A	7		DGSVVVLGFTDR	255	12	3	26.28	b3b4y5	1264.64	70.970	2697	2	632.82	-14.00
P02936 OMPA_SALTY Outer membrane protein A	8		IGSDAYNQGLSEK	267	13	3	20.67	b4b11y8	1381.67	38.825	12548	2	691.34	4.15
P02936 OMPA_SALTY Outer membrane protein A	9		FGQQEAAPVVAPAPAPAPEVQTK	194	23	9	52.61	b4b9b11°b11y6y8y10y12y14	2303.24	54.691	9669	2	1152.12	16.01
P02936 OMPA_SALTY Outer membrane protein A	10		AQGVQLTAKLGYPTDDLDVYTR	94	23	3	22.09	b3b4y8	2537.31	125.901	6110	3	846.44	-7.60
P02936 OMPA_SALTY Outer membrane protein A	11		GDNINGAYKAQGVQLTAK	85	18	3	22.76	b4b11b14	1847.94	102.911	5323	2	924.47	-12.75
P02936 OMPA_SALTY Outer membrane protein A	12		DGSVVVLGFTDRIGSDAYNQGLSEK	255	25	5	21.96	b5°b5b6y7*y7	2627.29	67.010	4820	4	657.58	-1.95
P02936 OMPA_SALTY Outer membrane protein A	13	Phosphoryl STY(7)	GVKDVVVTQPQA	339	11	3	31.32	b4b5b8	1221.59	31.620	112034	2	611.30	11.49
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		IGSFEAALLAYVDRDHAPLMQEINQSGGYNDEIEGK	463	36	13	35.31	b2b6b20b23b25y2y3°y3y7°y7y8y11y36	3950.89	96.001	97965	4	988.48	0.87
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	11	56.64	b2b3b12b13y4*y4y5y6*y6y8y19	2098.97	69.692	50617	3	700.33	-5.47
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3		IAQFNVSSEAHNEGATIVSVSDGVI R	15	25	4	12.42	b10y8y22y25	2641.32	75.126	48718	3	881.11	-14.88
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4		ILEVPVGR	93	8	5	40.9	b2y4y5y6y8	882.53	53.085	48643	2	441.77	-10.65
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		MQLNSTEISELIK	0	13	10	45.58	b2b3y2y3y8y10y11*y11y13*y13	1505.79	77.601	48597	2	753.40	0.49
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6		AVDSMIPIGR	151	10	8	58.17	b2b4°b4y4y6y7y8y10	1058.56	60.509	39595	2	529.78	-5.42
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		QSVDQPQVTGYK	139	12	18	122.12	b3*b3b4°b4°b4b7°b7y1y4y5*y5y6y7y8*y8y9y10y12	1349.67	34.847	30524	2	675.34	0.27
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		GYLADVELAK	453	10	7	55.62	b2b3b5y6y7y8y10	1078.57	61.099	29306	2	539.79	-3.73
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9		QYAPMSVAQQLVFLAAER	434	19	6	22.74	b3b19y5°y5y6y19	2109.10	94.014	27974	2	1055.06	11.81
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		ELAAFSQFASDLDDATRK	401	18	4	24.52	b2y9y10y13	1984.94	84.059	18780	3	662.32	-8.92
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		DSVGAVVMGPYADLAEGMK	68	19	9	39.46	b2b4b12b13y1y7°y7y8y19	1909.90	80.268	16229	2	955.45	-4.35
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12		QLNSTEISELIK	1	12	5	29.51	b7b9b10°b10y12	1374.74	81.984	15586	2	687.87	-6.30
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		GILDSFK	501	7	6	56.74	b4b6°b6y4y5y7	779.42	66.232	6517	2	390.21	-9.79
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		TALAIDAIIINQRDSGIK	175	17	7	33.75	b1b4°b4b5°b5b7b13	1799.00	104.741	5370	2	900.00	-1.90
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		TALAIDAIIINQR	175	12	5	29.51	y3*y3y4*y4y8	1298.74	74.797	25400	2	649.88	0.00
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16		ELAAFSQFASDLDDATR	401	17	8	92.91	y3y4y5y6y10y11y13y15	1856.88	89.325	23841	2	928.94	7.03
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17		VGGAAQTK	376	8	3	40.9	b3b4b6	731.40	33.486	16457	1	731.40	-4.67
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18		GPVDNDGFSAVEAIPGVIDR	118	21	3	22.34	b10y6y7	2099.06	82.819	5499	2	1050.04	11.40

Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	19		TALAQYR	394	7	4	37.49	b5*b5y3y4	822.43	28.386	2227	2	411.72	-18.55
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	20		VVNTLGAPIDGKGVPVDNDGFSAV EAIAPGVIDR	106	33	15	105.5	b7*b7b25y4y6*y6y7y8y9y1 0y11y16y17y24y26	3263.70	85.061	59396	3	1088.57	3.67
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	21		DHAPLMQEINQSGGYNDEIEGKL K	477	24	3	19.03	b4b11b13	2686.31	93.832	26383	3	896.11	12.81
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	22		DRGEDALIYDDLK	250	15	3	24.18	b8y5y6	1722.87	74.588	21302	2	861.94	6.87
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	23		IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	5	12.66	b5b13y7y9*y9	3950.85	85.154	20490	3	1317.62	-8.90
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	24		VNADYVEAFTKGEVK	303	15	3	18.16	b8b11y9	1669.86	103.452	5602	2	835.43	7.46
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	25	Carbamidomethyl+C(32) ;Oxidation+M(34)	LEEHGALANTIVVVATASESAALQ YLAPYAGCAMEGEYFR	211	39	4	23.44	b3*b3b4b7	4159.96	81.505	4430	4	1040.75	-11.15
Q8ZLD7 UA_SALTY Universal stress protein A	1		ISEETHHALTELSTNAGYPITETLS GSGDLGQVLVDAIK	61	39	9	38.25	b8b12*b12y3y4y12y14y15 y39	4067.06	98.886	140020	4	1017.52	2.52
Q8ZLD7 UA_SALTY Universal stress protein A	2		QLINTVHVDMILIVPLRDEEE	124	20	11	49.6	b2*b2b10b11*b11y1y7y8y 9y20*y20	2363.22	87.273	82889	3	788.41	-3.41
Q8ZLD7 UA_SALTY Universal stress protein A	3		AVSMARPYNAK	22	11	8	55.56	b9b10y1y5y7*y7y9y11	1207.62	31.803	76075	2	604.31	-2.53
Q8ZLD7 UA_SALTY Universal stress protein A	4		ISEETHHALTELSTNAGYPITETLS GSGDLGQVLVDAIKK	61	40	12	57.95	b11*b11b12b15b16b17y2y 4y7y22y24y40	4195.15	94.994	48343	4	1049.54	2.79
Q8ZLD7 UA_SALTY Universal stress protein A	5	Carbamidomethyl+C(9)	KYDMDLVVCGHHQDFWSK	100	18	3	15.6	b7b10y9	2264.99	65.372	3889	4	567.00	-12.18
Q8ZLD7 UA_SALTY Universal stress protein A	6		MAYKHILIAVDLSPESK	0	17	4	22.96	b3b5y5y8	1915.01	83.861	1748	3	639.01	-11.79
Q8ZLD7 UA_SALTY Universal stress protein A	7		SMARPYNAK	24	9	3	31.32	b4b6b7	1037.51	31.799	80619	2	519.26	-5.06
Q8ZLD7 UA_SALTY Universal stress protein A	8		VSMARPYNAK	23	10	0	2.42		1136.58	31.841	9277	2	568.79	-6.98
Q8ZLD7 UA_SALTY Universal stress protein A	9		AVSMARPYNAK	22	11	0	2.42		1189.60	31.801	4910	3	397.21	-4.93
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	1	Carbamidomethyl+C(13)	ISVMGHGMGIPSCSIYTK	57	18	5	26.61	b5b6*b6b12y5	1937.93	98.900	4635	2	969.47	1.95
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	2	Carbamidomethyl+C(13)	ISVMGHGMGIPSCSIYTKELITDFG VK	57	27	9	75.76	b2b6b7b8*b8b9b10b11y3	2940.50	112.499	3281	3	980.84	10.05
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	3	Carbamidomethyl+C(5)	ALTICTVSDHIR	196	12	3	26.28	b8b9y10	1385.71	47.293	1903	3	462.57	-8.46
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	4		YGVLGVEMEAAGIYGVAAEFGAK	173	23	5	33.63	b8b12b14y9y10	2302.10	81.925	9261	3	768.04	-16.65
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	5		EVNNVR	38	6	1	13.63	b3	730.38	31.597	6967	1	730.38	-0.33
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	6		QTTFNMIK	218	9	3	30.51	b4y5y6	1097.53	51.700	1510	3	366.51	0.56
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	7	Carbamidomethyl+C(14)	KISVMGHGMGIPSCSIYTK	56	19	3	14.96	b10y10y12	2066.00	85.560	4447	2	1033.50	-10.64
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	8		THEQTTAERQTTFNMIK	208	19	5	25.9	b13y5y6y11*y11	2222.03	93.781	2891	2	1111.52	-10.77
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	9		EVNNVRGMLGFTGTYK	38	16	3	17.18	b8y3y7	1785.91	50.335	2588	2	893.46	6.08
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	10	Carbamidomethyl+C(5)	ALTICTVSDHIRTHEQTTAER	196	22	3	13.45	b9y8y10	2510.23	88.702	2021	3	837.41	-4.96
Q8ZJV7 DEOD_SALTY Purine nucleoside phohorylase deoD-type	11	Carbamidomethyl+C(11) ;Oxidation+M(8)	LRDVVIMGACTDSK	100	15	3	26.24	y3y4y12	1637.80	69.373	4972	2	819.40	-0.75

P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	1		SLTDAAQQVVAAVEGK	372	16	10	46.68	b6°b6b13b14y2y3°y3y5y6y16	1586.83	89.172	45735	2	793.92	-2.38
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	2		VALDPLTGPMPLYQGR	146	15	6	26.24	b2y2y5y7y9y15	1614.84	71.706	30314	2	807.92	4.31
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	3		LHGGEPANFLDVGGGATK	277	18	7	21.78	b2b5b9°b9y6y16y18	1739.86	59.846	29276	3	580.62	-9.05
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	4		DLALIEINPLVITK	191	14	11	86.26	b2b3b4b5y2y3y4y6y7y9y14	1551.94	98.308	21564	2	776.47	2.75
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	5		LVTYQTDANGQPVNQILVEAATDIGNKELYLGAVVDR	80	36	11	42.44	b2b8°b8y1y4y6y7y8y23y25y36	3874.06	122.151	17147	3	1292.02	9.14
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	6		LEGNNaelGAK	348	11	4	31.32	y6y9y10y11	1115.56	29.914	15580	2	558.29	-5.03
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	7		LHGGEPANFLDVGGGATKER	277	20	4	23.81	b4b8b9b20	2025.00	81.325	9716	3	675.67	-6.93
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	8	Carbamidomethyl+C(11)	YGLPAPVGyACTTPR	14	15	3	18.16	b3b7y9	1622.79	46.847	2905	3	541.60	-8.80
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	9		IFMGLATIFLER	179	12	3	22.3	b11y7y10	1410.78	109.444	15411	2	705.89	-1.30
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	10		IILSDDNVK	303	9	4	45	b6b7y5y8	1016.54	36.050	2894	2	508.78	-18.37
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	11		RVVFMasteGGVEIEK	119	16	3	25.56	y5y12y13	1751.89	79.846	11837	2	876.45	-4.11
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	12		LADsGLNIIAAKSLTDAAQQVVAAVEGK	360	28	6	36.02	b3b6°b6b7b8y7	2753.48	73.496	4080	3	918.50	-10.55
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	13		MNLHEYQAKQLFAR	0	14	3	24.75	b9b10y11	1748.90	79.969	3856	2	874.95	4.33
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	14		EAEeAASKIGAGPWVVK	29	17	5	33.75	b3b8b11°b11b12	1741.90	82.443	3426	2	871.45	-8.69
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	15	Carbamidomethyl+C(20);Oxidation+M(32)	EAQAaQWELNYValDGNIGCMVNGAGLAMGTMDIVK	241	36	4	10.9	b4b14y7°y7	3826.84	84.178	1821	3	1276.29	13.78
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	16	Oxidation+M(4)	VVFMasteGGVEIEK	120	15	6	51.62	b8b14y6y9y10y11	1611.77	136.559	1539	1	1611.77	-14.77
Q8ZRP4 DAPD_SALTY 2	1		MQQLQNVIETAFER	0	14	10	81.2	b8°b8b10y3y6y7y9y10y11y14	1706.87	86.761	55819	2	853.94	8.80
Q8ZRP4 DAPD_SALTY 2	2		IDGQWVTHQWLK	48	12	7	47.97	b2b3b4b6b7y1y12	1510.77	91.212	51420	2	755.89	-9.78
Q8ZRP4 DAPD_SALTY 2	3		INDNQVIDGAESR	68	13	10	62.79	b2b3y1y5y6y7°y7y8y10y13	1430.69	41.960	21386	2	715.85	2.05
Q8ZRP4 DAPD_SALTY 2	4		SEVVEGVIVEEGSVISMGVYLGS TK	187	26	3	21.93	b11y10y11	2696.39	101.758	3004	3	899.47	7.52
Q8ZRP4 DAPD_SALTY 2	5		FADYDEAR	89	8	4	33.12	b3b4°b4y7	986.42	35.259	10738	2	493.72	3.59
Q8ZRP4 DAPD_SALTY 2	6		EAVNQVISLLDSGALR	28	16	7	65.85	b14y4y5y6y9y10y13	1684.90	92.799	5131	3	562.30	-15.50
Q8ZRP4 DAPD_SALTY 2	7	Carbamidomethyl+C(28)	NVHLsGGVGIGGVLEPLQANPTIIE DNCFIGAR	154	33	4	11.06	b15°b15y8y14	3417.73	96.776	3567	5	684.35	-8.71

Q8ZRP4 DAPD_SALTY 2	8		ETGEVHYGR	217	9	5	30.51	b5°b5b8y6°y6	1047.48	32.627	1521	2	524.24	-7.34
Q8ZRP4 DAPD_SALTY 2	9		YFDKVPMK	81	8	3	36.13	b6y5y7	1027.52	55.570	4836	2	514.27	-3.56
Q8ZRP4 DAPD_SALTY 2	10		IYDRETGEVHYGR	213	13	4	32.35	b7y6y7y9	1594.77	60.910	1756	2	797.89	6.43
Q8ZRP4 DAPD_SALTY 2	11		VPMKFADYDEAR	85	12	4	34.29	b3b4b7y5	1441.67	66.207	1654	2	721.34	-3.39
Q8ZRP4 DAPD_SALTY 2	12	Phosphoryl STY(5)	VPAGSVVVSGNLP SK	226	15	3	18.16	b4b7y12	1490.77	81.006	2891	2	745.89	14.49
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	1	Carbamidomethyl+C(7)	LWVNPDCLK	719	10	7	68.17	b2y4y5y6y7y8y10	1201.60	61.270	50143	2	601.30	-1.52
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	2		AQESYWAGNTTR	21	12	5	32.23	b6b9y4y7y12	1383.63	30.214	28800	2	692.32	3.53
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	3		LAAITAQDSQRENPYEVR	395	18	8	36.61	b2b3y2y14*y14y15y16y18	2061.03	48.078	26974	3	687.68	-4.62
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	4		LTWTQLLEEVDEALALGHK	137	19	9	44.33	b2b5y1y5y6y9y13y17y19	2166.13	119.564	25867	3	722.71	-6.54
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	5		QAGIDLLPVGDFAWYDHVLTTSLLGNV PAR	52	31	11	41.69	b5°b5*b5b7*b7y3y5y6y7y24y31	3351.79	120.036	25454	3	1117.94	5.83
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	6		DALNSGETAALEEWSAPIQAR	360	21	6	18.95	b2b5b16y5y19y21	2229.10	81.112	24122	2	1115.05	10.40
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	7	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPREDVTR	549	21	6	30.04	b2y3y14y16y17y21	2435.22	98.356	23456	3	812.41	-0.30
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	8	Carbamidomethyl+C(1)	CVKPPVVIGDISRPAPITVEWAK	515	23	12	83.03	b2b3b4b6b7y3y4y6y15y16y20y23	2532.40	76.463	19609	3	844.81	0.19
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	9		LPVDWLLSAGLINGR	279	15	5	18.16	b2b6y3y12y15	1623.93	102.196	18020	2	812.47	5.79
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	10		QAIIEQER	466	8	8	40.9	b2*b2y4°y4y5°y5y6y8	986.52	31.687	17473	2	493.76	-6.93
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	11	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	7	35.49	b2b7b14y1y5y6y9	1834.94	105.926	15881	2	917.97	2.46
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	12		LAAITAQDSQR	395	11	11	113.72	b2b3y3y4y5y6y7y8y9y10y11	1173.62	34.839	14745	2	587.31	-1.46
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	13		WFNTNYHYIYPEFSK	117	15	4	26.24	y4°y4y5y8	1944.91	78.785	35853	3	648.97	-9.73
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	14		LPAPWTTTIGSFPTTEIR	422	19	3	34.55	y8y9y10	2116.08	67.730	21782	3	706.03	-14.42
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	15		TGIAEHIK	458	8	4	54.13	b4b7y5y7	868.47	23.733	10813	2	434.74	-20.94
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	16	Carbamidomethyl+C(1)	CGELALLR	352	8	3	36.13	b4b7y6	931.50	50.559	9588	2	466.25	-2.23
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	17		DEVADLEAAGIGIIQIDEPALR	582	22	3	23.33	b14b15b18	2308.15	93.021	7207	3	770.06	-21.15
Q9L6N1 METE_SALTY 5-methyltetrahydropteroylriglutamate--homocysteine methyltransferase	18		GQQFR	132	5	3	26.46	b3y3*y3	635.32	42.494	5020	1	635.32	-4.71

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	19	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETR	315	22	4	13.45	b5b7°b7y11	2441.25	88.437	2676	3	814.42	-1.30
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	20		FKLPAWPTTTIGSFPQTTEIR	420	21	5	26.78	b3b14y5y7y10	2391.27	88.531	35167	3	797.76	-1.43
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	21		GNLDANHYRTGIAEHK	449	17	3	16.34	b6b15y4	1908.98	121.320	25259	2	954.99	6.20
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	22		KAQESYWAGNTTR	20	13	5	29.91	y6y9°y9y12°y12	1511.74	88.585	5425	2	756.37	10.50
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	23		VKGEPFDR	172	8	3	36.13	b5y3y5	947.51	42.473	4169	2	474.26	14.04
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	24		ADLTEKYAQINAIVGK	298	16	3	23.72	b12y3y4	1733.93	51.426	3933	3	578.65	-10.00
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	25		SDWDAYLEWGVAEFRINAATAVAK	611	22	3	22.2	b12y3y4	2511.22	93.948	3632	3	837.74	-5.15
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	26	Carbamidomethyl+C(1); Phosphoryl STY(13)	CGELALLRDALNSGETAALEEWS APIQAR	352	29	6	25.16	b12b14y10y11y13*y13	3221.51	100.282	5385	4	806.13	-4.70
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	27		RPAPITVEWAK	527	11	0	7.26		1267.70	76.514	23991	2	634.35	-14.73
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	28		LNSGETAALEEWSAPIQAR	362	19	1	7.64	b13	2043.03	81.066	19624	3	681.68	8.07
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		AYGSTNPINVVR	126	12	17	138.37	b2b3b9b11*b11y2y3y4y5y6y7y8y9*y9y10*y10y12	1290.68	51.727	128865	2	645.84	-3.69
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		VFMQPASEGTGIIAGGAMR	93	19	23	192.3	b1b2b3b4b11b12b13b14b16°b16y1y4y5y6y7y11y12y13y14y15y16*y16y19	1892.94	68.772	102798	2	946.98	3.80
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		ATIDGLENMNSPEMVAAK	138	18	14	78.49	b15b18y2y3y4y8y11y12°y12*y12y14y15°y15y18	1890.91	64.010	61108	2	945.96	7.62
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		SVEEILGK	159	8	5	40.9	b1y3y5y6y8	874.48	50.837	52811	2	437.74	-8.17
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		ATIDGLENMNSPEMVAAKR	138	19	9	69.02	y1y3y4y8y10*y11y15y16y17	2046.99	59.765	35589	3	683.00	-4.41
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		VGFGYGK	45	7	6	40.5	b5b7y2y3y6y7	727.37	40.234	19679	2	364.19	-7.97
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		AREVPAAIQK	52	10	3	33.93	b6b7b9	1082.63	29.192	5026	2	541.82	-5.86
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		AVLEVAGVHNVLAK	112	14	9	100.46	b3b4b13y3y6y8y9y10y12	1419.80	61.011	107995	3	473.94	-20.72
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		LIAVNR	14	6	2	26.87	y4y5	685.43	33.390	9542	1	685.43	-5.61
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		AHIEK	1	5	3	39.69	b3b4y4	597.33	23.719	8475	1	597.33	-9.40
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		IFSFTALTTVVGDNRGVFGYGK	29	23	3	22.09	b5y4y5	2362.24	73.611	191825	4	591.31	7.03
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12	Oxidation+M(3)	VFMQPASEGTGIIAGGAMR	93	19	4	20.73	b5b9y4y6	1908.91	40.714	54869	3	636.97	-11.64

[P0A7W4]RS5_SALTY 30S ribosomal protein S5	13		MNSPEMVAAKR	146	11	0	5.65		1233.59	59.806	53366	3	411.87	-12.96
[P0A7W4]RS5_SALTY 30S ribosomal protein S5	14		AYGSTNPINVVR	126	12	0	2.82		1273.64	51.697	1670	2	637.33	-5.08
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	1		LSIAYGIAQAMHREGAELAFYQNDK	17	26	8	25.6	b4°b4b21*b21y3°y3y4y26	2897.44	107.392	140071	4	725.11	4.30
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	2		YMANAMGPEGVR	171	12	10	61.2	b12*b12y5y6y7°y7y8y11°y11*y11	1295.60	51.384	80034	2	648.31	13.66
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	3		AIPNYNVMLAK	151	12	6	40.31	b8b9b10y1y3y12	1290.69	58.528	26443	2	645.85	3.12
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	4		TMLNPGSALLTLSYLGAER	132	19	11	53.78	b2b6b14y1y3°y3y4y6y7y15y19	2007.08	101.863	10621	2	1004.04	9.97
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	5		ILVTGVASK	8	9	3	38.3	y4y6y7	887.55	42.452	7104	2	444.28	-9.63
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	6		FDGFVHSIGFAPGDQLDGDYVNAVTR	84	26	4	12.15	b3b9°b9y12	2797.33	83.980	4840	4	700.09	2.36
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	7		VAHDISSYSFVAMAK	114	15	3	18.16	b4b10y8	1625.79	77.715	3521	2	813.40	-6.83
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	8		EGAEALFTYQNDK	30	13	4	25.44	b8y6*y6y7	1485.71	65.947	8776	3	495.91	15.28
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	9		MGFLSGK	0	7	4	40.5	b3b5b6°b6	739.39	35.328	8047	1	739.39	18.24
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	10		EGFKVAHDISSYSFVAMAK	110	19	4	14.96	b10°b10y8y12	2087.01	101.314	2116	2	1044.01	-9.24
[P16657]FABI_SALTY Enoyl-[acyl-carrier-protein] reductase [NADH]	11		VAHDISSYSFV	114	11	1	7.26	y4	1224.59	77.674	2047	2	612.80	3.09
[P60446]RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	10	68.17	b2y2y4°y4y5y6y7°y7y8y10	1115.63	57.240	80296	2	558.32	-8.86
[P60446]RL3_SALTY 50S ribosomal protein L3	2		IFTEDGVSIPTVIEVEANR	13	20	9	37.65	b1b7b10y4*y4y5y11y13y20	2188.17	88.967	46795	2	1094.59	10.71
[P60446]RL3_SALTY 50S ribosomal protein L3	3		DLANDGYR	38	8	7	62.59	b5y3y5y6°y6y7y8	923.42	32.508	23036	2	462.22	1.92
[P60446]RL3_SALTY 50S ribosomal protein L3	4		TQDATHGNSLSHR	128	13	10	74.83	b2y1y2y3y4y5y6y7y11y13	1423.65	15.546	10979	3	475.22	-13.55
[P60446]RL3_SALTY 50S ribosomal protein L3	5		LAEGEEYTVGQSIISVELFADVKK	83	23	4	19.47	b6b11b15*b15	2512.26	91.115	4824	4	628.82	-10.01
[P60446]RL3_SALTY 50S ribosomal protein L3	6		NLLLVK	184	6	3	40.1	b3y3y4	699.47	56.854	17956	1	699.47	-5.50
[P60446]RL3_SALTY 50S ribosomal protein L3	7		GLWEFR	77	6	2	26.87	b3y4	807.40	70.466	17271	2	404.21	-13.98
[P60446]RL3_SALTY 50S ribosomal protein L3	8		LAEGEEYTVGQSIISVELFADV K	83	22	10	54.92	b3b7b11°b11b12°b12b14y9y20y21	2384.20	136.469	3147	2	1192.60	3.69
[P60446]RL3_SALTY 50S ribosomal protein L3	9		WNFR	124	4	1	12.83	b3	622.31	46.055	2495	1	622.31	-5.79
[P60446]RL3_SALTY 50S ribosomal protein L3	10		VDAER	179	5	1	13.23	y4	589.29	68.061	1795	1	589.29	1.14
[P60446]RL3_SALTY 50S ribosomal protein L3	11	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	6	53.48	b3b4y5y6y7y13	1809.97	56.903	57141	3	603.99	-13.02
[P60446]RL3_SALTY 50S ribosomal protein L3	12		IFTEDGVSIPTVIEVEANRVTQVK	13	25	4	23.12	b3b4b10y16	2743.48	95.708	23493	3	915.17	-2.31
[P60446]RL3_SALTY 50S ribosomal protein L3	13		VTVQSLDVVRVDAER	169	15	3	24.18	b7b8y9	1685.91	119.804	8071	2	843.46	-6.01
[P60446]RL3_SALTY 50S ribosomal protein L3	14		TQDATHGNSLSHRVPGSIGQNQT PGK	128	26	3	12.15	b14y11y15	2687.31	100.367	1693	2	1344.16	-6.54
[P60446]RL3_SALTY 50S ribosomal protein L3	15	Phosphoryl STY(8)	IFTEDGVSIPTVIEVEANR	13	20	3	14.39	b7b12_HPO3 b12y14	2268.10	75.254	32293	3	756.70	-4.52
[P60446]RL3_SALTY 50S ribosomal protein L3	16	Phosphoryl STY(8)	LAEGEEYTVGQSIISVELFADV K	83	22	3	22.2	b6b7y11	2464.11	108.290	3283	3	822.04	-14.27

[P60446]RL3_SALTY 50S ribosomal protein L3	17		LANDGYR	39	7	0	1.21		808.40	32.496	10009	2	404.70	7.32
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1	Carbamidomethyl+C(3)	FACGVIEK	169	8	11	75.83	b2b6y1y2*y2y3y4y5y6y7y8	923.46	41.593	172261	2	462.23	-9.72
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2		EVPALMAGGHLDPEK	84	15	13	58.96	b2b3*b3b6b11b12*b12y1y2y3y9y13y15	1563.76	58.010	38581	3	521.93	-13.58
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3		GGDNYSDKPAPLGGGGAR	151	18	16	144.69	b4*b4b5*b5b7b10*b10y3y4y5y6y7y8y9y10y11	1688.77	33.990	95651	3	563.60	-16.34
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	4		HLGPYNDKGHLGDLPLVNVADGTATYPLLAPR	102	33	5	24.45	b11b16*b16y5y6	3441.78	81.868	45549	4	861.20	-3.62
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	5		EVPALMAGGHLDPEKTGK	84	18	7	40.87	b6b12y4y6*y6y7y16	1849.93	53.304	32993	3	617.31	-11.15
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	6	Oxidation+M(6)	EVPALMAGGHLDPEK	84	15	3	18.16	b10y6y11	1579.78	55.082	2124	2	790.39	-0.31
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	7		PALMAGGHLDPEK	86	13	2	14.93	b3b9	1335.68	58.033	7680	2	668.34	7.49
[P53636]SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	8		EVPALMAGGHLDPEK	84	15	0	4.03		1545.76	58.009	8358	3	515.92	-7.98
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	1		EFDVAVVIGAGGAGMR	6	15	7	37.14	b5b9b13b15y6y8y15	1449.70	58.048	49730	3	483.91	-8.00
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	2		TGPEAILELEHMGLPFSR	90	18	18	176.68	b5b6y1y3*y3y4y6y7y8y10y11y12y13y14*y14y15y16y18	1996.99	94.532	45595	3	666.34	-10.88
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	3	Carbamidomethyl+C(18)	TFAHVDPVKEPIPIPTCHYMMGGIPTK	335	28	7	31.19	b5b6b9y2y3y5y10	3135.55	74.353	43894	4	784.64	-10.28
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	4		DASESDVEGSLER	430	13	5	29.91	y5*y5y7y9y13	1393.62	42.512	8229	2	697.31	10.34
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	5	Carbamidomethyl+C(13)	FDFPERDDANWLCHTLYQPQTESMTR	542	26	4	26.54	y3y6y8y11	3257.48	81.012	5903	3	1086.50	11.02
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	6	Carbamidomethyl+C(5)	ALQECMQHNFSVFR	461	14	5	24.75	b4*b4y7y8y14	1766.82	64.399	5122	2	883.91	6.15
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	7	Carbamidomethyl+C(29)	AGVPVQDMEMWQFHPTGIAGAGVLVTEGCR	228	30	7	19.35	b7*b7*b7b9b11y3y7	3213.56	93.790	3949	5	643.52	10.48
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	8	Carbamidomethyl+C(3)	VECLELDNLMETAYATAVSANFR	510	23	4	20.15	b10y5y8y10	2617.22	110.488	2147	3	873.08	-4.20
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	9		LGGNSLLDLVVFGRR	399	14	3	27.09	y4y5y8	1459.83	104.575	21891	2	730.42	3.60
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	10	Carbamidomethyl+C(7)	DDANWLCHTLYQPQTESMTR	548	20	3	21.18	y5y7y9	2466.12	69.268	16242	3	822.71	13.66
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	11		DLAGR	281	5	2	26.46	b4y4	531.29	28.951	11600	1	531.29	5.05
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	12		ATVLATGGAGR	196	11	3	36.09	y3y5y7	973.53	31.638	9224	2	487.27	-9.72
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	13		LPVR	2	4	1	12.83	b3	484.32	77.566	8315	1	484.32	-9.89
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	14		IYQRPFGGQSK	113	11	5	36.09	y3*y3*y3y7y10	1280.65	35.310	7805	2	640.83	-22.21
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	15		TFAHVDPVK	335	9	5	30.51	b3*b3b7*b7y3	1013.55	53.154	4545	2	507.28	11.20
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	16		TESR	533	4	2	12.83	b3*b3	492.24	36.909	4396	1	492.24	-9.05
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	17		NHTTIFSEWYALDLVK	155	16	6	42.7	b5b8b9*b9b10y9	1936.98	96.129	1833	3	646.33	-1.95
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	18		AAGLHLQESIAEQGVLR	413	17	4	23.33	b12y10y11*y11	1791.97	63.226	1633	2	896.49	-0.89
[Q8ZQU3]DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	19		IYQRPFGGQSKNFGGEQAAR	113	20	6	32.25	b7b9b10*b10b18y14	2211.09	68.586	454964	3	737.70	-6.85

Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	20		EGDAMAKGLEQLK	475	13	5	34.48	b10°b10b11y4y12	1389.69	63.771	6041	2	695.35	-13.35
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	21	Carbamidomethyl+C(15)	LDDTSSEFNTQRVECLELDNLME TAYATAVSANFR	498	35	8	28.95	b12y5y7y8y10°y10*y10y13	4010.88	110.933	5431	3	1337.63	10.35
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	22		LDDGRIYQRPFGGQSK	108	16	3	17.18	b5y4y11	1836.91	78.677	4634	3	612.97	-13.69
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	23	Carbamidomethyl+C(9); Oxidation+M()	EIPVPIPTCHYMMGGIPTK	344	19	5	42.09	b9b10b11y3y10	2157.08	83.368	42773	2	1079.04	12.56
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	24	Oxidation+M(12)	TGPEAILELEHMGLPFSR	90	18	4	29.18	b5b12y10y11	2013.02	70.884	6226	3	671.68	4.24
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	25	Carbamidomethyl+C(3); Oxidation+M(10)	VECLELDNLMETAYATAVSANFR	510	23	5	24.6	b10b22y3y5y10	2633.19	70.807	4616	3	878.40	-10.85
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	26	Oxidation+M(14)	EFDVVIGAGGAGMR	6	15	4	18.16	b8b11°b11y9	1465.72	65.385	2216	2	733.36	7.25
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	27		EFDVVI	6	7	1	7.26	y5	792.42	58.022	2207	2	396.72	12.32
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	1		VDQLSNDVNAMR	40	12	6	34.29	b4y4*y4y7y8y12	1361.65	49.436	32622	2	681.33	1.88
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	2		SDVQAAKDDAAR	52	12	5	49.74	b3y3y4y6y9	1246.59	18.753	24149	3	416.20	-13.81
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	3		IDQLSSDVQTLNAK	26	14	3	19.31	b3b5y9	1531.80	53.514	7089	2	766.41	4.46
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	4		VDQLSNDVNAMRSDVQAAK	40	19	3	14.96	b5b11y5	2060.99	57.110	2707	3	687.67	-4.15
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	5		IDQLSSDVQTLNAKVDQLSNDVN AMR	26	26	4	18.31	b10y3y6y9	2874.42	92.125	1669	3	958.81	-1.87
P0A2S0 LRP_SALTY Leucine-reonsive regulatory protein	1		TYVVMEEVK	145	9	7	30.51	b2b8y2y5°y5y7y9	1097.55	53.130	24457	2	549.28	-3.11
P0A2S0 LRP_SALTY Leucine-reonsive regulatory protein	2	Carbamidomethyl+C(8)	VGLSPTCLER	37	11	7	56.02	b2b4y4y5y7y8y11	1228.63	52.414	17186	2	614.82	-1.19
P0A2S0 LRP_SALTY Leucine-reonsive regulatory protein	3		LVIK	158	4	1	12.83	y3	472.35	56.857	9049	1	472.35	-6.65
P0A2S0 LRP_SALTY Leucine-reonsive regulatory protein	4	Carbamidomethyl+C(22)	GAPDVFEQFNAAVQKLEEIQECHL VSGDFDYLLK	84	34	3	10.99	b5b8y12	3909.90	118.462	10561	4	978.23	-0.75
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	10	82.89	b2b3b4y2y3y4y6y8y9y12	1377.65	78.988	102178	2	689.33	0.71
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AVVESIQR	69	8	9	49.36	b2b5y4*y4y5°y5y6*y6y8	901.50	33.484	80421	2	451.26	-7.24
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3		AAVTMPSSK	22	9	7	57.55	y3y4°y4y6y7°y7y9	891.46	32.038	75104	2	446.24	2.94
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4		MSMQDPIADMLTR	0	13	3	25.44	b4y4y5	1508.70	47.354	1731	3	503.57	8.09
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	1		LTANQTYQHFLSGFTAK	371	17	16	91.74	b1b2b8°b8b11y1y2y3°y3y6 y10y12y14y15y16y17	1926.95	68.607	37965	3	642.99	-12.54
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	2		NTYASPEQWQEK	495	12	3	35.53	y8y9y10	1480.69	45.302	22071	2	740.85	13.52
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	3		MQAAGAQAYL VNTGWNGTGKR	426	21	5	18.95	b2b8b12y11y19	2194.08	60.581	21230	3	732.03	0.78
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	4		GVLTNLGAVAVDTGIFTGR	45	19	9	52.26	b19y1y2y7y8°y8y9y10y18	1861.03	94.542	17694	2	931.02	4.66
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	5		GMFSVMNYLLPLK	212	13	3	25.44	b10y3y4	1512.80	109.748	16147	2	756.90	1.69

[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	6		YIVRDDTTTRDTLWWS DK	69	17	3	16.34	b8y5y7	2170.07	99.764	11100	3	724.03	4.61
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	7		AYGINDVQDIVYNPSYDTLYQEEL NPGLEGYER	12	33	10	34.76	b3b5b7b10°b10y2y4y7y8°y8	3837.81	91.723	8511	3	1279.94	8.40
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	8		IQLIGGTWYGGEMK	197	14	3	27.09	y5y11y12	1552.78	77.097	7005	2	776.90	0.94
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	9		EQGLNSEN FVAFNLTER	180	17	10	42.81	b11°b11b13y2°y2y3y10°y10y11y14	1967.94	85.154	3762	3	656.65	-1.12
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	10		DALLENVTVREDGTVD FDDGSK	305	22	4	13.45	b6b8°b8y6	2395.09	71.346	2707	3	799.04	-13.35
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	11		MQAAGAQA YLVNTGWNGTGK	426	20	6	14.39	b11°b11y2y5y11°y11	2038.00	65.417	2187	2	1019.50	9.40
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	12		AIIDAILNGSLD NAETFR	454	18	5	24.85	b5y2y3y5y7	1932.98	112.570	1689	2	966.99	-11.11
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	13		VSYPYIHIDNIVKPVSK	332	17	7	44.64	b6b7°b7b10°b10b11y9	1972.05	66.226	44464	4	493.77	-20.24
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	14		VNNLTPQDLK	2	10	3	28.7	b3y4y5	1141.62	44.888	13704	2	571.31	-2.89
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	15	Carbamidomethyl+C(21)	LIGDDEHG WDDDG VFNFE GG CYAK	263	24	7	27.62	b8b14y9°y9y13°y13y14	2716.15	80.084	13438	3	906.05	7.37
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	16		YTDTPAGEALVSAGPK	521	16	3	24.89	b6b8b14	1576.78	62.691	7244	2	788.89	-4.10
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	17		NDNKPLSQETWQH LK	90	15	5	25.83	b5°b5b10y5y7	1837.92	80.247	2838	2	919.46	1.66
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	18		GDVAVFFGLSGTGK T TLSTD PK	239	22	9	42.89	b4b8°b8b11b20y3y5y8°y8	2198.10	116.161	35968	3	733.37	-13.44
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	19		NDNKPLSQETWQH LKGLVTHQLSGK	90	25	4	18.64	b4b9°b9b11	2858.49	81.921	3436	3	953.50	0.17
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	20	Phosphoryl STY(7)	EAEPEIYHAIR	293	11	3	36.09	y3y6y10	1407.63	136.516	2965	1	1407.63	8.85
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	21	Carbamidomethyl+C(7); Oxidation+M(5)	GIASMHC SANVGEK	225	14	4	19.31	b4°b4b6y8	1476.66	42.520	6260	2	738.84	4.30
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	22		DALLENVTVREDGTVD FDDG	305	20	0	6.86		2180.03	71.371	6840	2	1090.52	14.89
[P41033]PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	23		TANQTQYHFLSGFTAK	372	16	5	20.89	b3°b3b4°b4°b4	1813.86	68.572	1784	2	907.43	-14.40
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	1		NIANPIAQILSLALLLR	293	17	7	33.75	b1b2y5y7y8y13y17	1833.15	137.380	7231	2	917.08	9.86
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	2		EIVNDVAK	206	8	8	64.36	b5b6b7y5°y5y6°y6y8	887.47	33.523	5688	2	444.24	-9.97

[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	3	Carbamidomethyl+C(12)	ADIAANGFDILCVR	124	14	5	19.31	b8°b8b10°b10y3	1534.79	81.021	61570	2	767.90	15.59
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	4		NYHIAVLPGDGIGPEVMAQALK	3	22	5	24.25	b10b11b14y15°y15	2293.16	101.897	21327	3	765.06	-18.52
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	5	Carbamidomethyl+C(9)	LYQGLEAFCLPLR	112	12	3	29.51	y5y8y9	1466.78	72.931	9579	3	489.60	19.72
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	6		GAAAVSTDEMGDIAR	341	16	3	17.18	b14y8y12	1576.79	82.738	3696	3	526.27	13.94
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	7	Carbamidomethyl+C(6)	ATVEGCEQADAILFGSVGGPK	59	21	4	22.34	b5°b5b6y13	2106.00	51.343	2408	4	527.26	-6.84
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	8		ELTGGIYFGQPK	138	12	4	22.3	b7b9y6°y6	1309.67	47.470	1966	2	655.34	-6.52
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	9		YSLDANDAATAIEQAINR	310	18	7	40.72	b3b4b5b12°b12y13°y13	1935.96	85.119	1784	3	645.99	9.96
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	10	Carbamidomethyl+C(9); Carbamidomethyl+C(24)	LYQGLEAFCLRADIAANGFDILCVR	112	26	5	22.82	y9°y9y10*y10y13	2982.45	71.524	2739	4	746.37	-14.00
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	11		AFDTEVYHRFEIER	160	14	3	19.31	b4y5y7	1811.87	72.224	2712	2	906.44	1.08
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	12		WENLPPEQPPEGALLPLR	80	19	4	24.13	b8b9°b9b11	2202.14	80.005	2565	3	734.72	-12.97
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	13	Oxidation+M(10)	GAAAVSTDEMGDIAR	341	16	5	42.7	b9y9y12y13y14	1592.75	80.038	30837	2	796.88	-2.76
[P55900]SERC_SALTY Phohoserine aminotransferase	1	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	16	106.28	b1b8b10b12°b12y1y3y4y5°y5y8y9y10y11y12°y12	2567.18	74.810	46465	4	642.55	-13.88
[P55900]SERC_SALTY Phohoserine aminotransferase	2		AQVFNFSSGPAMLPAEVLK	1	19	10	47.89	b2°b2b3b6b14y3y5y6y14y19	2006.06	92.181	27201	2	1003.53	7.79
[P55900]SERC_SALTY Phohoserine aminotransferase	3		ASIYNAMPIEGVK	335	13	4	35.14	y8y9y10y13	1392.72	65.554	23574	2	696.86	2.02
[P55900]SERC_SALTY Phohoserine aminotransferase	4		GKEFIQVAEEAEQDFR	42	16	7	37.4	b2b13y5*y5y6y7y16	1895.93	53.142	23153	3	632.65	11.01
[P55900]SERC_SALTY Phohoserine aminotransferase	5		ALTDFMIDFER	348	11	5	35.34	b2b5b8y3y6	1357.64	91.209	12108	2	679.32	-3.78
[P55900]SERC_SALTY Phohoserine aminotransferase	6		VFLEESFAAGLHALK	311	15	4	18.16	b5°b5b10y3	1631.88	88.976	3517	3	544.63	-0.15
[P55900]SERC_SALTY Phohoserine aminotransferase	7		EFIQVAEEAEQDFRDLLNIPSNYK	44	24	6	26.19	b5°b5b11°b11y5y6	2868.40	118.999	3076	3	956.80	-2.55
[P55900]SERC_SALTY Phohoserine aminotransferase	8		TTADYVDAGYWAASAIK	91	17	4	22.96	b5b9y11y13	1802.87	83.883	2825	2	901.94	4.06
[P55900]SERC_SALTY Phohoserine aminotransferase	9		AQGGVAAMHK	257	10	3	33.93	y3y7y8	969.48	95.427	1858	2	485.24	-14.73
[P55900]SERC_SALTY Phohoserine aminotransferase	10	Carbamidomethyl+C(3)	KYCAPQIIDAK	111	11	5	41.54	b7b8b9y10*y10	1306.67	67.611	76511	2	653.84	-7.47
[P55900]SERC_SALTY Phohoserine aminotransferase	11		MNVVPQLADNTLDKVFLEESFAAGLHALK	297	29	5	24.26	b3y4y12y14y26	3218.63	109.323	34358	4	805.41	-6.52
[P55900]SERC_SALTY Phohoserine aminotransferase	12		AELLYGVIDNSDFYRNDVAQANR	272	23	11	55.24	b3b5b12°b12y10y13°y13*y13y14y19y20	2643.30	80.005	20390	3	881.77	6.56
[P55900]SERC_SALTY Phohoserine aminotransferase	13		GQFAGVPLNLLGDKTTADYVDA GYWAASAIK	77	31	6	25.24	b3b4b6°b6b25y25	3212.65	97.863	19394	3	1071.56	8.89
[P55900]SERC_SALTY Phohoserine aminotransferase	14		ASIYNAMPIEGVKALTDFMIDFER	335	24	5	23.45	b3b11b12°b12y14	2731.35	90.772	5253	3	911.12	1.07
[P55900]SERC_SALTY Phohoserine aminotransferase	15	Carbamidomethyl+C(14)	DLLNIPSNYKVLFCGGGR	58	19	5	14.96	b3y3y13°y13*y13	2160.12	100.730	3761	4	540.79	9.49
[P55900]SERC_SALTY Phohoserine aminotransferase	16		SRMNVVPQLADNTLDK	295	16	4	35.11	b8b10b11b13	1848.94	92.296	2682	4	462.99	6.87
[P55900]SERC_SALTY Phohoserine aminotransferase	17		ALTDFMIDFERR	348	12	5	26.28	b6°b6y6°y6y7	1513.74	60.919	2342	2	757.37	-6.21

[P55900]SERC_SALTY Phohoserine aminotransferase	18		INQKKAELLYGVIDNSDFYR	267	20	3	22.52	b3b4y8	2386.19	115.053	1784	3	796.07	-5.93
[P55900]SERC_SALTY Phohoserine aminotransferase	19	Carbamidomethyl+C(7); Oxidation+M(17)	LAQQELCDWHGLGTSVMEISHR	20	22	3	13.45	b7b14y11	2583.18	92.342	4350	4	646.55	-9.07
[P55900]SERC_SALTY Phohoserine aminotransferase	20	Oxidation+M(1)	MNVPFQLADNTLDK	297	14	4	19.31	b4y5y8*y8	1621.77	69.370	2444	4	406.20	-13.92
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		AAIEEMMASLPAQWR	58	15	11	52.42	b4b6°b6b8b13°b13y2y5y9°y9y15	1703.83	91.301	10637	2	852.42	6.09
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		TYENTTALTPEDITEAVWWVATLPAHVNINTVEMMPVTQSFAGLSVHR	199	48	6	21.78	b2b14b24b25y14y48	5340.63	136.532	4955	4	1335.91	-1.01
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		VTDIEPGLVGGTEFSSVR	171	18	5	47.38	y5y7y8y9y13	1862.96	69.964	27563	2	931.98	6.03
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4		ASVEDWETMIDTNNK	93	15	6	25.83	b5°b5b8y8°y8y11	1752.81	72.859	12036	2	876.91	17.55
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		LQALK	36	5	1	13.23	b3	572.37	56.622	4418	1	572.37	-3.09
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		AGKTYENTTALTPEDITEAVWWVATLPAHVNINTVEMMPVTQSFAGLSVHR	196	51	5	11.66	b11°b11b18y10*y10	5596.79	102.299	10079	5	1120.16	0.17
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		NRGHIINIGSTAGSWPYAGGNVYGATK	124	27	4	25.91	y9y12y14y23	2761.39	100.770	7022	3	921.14	4.51
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	8	Carbamidomethyl+C(15);Phosphoryl STY(6)	MIVLVTGATAGFGECIAR	0	18	3	15.6	b7y6y12	1945.94	96.620	1782	2	973.48	13.05
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	9	Oxidation+M(9)	ASVEDWETMIDTNNK	93	15	4	18.16	b4y3y8*y8	1768.76	36.861	3849	4	442.95	-4.69
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	10		TYENTTALTPEDITEAVWWVATLPAH	199	26	2	27.57	y8y9	2929.39	136.539	4015	3	977.14	-10.75
[P58661]AAT_SALTY Aartate aminotransferase	1		LREEFGVYAVASGR	360	14	8	39.08	b10°b10b12b14y3y4y11y14	1553.79	72.192	23576	2	777.40	-11.31
[P58661]AAT_SALTY Aartate aminotransferase	2		MFENITAAPADPILGLADLFR	0	21	15	47.93	b2b5°b5°b5b6°b6b8°b8y1y2y3y5y7y13y21	2275.20	121.298	17489	2	1138.10	10.19
[P58661]AAT_SALTY Aartate aminotransferase	3		VWVSNPSWPNHK	122	12	3	22.3	b6b8y4	1450.71	54.190	11525	3	484.24	-11.70
[P58661]AAT_SALTY Aartate aminotransferase	4		NYLGIDGIPEFAR	63	13	10	54.62	b2b4°b4b5b8°b8b12y5y8y13	1464.75	81.553	11152	2	732.88	-0.08
[P58661]AAT_SALTY Aartate aminotransferase	5		ELIVASSYSK	236	10	5	36.94	b2y6y7y8°y8	1096.58	47.316	10183	2	548.79	-10.13
[P58661]AAT_SALTY Aartate aminotransferase	6		TAQTPGGTGALR	96	12	7	68.41	b4b5y7y8y9y10*y10	1129.59	30.335	13144	2	565.30	-4.75
[P58661]AAT_SALTY Aartate aminotransferase	7		NFGLYNER	246	8	5	36.13	b3b7y6°y6*y6	1012.48	51.319	5172	2	506.74	-7.11
[P58661]AAT_SALTY Aartate aminotransferase	8	Carbamidomethyl+C(4)	VGACTLVADAETVDR	254	16	7	52.82	b3b4b9b10°b10y6y12	1647.81	55.569	4616	2	824.41	6.30
[P58661]AAT_SALTY Aartate aminotransferase	9		GWLPLFDFAYQGFR	204	15	6	37.14	b3b7y3y5y7*y7	1787.88	33.511	2148	4	447.73	-6.14
[P58661]AAT_SALTY Aartate aminotransferase	10	Carbamidomethyl+C(15)	VNVAGMTPDNMAPLCEAIVAVL	374	22	3	13.45	b8y8y10	2285.17	109.692	2083	3	762.39	15.28
[P58661]AAT_SALTY Aartate aminotransferase	11	Carbamidomethyl+C(1)	CTQELLFGKGSALINDK	76	17	3	24.99	b7b8b12	1893.95	98.401	103557	3	631.99	-12.50

P58661 AAT_SALTY Aartate aminotransferase	12		TAQTPGGTGALRIAADFLAK	96	20	4	21.18	b6*b6b9b16	1959.04	103.486	15396	2	980.02	-13.02
P58661 AAT_SALTY Aartate aminotransferase	13		AEQYLLNETTKNYLGIDGIPEFAR	51	25	3	12.42	b3b9y4	2884.47	63.811	7662	5	577.70	12.19
P58661 AAT_SALTY Aartate aminotransferase	14		AFSQMKSAIR	270	10	4	28.7	b4°b4b5y3	1138.60	31.686	7342	2	569.80	-1.82
P58661 AAT_SALTY Aartate aminotransferase	15	Carbamidomethyl+C(4)	VGACTLVAADAETVDRAFSQMK	254	22	3	13.45	b16y7y12	2340.12	104.579	6640	3	780.71	-6.26
P58661 AAT_SALTY Aartate aminotransferase	16		AIWEQELTDMRQR	304	13	4	34.11	b7y5y8y10	1675.82	84.103	1698	3	559.28	-0.66
P58661 AAT_SALTY Aartate aminotransferase	17		KAEQYLLNETTK	50	13	3	20.67	b6y5y7	1566.79	63.906	1551	3	522.93	-8.26
P58661 AAT_SALTY Aartate aminotransferase	18		VWVSNPSWPNH	122	11	0	2.82		1322.63	54.189	13282	3	441.55	2.58
P58661 AAT_SALTY Aartate aminotransferase	19		NYLGIDGIPEFAR	63	13	0	3.23		1447.72	81.574	1591	2	724.36	2.53
P77983 KPYK1_SALTY Pyruvate kinase I	1		GDLGVEIPVEEVIFAQK	244	17	6	34.05	b3b6b7y3y10y17	1843.00	95.550	27286	2	922.00	8.08
P77983 KPYK1_SALTY Pyruvate kinase I	2		MLDAGMNVMR	22	10	9	43.18	b2b4°b4y1y2y7y8y9y10	1137.52	57.986	21918	2	569.26	-2.47
P77983 KPYK1_SALTY Pyruvate kinase I	3		AGQTFTFTTDK	86	11	3	24.33	b10y6y10	1216.57	59.190	13800	3	406.19	-12.44
P77983 KPYK1_SALTY Pyruvate kinase I	4		IENQEGLNNFDEILEASDGIMVAR	220	24	8	47.04	y2y3y4y6y8y10y13y24	2677.29	97.201	13767	3	893.10	6.20
P77983 KPYK1_SALTY Pyruvate kinase I	5		AHGGENIQISK	208	12	6	26.28	b2b6b7b8°y2y4	1266.68	40.226	6761	2	633.84	-2.02
P77983 KPYK1_SALTY Pyruvate kinase I	6		AEAGDVANAILDGTDAVMLSGESAK	292	25	6	22.77	b4b8b15y2y9y24	2405.17	118.976	1643	3	802.40	9.64
P77983 KPYK1_SALTY Pyruvate kinase I	7	Carbamidomethyl+C(13)	YPLEAVSIMATICER	319	15	4	26.24	y5°y5y6y14	1752.87	83.469	14311	2	876.94	4.87
P77983 KPYK1_SALTY Pyruvate kinase I	8		GAVETAEK	360	8	5	36.13	b3b6°b6y3°y3	804.42	68.567	6075	1	804.42	14.34
P77983 KPYK1_SALTY Pyruvate kinase I	9		VVITATQMLDSMIK	272	14	5	27.61	b8°b8b10y5y13	1549.83	102.303	4950	2	775.42	-0.39
P77983 KPYK1_SALTY Pyruvate kinase I	10		AEAGDVANAILDGTDAVMLSGESAKGK	292	27	5	22.77	b4°b4b12b13°b13	2590.24	51.388	61960	3	864.09	-9.52
P77983 KPYK1_SALTY Pyruvate kinase I	11		TESEEMLSKMLDAGMNVMR	13	19	12	50.11	b10b11°b11b13°b13y6y9°y9°y9y10°y10y12	2171.99	83.871	56115	3	724.67	3.71
P77983 KPYK1_SALTY Pyruvate kinase I	12		DVALQSGLAQKGDVVVMVSGALVPSGTTNTASVHVL	434	36	3	10.9	b23y19y23	3520.83	86.552	11041	3	1174.28	-12.07
P77983 KPYK1_SALTY Pyruvate kinase I	13		KYFPDATILALTTNEVTAR	388	19	3	14.96	b5y3y10	2124.11	83.424	10477	3	708.71	-9.77
P77983 KPYK1_SALTY Pyruvate kinase I	14	Carbamidomethyl+C(3)	IVCTIGPKTESEEMLSK	5	17	5	24.99	y6°y6y7°y7y10	1921.96	67.652	1909	3	641.33	0.83
P77983 KPYK1_SALTY Pyruvate kinase I	15	Carbamidomethyl+C(13) ;Oxidation+M(9)	YPLEAVSIMATICER	319	15	6	43.16	b6°b6b7y4y5y7	1768.89	101.415	5273	2	884.95	13.73
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	1		LGSVFSSTGTGGGQEQTITSTWTTLAHHGMVIVPIGYAAQELFDVSQVR	106	49	19	69.2	b3°b3b7b11°b11b33y1y2y3y4°y4°y4y5y6°y6y7y12y29y49	5134.56	116.999	28964	4	1284.40	0.38
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	2		TQNAPVATPQELADYDAIIFGTPTR	54	25	8	50.32	b2b11b12y5y6y7y13y25	2689.35	90.757	14488	3	897.12	2.63
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	3		GGTPYGATTIAGGDGSR	155	17	3	16.34	b6y4y12	1537.73	41.571	3241	2	769.37	4.45
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	4		TFLDQTGGLWASGSLYGK	88	18	4	24.52	b5b11b12°b12	1900.93	118.603	2050	2	950.97	-5.46
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	5		VPETMPPEIFAK	38	12	5	37.3	b3b7°b7b10y8	1358.71	47.406	7908	2	679.86	8.45

Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	6		YQGEYVAGLAVK	183	12	5	34.29	b3b4*b4b8y10	1297.68	46.951	2225	2	649.34	-1.88
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	7		TQNAPVATPQELADYDAIIFGTPT RFGNMSGQMR	54	34	5	21.53	b8*b8b9b11y21	3697.83	122.791	18337	4	925.21	13.93
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	8		TPYGATTIAGDGSR	157	15	7	64.01	b5b6b7b8b10*b10b13	1423.69	41.595	41544	3	475.24	7.46
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	9		GGTPYGATTIAG	155	12	1	7.28	y10	1065.52	41.519	9629	2	533.26	-3.09
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	10		LGSVFSSTGTGGGQEQTITSTWTT LA	106	26	4	16.84	y6y8°y8y13	2587.25	116.993	5514	3	863.09	-2.17
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	1		YLSLLPYTDR	63	10	8	58.17	b2b3y1y5y6y7y8y10	1240.65	75.726	58637	2	620.83	-4.03
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	2		FTAEGVQEIDYKDIATLK	12	18	4	15.6	b3b6°b6y10	2041.06	75.278	1833	3	681.02	3.83
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	3		NYITESGK	30	8	5	36.13	b4°b4*b4y4y7	911.45	74.134	1947	1	911.45	7.37
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	4		FTAEGVQEIDYK	12	12	7	62.21	b3b4b10y5y6y7*y7	1399.67	46.096	1624	2	700.34	0.44
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	5		DIATLKNYITESGK	24	14	4	31.57	b11y4y8y12	1552.81	72.551	5420	3	518.28	-5.11
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	6	Carbamidomethyl+C(2)	FCRFTAEGVQEIDYK	9	15	3	18.16	b9y4y7	1862.90	49.538	4902	3	621.64	14.35
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	1		AVGWAALQYVQPGTIVGVGTGST AAHFIDALGTMK	8	35	24	205.26	b3b4b5b6b7b9b10b11y3y4 y6y7y9y11°y11y14y19y20y 24y26y27y28y30y35	3487.82	108.271	66392	3	1163.28	3.57
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	2	Carbamidomethyl+C(3)	FICIADASK	112	9	8	74.98	b2b8y3y4y5y6y7y9	1024.51	51.745	40807	2	512.76	-6.08
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	3		GADVALIGTPDGVK	201	14	5	19.31	b4b6y2y5y14	1312.71	58.099	21205	2	656.86	-1.49
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	4		GQIEGAVSSSDASTEK	43	16	6	27.7	b11y2y7y9y12y16	1565.74	32.497	9087	2	783.37	7.80
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	5		FPLPVEVIPMAR	128	12	4	44.96	y3y5y8y9	1368.75	91.629	9164	2	684.88	-13.20
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	6		QVDILGKFPLPVEVIPMAR	121	19	5	41.17	y3y4y6y7°y7	2122.19	100.714	40269	3	708.07	-7.59
P66955 TALB_SALTY Transaldolase B	1		LSYDTEASIAK	100	11	8	64.02	b3b8y3y7°y7y8y9y11	1197.60	45.044	19099	2	599.30	0.20
P66955 TALB_SALTY Transaldolase B	2	Carbamidomethyl+C(11)	NVGEILELAGCDR	228	13	4	34.11	b3y5y8y11	1445.71	74.690	15086	2	723.36	5.24
P66955 TALB_SALTY Transaldolase B	3		ELAESEGAIER	250	11	9	71.01	b3y2y3°y3y4y7y8y9y11	1203.59	37.345	14201	2	602.30	5.88
P66955 TALB_SALTY Transaldolase B	4		ISTEVDAR	92	8	7	49.36	b7b8y2y4y6y7y8	890.45	28.911	13348	2	445.73	-10.83
P66955 TALB_SALTY Transaldolase B	5		LYQPQDATTNPSLILNAAQIPEYR	25	24	9	51.04	b4*b4b5b10b11b12y1y3y2 4	2716.39	96.707	6368	3	906.13	-2.88
P66955 TALB_SALTY Transaldolase B	6		QHGYETVVMGASFR	214	14	3	27.09	y3y4y9	1581.77	56.643	5367	2	791.39	11.34
P66955 TALB_SALTY Transaldolase B	7		LASTWQGIR	132	9	3	38.3	y4y6y7	1031.55	52.635	18156	2	516.28	-8.17
P66955 TALB_SALTY Transaldolase B	8		LYNDAGISNDR	117	11	5	47.56	y3y4y5°y5y9	1237.60	80.759	10115	3	413.20	11.94
P66955 TALB_SALTY Transaldolase B	9		LIDDAVAWAK	50	10	5	26.94	b6°b6b9°b9y6	1101.58	61.775	8897	2	551.29	-14.96
P66955 TALB_SALTY Transaldolase B	10		DYAPAEDPGVVSVTEIYEYYK	193	21	6	21.72	b3°b3b5b11y5°y5	2408.11	93.221	7245	3	803.38	-1.93
P66955 TALB_SALTY Transaldolase B	11		ANTDK	187	5	1	13.23	b4	548.27	74.794	2412	1	548.27	6.12

P66955 TALB_SALTY Transaldolase B	12		ITEAEFLWQHHQDPMASVDK	275	19	4	23.68	b6y5y8y10	2295.11	47.416	2207	3	765.71	12.45
P66955 TALB_SALTY Transaldolase B	13		KFAVDQEK	300	8	4	33.12	b5°b5b6y6	964.52	55.629	8581	2	482.76	10.00
P66955 TALB_SALTY Transaldolase B	14	Phosphoryl STY(5)	ELAESEGAIERK	250	12	4	22.3	b4y8°y8y11	1411.64	51.377	5747	3	471.22	1.30
P66955 TALB_SALTY Transaldolase B	15	Oxidation+M(15)	QFTTVVADTGDIAAMK	9	16	4	24.3	b4b13y8y10	1683.83	75.472	1549	2	842.42	1.45
P66955 TALB_SALTY Transaldolase B	16		STEVDAR	93	7	1	9.67	b4	777.38	28.933	1716	1	777.38	5.02
Q7CPG1 YICS_SALTY Uncharacterized protein yicS	1		IMASEGNQQHIR	59	12	8	73.76	b2b9y3y5y7*y7y9y10	1383.67	27.300	18857	3	461.89	-7.32
Q7CPG1 YICS_SALTY Uncharacterized protein yicS	2		GALTDEAWEEK	48	11	5	24.33	b4°b4b6y8y11	1247.63	62.811	11983	2	624.32	4.31
Q7CPG1 YICS_SALTY Uncharacterized protein yicS	3		GALTDEAWEK	48	10	4	54.94	y3y4y7y9	1119.54	50.385	9772	2	560.27	4.91
Q7CPG1 YICS_SALTY Uncharacterized protein yicS	4	Oxidation+M(2)	IMASEGNQQHIR	59	12	3	22.3	b5y8y10	1399.68	40.802	7765	2	700.35	7.06
P66643 RS9_SALTY 30S ribosomal protein S9	1		GGGISGQAGAIR	68	12	5	40.31	b3y7y8y9y12	1043.55	34.116	23920	2	522.28	-6.32
P66643 RS9_SALTY 30S ribosomal protein S9	2		SLEQYFGRETAR	33	12	5	34.29	b3°b3b4b6y6	1456.72	33.553	2395	2	728.86	1.42
P66643 RS9_SALTY 30S ribosomal protein S9	3		AENQYYGTGR	1	10	4	28.7	b4°b4b5y5	1158.54	27.648	28343	2	579.77	20.02
P66643 RS9_SALTY 30S ribosomal protein S9	4		ALMEYDESLR	85	10	3	26.94	b8y3y8	1226.57	41.066	5415	2	613.79	-1.69
P66643 RS9_SALTY 30S ribosomal protein S9	5		QPLELVDMVEK	49	11	4	24.33	b4*b4b7y8	1300.71	27.812	4887	2	650.86	20.18
P66643 RS9_SALTY 30S ribosomal protein S9	6		ALMEYDESLRGELR	85	14	4	19.31	b10°b10y11y13	1681.83	103.578	3464	3	561.28	3.12
P62405 RL5_SALTY 50S ribosomal protein L5	1		LLDNAAADLT AISGQKPLITK	48	21	11	87.55	b3b5y5y6y9y11y12y16y17y19y21	2153.21	76.097	40945	3	718.41	-5.78
P62405 RL5_SALTY 50S ribosomal protein L5	2		LMTEFNYSVMQVPR	15	15	9	60.65	b12b13°b13y2y7y8y11y12y15	1828.89	76.891	13885	2	914.95	10.08
P62405 RL5_SALTY 50S ribosomal protein L5	3		ITLNMGVGEAIADK	33	14	5	19.31	b7b11y11°y11y14	1431.76	66.067	3123	2	716.38	7.84
P62405 RL5_SALTY 50S ribosomal protein L5	4		GNYSMGVREQIIFPEIDYDK	125	20	4	25.28	b8y6y8y9	2374.16	98.968	2257	2	1187.58	7.40
P62405 RL5_SALTY 50S ribosomal protein L5	5		EQIIFPEIDYDK	133	12	3	22.3	b7y6y8	1509.74	62.484	1634	3	503.92	-6.39
P62405 RL5_SALTY 50S ribosomal protein L5	6		LHDYYK	3	6	1	13.63	b5	838.40	106.633	1526	1	838.40	-6.26
P62405 RL5_SALTY 50S ribosomal protein L5	7	Carbamidomethyl+C(7)	QGYPIGCKVTLR	80	12	4	22.3	b8y3y7°y7	1391.76	33.398	2874	3	464.59	11.05
P62405 RL5_SALTY 50S ribosomal protein L5	8		GLDITITTTAKSDEEGR	150	17	3	16.34	b5b12y9	1806.91	39.732	1550	2	903.96	-0.61
P62405 RL5_SALTY 50S ribosomal protein L5	9	Phosphoryl STY(2)	ITLNMGVGEAIADKK	33	15	3	18.16	b13y12y14	1639.80	67.665	16237	3	547.27	-4.69
P64267 GNS_SALTY Protein gns	1		TGQEVSEIEFAPR	28	13	5	39.34	b4y8y9°y9y10	1462.72	57.860	12322	2	731.86	2.17
P64267 GNS_SALTY Protein gns	2		TGQEVSEIEFAPRETMK	28	17	5	16.34	b1b3y3y6y17	1951.95	46.097	7646	2	976.48	2.56
P64267 GNS_SALTY Protein gns	3		AEEEEIALISK	9	11	3	36.09	b3b5b9	1173.61	83.869	3810	2	587.31	-20.07
P64267 GNS_SALTY Protein gns	4		ETMK	41	4	1	12.83	y3	508.25	80.818	3579	1	508.25	14.23
P64267 GNS_SALTY Protein gns	5		NSEELTHKAEIEEIALISK	1	19	3	21.91	b8b11b13	2112.07	75.302	11547	3	704.69	-7.05
P64267 GNS_SALTY Protein gns	6		TGQEVSEIEFAPRETMK	28	17	6	32.8	b3b5°b5b13y6y11	1951.93	85.143	3328	3	651.32	-5.19
P64267 GNS_SALTY Protein gns	7	Phosphoryl STY(6)	TGQEVSEIEFAPRETMK	28	17	3	16.34	b5y4y11	2031.92	89.826	4063	3	677.98	7.81
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	1		SVDGIQVGEGR	266	11	5	36.77	b7y2y5y6y9	1116.56	42.157	22151	2	558.79	-0.33
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	2		AAPNTIPTAAK	149	11	9	68.58	y1y2y3y5y7°y7y8y9y11	1054.59	32.912	14834	2	527.80	-1.27

[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	3		IQQAFFGLFTGETEDK	284	16	3	17.18	b9y4y10	1830.89	76.885	11263	2	915.95	-0.93
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	4		DGVLFTPPFTSSALPGITR	204	19	3	14.96	b6b9y14	1976.05	93.757	14096	2	988.53	-0.99
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	5		ADYIWFNGEMVR	5	12	3	22.3	b3b7y5	1500.70	69.376	5697	3	500.90	3.74
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	6		WGWLDPVNS	300	9	3	30.51	b6b8y5	1073.50	68.077	3869	2	537.25	-6.14
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	7		ESLYLADEVFMSGTAAEITPVR	244	22	4	13.45	b10b12y13°y13	2399.17	128.566	3172	3	800.40	-3.77
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	8	Carbamidomethyl+C(14)	FPVSQSIDELMEACR	69	15	4	29.48	b6y7y10y11	1781.86	83.285	1930	3	594.62	19.80
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	9		VHVMSHALHYGTSVFEGIR	22	19	5	33.39	b5b8b10b11y15	2140.04	75.551	1689	4	535.77	-14.72
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	10		KADYIWFNGEMVR	4	13	3	20.67	b3y6y9	1628.80	72.385	3834	3	543.61	8.39
[P0A1A5]ILVE_SALTY Branched-chain-amino-acid aminotransferase	11	Phosphoryl STY(12)	DGVLFTPPFTSSALPGITR	204	19	8	51.87	b6°b6b11b13_HPO3 b13b15y9y13_H3PO4 y13y14	2055.98	94.511	2560	2	1028.50	-10.09
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	1		TGYLPITTAAYELTR	343	15	7	55.64	b3y4y6y7y9y11y15	1669.89	85.729	64699	2	835.45	3.36
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	2		LGNMPQIR	389	8	6	49.36	b6°b6y4y5y7*y7	928.50	48.366	37385	2	464.75	-8.74
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	3		TIVDEELESVWTGKK	397	15	8	55.64	b5y3y4y8y11°y11y13y15	1733.88	76.351	17273	3	578.63	-9.15
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	4		FNYGVGMMPYDADIK	282	15	5	31.85	b2b4b5y7y11	1720.78	75.411	15363	2	860.90	7.66
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	5		FNQANPDYK	47	9	6	38.3	b2y2y3y4y8y9	1096.50	29.399	14527	2	548.76	-1.00
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	6		GNYEQNLASAGIAFR	62	15	7	55.42	b7b10b11*b11b12b13y15	1610.80	74.093	13647	2	805.90	6.29
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	7		TIVDEELESVWTGK	397	14	5	27.88	b5°b5b7b11°b11	1605.82	78.262	3171	2	803.41	12.47
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	8		GAPQNAIIGGASLWVMQGKDKET YTGVAK	297	29	4	21.95	b14b15°b15y11	2990.51	105.519	3012	4	748.38	-11.27
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	9		SGHLLSQPFNSSTPVLYYNK	132	20	3	14.39	b3b7y3	2252.12	68.991	42334	3	751.38	-8.56
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	10	Carbamidomethyl+C(6)	FYNGDCAMTTASSGSLANIR	258	20	4	21.18	y4y11°y11y14	2135.97	61.909	11358	2	1068.49	8.34
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	11		DAGINFDESQFVPTVAGYYTDAK	109	23	5	29.51	b5y3y6y8y11	2508.18	62.099	5431	3	836.73	7.88
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	12		NNGFDGTDAVLEFNKPEQVK	212	20	8	56.19	y6y8°y8y9°y9y10y16y18	2222.10	66.246	4615	2	1111.55	10.33
[Q7CPK0]UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	13		FLDFLAKPENAAEWHQK	326	17	3	23.33	b8b9y14	2044.03	82.406	2322	3	682.01	-0.90

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	14		TWQELADYTAK	167	11	3	27.34	b10y6y7	1325.66	61.819	1898	2	663.33	15.65
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	15		AGLDPEQPPKTWQELADYTAK	157	21	5	29.8	b4b7y4y5y17	2358.16	73.498	26194	3	786.73	1.14
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	16		EQGYDKNPGADIATR	358	16	4	25.56	y3y4y9*y9	1797.84	41.011	25655	3	599.95	-1.29
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	17		EVDSLAQRFNQANPDYK	39	17	9	52.65	b5b10b12y6°y6y9°y9y12y13	1994.95	94.557	10404	3	665.66	-1.77
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	18		ETYTGVAKFLDFLAKPENAAEWHQK	318	25	3	12.42	b4b11y10	2893.46	116.927	3032	3	965.16	2.28
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	19		LGNMPQIRTIVDEELESVWTGK	389	22	3	23.33	y10y12y13	2515.27	115.248	2178	3	839.10	-6.21
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	20		VDEELESVWTGKK	399	13	2	14.93	b5b9	1519.77	76.357	3694	2	760.39	2.41
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	1		LNSAVFPSAQGGPLMHVIAGK	251	21	8	21.72	b2b4*b4y3y13y15°y15y21	2094.11	79.047	70914	3	698.71	-4.08
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	2		VMQAQGSQLTNK	42	12	17	125.13	b2b3b6*b6b10*b10y2*y2y3y4y5y6y7y9y10*y10y12	1304.66	30.537	46865	2	652.83	-4.12
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	3		SPFVTSGIR	354	9	6	45.51	b1b7y5y6y7y9	963.52	49.613	45038	2	482.26	-4.05
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	4		EMNIADYDAELWQAMEQEK	4	19	9	58.02	b3y4°y4y6y7y9y10y12y19	2314.03	93.426	36563	2	1157.52	12.66
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	5	Carbamidomethyl+C(7)	ELAGWMCDVLDNINDEATIER	380	21	6	30.04	y4y5y8y11°y11y21	2464.15	102.104	28981	2	1232.58	14.86
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	6		AVALKEAMEPEFK	272	13	3	20.67	b3b11y3	1462.76	60.153	24309	2	731.88	-0.83
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	7		EAMEPEFK	277	8	4	36.13	b5y2y4y6	980.44	44.073	16933	2	490.72	1.31
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	8		VVSGGTENHLFLDLVDK	308	18	5	24.52	b6°b6b7°b7b13	1956.04	74.687	90943	2	978.52	-3.06
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	9		FPVYA	412	5	1	13.23	b4	596.30	58.037	23953	1	596.30	-7.98
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	10		QEEHIELIASENYTSR	25	17	4	16.34	b9b11y10*y10	2016.01	81.040	3356	2	1008.51	20.95
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	11		YAEGYPGK	54	8	3	40.9	y4y6y7	884.41	27.813	1832	2	442.71	-1.86
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	12		GYKVVSOGGTENHLFLDLVDK	305	21	3	13.89	b10b12y11	2304.22	102.028	63979	2	1152.61	-3.28
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	13		EMNIADYDAELWQAMEQEKVR	4	21	4	23.54	b5°b5b19b20	2569.14	75.233	56969	3	857.05	-13.30
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	14		LYNIVPYGIDESGKIDYDEMAK	138	22	4	26.95	b3b13y17y18	2533.22	77.232	49498	3	845.08	2.12
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	15		NSVPNDPKSPFVTSGIR	346	17	4	26.18	b3y8y11y14	1814.92	52.894	21450	3	605.65	-10.16
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	16		AVALKEAMEPEFK	272	13	3	28.15	y4y7y8	1462.76	56.574	8912	2	731.88	-2.50
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	17		MIIGGFSAYSGVVDWAKMR	168	19	3	24.13	y6y9y10	2088.02	105.390	5901	2	1044.51	-9.94
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	18		NLTGKEADAALGR	326	13	3	29.91	y3y6y9	1315.70	61.665	3744	2	658.35	1.48

P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	19		VRQEEHIELIASENYTSR	23	19	5	14.96	b6°b6y6°y6y8	2271.11	77.893	2394	4	568.53	-13.22
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	20	Oxidation+M(15)	LNSAVFPSAQGGPLMHVIAGK	251	21	6	24.73	b3°b3b4°b4b10y3	2110.09	85.387	46600	3	704.03	-12.15
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	21	Oxidation+M(3)	REMNIADYDAELWQAMEQEK	3	20	3	22.52	b5y5y6	2486.12	77.768	3391	4	622.29	10.90
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	22	Oxidation+M(1)	MIIGGFSAYSQVVDWAK	168	17	7	51.18	b14y8y9y11y12°y12y14	1816.88	83.903	1733	2	908.95	-5.78
P22107 TRAT_SALTY TraT complement resistance protein	1		FEEAKPVLEEQLAK	223	14	7	27.88	b2y2y6*y6y9y13y14	1630.86	53.953	40945	3	544.29	-7.78
P22107 TRAT_SALTY TraT complement resistance protein	2		ATVTTDNVAALR	177	12	11	75.9	b4b9y1y5y6y8°y8y9°y9y10y12	1231.66	46.245	33482	2	616.34	-0.89
P22107 TRAT_SALTY TraT complement resistance protein	3		ESQGWLNR	107	8	6	48.68	y3y5*y5y7y8*y8	989.48	44.287	27727	2	495.24	-3.95
P22107 TRAT_SALTY TraT complement resistance protein	4		GYTVVTSPDK	79	10	5	36.94	b2y5y6y7y10	1066.54	36.884	10307	2	533.78	1.49
P22107 TRAT_SALTY TraT complement resistance protein	5		IQTSTETGNQHK	196	12	3	29.51	y5y6y10	1343.63	15.178	7062	3	448.55	-17.17
P22107 TRAT_SALTY TraT complement resistance protein	6		ATVTTDNVAALRQGTSGAK	177	19	6	14.96	b9°b9°b9y3y7*y7	1861.00	53.186	168152	3	621.01	14.37
P22107 TRAT_SALTY TraT complement resistance protein	7		DIQAKGYTVVTSPDK	74	15	3	24.18	b9b10y5	1621.82	65.770	6265	2	811.41	-13.17
P22107 TRAT_SALTY TraT complement resistance protein	8	Carbamidomethyl+C(16) ;Oxidation+M()	LMMVTLVSSTLALSGCGAMSTAI KK	5	25	3	12.42	b5b24y7	2586.36	77.045	315909	3	862.79	8.31
P22107 TRAT_SALTY TraT complement resistance protein	9	Carbamidomethyl+C(16) ;Oxidation+M()	LMMVTLVSSTLALSGCGAMSTAI K	5	24	3	22.02	b3b4y12	2458.23	77.244	4226	3	820.08	-3.48
P22107 TRAT_SALTY TraT complement resistance protein	10		YTVVTSPDK	80	9	2	20.7	b4b8	1009.53	36.932	1790	2	505.27	11.12
P04787 LEUD1_SALTY 3-isopropylmalate dehydratase small subunit 1	1		FTQHTGLVPLDAANVDTDAIIPK	4	24	7	16.89	b9b21y2y3y10*y10y24	2535.34	81.529	28221	3	845.79	-1.25
P04787 LEUD1_SALTY 3-isopropylmalate dehydratase small subunit 1	2		GQQPNPEFVLNFPEYQGASILLAR	53	24	5	12.28	b2b13°y12y14y24	2688.38	99.066	12559	3	896.80	-0.18
P04787 LEUD1_SALTY 3-isopropylmalate dehydratase small subunit 1	3		TGFGAHLFNDWR	36	12	11	59.2	b1b4°b4b5b7°b7y2y3y5y7y12	1420.66	73.433	12098	3	474.22	-14.09
P04787 LEUD1_SALTY 3-isopropylmalate dehydratase small subunit 1	4		EHAPWALTDYGFK	86	13	6	20.67	b2°b2b3y10y12y13	1534.75	73.428	11723	2	767.88	8.91
P04787 LEUD1_SALTY 3-isopropylmalate dehydratase small subunit 1	5		QPAFMR	195	6	1	13.63	b5	749.37	31.974	11762	1	749.37	-4.64
P04787 LEUD1_SALTY 3-isopropylmalate dehydratase small subunit 1	6	Carbamidomethyl+C(3)	RHCMLNGLDSIGLTLQHEDAIAAY ENK	168	27	3	18	b6b10b23	3069.51	133.498	8981	3	1023.84	7.32
P04787 LEUD1_SALTY 3-isopropylmalate dehydratase small subunit 1	7		VTRTGFGAHLFNDWR	33	15	5	26.24	y3°y3y6y10°y10	1776.88	67.657	4571	3	592.96	-9.48
P04787 LEUD1_SALTY 3-isopropylmalate dehydratase small subunit 1	8		TGFGAHLFNDWRFLDEK	36	17	5	23.74	b4b10b12°b12°b12	2053.02	80.098	3584	2	1027.01	12.96
Q9F7A2 NUDD_SALTY GDP-mannose mannosyl hydrolase	1		AYFSPDAPAVGL	145	12	5	37.3	b3b8b10y11°y11	1207.59	67.714	3071	2	604.30	-10.21
Q9F7A2 NUDD_SALTY GDP-mannose mannosyl hydrolase	2		DETLEAAFAR	54	10	7	28.7	b2b3b4b10y6°y6y10	1122.55	49.873	2565	2	561.78	5.55
Q9F7A2 NUDD_SALTY GDP-mannose mannosyl hydrolase	3		WLTPEQLLASDNVHENS	127	18	5	15.6	b1b7y4y6°y6	2109.04	71.359	2057	2	1055.02	3.13

Q9F7A2 NUDD_SALTY GDP-mannose mannosyl hydrolase	4		LPDAQHGSYR	117	10	5	26.94	b4°b4b6*b6y7	1143.54	75.271	10788	2	572.27	-13.66
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	1		FQDGADFNAAAVK	97	13	7	46.15	y1y4y5y10y11*y11y13	1353.65	50.287	26485	2	677.33	1.62
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	2		YISMNVTQKPFDNPK	269	15	8	40.72	y4y5y6*y6y9*y9*y9y15	1781.86	56.315	24574	3	594.63	-13.98
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	3		NLTGFWIMPDTGFSDDADLK	491	21	5	27.4	b6b11y2y13y14	2390.13	107.540	22727	2	1195.57	11.54
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	4		DIGFHPVGTGPYQLETWNQTDFV K	176	24	4	22.02	b10y10y11y24	2749.34	83.962	22550	3	917.12	5.24
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	5		AAMLQTGEAQFAFPIPEQAALLA K	229	25	4	22.9	b6°b6b11b12	2679.40	97.872	9902	3	893.81	7.38
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	6		LDSITWRPVTDNNTNTR	214	15	5	41.52	y2y4y6y11y13	1787.91	57.506	5965	2	894.46	3.76
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	7		NLELVASPSIMQR	256	13	4	29.71	b8b12y4y7	1457.78	53.196	3195	3	486.60	0.08
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	8		SFYQGLFGLDKDMK	56	14	4	27.09	b2y4y7y8	1648.79	71.245	1947	3	550.27	-10.66
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	9		EAQDIIWKESPWIPLVVEK	465	19	5	21.91	b5°b5b7b11y2	2280.20	93.092	1811	3	760.74	-13.92
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	10		TEVVDPATVK	134	10	4	26.94	b4°b4b9y5	1058.57	39.754	18692	2	529.79	-5.07
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	11		FAGYWQQGLPK	203	11	3	24.33	b6b10y9	1294.66	48.859	16337	2	647.83	2.45
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	12		MTQFITHK	0	8	8	65.6	b3b4b6°b6b7°b7*b7y5	1005.51	66.158	2744	2	503.26	-5.46
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	13		EAGYPDGFSTTLWSSHNHSTAQK	339	23	3	13.06	b8b10y13	2521.16	91.038	2515	4	631.04	7.36
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	14		QGVKFQDGADFNAAAVK	93	17	6	39.79	b8b10b12*b12y11y12	1765.87	80.014	11473	2	883.44	-8.64
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	15		NIakteVVDPATVK	130	14	3	24.75	b6y7y8	1484.84	58.550	6646	2	742.92	2.38
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	16		FAGYWQQGLPKLDSITWRPVTDN NTR	203	26	3	12.15	b9b16y10	3063.56	84.167	3972	4	766.65	6.14
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	17		FQDGADFNAAAVKANLDR	97	18	3	15.6	b4b14y3	1922.96	81.026	3965	2	961.98	11.68
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	1		TFDTPTYPNLSALSADGK	308	18	5	15.6	b3y2y11y14y18	1897.94	66.505	25903	2	949.47	9.91
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	2		EQEATQPDDVIR	338	12	8	64.21	y1y2y3y6y8y9y10y12	1400.66	40.199	19567	2	700.84	-0.87
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	3		QAGQVSVIDAK	291	11	4	24.33	b9y4y9y11	1115.60	38.288	19279	2	558.30	-2.95
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	4		MSTGLALDSK	185	10	4	28.7	b5b6y7y10	1022.52	46.828	11629	2	511.76	-2.15
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	5		IAAPASLAVLFNPTR	268	15	8	24.18	b1b6y1y5°y5*y5y6y15	1540.88	90.626	8587	2	770.94	-1.90
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	6		EHFFINLSLDTAGHR	229	15	4	18.16	b3b10y1y10	1756.90	96.661	7604	2	878.95	13.55
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	7		ELVADAATNTIYISGVGKESAIWV VDGETIK	144	31	6	35.45	b14b15y2y12y13y31	3249.71	105.107	4798	3	1083.91	5.78
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	8		LLDDGKEHFFINLSLDTAGHR	223	21	4	24.73	b4b7b8y19	2398.18	93.223	3130	3	800.07	-13.84
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	9		LLDDGK	223	6	1	13.63	y4	660.36	34.639	4400	1	660.36	2.03
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	10		ESAIWVVVDGETIK	162	13	3	20.67	b4y9y11	1446.72	44.102	3748	2	723.87	-16.79
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	11		ELVADAATNTIYISGVGK	144	18	3	22.76	b4b9b13	1821.93	136.286	2331	2	911.47	-16.08

Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	12		LVL DAR	126	6	1	13.63	y5	686.41	40.226	1534	2	343.71	-7.47
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	13		NEAYVTHRQAGQVSVIDAK	283	19	4	14.96	b6°b6b12y8	2086.07	65.190	10373	3	696.03	2.46
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	14		MSTGLALDSKAQR	185	13	4	32.35	b6b11b12y6	1377.73	73.400	10231	2	689.37	12.49
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	15		GAYEMAWSQQENALWLATSQSR K	41	23	3	13.06	b3y7y20	2655.24	55.645	5678	3	885.75	-9.47
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	16		AQRLYTTNADGEFITIDTASNK	195	22	5	13.45	b8b10*b10y6*y6	2429.16	96.233	1916	2	1215.08	-14.67
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	17		AVGKGAYEMAWSQQENALWLAT SQSR	37	26	4	18.3	b5b10b12°b12	2882.42	100.369	1751	4	721.36	12.11
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	18	Phosphoryl STY(11)	ESAIWVVDGETIK	162	13	4	29.71	b6b10y3y7	1526.71	35.976	2227	3	509.58	6.64
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	19	Oxidation+M(1)	MSTGLALDSK	185	10	5	41.14	b6b7y3y9°y9	1038.51	47.905	9904	2	519.76	-2.12
P37589 PMRD_SALTY Signal transduction protein pmrD	1	Carbamidomethyl+C(2); Carbamidomethyl+C(8)	ACHVLVLCDSGGSLK	14	15	4	29.48	b5b6b9y12	1615.81	66.204	12614	2	808.41	12.69
P37589 PMRD_SALTY Signal transduction protein pmrD	2	Carbamidomethyl+C(26)	MIAEANSMILLSPGDILSPLQDAQY CINR	29	29	9	66.16	b5b7y1y6y7y8y9y10y13	3233.56	117.017	3020	3	1078.52	-13.59
P37589 PMRD_SALTY Signal transduction protein pmrD	3	Carbamidomethyl+C(2); Carbamidomethyl+C(8); Carbamidomethyl+C(41)	ACHVLVLCDSGGSLKMIAEANS MILLSPGDILSPLQDAQYCINR	14	44	3	16.52	b8b10b13	4830.36	107.673	7790	4	1208.35	-2.33
P37589 PMRD_SALTY Signal transduction protein pmrD	4	Carbamidomethyl+C(26) ;Phosphoryl STY(12)	MIAEANSMILLSPGDILSPLQDAQY CINR	29	29	7	29.02	b6b11b12b20y5y8*y8	3313.59	101.926	8500	3	1105.20	10.90
P37589 PMRD_SALTY Signal transduction protein pmrD	5	Carbamidomethyl+C(26) ;Oxidation+M()	MIAEANSMILLSPGDILSPLQDAQY CINR	29	29	6	22.15	b13y3*y3y7*y7y8	3249.58	78.868	11850	3	1083.87	-3.61
P0A277 XGPT_SALTY Xanthine phohoribosyltransferase	1		LMPSEQWK	22	8	3	36.13	b7y3y6	1018.50	48.517	16775	2	509.75	-0.24
P0A277 XGPT_SALTY Xanthine phohoribosyltransferase	2		GGLVPGALLAR	37	11	4	24.33	b3y2y3y7	1023.62	69.776	9531	2	512.31	-10.37
P0A277 XGPT_SALTY Xanthine phohoribosyltransferase	3	Carbamidomethyl+C(6)	HVDTVCISSYDHDNQR	53	16	8	64.79	b3°b3b4b5b6y4y5°y5	1945.83	39.769	3911	3	649.28	-6.65
P0A277 XGPT_SALTY Xanthine phohoribosyltransferase	4		AEGDGEFVIDDLVDTGGTAVAI R	76	25	3	21.96	b14y14y15	2490.23	81.032	1936	3	830.75	-4.12
P0A277 XGPT_SALTY Xanthine phohoribosyltransferase	5	Carbamidomethyl+C(6)	HVDTVCISSYDHDNQRELK	53	19	7	45.7	b6b8y8y9*y9y10y12	2316.05	74.128	17428	3	772.69	-7.17
P0A277 XGPT_SALTY Xanthine phohoribosyltransferase	6		RAEGDGEFVIDDLVDTGGTAV AIR	75	26	3	18.3	b4b6b10	2646.32	75.383	7776	3	882.78	-6.18
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	1		LYTSLGDAAVGR	22	12	5	29.51	y6°y6y7y10y12	1222.64	53.189	19401	2	611.83	1.70
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	2		LFAGNATPELAQR	5	13	8	64.16	b3b4y5y6y10y11°y11y13	1387.74	54.541	16203	2	694.37	5.81
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	3		VFAYATHPIFSGNAANNLR	243	19	4	23.68	b13y8y10y16	2063.03	65.979	14066	3	688.35	-9.82
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	4	Carbamidomethyl+C(10)	NSVIDEVVVCDTIPTLDEIK	262	20	8	28.05	b3b8°b8*b8b11y7y12y20	2259.17	89.029	8853	2	1130.09	11.35
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	5		ITAVIPYFGYAR	84	12	3	22.3	b4y7y10	1370.74	81.355	16080	2	685.88	-2.14
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	6		ANVSQVMHIIGDVAGR	198	16	4	35.11	b3b9b12b13	1666.84	80.003	11409	3	556.28	-18.24
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	7	Carbamidomethyl+C(2); Carbamidomethyl+C(16)	DCVLVDDMIDTGGTLCK	214	17	5	29.95	b4b6°b6y6y7	1911.87	80.249	3120	3	637.96	9.83
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	8		RISNEESISAMFEH	301	14	3	19.31	b4y10y13	1649.75	93.271	2253	3	550.59	-8.14

P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	9	Phosphoryl STY(6)	VFAYATHPIFSGNAANNLR	243	19	3	24.13	b4b5b9	2142.98	58.070	8719	4	536.50	-9.91
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	10	Oxidation+M(7)	LLNDTDMAIIDKR	182	13	5	32.35	b3b10b11*b11y9	1533.78	70.533	7560	2	767.39	-7.96
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	1	Carbamidomethyl+C(22)	TSEGGIFNNAAQVWNHTFYWNCL APNAGGEPTGK	58	34	9	24.31	b2b6°b6y2y4y10y11y13y3 4	3708.72	97.116	23497	3	1236.91	8.56
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	2		SFELPALPYAKDALAPHISAETLEY HYGK	1	29	7	19.93	b1b9b11b17y1y8y10	3231.63	82.052	19896	4	808.66	-0.68
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	3		DALAPHISAETLEYHYGK	12	18	4	15.6	b5°b5y9y11	2015.00	76.697	34950	2	1008.00	7.39
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	4		NARPNYLEHFWALVNWEFVAK	168	21	6	23.54	b3b4*b4b10°b10*b10	2604.30	105.160	10915	3	868.77	-4.22
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	5		LADAIAASFGSFAEFK	92	16	9	59.06	b3b5b10b11°b11b14y3y6°y 6	1644.79	105.966	5681	2	822.90	-22.19
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	6		NFGSGWTWLVK	117	11	5	50.57	b3b4b6b10*b10	1294.68	53.102	4385	2	647.84	18.39
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	7		AQFTDAAIKNFGSGWTWLVK	108	20	4	22.52	b9y11y12*y12	2240.12	73.357	74405	3	747.38	-11.23
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	8		GTAFEGKSLEEIVR	44	14	3	19.31	b3y4y10	1535.82	63.109	7537	3	512.61	9.78
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	9		NARPNYLEHFWALVNWEFVAKN LAA	168	25	4	12.42	b6b9°b9y11	2973.51	112.415	2871	3	991.84	-1.48
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	10	Phosphoryl STY(7)	NFGSGWTWLVK	117	11	5	36.77	b3y3y4y6°y6	1374.63	43.131	34079	3	458.88	13.14
O54296 RS11_SALTY 30S ribosomal protein S11	1	Carbamidomethyl+C(1)	CADAVKEYGIK	69	11	7	31.32	b1b2b3b4b10y2y11	1253.60	37.850	26297	3	418.54	-13.92
O54296 RS11_SALTY 30S ribosomal protein S11	2		ALNAAGFR	98	8	5	40.9	y3y5y6*y6y8	819.45	42.522	21467	2	410.23	1.42
O54296 RS11_SALTY 30S ribosomal protein S11	3		STPFAAQVAAER	57	12	5	44.96	b2y4y7y8y10	1247.64	50.273	17670	2	624.32	-1.86
O54296 RS11_SALTY 30S ribosomal protein S11	4		QGNALGWATAGGSGFR	37	16	3	24.89	y8y11y14	1549.76	66.795	7601	2	775.38	7.72
O54296 RS11_SALTY 30S ribosomal protein S11	5		EYGIK	75	5	1	13.23	y3	609.32	66.206	7072	1	609.32	-13.62
O54296 RS11_SALTY 30S ribosomal protein S11	6		QVSDGVAHIHASFNNITIVTITDR	14	23	9	35.36	b6°b6b10b12y12*y12y13y 19*y19	2495.29	68.549	2648	3	832.43	9.88
O54296 RS11_SALTY 30S ribosomal protein S11	7	Phosphoryl STY(16)	QVSDGVAHIHASFNNITIVTITDR	14	23	5	20.15	b8b12*b12b15y9	2575.22	111.183	4375	3	859.08	1.61
P26976 PHON_SALTY Non-ecific acid phohatase	1		IFSPVVGAK	85	9	5	38.3	b2y3y4y6y9	917.54	51.811	28225	2	459.27	-8.58
P26976 PHON_SALTY Non-ecific acid phohatase	2		QAAEDADVSVENIAR	70	15	8	45.59	b2b4b12°b12y10y11*y11y 12	1587.77	51.361	9740	2	794.39	3.38
P26976 PHON_SALTY Non-ecific acid phohatase	3	Carbamidomethyl+C(3)	VICGAHWQSDVDAGR	191	15	4	18.16	b8y3y9y15	1670.78	45.965	4861	2	835.89	3.80
P26976 PHON_SALTY Non-ecific acid phohatase	4		LQTIPAFQK	215	9	3	38.3	y4y5y7	1045.60	55.731	34116	2	523.30	-6.77
P26976 PHON_SALTY Non-ecific acid phohatase	5		NGSYPSGHTAYGTLLALVLSEARP ER	150	26	5	21.93	b3°b3b4°b4y8	2759.38	96.999	29127	4	690.60	-12.30
P26976 PHON_SALTY Non-ecific acid phohatase	6		YVGAVEFAR	206	9	4	30.51	b3y4°y4y7	1011.52	51.986	15837	2	506.26	-9.59
P26976 PHON_SALTY Non-ecific acid phohatase	7		NLLTMGGYYATASAK	108	15	4	25.83	b8b13y3y8	1560.74	74.732	2727	2	780.88	-19.01
P26976 PHON_SALTY Non-ecific acid phohatase	8		EELNDK	230	6	4	26.87	b3°b3b4°b4	747.36	79.857	1595	1	747.36	11.35
P26976 PHON_SALTY Non-ecific acid phohatase	9		WKQAAEDADVSVENIAR	68	17	3	23.33	b8b9y9	1901.94	55.058	5690	2	951.48	4.94
P26976 PHON_SALTY Non-ecific acid phohatase	10	Carbamidomethyl+C(3)	VICGAHWQSDVDAGRYVGAVEF AR	191	24	5	16.89	b3b22y9y13°y13	2663.25	77.030	3793	4	666.57	-9.44

P26976 PHON_SALTY Non-ecific acid phohatase	11		NNLLSKEDHPK	236	11	3	24.33	b3b7y6	1294.67	61.976	1933	3	432.23	-1.70
P65599 ORN_SALTY Oligoribonuclease	1		SADENNLIWIDLEMTGLDPER	1	21	4	21.72	b8y5y7y11	2431.15	83.441	12295	3	811.05	2.21
P65599 ORN_SALTY Oligoribonuclease	2		THTGSGLVDR	64	10	5	41.71	b3b6b8°b8y10	1042.52	32.541	3034	3	348.18	-5.27
P65599 ORN_SALTY Oligoribonuclease	3		SADENNLIWIDLEMTGLDPERDR	1	23	8	17.51	b1°b1b3b12°b12y5°y5y9	2702.25	93.217	2517	4	676.32	-7.41
P65599 ORN_SALTY Oligoribonuclease	4	Carbamidomethyl+C(4)	SPICGNSIGQDR	101	12	3	26.28	b8b9y10	1303.62	72.243	1801	3	435.21	7.40
P65599 ORN_SALTY Oligoribonuclease	5	Carbamidomethyl+C(11)	TWVPAGKSPICGNSIGQDR	94	19	4	14.96	b12°b12y6y11	2043.04	69.760	48783	3	681.68	13.50
P65599 ORN_SALTY Oligoribonuclease	6		SADENNLIWIDLEMTGLDPERDR	1	23	6	40.04	b10b11b12°b12y5y10	2702.25	93.835	22544	4	676.32	-7.77
P65599 ORN_SALTY Oligoribonuclease	7		ESVAELAYYREHFIK	165	15	4	34.7	b3b4°b4b5	1854.94	83.300	1775	2	927.97	0.13
P65599 ORN_SALTY Oligoribonuclease	8	Oxidation+M(1)	MSADENNLIWIDLEMTGLDPERD R	0	24	6	42.91	b11y5y6y7y9y13	2849.28	89.715	5467	4	713.08	-9.34
P65599 ORN_SALTY Oligoribonuclease	9		SADENNLIWIDLEMTGLDPER	1	21	0	6.45		2414.13	83.433	39125	3	805.38	7.69
P43019 SODM_SALTY Superoxide dismutase [Mn]	1		LAVVSTANQDSPLMGEAISGASGF PILGLDVWEHAYYLK	138	39	6	15.69	b2b3b12y4y9y11	4120.10	116.927	8428	3	1374.04	7.11
P43019 SODM_SALTY Superoxide dismutase [Mn]	2		SYTLPSLPYAYDALEPHFDK	1	20	8	45.91	b1b3b11b12b14y5y11y13	2327.10	88.714	8301	3	776.37	-7.87
P43019 SODM_SALTY Superoxide dismutase [Mn]	3		RPDYIKEFWNVVNWDEAAAR	181	20	4	19.79	b4b8y3y19	2479.19	104.031	1720	4	620.55	-11.32
P43019 SODM_SALTY Superoxide dismutase [Mn]	4		AAIER	100	5	1	13.23	y4	559.31	46.135	14674	1	559.31	-9.93
P43019 SODM_SALTY Superoxide dismutase [Mn]	5		MSYTLPSLPYAYDALEPHFDK	0	21	5	18.95	b4b6y6°y6y9	2458.20	65.248	4824	4	615.31	14.50
P43019 SODM_SALTY Superoxide dismutase [Mn]	6		SYTLPSLPYAYDALEPHFDKQTME IHHTK	1	29	7	24.26	b3°b3y3°y3y12y22y25	3432.62	79.870	69084	5	687.33	-10.74
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	1		IVELEAPQLPR	178	11	7	53.01	b1b3y5y6y7y9y11	1264.72	67.041	59330	2	632.86	-5.89
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	2		LKDGVGLLPTSLDIVENPK	156	19	8	46.24	y2y4y5y7y10°y10y11y19	2008.12	80.035	40314	3	670.04	-7.96
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	3		DGIFVEDKDSPYVNLIVTR	215	19	3	14.96	b8b11y17	2180.10	80.000	7674	3	727.37	-10.08
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	4		FVQAYQSDEVYEAANK	245	16	5	17.18	b4y8°y8y11y16	1861.88	84.186	7316	2	931.45	12.78
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	5		GDIDANAFQHKKPYLDQQIK	78	19	3	22.74	b3b4y7	2201.08	66.976	4289	2	1101.04	-10.76
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	6		DSPYVNLIVTR	223	11	4	31.32	b5b6b10°b10	1276.70	62.039	3969	3	426.24	9.56
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	7		DGSQVAVPNDPTNLGR	128	16	5	37.92	b6b8b9b11y10	1639.80	65.219	5443	3	547.27	-4.17
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	8		DAENVK	238	6	2	13.63	b5°b5	675.33	65.066	4792	1	675.33	0.27
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	9		DGIFVEDK	215	8	3	36.13	b7y5y7	922.46	86.782	1513	1	922.46	3.71

Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	10		FVQAYQSDEVYEAAKVFNGGA VK	245	24	8	32.95	b3b10y4y6y7*y7y22°y22	2634.29	78.364	24815	3	878.77	3.34
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	11		SLDELKDGSQLVAVPNDPTNLGR	122	22	6	25.64	b3°b3b13y6y9y19	2325.19	58.570	4621	2	1163.10	9.66
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	12	Phosphoryl STY(10)	LKDGVLTLPTSLDIVENPK	156	19	3	14.96	b10y7y9	2088.11	85.390	179934	3	696.71	8.89
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	13	Phosphoryl STY(13)	YGLDVELVTFNDYVLPNEALSK	56	22	7	18.2	b3b11y7*y7y11_H3PO4 y11°y11*y11	2579.25	117.003	1800	3	860.42	9.09
P0A212 GYRI_SALTY DNA gyrase inhibitory protein homolog	1		IVPVEWIAVYYDNPDPVPAEK	41	21	7	30.04	b2y4y8y11°y11y12y21	2416.24	97.210	19353	3	806.09	-0.30
P0A212 GYRI_SALTY DNA gyrase inhibitory protein homolog	2		IAGFHMVGPWEHTVK	12	15	9	66.32	b3b10b11b12°b12b13y5y8 y15	1708.89	90.655	9989	3	570.30	13.22
P0A212 GYRI_SALTY DNA gyrase inhibitory protein homolog	3	Carbamidomethyl+C(1)	CDTVVSVAENFILPDNSEGVIVTAI EGGEYATAVAR	64	36	4	10.9	b11y2y8y23	3766.81	93.787	3380	4	942.46	-9.14
P0A212 GYRI_SALTY DNA gyrase inhibitory protein homolog	4		DYEIR	1	5	1	13.23	y3	695.34	49.634	1705	1	695.34	12.11
P0A212 GYRI_SALTY DNA gyrase inhibitory protein homolog	5		IAGFHMVGPWEHTVKQGFEQLM TWVDR	12	27	4	21.92	b10b11y11°y11	3199.53	84.418	28708	4	800.64	-8.78
P0A212 GYRI_SALTY DNA gyrase inhibitory protein homolog	6		VEDRDFAKPWER	100	12	4	37.3	b5b9b11y10	1547.77	80.486	5845	2	774.39	9.46
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	1		MYAVFQSGGK	0	10	7	52.61	b3b7y5y6y8*y8y10	1087.52	53.015	54077	2	544.26	-4.04
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	2		IGVPFVDGGVIK	48	12	5	32.52	y2y5y7y9y12	1200.69	77.596	50888	2	600.85	-3.86
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	3		LDIATGETIEFAEVLMIANGEEVK	24	24	6	23.65	b3°b3b11y3y5y9	2592.27	117.946	27950	3	864.76	-16.76
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	4		QQGHRQWFTDVK	85	12	4	22.3	b10y8y10*y10	1529.76	70.610	8116	2	765.38	-0.48
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	5	Oxidation+M(16)	LDIATGETIEFAEVLMIANGEEVK	24	24	4	22.02	b7°b7y10y11	2608.30	63.294	6251	4	652.83	-2.43
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	1		ELLTQMGQLYGHVADELATPSSAI LDIER	174	29	8	29.02	b17b19y3y5y10y11y29*y2 9	3170.62	105.821	31996	3	1057.54	4.47
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	2	Carbamidomethyl+C(14)	ILNTASVIPVDGLCVR	252	16	6	37.92	b5y5y8y9y11y16	1726.96	78.585	27615	2	863.98	5.23
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	3		MKDDAIILDPVNQDVITDGLNNG VK	103	26	7	21.93	b8y9°y9*y9y10*y10y26	2810.48	86.669	19460	3	937.50	5.91
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	4		LNMGPFLSAFTVGDQLLWGAAE PLRR	335	27	7	25.91	b4*b4b7°b7*b7b10b12	2988.55	119.164	17236	3	996.85	3.19
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	5	Carbamidomethyl+C(8)	ALDIIVTCQGGDYTNEIYPK	65	20	3	14.39	b8y6y11	2270.08	84.202	16032	3	757.36	-9.46
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	6		GMVGSVLMQR	10	10	6	28.7	b2b8b9b10y7*y7	1077.54	59.204	11627	2	539.28	-8.84
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	7		NVGFIGWR	2	8	4	18.13	b4*b4y6y8	948.50	70.786	10915	2	474.75	-8.94
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	8		DFDAIRPVFFSTSQFGQAAPTFGD TSTGTLQDAFDLDALK	25	40	4	12.06	b7b9y3y9	4298.10	106.877	5278	3	1433.37	9.66
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	9		ELTPAAVTGTLTTPVGR	315	17	4	26.18	b9y4y9y14	1683.93	69.488	24261	2	842.47	2.97
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	10		LNMGPFLSAFTVGDQLLWGAAE PLR	335	26	3	18.3	b3b6b13	2832.47	94.506	13528	3	944.83	9.31
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	11		SGELPVDNFGVPLAGSLIPWIDK	210	23	3	13.06	b3b13y3	2424.31	112.390	3598	2	1212.66	13.80
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	12		ESGWQGYWIDAASTLR	87	16	3	17.18	b3b12y6	1839.91	78.248	1975	3	613.97	22.16

[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	13		VVPNDRDITMR	304	11	3	24.33	b5b8y9	1315.69	31.117	27417	3	439.24	9.00
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	14		SGELPVDNFGVPLAGSLIPWIDKQ LDNGQSR	210	31	4	11.26	b13y9y11*y11	3322.72	111.693	8077	3	1108.24	3.01
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	15		EVSIPTVEELLAAHNPWAKVVPN DR	285	25	4	12.42	b10b17°b17y7	2784.48	100.287	5507	3	928.83	3.07
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	16		QLDNGQSREEWK	233	12	3	26.28	b9b10y4	1489.70	53.084	4159	3	497.24	-1.31
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	17		GMVGSVLMQRMVEER	10	15	3	18.16	b10y5y14	1721.84	72.226	3945	3	574.62	-4.32
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	18	Phosphoryl STY(9)	LNMGPPEFLSAFTVGDQLLWGAAE PLRR	335	27	3	21.92	b7b8y3	3068.49	78.855	12789	3	1023.50	-0.88
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	19	Phosphoryl STY(12)	ELTPAAVTGTLTTPVGR	315	17	6	26.18	b6°b6b10°b10b12y9	1763.88	78.590	5286	2	882.44	-2.63
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	20	Phosphoryl STY(15)	DITMRELTPAAVTGTLTTPVGR	310	22	5	25.64	b7b12y7y9y11	2380.16	112.566	3589	3	794.06	-8.41
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	21	Oxidation+M(3)	LNMGPPEFLSAFTVGDQLLWGAAE PLR	335	26	4	22.83	b9b10b22y9	2848.42	91.649	23286	3	950.14	-5.74
[P0A1F8]DHAS_SALTY Aartate-semialdehyde dehydrogenase	22		MKDDAIIMDPVNQDVITD	103	19	1	8.48	y11	2128.10	86.630	4597	3	710.04	5.62
[Q8ZL56]GPMI_SALTY 2	1		TFFANPVLटनाVDQAK	91	16	7	46.01	b2b3b5b9y11y12y14	1735.91	77.470	28650	2	868.46	2.11
[Q8ZL56]GPMI_SALTY 2	2		LSDIAPTMSLMGMEIPQEMTGKP LFIVE	485	29	13	49.47	b2b3°b3b4°b4b5°b5b8b9y1 y2°y2y13	3191.61	121.889	12407	3	1064.54	0.69
[Q8ZL56]GPMI_SALTY 2	3		AFVNADFDFGAR	272	12	6	44.96	b2y5y6y9y11°y11	1329.64	72.256	10451	2	665.32	14.60
[Q8ZL56]GPMI_SALTY 2	4		IVYQDLTR	75	8	3	33.12	b5b6y5	1007.54	56.577	4913	2	504.28	-8.06
[Q8ZL56]GPMI_SALTY 2	5		TPVMDALWAK	31	10	3	26.94	b8y6y8	1131.59	72.362	17366	2	566.30	1.83
[Q8ZL56]GPMI_SALTY 2	6		DPATGQAHTAHTNLPVPLIYVGE K	452	24	4	23.01	b9°b9b10b12	2529.30	85.190	15390	3	843.77	-4.54
[Q8ZL56]GPMI_SALTY 2	7		AVESVGGQLLITADHGNAEQMR	430	22	4	23.33	b3b5b6°b6	2296.15	83.253	10336	3	766.05	5.32
[Q8ZL56]GPMI_SALTY 2	8		TAVAYPPASLANTFGEWMAK	303	20	4	14.39	b7b12°b12y4	2125.06	96.513	8057	2	1063.03	7.58
[Q8ZL56]GPMI_SALTY 2	9		VATYDLQPEMSSAELTEK	364	18	4	15.6	b5y3y7°y7	2011.97	91.150	4481	2	1006.49	8.98
[Q8ZL56]GPMI_SALTY 2	10		QMGNSEVGHVNLGAGR	59	16	4	30.83	b3b4y3y5	1625.81	97.866	3199	2	813.41	17.72
[Q8ZL56]GPMI_SALTY 2	11		VVNLNFVMLTEYAADIK	286	17	3	24.99	y5y6y11	1939.99	70.206	3181	2	970.50	-15.79
[Q8ZL56]GPMI_SALTY 2	12		LDVEIK	83	6	1	13.63	b4	716.42	78.412	2892	1	716.42	2.22
[Q8ZL56]GPMI_SALTY 2	13		AYDLMTLAQGEFQADTAVAGLQ AAYAR	202	27	3	11.92	b6b10y13	2845.35	74.291	2295	4	712.09	-11.58
[Q8ZL56]GPMI_SALTY 2	14		DPATGQAHTAHTNLPVPLIYVGE KNVK	452	27	3	22.77	b4b10b11	2870.50	110.756	59826	3	957.50	-5.44
[Q8ZL56]GPMI_SALTY 2	15		RPHTLIDASGLEVGLPDRQMGNSE VGHVNLGAGR	41	34	5	36.49	y6y13*y13y14y15	3552.80	93.887	11038	3	1184.94	-1.37
[Q8ZL56]GPMI_SALTY 2	16		QMGNSEVGHVNLGAGRIVYQDL TR	59	24	3	12.72	b22y4y8	2614.35	88.782	4319	3	872.12	12.33
[Q8ZL56]GPMI_SALTY 2	17		FEDKFAALGK	168	10	3	33.93	b6b8b9	1125.60	50.617	4025	3	375.87	1.08
[Q8ZL56]GPMI_SALTY 2	18		DTPPSAEASLK	155	12	4	32.52	b4°b4b7b10	1271.65	40.763	2460	3	424.56	-6.62
[Q8ZL56]GPMI_SALTY 2	19	Oxidation+M(1)	MSVSKKPMVLVILDGYGYR	0	19	5	23.68	b4y3y7y11°y11	2172.18	106.019	8422	3	724.73	11.46
[P66738]RRF_SALTY Ribosome-recycling factor	1		QLASVTVEDSR	52	11	6	36.09	b2b11y5y6y7y11	1204.62	40.658	25026	2	602.81	4.36
[P66738]RRF_SALTY Ribosome-recycling factor	2		VDAALADKEAELMQF	170	15	6	37.14	b1b4b7b11y10y12	1650.81	79.758	7238	2	825.91	4.29
[P66738]RRF_SALTY Ribosome-recycling factor	3		ASPSLLDGIVVEYYGTPTPLR	31	21	4	37.45	y5y10y11y12	2248.21	94.132	37445	2	1124.61	10.32
[P66738]RRF_SALTY Ribosome-recycling factor	4		AIMASDLGLNPSSAGTDIR	80	19	4	34.55	y9y10°y10y11	1888.95	68.200	14805	2	944.98	4.91
[P66738]RRF_SALTY Ribosome-recycling factor	5		AIMASDLGLNPSSAGTDIRVPLPPL TEER	80	29	7	35.39	b4b7y4y6y12y21y22	3020.59	87.175	41512	3	1007.54	6.63
[P66738]RRF_SALTY Ribosome-recycling factor	6		VDAALADKEAELMQF	170	15	4	29.48	b6b9b13y13	1650.83	84.123	22689	3	550.95	14.72

P66738 RRF_SALTY Ribosome-recycling factor	7	Oxidation+M(3)	AIMASDLGLNPSSAGTDIR	80	19	8	31.67	b5b8y8°y8y9y13°y13*y13	1904.95	67.641	10477	3	635.65	5.70
P66738 RRF_SALTY Ribosome-recycling factor	8	Oxidation+M(13)	VDAALADKEAELMQF	170	15	3	18.16	b9y7y14	1666.81	77.853	3325	3	556.28	7.84
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	1		HGHAFNDLDLGK	37	12	9	54.21	b3b4y9°y9y10°y10y11*y11y12	1323.66	56.135	12806	2	662.33	13.46
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	2		MAESFTTTNR	0	10	4	39.38	b3b9y5y7	1157.51	43.180	1568	3	386.51	-11.81
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	3		EAQLLERHGHAFNDLDLGK	30	19	5	20.73	b3b10°b10y10y14	2163.08	74.689	31532	3	721.70	-6.77
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	4		HGHAFNDLDLGKR	37	13	3	29.91	y3y7y9	1479.75	37.143	3428	3	493.92	4.45
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	5		AESFTTTNRYFDNK	1	14	4	38.56	b3b4b5y6	1693.79	37.328	2180	3	565.27	6.99
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	6		MAESFTTTNRYFDNK	0	15	5	29.48	b10y4y8y9*y9	1824.81	92.847	1846	3	608.94	-4.28
Q9L9J1 THIG_SALTY Thiazole biosynthesis protein thiG	1	Carbamidomethyl+C(6)	LEEVGCAAVMPLGAPIGSNQGLE TK	139	25	4	18.86	b5b11b15y13	2541.24	123.823	3029	3	847.75	-10.76
Q9L9J1 THIG_SALTY Thiazole biosynthesis protein thiG	2	Carbamidomethyl+C(9); Carbamidomethyl+C(16)	QGFVVLPCYGADPVLCK	121	17	3	23.33	b10b11y11	1922.93	92.248	1737	3	641.65	-8.89
Q9L9J1 THIG_SALTY Thiazole biosynthesis protein thiG	3		TFDSLHTGTGK	7	12	3	22.3	b4b10y6	1310.62	48.864	28749	3	437.54	-16.67
Q9L9J1 THIG_SALTY Thiazole biosynthesis protein thiG	4	Carbamidomethyl+C(6); Oxidation+M(10)	LEEVGCAAVMPLGAPIGSNQGLE TK	139	25	5	27.44	b3b6b11b13y8	2557.29	80.314	1721	3	853.10	9.07
P0A2B3 RS7_SALTY 30S ribosomal protein S7	1		STAESIVYSALETLAQR	36	17	12	65.2	b2°b2b8y2y3y5y6°y6y7y9y11y17	1838.96	107.007	43054	2	919.98	4.45
P0A2B3 RS7_SALTY 30S ribosomal protein S7	2		FVNILMVDGK	25	10	6	41.71	b2y2y3y5y8y10	1135.61	76.356	25102	2	568.31	-7.85
P0A2B3 RS7_SALTY 30S ribosomal protein S7	3		VGGSTYQVPVEVRPVR	79	16	5	27.7	b1b3b12b14y3	1742.98	76.956	17049	2	871.99	12.12
P0A2B3 RS7_SALTY 30S ribosomal protein S7	4		LANELSDAADNK	119	12	9	34.29	b7b12°b12y3y4*y4y11°y11y12	1260.63	65.150	8380	2	630.82	14.91
P0A2B3 RS7_SALTY 30S ribosomal protein S7	5		SELEAFEVALENVRPTVEVK	56	20	4	23.81	b3°b3b4b11	2259.18	92.378	6355	2	1130.09	-2.92
P0A2B3 RS7_SALTY 30S ribosomal protein S7	6		FGSELLAK	17	8	4	49.36	b5y3y4y7	864.47	52.046	51336	2	432.74	-15.53
P0A2B3 RS7_SALTY 30S ribosomal protein S7	7		NALAMR	96	6	1	13.63	y5	675.36	36.616	5916	1	675.36	-2.62
P0A2B3 RS7_SALTY 30S ribosomal protein S7	8		VIGQR	5	5	1	13.23	y4	572.34	33.434	2648	1	572.34	-13.33
P0A2B3 RS7_SALTY 30S ribosomal protein S7	9		LANELSDAADNKGTAVK	119	17	18	196.05	b5b7b8b9b10y5y7y8*y8y9y10°y10y11y12y13y14y15y16	1716.86	39.722	103375	3	572.96	-12.16
P0A2B3 RS7_SALTY 30S ribosomal protein S7	10		RVGGSTYQVPVEVRPVR	78	17	7	64.27	b6°b6b7b8b9y8y9	1899.04	49.703	41456	3	633.68	-10.41
P0A2B3 RS7_SALTY 30S ribosomal protein S7	11		SGKSELEAFEVALENVRPTVEVK	53	23	3	13.06	b7b9y3	2531.32	88.390	16984	3	844.44	-7.04
P0A2B3 RS7_SALTY 30S ribosomal protein S7	12		NALAMRWIVEAAR	96	13	4	29.71	b7b12y7y10	1500.80	72.299	14095	2	750.90	-8.78
P0A2B3 RS7_SALTY 30S ribosomal protein S7	13		KSTAESIVYSALETLAQR	35	18	3	23	b6b7y6	1967.02	98.642	9984	3	656.34	-12.91
P0A2B3 RS7_SALTY 30S ribosomal protein S7	14		EDVHRMAEANK	138	11	5	38.35	b3b5y5*y5y6	1299.62	73.631	8235	3	433.88	3.29
P0A2B3 RS7_SALTY 30S ribosomal protein S7	15		GDKSMALR	111	8	3	48.68	y3y5y7	877.45	28.992	4683	2	439.23	-7.16
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	1		YAHQAGWELTENGR	214	14	7	33.05	b1b7b8y2y7y11y14	1631.77	47.368	8792	2	816.39	11.30

Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	2	Carbamidomethyl+C(11)	EHDPLIEWIPCPIPTDELYK	71	20	4	14.39	b11y7°y7y11	2465.20	97.952	3798	2	1233.10	-4.16
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	3		QEPPAWSASLHILPHR	198	16	3	17.18	b4b10y3	1838.93	36.888	94568	4	460.49	-18.25
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	4		DALLQK	161	6	2	26.87	b3y3	687.40	44.567	17800	1	687.40	-3.91
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	5	Carbamidomethyl+C(5)	DGILCALAWIGDEVVVEHFN	175	21	5	31.23	b13y4y7y11y12	2413.23	88.518	5515	3	805.08	13.05
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	6		QVINEEELELSSPLPFHR	137	18	3	15.6	b9b12y9	2137.14	73.342	3447	3	713.05	21.13
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	7		TIDAFSGITNPVEMLK	49	16	4	28.37	b3b6b7y10	1735.87	101.920	1726	2	868.44	-12.73
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	8		YAHQAGWELTENGRR	214	15	4	18.16	b6y4y8°y8	1787.86	66.282	4727	2	894.43	2.73
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	9	Carbamidomethyl+C(17)	LVHEPREHDPLIEWIPCPIPTDELYK	65	26	3	12.15	b8y5y7	3196.57	90.541	4314	3	1066.20	-12.53
Q9ZFU6 YPFL_SALTY Uncharacterized protein ypfL	10	Carbamidomethyl+C(3); Carbamidomethyl+C(8)	IPCKNPQCSHFILPATAAR	4	19	3	22.74	b8y13y14	2181.10	78.493	3239	3	727.70	-2.69
P40783 QOR_SALTY Quinone oxidoreductase	1		AIGINFIDTYIR	36	12	8	34.29	b2b3y2y5y6y10y12*y12	1395.76	88.476	34444	3	465.92	-4.20
P40783 QOR_SALTY Quinone oxidoreductase	2		GLMVSFGNASGPVTGVNLGILNQK	232	24	6	36.78	b10*b10b12b13b14y24	2373.26	79.208	17498	3	791.76	1.13
P40783 QOR_SALTY Quinone oxidoreductase	3		AAILPDAISFEQAAASFLK	105	19	4	22.74	b11b12y2y9	1963.03	103.639	4841	2	982.02	-10.07
P40783 QOR_SALTY Quinone oxidoreductase	4	Carbamidomethyl+C(9)	DTWEASLDCLQR	219	12	3	29.51	y5y6y8	1493.66	72.087	1857	3	498.56	-8.09
P40783 QOR_SALTY Quinone oxidoreductase	5		ALDAGAWQVINYR	180	13	3	20.67	b5b8y7	1476.73	54.055	7845	2	738.87	-20.09
P40783 QOR_SALTY Quinone oxidoreductase	6		VVYAQSTLGAYSSVHNVTADK	84	21	5	29.8	b7b12y7y8y15	2210.07	88.936	4464	4	553.27	-16.57
P40783 QOR_SALTY Quinone oxidoreductase	7		HGGPEVLQTVFTPAEPAEHEIQVENK	9	27	4	11.92	b4y12*y12y14	2985.47	67.287	2547	3	995.83	3.27
P40783 QOR_SALTY Quinone oxidoreductase	8		ALDAGAWQVINYREESIVER	180	20	3	14.39	b4b8y7	2319.21	85.453	2619	2	1160.11	14.63
P40783 QOR_SALTY Quinone oxidoreductase	9	Phosphoryl STY(12)	ALDAGAWQVINYREESIVER	180	20	3	14.39	b9b11y7	2399.11	99.541	122464	3	800.38	-6.92
P40783 QOR_SALTY Quinone oxidoreductase	10	Phosphoryl STY(13)	VVYAQSTLGAYSSVHNVTADK	84	21	4	13.89	b5y7°y7y9	2290.07	78.403	19602	3	764.03	1.92
P40783 QOR_SALTY Quinone oxidoreductase	11	Phosphoryl STY(6)	GLTVFYLLR	124	9	3	30.51	b4b6_H3PO4 b6y5	1161.58	31.600	2212	2	581.30	-12.30
P40783 QOR_SALTY Quinone oxidoreductase	12		GINFIDTYIR	38	10	1	7.6	b5	1211.65	88.480	16050	2	606.33	5.74
P41784 PRGI_SALTY Protein prgI	1		FDTGVDNLQTQVTEALDK	15	18	6	40.72	b11b15b16*b16b17y9	1993.96	74.679	26484	3	665.33	-3.80
P41784 PRGI_SALTY Protein prgI	2		DIDAAIQNFR	69	11	5	31.32	b6b7°b7b10*b10	1275.68	75.338	4368	2	638.34	7.66
P41784 PRGI_SALTY Protein prgI	3		MATPWSGYLDDVSAK	0	15	3	18.16	b10b12y8	1640.79	69.415	15090	2	820.90	18.67
P41784 PRGI_SALTY Protein prgI	4		ATPWSGYLDDVSAK	1	14	3	24.75	b10y10y11	1509.73	89.977	14425	2	755.37	1.94
P41784 PRGI_SALTY Protein prgI	5		LSEYNLYR	50	8	6	54.13	b4b6y4*y4y7*y7	1057.52	30.887	1670	3	353.18	-11.31
P41784 PRGI_SALTY Protein prgI	6		FDTGVDNLQTQVTEALDKLAACP SDPALLAAYQSK	15	35	4	10.93	b12b15y16°y16	3718.93	136.660	4147	3	1240.32	4.60
P41784 PRGI_SALTY Protein prgI	7		LAAKPSDPALLAAYQSKLSEYNLYR	33	25	7	28.11	b3y4y5y8°y8*y8y12	2782.45	136.217	2266	3	928.15	-10.70
P41784 PRGI_SALTY Protein prgI	8	Oxidation+M(1)	MATPWSGYLDDVSAK	0	15	3	18.16	b14y10y12	1656.74	80.035	9114	3	552.92	-11.86
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	1		THLVSPAMAAAAAVTGHFADIR	441	22	4	18.2	b3b13y7y17	2207.11	85.787	23353	3	736.38	-12.28
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	2		AGLVAPDETTFNYYVK	229	15	5	37.93	b3y10y11y12y15	1624.84	66.397	16860	2	812.92	8.94

P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	3	Carbamidomethyl+C(14)	TGSAGGTGHVVEFCGDAIR	190	19	5	31.62	y3y8y9y18y19	1890.87	51.654	14681	3	630.96	-2.78
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	4	Carbamidomethyl+C(4)	MTLCNMAIEMGAK	216	13	5	20.67	b8°b8y3y5°y5	1469.68	72.311	8988	2	735.34	8.97
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	5		AQAEAEGLDK	383	10	9	60.39	b4*b4b7°b7b9y2°y2y7y9	1031.51	32.541	7121	2	516.26	6.04
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	6		HLVHEVTSPQAFDGLR	29	16	6	24.3	b12°b12b14y4°y4y12	1805.95	84.243	15322	4	452.24	9.26
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	7		IQMQELIK	80	8	3	33.12	b4b5y6	1002.56	60.211	8621	2	501.78	-5.72
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	8		LFDAHVVFEAPNETPLLYIDR	8	21	4	37.45	b3b4b5b10	2459.22	96.834	4453	3	820.41	-15.69
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	9		IEDLR	351	5	1	13.23	b4	645.36	31.467	1595	2	323.18	6.15
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	10	Carbamidomethyl+C(26)	ALAYMGLQPGVPLTDVAIDKVFI GSCTNSR	321	30	6	37.02	b5b6y4y8y11y22	3193.65	96.133	7571	3	1065.22	4.59
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	11	Carbamidomethyl+C(4); Carbamidomethyl+C(7)	LPGCSMCLAMNNDRLNPGER	403	20	3	14.39	b3y4y9	2305.04	60.143	7048	3	769.02	3.07
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	12		GGRTHLVSPMAAAAAVTGHFA DIR	438	25	4	23.12	b11y3y6y7	2477.30	94.754	4153	3	826.44	5.72
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	13	Carbamidomethyl+C(11)	ALSMGRMTLCNMAIEMGAK	209	20	4	36.05	b6b7y6y7	2214.03	116.148	2695	3	738.68	6.18
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	1		NPALITMFD RPTFSAGAVYIDPDV NISGTSPSR	57	33	4	11.06	b3b16y16y33	3509.77	108.273	28045	4	878.20	8.07
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	2		FAGDLGQLVAAQN PALAPVAGQI PSDTK	182	28	4	11.71	b6y9y22y28	2749.45	85.969	16139	3	917.15	-1.69
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	3		LNEAWSFGLGFD AVYAR	160	17	6	39.19	b4*b4b5b6°b6b10	1915.93	98.425	4017	3	639.31	-2.93
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	4		TGIAFDDSPVPAQNR	356	15	5	29.48	b12y5y6°y6y10	1587.77	47.280	3064	2	794.39	-1.61
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	5		FWLSAGTTYAFNKDASVDVGVSY MHGQSVK	380	30	3	11.39	b14y8y10	3265.56	84.420	1982	3	1089.19	-0.22
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	6		FWLSAGTTYAFNK	380	13	3	29.91	y4y6y10	1505.76	67.954	11569	3	502.59	9.49
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	7		INEGPYQFESEGK	410	13	3	20.67	b7y5y10	1497.68	41.370	7150	2	749.34	-6.36
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	8		AYSGEAIA DDAGNVSR	40	17	3	16.34	b4b9y7	1652.75	30.837	5703	3	551.59	0.30
Q8ZNA5 FADL_SALTY Long-chain fatty acid tranort protein	9		SISIPDQDRFWLSAGTTYAFNK	371	22	6	34.39	b11b12y5y9°y9y11	2517.22	102.420	6960	3	839.75	-8.15
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	1		RELSVNEEVIK	139	11	7	24.33	b6b9°b9b11y1y2y10	1315.71	57.432	40222	2	658.36	-10.86
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	2		VLVVEDNALLR	3	11	6	56.02	b2b3y6y7y8y9	1240.72	68.284	17106	2	620.86	-6.10

P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	3		SSDVSLPVLVLTAR	68	14	5	27.61	b3°b3b6y4y8	1456.84	87.484	16724	2	728.92	1.26
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	4		NSGLASQVINIPPFQVDLSR	119	20	6	23.81	b2b5°b5b7b8*b8	2155.15	103.973	3005	3	719.05	-2.15
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	5		LTAFEYTIMETLIR	150	14	4	27.61	b9b11y6y11	1700.87	108.362	1935	3	567.63	-14.57
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	6		VQLQDSGHQVDAEDAR	18	17	5	27.43	b8*b8y4y5y8	1838.84	27.732	53701	3	613.62	-13.81
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	7		IQAQYPHDVITTVR	201	14	5	30.78	b6y9y10y12*y12	1640.85	52.085	23926	3	547.62	-15.62
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	8		DSLMLQLYPDAELR	172	14	6	27.61	b3°b3b11°b11y5y8	1663.81	67.669	3695	3	555.27	-17.61
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	9		ESHTIDVLMGR	186	11	3	24.33	b4b9y8	1257.64	43.696	3486	2	629.32	8.93
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	10		VEVLSSGADDYVTKPFHIEEVMAR	88	24	5	37.23	b12b13b14b22y7	2692.35	92.337	2439	3	898.12	7.80
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	11		EGWQDKVEVLSSGADDYVTKPFHIEEVMAR	82	30	6	28.41	b4b7y6y7y10y12	3435.64	84.609	30516	4	859.67	-3.91
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	12		HHLKVQLQDSGHQVDAEDAR	14	21	3	13.89	b6y5y8	2354.15	114.296	5086	3	785.39	-6.02
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	13		ELSVNEEVIKLTAFEYTIMETLIR	140	24	3	12.72	b9y4y12	2841.47	67.023	3932	3	947.83	-7.39
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	14	Phosphoryl STY(12)	VVSKDSLMLQLYPDAELR	168	18	3	24.52	y5y6y9	2157.07	55.613	1612	3	719.69	6.00
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	15	Oxidation+M(4)	DSLMLQLYPDAELR	172	14	11	62.22	b7b8°b8b10°b10*b10b11*b11y9*y9y10	1679.83	68.566	2055	3	560.61	-1.45
P58663 RCSB_SALTY Capsular synthesis regulator component B	1		LGVENDIALLNYSVTLSPTDKE	192	24	8	42.91	b4y2y3y7y8y9y11y24	2591.35	109.888	8018	2	1296.18	2.07
P58663 RCSB_SALTY Capsular synthesis regulator component B	2		LGVENDIALLNYSVTLSPTDK	192	23	5	20.15	b1b3b6b11y4	2462.28	85.526	3292	4	616.33	-8.92
P58663 RCSB_SALTY Capsular synthesis regulator component B	3		LDAHVLITDLSMPGDK	47	16	4	42.89	b3b4b11b12	1724.86	90.643	9324	3	575.62	-18.82
P58663 RCSB_SALTY Capsular synthesis regulator component B	4		ESEVLR	154	6	1	13.63	b4	732.38	106.491	3649	1	732.38	-12.25
P58663 RCSB_SALTY Capsular synthesis regulator component B	5		SLEQIEWVNVVGEFEDSTALINNL PK	21	26	3	22.82	b6b8b9	2944.52	69.077	2473	4	736.89	9.45
P58663 RCSB_SALTY Capsular synthesis regulator component B	6		ISAGGYGDK	140	9	4	30.51	b6°b6y6y8	867.42	91.342	1908	1	867.42	-2.04
P58663 RCSB_SALTY Capsular synthesis regulator component B	7		SAMMKLGVENDIALLNYSVTLSPTDK	187	28	10	40.8	b8°b8b9b10°b10*b10b21°b21*b21b26	3010.54	115.106	30175	3	1004.19	-1.87
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	1	Carbamidomethyl+C(9)	VTINGAHNCR	43	10	10	68.17	b2°b2y2y3y4y6y7*y7y8y10	1141.55	21.199	5590	2	571.28	0.53
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	2		VEIDPSLLEDDKEMLEDLVAAAFNDAAR	54	28	6	17.73	b2y5y8y10°y10*y10	3089.50	127.621	4728	3	1030.51	2.05
P0A8B8 YBAB_SALTY UPF0133 protein ybaB	3		MQEEIAQLEVTGESGAGLVK	23	20	4	19.79	b11b18y13y15	2089.06	83.846	3678	3	697.03	8.06

[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	4		MASVSSGMQLPPGFK	91	15	6	37.14	b5b12y11y12y14*y14	1536.78	91.309	1941	2	768.89	15.25
[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	5		IEETQK	83	6	2	29.88	b3b5	747.38	41.957	1545	1	747.38	-6.29
[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	6		MASVSSGMQLPPGFKMPF	91	18	6	34.7	b10*b10y3y5y6y8	1911.90	53.127	16357	3	637.97	-8.62
[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	7		GGLGNLMKQAQQMQEK	4	16	5	28.37	b4y5y10*y10y11	1760.90	73.662	6849	2	880.95	10.61
[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	8	Carbamidomethyl+C(29)	MQEEIAQLEVTGESGAGLVKVTIN GAHNCR	23	30	3	11.39	b8b23y8	3211.60	110.031	6775	4	803.66	6.23
[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	9		QAQQMQEKMQK	12	11	3	24.33	b4y3y6	1377.65	29.646	1703	2	689.33	-8.51
[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	10	Oxidation+M(2)	EMLEDLVAAAFNDAARR	66	17	3	23.33	b9b10y9	1907.93	73.646	143977	3	636.65	2.37
[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	11	Carbamidomethyl+C(8)	TINGAHNCR	44	9	1	8.26	b7	1042.48	21.185	3848	2	521.74	-6.79
[P0A8B8 YBAB_SALTY UPF0133 protein ybaB	12	Carbamidomethyl+C(7)	INGAHNCR	45	8	0	2.02		941.43	21.175	2895	2	471.22	-3.50
[P40720 FUMA_SALTY Fumarate hydratase class I	1		SNKPFFYQDPFPLK	1	14	8	27.09	b1b5°b5b6°b6b11°b11y14	1727.89	59.205	90740	3	576.63	5.58
[P40720 FUMA_SALTY Fumarate hydratase class I	2		MSNKPFFYQDPFPLK	0	15	4	26.24	y6y9y10y15	1858.90	75.902	15785	2	929.95	-10.51
[P40720 FUMA_SALTY Fumarate hydratase class I	3		VAPEALTLLAR	41	11	3	24.33	b4y7y9	1153.69	73.626	14235	2	577.35	-6.03
[P40720 FUMA_SALTY Fumarate hydratase class I	4		VWTGGGDEAALAR	120	13	3	20.67	b12y6y11	1302.64	48.719	9557	2	651.82	-1.87
[P40720 FUMA_SALTY Fumarate hydratase class I	5		EVNTGTNLPAQIDLYSVDGDEYK	156	23	4	17.51	b3b6y3y12	2541.23	88.667	6936	2	1271.12	13.83
[P40720 FUMA_SALTY Fumarate hydratase class I	6		TYLYQETK	192	8	3	40.9	y4y6y7	1045.52	39.845	6761	2	523.26	-4.32
[P40720 FUMA_SALTY Fumarate hydratase class I	7	Carbamidomethyl+C(5); Carbamidomethyl+C(13)	HGASCPVGMGVSCSADR	305	17	6	36.97	b2b7y8y9y10y17	1747.72	37.049	6195	3	583.25	-5.24
[P40720 FUMA_SALTY Fumarate hydratase class I	8		DHPIYYAGPAK	415	11	6	27.34	b2b3b4°b4y7y11	1231.60	26.298	3568	3	411.20	-12.39
[P40720 FUMA_SALTY Fumarate hydratase class I	9		GVYNTYIEDNLR	133	12	7	32.23	b4b9°b9b12y7°y7y9	1456.72	78.428	3166	3	486.24	8.38
[P40720 FUMA_SALTY Fumarate hydratase class I	10		DDTEYYLLTSEHVSVAEFEGQEIL K	16	25	3	21.96	b10b11y11	2915.40	86.274	3062	4	729.61	5.19
[P40720 FUMA_SALTY Fumarate hydratase class I	11		YYDALPTEGNEHGQAFR	251	17	4	27.43	b6y6y12y13	1967.87	92.691	25473	3	656.63	-7.01
[P40720 FUMA_SALTY Fumarate hydratase class I	12		IEVEDFPFILVDDK	515	15	6	43.16	b3b4b8y3°y3y4	1749.91	59.216	9054	2	875.46	8.79
[P40720 FUMA_SALTY Fumarate hydratase class I	13	Carbamidomethyl+C(13)	GNDFFQIQSSQCGAALS NVAAL R	530	24	3	12.72	b3b15y15	2582.27	97.644	8258	4	646.32	9.64
[P40720 FUMA_SALTY Fumarate hydratase class I	14	Carbamidomethyl+C(7)	TLGTAACPPYHIAFVIGGTSAEAN LK	217	26	7	21.97	b7b10°b10b13°b13y11y24	2659.31	114.589	7102	3	887.11	-15.15
[P40720 FUMA_SALTY Fumarate hydratase class I	15	Carbamidomethyl+C(3)	LECVEYPELGMEAIWK	499	16	3	25.56	y6y7y9	1966.95	112.466	3008	3	656.32	12.91
[P40720 FUMA_SALTY Fumarate hydratase class I	16		DIELEK	268	6	1	13.63	b5	746.40	35.780	2807	1	746.40	7.69
[P40720 FUMA_SALTY Fumarate hydratase class I	17		VDLNRPMSEILQQLSQYPVSTR	360	22	4	13.45	b3b6y9*y9	2574.35	88.523	2294	3	858.79	4.55
[P40720 FUMA_SALTY Fumarate hydratase class I	18		YSQNAALDMYK	145	11	3	36.09	y4y6y10	1303.62	60.169	2235	2	652.32	18.92
[P40720 FUMA_SALTY Fumarate hydratase class I	19		TPEGYASGSLGPTTAGR	426	17	5	22.96	b3°b3b11y7y15	1621.81	88.744	1529	2	811.41	14.53
[P40720 FUMA_SALTY Fumarate hydratase class I	20		VWTGGGDEAALARGVYNTYIED NLR	120	25	10	33.48	b7°b7b11b15°b15y7y8*y8y11°y11	2740.33	94.481	76526	3	914.12	0.09

P40720 FUMA_SALTY Fumarate hydratase class I	21		GGNMIRYFAGER	554	12	3	32.52	y3y6y11	1370.68	62.757	74668	3	457.56	11.40
P40720 FUMA_SALTY Fumarate hydratase class I	22		DHPIIYAGPAKTPEGYASGSLGPT TAGR	415	28	6	24.96	b9y7y11°y11y15y17	2834.40	92.802	20747	3	945.47	10.42
P40720 FUMA_SALTY Fumarate hydratase class I	23		YIPEALRQAGEGEAVR	344	16	7	37.92	b8*b8b9b12*b12b14y7	1758.90	67.136	18622	2	879.95	-8.81
P40720 FUMA_SALTY Fumarate hydratase class I	24	Carbamidomethyl+C(26)	EVNTGTNLP AQIDLYSVDGDEYK FLCIAK	156	29	5	14.54	b10°b10b16y10y12	3273.61	104.314	6646	3	1091.87	2.39
P40720 FUMA_SALTY Fumarate hydratase class I	25	Carbamidomethyl+C(11)	GNRSQQVTDACK	463	12	4	32.52	b3b7b10°b10	1363.64	99.076	2532	2	682.33	3.67
P40720 FUMA_SALTY Fumarate hydratase class I	26		KDDTEYYLLTSEHVSVAEFEGQEI LK	15	26	4	12.15	b9°b9y8y10	3043.47	65.311	2333	4	761.62	-3.05
P40720 FUMA_SALTY Fumarate hydratase class I	27	Carbamidomethyl+C(4)	RLECVEYPELGMEAIWK	498	17	4	36.97	b6b7b8y10	2123.02	55.598	2171	4	531.51	-2.64
P40720 FUMA_SALTY Fumarate hydratase class I	28		TPEGYASGSLGPTTAGRMDSYVD QLQSQGGSMIMLAK	426	37	9	22.99	b3b13y10°y10y12°y12*y12 y13*y13	3804.77	106.008	1859	4	951.95	-4.30
P40720 FUMA_SALTY Fumarate hydratase class I	29	Phosphoryl STY(6)	GVYNTYIEDNLR	133	12	3	26.28	b4b5y5	1536.65	43.868	2005	3	512.89	-9.69
P40720 FUMA_SALTY Fumarate hydratase class I	30	Oxidation+M(9)	YSQNAALDMYK	145	11	4	27.34	b8y7°y7y8	1319.61	64.418	3163	2	660.31	9.34
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	1		VLRDGNTLLVQVK	76	13	4	20.67	b6y3y11y13	1454.86	64.439	16351	2	727.93	-8.56
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	2		VAVGAALLSMPVR	36	13	5	32.35	b3y5°y5y6y11	1283.75	77.664	13418	2	642.38	-3.99
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	3		QMEGAWLGSDLVDQGKER	370	18	7	15.6	b12b18y6°y6*y6y11°y11	2018.94	68.579	11973	3	673.65	-10.64
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	4		DEVPWWNVVGDRK	200	13	4	25.44	b4b5°b5y7	1599.78	62.747	6431	2	800.39	-5.88
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	5		LSNMQPQIAMDR	535	12	6	29.51	b2°b2y5y7y8y12	1403.68	51.829	6242	2	702.35	4.17
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	6		IFYNDFQADDADLSDYTNK	488	19	4	14.96	b2b7y7y12	2255.01	72.877	5443	2	1128.01	14.29
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	7		LSGVQVSGNLAGHSAEIENLTK	267	22	7	30.32	b3°b3b5b10b11y2y5	2224.13	63.280	4497	3	742.05	-9.88
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	8		VPGSPDQVDVVYK	404	13	7	53.15	b2b8b9y2y8y9y10	1402.73	65.288	4352	3	468.25	9.49
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	9		DIHFEGLQR	27	9	5	30.51	b7y4y7y9*y9	1114.56	53.208	3873	2	557.78	-1.75
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	10		FNIDSTQVSLTPDKK	237	15	4	26.24	b3b5°b5b6	1692.90	64.425	3567	3	564.97	9.23
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	11		LGFFETVDTDTQR	391	13	4	20.67	b1b5y4y10	1528.72	74.170	2810	3	510.25	-2.16
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	12		SYGTDVTLGFPINEYNTLR	507	19	4	14.96	b9b11°b11y9	2160.09	85.819	5874	2	1080.55	15.37
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	13		IQQINIVGNHAFSTEELISHFQLR	176	24	3	12.72	b3b5y10	2794.45	95.173	4420	3	932.16	-3.06

Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	14		VTIPGSDNEYK	594	12	4	35.53	b6b7b8°b8	1385.67	50.564	3404	2	693.34	6.70
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	15		VGESLDR	120	7	5	37.49	b6°b6y4y5°y5	775.40	36.973	1607	2	388.20	5.82
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	16		TTLSDIEKGLDFYYSVGK	127	19	5	29.46	b5b8y6y8y13	2165.08	82.029	75576	2	1083.05	9.13
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	17		LNRLGFFETVDTDTQR	388	16	5	27.7	b13y4*y4y7y9	1911.95	90.684	17705	2	956.48	-4.47
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	18		GYFPTDGSRVNLTGK	579	15	8	69.33	b4b8b10b11b13y11°y11y12	1611.80	55.638	11201	2	806.40	-10.83
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	19		QMEGAWLGSDLVDQGKER	370	18	12	61.89	b3b5b7°b7y6y9y11y13°y13y14°y14*y14	2018.98	94.529	7183	3	673.67	12.03
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	20		IEPGELYNGTKVTK	289	14	4	27.88	b5°b5b7b11	1548.82	36.959	4288	3	516.94	-7.41
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	21		LSGVQVSGNLAGHSAEIENLTKIE PGELYNGTK	267	33	4	25.83	y4y6y7y9	3425.72	114.545	3785	3	1142.58	-9.76
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	22		LAGDLETLSYYLDR	218	15	3	18.16	b4y4y10	1784.91	80.919	2445	3	595.64	-3.08
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	23		LDRGYFPTDGSR	576	12	4	37.3	b9y4y6y9	1383.68	62.048	1749	2	692.34	7.32
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	24	Oxidation+M(2)	QMEGAWLGSDLVDQGKER	370	18	3	23	b11b12y12	2034.97	72.913	2068	3	679.00	9.36
Q8ZRP0 YAET_SALTY Outer membrane protein assembly factor yaeT	25		PQIAMDR	540	7	0	2.82		830.42	51.802	6563	1	830.42	7.13
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1		LVDIEQVSSTHAK	12	13	6	28.15	b2y1y5°y5y7y8	1426.73	46.056	43222	3	476.25	-14.29
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2		VTLEPLER	25	8	6	54.13	y1y4y5y6y7y8	956.53	52.762	41428	2	478.77	-11.36
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3	Carbamidomethyl+C(6)	LLVDACYSPVER	170	12	9	83.98	b2b7y4y5y7y8y9y10y12	1421.71	60.105	34177	2	711.36	3.01
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4		EGVQEDILEILLNLK	71	15	10	58.65	b2b7y1y2y3y4y5y6y8y15	1725.97	122.853	17543	2	863.49	5.38
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5		MQGSVTEFLKPR	0	12	3	32.52	y4y7y9	1392.71	59.743	47063	3	464.91	-16.30
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		IHSEEDERPIGR	158	12	4	36.2	b3b4y6y11	1437.72	66.996	26964	2	719.36	6.79
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		LVIEMETNGTIDPEEAIR	200	18	6	15.6	b7b9°b9*b9y13°y13	2030.03	84.369	25497	3	677.35	9.08

P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8	Carbamidomethyl+C(10)	RILLSSMPGCAVTEVEIDGVLHEY STK	44	27	11	62.38	b10°b10b11b12°b12y4y7°y7y9y13y26	3004.49	115.107	156052	4	751.88	-6.91
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9	Carbamidomethyl+C(26)	EEKPEFDPILLRPVDDLELTVRSAN CLK	243	28	3	11.71	b4b10y6	3296.71	85.831	21979	5	660.15	-1.63
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	10		VEQRTDLDK	191	9	4	30.51	b4°b4y4y5	1103.56	67.107	6943	2	552.28	-12.17
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	11		GLSLGMRLNWPPASIADE	310	19	4	14.96	b6°b6b8y5	2056.02	50.581	4488	3	686.01	2.02
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	12	Carbamidomethyl+C(6)	LLVDACYSPVERIAYNVEAAR	170	21	4	22.34	b10b11y7°y7	2409.20	80.296	2342	2	1205.11	-7.80
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	13		DIEQVSSTHAK	14	11	0	3.23		1214.60	46.087	6913	2	607.80	-0.40
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	1		LGYSNGTTDPKEIAAYEELK	179	21	4	13.89	b8y5y10y21	2328.09	82.411	28260	3	776.70	-14.79
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	2		EVAETIGYPTPNLAAR	285	16	5	34.59	b2°b2y8y9y10	1701.89	61.827	16590	2	851.45	8.25
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	3		LTFNHNLDPMLNKPFDPNNDYS VPYIWGATAIGVNSDAIDPK	103	43	7	21.45	b2b9y1y2y7y8y10	4803.34	95.633	11005	4	1201.59	8.54
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	4		LMPNVAAFNSDNPANPYMEGEV NLGMVWNGSAFVAR	201	36	10	37.54	b2b3b9°b9b10°b10b14b15y14°y14	3882.80	99.686	8864	4	971.46	-1.45
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	5		TYKDGAYDLVVPSTYYVDK	70	19	5	22.74	b6b7°b7y8°y8	2197.07	77.632	8536	3	733.03	1.89
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	6		TITSWADLWKPEYK	146	14	3	27.09	y4y8y9	1737.85	83.314	43732	3	579.96	-18.26
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	7		EGGIFWMDSLAIPANAK	249	17	5	16.34	b5°b5b15°b15y13	1819.92	94.467	35659	2	910.46	8.45
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	8		NSLLLTDDAR	160	10	3	26.94	b6y5y7	1117.59	69.717	7238	2	559.30	2.29
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	9		EVFQMALR	170	8	4	40.9	b3b6°b6b7	993.52	77.064	2360	2	497.27	4.12
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	10		DGAYDLVVPSTYYVDK	73	16	4	24.89	y4°y4y7y10	1804.83	67.610	1971	3	602.28	-18.26
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	11		EGALK	268	5	1	13.23	b4	517.30	46.034	1546	1	517.30	6.14
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	12		SLYPDAQTISKGEWQNDVGDASA IYEEYYQK	312	31	7	24.45	b3b4b12°b12y10y13°y13	3568.69	81.970	6014	3	1190.23	13.34
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	1		IQVTGSEGELGIYPGHAPLLTAIKP GMIR	23	29	11	42.92	b2°b2b3b13y2y4y5y12y13y27y29	3018.61	82.710	73384	4	755.41	-9.87
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	2		AMTYHLDVVSAEQQMFGSLVEK	1	22	12	66.22	b4b8b9b11°b11b12y3y8y9°y9y12y22	2483.19	91.078	29576	3	828.40	-1.87

P0A1B7 ATPE_SALTY ATP synthase epsilon chain	3		SSHGDVDYAQASAE LAK	107	17	4	29.95	b7b8y6y8	1748.79	45.982	23560	3	583.60	-11.87
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	4		AEEHIKSSHGDVDYAQASAE LAK	101	23	3	13.06	b13y6y11	2456.18	74.533	6916	4	614.80	4.08
Q8ZNW0 KPYK2_SALTY Pyruvate kinase II	1		ISSGLPIFAMSR	397	12	3	29.51	y4y5y7	1278.68	81.383	9763	2	639.84	-7.83
Q8ZNW0 KPYK2_SALTY Pyruvate kinase II	2		GDLGVEIGDPELVGIQK	250	17	3	23.74	b8b10b12	1738.91	100.403	7330	2	869.96	-5.55
Q8ZNW0 KPYK2_SALTY Pyruvate kinase II	3		GVTPVHFDSAADGVVAAHEAVN LLR	421	25	5	18.64	b2b3b12b20y2	2545.30	80.200	4870	3	849.11	-5.76
Q8ZNW0 KPYK2_SALTY Pyruvate kinase II	4		LDVQFDNVEEAIAMSAMYAANH LK	353	24	7	26.19	b7*b7b11y1y11y12*y12	2680.28	111.289	4678	3	894.10	2.28
Q8ZNW0 KPYK2_SALTY Pyruvate kinase II	5		AVITATQMMESMITNPMPT R	278	20	4	14.39	b11*b11y4y8	2223.09	70.791	1576	2	1112.05	11.42
Q8ZNW0 KPYK2_SALTY Pyruvate kinase II	6		DKGYLVSGDLVIVTQGDVMSTV GSTNTTR	446	29	3	11.54	b4y7y11	3013.49	76.415	10822	4	754.13	-8.34
Q8ZNW0 KPYK2_SALTY Pyruvate kinase II	7	Oxidation+M(8)	AVITATQMMESMITNPMPT R	278	20	6	30.68	b8*b8b12b13y4y11	2239.06	85.252	4278	2	1120.03	1.20
Q8ZPU5 NADE_SALTY NH(3)-dependent NAD(+) synthetase	1		TIEGWYVK	249	8	3	33.12	b6b7y5	995.53	38.271	7492	2	498.27	9.99
Q8ZPU5 NADE_SALTY NH(3)-dependent NAD(+) synthetase	2		AQYSIAGMTHGVVVGTDHAAEAI TGFFTK	144	29	8	35.8	b6*b6b7*b7b8*b8b11y11	2979.50	99.571	6340	3	993.84	11.88
Q8ZPU5 NADE_SALTY NH(3)-dependent NAD(+) synthetase	3		SVDFLK	25	6	1	13.63	b5	708.39	60.500	10815	1	708.39	-9.91
Q8ZPU5 NADE_SALTY NH(3)-dependent NAD(+) synthetase	4		LSQMAIAELR	58	10	4	40.17	b6y5y7y8	1131.60	30.612	2290	3	377.87	-20.17
Q8ZPU5 NADE_SALTY NH(3)-dependent NAD(+) synthetase	5		TIEGWYVKTEHK	249	12	3	22.3	b8y3y11	1490.78	73.422	6418	2	745.89	7.62
Q8ZPU5 NADE_SALTY NH(3)-dependent NAD(+) synthetase	6		GTDHAAEAITGFFTK	158	15	5	17.5	b6*b6b9b13*b13	1565.75	99.590	3044	3	522.59	-2.96
P65933 PYRH_SALTY Uridylate kinase	1		VDGVFTADPAK	166	11	3	27.34	b6y6y7	1119.56	46.761	13968	2	560.28	-11.23
P65933 PYRH_SALTY Uridylate kinase	2		VDGVFTADPAKDPSATMYDQLT YSEVLDKELK	166	32	5	22.8	b1b10*b10b12b13	3546.70	82.938	12452	4	887.43	-5.58
P65933 PYRH_SALTY Uridylate kinase	3		VVGDHMGMLATVMNGLAMR	73	19	6	33.39	b1b3b6b14b15y7	2002.97	93.195	3781	3	668.33	0.37
P65933 PYRH_SALTY Uridylate kinase	4		VDGVFTADPAKDPSATMYDQLT YSEVLDK	166	29	4	22.73	b10*b10b13b14	3176.52	91.754	3124	3	1059.51	5.69
P65933 PYRH_SALTY Uridylate kinase	5	Carbamidomethyl+C(11)	LMSAIPLNGVCDNYSWAE AISLLR	103	24	6	27.62	b3b13y12y13*y13y23	2693.31	95.660	11017	3	898.44	-10.70
P65933 PYRH_SALTY Uridylate kinase	6		LPIR	212	4	1	12.83	b3	498.34	91.216	3133	1	498.34	-4.53
P65933 PYRH_SALTY Uridylate kinase	7		GIEIEADVVLK	152	11	3	27.34	b4b5y5	1185.65	70.703	2935	2	593.33	-16.16
P65933 PYRH_SALTY Uridylate kinase	8		LSGEALQGTGFGIDASILDRMAQ EIK	15	27	3	11.92	b8b11y4	2849.40	93.511	3439	3	950.47	-12.08
P65933 PYRH_SALTY Uridylate kinase	9	Carbamidomethyl+C(17)	AYVNARLMSAIPLNGVCDNYSWA E AISLLR	97	30	4	14.19	b9b14y9y13	3367.70	86.770	2716	3	1123.24	2.03
P65933 PYRH_SALTY Uridylate kinase	10	Oxidation+M(18)	VVGDHMGMLATVMNGLAMR	73	19	6	29.46	b6*b6b9b12y6y9	2018.95	72.907	12219	2	1009.98	-5.80
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	1		TADKDSATSQFFINVADNAFLDH GQR	116	26	12	56.27	b2b7b10*b10y3y4*y4y5y7y11y12*y12	2868.33	86.754	82088	4	717.84	-9.19
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	2		NFVDYVNSGFYNNTTFHR	54	18	7	44.37	b2y6y8y9y12y14y18	2194.98	75.430	42955	3	732.33	-5.67
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	3		VIPGFMIQGGGFNEQM QK	72	19	5	21.91	b2y8y11y17y19	2109.05	77.392	41372	2	1055.03	11.23
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	4		ISQVPTHDVGPYQNVPTKPVVILS AK	161	26	6	15.82	b1b7b12y8y11y26	2787.51	62.789	20072	4	697.63	-12.61

P20753 PIIA_SALTY Peptidyl-prolyl cis-trans isomerase A	5		GMDVADKISQVPTHDVGPYQNV PTKPVVILSAK	154	33	10	51.03	b3b5b9b13b16y3y6y8y11y31	3503.84	69.114	79456	4	876.71	-5.50
P20753 PIIA_SALTY Peptidyl-prolyl cis-trans isomerase A	6		NTRGTIAMAR	106	10	5	40.17	b3b6*b6b7y7	1090.58	77.907	15465	2	545.80	3.92
P00929 TRPA_SALTY Tryptophan synthase alpha chain	1	Carbamidomethyl+C(9)	HNIAPIFICPPNADDDLRL	145	19	4	14.96	b13y10y12y19	2191.12	97.131	15909	2	1096.06	11.03
P00929 TRPA_SALTY Tryptophan synthase alpha chain	2		EGAFVPFVTLGDPGIEQSLK	15	20	8	30.68	b4b5*b5b7*b7y8y10y20	2104.12	94.939	12044	2	1052.56	9.28
P00929 TRPA_SALTY Tryptophan synthase alpha chain	3		HPTIPIGLLMYANLVFNNGIDAFY AR	91	26	6	36.54	y1y5y9y10y11y26	2920.50	105.977	11222	4	730.88	-4.68
P00929 TRPA_SALTY Tryptophan synthase alpha chain	4	Carbamidomethyl+C(11)	AFAAGVTPAQCFEMLALIR	70	19	6	36.32	b2b4y12y13y14y19	2066.06	102.172	8764	2	1033.54	3.19
P00929 TRPA_SALTY Tryptophan synthase alpha chain	5		QVASYGRGYTYLLSR	164	15	4	37.93	b6b7b8y7	1733.89	44.281	1868	3	578.64	-2.96
P00929 TRPA_SALTY Tryptophan synthase alpha chain	6		GYTYLLSRSGVTGAENR	171	17	3	24.99	y5y6y11	1843.94	74.045	1560	2	922.48	7.48
P00929 TRPA_SALTY Tryptophan synthase alpha chain	7	Phosphoryl STY(10)	REGAFVPFVTLGDPGIEQSLK	14	21	6	40.93	b6*b6b10y10_H3PO4 y9y10y11	2340.15	55.645	9745	3	780.72	0.21
P00929 TRPA_SALTY Tryptophan synthase alpha chain	8	Phosphoryl STY(4)	LKEYHAAPALQGFGISSPEQVSAA VR	199	26	3	12.15	b3y16y22	2806.39	67.960	7006	4	702.35	3.74
P00929 TRPA_SALTY Tryptophan synthase alpha chain	9	Phosphoryl STY(9)	EGAFVPFVTLGDPGIEQSLK	15	20	5	45.26	b4b7b10b11b12	2184.07	93.234	4672	3	728.70	8.27
O68926 BFR_SALTY Bacterioferritin	1		ILFLEGIPNLQDLGK	61	15	7	29.48	b2b5y3y8y11*y11y15	1669.96	101.421	9457	2	835.48	1.54
O68926 BFR_SALTY Bacterioferritin	2		LGIGEDVEEMLR	76	12	5	32.52	y5*y5y7y9y12	1360.68	83.311	7751	2	680.84	2.87
O68926 BFR_SALTY Bacterioferritin	3		LLGNELVAINQYFLHAR	13	17	3	16.34	b3y8y10	1971.07	96.659	12884	3	657.69	-7.68
O68926 BFR_SALTY Bacterioferritin	4		EAIAYADSVHDYVSR	102	15	5	37.14	b3b6b10y4y6	1695.80	84.322	2816	3	565.94	-0.29
O68926 BFR_SALTY Bacterioferritin	5		DMMIEILADEEGHIDWLETDLI AK	117	26	4	22.82	b6*b6b7b9	3042.41	115.109	2658	5	609.29	-19.66
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	1		VTAEDVLKPGTADILVPR	842	18	6	29.18	b5*b5b6y3y5y18	1894.04	72.985	14495	3	632.02	-12.18
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	2		FTDMIDGQTITR	1036	12	6	34.29	b5b10b11y7y12*y12	1397.67	58.390	13053	2	699.34	0.17
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	3		IALASPD MIR	21	10	5	51.93	y3y5y6y7y10	1086.59	61.751	10895	2	543.80	-9.55
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	4		EGLNVLYQYFISTHGAR	764	16	4	17.18	b3b8y10y16	1804.94	91.844	8256	2	902.98	5.21
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	5		SWSFGEVK	31	8	4	40.9	b2y3y4y5	939.45	33.478	4707	2	470.23	-7.67
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	6	Carbamidomethyl+C(10) ;Carbamidomethyl+C(12))	IFGPVKDYECLCGK	60	14	4	27.61	b9b13y3y10	1685.79	94.565	3731	2	843.40	-5.36
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	7		ASLATESFISAASFQETTR	1311	19	5	23.68	b9*b9b12b15y13	2017.01	90.497	3714	2	1009.01	13.31
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	8		HEIISEAEAEVAIEQEQFSGLVTA GER	650	28	6	31.19	b7b11b12y5y8y13	3070.51	115.131	2900	3	1024.17	3.90
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	9		AAGEQPATPQVTAEDASASLAELL NAGLGGSDNE	1373	34	4	22.92	b10b12b13y34	3254.58	117.800	2290	3	1085.53	13.95

P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	10		SGASVGIDDMVPEK	634	15	3	18.16	b3b12y9	1517.79	47.394	73813	2	759.40	22.36
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	11		GLMAKPDGSIETPITANFR	744	20	5	34.6	y8y9°y9y10°y10	2131.12	96.581	32269	3	711.05	-0.57
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	12	Carbamidomethyl+C(9)	NTLLHEQWCDLLEANSVDAVK	860	21	8	40.64	b6°b6*b6b7b9y4y9y10	2455.20	67.661	14574	4	614.56	2.98
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	13		LGIQAFEPVLIEGK	431	14	5	30.78	b4y4y9y10°y10	1513.86	86.673	11748	2	757.43	-0.97
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	14	Carbamidomethyl+C(5)	DGLFCAR	53	7	3	37.49	b4y5y6	838.38	110.921	9368	1	838.38	-11.28
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	15		ALMMSTNNILSPANGEPHIIVPSQD VVGLGYYMTR	481	34	6	17.41	b6b18y3y6°y6y8	3707.92	101.368	6715	5	742.39	8.30
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	16		TFHIGGAASR	933	10	3	26.94	b6b9y9	1016.52	34.849	5699	2	508.76	-8.89
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	17		QTDELTLGLSSLVVLDSAER	1048	19	7	29.46	b9*b9b12b14y13°y13y18	2033.06	87.564	4166	2	1017.03	10.81
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	18	Carbamidomethyl+C(4)	GVICEK	81	6	3	40.1	b3b4b5	705.36	41.589	4147	1	705.36	-3.72
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	19		LVITPVDGSDPYEEMIPK	1174	18	3	23	b10b11y6	2003.00	74.107	3615	3	668.34	-2.38
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	20		IPQESGGTK	1123	9	6	67.77	b4°b4b8y3y5y7	916.49	39.737	3561	2	458.75	13.72
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	21		LIPAGTGYAYHQDR	1355	14	4	38.77	y3y7y8y10	1561.81	48.164	3213	3	521.27	20.79
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	22		IVDAQGNDVLIPTDMPAQYFLP GK	1079	25	4	16.33	b4b7y10y14	2659.36	89.764	3042	2	1330.18	4.77
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	23		GVHAVTR	1224	7	3	40.5	b3b4b5	739.43	43.130	3038	2	370.22	8.17
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	24		VLTEAAVAGK	1330	10	3	28.7	b6y7y8	958.55	36.465	2957	2	479.78	-6.11
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	25		VPYGAVMAK	996	9	3	38.3	y4y5y7	935.51	36.888	2716	2	468.26	7.05
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	26		DGQEEQQVSFNSIYMMADSGAR	709	22	4	24.25	b8y7y8y12	2463.11	64.600	2690	3	821.71	22.30
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	27		VLYFESYVVIEGGMTNLER	137	19	7	25.9	b8°b8b9°b9b11y4*y4	2219.08	60.108	2435	2	1110.04	-11.22
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	28		MLQEAVDALLDNGR	297	14	5	33.05	b4b5y5y8*y8	1544.75	136.603	2246	1	1544.75	-14.46

P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	29		AIVQLEDGVQISSGDTLAR	1104	19	4	24.13	y3y9°y9y10	1972.00	67.203	1995	2	986.50	-19.31
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	30	Carbamidomethyl+C(5)	MLNTCYRILGLKPTVIFADQMTYT GFAYAAR	603	31	7	29.6	b9b10°b10y4y11y23*y23	3585.81	109.916	25066	4	897.21	0.34
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	31		SWSFGEVKKPETINYR	31	16	3	17.18	b8b12y3	1940.97	85.969	14277	3	647.66	-7.55
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	32		HEIISEAAEVAEIQEQFQSGLVTA GERYNK	650	31	3	22.05	b11b12y7	3475.66	84.367	11647	4	869.67	-11.38
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	33		AQTKTEEFDAIK	9	12	4	22.3	b6*b6y5y10	1380.68	48.854	9066	3	460.90	-12.64
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	34		RVDYSGR	345	7	3	40.5	b3b5y6	852.44	77.672	7891	1	852.44	14.39
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	35		GEAIGVIAAQSIGEPGTQLTMRTF HIGGAASR	911	32	4	15.88	b4y5y12y23	3196.68	114.159	5425	4	799.92	7.33
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	36	Carbamidomethyl+C(4); Carbamidomethyl+C(7)	GVICEKCGVEVTQTK	81	15	4	26.24	b3b4b8°b8	1707.83	86.697	4166	3	569.95	-7.51
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	37		ENVIVGRLIPAGTGYAYHQDR	1348	21	3	23.54	y5y6y13	2329.22	133.439	2775	3	777.08	6.60
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	38		VERGDVISDGPEAPHDILR	1203	19	4	14.96	b5°b5b8y7	2075.05	54.018	2536	4	519.52	-0.82
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	39		DIERVLYFESYVVIEGGMTNLER	133	23	3	13.06	b10y7y10	2732.35	99.473	2206	4	683.84	-5.27
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	40	Phosphoryl STY(10)	MGHIELASPTAHIWFLK	101	17	4	23.74	b4b8°b8b10	2030.97	71.440	9542	3	677.66	-7.51
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	41	Phosphoryl STY(10)	QTDELTLGLSSLVVLDSAER	1048	19	7	40.93	b3°b3b17y6y8y11y15	2112.98	67.177	3147	4	529.00	-6.01
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	42	Phosphoryl STY(4)	TANSGYLTRR	789	10	3	26.94	b3b9_H3PO4 b9y8_HPO3 y8	1218.57	58.409	1834	2	609.79	12.92
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	43	Oxidation+M(7)	VPYGAVMAK	996	9	3	30.51	b5y3y8	951.51	44.215	41264	2	476.26	14.37
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	44	Oxidation+M()	ALMMSTNNILSPANGEPHIIVPSQD VVLGLYYMTR	481	34	3	10.99	b10y5y13	3723.86	107.968	7323	3	1241.96	-4.26
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	45	Oxidation+M(4)	GEGMVLTPKEAER	521	14	6	31.57	b3°b3b6°b6b11y5	1489.74	97.597	3802	2	745.37	3.03
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	1	Carbamidomethyl+C(5)	IADVCVTTTEEQR	271	13	4	20.67	b3b12y10y13	1521.73	67.227	34169	2	761.37	4.81
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	2		QWSNAVEFLPEMPWR	40	16	3	17.18	b8b10y11	1990.94	71.254	9996	2	995.98	-2.45
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	3	Carbamidomethyl+C(7)	TILDVGCSGGYHLWR	124	15	3	18.16	b9b11y9	1733.85	89.138	3209	2	867.43	2.53
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	4		LDLLHSVTAESETPLSEGQLK	56	21	5	13.89	b11y2y10y13°y13	2267.15	99.452	3122	2	1134.08	-10.01

Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	5		DQLVNEGELVLETLVIDGDENTV LVPGDR	213	29	4	21.95	b6y11*y11y12	3151.60	95.561	3059	3	1051.20	-0.54
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	6		NLMPWRK	84	7	6	56.74	b1b4b6y3y4y7	944.51	34.908	2822	2	472.76	-1.55
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	7		NHLSHWLETLPAQIASWQR	13	19	4	36.32	b6y3y4y5	2287.13	72.290	25678	3	763.05	-17.72
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	8		TEWMVTESLADFLDPNDR	285	18	6	47.38	y4y5°y5y6y8y12	2139.01	78.485	15969	3	713.67	18.15
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	9		GPFSLYGVDIDTEWR	91	15	6	29.48	b4y3°y3y4y6°y6	1754.81	74.621	10944	2	877.91	-17.25
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	10		AFDTVFSMGVLYHR	188	14	4	31.57	b6b8b10y3	1642.84	62.086	9342	3	548.28	19.69
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	11	Carbamidomethyl+C(20)	MIGAGAHLAVGIDPTQLFLCQFEA VR	139	26	4	12.15	b8b11y9°y9	2814.43	91.776	4039	3	938.81	-5.38
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	12		SKTVEGYAPQR	303	12	4	34.29	b5b9b10y3	1332.69	56.259	27761	3	444.90	-1.74
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	13		GPFSLYGVDIDTEWRSDWK	91	19	9	64.73	b4b8b9y4°y4y7y8y9y12	2271.07	81.947	3343	2	1136.04	-1.08
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	14		KGPFSLYGVDIDTEWR	90	16	3	25.56	y8y10y11	1882.92	80.424	3004	2	941.97	-4.86
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	15	Oxidation+M(1)	MIEFGNFYQLIAK	0	13	3	25.44	b4b5y5	1589.80	51.643	25067	2	795.40	-0.61
Q8ZNV1 CMOB_SALTY tRNA (mo5U34)-methyltransferase	16	Oxidation+M(4)	TEWMVTESLADFLDPNDR	285	18	4	15.6	b3b6y10*y10	2154.98	102.992	6508	4	539.50	9.29