

MA6926 LC-MS run 1: 6926_220709_1a2_01

Protein name	Peptide Rank	Modification	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	23	185.41	b2b3b4b5*b5b6*b6y2y3°y3y4y5y6y7°y7y8y9y10*y10y11*y11y12y13	1244.69	59.326	667470	2	622.85	-4.51
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVGFGTFK	22	29	53	419.92	b2b3b4°b4b7b8°b8b9°b9b10b14b18b20b22b23°b23b24b25b26b27b28°b28b29y1y2y3y4°y4y5°y5y6°y6y7y8y10y11y12*y12y13°y13y14*y14y15°y15*y15y17y18y21y22y23y25y26y29	2966.56	114.060	574938	3	989.53	-3.87
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	3		AALESTLAAITESLK	22	15	11	104.06	b3b4b6b8b9b14y5y7y8y12y15	1517.84	96.507	57978	2	759.42	-2.25
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	4		NPQTGK	61	6	3	27.43	b4b5°b5	644.33	36.859	32279	1	644.33	-4.83
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	5		EGDAVQLVGFGTFK	37	14	6	31.73	b8°b8y6y7y9*y9	1467.75	77.982	21975	2	734.38	-0.17
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	6		TQLIDVIADK	3	10	5	40.43	b4b6y3°y3y7	1115.64	45.196	5235	2	558.32	4.60
[P0A1H5]EFTU_SALTY Elongation factor Tu	1		AIDKPFLLPIDVFSISGR	205	19	34	281.3	b2b4°b4b5b6b7b8b9b10b11b12b14b15y1y2y3y4y5°y5y6°y6y7°y7y8°y8y9°y9y10°y10y11°y11y12y15y19	2117.15	103.646	869155	3	706.39	-8.76
[P0A1H5]EFTU_SALTY Elongation factor Tu	2		ELLSQYDFPGDDTPIVR	155	17	27	182.17	b2°b2b3°b3b4°b4b5°b5b6b13°b13y1y2y3y4y5y6y8y9y10°y10y11y12°y12y13y17	1964.97	76.539	452205	2	982.99	5.59
[P0A1H5]EFTU_SALTY Elongation factor Tu	3		AGENVGVLLR	270	10	18	132.39	b4°b4b5°b5b6°b6y1y2y3y4y5y6y7*y7y8*y8y9y10	1027.58	55.940	427810	2	514.29	-14.02
[P0A1H5]EFTU_SALTY Elongation factor Tu	4		IIELAGFLDSYIPEPER	188	17	33	307.87	b2b3b4b5b6b7b8b9b11°b11b12°b12b14y1y2y3°y3y4°y4y5°y5y6y7y8°y8y9y10y11y12y13y14y15y17	1962.03	101.463	424624	2	981.52	5.35
[P0A1H5]EFTU_SALTY Elongation factor Tu	5		GITINTSHVEYDTPTR	59	16	30	213.9	b2b3°b3b9b10b12b13b16y3°y3y4°y4y5°y5y6y7y8y9y10°y10y11y12°y12*y12y13*y13y14°y14*y14y16	1803.86	49.178	421030	3	601.96	-14.01
[P0A1H5]EFTU_SALTY Elongation factor Tu	6		TTLTAAITTVLAK	25	13	20	150.57	b2°b2b3°b3b4°b4b6°b6b13y2y3y4y5y6y7y8y9y10y11y13	1303.78	84.118	395171	2	652.39	-4.49
[P0A1H5]EFTU_SALTY Elongation factor Tu	7		QVGVPYIIVFLNK	124	13	15	120.51	b3°b3b4b6b13y1y4*y4y5y6y7y8y9y11y13	1489.88	98.622	391011	2	745.44	0.25
[P0A1H5]EFTU_SALTY Elongation factor Tu	8		TTDVTGTIELPEGVEMVMPGDNIK	334	24	45	291.79	b1b2°b2b3°b3b4b5°b5b7°b7b8°b8b9°b9b10°b10b12b14b17°b17b18y1y2y3y4y5*y5y6°y6*y6y7°y7*y7y8y9y10°y10*y10y11y12y14y15y16y17y24	2546.26	86.590	278345	2	1273.63	7.96

P0A1H5 EFTU_SALTY Elongation factor Tu	9		ALEGDAEWEAK	177	11	10	83.43	b2y2y3y4y5y6y8y9°y9y11	1218.55	45.795	162124	2	609.78	-7.21
P0A1H5 EFTU_SALTY Elongation factor Tu	10		VGEEVEIVGIK	238	11	14	117.02	b3b4°b4y1y2y3y4y5y7y8y9°y9y10y11	1171.65	59.910	147395	2	586.33	-6.98
P0A1H5 EFTU_SALTY Elongation factor Tu	11	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	16	89.59	b2°b2b6y1y2y3y4°y4y5y6°y6y7°y7y8°y8y10	1187.51	52.377	132055	2	594.26	-3.60
P0A1H5 EFTU_SALTY Elongation factor Tu	12	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEV	137	18	21	168.57	b2b3b5b8b9b11b12y1y2y3y4y5°y5y6y7y8°y8y9y13y14y18	2224.00	105.670	127888	2	1112.50	9.22
P0A1H5 EFTU_SALTY Elongation factor Tu	13		NMITGAAQMDGAILVVAATDGPMPQTR	90	27	4	23.08	y6y7y10*y10	2729.34	126.218	3331	3	910.45	-2.06
P0A1H5 EFTU_SALTY Elongation factor Tu	14		MVVTLIHPIAMDDGLR	358	16	26	246.4	b3b4°b4b5°b5b6b7°b7b11b13y3y4°y4y5°y5y6y7y8y9°y9y10°y10y11y12y13y15	1780.91	78.437	789172	3	594.31	-17.07
P0A1H5 EFTU_SALTY Elongation factor Tu	15		EHILLGR	117	7	6	68.39	b3°b3b4y3y4y5	837.48	38.988	111061	2	419.24	-20.33
P0A1H5 EFTU_SALTY Elongation factor Tu	16		GQVLAKPGTIKPHTK	289	15	13	91.2	b4°b4y3°y3y4°y4y5°y5y6y8y9°y9y10	1574.91	27.870	84383	3	525.64	-15.89
P0A1H5 EFTU_SALTY Elongation factor Tu	17		LLDEGR	264	6	4	40.96	b4°b4y4y5	702.37	26.700	3927	1	702.37	-12.86
P0A1H5 EFTU_SALTY Elongation factor Tu	18	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	3	18.79	b6b9y9	1768.78	79.607	3414	3	590.26	-5.94
P0A1H5 EFTU_SALTY Elongation factor Tu	19		HTPFFK	319	6	4	27.43	b4°b4b5°b5	776.40	52.339	1629	2	388.70	-10.69
P0A1H5 EFTU_SALTY Elongation factor Tu	20	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLELVEMEV	124	31	4	50.3	y4y5y6y7	3694.86	127.457	31937	3	1232.29	4.49
P0A1H5 EFTU_SALTY Elongation factor Tu	21		GTVVTGRVER	224	10	5	59.52	b9y3y6y7y8	1073.60	25.225	20110	2	537.30	-7.96
P0A1H5 EFTU_SALTY Elongation factor Tu	22		IIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGR	188	36	9	60.01	b3b5y3y4y6y7y11y12y24	4060.17	122.499	16583	4	1015.80	0.84
P0A1H5 EFTU_SALTY Elongation factor Tu	23		FESEVYILSKDEGGR	304	15	4	37.67	b7b8b11b13	1728.84	85.719	7034	2	864.93	-0.64
P0A1H5 EFTU_SALTY Elongation factor Tu	24		TYGGAARAFDQIDNAPEEK	38	19	10	81.81	b7b9b10b11b12°b12b15y4y5y7	2052.95	95.684	3097	2	1026.98	-5.47
P0A1H5 EFTU_SALTY Elongation factor Tu	25		GYRPQFYFRTTDTGTIELPEGVE MVMPGDNIK	325	33	3	23.02	b8b9b11	3760.80	99.412	2541	3	1254.27	-8.57
P0A1H5 EFTU_SALTY Elongation factor Tu	26	Phosphoryl STY(4)	MVVTLIHPIAMDDGLR	358	16	4	31.73	b5_H3PO4 b5b6y6y11	1860.91	105.960	62103	3	620.97	3.08
P0A1H5 EFTU_SALTY Elongation factor Tu	27		TINTSHVEYDTPTR	61	14	8	43.79	b3°b3b4°b4b9b10°b10°b10	1633.79	49.174	22362	2	817.40	5.01
P0A1H5 EFTU_SALTY Elongation factor Tu	28		INTSHVEYDTPTR	62	13	3	14.67	b3°b3b9	1532.73	49.203	3084	2	766.87	-1.12
P0A1H5 EFTU_SALTY Elongation factor Tu	29		GITINTSHVEYDTPTR	59	16	0	4.15		1785.85	49.175	21585	3	595.96	-11.69
P66593 RS6_SALTY 30S ribosomal protein S6	1		AHYVLMNVEAPQEVIDELETFR	56	23	34	302.78	b2b3b4b5b6b7b8b9b10°b10b13b14b18b19y1y2y3y4y5°y5y6y7°y7y8°y8y9y10y11y12*y12y13*y13y14y23	2704.33	109.565	192789	3	902.11	0.00
P66593 RS6_SALTY 30S ribosomal protein S6	2		YSAAITGAEGK	24	11	24	164.59	b1b2°b2b3°b3b4b7b8°b8b10y1y2y3°y3y4y5y6°y6y7°y7y9°y9y10y11	1067.53	33.074	93621	2	534.27	-7.78
P66593 RS6_SALTY 30S ribosomal protein S6	3		HAVTEASPMVK	93	11	23	191.64	b1b2b3b4°b4b5°b5b6°b6b7°b7b9°b9b10y4y5y6y7°y7y8y9y10y11	1169.59	29.854	59544	2	585.30	-8.56

P66593 RS6_SALTY 30S ribosomal protein S6	4		HYEIVFMVHPDQSEQVPGMIER	2	22	18	122.35	b3°b3b4b5b6b7b13°b13b16y4y5y6°y6y8y11°y11*y11y13	2641.21	73.782	124483	4	661.06	-17.38
P66593 RS6_SALTY 30S ribosomal protein S6	5		FNDAVIR	79	7	7	84.93	b3b5y3y4y5y6*y6	834.43	41.507	92456	2	417.72	-15.51
P66593 RS6_SALTY 30S ribosomal protein S6	6		LEDWGR	38	6	4	54.49	b3y3y4y5	775.37	37.843	5869	2	388.19	-4.80
P66593 RS6_SALTY 30S ribosomal protein S6	7		RQLAYPINK	44	9	6	46.59	b3*b3b4b7y4*y4	1102.63	36.463	35278	2	551.82	-6.53
P66593 RS6_SALTY 30S ribosomal protein S6	8		AHYVLMNVEAPQEVIDELETTRFNDAVIR	56	30	6	25.62	b3b7y4y20*y20y21	3519.73	114.629	17833	4	880.69	-6.59
P66593 RS6_SALTY 30S ribosomal protein S6	9		HYEIVFMVHPDQSEQVPGMIERYSAAITGAEGK	2	33	6	18.6	b4b6b8y4°y4y10	3689.79	119.514	2534	5	738.76	4.96
P66593 RS6_SALTY 30S ribosomal protein S6	10		HAVTEASPMVK	93	11	0	2.26		1151.57	29.848	1677	3	384.53	-11.98
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	1		AAADLQLQGV PAMFVNGK	158	18	28	247.84	b2b4b5b6b7b8b9b10b13b14b16y2y3*y3y4y5*y5y7*y7y8y10y11*y11y12*y12y13y14y18	1829.96	80.673	187876	2	915.48	-1.33
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	2		YQINPQGM DTSSMDVFVQQYADTVK	176	25	17	98.26	b2*b2b3b4*b4b14b15y2y3y4y5y6y7°y7*y7y10y25	2865.31	86.343	108294	3	955.78	1.96
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	3		YHVEFLGPLGK	77	11	8	52.12	b2b3b4y2y3y5y6y11	1259.67	68.622	104697	2	630.34	-7.17
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	4		TQTVQSAADIR	116	11	22	126.74	b1°b1b2°b2*b2b3°b3*b3b6b7y2y3y4y5y6y7°y7*y7y8y9*y9y11	1189.61	34.916	66514	2	595.31	-5.34
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	5		ELTQAWAVAMALGVEDK	88	17	3	16.91	b11y4y7	1831.90	71.065	1640	2	916.45	-15.53
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	6		ELTQAWAVAMALGVEDKVTVPLFEAVQK	88	28	8	21.44	b5°b5*b5b7*b7y6y8y23	3043.62	115.679	33790	3	1015.21	0.00
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	7		VFVDAGVKGEDYDAAWNSFVVK	128	22	3	23.77	b3b4b13	2416.16	81.052	5223	2	1208.58	-8.29
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	8	Oxidation+M(21)	YHVEFLGPLGKELTQAWAVAMALGVEDK	77	28	4	25.73	b8b11y12y13	3088.62	85.402	11490	4	772.91	13.91
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	9		PAMFVNGK	168	8	1	7.29	b5	863.43	80.654	4596	1	863.43	-12.65
P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	10		YQINPQGM DTSSMDVFVQQYA	176	21	0	7.54		2422.06	86.317	1531	4	606.27	-1.92
P25077 MDH_SALTY Malate dehydrogenase	1		NQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVK	21	33	26	95.35	b1b2*b2b3*b3b8°b8b9*b9b10°b10*b10b13b15°b15y1y2y3y5y12y15y16y18y19y30y33	3388.82	93.673	234180	3	1130.28	6.27
P25077 MDH_SALTY Malate dehydrogenase	2	Carbamidomethyl+C(2)	ACVGITNPVNTTVAIAAEVLKK	111	23	16	123.4	b2b3b4b5b6b12y2y3y4y6y15y16y18y20y21y23	2382.33	104.331	181513	3	794.78	-4.92
P25077 MDH_SALTY Malate dehydrogenase	3		VAVLGAAGGIGQALALLK	2	19	32	367.51	b2b3b4b5b6b7b8b9b10b11b15b16b17b18b19y1y2y3y4y5y6y7y9y10y11y12y13y14y15y16y17y19	1735.09	119.476	181277	2	868.05	2.74

P25077 MDH_SALTY Malate dehydrogenase	4		FFSQPLLLGK	262	10	8	69.52	b2y2y3y4y6y7y8y10	1149.66	75.411	150507	2	575.33	-7.96
P25077 MDH_SALTY Malate dehydrogenase	5		DIQLGEDFINK	301	11	14	89.17	b2°b2b3y3y4y6°y6y7y8y9°y9°y9y11*y11	1291.64	67.550	134656	2	646.33	-6.62
P25077 MDH_SALTY Malate dehydrogenase	6		SIGTLSAFEQHSLDAMLDTLKK	279	22	14	70.72	b2°b2b10b13y2y3y11y12y15y17y18y20y22*y22	2405.22	94.144	123149	3	802.41	-7.71
P25077 MDH_SALTY Malate dehydrogenase	7		IQNAGTEVVEAK	205	12	24	143.66	b2*b2b3*b3b4y1y2y3°y3y4y5y6y7y8°y8y9y10°y10*y10y11°y11*y11y12*y12	1258.66	34.341	107890	2	629.83	-6.59
P25077 MDH_SALTY Malate dehydrogenase	8		LFGVTTLDIIR	142	11	9	56.89	b2b3b4y1y2y3y6y9y11	1247.73	88.567	67940	2	624.37	-5.58
P25077 MDH_SALTY Malate dehydrogenase	9		AGGGSATLSMGQAAAR	217	16	17	98.87	b5b8°b8b15b16y2y6y7y8y9°y9°y9y10°y10y11°y11y16	1405.68	39.749	62853	2	703.34	-4.60
P25077 MDH_SALTY Malate dehydrogenase	10		SDLFNVNAGIVK	87	12	12	77.79	b2b3°b3b5°b5y2y4y6y7y8y9y12	1276.68	69.254	61861	2	638.84	-6.79
P25077 MDH_SALTY Malate dehydrogenase	11	Carbamidomethyl+C(2)	ACVGITNPVNTTVAIAAEVLK	111	22	6	22.65	b2b4b5y1y2y8	2254.23	112.999	9699	3	752.08	-8.77
P25077 MDH_SALTY Malate dehydrogenase	12		GFSGEDATPALEGADVVLISAGVAR KPGMDR	56	31	3	22.26	b3b4y7	3086.56	82.571	3013	3	1029.52	-0.55
P25077 MDH_SALTY Malate dehydrogenase	13		NLVQQIAK	99	8	3	36.94	b3y3y6	913.53	48.489	69036	2	457.27	-15.83
P25077 MDH_SALTY Malate dehydrogenase	14		GFSGEDATPALEGADVVLISAGVAR	56	25	3	19.01	b4b15b22	2402.27	106.109	6757	3	801.43	19.11
P25077 MDH_SALTY Malate dehydrogenase	15		SIGTLSAFEQHSLDAMLDTLK	279	21	3	14.36	b8b13y12	2277.18	82.283	3133	3	759.73	18.33
P25077 MDH_SALTY Malate dehydrogenase	16		NGVEER	272	6	1	13.9	y4	703.34	31.842	1689	2	352.17	-1.74
P25077 MDH_SALTY Malate dehydrogenase	17		IKGFSGEDATPALEGADVVLISAGVAR	54	27	6	63.49	b14y4y5y6y7y8	2643.39	86.816	51442	3	881.80	-3.23
P25077 MDH_SALTY Malate dehydrogenase	18		RIQNAGTEVVEAK	204	13	5	30.68	b3b11y3°y3y8	1414.77	31.732	13255	2	707.89	0.17
P25077 MDH_SALTY Malate dehydrogenase	19		AGGGSATLSMGQAAARFGLSLVR	217	23	4	29.55	b7b8b10b14	2178.12	77.343	2816	2	1089.56	-12.44
P25077 MDH_SALTY Malate dehydrogenase	20		KPGMDRSDLFNVNAGIVK	81	18	3	25.07	b8b11b12	1961.04	103.331	2714	3	654.35	6.91
P25077 MDH_SALTY Malate dehydrogenase	21		SIGTLSAFEQHSLDAMLDTLKK	279	22	4	18.94	b10b13y12y19	2405.22	81.622	2526	3	802.41	-8.93
P25077 MDH_SALTY Malate dehydrogenase	22	Oxidation+M(16)	SIGTLSAFEQHSLDAMLDTLK	279	21	3	24.02	b10b19b20	2293.15	100.835	32259	3	765.06	6.18
P25077 MDH_SALTY Malate dehydrogenase	23		GTLSAFEQHSLDAMLDTLKK	281	20	1	7.64	b9	2205.10	94.135	7753	3	735.70	-11.63
P0A1D5 CH10_SALTY 10 kDa chaperonin	1		VGDIVIFNDGYGVK	60	14	20	178	b2b3b4b5°b5b13°b13y1y3y4y5y6°y6y7y8y9y10y12y13y14	1495.77	73.081	295256	2	748.39	-3.75
P0A1D5 CH10_SALTY 10 kDa chaperonin	2		ILDNGTVQPLDVK	47	13	29	219.45	b2b3b5°b5b8°b8b10b11°b11b12y1y2y3°y3y4y5y6°y6°y6y7y8y9y10y11°y11*y11y12y13*y13	1411.78	57.114	272282	2	706.39	-1.64
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	16	114.65	b2b4°b4b6°b6b7y2y3y4y6y7y8y9°y9y12y14	1188.65	43.528	160325	2	594.83	-8.01
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIAVGK	37	8	7	79.28	b4b5y3y4y5y6y8	786.46	41.208	51293	2	393.73	-14.36
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		STRGEIIAVGK	34	11	12	140.27	b3b4b5b6°b6b7b8b9b10y3y4y8	1130.64	36.860	88168	2	565.83	-8.31

P0A1D5 CH10_SALTY 10 kDa chaperonin	6		VGDIVIFNDGYGVKSEK	60	17	4	23.83	b10b13y8y10	1839.95	92.104	12608	2	920.48	0.66
P64076 ENO_SALTY Enolase	1	Carbamidomethyl+C(16)	AAGYELGKDITLAMDCAASEFYK D GK	231	26	26	211.06	b2b3b4b5b6b7b9°b9b13b14y2y3°y3y4y6°y6y7y8y9y10y11y12y13y15y24y26	2824.28	97.281	321448	4	706.83	-13.14
P64076 ENO_SALTY Enolase	2		AFTSEEFTHFLEELTK	266	16	29	212.65	b2b3°b3b5°b5b6b11b13b16°b16y1y2°y2y3y4y5°y5y6y7y8y9y10°y10y11°y11y12y13y14y16	1928.91	102.423	289395	3	643.64	-11.71
P64076 ENO_SALTY Enolase	3		FNQIGSLTETLAAIK	342	15	33	271.31	b2°b2b3°b3b4°b4b5b6°b6b7°b7b8b11b12°b12b14°b14y1y2y3y4y5y6y7y8y9y10y11y12y13°y13y15°y15	1605.89	85.443	284039	2	803.45	0.46
P64076 ENO_SALTY Enolase	4		SGETEDATIADLAVGTAAGQIK	371	22	27	214.44	b2b3b7°b7b8°b8b11b14°b14b16b22y2y3y4y5y6y7y8y9y10y12°y12y13y14y15y16y22	2118.07	75.218	261280	2	1059.54	6.45
P64076 ENO_SALTY Enolase	5		YSMPVPMMNINGGEHADNNVDI QEFMIQPVGAK	143	34	22	140.95	b2°b2b3°b3b4b5b10b13b23y3y5y6°y6y7y8y9y10y12y13y29y31y34	3759.80	98.213	195361	3	1253.94	8.57
P64076 ENO_SALTY Enolase	6		GMNTAVGDEGGYAPNLGSNAEA LAVIAEAVK	200	31	22	134.52	b2b4b5°b5°b5b6°b6b8b13y1y2y3y7y8y9y10y12y13y14y15y24y31	2989.46	94.865	174497	3	997.16	1.39
P64076 ENO_SALTY Enolase	7		AVGAVNGPIAQAILGK	66	16	4	43.79	y5y6y10y11	1478.87	74.926	165962	2	739.94	-1.73
P64076 ENO_SALTY Enolase	8		DAGYTAVISHR	360	11	19	148.05	b2b3°b3b4b6°b6b7b8y2y3°y3y4y5y6°y6y7y9°y9y11	1189.59	40.986	96762	2	595.30	-4.31
P64076 ENO_SALTY Enolase	9		IQLVGDDLFTVNTK	311	14	20	137.72	b2°b2b3°b3b8y2y3y4y5°y5y6y8°y8y9y10°y10y11°y11y12y14	1562.85	77.329	83684	2	781.93	2.27
P64076 ENO_SALTY Enolase	10		YVLAGEGNK	257	9	9	82.67	b2y3y4y5y6°y6y7y8y9	950.49	32.887	70679	2	475.75	-9.25
P64076 ENO_SALTY Enolase	11		IEEALGEK	411	8	8	65.76	b3b4y1y3°y3y6y7y8	888.46	30.698	45459	2	444.73	-10.44
P64076 ENO_SALTY Enolase	12	Carbamidomethyl+C(16)	AAGYELGKDITLAMDCAASEFYK	231	23	13	78.37	b4b5b11°b11b13y3y4°y4y5y7y8y11y23	2524.17	100.858	38290	3	842.06	-3.29
P64076 ENO_SALTY Enolase	13		ILKEGIEK	325	8	7	55.24	b2y4y5°y5y6y7y8	929.56	28.456	33360	2	465.28	-8.27
P64076 ENO_SALTY Enolase	14		GNPTVEAEVHLEGFGVMAAAPS GASTGSR	16	30	5	22.52	b7b9b10y6y30	2856.38	91.970	28906	3	952.80	6.41
P64076 ENO_SALTY Enolase	15		QYPIVSIEDGLDESDDWGFAYQTK	282	24	5	23.4	y4°y4°y4y5y8	2776.28	93.565	28401	2	1388.64	6.33
P64076 ENO_SALTY Enolase	16	Carbamidomethyl+C(8)	DITLAMDCAASEFYKDGK	239	18	5	23.55	b2b8b9y2y5	2034.93	62.231	7888	3	678.98	6.00
P64076 ENO_SALTY Enolase	17		GMPLYEHIAELNGTPGK	126	17	4	23.83	b6b10y3y5	1826.88	66.538	130399	3	609.63	-16.24
P64076 ENO_SALTY Enolase	18		GIANSILIK	333	9	4	55.62	y3y5y6y7	928.57	59.912	102992	2	464.79	-16.10
P64076 ENO_SALTY Enolase	19		MGSEVFHHLAK	184	11	9	104.46	b4b8b10y3y4y6y9y10°y10	1255.60	41.207	97674	3	419.21	-19.35
P64076 ENO_SALTY Enolase	20		AAGYELGK	231	8	4	36.94	b3b5y7°y7	808.42	30.661	2709	2	404.71	-2.49
P64076 ENO_SALTY Enolase	21		VLGDKIQLVGDDLFTVNTK	306	19	6	48.36	b7b8y3y4y6y8	2075.12	79.252	75144	3	692.38	-8.71
P64076 ENO_SALTY Enolase	22		DGKYVLAGEGNK	254	12	7	38.3	b4°b4b9°b9b11y9°y9	1250.63	43.406	60163	2	625.82	-9.37
P64076 ENO_SALTY Enolase	23		DQAGIDKIMIDLGTENK	85	18	4	39.47	y5y7y8y9	1975.95	75.387	29110	3	659.32	-8.71
P64076 ENO_SALTY Enolase	24		GKGMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	198	33	9	41.97	b4b5°b5b6°b6b12b15y3y15	3174.59	89.671	27784	3	1058.87	4.46

P64076 ENO_SALTY Enolase	25		GMPLYEHIAELNGTPGKYSMPPV MMNIINGGEHADNNVDIQEFMIQP VGAK	126	51	6	22.07	b22y5y6*y6y11*y11	5567.69	97.458	8062	4	1392.68	5.26
P64076 ENO_SALTY Enolase	26		YVLAGEGNKAFTEEFTHFLEELT K	257	25	7	30.47	b7°b7b11b14y5y11y22	2860.43	81.489	7699	3	954.15	8.45
P64076 ENO_SALTY Enolase	27		DAGYTAVISHRSGETEDATIADLA VGTAAGQIK	360	33	3	11.22	b3b10y8	3288.62	126.860	5574	3	1096.88	-4.53
P64076 ENO_SALTY Enolase	28		YSMPVPMMNINGGEHADNNVDI QEFMIQPVGAQTVK	143	37	3	16.57	b6b9b13	4087.98	106.000	2609	4	1022.75	1.31
P64076 ENO_SALTY Enolase	29		EIIDSRCNPTVEAEVHLEGGFVGM AAAPSGASTGSR	10	36	3	10.98	b24y8y11	3569.69	107.334	1866	4	893.18	-10.26
P64076 ENO_SALTY Enolase	30	Carbamidomethyl+C(8)	DITLAMDCAASEFYKDGK	239	18	3	16.15	b11y3y7	2034.94	50.920	1502	4	509.49	14.04
P64076 ENO_SALTY Enolase	31	Oxidation+M(27)	YSMPVPMMNINGGEHADNNVDI QEFMIQPVGAK	143	34	4	22.43	b10b11°b11y10	3775.81	91.899	3361	3	1259.27	12.41
P64076 ENO_SALTY Enolase	32		GYTAVISHR	362	9	2	8.01	b3°b3	1003.53	40.997	35522	2	502.27	-6.57
P64076 ENO_SALTY Enolase	33		LKEGIEK	326	7	0	1.13		816.47	28.457	26028	2	408.74	-11.29
P64076 ENO_SALTY Enolase	34		LAGEGNK	259	7	0	1.51		688.36	32.881	6457	1	688.36	-7.71
P64076 ENO_SALTY Enolase	35		TSEEFTHFLEELTK	268	14	12	98.57	b3°b3b4°b4b5°b5b8b10b11 b12b13°b13	1710.83	102.429	5554	2	855.92	5.42
P64076 ENO_SALTY Enolase	36		DGFAYQTK	298	8	0	7.17		929.44	93.528	4059	1	929.44	8.34
P64076 ENO_SALTY Enolase	37		TAVISHR	364	7	1	8.01	b3	783.44	41.018	3300	2	392.22	-12.46
P64076 ENO_SALTY Enolase	38		AFTSEEFTHFLEELTK	266	16	0	4.15		1910.90	102.424	11773	3	637.64	-8.69
P64076 ENO_SALTY Enolase	39		DAGYTAVISHR	360	11	0	2.26		1171.56	40.949	2769	3	391.19	-13.65
P06179 FLIC_SALTY Flagellin	1		AQILQQAGTSVLAQANQVPQNVL SLLR	468	27	38	267.02	b2*b2b3b4*b4b5*b5b6*b6 b7*b7b10*b10b11°b11b12 b14b15b17b18*b18y1y2y3 y4y5y6y7y9y10y11y12*y1 2y13*y13y14y24y27	2860.61	105.086	126197	3	954.21	2.48
P06179 FLIC_SALTY Flagellin	2		FNSAITNLGNTVNNLTSAR	432	19	18	105.75	b2b3°b3b4b5°b5b12b13°b 13y3y4y7*y8y11y12y14°y1 4y19	2007.04	78.095	96846	2	1004.02	6.20
P06179 FLIC_SALTY Flagellin	3		SQSALGTAIER	20	11	8	51.6	b2*b2y4y6y7y9°y9y11	1132.59	41.699	71454	2	566.80	-7.33
P06179 FLIC_SALTY Flagellin	4		AQVINTNSLSLLTQNNLNK	1	19	14	59.59	b1b2°b2b3b4y1y2y6*y6y7 y10y13y15y19	2085.14	74.610	57331	2	1043.07	3.16
P06179 FLIC_SALTY Flagellin	5		VSGQTQFNGVK	125	11	8	32.05	b2°b2y7*y7y9y10*y10y11	1164.59	32.949	54296	2	582.80	-6.71
P06179 FLIC_SALTY Flagellin	6		IDAALAQVDTLR	411	12	18	181.5	b2b3b4b5b7b8°b8*b8b9y3 y4y6y7y9y10y11°y11y12	1285.70	60.971	52835	2	643.36	-5.22
P06179 FLIC_SALTY Flagellin	7		NANDGISIAQTTEGALNEINNQL R	66	25	12	23.73	b1°b1b2b4b6°b6y2y3y6*y 6y9y25	2670.33	86.488	50961	2	1335.67	9.78
P06179 FLIC_SALTY Flagellin	8		INSAKDDAAGQAIANR	37	16	14	112.1	b6b10y1y3*y3y4y5y7*y7y 8y9y10y11y16	1614.80	29.767	44732	3	538.94	-14.36
P06179 FLIC_SALTY Flagellin	9		QINSQTLGLDTLNVQQK	161	17	11	51.26	b7b8°b8b17y1y5*y5y6y10 y12y17	1900.02	65.088	35302	2	950.51	4.30
P06179 FLIC_SALTY Flagellin	10		SDLGAVQNR	423	9	8	31.3	b1b4°b4b7°b7°b7y8y9	959.50	36.360	19265	2	480.25	6.36
P06179 FLIC_SALTY Flagellin	11		TEVVSIGGK	370	9	5	31.3	b3b4°b4y8y9	889.49	38.283	7476	2	445.25	-4.94
P06179 FLIC_SALTY Flagellin	12		VSDTAATVTGYADTTIALDNSTF K	180	24	6	19.42	b1y1y3y7y10*y10	2462.23	111.540	3659	3	821.41	14.87
P06179 FLIC_SALTY Flagellin	13		ELAVQSANSTNSQSDLSIQAEIT QR	93	26	3	12.49	b13y3y6	2805.34	70.261	16062	3	935.78	-4.35
P06179 FLIC_SALTY Flagellin	14		IEDSDYATEVSNMSR	453	15	3	18.79	b10y7y10	1716.74	53.133	11246	2	858.88	2.77
P06179 FLIC_SALTY Flagellin	15		ASATGLGGTDQK	204	12	11	94.05	b6°b6b7b8b9°b9y4y7*y7y8 y9	1105.54	32.462	1586	2	553.27	-10.38
P06179 FLIC_SALTY Flagellin	16		SRIEDSDYATEVSNMSR	451	17	12	113.41	b4b5b7b8b10°b10b11y3y5 y6y8y12	1959.85	50.300	81317	3	653.95	-11.46

P06179 FLIC_SALTY Flagellin	17		YKVSDTAATVTGYADTTIALDNS TFK	178	26	5	18.95	b9°b9y4y7y15	2753.35	136.594	8928	3	918.46	0.53
P06179 FLIC_SALTY Flagellin	18		YTADDGTSKTALNK	349	14	5	25.4	b12b13°b13°b13y13	1484.70	91.470	6394	2	742.85	-14.63
P06179 FLIC_SALTY Flagellin	19		TYAASKAEGHNFK	379	13	4	26.12	b10°b10b11y12	1423.70	74.414	4283	2	712.35	2.74
P06179 FLIC_SALTY Flagellin	20		ASATGLGGTDQKIDGDLK	204	18	3	25.07	b9b11b12	1746.87	76.519	3940	2	873.94	-8.80
P06179 FLIC_SALTY Flagellin	21		AEGHNFKAQPDLAEEAAATTENP LQK	385	26	3	12.49	b5b23y14	2752.37	88.299	2057	3	918.13	4.97
P06179 FLIC_SALTY Flagellin	22	Phosphoryl STY()	AQVINTNSLSLLTQNNLNK	1	19	13	77.14	b3b8°b8b11°b11b12b13°b 13y10y11°y11y12°y12	2165.07	81.105	84627	2	1083.04	-6.99
P06179 FLIC_SALTY Flagellin	23	Phosphoryl STY(22)	TNGEVTLAGGATSPLTGGLPATA TEDVK	252	28	11	30.86	b7°b7°b7b8°b8°b8b11°b1 1b22y5y14	2708.26	123.855	26621	4	677.82	-13.97
P06179 FLIC_SALTY Flagellin	24	Phosphoryl STY()	MAQVINTNSLSLLTQNNLNK	0	20	3	14.89	b3b9y11	2296.10	77.411	3033	4	574.78	-12.97
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	48	303.52	b1b2b3°b3b4°b4b5°b5°b5 b6°b6°b6b7°b7°b7y2°y2y3 y4y6°y6y7°y7°y7y8°y8°y8 y9y10°y10y11y14y15°y15° y15y16°y16y17y18y19y20 y21y22°y22y23°y23y24°y2 4	2574.32	97.685	502788	3	858.78	-2.66
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	2		LVSWYDNETGYSNK	307	14	8	90.3	y4y5y6y9y10y11y12y14	1675.77	57.882	270371	2	838.39	4.15
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	3		AGIALNDNFVK	296	11	14	86.95	b3b4y2y4y5°y5°y5y6y7°y7 °y7y8°y8y11	1161.62	61.098	242479	2	581.31	-6.94
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	4		VLDLIAHISK	321	10	10	89.59	b2b3y3y4y5°y5y6y7y8y10	1108.66	64.206	201985	2	554.84	-7.60
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	5		GASQNIIPSSTGAAK	198	15	20	125.55	b3b5°b5°b5b6°b6°b6b7°b 7y2y4y5y7y8°y8y9y10y11y 15°y15	1401.72	40.720	164163	2	701.36	-8.36
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	6		VPTPNVSVVDLTVR	232	14	18	133.74	b3°b3b5°b5°b5b12y1y2y3y 4y5y8y9y10y11y12°y12y14	1495.85	70.700	150705	2	748.43	-0.49
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	7		AATYEQIK	249	8	3	41.71	y4y5y6	923.47	30.364	97338	2	462.24	-12.29
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	8		SDIEIVAINDLLDAEYMAYMLK	24	22	26	213.26	b2b3b4°b4b5°b5b6°b6b7°b 7b8b11y1y2y3y4y5y6y7y8 y9y10y11y12y14y22	2530.24	125.418	86913	3	844.08	-2.41
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	9		VLPELNGK	217	8	11	55.24	b2y2y3y4°y4y5°y5y6°y6y 8°y8	869.50	44.442	61775	2	435.25	-13.20
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	10		VVLTPGSKDNTPMFVK	116	16	10	46.53	b3b12y3y7°y7°y7y13°y13y 14y16	1732.91	57.060	52135	3	578.31	-11.90
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	11	Carbamidomethyl+C(12) ;Carbamidomethyl+C(16)	YEQDIVSNASCTTNCLAPLAK	138	22	6	18.94	b4b14b22y2y3y14	2412.12	97.490	3447	4	603.79	1.32
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	12		LTGMAFR	225	7	3	41.34	y3y5y6	795.40	48.392	89222	2	398.20	-21.03
P0A1P0 G3P1_SALTY Glyceraldehyde-3- phohate dehydrogenase	13		VGINGFGR	4	8	3	49.49	y3y5y7	819.43	47.095	61092	2	410.22	-19.81

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14	Carbamidomethyl+C(20)	GVLGYTEDDVVSTDFNGEVCTSV FDAK	269	27	5	23.08	b7°b7b8b13°b13	2924.31	97.104	2500	4	731.83	-0.75
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEQDIVSNASCTTNCL APLAK	132	28	33	248.47	b3b4b5b7°b7°b7b8b11b12 b13°b13°b13b16b24°b24b 27y3y4y5y6y9°y9y10y11*y 11y12°y12*y12y13y14y15 *y15y16	3044.42	66.180	295528	3	1015.48	2.09
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		VPTPNVSVVDLTVRLEK	232	17	4	16.91	b3b5*b5y14	1866.05	76.008	47630	3	622.69	-12.63
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		RSDIEIVAINDLLDAEYMayMLK	23	23	11	108.43	b3b5b6b7b8y3y4y6y7y10y 11	2686.35	117.622	31774	3	896.12	1.00
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		SDIEIVAINDLLDAEYMayMLKYD STHGR	24	29	6	17.49	b10y6y8°y8y10°y10	3346.64	72.886	17471	4	837.42	14.01
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19	Carbamidomethyl+C(28)	AAAEGEMKGVLGYTEDDVVSTD FNGEVCTSVFDAK	261	35	5	24.75	b3b12b13b17y8	3711.71	101.985	3955	4	928.68	10.06
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20		KHITAGAK	107	8	3	41.71	y3y4y5	825.49	12.743	2089	2	413.25	-8.06
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	21		DNTPMFVKGANFDK	124	14	5	28.56	b4b8y6°y6y10	1583.75	88.122	1890	3	528.59	-1.54
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	22		LDLIAHISK	322	9	1	8.42	b3	1009.59	64.202	56943	2	505.30	-10.64
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	23		DLIAHISK	323	8	3	37.7	b3b4b5	896.51	64.211	56766	2	448.76	-13.62
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	24		LNDNFVK	300	7	1	8.01	b6	849.44	61.112	8356	1	849.44	-9.41
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	25		LIAHISK	324	7	1	8.42	b4	781.49	64.212	3578	2	391.25	-5.94
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	26		AATYEQIK	249	8	0	1.13		906.46	30.358	26413	2	453.73	3.23
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	27		VVLTGPSKDNTPMFVK	116	16	0	4.15		1715.88	57.072	1509	3	572.63	-12.59
P0A1S2 HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	42	310.2	b2°b2b3°b3b4°b4b5°b5b6° b6b7°b7b8°b8b9°b9b11°b1 1b12°b12b21y1y2y3y4y5y 6y7*y7y8y9y10y12*y12y1 3y14y15°y15y16y17y18y21	2216.10	96.692	468363	2	1108.56	4.63
P0A1S2 HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	12	102.7	b2b3°b3y2y4y5y6y7y8y9y1 0y11	1304.55	32.563	138508	2	652.78	-8.05
P0A1S2 HNS_SALTY DNA-binding protein H-NS	3		REEESAAAAEVEER	40	14	21	158.73	b2b3°b3b5°b5b6°b6b7b8b1 0b12y2y3°y3y4°y4y5°y5y6 y7y14	1575.71	31.359	120753	3	525.91	-11.39
P0A1S2 HNS_SALTY DNA-binding protein H-NS	4		LEVVVNER	32	8	4	36.94	b7y4°y4y6	957.53	42.388	17826	2	479.27	-7.20

P0A1S2 HNS_SALTY DNA-binding protein H-NS	5		SEALK	1	5	2	27.05	b3y4	547.30	43.084	7504	1	547.30	-12.27
P0A1S2 HNS_SALTY DNA-binding protein H-NS	6	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	5	21.35	b9y7°y7y9°y9	1624.76	88.163	3216	3	542.26	12.17
P0A1S2 HNS_SALTY DNA-binding protein H-NS	7	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEVVVNER	19	21	34	284.19	b3°b3b4°b4b6b7°b7b9b12° b12y3°y3°y3y4°y4y5°y5°y 5y6y7°y7°y7y8y9y10y11y1 2y13y14y15y16y17y18y19	2563.26	123.142	212879	3	855.09	-0.86
P0A1S2 HNS_SALTY DNA-binding protein H-NS	8		QLEDFLIKE	128	9	3	39.08	y3y6y7	1134.59	70.966	186791	2	567.80	-12.37
P0A1S2 HNS_SALTY DNA-binding protein H-NS	9		YSYVDENGETKKTWTGQGR	96	18	17	154.78	b3°b3b6y4y5°y5y6°y6y8°y 8y11y12y13y14y15y16y17	2090.92	46.417	105008	3	697.65	-8.76
P0A1S2 HNS_SALTY DNA-binding protein H-NS	10		EMLIADGIDPNELLNSMAAAKSGT K	62	25	4	19.53	b4b7b11y5	2589.30	82.675	35964	3	863.77	5.00
P0A1S2 HNS_SALTY DNA-binding protein H-NS	11		LQYREMLIADGIDPNELLNSMAA AK	57	26	5	28.45	b6b8b12b13y5	2904.50	99.338	4984	4	726.88	12.78
P0A1S2 HNS_SALTY DNA-binding protein H-NS	12		AARPAKYSYVDENGETK	90	17	4	27.05	b12y6y14y16	1898.91	104.540	2808	2	949.96	-5.72
P0A1S2 HNS_SALTY DNA-binding protein H-NS	13	Oxidation+M(2)	EMLIADGIDPNELLNSMAAAK	62	21	7	32.3	b8y3y7°y7y12°y12y13	2232.11	91.370	17241	2	1116.56	10.83
P0A1S2 HNS_SALTY DNA-binding protein H-NS	14	Carbamidomethyl+C(6); Oxidation+M(14)	AQARECTLETLEEMLEK	15	17	4	16.91	b5y5y7°y7	2066.97	108.961	2645	3	689.66	-0.71
P65702 PGK_SALTY Phohoglycerate kinase	1	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	13	94.99	b2b3b7b8y4y5°y5y8y9y13y 14y15y20	2002.04	98.724	224640	2	1001.53	6.28
P65702 PGK_SALTY Phohoglycerate kinase	2		SVNDVKEDEQILDIGDASAQQLAE ILK	272	27	30	195.28	b1b2b4b5°b5°b5b8b9b11b 12b13°b13b14b18b22b25b 26y1y2y3y4y5y7y10y13°y 13y14y15°y15y27	2941.50	99.629	198090	3	981.17	0.58
P65702 PGK_SALTY Phohoglycerate kinase	3		VMVTSHLGRPTEGEYNEEFSLPV VNYLK	53	29	18	127.69	b2b6b14b17b18b19b20°b2 0b21°b21b22y3y4y5y7y8y 10y29	3321.66	91.813	154138	4	831.17	-7.50
P65702 PGK_SALTY Phohoglycerate kinase	4		VLPVAMLEER	373	11	3	36.82	y4y5y6	1227.67	79.708	143761	2	614.34	-7.95
P65702 PGK_SALTY Phohoglycerate kinase	5	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	17	107.08	b2b3b6°b6b7°b7b9°b9y1y2 y5y7y8y10y11y12y14	1599.84	68.438	126501	2	800.43	1.75
P65702 PGK_SALTY Phohoglycerate kinase	6		VATEFSETAPATLK	258	14	17	147.94	b2b3b4°b4b5b12b14y2y3y 5y6y7y9y10y11y12y14	1464.76	52.423	100094	2	732.88	0.50
P65702 PGK_SALTY Phohoglycerate kinase	7		TILWNGPVGVFEPNFR	302	17	22	137.76	b2b13°b13y1y3°y3y4°y4y 5y6°y6y7y10y11°y11y12°y 12°y12y13°y13y14y17	1993.05	106.047	92132	2	997.03	6.68
P65702 PGK_SALTY Phohoglycerate kinase	8		ADLNPVKEGK	19	11	15	113.22	b2b4°b4b5b9y1y3°y3y4°y4 y5y6y7y8y11	1169.65	36.426	73524	2	585.33	-3.86
P65702 PGK_SALTY Phohoglycerate kinase	9		ASLPTIELALK	38	11	6	66.89	y3y4y5y7y8y11	1155.69	76.943	70860	2	578.35	-7.08
P65702 PGK_SALTY Phohoglycerate kinase	10		LVKDYLDGVDVAEGELVVLENV R	90	23	15	84.28	b2b7b10b13b14b15°b15b1 7y2y3y4°y4y5y11y23	2544.35	96.480	70675	3	848.79	-3.36
P65702 PGK_SALTY Phohoglycerate kinase	11		LTVLDSLK	197	9	9	58.63	b2°b2y1y2y4y5y7y8y9	975.56	61.546	70345	2	488.28	-10.01
P65702 PGK_SALTY Phohoglycerate kinase	12		TILWNGPVGVFEPNFRK	302	18	9	76.37	b2y5y6y10y13y14y15y16y 18	2121.11	96.376	50292	3	707.71	-8.98

P65702 PGK_SALTY Phohoglycerate kinase	13		MTDLDLAGKR	5	10	7	72.53	y2y3y4y5y7y9y10	1119.58	42.137	44014	2	560.29	-3.27
P65702 PGK_SALTY Phohoglycerate kinase	14	Carbamidomethyl+C(5)	YAAALCDVFVMDAFGTAHR	128	18	14	107.26	b2b3b5b7b9y1y4y5y6y7y9y12y13y18	2043.94	89.695	30654	3	681.98	-2.69
P65702 PGK_SALTY Phohoglycerate kinase	15		IADQLIVGGGIANTFVAAQGHSVGK	206	25	10	56.59	b3b4b5y2y11*y11y13*y13y14y18	2423.29	77.933	30086	3	808.44	-5.44
P65702 PGK_SALTY Phohoglycerate kinase	16		DYLDGVDVAEGELVVLENVR	93	20	6	20.59	b10b19y1y7y16y20	2204.13	115.288	13944	3	735.38	8.09
P65702 PGK_SALTY Phohoglycerate kinase	17		SVNDVK	272	6	2	27.43	b4b5	661.35	28.068	40716	1	661.35	-9.51
P65702 PGK_SALTY Phohoglycerate kinase	18		SLYEADLVDEAK	231	12	5	33.23	b5°b5b7y3y8	1352.66	58.081	14830	2	676.83	0.99
P65702 PGK_SALTY Phohoglycerate kinase	19		ADLNVPVK	19	8	4	36.94	b7°b7y3y7	855.49	42.301	12292	2	428.25	-8.85
P65702 PGK_SALTY Phohoglycerate kinase	20		ISYISTGGGAFLEFVEGK	355	18	5	33.93	b3b4b12y8y11	1874.91	47.814	2309	3	625.64	-22.01
P65702 PGK_SALTY Phohoglycerate kinase	21		VMVTSHLGRPTEGEYNEEFSLLPV VNYLKDK	53	31	6	22.35	b6b12°b12b13°b13y27	3564.79	95.699	22644	4	891.95	-3.97
P65702 PGK_SALTY Phohoglycerate kinase	22	Carbamidomethyl+C(6)	RLLTTCDIPVPTDVR	243	15	3	24.81	b7b8y7	1755.92	64.002	6180	3	585.98	-13.07
P65702 PGK_SALTY Phohoglycerate kinase	23	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGKALK	156	23	3	35.33	b12b13b14	2314.25	123.993	4931	3	772.09	0.21
P65702 PGK_SALTY Phohoglycerate kinase	24		EPARPMVAIVGGSKVSTK	179	18	3	23.31	b4b6b16	1827.02	84.951	1624	2	914.01	2.61
P65702 PGK_SALTY Phohoglycerate kinase	25		DLDLAGKR	7	8	1	8.42	b3	887.50	42.123	24279	2	444.25	6.05
P65702 PGK_SALTY Phohoglycerate kinase	26		TDLDLAGKR	6	9	1	8.42	b4	988.54	42.135	18320	2	494.77	-6.54
P52616 FLJB_SALTY Phase 2 flagellin	1		AQILQQAGTSVLAQANQVPQNVLSLLR	479	27	38	267.02	b2*b2b3b4*b4b5*b5b6*b6b7*b7b10*b10b11°b11b12b14b15b17b18*b18y1y2y3y4y5y6y7y9y10y11y12*y12y13*y13y14y24y27	2860.61	105.086	126197	3	954.21	2.48
P52616 FLJB_SALTY Phase 2 flagellin	2		SQSALGTAIER	20	11	8	51.6	b2*b2y4y6y7y9°y9y11	1132.59	41.699	71454	2	566.80	-7.33
P52616 FLJB_SALTY Phase 2 flagellin	3		AQVINTNSLSLLTQNNLNK	1	19	14	59.59	b1b2*b2b3b4y1y2y6*y6y7y10y13y15y19	2085.14	74.610	57331	2	1043.07	3.16
P52616 FLJB_SALTY Phase 2 flagellin	4		VSGQTQFNGVK	125	11	8	32.05	b2°b2y7*y7y9y10*y10y11	1164.59	32.949	54296	2	582.80	-6.71
P52616 FLJB_SALTY Phase 2 flagellin	5		NANDGISIAQTTEGALNEINNLR	66	25	12	23.73	b1*b1b2b4b6*b6y2y3y6*y6y9y25	2670.33	86.488	50961	2	1335.67	9.78
P52616 FLJB_SALTY Phase 2 flagellin	6		INSAKDDAAGQAIANR	37	16	14	112.1	b6b10y1y3*y3y4y5y7*y7y8y9y10y11y16	1614.80	29.767	44732	3	538.94	-14.36
P52616 FLJB_SALTY Phase 2 flagellin	7		SDLGAVQNR	434	9	8	31.3	b1b4°b4b7°b7*b7y8y9	959.50	36.360	19265	2	480.25	6.36
P52616 FLJB_SALTY Phase 2 flagellin	8		AQPELAEEAAK	403	11	6	25.06	b3b8°b8*b8y1y7	1098.59	36.439	11455	2	549.80	14.33
P52616 FLJB_SALTY Phase 2 flagellin	9		DTPAVVSADAK	288	11	4	25.06	b3b6y2y3	1073.54	26.817	2683	2	537.27	-6.14
P52616 FLJB_SALTY Phase 2 flagellin	10		FNSAITNLGNTVNNLSEAR	443	19	5	26.72	b4°b4b11b12y11	2035.01	74.411	2233	2	1018.01	-5.64
P52616 FLJB_SALTY Phase 2 flagellin	11		TTMPAGATTK	271	10	4	27.7	b4b9°b9y5	978.49	35.487	14005	2	489.75	-4.24
P52616 FLJB_SALTY Phase 2 flagellin	12		FTANIK	53	6	1	13.9	y3	693.38	33.376	11892	2	347.20	-13.38
P52616 FLJB_SALTY Phase 2 flagellin	13		TAANQLGGVDGK	369	12	5	38.3	b4*b4y3y5y8	1130.60	50.384	5686	2	565.80	18.90

P52616 FLJB_SALTY Phase 2 flagellin	14		AYANNGTTLDVSLDDAAIK	189	20	3	21.68	b3b10b13	2009.02	75.680	4794	3	670.34	18.90
P52616 FLJB_SALTY Phase 2 flagellin	15		IDAALAQVDALR	422	12	4	30.21	b3°b3b9b10	1255.69	103.582	4128	2	628.35	-11.47
P52616 FLJB_SALTY Phase 2 flagellin	16		AYDVK	177	5	4	40.58	b3b4y4°y4	595.30	32.454	3492	1	595.30	-12.30
P52616 FLJB_SALTY Phase 2 flagellin	17		YFVTIGGFTGADAAK	234	15	6	44.38	b4°b4b7b10y11y12	1517.74	47.884	2456	2	759.37	-15.60
P52616 FLJB_SALTY Phase 2 flagellin	18		AATGGTNGTASVTGGAVKFDAD NNK	209	25	7	23.73	b11b20b24y4*y4y13°y13	2324.11	96.597	210318	2	1162.56	-2.73
P52616 FLJB_SALTY Phase 2 flagellin	19		AYANNGTTLDVSGLDAAIKAAT GGTNGTASVTGGAVK	189	38	3	10.89	b11y19y33	3509.76	107.344	33724	4	878.19	5.70
P52616 FLJB_SALTY Phase 2 flagellin	20		TEVVTIDGKTYNASK	381	15	4	32.78	b6b7y5y8	1625.83	70.194	9255	2	813.42	-6.16
P52616 FLJB_SALTY Phase 2 flagellin	21		AAGHDFKAQPELAEAAAK	396	18	3	16.15	b4y7y11	1824.95	48.643	6752	3	608.99	14.05
P52616 FLJB_SALTY Phase 2 flagellin	22		VLAQDNTLTIQVGANDGETIDIDL KQINSQTLGLDSLNVQK	136	41	4	25.55	b5b7b15b16	4395.23	113.177	4298	3	1465.75	-13.11
P52616 FLJB_SALTY Phase 2 flagellin	23		AGDKYYAADYDEATGAIK	337	18	7	68.59	b3b5°b5b6b7b8b9	1921.88	119.177	3013	2	961.44	-3.18
P52616 FLJB_SALTY Phase 2 flagellin	24		FDADNNKYFVTIGGFTGADAAK	227	22	3	13.9	b13y6y8	2322.13	80.515	2019	3	774.71	11.04
P52616 FLJB_SALTY Phase 2 flagellin	25		TAANQLGGVDGKTEVVTIDGK	369	21	3	14.36	b13y3y14	2073.08	84.406	1552	3	691.70	-2.24
P52616 FLJB_SALTY Phase 2 flagellin	26	Phosphoryl STY(11)	NALIAGGV DATDANGAELVK	299	20	6	29.14	b5b9°b9y6y9y15	1978.92	78.926	2915	2	989.96	-8.82
P52616 FLJB_SALTY Phase 2 flagellin	27	Phosphoryl STY(6)	QINSQTLGLDSLNVQK	161	16	5	25.19	b5°b5b9_H3PO4 b9y9y12_H3PO4 y12	1837.88	71.303	1830	3	613.30	-11.29
P52616 FLJB_SALTY Phase 2 flagellin	28	Phosphoryl STY(11)	FNSAITNLGNTVNNLSEAR	443	19	5	32.44	b3_H3PO4 b3°b3b4b10b12_H3PO4 b12	2114.98	59.685	1643	3	705.67	2.31
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	25	159.48	b1b2°b2b3°b3b4°b4b5b13* b13b19y3y4°y4y6y9y11°y1 1*y11y12y13y15y16y17y1 9	2130.16	92.210	301070	3	710.72	-7.68
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		MVAPVDGTIGK	59	11	17	126.74	b2b3b4b6°b6y2y3y5°y5y6y 7y8°y8y9°y9y10y11	1087.57	46.003	189762	2	544.29	-11.67
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		VGDPVIEFDLPLEEK	115	16	20	189.28	b3b4b5°b5b6b7°b7b8°b8b1 0b12b15y3°y3y6y9y10y11y 13y16	1812.97	99.363	133814	2	906.99	2.56
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		LSGSVTVGETPVIR	152	14	7	48.11	b7b10y1y7y8y9y14	1414.78	55.421	62144	2	707.90	-4.83
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		STLTPVVISNMDEIK	133	15	5	24.81	b1b4y2y11y12	1646.87	72.841	19490	2	823.94	0.96
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		DTGTIEIVAPLSGEIVNIEDVPDVV FAEK	16	29	4	15.1	b4b8y4y8	3069.61	111.136	11813	3	1023.87	7.24
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		IVGDGIAIKPTGNK	45	14	19	129.12	b5°b5y3y4°y4y5°y5°y5y6y 7y8°y8*y8y10y12°y12*y12 y13°y13	1382.77	43.334	175609	3	461.60	-20.48
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		IAEEGQR	106	7	5	41.34	b3°b3b5y6°y6	802.40	36.855	3710	2	401.70	-8.75
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9		VKVGDPVIEFDLPLEEK	113	18	19	170.79	b5°b5b6b7b8b9b11b12y3° y3y4°y4y6y7y8°y8y9y10y1 3	2040.10	94.818	127137	3	680.71	-10.83

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	10		PVDGTIGK	62	8	4	48.59	b3b4b5b7	786.43	46.005	3838	1	786.43	-5.59
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	11		STLTPVVISNMDEIKELIK	133	19	0	5.28		2112.15	92.202	3447	3	704.72	-5.43
P0A1E3 CYSK_SALTY Cysteine synthase A	1		LTLTMPETMSIER	87	13	18	108.53	b2°b2b5°b5b12y1y2°y2y4°y4y6y7y8y9°y9y10y11y13	1521.77	73.764	139645	2	761.39	0.80
P0A1E3 CYSK_SALTY Cysteine synthase A	2		YLLLQQFSNPANPEIHEK	137	18	16	150.42	b2b3b4y3y4y6y7y9y10°y10y11y12y15°y15y16y18	2141.08	73.628	125431	3	714.36	-10.83
P0A1E3 CYSK_SALTY Cysteine synthase A	3		IQGIGAGFIPGNLDLK	226	16	19	132.16	b2°b2b3b4b6b8b9b14y2y3y7°y7°y7y8y10y12y14°y14y16	1612.91	83.180	118289	2	806.96	2.42
P0A1E3 CYSK_SALTY Cysteine synthase A	4		YLSTALFADLFTEKELQQ	305	18	24	149.48	b2b5b11b13°b13b15b16y2°y2y3°y3y4°y4y5y7°y7y9y10°y10y11y12°y12y13y18	2117.10	101.945	93842	2	1059.05	7.50
P0A1E3 CYSK_SALTY Cysteine synthase A	5		GVLKPGVELVEPTSGNTGIALAYV AAAR	56	28	16	136.68	b2b3b11y3y4y5y6y7y8y9y11y13y14y17y18y28	2753.52	81.107	86847	3	918.51	-1.06
P0A1E3 CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	12	113.59	b2b3°b3b4b5b6y6y7y8y9y10y12	1283.73	63.672	73305	2	642.37	-3.42
P0A1E3 CYSK_SALTY Cysteine synthase A	7		IYEDNSLTIGHTPLVR	3	16	11	81.06	b2y2y4y7y8y9y11y14°y14y15y16	1827.94	61.266	63760	3	609.98	-12.15
P0A1E3 CYSK_SALTY Cysteine synthase A	8		ALGANLVLTEGAK	105	13	12	63.97	b2b5°b5b12y1y2y5y7y9°y9y11y13	1256.72	61.021	28361	2	628.87	3.01
P0A1E3 CYSK_SALTY Cysteine synthase A	9		VVGITNEEAISTAR	246	14	12	108.33	b3b4y2y4y5y6y7y9°y9y10y12y14	1459.77	49.368	22800	2	730.39	-2.26
P0A1E3 CYSK_SALTY Cysteine synthase A	10		YLSTALFADLFTEK	305	14	12	76.62	b2b5°b5b7°b7y9y10°y10y11y12y13y14	1618.85	102.832	22456	2	809.93	5.66
P0A1E3 CYSK_SALTY Cysteine synthase A	11		IGANMIWDAEK	44	11	8	37.8	b1b5y1y2°y2y5y6y10	1247.61	65.075	19877	2	624.31	-0.20
P0A1E3 CYSK_SALTY Cysteine synthase A	12		IGANMIWDAEKR	44	12	5	35.29	b6y7y8y10y12	1403.69	62.942	15477	2	702.35	-11.04
P0A1E3 CYSK_SALTY Cysteine synthase A	13		NPSFSVK	35	7	5	41.34	b3°b3°b3y3y6	778.40	36.871	42567	2	389.70	-16.62
P0A1E3 CYSK_SALTY Cysteine synthase A	14		TDLITVAVEPTDSPVIAQALAGEEI KPGPHK	195	31	4	22.35	b3b4b10y5	3196.69	84.686	38373	4	799.93	-6.87
P0A1E3 CYSK_SALTY Cysteine synthase A	15		AEEIVASDPQK	126	11	7	89.17	b4y4y5y6y7y8y9	1186.59	31.369	3017	1	1186.59	-2.47
P0A1E3 CYSK_SALTY Cysteine synthase A	16		GKTDLITVAVEPTDSPVIAQALAGEEIKPGPHK	193	33	14	87.37	b6b7°b7b9b11y3y4y5y10y11y13y15y18y22	3381.80	79.364	122982	4	846.21	-7.72
P0A1E3 CYSK_SALTY Cysteine synthase A	17		LIDKVVGITNEEAISTAR	242	18	11	82.22	b6b8y4y6y7°y7y8y10y12°y12y13	1929.05	59.197	60641	3	643.69	-8.92
P0A1E3 CYSK_SALTY Cysteine synthase A	18		SKIYEDNSLTIGHTPLVR	1	18	3	23.55	b9y4y5	2043.08	57.405	44251	3	681.70	-5.38
P0A1E3 CYSK_SALTY Cysteine synthase A	19		AEEIVASDPQKYLLLQQFSNPANPEIHEK	126	29	7	48.04	b6y3y6y8y9y10y12	3308.66	76.887	26235	4	827.92	-6.05
P0A1E3 CYSK_SALTY Cysteine synthase A	20		GAIQKAEEIVASDPQK	121	16	5	36.01	b6b9y3y7y10	1683.89	55.165	19749	2	842.45	1.23
P0A1E3 CYSK_SALTY Cysteine synthase A	21		VVGITNEEAISTARR	246	15	3	18.79	b7y3y9	1615.87	54.595	14879	3	539.29	-5.89
P0A1E3 CYSK_SALTY Cysteine synthase A	22		LQEDESFTNKNIVVILPSSGER	283	22	6	36.4	b4b10y3y5y6y8	2475.26	69.304	10635	3	825.76	-4.04
P0A1E3 CYSK_SALTY Cysteine synthase A	23		IGANMIWDAEKR	44	12	3	26.99	b10y5y6	1403.70	66.359	9988	2	702.36	-4.44

[P0A1E3]CYSK_SALTY Cysteine synthase A	24		GYKLTLTMPETMSIER	84	16	3	17.79	b14y6y9	1869.97	97.046	6624	3	623.99	13.58
[P0A1E3]CYSK_SALTY Cysteine synthase A	25		LMEEEGILAGISSGAAVAALKLQ EDESFTNK	261	32	8	42.5	b4b8b10b11b12y10y12°y12	3292.61	106.014	1928	3	1098.21	-14.46
[P0A1E3]CYSK_SALTY Cysteine synthase A	26	Phosphoryl STY(5)	VVGITNEEAISTARR	246	15	3	26.87	b3b5b10	1695.83	52.282	23104	3	565.95	-1.30
[P0A1E3]CYSK_SALTY Cysteine synthase A	27	Phosphoryl STY(12)	IYEDNSLTIGHTPLVR	3	16	5	28.6	b7b11b13_HPO3 b13y13*y13	1907.93	91.437	1871	2	954.47	6.46
[P0A1E3]CYSK_SALTY Cysteine synthase A	28	Oxidation+M(9)	LTLTMPETMSIERR	87	14	3	25.4	b5y10y11	1693.88	90.840	1879	2	847.44	10.38
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	1		TQFMGPEGVANVSLSNIAGESAE GLLVTKPK	240	31	25	151.72	b2b3b4b5°b5°b5b10*b10b12b15y2y4y5y6y8y13y14y19°y19y22y26y27y28y29y31	3144.63	88.284	270142	3	1048.88	2.95
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	2	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILM ITPAATAPELTAR	92	38	24	172.9	b2b5b7b10b11°b11b12°b12b14b23b24b25b26b27y4y6y7y8y10y11y12y13y15y38	4078.01	89.169	240855	3	1360.01	7.30
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	3		ENIDFVYYGGYHPEMGQILR	212	20	17	143.21	b2°b2b6°b6°b6y3y5y6y8y10y12y13y14y15y16y17y20	2401.12	79.702	140407	3	801.04	-3.97
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	4		TTGLDSQDGPTAAK	137	14	30	233.36	b1°b1b2°b2b3°b3b5°b5b7b8b10b11b12°b12b13°b13y1y3y5y6y8y9y10°y10°y10y11y12*y12y13y14	1361.65	29.253	137065	2	681.33	-3.14
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	5		VAVVGAMSGPVAQYGDQEFTGA EQAIADINAK	25	32	20	129.73	b3b6b9b11b16b26y2y3*y3y5y6°y6y7y8y11y12°y12y13y14y32	3207.59	89.802	136286	3	1069.87	7.31
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	6		QQYGEGLAR	168	9	14	63.12	b2°b2b3°b3b9y1y2y4y5°y5y6°y6y7y9	1021.50	32.512	116187	2	511.25	-8.90
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	7		GGVNVVFFDGITAGEKDFSTLVAR	185	24	18	147	b4°b4b5°b5b6b7b14b15y2y3y4y7y8y12y13y18y19y24	2499.28	101.354	101634	3	833.76	-3.81
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	8		IAIHDK	161	7	6	41.34	y2y3°y3y5y6y7	809.48	32.088	27832	2	405.24	-11.46
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	9		GATVDTVMGPLSWDEK	326	16	7	53.06	b3b4b8b12°b12y10y11	1705.82	78.036	16357	2	853.42	7.51
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	10		GFEFGVFDWHANGTATDAK	346	19	5	47.35	y3y5y7y8y9	2069.92	89.101	3663	3	690.64	-8.26
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	11		NYDQVPANKPIVDAIK	271	16	12	96.38	b3°b3b5b8b9y3y4y5y7y10y11°y11	1784.92	53.416	260852	3	595.65	-16.55
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	12	Carbamidomethyl+C(6)	TLLAGCIALSLSHMAFADDIK	4	21	4	14.36	b8°b8y13y18	2247.14	67.278	6736	3	749.72	-3.15
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	13		GGVNVVFFDGITAGEK	185	16	3	25.49	b4b12b14	1609.79	68.858	1973	3	537.27	-19.87
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	14		KQDPSGAFVWTTYAALQSLQAGL NHSDDPAEIAK	289	34	45	340.15	b3°b3b6b7°b7°b7b8°b8b9b10b11°b11°b11b12°b12b13°b13b14b15y3y6y9°y9y10y11y12y13°y13°y13y14°y14y15°y15°y15y16y17y18*y18y19y20°y20y21y22y24y25	3629.77	101.997	352014	4	908.20	-4.98
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	15		GDLKGFEFGVFDWHANGTATDAK	342	23	3	22.51	b10b11y3	2483.16	81.934	3615	3	828.39	-1.28
[P17215]LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	16		YLKGATVDTVMGPLSWDEK	323	19	4	15.48	b13°b13y7y16	2110.04	96.533	2314	3	704.02	-4.98

P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	17	Carbamidomethyl+C(6); Oxidation+M(14)	TLLAGCIALSLSHMAFADDIK	4	21	3	14.36	b8y7y18	2263.15	59.069	3006	3	755.06	2.16
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	18		QQYGEGLAR	168	9	1	9.02	y3	1003.49	32.533	11576	2	502.25	-5.23
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTASPYASYLQYGHIANIDD IIAGKKPATDLGVK	125	38	27	144.88	b2b3b5b6°b6b8°b8°b8b9°b9b10°b10b20y1y2y3y4y8y9y11y12y22y23y27y30y31y38	4001.01	82.892	229426	5	801.01	-13.42
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		AEQQLDKDSAIVPVYYVYNAR	494	21	13	84.92	b5b7b8b11b12°b12y4y5y7°y7y9y10y21	2442.21	72.626	131256	3	814.74	-7.90
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3	Carbamidomethyl+C(4)	AGWCADYNEPTSLNTMLSDSSN NTAHYK	439	29	11	57.82	b4y2y10°y10y11y13y14y15y22y24y29	3294.43	89.896	122771	3	1098.81	5.63
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4		WSDGTPVTAHDFVYSWQR	107	18	20	180.76	b2°b2y3°y3y4y5°y5y6y7y8°y8y9y10y11y12y13y16y17y18°y18	2151.97	71.751	105151	3	718.00	-7.49
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		LVEPEWFK	352	8	10	82.29	b2b3b7y2y3y5y6°y6y7y8	1047.54	70.614	94532	2	524.28	-7.57
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		ALDDHTFEVTLSEPVPYFYK	163	20	16	105.47	b5b6b7b9b10°b10b13°b13y2y4y5y7y8y9°y9y20	2371.14	85.717	92018	3	791.05	-3.71
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7		TVINQVTYLPISSEVTDVNR	241	20	27	214.42	b1b2b5b8°b8b9b10b12y1y2y3°y3y4y5y6y7y8°y8y9y11°y11y12y13y14y15y18y20	2248.20	76.953	83840	2	1124.60	8.25
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		LVKPWVGGYTGKDPLDNIYVK	515	21	8	54.23	b2y1y3y5y6y8y9y18	2362.28	72.337	72429	3	788.10	-0.62
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9		SGEIDMTYNNMPIELFQK	263	18	11	42.31	b2b3b13y2y3y5y10y11°y11°y11y18	2130.01	86.450	69489	2	1065.51	9.17
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		NQGDLPAYSYPYTDGAK	333	19	11	49.42	b1°b1b4y2y8y9y11y12°y12y14y19	2057.96	59.042	60562	2	1029.48	7.83
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	12	47.75	b3b7b8°b8y1y2y3y4y15y17y22y29	3091.56	88.176	60260	3	1031.19	6.08
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		LLAEAGFTADKPLTFDLLYNTSDL HKK	372	27	7	37.17	b2b4y1y8y9y10y12	3021.57	83.255	48467	4	756.15	-6.79
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	13		NLGVNVNLENQEWK	410	14	12	82.37	b6b7b9y7°y7y8°y8y10y11y12°y12y14	1656.84	66.346	45479	2	828.92	2.21
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	14		HQGTFDVAR	430	9	9	66.13	b2b6y2y3y4y7y8°y8y9	1030.50	30.778	44440	2	515.75	-6.52
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	15		DLFEGLLISDVEGHPSPGVAEK	67	22	6	21.64	b2b12y8y11y15y22	2309.16	89.001	25475	3	770.39	-2.43
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	16		LIADTLK	474	7	6	54.86	y2y3y4y5y6y7	773.47	43.082	21113	2	387.24	-13.41
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	17	Carbamidomethyl+C(6)	VDPYLCTYYYEINNQK	291	16	5	29.27	b1b5y6y7y9	2082.97	70.470	10632	2	1041.99	8.56

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	18		WTQPANIVTNGAYK	204	14	5	25.4	b1b13*b13y5y6	1562.81	82.139	2896	2	781.91	6.87
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	19		IEGVPESNVSR	56	11	3	25.06	b3y5y7	1186.62	72.276	22227	2	593.81	11.52
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	20		DIIVNK	325	6	1	13.9	y3	701.41	55.080	12718	1	701.41	-10.27
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	21		SLIAAGILTALIAASAATAADVPAG VQLADK	7	31	4	22.35	b15b18b19y16	2863.59	136.705	2248	3	955.20	-6.82
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	22		DSAIVPVYYYVNAR	501	14	7	52.09	b5b7b8y5y7y8*y8	1629.84	106.021	1500	2	815.42	6.89
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	23		FGDKWTQPANIVTNGAYK	200	18	16	92.36	b5°b5b7°b7b8b10°b10°b10°y4y5y6y7y9*y9y11*y11	2010.00	62.284	87754	3	670.67	-5.71
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	24		NNGSEVQSLDPHKIEGVPESNVSR	43	24	10	73.09	b4b5b9b10°b10b11y5y11y14y22	2592.23	50.963	83868	4	648.81	-12.90
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	25	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYYEINNQK	284	23	8	51.5	b7b9b15y4y8y9y11y21	2920.39	75.858	45948	3	974.14	3.01
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	26		NPQYWDNAKTVINQVTYLPISSEV TDVNR	232	29	4	11.8	b12b22°b22y8	3364.70	101.329	28042	3	1122.24	6.75
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	27		TVINQVTYLPISSEVTDVNRYSR	241	22	3	20.41	y13y16y19	2567.35	76.760	20320	3	856.45	1.24
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	28	Carbamidomethyl+C(6)	VDPYLCTYYYYEINNQKAPFNDVR	291	23	4	13.48	b5°b5y5y13	2882.35	76.040	17359	3	961.45	-0.08
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	29		LKNWVVNER	218	9	4	31.3	b6y6y7°y7	1157.63	43.408	11790	2	579.32	-7.59
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	30		DLFEGLLISDVEGHSPGVAEKWE NK	67	26	7	49.82	b3b4y6y8y9y11y25	2866.44	99.383	8029	3	956.15	5.79
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	31		LVEPEWFKWSQQK	352	13	7	47.43	b7b10b11°b11y4y5°y5	1704.86	72.341	2160	2	852.93	-10.53
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	32	Phosphoryl STY(21)	LLAEAGFTADKPLTFDLLYNTSDL HKK	372	27	4	23.19	b11y3y6y7	3101.57	136.539	2971	2	1551.29	5.04
P02910 HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTQTETFGNEHWAPK	135	20	16	135.73	b1b2b4b5y3y4y5y6y8y9y10°y10y11y12y19y20	2199.07	63.040	148780	3	733.70	-4.77
P02910 HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	16	129.26	b2b4y3°y3y5°y5y6°y6y7y8y9y10y11°y11y12y13	1425.69	55.303	127569	2	713.35	-1.71
P02910 HISJ_SALTY Histidine-binding periplasmic protein	3		NSDIQPTVASLK	120	12	19	131.89	b2°b2°b2b3°b3°b3b4b5b6y3y4y5y8°y8°y8y9y10*y10y12	1272.67	47.956	104647	2	636.84	-6.81
P02910 HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	18	122.31	b3°b3b10b15b16°b16y1y2y3y4°y4y5y6y7y9y10y11y20	2273.21	103.489	87660	2	1137.11	10.10
P02910 HISJ_SALTY Histidine-binding periplasmic protein	5		NAQGELVGFDIDLAK	42	15	8	26.76	b7°b7°b7b10y1y8y12y15	1589.82	79.057	63362	2	795.42	4.22

P02910 HISJ_SALTY Histidine-binding periplasmic protein	6		LFGVGTGMGLR	211	11	6	28.07	b2b3y2y9y10y11	1107.59	71.737	59594	2	554.30	-9.59
P02910 HISJ_SALTY Histidine-binding periplasmic protein	7		FGGPAVKDEK	201	10	17	140.17	b2b3b6b8°b8b9y1y2°y2y3y4°y4y5y7y8y9y10	1047.54	26.139	41452	2	524.27	-5.48
P02910 HISJ_SALTY Histidine-binding periplasmic protein	8		IDAIMSSLSITEKR	85	14	5	56.26	b3b6b7b8b12	1563.83	98.796	23126	2	782.42	-7.34
P02910 HISJ_SALTY Histidine-binding periplasmic protein	9	Carbamidomethyl+C(18)	NAQGELVGFDIDLAKELCK	42	19	8	47.35	b1b6b10b11b13°b13b14y19	2120.07	104.561	8489	2	1060.54	2.42
P02910 HISJ_SALTY Histidine-binding periplasmic protein	10		GIEIVSYQGQDNIYSDLTAGR	155	21	4	22.49	b13y3y7y14	2299.15	78.609	15862	2	1150.08	11.47
P02910 HISJ_SALTY Histidine-binding periplasmic protein	11		AFAEMR	234	6	1	13.9	y5	724.34	35.473	3016	2	362.67	-11.54
P02910 HISJ_SALTY Histidine-binding periplasmic protein	12		IDAAFQDEVAASEGFLKQPVGK	176	22	7	44.14	b4b5b9b13y4y18y20	2320.17	77.915	67226	3	774.06	-5.37
P02910 HISJ_SALTY Histidine-binding periplasmic protein	13	Carbamidomethyl+C(18)	NAQGELVGFDIDLAKELCK	42	19	4	24.5	b3y3y11y13	2120.06	85.954	14914	3	707.36	-3.92
P02910 HISJ_SALTY Histidine-binding periplasmic protein	14		RVGVLQGTQTQETFGNEHWAPK	134	21	5	39.7	b4b5b6b17y10	2355.15	57.731	13996	4	589.54	-14.51
P02910 HISJ_SALTY Histidine-binding periplasmic protein	15		DEKLFGVGTGMGLR	208	14	5	32.52	b4°b4b7b13y10	1479.74	70.390	5156	2	740.38	-11.96
P02910 HISJ_SALTY Histidine-binding periplasmic protein	16		EALNKAFAMR	229	11	6	54.34	b9y6y8°y8y9y10	1279.63	80.594	3816	2	640.32	-9.16
P02910 HISJ_SALTY Histidine-binding periplasmic protein	17	Oxidation+M(8)	LFGVGTGMGLR	211	11	3	28.07	b7b8y9	1123.59	42.048	6428	2	562.30	-3.37
P02910 HISJ_SALTY Histidine-binding periplasmic protein	18		GGPAVKDEK	202	9	5	52.98	b3b4b5b7°b7	900.47	26.139	15248	2	450.74	-6.98
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	1		TLWFYNPFVEQATATWLK	85	18	24	157.93	b2b3°b3b4°b4b5°b5b6°b6°b6b8y1y2y3y4y5y6y7y9°y9y12y13y14y18	2215.14	115.603	41613	2	1108.07	6.72
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	2		DATGNTPFMLIAR	103	13	7	46.85	b3y3y4y7y10y13*y13	1406.71	78.239	34494	2	703.86	-1.91
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	3		QFTINVGR	146	8	9	50.47	b2°b2b7°b7y4*y4y5y6y8	934.50	53.163	33859	2	467.75	-10.06
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	4		VSSFHATFTQK	33	11	6	25.06	b5b10y1y9°y9y11	1252.61	40.496	21106	3	418.21	-14.42
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	5		VTDGSGAAVQEGQGDLWVK	44	19	5	24.66	b1y9y10y12y19	1916.95	56.976	18245	2	958.98	7.96
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	6		RPNLFNWHMTQPDESILVSDGK	63	22	9	61.65	b8b9b11b13y2y4y5y6y11	2584.26	76.346	12174	3	862.09	1.04
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	7		VTDGSGAAVQEGQGDLWVKRPNLFNWHMTQPDESILVSDGK	44	41	6	15.7	b8b10°b10b14y3y13	4482.19	92.601	2741	3	1494.74	3.38
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	8	Carbamidomethyl+C(5)	MAIACALLSSVVASSVWADAASSLK	3	25	3	23.27	b8b9b12	2508.32	74.092	4302	2	1254.67	15.87
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	9		NQASDWQQYNIKQDGDNFVLTPK	116	23	5	29.55	y3y12°y12y20y21	2709.29	67.677	39712	3	903.77	-1.17
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	10		ASNGNLKQFTINVGR	139	15	3	18.79	b10y3y7	1618.87	52.717	2736	2	809.94	4.52

Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	11		SQQNGAVDPSKFTFTPPQGVTTIDDQR	176	26	5	23.16	b3b4°b4b9°b9	2833.40	86.583	1718	2	1417.20	8.19
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	12		SAYQLKSQQNGAVDPSK	170	17	11	55.66	b3b4°b4*b4b6°b6y3y6y7°y7y9	1820.94	38.338	1596	3	607.65	12.40
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	13	Phosphoryl STY(10)	FTFTPPQGVTTIDDQRK	187	16	3	17.79	b9y8y10	1929.91	72.371	42164	3	643.97	3.48
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	14	Oxidation+M(27)	TLWFYNPFVEQATATWLKDATGNTPFMLIAR	85	31	4	35.97	b5b6b7y12	3618.86	130.779	3335	3	1206.96	13.63
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	15	Oxidation+M(9)	RPNLFNWHMTQPDESILVSDGK	63	22	3	13.9	b3b11y13	2600.29	110.340	1692	3	867.44	14.18
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	16		SSFHATFTQK	34	10	0	2.26		1153.56	40.496	5846	2	577.28	-6.46
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		VANLGSLGDQVNVK	8	14	24	178	b1b2b3b5°b5b6b12b13°b13*b13b14y2y3y4y6y7°y7y8y9y10°y10y11y12y14	1413.76	56.501	122675	2	707.39	-4.75
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		MQVILLDK	0	8	8	68.77	b2°b2b3b5y4y5y6y8	959.55	63.795	91889	2	480.28	-14.18
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		DIADAVTAAGVDVAK	97	15	11	118.71	b2b6b8y3y4y6y7y9y10y11y13	1415.74	65.944	70279	2	708.37	0.17
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		INALETVTIASK	71	12	5	26.99	b2b3b4y5y12	1259.72	60.847	61057	2	630.36	-3.49
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		NVEYFEAR	42	8	8	41.71	b2°b2y2y4y5y6°y6y8	1027.48	46.195	53120	2	514.24	-5.47
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		NVEYFEARR	42	9	5	31.3	b1b8y4y6y9	1183.57	51.799	7907	2	592.29	-13.41
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		TTGEHEVNFQVHSEVFAK	123	18	3	25.07	b7b8b10	2058.97	72.849	3306	2	1029.99	-6.64
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		LADVLAAANAR	57	11	4	36.37	b4b7y4y10	1084.60	53.035	4172	1	1084.60	-13.06
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	9		LADVLAAANARA EK	57	14	3	25.4	b3b4y6	1412.77	59.333	7260	2	706.89	-12.70
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	10		DIADAVTAAGVDVAKSEVR	97	19	3	35.07	b5b6b7	1886.96	74.544	5088	3	629.66	-11.71
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	11		LFGSIGTRDIADAVTAAGVDVAK	89	23	4	22.51	b4b5°b5y14	2247.19	94.864	3657	3	749.74	-2.50
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	12		NVEYFEARR	42	9	5	46.08	b3°b3b4y3y7	1183.57	62.366	2088	2	592.29	-14.13
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	13	Phosphoryl STY(8)	INALETVTIASK	71	12	3	23.01	b3y4y6_H3PO4 y6	1339.69	28.657	6319	2	670.35	10.84
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	14	Phosphoryl STY(6)	VANLGSLGDQVNVK	8	14	4	25.4	b5°b5y10y11	1493.74	81.575	2546	2	747.37	7.93
P67091 UF_SALTY Universal stress protein F	1		TILVPIDISDSELTQR	3	16	17	138.18	b2b3b4y2y3y4y6°y6y8y9y11°y11y12°y12y13y14y16	1799.98	81.903	143220	2	900.49	1.49
P67091 UF_SALTY Universal stress protein F	2	Carbamidomethyl+ C(4)	HAECSVLVVR	134	10	14	110.1	b2b3°b3b4b7b9b10y2y3y4y8°y8y9y10	1169.60	40.794	61581	2	585.30	-7.51
P67091 UF_SALTY Universal stress protein F	3		SQLEAIKK	69	9	12	63.12	b2°b2*b2b3°b3°b3y2y3y4y5y7y9	1029.62	44.005	44103	2	515.32	-6.05
P67091 UF_SALTY Universal stress protein F	4		VISHVEAEAK	19	10	15	118.86	b2b6b7b8y1y2y3°y3y4y5°y5y6y7y8y10	1082.58	23.529	40806	2	541.79	-5.86
P67091 UF_SALTY Universal stress protein F	5		VQAHVAEGSPK	85	11	11	89.17	b5y2y4°y4y5y6°y6y7y8y9y11	1122.58	18.279	10814	2	561.79	-11.74

P67091 UF_SALTY Universal stress protein F	6		VHFLTVPISLPYYASLGLAYSaelPAMDDLK	34	31	4	17.33	y6y9°y9y11	3394.80	125.921	2620	3	1132.27	9.06
P67091 UF_SALTY Universal stress protein F	7		SQLEAIIK	69	8	6	50.47	b3°b3b5b6°b6y4	901.52	53.229	22626	2	451.27	-13.40
P67091 UF_SALTY Universal stress protein F	8		ILEMAK	98	6	1	13.9	y4	704.40	37.762	12319	1	704.40	-8.23
P67091 UF_SALTY Universal stress protein F	9		LPADMVIIASHRPDITTYLLGSNAaAVVR	105	29	3	11.8	b6y5y9	3064.63	88.809	7107	4	766.91	-10.99
P67091 UF_SALTY Universal stress protein F	10		VHFLTVPISLPYYASLGLAYSaelPAMDDLKAEAK	34	35	8	37.79	b3b6°b6b7y4y10y11y14	3793.97	111.071	48587	4	949.25	-2.12
P67091 UF_SALTY Universal stress protein F	11		ISHVEAEAK	20	9	3	22.92	b7°b7b8	983.51	23.524	18891	2	492.26	-9.18
P67091 UF_SALTY Universal stress protein F	12		QAHVAEGSPK	86	10	2	8.01	b3*b3	1023.51	18.273	2554	2	512.26	-8.11
P0A1P8 GLRX1_SALTY Glutaredoxin-1	1		TVGKPVETVPQIFVDQK	50	17	10	47.28	b3b9y2*y2y4y6*y6y8y13y17	1885.02	64.647	52251	3	629.01	-11.07
P0A1P8 GLRX1_SALTY Glutaredoxin-1	2	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	MFTVIFGRPGCPYCVR	0	16	13	105.41	b2b3°b3b7b10y5y8y10y11y12y13y14y16	1959.92	76.096	41352	3	653.98	-10.09
P0A1P8 GLRX1_SALTY Glutaredoxin-1	3		LSKERDDFNyR	23	11	3	25.06	b4y3y5	1442.70	51.417	2384	3	481.57	-1.02
P0A1P8 GLRX1_SALTY Glutaredoxin-1	4		YIDIHAEGITK	34	11	3	28.07	b3y6y7	1259.64	48.408	20569	3	420.55	-18.61
P0A1P8 GLRX1_SALTY Glutaredoxin-1	5	Carbamidomethyl+C(5)	HIGGCTDFEAWAK	67	13	4	35.09	b4b6b11y6	1491.65	36.752	2684	2	746.33	-14.48
P0A1P8 GLRX1_SALTY Glutaredoxin-1	6	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14))	MFTVIFGRPGCPYCVRAK	0	18	4	16.15	b12°b12y8y11	2159.09	73.157	6540	3	720.37	10.06
P0A1P8 GLRX1_SALTY Glutaredoxin-1	7	Carbamidomethyl+C(5)	HIGGCTDFEAWAKENLNLFA	67	20	4	28.72	b4b13y8y9	2293.06	51.879	2732	3	765.02	-6.71
P0A1P8 GLRX1_SALTY Glutaredoxin-1	8		PQIFVDQK	59	8	1	7.26	b3	974.54	64.658	9034	1	974.54	12.21
P0A1H3 EFG_SALTY Elongation factor G	1		IATDPFVGnLTFFR	323	14	19	129.64	b2b4°b4b6b7b12b14y1y2y3y4y6y7*y7y10*y10y11y12y14	1597.84	93.030	121205	2	799.42	-1.45
P0A1H3 EFG_SALTY Elongation factor G	2		IHAeVPLSEMFGYATQLR	653	18	20	159.02	b2b3b4b5b6b7b9y1y2y3*y3y4y5y6y7*y7y8y13y16y18	2062.03	89.041	96883	3	688.01	-8.17
P0A1H3 EFG_SALTY Elongation factor G	3		VYSGVNSGDTVLNSVK	337	17	19	143.36	b2b4b5b7b14b15*b15y4*y4y5y9y10y11°y11*y11y12y14y15y17	1737.90	61.854	88933	2	869.46	0.70
P0A1H3 EFG_SALTY Elongation factor G	4		SGPLAGYPVVDLGVR	562	15	15	95.03	b2°b2b3°b3b5°b5b7°b7y3y4y8y9y10y11y15	1499.82	76.335	67213	2	750.41	-0.98
P0A1H3 EFG_SALTY Elongation factor G	5		MEFPEPVISIAVEPK	408	15	10	60.77	b2b3b9b10b12y2y10y12y13y15	1685.88	85.687	65458	2	843.45	1.45
P0A1H3 EFG_SALTY Elongation factor G	6		IGEVHDGAATMDWMEQEQR	39	20	12	57.21	b2b8b11°b11b12°b12b13y1y6y7y9y20	2331.99	61.668	64439	3	778.00	-3.14
P0A1H3 EFG_SALTY Elongation factor G	7		GQYGHVVIDMYPLEPGSNPK	512	20	20	137.96	b2°b2b4b6b7°b7b8b9b11b12y5y6*y6y7°y7*y7y9y10°y10y11	2201.06	69.796	48815	3	734.36	-5.44
P0A1H3 EFG_SALTY Elongation factor G	8		HASDDEPFSALAFK	309	14	5	19.96	b2b6y9y12y14	1534.73	69.668	42846	2	767.87	10.02
P0A1H3 EFG_SALTY Elongation factor G	9		LHFGSYHDVDSSELAFK	577	17	10	37.36	b1b2b6b7b9°b9b11y1y10y17	1951.91	62.357	42162	3	651.31	-6.07
P0A1H3 EFG_SALTY Elongation factor G	10		VEVETPEENTGDVIGDLSR	618	19	5	32.44	y3y5y6y14y19	2059.00	66.599	40374	2	1030.00	6.52
P0A1H3 EFG_SALTY Elongation factor G	11		GQSEVTGVK	643	10	7	62.53	b2b8y3y4y7°y7y8	1033.50	25.251	40203	2	517.25	-13.11

P0A1H3 EFG_SALTY Elongation factor G	12	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	9	65.71	b5°b5b6b7y6y9y11y12y14	2621.29	85.814	35706	3	874.43	1.02
P0A1H3 EFG_SALTY Elongation factor G	13		ILFYTGvNHNK	29	10	7	69.52	y3*y3y5y6y7y8y10	1191.64	54.309	32000	2	596.32	-8.81
P0A1H3 EFG_SALTY Elongation factor G	14		LGANPVPLQLAIGAEEGFTGVVDL VK	161	26	8	50.96	b4b5b6*b6y4y5y7y26	2607.43	119.879	30570	3	869.82	-2.90
P0A1H3 EFG_SALTY Elongation factor G	15	Carbamidomethyl+C(11)	VLNNEILVTCGSAFK	255	16	8	47.5	b4b5*b5b12y6y8y10y16	1777.96	78.917	25259	2	889.48	4.33
P0A1H3 EFG_SALTY Elongation factor G	16	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTTGDTLCDPEN PIILER	378	30	17	80.32	b3b5°b5b6°b6b7°b7b9b17b 27y2°y2y3y4y6y10y13	3138.62	84.981	21704	3	1046.88	5.29
P0A1H3 EFG_SALTY Elongation factor G	17		GVQAMLDavidYLPSPVDVPAIN GILDDGKDTPAER	273	36	16	76.73	b2b3*b3b4b6b7b9b11*b11 y1y4y5y6y9y11y23	3764.93	121.906	16688	3	1255.65	7.65
P0A1H3 EFG_SALTY Elongation factor G	18		GGVIPGEYIPAVDK	541	14	5	25.4	b2b4y9y10y14	1414.75	65.220	8821	2	707.88	-3.71
P0A1H3 EFG_SALTY Elongation factor G	19		AINWNDADQGVTFEYEDIPADMQ DLANEWHQNLIESAEESEELME K	189	47	22	169.83	b3b4b5b6°b6b7b11°b11y2 °y2y3y4y5y6°y6y7y8y9y10 y12y13y29	5380.42	125.878	8384	4	1345.86	5.81
P0A1H3 EFG_SALTY Elongation factor G	20		VEVETPEENTGDVIGDLSRR	618	20	3	21.68	b5b16b18	2215.09	82.245	1888	3	739.03	1.10
P0A1H3 EFG_SALTY Elongation factor G	21		EFNVEANVGKPKVAYR	475	16	10	71.66	b6b9b11y3y6y8*y8y9y11* y11	1820.90	53.148	73193	3	607.64	-15.35
P0A1H3 EFG_SALTY Elongation factor G	22		YDDAPNNVAQAVIEAR	686	16	4	17.79	b4y3°y3y8	1745.85	64.930	23817	2	873.43	4.13
P0A1H3 EFG_SALTY Elongation factor G	23	Carbamidomethyl+C(9)	DVTTGDTLCDPENPIILER	389	19	4	24.66	y3y10y11*y11	2158.05	70.441	19114	2	1079.53	9.05
P0A1H3 EFG_SALTY Elongation factor G	24		VVGQIK	153	6	1	13.9	b4	643.41	44.712	12060	1	643.41	-9.39
P0A1H3 EFG_SALTY Elongation factor G	25		MGLALGR	430	7	3	41.34	y3y4y6	717.39	49.493	10688	2	359.20	-18.97
P0A1H3 EFG_SALTY Elongation factor G	26		TTPIAR	3	6	1	13.9	y3	658.38	33.610	7185	1	658.38	-11.03
P0A1H3 EFG_SALTY Elongation factor G	27		ADQEK	425	5	2	13.53	y4*y4	590.28	58.276	5240	1	590.28	11.68
P0A1H3 EFG_SALTY Elongation factor G	28		NIGISAHIDAGK	11	12	9	64.26	b7°b7b9y4°y4y5y7°y7y8	1195.62	36.323	2748	2	598.31	-22.26
P0A1H3 EFG_SALTY Elongation factor G	29		GVQAMLDavidYLPSPVDVPAIN GILDDGK	273	30	6	20.18	b4b7y3y8°y8y10	3095.55	105.107	2166	3	1032.52	-16.72
P0A1H3 EFG_SALTY Elongation factor G	30		QYEPHR	77	6	1	13.9	y3	829.39	116.029	1559	1	829.39	-7.51
P0A1H3 EFG_SALTY Elongation factor G	31		YLGGEELTEEEIKQALR	236	17	10	82.26	b5°b5b7b12y3y4y5y10y11 y15	1977.99	73.026	91583	3	660.00	-13.52
P0A1H3 EFG_SALTY Elongation factor G	32		ASYTMEFLKYDDAPNNVAQAVIE AR	677	25	11	86.76	b8b9b11b12b13y3y4y5°y5 y8y12	2816.36	83.989	67417	3	939.46	1.56
P0A1H3 EFG_SALTY Elongation factor G	33		GGVIPGEYIPAVDKGIQEQLK	541	21	4	25.5	b3b4b11y12	2211.18	73.991	24861	3	737.73	-7.95
P0A1H3 EFG_SALTY Elongation factor G	34		AKPVLLEPIMKVEVETPEENTGDV IGDLSR	607	30	5	26.89	y5y6y10y14°y14	3278.69	83.531	19671	4	820.43	-8.12
P0A1H3 EFG_SALTY Elongation factor G	35		NIGISAHIDAGKTTTTER	11	18	4	27.46	b3b4b11y9	1884.98	63.030	4468	3	629.00	3.24
P0A1H3 EFG_SALTY Elongation factor G	36		EFNVEANVGKPKVAYREAIR	475	20	6	38.56	b4b10b11*b11b12*b12	2290.19	101.979	2391	2	1145.60	-0.75
P0A1H3 EFG_SALTY Elongation factor G	37		GQSEVTGvKIHAEVPLSEMFGY ATQLR	643	28	5	27.36	b6b9b10b12y16	3076.54	119.957	2060	3	1026.19	0.40
P0A1H3 EFG_SALTY Elongation factor G	38	Oxidation+M(5)	GVQAMLDavidYLPSPVDVPAIN GILDDGK	273	30	4	26.89	b3b6b7b10	3111.64	86.949	78221	4	778.66	14.20

P0A1H3 EFG_SALTY Elongation factor G	39	Carbamidomethyl+C(10) ;Oxidation+M(7)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	3	13.11	b11y5y7	2637.27	94.515	15730	3	879.76	-3.80
P0A1H3 EFG_SALTY Elongation factor G	40	Oxidation+M(10)	GQYGHVVIDMYPLEPGSNPK	512	20	4	21.68	y6°y6y10y14	2217.09	87.838	4477	2	1109.05	13.65
P0A1H3 EFG_SALTY Elongation factor G	41		TPEENTGDVIGDLSRR	622	16	1	7.43	b11	1758.89	82.220	15370	2	879.95	13.74
P0A1H3 EFG_SALTY Elongation factor G	42		FYTGVDNHK	31	8	0	1.89		965.48	54.299	11666	2	483.24	-7.40
P0A1H3 EFG_SALTY Elongation factor G	43		VEVETPEENTGDVIGD	618	16	0	5.66		1702.77	82.224	8793	2	851.89	1.79
P0A1H3 EFG_SALTY Elongation factor G	44		PFSALAFK	315	8	0	3.4		880.49	69.703	3516	2	440.75	-8.32
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	18	164.33	b2b3b7b11y2y3y4y5y6y7y 10y11y12y14y16°y16y17y1 8	1970.00	63.020	209042	3	657.34	-10.10
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		ESSVPFSYYDNQQK	47	14	19	129.64	b3°b3b4°b4b7b11°b11y4y 5*y5y6y7y8*y8y9°y9y10*y 10y14	1691.75	55.314	194992	2	846.38	-0.36
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		VVGYSQDYSNAIVEAVK	61	17	11	67.48	b2b8b13b16y1y4y5y11y13 y15y17	1841.93	67.471	153243	2	921.47	3.78
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		AVAFMMDDALLAGER	198	15	13	121.57	b3b5b11b12°b12y3y4y5y1 0y11y12y13y15	1609.78	84.339	144585	2	805.39	4.70
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5		NGVIVVGHR	38	9	13	91.43	b2°b2b3°b3b4°b4y2y3y4y 5y6y7y9	950.54	31.817	108043	2	475.77	-14.77
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(19)	KPDNWEIVGKPQSQEAYGCMLRK	217	23	14	92.95	b5b7b8°b8b11b13b16y5y6 y8y11y13y15y23	2734.31	55.836	105096	4	684.33	-12.68
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7		LIPITSQNR	89	9	5	39.08	b2y4y5y6y9	1041.60	42.608	72262	2	521.30	-8.32
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8	Carbamidomethyl+C(19)	KPDNWEIVGKPQSQEAYGCMLR	217	22	17	126.6	b2b5°b5b6b7b10y2y4y5y6 y8y9y10y11°y11y12y22	2606.21	61.130	59167	4	652.31	-13.58
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9		QAAFSDTIFVVGTR	122	14	10	62.01	b2b3b14y1y3y5y6y10y12y 14	1511.79	76.512	51742	2	756.40	3.96
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTTNLER	98	22	22	138.41	b2b3b4b5y1y2y3y4°y4y5° y5y6°y6°y6y8°y8y9°y9y10 y11y12y22	2526.22	81.539	51428	2	1263.61	9.86
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11		AVVVTSGTTSEILLHK	154	16	6	36.68	b3b4b10y4y12°y12	1654.94	57.505	26338	3	552.32	4.50
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12	Carbamidomethyl+C(21)	AKKPDNWEIVGKPQSQEAYGCML R	215	24	11	61.5	b2b7y4y5y7y8y10°y10y12y 16y24	2805.39	57.080	22114	3	935.80	3.66
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	13		LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	3	22.97	y8y9y12	2869.43	86.131	15395	3	957.15	-3.57
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	14		GGDIKDFPDLK	141	11	6	54.34	b4b5b6b10y7y11	1204.61	35.489	7128	2	602.81	-5.67
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	15		IISAKDHGDSFR	180	12	5	30.21	y4°y4y10y11y12	1345.67	68.809	4343	2	673.34	-11.34

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	16		LMDDTIAQAQTSGEAEK	247	17	3	16.91	b9y7y9	1807.85	46.068	11272	2	904.43	4.05
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	17		NDPEFK	240	6	1	13.9	y5	749.34	79.448	4769	1	749.34	-3.01
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	18		DFPDLK	146	6	1	13.9	b4	734.36	103.494	2368	1	734.36	-11.64
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	19		APNDK	294	5	2	13.53	y4*y4	544.27	29.202	2206	1	544.27	-11.10
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	20	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTT NNLER	89	31	7	35.06	b3b10y6y9y10y13y29	3548.79	86.735	344872	3	1183.60	3.51
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	21		LMDDTIAQAQTSGEAEKWFDK	247	21	3	14.36	b12y7y9	2384.14	85.030	4467	3	795.39	14.85
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	22	Oxidation+M(2)	LMDDTIAQAQTSGEAEK	247	17	4	27.05	b10y7y9y13	1823.85	80.573	8211	3	608.62	10.64
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	23	Oxidation+M(5)	LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	4	22.23	b4b5°b5y25	2885.41	111.427	6621	3	962.47	-11.42
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	24		PITSQNR	91	7	1	9.02	b6	815.43	42.611	21911	2	408.22	-11.90
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	25	Carbamidomethyl+C(13)	IVGKPQSQEAYGCMLRK	223	17	1	7.76	b9	1965.00	55.833	4627	3	655.67	-4.47
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	1		DLVESAPAALK	85	11	8	72.63	b10y2y5y7y8y9y10y11	1113.61	53.331	60340	2	557.31	-7.23
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		DQIIEAVSAMSVM DVVELISAMEE K	5	25	26	173.18	b2°b2*b2b3b4*b4b5b6*b6 b7b8°b8b10y2°y2y3y4y5y6 y7y9y10y12y13°y13y25	2737.34	137.064	46462	3	913.12	0.89
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	3		SLEEAGAEVEVK	109	12	4	30.21	b4b5°b5b9	1260.63	47.029	2104	2	630.82	-0.39
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	4		SITK DQIIEAVSAMSVM DVVELISA MEEK	1	29	4	36.93	y4y6y7y8	3166.62	136.331	6485	3	1056.21	7.02
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	5		AAGANKVAVIK	60	11	3	28.07	b3y4y5	1041.63	28.780	6462	2	521.32	-11.48
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	6	Phosphoryl STY(8)	EAKDLVESAPAALK	82	14	4	28.56	b7b11y7y9	1521.73	66.133	52675	2	761.37	-13.32
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	7	Oxidation+M()	MSITK DQIIEAVSAMSVM DVVELI SAMEEK	0	30	6	30.78	b6b7y5y7y9°y9	3313.59	100.899	8389	3	1105.20	-11.79
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	8	Oxidation+M(22)	DQIIEAVSAMSVM DVVELISAMEE K	5	25	5	26.54	b3b4y7°y7y9	2753.36	110.675	4395	3	918.46	12.06
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	1		SGFAEDEVVAVSK	35	13	12	102.21	b3°b3b4b10y2y4y5y8y9y1 0y12y13	1337.65	54.177	84501	2	669.33	-3.65
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	2		EIPMEVKPEVR	55	11	7	66.89	y2y4y6y7y8y9y11	1326.71	48.034	58522	2	663.86	-0.37
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	3		AANDDLLNSFWLLDSEK	9	17	5	16.91	b6b12y2y13y17	1950.96	87.652	57373	2	975.98	8.95
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	4		FNSLTPEQQR	106	10	14	115.85	b2°b2b5b8b9y2y3y5°y5y6 y7y8y9y10	1219.60	37.635	52326	2	610.30	-8.21
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	5		MITGIQITK	0	9	9	90.18	b3°b3y3y4°y4y5y6y7y8	1004.57	54.671	94436	2	502.79	-15.19

Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	6		VEGGQHNLNVNVL	66	13	11	125.07	b6b8y3y4y5y6*y6y7y8y11y12	1434.75	49.580	87644	3	478.92	-18.89
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	7		AANDDLLNSFWLLDSEKGEAR	9	21	28	261.91	b3b5°b5*b5b6°b6b7*b7b9y3y4y5y7°y7y8y9y10y11y12y13y14*y14y15*y15y16y17y18y19	2364.14	92.271	212972	3	788.72	-3.92
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	8		MITGIQITKAANDDLLNSFWLLDSEK	0	26	6	28.45	b21y3°y3y7y8y12	2936.52	105.121	14899	3	979.51	5.65
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	9		VSGYAVRFNSLTPEQQR	99	17	4	16.91	b4y4°y4y9	1952.01	59.192	3024	3	651.34	4.38
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	10		PMEVKPEVR	57	9	3	32.05	b3b4b7	1084.58	48.025	58518	2	542.79	-5.29
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor	11		EIPMEVKPEVR	55	11	0	2.26		1308.68	48.015	18291	3	436.90	-13.06
P41031 CY_SALTY Thiosulfate-binding protein	1		AYLNLWLYSPQAQTIIITHYYR	265	21	27	230.71	b2b3b4*b4b6°b6b9y2y3y4y5y6y7y8y9y10y11°y11y13y14y15y16y17y19°y19y21*y21	2664.32	92.752	180847	3	888.78	-2.20
P41031 CY_SALTY Thiosulfate-binding protein	2		GLGDVLISFESEVNNIRK	208	18	25	180.49	b2b4b5°b5b6b12y2y4*y4y5y6y8*y8y9°y9*y9y10y11°y11*y11y12y13y14y16y18	1990.03	100.715	157957	3	664.02	-13.25
P41031 CY_SALTY Thiosulfate-binding protein	3		ELFAALNPPFEQQWAK	37	16	16	72.33	b3b5b6°b6b7*y1y4*y4y6y9*y9y12y13°y13*y13y16	1888.97	89.640	141119	2	944.99	7.17
P41031 CY_SALTY Thiosulfate-binding protein	4		LPNNSSPFYSTMGFLVR	110	17	20	180.9	b4b5°b5b6°b6y1y2y3y4y5y6y8y9y11°y11y12y13y14y15y17	1929.96	91.761	112331	2	965.48	3.86
P41031 CY_SALTY Thiosulfate-binding protein	5		FGSWPEVMK	311	9	8	58.63	b2y1y2y3y5y7y8y9	1080.51	68.112	107412	2	540.76	-8.47
P41031 CY_SALTY Thiosulfate-binding protein	6		VNNPEIMGK	286	9	12	93.19	b2*b2b3b5b6y3y6y7*y7y8*y8y9	1001.50	35.836	102481	2	501.25	-11.70
P41031 CY_SALTY Thiosulfate-binding protein	7		TEQFMTQFLK	179	10	8	62.53	b2b4°b4y3y5y7y8y10	1272.62	75.036	99240	2	636.82	-4.22
P41031 CY_SALTY Thiosulfate-binding protein	8		NIHDWSDLVR	132	10	15	115.85	b1*b1b3°b3b4b7y1y2y3y4y5y6y7y8y10	1254.62	62.059	84703	2	627.81	-5.94
P41031 CY_SALTY Thiosulfate-binding protein	9		QYEAQGFVVIK	226	13	14	93.24	b2*b2b3°b3b7b13y2y3y5y8y9y10y11y13	1507.77	69.586	82451	2	754.39	-3.72
P41031 CY_SALTY Thiosulfate-binding protein	10		NVEVFDTGGR	189	10	10	72.26	b1b2b5b8y4y6y7y8°y8y10	1093.52	46.836	67199	2	547.26	-5.02
P41031 CY_SALTY Thiosulfate-binding protein	11		QALAILQLK	71	10	11	76.06	b2*b2b3°b3b10y1y3y4y5y6y7	1054.65	74.580	65283	2	527.83	-11.81
P41031 CY_SALTY Thiosulfate-binding protein	12		GATTTFAER	199	9	6	55.62	y1y3y4y5y7y9	953.46	30.292	29058	2	477.23	-9.92
P41031 CY_SALTY Thiosulfate-binding protein	13		GLGDVLISFESEVNNIR	208	17	5	30.82	b6b13y10*y10y11	1861.97	106.797	25587	2	931.49	2.29
P41031 CY_SALTY Thiosulfate-binding protein	14		ADVVTYNQVTDVQILHDK	81	18	6	22.62	b2b3b12y3y7y18	2058.04	63.598	15659	3	686.68	-6.76
P41031 CY_SALTY Thiosulfate-binding protein	15		YTYLAAWGAADNADGGDK	159	18	3	16.15	b6b8y4	1858.84	53.149	5311	4	465.47	10.31
P41031 CY_SALTY Thiosulfate-binding protein	16		ELFAALNPPFEQQWAKDNGGDK	37	22	3	13.9	b15b20y12	2475.21	92.050	2403	4	619.56	5.92
P41031 CY_SALTY Thiosulfate-binding protein	17		LIFPNPK	146	7	4	41.34	b5y3y5*y5	828.48	55.587	78375	2	414.75	-16.06
P41031 CY_SALTY Thiosulfate-binding protein	18		TNILAEFPVAWVDKNVQANGTEK	239	23	17	165.68	b3b4b5b6y4y6y7*y7y9y11y12*y12y16y17y18y19y20	2544.30	90.289	159609	3	848.77	-2.49

P41031 CY_SALTY Thiosulfate-binding protein	19		YTYLAAWGAADNADGGDKAK	159	20	7	54.11	b4b19y6y9y11y15y18	2057.94	61.746	104391	3	686.65	-8.90
P41031 CY_SALTY Thiosulfate-binding protein	20		KQYEAQGFEVVIPK	225	14	6	43.71	b4*b4b8b11b12y3	1635.86	62.812	30946	3	545.96	-11.27
P41031 CY_SALTY Thiosulfate-binding protein	21		NVEVFDTGGRGATTTFAER	189	19	3	24.66	y6y7y11	2027.97	68.022	26768	3	676.66	-4.94
P41031 CY_SALTY Thiosulfate-binding protein	22		ADVVTYNQVTDVQILHDKGK	81	20	5	26.08	b3b4b11y5°y5	2243.15	58.401	25409	3	748.39	-5.55
P41031 CY_SALTY Thiosulfate-binding protein	23		THFASGGELDKLLAAGR	320	17	3	23.9	b10y4y5	1742.89	65.412	16478	3	581.64	-13.80
P41031 CY_SALTY Thiosulfate-binding protein	24		AYLNWLYSPPQAQTIITHYYRVN NPEIMGK	265	30	6	41.06	b6b8b9b10b12°b12	3646.80	84.138	7681	5	730.17	-4.42
P41031 CY_SALTY Thiosulfate-binding protein	25		FGSWPEVMKTHFASGGELDK	311	20	4	23.44	b12y6y9y12	2223.06	69.767	7507	3	741.69	1.54
P41031 CY_SALTY Thiosulfate-binding protein	26		TSGNARYTYLAAWGAADNADGG DK	153	24	3	19.42	b7b10b12	2445.08	100.030	6660	3	815.70	-10.18
P41031 CY_SALTY Thiosulfate-binding protein	27		VEEKFGSWPEVMK	307	13	5	26.12	b10b11°b11y11°y11	1565.78	87.257	5104	2	783.39	9.67
P41031 CY_SALTY Thiosulfate-binding protein	28		GNPKNIHDWSDLVR	128	14	4	25.4	b8b9°b9y8	1650.82	52.725	2910	2	825.91	-7.99
P41031 CY_SALTY Thiosulfate-binding protein	29		QADKFPQTELFR	295	12	3	23.01	b5b11y5	1479.76	82.003	1918	2	740.38	0.50
P41031 CY_SALTY Thiosulfate-binding protein	30		AKTEQFMTQFLK	177	12	4	26.99	b4y10y11°y11	1471.77	39.293	1771	2	736.39	6.47
P41031 CY_SALTY Thiosulfate-binding protein	31		NIHDWSDLVRSDVK	132	14	5	31.73	b3b10b11°b11y9	1683.84	81.111	1736	2	842.42	-5.07
P41031 CY_SALTY Thiosulfate-binding protein	32		GSWPEVMK	312	8	1	9.02	b4	933.44	68.114	4478	1	933.44	-6.93
P41031 CY_SALTY Thiosulfate-binding protein	33		TTTFAER	201	7	1	9.02	b4	825.40	30.342	3335	2	413.20	-9.32
P41031 CY_SALTY Thiosulfate-binding protein	34		NVEVFDTG	189	8	0	1.89		880.41	46.839	2548	1	880.41	0.42
P41031 CY_SALTY Thiosulfate-binding protein	35		AALNPPFEQQWAK	40	13	0	4.15		1499.78	89.635	1560	2	750.39	8.38
P41031 CY_SALTY Thiosulfate-binding protein	36		NIHDWSDLVR	132	10	0	1.89		1237.59	62.049	3725	3	413.20	-4.73
P41031 CY_SALTY Thiosulfate-binding protein	37		QALAILQGLK	71	10	0	1.89		1037.62	74.575	1919	2	519.32	-8.12
P67904 RS10_SALTY 30S ribosomal protein S10	1		FTVLISPHVNKDAR	48	14	13	76.62	b4b12y2y5*y5y6y7°y7*y7y8y9*y9y14	1596.86	52.704	100222	3	532.96	-14.07
P67904 RS10_SALTY 30S ribosomal protein S10	2		LIDQSTAEIVETAKR	16	15	17	170.08	b9*b9b10y1y3y4y5y6y7y8y9y10y11°y11y12y13y15	1673.88	51.823	91228	3	558.63	-14.29
P67904 RS10_SALTY 30S ribosomal protein S10	3		LIDQSTAEIVETAK	16	14	14	112.59	b2b10y2y3y4y5y7y8y9y10°y10y11*y11y14	1517.80	55.359	71124	2	759.40	-3.70
P67904 RS10_SALTY 30S ribosomal protein S10	4		LVDIVEPTEK	72	10	6	62.53	b3y4y6y8y9y10	1142.62	51.636	45875	2	571.82	-4.81
P67904 RS10_SALTY 30S ribosomal protein S10	5		GPIPLPTRK	37	9	6	39.08	b2y4°y4y5y6y9	978.60	42.595	43534	2	489.80	-9.42
P67904 RS10_SALTY 30S ribosomal protein S10	6		FTVLISPHVNKDARDQYEIR	48	20	4	14.89	b8y6°y6y11	2401.26	68.805	2067	2	1201.13	-1.53
P67904 RS10_SALTY 30S ribosomal protein S10	7		FTVLISPHVNVK	48	11	6	66.89	y3*y3y4y6y7y8	1254.70	57.720	48483	3	418.90	-17.41
P67904 RS10_SALTY 30S ribosomal protein S10	8		DQYEIR	62	6	3	27.43	y4y5*y5	823.38	31.095	19965	2	412.20	-12.38
P67904 RS10_SALTY 30S ribosomal protein S10	9		RLVDIVEPTEK	71	11	8	100.48	b3b4b5b6b7b10y4y6	1298.73	50.333	56464	2	649.87	-4.70
P67904 RS10_SALTY 30S ribosomal protein S10	10		IPLPTRK	39	7	0	1.51		824.52	42.601	8098	2	412.77	-12.73

P67904 RS10_SALTY 30S ribosomal protein S10	11		VLISPHVNKDAR	50	12	0	3.4		1348.75	52.700	7825	3	450.26	-12.67
P67904 RS10_SALTY 30S ribosomal protein S10	12		ISPHVNKDAR	52	10	0	3.4		1136.61	52.699	6545	2	568.81	-8.38
P67904 RS10_SALTY 30S ribosomal protein S10	13		TVLISPHVNKDAR	49	13	0	3.4		1449.81	52.683	3034	3	483.94	-8.08
P02906 SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQEIAAK	263	13	19	150.57	b2b3b4°b4b7b10y2y3y4y5y7y8°y8°y8y9°y9y10y11y13	1468.73	50.510	64449	2	734.87	-1.83
P02906 SUBI_SALTY Sulfate-binding protein	2		LFTIDEVFGGWAK	298	13	12	78.47	b2b3°b3b4b13y2y3y4y5y7y8y13	1482.76	101.497	45636	2	741.88	-0.74
P02906 SUBI_SALTY Sulfate-binding protein	3		NVEVLDSGAR	183	10	11	90.56	b2b3°b3b4y2y4y5y6y7y8y10	1059.54	39.764	35301	2	530.27	-3.23
P02906 SUBI_SALTY Sulfate-binding protein	4		AVAEAYLK	255	8	6	41.71	y1y2y4y5y6y8	864.47	40.535	25425	2	432.74	-12.21
P02906 SUBI_SALTY Sulfate-binding protein	5		QETGDNVVIR	48	10	7	56	b10y3y4y7°y7y8y10	1130.57	35.035	19550	2	565.79	-6.05
P02906 SUBI_SALTY Sulfate-binding protein	6		DHFANGGTFDQISKR	314	15	8	30.4	b2b3y3y6°y6y7°y7y15	1692.79	43.644	15364	3	564.93	-11.75
P02906 SUBI_SALTY Sulfate-binding protein	7		QATSVINGIEADVVTALAYDVD AIAER	66	28	13	93.37	b2b3°b3b4b17y3°y3y5y6y7y8y9y10	2917.52	127.851	12249	3	973.18	0.17
P02906 SUBI_SALTY Sulfate-binding protein	8		AQKDHFANGGTFDQISK	311	17	5	30.82	b4°b4b9y10y11	1863.91	55.950	6718	3	621.98	8.78
P02906 SUBI_SALTY Sulfate-binding protein	9		DIQLLNVSYPDTRELYEQYNK	20	21	5	24.02	y4y5°y5y7y21	2601.30	81.505	1516	3	867.77	7.60
P02906 SUBI_SALTY Sulfate-binding protein	10		WNYLAAWGYALHHNNNDQAK	153	20	12	88	b3b5b6y8y9y11y13°y13°y13y14y16y18	2386.06	78.018	64453	4	597.27	-19.95
P02906 SUBI_SALTY Sulfate-binding protein	11		GSTNTFVER	193	9	8	66.13	b4°b4b5b7b8°b8°b8y3	1010.48	31.595	26983	2	505.75	-6.22
P02906 SUBI_SALTY Sulfate-binding protein	12		ELYEQYNK	33	8	8	68.77	b3b4b7°b7y4°y4y6°y6	1086.49	34.968	7452	2	543.75	-18.31
P02906 SUBI_SALTY Sulfate-binding protein	13		QIHDWNLIKPGVSVITPNPK	126	21	10	85.11	b5b6b7b9b12°b12b14y4y5y6	2371.30	72.293	4307	2	1186.15	10.09
P02906 SUBI_SALTY Sulfate-binding protein	14		GIGDVLIAWENEALLATNELGK	202	22	3	13.9	b5b10y13	2326.18	113.257	2891	3	776.07	-19.00
P02906 SUBI_SALTY Sulfate-binding protein	15		RLPDNSAPYTSTIVFLVR	103	18	9	88.53	b4b5b6b7b9y3y4y5y11	2049.09	82.340	43084	3	683.70	-10.37
P02906 SUBI_SALTY Sulfate-binding protein	16		NVEVLDSGARGSTNTFVER	183	19	5	35.07	b7°b7b8°b8b9	2051.00	108.989	2956	3	684.34	-7.74
P02906 SUBI_SALTY Sulfate-binding protein	17		QSHGGSGKQATSVINGIEADVVTL ALAYDVD AIAER	58	36	4	22.59	b9°b9b10y12	3655.81	125.967	2446	3	1219.27	-13.89
P02906 SUBI_SALTY Sulfate-binding protein	18		AFSAHWKQETGDNVVIR	41	17	3	16.91	b7y7y12	1958.01	72.247	2191	2	979.51	9.16
P02906 SUBI_SALTY Sulfate-binding protein	19		IQLLNVSYPDTRELYEQYNK	21	20	0	6.04		2486.23	81.532	4974	3	829.41	-11.98
P02906 SUBI_SALTY Sulfate-binding protein	20		FDQISKR	322	7	0	3.77		893.49	43.660	3923	2	447.25	2.94
P66038 RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	25	160.81	b3b4b8b9°b9b10°b10b11°b11b12°b12b13°b13°b13b14°b14y2y3y4y9y11y12y15y16y29	3110.70	98.135	82056	3	1037.57	5.81
P66038 RISB_SALTY 6	2		GAEAALTALEMINVLK	136	16	21	122.91	b2b4°b4b5b6b7°b7b8°b8b12°b12b13°b13°b13b14°b14y2y4y6y10y16	1643.91	102.561	69364	2	822.46	1.11
P66038 RISB_SALTY 6	3		FNQFINDSLLDGAVDALTR	21	19	16	131.17	b2b3b5b8y2y3y4y5y8y9y10y13y14y15y19°y19	2109.07	100.883	59692	2	1055.04	6.14
P66038 RISB_SALTY 6	4		VAIT IAR	14	7	6	54.86	y2y3y4y5y6y7	743.47	43.903	7427	2	372.24	-12.56

[P66038]RISB_SALTY 6	5		ANVAAPDAR	5	9	8	46.59	b2*b2b8y1y2y5y6y7	884.45	22.633	6385	2	442.73	-10.08
[P66038]RISB_SALTY 6	6		YDAVVALGTVIR	72	12	5	51.03	b3b6b7b9y5	1276.70	60.974	4567	3	426.24	-19.98
[P66038]RISB_SALTY 6	7		AGNKGAEAAALTALEMINVLK	132	20	5	42.56	b7b16y3y4y5	2014.08	96.708	28253	3	672.03	-10.00
[P66764]METK_SALTY S-adenosylmethionine synthetase	1		SLQEAVMEEIHKPILPSEWLNSTSTK	197	25	26	156.75	b2b5°b5b10*b10b11*b11b12b13b15b18y1y2y3y4y5°y5y7y10y11y12*y12y13*y13y14y25	2856.52	110.822	59893	3	952.85	5.04
[P66764]METK_SALTY S-adenosylmethionine synthetase	2		FFINPTGR	222	8	5	36.94	b2b4b7y4y8	951.49	59.905	54866	2	476.25	-13.02
[P66764]METK_SALTY S-adenosylmethionine synthetase	3	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGR	230	15	7	26.87	b2y2y6°y6y12y13y15	1536.73	68.426	31063	2	768.87	0.79
[P66764]METK_SALTY S-adenosylmethionine synthetase	4	Carbamidomethyl+C(10)	FVIGGPMGDCGLTGRK	230	16	9	57.83	b2b13b14y9y11°y11y12°y12y13	1664.81	61.590	17155	3	555.61	-8.14
[P66764]METK_SALTY S-adenosylmethionine synthetase	5		EFFDLRPYGLIQMLDLLHPIYK	331	22	9	45.15	b7b9b11b12y1y2y4y5y22	2721.41	121.384	13939	4	681.11	-12.74
[P66764]METK_SALTY S-adenosylmethionine synthetase	6		VPAEQLILLVR	320	11	6	37.8	b2b5y2y5y8y9	1250.78	83.259	9289	2	625.90	-0.10
[P66764]METK_SALTY S-adenosylmethionine synthetase	7	Carbamidomethyl+C(1)	CEIQVSYAIGVAEPTSIMVETFGTEK	294	26	5	18.95	b4b11*b11b13y13	2859.36	93.617	8670	3	953.79	-6.49
[P66764]METK_SALTY S-adenosylmethionine synthetase	8		ADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHR	109	35	3	16.75	y5y7y9	3749.78	90.867	7552	3	1250.60	6.32
[P66764]METK_SALTY S-adenosylmethionine synthetase	9		IVGIDAVVLSTQHAEDIDQK	177	20	6	34.59	b3y3y5y13*y13y18	2151.11	72.294	7052	3	717.71	-6.92
[P66764]METK_SALTY S-adenosylmethionine synthetase	10		TGMVLVGGEITTSAWVDIEEITR	47	23	4	13.48	b12°b12y8y10	2477.28	79.885	2914	5	496.26	8.67
[P66764]METK_SALTY S-adenosylmethionine synthetase	11		IIVDTYGGMAR	246	11	4	32.05	y4y7°y7y8	1195.60	41.197	1549	2	598.31	-7.86
[P66764]METK_SALTY S-adenosylmethionine synthetase	12	Carbamidomethyl+C(20)	NTVREIGYVHSDMGFDANSCAVLSAIGK	70	28	4	12	b27y11y15°y15	3011.45	94.916	214102	3	1004.49	4.05
[P66764]METK_SALTY S-adenosylmethionine synthetase	13		QSPDINQGVDRADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHR	98	46	8	30.97	b3b5b7b9y3y7y9y10	4959.37	88.150	26675	4	1240.60	8.66
[P66764]METK_SALTY S-adenosylmethionine synthetase	14		SAAYAARYVAK	273	11	3	25.06	b6b10y8	1170.64	43.335	22888	2	585.82	12.72
[P66764]METK_SALTY S-adenosylmethionine synthetase	15	Carbamidomethyl+C(18)	FFINPTGRFVIGGPMGDCGLTGR	222	23	7	35.27	b4b5b7°b7b15y6y20	2469.19	80.545	19176	3	823.74	-10.38
[P66764]METK_SALTY S-adenosylmethionine synthetase	16		MAKHLFTSESVSEGHPPDK	0	18	5	33.93	b9b15y12y13y15	1999.98	79.129	12510	3	667.33	13.79
[P66764]METK_SALTY S-adenosylmethionine synthetase	17		IIVDTYGGMARHGGGAFSGK	246	20	6	33.34	b7b10b12b13y8°y8	1994.00	90.912	2655	3	665.34	4.29
[P66764]METK_SALTY S-adenosylmethionine synthetase	18	Carbamidomethyl+C(1); Oxidation+M(18)	CEIQVSYAIGVAEPTSIMVETFGTEK	294	26	4	16.46	b6b12y11y14	2875.35	75.881	5290	3	959.12	-8.58
[P66764]METK_SALTY S-adenosylmethionine synthetase	19	Oxidation+M(3)	TGMVLVGGEITTSAWVDIEEITR	47	23	3	13.48	b5b13y3	2493.25	68.779	1775	2	1247.13	-3.23
[P66764]METK_SALTY S-adenosylmethionine synthetase	20		SLQEAVMEEIHKPILPSE	197	18	0	7.54		2026.05	110.799	3261	3	676.02	-11.99
[P0AA28]THIO_SALTY Thioredoxin-1	1		MIAPILDEIADEYQGK	37	16	17	149.94	b2b3b8y2y3*y3y4y5y6y8y9°y9y10y11y13y14y16	1805.91	93.414	240653	2	903.46	5.00
[P0AA28]THIO_SALTY Thioredoxin-1	2		LNIDQNPGTAPK	58	12	27	170.71	b2*b2b4*b4b5*b5b6°b6*b6b7*b7b10y1y2y4y5y6y7y8*y8y9°y9*y9y10°y10y11y12	1267.65	38.303	126813	2	634.33	-8.86
[P0AA28]THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	10	76.65	b2b3y1y2y3y4y5y6y7y9	1001.63	90.210	71876	2	501.32	-10.91
[P0AA28]THIO_SALTY Thioredoxin-1	4		IIHLTDDSFDTDVLK	4	15	9	96.15	b3b6y3y5y6y10y11y12y13	1731.85	71.078	26898	3	577.96	-16.99

P0AA28 THIO_SALTY Thioredoxin-1	5		MIAPILDEIADEYQGKLTVAK	37	21	6	32.3	b3y12*y12y16y18y19	2318.22	94.471	47606	3	773.41	-4.63
P0AA28 THIO_SALTY Thioredoxin-1	6		SDKIIHLTDDSFDTDVLK	1	18	3	25.07	y7y11y12	2062.02	67.239	39039	3	688.01	-5.68
P0AA28 THIO_SALTY Thioredoxin-1	7	Oxidation+M(1)	MIAPILDEIADEYQGK	37	16	5	42.92	b5y3y6y12y14	1821.89	84.995	1689	2	911.45	-2.28
P0AA28 THIO_SALTY Thioredoxin-1	8		GIPTLLLFK	74	9	0	1.51		983.64	90.207	1527	2	492.32	13.71
O33921 AGP_SALTY Glucose-1-phohatase	1		TPIGGQLVFQR	335	11	10	89.96	b2b4b5y2y3y5y7y8y9y11	1215.68	61.161	94470	2	608.34	-3.61
O33921 AGP_SALTY Glucose-1-phohatase	2		MGTMDPTFNPVITDDSAAFR	141	20	20	149.68	b1b3*b3b5b12y1y2y3y4y5y6y7y9y11y12y13*y13y15y16y20	2186.01	78.405	92644	2	1093.51	7.37
O33921 AGP_SALTY Glucose-1-phohatase	3	Carbamidomethyl+C(14)	EWLVQAQGLIPSGECPAPDTVYAYANSLQR	87	29	23	133.02	b3*b3b4b5b6b7*b7*b7b9*b9b14b16y2y3y6y9y10y13*y13y15y20y21y29	3205.58	93.702	57278	3	1069.20	5.64
O33921 AGP_SALTY Glucose-1-phohatase	4		IEYVYQSAR	358	9	11	76.65	b2b3y2y3y5y6y7y8*y8y9*y9	1128.56	42.203	53654	2	564.79	-3.03
O33921 AGP_SALTY Glucose-1-phohatase	5		DTFSANYQQEPGVQGPLK	208	18	7	33.93	b10b13y2y8y12y13y18	1978.97	56.451	43523	2	989.99	7.83
O33921 AGP_SALTY Glucose-1-phohatase	6	Carbamidomethyl+C(14)	LLEQITHYQDSPCK	182	15	6	41.65	y2y5y8y9y10y15	1818.85	51.180	43461	3	606.95	-13.02
O33921 AGP_SALTY Glucose-1-phohatase	7		APLANNGSVLAQSTPNAWPAWDVPGGQLTTK	43	31	14	71.79	b2b3b4b8b9*b9b18y3y8*y8y9y13y14y31	3161.61	83.524	35013	3	1054.54	4.09
O33921 AGP_SALTY Glucose-1-phohatase	8		SQLHLDSEYK	172	10	10	74.02	b7b8*b8y2y4*y4y6y7y8y10	1219.59	39.808	24346	2	610.30	-6.21
O33921 AGP_SALTY Glucose-1-phohatase	9	Carbamidomethyl+C(14)	LLEQITHYQDSPCKEK	182	17	6	37.36	b2b8y6y7y11y15	2075.99	47.463	17148	3	692.67	-6.70
O33921 AGP_SALTY Glucose-1-phohatase	10		NGYQDSLFTSPTVAR	266	15	4	30.4	b3b4b11y14	1655.79	72.289	3522	3	552.60	-4.50
O33921 AGP_SALTY Glucose-1-phohatase	11		VTVLVGHDSNIASLLTALDFKPYQLHDQYER	304	31	24	141.2	b4*b4b10b12*b12*b12b13*b13y3y4*y4*y4y5*y5y6y7y10y12y14y17y18y19y20*y20	3542.77	95.692	187194	5	709.36	-17.37
O33921 AGP_SALTY Glucose-1-phohatase	12		NVAAPLVK	281	8	4	55.24	y3y4y5y6	811.49	39.706	44228	2	406.25	-17.60
O33921 AGP_SALTY Glucose-1-phohatase	13	Carbamidomethyl+C(16)	TVATAQFFITGAFPGCDIPVHHQEK	116	25	4	19.53	b6b12b15y10	2771.33	83.061	7053	3	924.45	-11.72
O33921 AGP_SALTY Glucose-1-phohatase	14		GGVLEVYMGHYTR	74	13	5	44.42	b7b9y5y7y10	1481.75	70.724	3341	3	494.59	20.76
O33921 AGP_SALTY Glucose-1-phohatase	15	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	GCPVDANGFCPLDKFDNMNTAAK	389	24	8	62.47	b4y3y4y6y10y14y20y22	2641.18	78.315	97133	3	881.07	-1.02
O33921 AGP_SALTY Glucose-1-phohatase	16	Carbamidomethyl+C(8); Carbamidomethyl+C(16)	VTLELKGCPVDANGFCPLDK	383	20	5	26.08	b13y6*y6y8y9	2233.08	67.479	92706	3	745.03	-10.39
O33921 AGP_SALTY Glucose-1-phohatase	17		LKNGYQDSLFTSPTVAR	264	17	6	46.61	b6b9b10y4y6y7	1896.96	58.318	44804	3	632.99	-11.65
O33921 AGP_SALTY Glucose-1-phohatase	18		ARSQLHLDSEYK	170	12	5	23.01	b9*b9y4*y4y11	1446.71	75.958	26053	2	723.86	-14.34
O33921 AGP_SALTY Glucose-1-phohatase	19		HNLRAPLANNGSVLAQSTPNAWPAWDVPGGQLTTK	39	35	5	24.72	b12b22y12y13*y13	3681.86	77.441	22196	4	921.22	-7.63
O33921 AGP_SALTY Glucose-1-phohatase	20		VGNSLVDRAFTLQYYEGFPMQVAVGGIHTDRQWK	226	34	3	11.12	b10b12y6	3928.85	84.235	12242	3	1310.29	-6.28
O33921 AGP_SALTY Glucose-1-phohatase	21	Oxidation+M(19)	VGNSLVDRAFTLQYYEGFPMQVAVGGIHTDR	226	31	4	16.71	b4b8b14y6	3502.63	84.062	14553	4	876.41	-1.32
O33921 AGP_SALTY Glucose-1-phohatase	22		LHLDESYK	174	8	0	1.89		1004.49	39.844	3449	2	502.75	-14.10

O33921 AGP_SALTY Glucose-1-phohatase	23		LLEQITHY	182	8	0	4.53		1016.55	47.425	1563	2	508.78	12.25
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	1		ADAFAVIVK	238	9	5	46.59	b6y5y6y7y9	933.53	62.427	43919	2	467.27	-11.05
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	2		TQGAAAFEGAVIAYEPVWAIGTG K	152	24	9	29.76	b2*b2b3°b3b8b11b12y4y24	2407.25	93.561	38301	2	1204.13	9.43
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	3		SATPAQAQAVHK	176	12	17	112.62	b2b3°b3b7°b7y1y2y3y4y5*y5y6y7*y7y8y9y12	1208.63	18.896	30944	2	604.82	-6.97
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	4		DIGAQYIIIGHSER	84	14	4	27.74	b2y3y4y6	1571.81	61.632	11861	3	524.61	-6.60
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	5		AAAGSHIMLGAQNVDNLNSGAFT GETSAEMLK	52	32	4	11.33	b11y2y9y13	3204.54	100.647	1921	3	1068.85	-9.60
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	6	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	7	35.27	b6b7b9b13y3y10°y10	2433.23	88.205	25437	2	1217.12	12.44
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	7	Carbamidomethyl+C(9)	EQGLTPVLCIGETEAEENEAGK	117	21	6	25.5	b4b5°b5*b5b13y5	2245.11	55.942	3387	4	562.03	18.60
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	8		HPLVMGNWK	2	9	3	31.3	b7y4y6	1081.54	39.145	2984	2	541.28	-16.70
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	9	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAEENEAGKTEE VCAR	117	28	16	155.8	y3y4y5°y5y6y7y12y13°y13y16y18y20y21y23y24y26	3090.43	72.031	188968	3	1030.82	-0.63
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	10		TQGAAAFEGAVIAYEPVWAIGTG KSATPAQAQAVHK	152	36	9	22.69	b5b7°b7b11°b11*b11b13°b13*b13	3596.83	130.759	41916	4	899.96	-6.65
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	11		ADAKIAEQVIIQYGGSVNASAAE LFAQPDIDGALVGGASLK	196	42	3	10.86	b5y7y21	4172.14	92.102	2887	4	1043.79	-1.76
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	12		TPAQAQAVHK	178	10	4	30.21	b3°b3b4b8	1050.56	18.897	12218	2	525.78	-9.18
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	13		PAQAQAVHK	179	9	9	80.79	b3*b3b4b5*b5b6*b6b7b8	949.51	18.896	10568	2	475.26	-9.13
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	14		ATPAQAQAVHK	177	11	2	7.72	b3°b3	1121.60	18.896	1618	2	561.31	-2.39
P0A1Z2 SKP_SALTY Chaperone protein skp	1		IAIVNMGNLFQQVAQK	23	16	21	115.92	b2b3b4b6*b6b15y1y2*y2y3y5*y6*y6y7*y7y8y11y12y13y16*y16	1773.97	89.640	278957	2	887.49	3.51
P0A1Z2 SKP_SALTY Chaperone protein skp	2		TGVSNTLENEFK	39	12	15	112.62	b2b3b11y2y4y5°y5y6y7y8°y8*y8y9y10y12	1338.66	57.273	155414	2	669.83	1.19
P0A1Z2 SKP_SALTY Chaperone protein skp	3		VANDQSIDLVVDANTVAYNSSDV KDITADVLK	126	32	19	114.39	b4*b4b5b6b8b9b11b15b18y1y3y13y14*y14y15y16y25y27y32	3392.73	89.644	102521	3	1131.58	7.05
P0A1Z2 SKP_SALTY Chaperone protein skp	4		METDLQSK	59	8	9	41.71	b2b8y2y4y6°y6y7°y7y8	951.44	26.420	86323	2	476.22	-9.37
P0A1Z2 SKP_SALTY Chaperone protein skp	5		AQAFEKDR	97	8	10	65.76	b2b5*b5b6y1y2y3y5°y5y6	964.47	17.704	5288	2	482.74	-10.13
P0A1Z2 SKP_SALTY Chaperone protein skp	6		VANDQSIDLVVDANTVAYNSSDV K	126	24	4	13.11	b8b11y11*y11	2537.24	84.149	36859	3	846.42	0.48
P0A1Z2 SKP_SALTY Chaperone protein skp	7		TGVSNTLENEFKGR	39	14	15	115.6	b3y3y4y6y7°y7*y7y8*y8y9°y9y11°y11*y11y12	1551.75	52.953	175405	3	517.92	-14.71
P0A1Z2 SKP_SALTY Chaperone protein skp	8		KVANDQSIDLVVDANTVAYNSSD VK	125	25	4	22.33	b6y8°y8y9	2665.29	94.092	13313	4	667.08	-14.47
P0A1Z2 SKP_SALTY Chaperone protein skp	9		AAELQKMETDLQSK	53	14	4	19.96	b5*b5b12y12	1591.81	64.991	2748	3	531.28	8.13
P0A1Z2 SKP_SALTY Chaperone protein skp	10	Oxidation+M(6)	LEKDVMSQR	82	9	4	31.3	b4b6y5*y5	1121.57	62.124	1823	2	561.29	11.43
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	1		LVGVGFFTSGGNGAQEAGK	35	19	10	42.34	b2b6b17y1y3y7*y7y15y18y19	1795.92	89.641	121055	3	599.31	13.80

Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	2		QLGSMLVEMAAHQVDKEK	134	18	11	69.66	b8*b8b10b18y3y4y7y8y9y11y18	2013.99	73.329	108616	3	672.00	-11.39
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	3		AYPDLDAIIAPDANALPAAQAEE NLKR	209	28	14	104.41	b7b8b10b14y4y5y6y9y12y18y19y20y23y28	2863.49	87.500	94270	3	955.17	-0.34
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	4	Carbamidomethyl+C(12)	ILTWSDTKPECR	111	13	11	97.71	b1b2y2y4y6y8y9y10y11y12y13	1620.75	49.816	76082	3	540.92	-13.78
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	5		NMPMNVGDSLDPGIGK	284	17	12	77.79	b2b3b6b12b15b16y2y4y5y11y15y17	1757.86	79.566	70979	2	879.44	4.03
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	6		NNLAIVGFSTPNVMRPYVQR	237	20	20	122.31	b2*b2b3*b3b4*b4b5b10*b10y2*y2y3y5y10y12y14y15y16y17y20	2276.19	77.715	70938	3	759.40	-3.11
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	7		ISQEHPGWEIVTTQFGYNDATK	177	22	9	41.13	b10*b10b11*b11b13y6y12°y12y13	2521.20	72.393	61876	3	841.07	-1.07
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	8		SLQTAEGIIK	199	10	4	27.7	b8y4y7y10	1059.59	50.798	53926	2	530.30	-9.33
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	9		VAFFYSSPTVTDQNQWVK	154	18	8	62.83	b8b12y8y11y12y13y14y18	2117.05	77.449	52577	2	1059.03	9.69
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	10		ISVYVANALLK	273	11	8	66.89	b1b2y5y6y7y8y10y11	1190.70	73.297	49534	2	595.86	-9.02
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	11		VTVSPNSEQGYHYEAK	301	16	10	101.58	y4y5y7y8*y8y9y10y11y12y16	1808.82	36.147	42049	3	603.61	-12.15
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	12		EFGLWDVVQQGK	261	12	7	35.29	b2°b2b3y5y7y8y12	1405.71	82.260	35489	2	703.36	0.61
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	13		GNGIVLLPER	317	10	5	34.69	b2y3y5y6y10	1067.61	61.192	21355	2	534.31	-6.40
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	14		GTVKEFGLWDVVQQGK	257	16	4	17.79	b10b13y5y16	1790.92	75.794	14074	3	597.64	-14.65
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	15		VIFNKDNIDK	327	10	5	29.46	b7°b7b8*b8y8	1205.67	77.242	5906	2	603.34	14.48
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	16		VAFFYSSPTVTDQNQWVKEAK	154	21	6	22.49	b6b10b13*b13y12y21	2445.18	97.616	2728	3	815.73	-12.88
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	17		AYPDLDAIIAPDANALPAAQAEE NLK	209	27	3	35.87	b11b12b13	2707.36	64.572	11690	3	903.13	-11.90
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	18		QLGSMLVEMAAHQVDK	134	16	8	50.33	b3b5b8*b8b14y6y14°y14	1756.91	89.642	2404	3	586.31	19.52
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	19		AKISQEHPGWEIVTTQFGYNDAT K	175	24	6	22.41	b12°b12y11*y11y12°y12	2720.33	112.035	3744	2	1360.67	-1.35
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	20		SYIINQGTQPKQLGSMLVEMAAHQ VDK	124	26	6	37.48	b9y5y6y7y10*y10	2908.39	104.393	2173	4	727.85	-14.02
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	21	Oxidation+M(5)	QLGSMLVEMAAHQVDKEK	134	18	9	42.31	b4*b4b6b11b12y8°y8y10*y10	2030.00	66.845	3754	3	677.34	-1.20
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	22		EMAAHQVDKEK	141	11	3	13.76	b5b9°b9	1285.61	73.299	4902	2	643.31	-8.36
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB	23	Carbamidomethyl+C(10)	TWSDTKPECR	113	11	1	7.51	b3	1394.61	49.828	4834	2	697.81	6.13
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		GYLSPYFINKPETGAVELESPFILL ADKK	197	29	27	249.52	b2b3b4°b4b5b6°b6b7b10y2y3y4y5y6y7y8y9y10y11y12y13y19y23y25y26y27y29	3239.69	95.310	259756	4	810.68	-9.50
P0A1D3 CH60_SALTY 60 kDa chaperonin	2		ANDAAGDGTTTATVLAQSIITEGL K	80	25	21	134.39	b2*b2b3*b3b4°b4*b4b5*b5b7y1y3y4°y4y5y6y7y8y9y10y25	2418.22	92.005	215507	3	806.75	-4.64
P0A1D3 CH60_SALTY 60 kDa chaperonin	3		EMLPVLEAVAK	231	11	10	68.66	b2°b2b3b8y2y3y4y6y8y11	1199.66	79.768	157888	2	600.33	-7.94

IP0A1D3 CH60_SALTY 60 kDa chaperonin	4	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDL PK	501	25	41	275.6	b2b3°b3b4°b4b5°b5°b5b6°b6°b6b7°b7b8°b8°b8b10°b10°b10b11°b11b12°b12b13b14y2y3y4y5°y5y6°y6y7y8y9y10y11y12°y12y13y25	2670.32	123.861	156664	3	890.78	0.37
IP0A1D3 CH60_SALTY 60 kDa chaperonin	5	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	16	108.98	b3°b3b5b13y1y3y5y6y9y12*y12y13y14y15y18*y18	1957.02	61.545	110094	2	979.01	4.74
IP0A1D3 CH60_SALTY 60 kDa chaperonin	6		AVAAAVEELK	122	10	14	89.59	b1b2b3y1y2y3°y3y4°y4y5y6y7y8y10	1000.56	47.017	108277	2	500.78	-10.13
IP0A1D3 CH60_SALTY 60 kDa chaperonin	7		GVNVLADAVK	18	10	9	89.59	b7y1y3y4y5y6y7y8y10	985.55	55.693	83058	2	493.28	-13.25
IP0A1D3 CH60_SALTY 60 kDa chaperonin	8		VVINKDTTTIIDGVGEEAAIQGR	322	23	14	123.13	b10b11b12y2y3*y3y4y5y6y7°y7y8y9y13	2399.27	66.986	79299	3	800.43	-5.09
IP0A1D3 CH60_SALTY 60 kDa chaperonin	9	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	12	89.59	b2b3°b3y1y2y3y4y5y6y7y8y10	1063.50	35.005	73324	2	532.25	-6.08
IP0A1D3 CH60_SALTY 60 kDa chaperonin	10		GGDGNYGYNAAATEEYGNMIDMG ILDPTK	470	28	12	48.87	b2b5°b5y1y2y3y4y5y8y11y13y28	2966.32	88.233	71153	2	1483.66	12.84
IP0A1D3 CH60_SALTY 60 kDa chaperonin	11		SFGAPTITK	42	9	12	63.12	b2b3°b3y1y2°y2y3y5°y5y6y7y9	921.49	44.636	68392	2	461.25	-14.44
IP0A1D3 CH60_SALTY 60 kDa chaperonin	12		LIAEAMDK	160	8	5	41.71	y2y4y6y7y8	890.45	38.710	50787	2	445.73	-12.82
IP0A1D3 CH60_SALTY 60 kDa chaperonin	13		AVAAGMNPMDLK	105	12	7	37.21	b2b3b7y1y7y8y12	1217.60	58.047	48362	2	609.30	-1.20
IP0A1D3 CH60_SALTY 60 kDa chaperonin	14		AMEAPLR	445	7	6	41.34	b7y4y5°y5y6y7	787.40	36.399	40466	2	394.21	-10.77
IP0A1D3 CH60_SALTY 60 kDa chaperonin	15		VGKEGVITVEDGTGLQDELDDVVE GMQFDR	168	29	4	11.8	b2b13y5y10	3135.50	72.268	40243	4	784.63	-4.52
IP0A1D3 CH60_SALTY 60 kDa chaperonin	16		ATLEDLGQAK	311	10	10	72.26	b5°b5b8y1y4y6y7°y7y8y10	1045.55	43.894	37909	2	523.28	-6.77
IP0A1D3 CH60_SALTY 60 kDa chaperonin	17		GQNEQNNGVIK	430	11	8	42.57	b2°b2b3y7y8°y8y9y11	1201.58	26.767	34829	2	601.29	-3.05
IP0A1D3 CH60_SALTY 60 kDa chaperonin	18		VEDALHATR	395	9	11	76.65	b1b2b4y1y2y3y4y5y7y8y9	1011.51	25.745	34715	2	506.26	-9.65
IP0A1D3 CH60_SALTY 60 kDa chaperonin	19		AIAQVGTISANSDETVGK	142	18	7	16.15	b1b5°b5y10°y10y13*y13	1760.90	72.364	23490	2	880.95	-3.60
IP0A1D3 CH60_SALTY 60 kDa chaperonin	20		SFGAPTITKDGVSVAR	42	16	3	24.32	b7b8y7	1605.85	54.771	2173	3	535.95	-6.39
IP0A1D3 CH60_SALTY 60 kDa chaperonin	21		LAGGVAVIK	371	9	6	80.91	b5b6y3y4y7y8	827.52	44.714	69024	2	414.26	-18.66
IP0A1D3 CH60_SALTY 60 kDa chaperonin	22		DTTTIIDGVGEEAAIQGR	327	18	4	25.7	b7b12b14y10	1845.91	99.453	63576	3	615.97	-7.34
IP0A1D3 CH60_SALTY 60 kDa chaperonin	23		GYLSPYFINKPETGAVELESPFILL ADK	197	28	3	12	b14y3y18	3111.58	106.518	2450	4	778.65	-14.99
IP0A1D3 CH60_SALTY 60 kDa chaperonin	24		EIELEDKFENMGAMVK	58	17	16	122.12	b3°b3b5y4*y4y5y6y7y8y10*y10y11°y11*y11y12y15	2010.92	72.969	157523	3	670.98	-13.54
IP0A1D3 CH60_SALTY 60 kDa chaperonin	25		FENMGAMVKEVASK	65	15	4	37.67	b4b5b7b10	1668.78	34.984	78127	3	556.93	-14.48
IP0A1D3 CH60_SALTY 60 kDa chaperonin	26		LIAEAMDKVGK	160	11	6	66.89	y3y4y7y8°y8y9	1174.64	45.450	36617	2	587.82	-6.75
IP0A1D3 CH60_SALTY 60 kDa chaperonin	27		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	20	114.59	b3b4b5b6°b6b7b10b13°b13°b13y4y5y7*y7y9*y9y10y19y25y29	3675.88	121.839	36612	3	1225.97	3.25
IP0A1D3 CH60_SALTY 60 kDa chaperonin	28	Carbamidomethyl+C(21)	VTRSALQYAASVAGLMITTECMV TDLPK	498	28	4	15.51	b11b20y11y16	3026.51	114.051	28636	3	1009.51	-8.95
IP0A1D3 CH60_SALTY 60 kDa chaperonin	29		IADLKGQNEQNNGVIK	425	16	3	17.79	b13y4y11	1741.91	53.684	19535	2	871.46	0.14

P0A1D3 CH60_SALTY 60 kDa chaperonin	30	Carbamidomethyl+C(16)	AVAAAVEELKALSVPSCDSK	122	20	3	14.89	b18y6y18	2045.04	71.732	17939	3	682.35	-7.04
P0A1D3 CH60_SALTY 60 kDa chaperonin	31		AIAQVGTISANSDETVGKLI AEAMDK	142	26	4	18.95	b4y3y5y7	2632.36	91.464	13312	3	878.13	4.36
P0A1D3 CH60_SALTY 60 kDa chaperonin	32	Phosphoryl STY(13)	SFGAPTITKDGVSVAR	42	16	5	36.68	b11b15y5y11y12	1685.80	93.650	4163	2	843.40	-8.11
P0A1D3 CH60_SALTY 60 kDa chaperonin	33	Oxidation+M(9)	AVAAGMNPMDLK	105	12	5	55.81	b4b5b6b7y5	1233.59	57.631	197463	3	411.87	-8.11
P0A1D3 CH60_SALTY 60 kDa chaperonin	34	Oxidation+M(22)	EGVITVEDGTGLQDELDVVEGMQFDR	171	26	5	28.45	b3b4b9b14y6	2867.32	113.250	77064	3	956.45	-0.94
P0A1D3 CH60_SALTY 60 kDa chaperonin	35	Carbamidomethyl+C(18) ;Oxidation+M(13)	SALQYAASVAGLMITTECMVTDLPK	501	25	6	27.99	b7b8b12y4y11°y11	2686.35	115.299	8885	3	896.12	14.72
P0A1D3 CH60_SALTY 60 kDa chaperonin	36	Oxidation+M(9)	AVAAGMNPMDLKR	105	13	5	54.63	b3b5b8b12y9	1389.69	50.560	2632	3	463.90	-8.70
P0A1D3 CH60_SALTY 60 kDa chaperonin	37		EDALHATR	396	8	1	9.02	b6	912.44	25.741	24038	2	456.73	-9.70
P0A1D3 CH60_SALTY 60 kDa chaperonin	38		AAAVEELK	124	8	1	8.42	b6	830.45	47.009	16483	1	830.45	-11.10
P0A1D3 CH60_SALTY 60 kDa chaperonin	39		GAPTITK	44	7	0	1.51		687.40	44.637	13482	1	687.40	-11.45
P0A1D3 CH60_SALTY 60 kDa chaperonin	40		AIAQVGTISANSDETVG	142	17	1	7.29	y6	1632.80	72.369	12455	2	816.90	-6.43
P0A1D3 CH60_SALTY 60 kDa chaperonin	41		NVLADAVK	20	8	2	8.42	b6*b6	829.47	55.669	10008	1	829.47	-3.46
P0A1D3 CH60_SALTY 60 kDa chaperonin	42		DALHATR	397	7	1	9.02	b5	783.40	25.717	7210	2	392.21	-7.71
P0A1D3 CH60_SALTY 60 kDa chaperonin	43	Carbamidomethyl+C(4)	SVPSCDSK	134	8	0	1.89		879.39	35.001	3757	1	879.39	-0.14
P0A1D3 CH60_SALTY 60 kDa chaperonin	44		EMLPVLEAVAK	231	11	0	2.26		1181.65	79.743	8276	2	591.33	-6.10
P00924 ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	18	145.42	b2*b2b4*b4b5b6°b6b7y2y3y5y6y7y8y9y10*y10y12	1286.70	65.886	103888	2	643.86	-5.03
P00924 ENO1_YEAST Enolase 1	2		SIVPSGASTGVHEALEMR	32	18	17	126.37	b2y1y2y4y6°y6y7°y7y8y9y10y13y14°y14y15°y15y16	1840.90	60.886	80222	3	614.31	-11.21
P00924 ENO1_YEAST Enolase 1	3		VNQIGTLESSEIK	346	12	9	80.79	b2*b2b3y3y5y6y7y8y9y12	1288.71	54.163	67167	2	644.86	-3.13
P00924 ENO1_YEAST Enolase 1	4		TFAEALR	178	7	5	41.34	b1b6y3y5y7	807.42	45.096	57211	2	404.22	-13.91
P00924 ENO1_YEAST Enolase 1	5		TAGIQIVADDLTVTNPK	312	17	11	86.32	b9b14y2y3y4y6y9y10y11y13y17	1755.95	72.225	45227	2	878.48	0.07
P00924 ENO1_YEAST Enolase 1	6		IEEELGDNAVFAGENFHHGDK	415	21	7	39.7	b12y1y9y10y11y19y21	2328.03	57.179	37582	4	582.76	-9.96
P00924 ENO1_YEAST Enolase 1	7		AVDDFLISLDGTANK	88	15	12	60.77	b2b5b6b12b14y1y5*y5y6°y6y8y15	1578.80	82.001	35655	2	789.90	0.62
P00924 ENO1_YEAST Enolase 1	8		WLTGPQLADLYHSLMK	272	16	10	76.67	b12*b12y2y4y5y6y12°y12y13y14	1872.94	95.632	23886	3	624.99	-13.49
P00924 ENO1_YEAST Enolase 1	9		AADALLK	338	8	9	109.35	b5b6°b6b7y3y4y5y6y7	814.49	53.318	81592	2	407.75	-19.41
P00924 ENO1_YEAST Enolase 1	10		HLADLSK	132	7	3	38.33	b4b5y4	783.43	25.372	33282	2	392.22	-11.76
P00924 ENO1_YEAST Enolase 1	11		YDLDFK	258	6	2	27.43	b3y3	800.39	99.388	10692	1	800.39	7.63
P00924 ENO1_YEAST Enolase 1	12		GNPTVEVELTTEK	15	13	4	35.82	b3*b3b4b5	1416.69	65.894	3595	3	472.90	-20.42
P00924 ENO1_YEAST Enolase 1	13		TGAPAR	397	6	1	13.9	y5	572.31	27.526	3384	1	572.31	-0.96
P00924 ENO1_YEAST Enolase 1	14		YPIVSIEDPFAEDDWEAWSHFFK	289	23	4	13.48	b10y5y7°y7	2828.33	124.479	2914	3	943.45	15.37
P00924 ENO1_YEAST Enolase 1	15		AVDDFLISLDGTANKSK	88	17	5	23.83	b5b11y10y15°y15	1793.91	64.859	149880	2	897.46	-8.44
P00924 ENO1_YEAST Enolase 1	16		YDLDFKNPNSDK	258	12	3	26.99	b6y3y4	1455.69	81.976	9059	2	728.35	8.39
P00924 ENO1_YEAST Enolase 1	17		DQKAVDDFLISLDGTANK	85	18	5	27.46	b12y5y6°y6y13	1949.98	72.331	4829	3	650.67	-0.25

P00924 ENO1_YEAST Enolase 1	18		TFAEALRIGSEVYHNLK	178	17	4	16.91	b4b16y9*y9	1948.03	88.200	4286	3	650.02	2.26
P00924 ENO1_YEAST Enolase 1	19		SVYDSRGNPTVEVELTTEK	9	19	4	21.55	b6b12y4y10	2124.06	47.893	2387	3	708.69	6.90
P00924 ENO1_YEAST Enolase 1	20		IEEELGDNAVFAGENFHGDKL	415	22	8	60.6	b5y6y8*y8y9y10y11y13	2441.14	82.477	2066	3	814.38	-0.30
P00924 ENO1_YEAST Enolase 1	21	Oxidation+M(15)	WLTGSQLADLYHSLMKR	272	17	5	24.32	b4*b4b7*b7b10	2045.08	107.776	8120	3	682.36	6.63
P00924 ENO1_YEAST Enolase 1	22	Oxidation+M(15)	WLTGSQLADLYHSLMK	272	16	7	36.68	b6b14*b14y6y13*y13y14	1888.96	86.886	4452	3	630.33	-1.16
P00924 ENO1_YEAST Enolase 1	23		PSGASTGVHEALEMR	35	15	3	25.07	b8b9b13	1541.74	60.889	4990	2	771.37	3.09
O54297 RS4_SALTY 30S ribosomal protein S4	1		VVNIASYQVSPNDVVSIR	128	18	18	135.95	b2b3b8*b8b9b15b17y3y4y5y8*y8y9y10y13*y13y14y18	1960.06	71.962	62732	2	980.53	4.48
O54297 RS4_SALTY 30S ribosomal protein S4	2		AALELAEQR	156	9	10	77.9	b3b4*b4y4*y4y5y6*y6y7y9	1000.53	42.968	56202	2	500.77	-10.25
O54297 RS4_SALTY 30S ribosomal protein S4	3		REGTDLFLK	13	9	5	31.3	b5b6*b6y4y9	1078.59	50.934	13981	2	539.80	-3.40
O54297 RS4_SALTY 30S ribosomal protein S4	4		IEQAPGQHGAR	33	11	3	28.07	b7y8y9	1163.59	30.664	2001	3	388.53	-4.62
O54297 RS4_SALTY 30S ribosomal protein S4	5		LDNVVYR	97	7	4	41.34	b3b4*b4b6	878.46	32.421	63613	2	439.74	-10.14
O54297 RS4_SALTY 30S ribosomal protein S4	6		EAAR	77	4	1	13.15	y3	446.23	31.120	30881	1	446.23	-11.35
O54297 RS4_SALTY 30S ribosomal protein S4	7		EKPTWLEVDAGK	165	12	3	23.01	b5b10y3	1372.71	54.496	11456	2	686.86	-4.18
O54297 RS4_SALTY 30S ribosomal protein S4	8		SDLSADINEHLIVELYSK	188	18	4	22.62	b5b8y3y17	2046.04	79.017	4937	4	512.27	0.84
O54297 RS4_SALTY 30S ribosomal protein S4	9		GNTGENLLALLEGR	83	14	6	32.52	b7*b7b9*b9b12y13	1456.76	93.684	4466	2	728.89	-7.88
O54297 RS4_SALTY 30S ribosomal protein S4	10		LKGTGENLLALLEGR	81	16	5	38.3	b8y3*y3y4y5	1697.93	87.597	11689	3	566.65	-12.87
O54297 RS4_SALTY 30S ribosomal protein S4	11		LDNVVYRMGFGATR	97	14	4	19.96	b12*b12y9y13	1598.83	122.768	2435	2	799.92	11.15
O54297 RS4_SALTY 30S ribosomal protein S4	12	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	5	30.68	b5b7*b7y8y10	1451.70	60.937	1669	3	484.57	-13.96
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		VLVLVAAPEGIAALEK	155	16	11	84.67	b2b3b4b5b6b7y1y3y9y11y16	1592.97	85.913	33408	2	796.99	2.07
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		NEETLEPVVPYFQK	103	13	4	28.83	b1y5y7y8	1593.80	65.246	25141	2	797.40	13.86
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		AGLGMMEGVLENVPSAR	78	17	11	72.12	b11b13y1y2y4y5y7y11y12y13y17	1730.86	81.594	24879	2	865.94	3.60
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		ITVVPILR	70	8	5	41.71	y2y4y5y6y8	910.60	69.394	11868	2	455.80	-8.98
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		LVSNI DER	116	8	9	41.71	y2*y2y3*y3y6y7*y7y8*y8	945.49	34.942	5528	2	473.25	-7.10
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	6		AHPDVELYASIDQGLNEHGYYIP GLGDAGDK	171	32	4	17.15	b5b8*b8b13	3365.65	91.848	3709	3	1122.56	7.18
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	7		FRELASEVGSLTYEATADLETEK	27	24	5	28.61	b3b8b9y4y13	2672.37	102.018	2452	2	1336.69	13.34
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	8		ELASEVGSLTYEATADLETEK	29	22	9	45.75	b4b6*b6b9b13*b13b14y6y12	2369.20	88.544	4528	2	1185.10	17.42
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	9		AHPDVELYASIDQGLNEHGYYIP GLGDAGDKIFGTK	171	37	9	50.8	b4b6b7b8y4y10y11y14*y14	3911.95	88.526	40208	4	978.74	1.62
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	10		LGLMRENDISTK	14	12	3	23.01	b3b11y6	1376.73	39.263	8515	3	459.58	7.27
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	11	Phosphoryl STY(14)	FRELASEVGSLTYEATADLETEK	27	24	4	36.18	b18y8y9y10	2752.29	73.944	3796	4	688.83	0.80
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	1		ALAINLVDPAAGTVIEK	84	18	14	93.12	b2b3b4b5*b5b6y1y2*y2y11y12y13y14y18	1766.01	80.489	100567	2	883.51	1.87

P23905 DGAL_SALTY D-galactose-binding periplasmic protein	2		SSIPVFGVDALPEALALVK	250	19	15	109.2	b2b4b5°b5y1y2y3y5y8y10y11y13y14y16y19	1926.10	107.608	90808	2	963.55	2.79
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	3		SGAMAGTVLNDANNQAK	269	17	18	145.57	b2b3b4b6b9°b9y4y5*y5y6y7y8y9y10y12°y12y13y17	1661.79	45.971	85988	2	831.40	0.51
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	4		VPYVGVDKDNLSEFTQK	315	17	5	28.3	b3y5y6y9y17	1938.97	61.211	55854	3	646.99	-6.67
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	5		HWQANQGWDLNKDGK	148	15	10	75.55	b2b3b4b5b7y2y4y5y8y14	1796.82	45.976	43045	3	599.61	-13.11
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	6		DNLSEFTQK	323	9	7	31.3	b2b4°b4y6*y6y8*y8	1081.51	30.701	5888	2	541.26	-5.87
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	7		GIQTEQLALDTAMWDTAQAKDK	192	22	7	18.94	b3b14b22y2y6y8°y8	2434.16	80.548	5200	2	1217.58	-13.14
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	8		YDDNFMSVVR	34	10	4	42.47	y3y5y9*y9	1245.56	66.014	28061	2	623.28	2.74
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	9		ESGVIQGDLIAK	136	12	3	23.01	b9y3y8	1229.67	53.455	20441	2	615.34	-6.85
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	10		NLAEGK	293	6	1	13.9	b4	631.34	46.371	7818	1	631.34	-8.51
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	11		ELNDK	187	5	1	13.53	y4	618.30	48.955	3835	1	618.30	-8.09
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	12		GAADGTSWK	299	9	3	31.3	b3y4y6	892.43	68.119	1760	1	892.43	10.53
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	13		SAPDVQLLMNDSQNDQSKQNDQIDVLLAK	52	29	6	36.43	b12b13y4y5y21°y21	3227.60	77.985	36287	3	1076.54	5.45
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	14		DGKSAPDVQLLMNDSQNDQSK	49	21	5	24.02	b5°b5b6b13°b13	2290.06	77.405	19686	3	764.03	0.85
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	15		NLAEGKGAADGTSWK	293	15	4	18.79	b7y3°y3y7	1504.73	37.398	16178	3	502.25	-3.41
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	16		ALDSYDKAYYVGTDISK	120	16	7	52.34	b10y5y6°y6y7°y7y8	1795.83	47.797	11943	3	599.28	-6.59
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	17		ELNDKGIQTEQLALDTAMWDTAQAK	187	25	10	91.15	b12b22y3y5y6y7y8y9y10y12	2790.36	79.755	11033	3	930.79	-0.26
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	18		KALDSYDK	119	8	3	33.93	b4b5y3	939.48	47.546	3025	2	470.24	1.23
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	19		SGAMAGTVLNDANNQAKATFDLAK	269	24	4	26.88	b8b9y6y10	2408.17	76.906	2601	4	602.80	-8.72
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	20	Phosphoryl STY(15)	VPYVGVDKDNLSEFTQK	315	17	4	27.05	b9b12b14y3	2018.96	93.536	7051	3	673.66	12.39

P23905 DGAL_SALTY D-galactose-binding periplasmic protein	21	Phosphoryl STY(11)	AYYVGTDSKESGVIQGDLIAK	127	21	4	22.82	b9b10°b10y12	2294.12	67.397	5100	3	765.38	12.88
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	22	Oxidation+M(9)	SAPDVQLLMNDSQNDQSK	52	18	3	16.15	b13b17y9	2005.94	90.103	86798	2	1003.47	13.02
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	23	Oxidation+M(13)	GIQTEQLALDTAMWDTAQAKDK	192	22	5	13.9	b3*b3b5°b5y11	2450.22	128.396	2327	3	817.41	12.16
P64052 EFTS_SALTY Elongation factor Ts	1		ITDVEVLK	104	8	5	58.25	y3y4y6y7y8	916.52	48.341	170199	2	458.77	-11.85
P64052 EFTS_SALTY Elongation factor Ts	2		VASLEGDVLGSYQHGAR	134	17	14	142.53	b2b3y4y5y7y8*y8y9y10y12y13y15y16y17	1758.85	58.651	113152	3	586.96	-13.88
P64052 EFTS_SALTY Elongation factor Ts	3		FTGEVSLTGQPFVMEPSK	222	18	9	51.86	b3b5b12y1y3y5°y5y13y14	1953.97	74.568	79796	2	977.49	5.06
P64052 EFTS_SALTY Elongation factor Ts	4		IGENINIR	125	8	11	68.77	y2y3*y3y4*y4y5*y5y6y7*y7y8	928.51	44.195	67334	2	464.76	-11.24
P64052 EFTS_SALTY Elongation factor Ts	5		SVGQLLKEHNADVTGFIR	240	18	8	33.93	b1b4b6y2y4y9y10y18	1984.04	65.099	25548	3	662.02	-8.55
P64052 EFTS_SALTY Elongation factor Ts	6		ALTEANGDIELAIENMRK	25	18	3	23.31	y5y14y16	1987.99	74.070	25269	3	663.33	-12.83
P64052 EFTS_SALTY Elongation factor Ts	7		AGNVAADGVIK	52	11	9	75.65	b3y1y4y6°y6y8y9y10y11	1014.55	36.427	21728	2	507.78	-8.66
P64052 EFTS_SALTY Elongation factor Ts	8		ALTEANGDIELAIENMR	25	17	6	35.22	b7b13°b13y4y5y13	1859.93	80.541	11611	2	930.47	9.78
P64052 EFTS_SALTY Elongation factor Ts	9		DAGFQAFADK	85	10	7	61.74	b3b5b9°b9y6y8y10	1069.51	28.135	11451	2	535.26	12.33
P64052 EFTS_SALTY Elongation factor Ts	10		AQFEER	112	7	4	41.34	y3y4y5y7	908.40	24.733	8908	2	454.71	-6.99
P64052 EFTS_SALTY Elongation factor Ts	11	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	5	42.47	b2°b2y3y5y7	1098.47	20.834	6003	2	549.74	0.56
P64052 EFTS_SALTY Elongation factor Ts	12	Carbamidomethyl+C(13)	IDGNVAFILEVNCQTDFVAK	65	20	4	21.68	b3b8b10y1	2253.11	124.557	1530	3	751.71	-7.04
P64052 EFTS_SALTY Elongation factor Ts	13		AEITASLVK	1	9	4	46.59	b3y4y5y6	931.53	48.408	82891	2	466.27	-16.84
P64052 EFTS_SALTY Elongation factor Ts	14		IGVLVAAK	151	8	4	50.47	b3y3y6y7	770.50	46.814	54887	2	385.75	-20.91
P64052 EFTS_SALTY Elongation factor Ts	15		VLDAAVAGK	95	9	3	31.3	b4y3y7	843.48	33.344	35894	2	422.24	-15.27
P64052 EFTS_SALTY Elongation factor Ts	16		FEVGEGIEK	258	9	4	46.08	b7b8y4y8	1007.51	47.934	13773	2	504.26	3.88
P64052 EFTS_SALTY Elongation factor Ts	17		VALVAK	119	6	3	40.96	b4y4y5	600.41	46.811	3626	1	600.41	-2.03
P64052 EFTS_SALTY Elongation factor Ts	18		EHNADVTGFIRFEVGEGIEK	247	20	7	36.87	b11b12°b12°b12b13°b13y4	2247.13	68.891	266968	3	749.72	12.93
P64052 EFTS_SALTY Elongation factor Ts	19		FEVGEGIEKVETDFAAEVAAMSK	258	23	31	300.16	b3b4°b4b5b8°b8b9b10b11b13b15b17y3°y3y4y5°y5y6y7°y7y8°y8y9y10y11y12y13y14y15y20y21	2457.18	105.466	156016	3	819.73	-2.38
P64052 EFTS_SALTY Elongation factor Ts	20		KAGNVAADGVIK	51	12	8	84.32	b3b5b9b11y4y10y11°y11	1142.65	31.021	54047	2	571.83	-5.56
P64052 EFTS_SALTY Elongation factor Ts	21		RVASLEGDVLGSYQHGAR	133	18	3	16.15	b5b9y9	1914.96	53.945	13086	3	638.99	-9.43
P64052 EFTS_SALTY Elongation factor Ts	22		DAGFQAFADKVLDAAVAGK	85	19	6	26.72	b10°b10b11°b11b13y3	1893.96	82.002	4247	3	631.99	-3.80
P64052 EFTS_SALTY Elongation factor Ts	23	Oxidation+M(14)	FTGEVSLTGQPFVMEPSK	222	18	3	16.15	b10y3y9	1969.93	68.918	10222	4	493.24	-11.46

P64052 EFTS_SALTY Elongation factor Ts	24	Oxidation+M(4)	QLAMHVAASKPEFVKPEDVSADV VEK	167	26	3	23.16	y10y11y20	2840.45	61.158	3621	3	947.49	0.69
P64052 EFTS_SALTY Elongation factor Ts	25	Oxidation+M(12)	VETDFAAEVAAMSK	267	14	3	19.96	b4b6y4	1484.67	136.612	2671	1	1484.67	-13.32
P64052 EFTS_SALTY Elongation factor Ts	26		GENINIR	126	7	1	9.89	b3	815.43	44.194	2065	1	815.43	-8.23
P64052 EFTS_SALTY Elongation factor Ts	27	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	1	8.42	b3	997.42	20.830	1618	2	499.22	-2.57
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	22	114.81	b2b5b7°b7b8b22b23b25y2 y3°y3y5y7°y7y8y10y11y12 *y12y13y14y36	3950.89	94.993	120628	4	988.48	1.61
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2		MQLNSTEISELIK	0	13	11	57.95	b2b3b12°b12y2y3y9y10y1 1y13*y13	1505.79	76.567	60477	2	753.40	0.65
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	13	87.3	b2b3b5b7b9b12y3y4*y4y6 y8y10y19	2098.97	68.562	54660	3	700.33	-4.65
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4		DSVGAVVMGPYADLAEGMK	68	19	13	121.41	b4b5b6°b6b8b9b12b13y10 y11y12y13y19	1909.92	83.477	43710	2	955.47	10.23
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		TALAIADAIINQR	175	12	9	30.21	b2°b2y1y2*y2y3y4y8y12	1298.74	73.804	40731	2	649.87	-5.55
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6		ILEVPVGR	93	8	6	41.71	b2y4y5y6°y6y8	882.53	52.228	36460	2	441.77	-13.42
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		GYLADVELAK	453	10	7	59.52	b7y2y3y6y7y8y10	1078.57	60.035	34983	2	539.79	-9.17
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		YAIALNLER	59	9	7	39.08	b1b2y1y3y5y6y9	1062.59	64.268	34698	2	531.80	-4.48
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9		ASTISNVVR	201	9	9	76.65	b2b7y2y3y4y5y6y7y9	946.53	36.898	32392	2	473.77	-6.58
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		ELAAFSQFASDLDDATR	401	17	11	91.09	b5b8y3°y3y4y5y8y9y12y13 y17	1856.88	88.309	30962	2	928.94	8.15
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		QSVDQPVPQTGYK	139	12	14	115.93	b2b8b12y3y4y5*y5y6y7y8 *y8y9y10y12	1349.67	33.860	23724	2	675.34	-2.89
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12		QYAPMSVAQQLVLFAAER	434	19	11	30.57	b2*b2b3°b3b9b11y2°y2y4 y6y19	2109.10	93.078	22993	2	1055.06	11.00
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		ELAAFSQFASDLDDATR	401	18	8	58.74	b2b11b12y3y4y9y10y18	1984.94	82.993	22119	3	662.32	-8.61
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		YAIALNLERDSVGAVVMGPYADL AEGMK	59	28	5	17.93	b10y5y9y11°y11	2953.45	98.113	16939	3	985.16	-9.67
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		EAFPGDVFYLHSR	283	13	4	28.83	b5b6b11y13	1537.75	76.342	9286	3	513.26	4.76
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16		AVDSMPIGR	151	10	4	52.98	y4y5y6y7	1058.56	59.624	41498	2	529.78	-8.53
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17		VNADYVEAFTK	303	11	4	25.06	b3b7y8°y8	1256.64	41.200	23703	2	628.82	16.42
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18		IAQFNVVSEAHNEGTVSVSDGVI R	15	25	5	12.79	b10b12°b12*b12y15	2641.39	93.086	11947	3	881.13	11.46
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	19		TALAQYR	394	7	4	41.34	b5*b5y3y5	822.46	41.941	7312	2	411.73	14.55
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	20		GPVDNDGFSAVEAIPGVIDR	118	21	7	24.02	b4°b4b5°b5*b5b11*b11	2099.08	85.005	3061	2	1050.04	18.84
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	21		DHAPLMQEINQSGGYNDEIEGK	477	22	3	23.77	y6y7y11	2445.12	100.425	2888	4	612.04	8.19
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	22		VGGAAQTK	376	8	3	33.93	b3y6y7	731.40	50.805	2608	1	731.40	-7.76
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	23		VVNTLGAPIDGKGPVDNDGFSAV EAIAPGVIDR	106	33	19	116.83	b3b4°b4b7°b7b26y3°y3y6y 9y10y11y13y14y15y17y26° y26y28	3263.71	84.168	55693	3	1088.57	5.91
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	24	Carbamidomethyl+C(33)	KLEEHGALANTIVVVATASESAAL QYLAPYAGCAMGEYFR	210	40	7	25.15	b12b14y3y5°y5y6y12	4272.11	121.987	33613	4	1068.78	0.11

Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	25		DRGEDALIYDDLSK	250	15	12	133.33	b6b7b8b10b11°b11b12b13y4y5y6y7	1722.86	73.411	33570	2	861.93	2.55
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	26		QKQYAPMSVAQQSLVLFAAER	432	21	7	30.86	b8°b8b12b13°b13y4y6	2365.22	85.659	12913	3	789.08	-7.43
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	27		VNADYVEAFTKGEVK	303	15	4	26.87	b3b6°b6b11	1669.86	103.303	7609	2	835.43	9.50
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	28	Carbamidomethyl+C(6)	DSGIKCIYVAIGQK	187	14	3	19.96	b5b8y13	1551.84	84.394	3871	2	776.42	12.11
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	29	Phosphoryl STY(10)	ELAAFSQFASDLDDATRK	401	18	4	16.15	b9°b9y6y8	2064.95	104.025	2850	4	516.99	14.54
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	30	Oxidation+M(8)	DSVGAVVMGPYADLAEGMK	68	19	4	24.5	b3y5y7y12	1925.92	90.171	10397	2	963.46	11.92
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	31	Oxidation+M(17)	YAIALNLERDSVGAVVMGPYADLAEGMK	59	28	3	18.02	y5y8y14	2969.47	123.150	5801	4	743.12	-0.25
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	32		ADVELAK	456	7	0	1.89		745.40	60.040	2086	1	745.40	-14.41
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	33		ASTISNVVR	201	9	0	1.51		928.51	36.894	4448	2	464.76	-3.75
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	34		ELAAFSQFASDLDDATRK	401	18	0	4.9		1966.92	82.992	2376	3	656.31	-13.59
P66738 RRF_SALTY Ribosome-recycling factor	1		ASPSLLDGIVVEYYGTPTPLR	31	21	12	84.69	b8b15b16y2y3y5y10y11y12y14y15y21	2248.21	93.198	42592	2	1124.61	9.01
P66738 RRF_SALTY Ribosome-recycling factor	2		QLASVTVEDSR	52	11	15	102.7	b2°b2b7y2y3°y3y4y5y6y7y8°y8y9y11°y11	1204.61	39.684	19748	2	602.81	-4.66
P66738 RRF_SALTY Ribosome-recycling factor	3		AIMASDLGLNPSSAGTDIR	80	19	4	35.07	y2y13y14y15	1888.95	67.216	15167	2	944.98	5.23
P66738 RRF_SALTY Ribosome-recycling factor	4		VDAALADKEAELMQF	170	15	4	18.79	b11y10°y10y12	1650.81	78.681	8600	2	825.91	5.47
P66738 RRF_SALTY Ribosome-recycling factor	5		SQEEVQK	155	7	4	38.33	b3°b3b4y3	847.42	35.490	1763	2	424.21	0.50
P66738 RRF_SALTY Ribosome-recycling factor	6		AIMASDLGLNPSSAGTDIRVPLPPLTEER	80	29	5	31.2	b6b7y12y22y26	3020.59	86.332	63307	3	1007.53	5.33
P66738 RRF_SALTY Ribosome-recycling factor	7		SMGPAVEKAIMASDLGLNPSSAGTDIR	72	27	4	18.31	b8°b8b12b16	2688.32	58.065	10058	4	672.84	-5.09
P66738 RRF_SALTY Ribosome-recycling factor	8		IVRGAEAQAR	115	10	8	102.6	b5b6b7y3°y3y5y7y9	1128.61	15.915	7928	2	564.81	-4.54
P66738 RRF_SALTY Ribosome-recycling factor	9	Oxidation+M(13)	VDAALADKEAELMQF	170	15	4	18.79	b4°b4b8y11	1666.79	60.947	2909	3	556.27	-6.37
P66738 RRF_SALTY Ribosome-recycling factor	10	Oxidation+M(3)	AIMASDLGLNPSSAGTDIR	80	19	3	15.48	b8b10y11	1904.96	92.645	1949	3	635.66	11.21
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	10	59.52	b2b3b10°b10y1y4y5y6y8y10	1193.60	80.485	59405	2	597.31	-2.15
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		GIMEGEYDHLPEQAFYMVGSIDEAVEK	429	27	10	61.24	b2b5y5y6°y6y8y9y11y12y27	3057.41	99.378	58106	3	1019.81	8.86
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		VALTGLTMAEK	219	11	10	89.17	b2b6y4y5y7y8y9°y9y10y11	1133.61	59.010	58033	2	567.31	-10.01
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4		QLDPLVVQGEHYDTAR	343	16	11	118.11	b16y3y4y5y6y8y9y10°y10y11y12	1840.90	57.400	54073	3	614.30	-11.21
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		TIAMGSSDGLR	53	11	10	36.37	b1b2°b2b5b10b11y7°y7y10y11	1107.56	50.977	49493	2	554.28	11.35
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		QIASLGIYPAVDPLDSTSR	324	19	9	72.8	b16y4y7y10y11y12y14y15y19	2003.06	80.483	47595	2	1002.03	5.55
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		VYDALEVQNGNEK	25	13	9	56.19	b2b3b10y2y5y7y8y11y13	1478.71	44.250	45198	2	739.86	1.49
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		YTLAGTEVSALLGR	247	14	10	68.84	b2°b2b4b8y4y6y7y10y11y14	1450.79	79.758	44915	2	725.90	-1.94
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		TVNMMELIR	156	9	7	76.65	b4y3y4y5y6y7y9	1106.56	75.540	43470	2	553.78	-8.71

Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		FLSQPFFVAEVFTGSPGK	399	18	14	90.14	b2b3°b3b4b6b10y2y3y6y7y11y14y16y18	1958.02	99.464	39087	2	979.52	9.29
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		MPSAVGYQPTLAEEMGVLQER	261	21	9	57.17	b3b5b12b14y6y9y11y13y21	2306.14	81.412	37304	2	1153.57	9.32
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		VGLFGGAGVGK	145	11	6	28.07	b9y1y2y7y8y11	961.54	58.603	33470	2	481.27	-9.84
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		GLDVKDLEHPIEVPVGK	65	17	7	30.82	b2b3b9y1y4y5y17	1844.99	66.892	28657	3	615.67	-12.70
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		AAPSYEELSNSQELLETKIK	112	20	8	48.11	b2b15y4y5y11y12y14y20	2179.05	73.604	27905	3	727.02	-10.53
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15		GVQSILQR	359	8	5	33.93	b2b3b4y4y8	900.52	39.226	22374	2	450.76	-7.79
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16		YVSLKDTIR	417	9	6	61.36	b6b7y3y4y5y9	1094.62	45.055	16651	2	547.81	-3.57
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17		DLEHPIEVPVGK	70	12	7	35.29	b4°b4b7b8y2y4y12	1332.70	55.405	12367	3	444.90	-14.84
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18		DEGRDVLLFVDNIYR	232	15	5	18.79	b7b12y7°y7y15	1823.91	70.684	11230	2	912.46	-11.78
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19		NIAIEHSGYSVFAGVGER	165	18	4	39.47	y8y11y12y13	1905.92	65.663	16237	3	635.98	-11.72
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20		DVLLFVDNIYR	236	11	3	28.07	b8y6y7	1366.71	90.912	9052	2	683.86	-17.06
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	21		IMNVLGEPVDMK	87	12	3	26.99	b6y5y6	1345.66	29.772	5089	3	449.23	-18.60
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	22		GVQSILQRYQELK	359	13	4	26.12	b5°b5b6y5	1561.87	53.603	57839	3	521.30	2.50
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	23		EGNDFYHEMTDSNVIDKVS LVYG QMNEPPGNR	185	32	4	39.89	y5y6y11y12	3655.63	84.326	17584	4	914.66	-2.47
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	24	Carbamidomethyl+C(6)	VIDLMCPFAKGGK	132	13	4	21.35	b6b8y11°y11	1435.73	74.399	16440	2	718.37	-6.63
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	25		IMNVLGEPVDMKGEIGEEER	87	20	3	24.31	y8y9y13	2245.07	69.236	13573	3	749.03	-6.52
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	26		VSLVYQMNEPPGNRLR	202	17	6	40.06	b8°b8b9b10b12°b12	1930.00	84.164	11249	2	965.50	2.15
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	27	Carbamidomethyl+C(26)	AAPSYEELSNSQELLETKIKVIDLM C PFAK	112	30	4	22.52	b5b8b9y8	3353.68	120.492	9485	3	1118.56	4.08
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	28		MPSAVGYQPTLAEEMGVLQERIT STK	261	26	4	37.17	b6b7b8b12	2836.43	107.916	1854	2	1418.72	4.56
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	29	Oxidation+M(11)	IMNVLGEPVDMK	87	12	3	26.99	b9y10y11	1361.67	59.884	3780	2	681.34	-11.03
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	30		QIASLGIYPAVDPLDS	324	16	4	24.66	y7°y7y12y13	1658.85	80.529	5521	2	829.93	-10.89
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	13	127.91	b2b3b5b11y2y3y5y6y7y8y9y10y12	1150.67	53.205	92672	2	575.84	-8.70
P66313 RL6_SALTY 50S ribosomal protein L6	2		ALLNSMVIGVTEGFTK	69	16	14	75.04	b2b4°b4b15y4y5y6y8°y8y12y13°y13°y13y16	1679.90	93.964	68790	2	840.45	-3.20
P66313 RL6_SALTY 50S ribosomal protein L6	3	Carbamidomethyl+C(26)	GNVVNLSLGFSHPVHDHQLPAGIT AECPTQTEIVLK	99	35	7	24.08	b2b3b25y3y9y10y35	3741.90	79.360	57438	4	936.23	-7.50
P66313 RL6_SALTY 50S ribosomal protein L6	4		INGQVITIK	18	9	7	66.13	b3y1y3y4y7y8y9	985.59	48.171	55576	2	493.30	-10.22
P66313 RL6_SALTY 50S ribosomal protein L6	5		YADEVVR	163	7	4	41.34	y3y5y6y7	851.42	29.976	47878	2	426.21	-12.40
P66313 RL6_SALTY 50S ribosomal protein L6	6		ALLNSMVIGVTEGFTKK	69	17	5	37.63	y3y7y9y15y17	1807.97	87.987	45138	3	603.33	-13.98
P66313 RL6_SALTY 50S ribosomal protein L6	7		DGYADGWAQAGTAR	55	14	6	25.4	b3y10°y10°y10y11y14	1438.64	49.669	43149	2	719.82	2.72
P66313 RL6_SALTY 50S ribosomal protein L6	8		HADNALTFGPR	44	11	13	97.93	b2b3°b3b5b6b7°b7y3y5y9y10°y10y11	1198.59	45.032	39604	2	599.80	-2.65

P66313 RL6_SALTY 50S ribosomal protein L6	9		QVIGQVAADLR	138	11	6	51.6	y1y2y5y6y8y9	1169.66	56.999	32708	2	585.33	-4.49
P66313 RL6_SALTY 50S ribosomal protein L6	10		LQLVGVGYSR	86	9	3	31.3	b3y5y7	1004.58	59.254	32599	2	502.79	-9.78
P66313 RL6_SALTY 50S ribosomal protein L6	11		RPEPYK	152	6	1	13.9	b3	789.44	34.083	4681	2	395.22	13.38
P66313 RL6_SALTY 50S ribosomal protein L6	12		GADKQVIGQVAADLR	134	15	6	60.92	b3b9y3y4y5y6	1540.82	58.016	35298	3	514.28	-13.31
P66313 RL6_SALTY 50S ribosomal protein L6	13		KLQLVGVGYSR	85	10	6	76.06	b4y3y4y5y6y8	1132.68	52.530	13821	2	566.84	-6.47
Q8ZLD7 UA_SALTY Universal stress protein A	1		ISEETHHALTELSTNAGYPITETLS GSGDLGQVLVDAIK	61	39	11	43.23	b2b12°b12b18b22y4y5y6y 11y15y39	4067.04	97.456	169081	4	1017.52	-0.48
Q8ZLD7 UA_SALTY Universal stress protein A	2		QLINTVHVDMLIVPLRDEEE	124	20	16	118.06	b10b11°b11b13°b13b20y1 y6y7y8y9y11y12y13y14y2 0	2363.21	86.300	124250	3	788.41	-5.58
Q8ZLD7 UA_SALTY Universal stress protein A	3		AVSMARPYNAK	22	11	16	66.61	b2b3°b3b8°b9°b9b10y1y5* y5y7*y7y9°y9*y9y11	1207.62	30.687	67391	2	604.31	-6.37
Q8ZLD7 UA_SALTY Universal stress protein A	4		ISEETHHALTELSTNAGYPITETLS GSGDLGQVLVDAIKK	61	40	4	12.33	b12b22y4y22	4195.14	93.868	45637	4	1049.54	-1.05
Q8ZLD7 UA_SALTY Universal stress protein A	5		ISLIHVDVNYSDLYTGLIDVNLGD MQK	33	27	3	12.23	b11y5y8	3035.50	104.068	2420	3	1012.51	-11.50
Q8ZLD7 UA_SALTY Universal stress protein A	6		VLVEK	17	5	1	13.53	y3	587.38	40.641	5597	1	587.38	4.26
Q8ZLD7 UA_SALTY Universal stress protein A	7		LMSSAR	118	6	2	13.9	b4°b4	664.34	36.849	2447	1	664.34	0.18
Q8ZLD7 UA_SALTY Universal stress protein A	8		AYKHILIAVDLSPESK	1	16	3	35.19	y8y9y10	1784.01	77.158	9245	3	595.34	8.69
Q8ZLD7 UA_SALTY Universal stress protein A	9		SMARPYNAK	24	9	3	32.05	b4b6b7	1037.51	30.688	71202	2	519.26	-9.06
Q8ZLD7 UA_SALTY Universal stress protein A	10		VSMARPYNAK	23	10	2	8.01	b3°b3	1136.58	30.686	7697	2	568.80	-4.08
Q8ZLD7 UA_SALTY Universal stress protein A	11		AVSMARPYNAK	22	11	0	2.26		1189.59	30.689	3626	3	397.20	-14.47
Q8ZKP1 ZAPB_SALTY Cell division protein zapB	1		VQQAIDTITLLQMEIEELKEK	12	21	25	219.77	b2b3b4°b4b5y2°y2y3y4y5 y6y8y9y10°y10y11°y11y1 2y13y15y16y17y18y21*y2 1	2472.32	98.351	177137	3	824.78	-0.99
Q8ZKP1 ZAPB_SALTY Cell division protein zapB	2		NNSLTQEVQSAQHQR	33	15	6	30.4	b9y3*y3y8y9y15	1739.82	40.224	42046	3	580.61	-12.91
Q8ZKP1 ZAPB_SALTY Cell division protein zapB	3		EKNNSLTQEVQSAQHQR	31	17	4	23.9	b11b12°b12y15	1996.97	89.500	29858	3	666.33	-5.32
Q8ZKP1 ZAPB_SALTY Cell division protein zapB	4		EELERENNSLK	48	11	4	36.37	b3b6y6y9	1360.67	82.041	11152	2	680.84	-0.45
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VVGQLGQVLGPR	122	12	10	83.8	b1b2y3y5y6y7y8y10°y10y 12	1222.72	58.865	132199	2	611.86	-7.79
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VGTVPNVAEAVK	141	13	11	80.9	b3°b3y3y8y9°y9y10y11y12 *y12y13	1284.71	47.936	89939	2	642.86	-3.33
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VAVFTQGPNAEAAK	74	14	11	88.39	b3b4b6y7y8y9°y9y10°y10y 11y14	1402.73	45.093	83230	2	701.87	0.26
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		QYDINEAIALLK	19	12	18	105.81	b2°b2b3°b3b4°b4°b4b9b1 1b12y1y2y3y4y5y6y8y12	1390.76	84.952	67155	2	695.88	-1.84
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		AAGAELVGMEDLADQIK	88	17	15	114.84	b2b3b5°b5b6b7b12y4y9y1 0y11y12y13*y13y17	1730.88	79.617	34854	2	865.94	7.05
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		GATVLPHTGTR	60	11	7	66.89	y2y4y5y6y7y9y11	1065.57	29.171	21402	2	533.29	-5.84

P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		GEMNFDVVIASPDAMR	106	16	5	39.12	b13y5y9y11y12	1751.80	71.534	8940	3	584.60	-7.46
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		ELATAK	31	6	2	13.9	b5°b5	632.35	28.141	6520	1	632.35	-13.22
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9		NGIHTTIGK	167	10	4	27.7	b3b8°b8y3	1053.60	38.709	3443	2	527.30	-5.45
P0A2A3 RL1_SALTY 50S ribosomal protein L1	10		SDQNVR	54	6	1	13.9	y4	718.35	59.576	2754	1	718.35	-1.70
P0A2A3 RL1_SALTY 50S ribosomal protein L1	11		VSISTTMGAGVAVDQAGLSASAN	211	23	3	13.48	b7y8y10	2107.03	55.866	1705	3	703.02	-1.39
P0A2A3 RL1_SALTY 50S ribosomal protein L1	12		KGEMNFDVVIASPDAMR	105	17	4	37.84	b5y7y8y9	1879.89	67.448	4726	2	940.45	-5.91
P0A2A3 RL1_SALTY 50S ribosomal protein L1	13		SDQNVRGATVLPHGTR	54	17	4	16.91	b5°b5b13y4	1764.91	75.952	4417	3	588.98	1.31
P0A2A3 RL1_SALTY 50S ribosomal protein L1	14	Oxidation+M(7)	VSISTTMGAGVAVDQAGLSASAN	211	23	12	72.39	b7b9b10°b10y4*y4y7y9y11*y11y14y20	2123.06	74.614	25800	3	708.36	14.49
P0A2A3 RL1_SALTY 50S ribosomal protein L1	15	Oxidation+M(9)	AAGAEVGMEDLADQIKK	88	18	3	25.07	b5b6b13	1874.97	75.116	18867	3	625.66	9.70
P0A2A3 RL1_SALTY 50S ribosomal protein L1	16		TVLPHGTR	62	9	0	2.26		937.51	29.172	20219	2	469.26	-7.88
P0A2A3 RL1_SALTY 50S ribosomal protein L1	17		VLPHGTR	63	8	0	2.26		836.46	29.173	5727	2	418.73	-14.81
P67093 UG_SALTY Universal stress protein G	1		HATLPVLVVR	132	10	13	74.02	b1b2b3°b3b4y1y2y4y7y8°y8y9y10	1104.68	59.715	77765	2	552.84	-8.40
P67093 UG_SALTY Universal stress protein G	2		NPSITTHLLGSNASSVVR	114	18	17	99.55	b2°b2b6b7°b7b10y5y8y9*y9y10*y10y11y12y14y18*y18	1852.96	58.285	59836	3	618.33	-12.65
P67093 UG_SALTY Universal stress protein G	3		TIIMPVDVFEMELSDK	3	16	7	36.68	b2b3b4b12y1y12y14	1866.94	104.248	52595	2	933.97	7.58
P67093 UG_SALTY Universal stress protein G	4		FGSVRDVVNEMGEELDADVVGSR	89	25	3	12.79	b6y5y10	2692.34	102.550	5105	3	898.12	5.71
P67093 UG_SALTY Universal stress protein G	5		LQTMVGHFSIDPSR	69	14	15	114.65	b4°b4°b4b5b11°b11y3°y3y4°y4y5y6y7y11y12	1587.77	63.061	84601	3	529.93	-17.76
P67093 UG_SALTY Universal stress protein G	6		FGSVRDVVNEMGEELDADVVGSR	89	25	3	23.27	b5b6b10	2692.30	123.861	121316	3	898.11	-7.44
P67093 UG_SALTY Universal stress protein G	7		DVVNEMGEELDADVVGSRNPSITTHLLGSNASSVVR	94	38	5	25.7	b3b4°b4b10b33	3980.01	102.598	110691	4	995.76	2.09
P67093 UG_SALTY Universal stress protein G	8		MYKTIIMPVDVFEMELSDK	0	19	5	23.26	b3y8°y8y9°y9	2289.15	81.472	12433	2	1145.08	12.05
P67093 UG_SALTY Universal stress protein G	9		FEEHLQHEAETRLQTMVGHFSIDPSR	57	26	3	12.49	b9y4y9	3094.50	77.518	1659	3	1032.17	5.52
P67093 UG_SALTY Universal stress protein G	10	Oxidation+M(24)	HAFLAQDQGVHLLHVLPGSASMSLHR	22	28	4	15.51	b9b12y8y20	3079.63	137.308	38594	3	1027.21	11.89
P67093 UG_SALTY Universal stress protein G	11	Oxidation+M(4)	LQTMVGHFSIDPSR	69	14	4	27.74	y9°y9y10y12	1603.79	55.744	2103	3	535.27	1.14
Q8ZQS2 GPMA_SALTY 2	1		AIHTLWNVLDELQAWLPVEK	62	21	20	122.42	b2b3b4b5b6b7b8°b8b11b16°b17y1y2°y2y4°y4y5y6y12y21	2490.29	117.075	42280	3	830.77	-3.82
Q8ZQS2 GPMA_SALTY 2	2		LSEKELPLTESLALTIDR	142	18	3	16.15	b3b5y4	2028.11	82.408	23035	3	676.71	-6.26
Q8ZQS2 GPMA_SALTY 2	3		VIIAAHGNSLR	178	11	8	66.89	b2y1y5y6y7y8y9y11	1150.66	36.729	16115	2	575.83	-6.37
Q8ZQS2 GPMA_SALTY 2	4		HYGALQGLNK	90	10	4	52.98	b4b5b6b9	1100.57	57.986	3153	2	550.79	-17.41
Q8ZQS2 GPMA_SALTY 2	5		AETAEK	100	6	1	13.9	y3	648.31	83.008	1724	1	648.31	-8.47
Q8ZQS2 GPMA_SALTY 2	6		MAVTK	0	5	1	13.53	b3	549.30	23.525	1564	1	549.30	-4.78
Q8ZQS2 GPMA_SALTY 2	7		AETAEKYGDEQVK	100	13	3	26.12	b4y6y7	1467.72	68.349	1615	2	734.36	14.72
Q8ZQS2 GPMA_SALTY 2	8	Phosphoryl STY(10)	GFAVTPPELTKDDER	117	15	5	30.4	b5b6°b6b9y5	1754.80	38.754	4316	3	585.60	3.76
Q8ZQS2 GPMA_SALTY 2	9		IAAHGNSLR	180	9	1	8.01	b3	938.51	36.716	16447	2	469.76	-10.21

IP0446 RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	15	115.85	b2b5b7b8y2y3y4y5y6°y6y7°y7*y7y8y10	1115.64	56.342	86751	2	558.32	-5.91
IP0446 RL3_SALTY 50S ribosomal protein L3	2		IFTEDGVSIPTVIEVEANR	13	20	15	92.35	b2b4b7b9°b9y3y4°y4y5y6°y6y7y11y13y20	2188.17	88.102	59814	2	1094.59	11.49
IP0446 RL3_SALTY 50S ribosomal protein L3	3	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	6	35.79	b2y4y6y8y15y18	1738.93	53.828	28656	3	580.31	-14.25
IP0446 RL3_SALTY 50S ribosomal protein L3	4		LAEGEETVQGSISVELFADVKK	83	23	9	29.55	b2b3b6°b6b11b17°b17y1y23	2512.27	117.073	17922	3	838.10	-4.08
IP0446 RL3_SALTY 50S ribosomal protein L3	5		DLANDGYR	38	8	11	50.47	b2°b2b5°b5b8y3y4°y4y6°y6y8	923.42	31.195	15059	2	462.22	3.44
IP0446 RL3_SALTY 50S ribosomal protein L3	6		VTKPEAGHFAK	59	11	8	83.43	y3y4y6y7°y7y8°y8y9	1184.62	23.436	35486	3	395.54	-20.30
IP0446 RL3_SALTY 50S ribosomal protein L3	7		NLLLVK	184	6	5	68.01	b3b4y3y4y5	699.47	55.801	21994	1	699.47	-7.59
IP0446 RL3_SALTY 50S ribosomal protein L3	8		GLWEFR	77	6	1	13.9	b3	807.41	61.597	6974	1	807.41	-2.19
IP0446 RL3_SALTY 50S ribosomal protein L3	9		VPGSIGQNQTGPK	141	13	5	30.59	y3y7y12°y12*y12	1282.69	57.741	4236	2	641.85	14.37
IP0446 RL3_SALTY 50S ribosomal protein L3	10		VDAER	179	5	1	13.53	b3	589.29	61.482	3546	1	589.29	-0.52
IP0446 RL3_SALTY 50S ribosomal protein L3	11	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	7	64.5	b14y5y6y7y8y12y16	1809.97	56.031	83896	3	603.99	-10.66
IP0446 RL3_SALTY 50S ribosomal protein L3	12		ANRVTKPEAGHFAK	56	14	3	25.4	b3b4y5	1525.81	53.827	6386	3	509.27	-9.44
IP0446 RL3_SALTY 50S ribosomal protein L3	13		VTVQSLDVVRVDAER	169	15	4	38.85	b5b6b7y3	1685.93	103.625	4023	2	843.47	4.34
IP0446 RL3_SALTY 50S ribosomal protein L3	14		LAEGEETVQGSISVELFADVKK	83	23	4	37.68	b3b10b11b12	2512.28	90.245	3963	4	628.82	-2.33
IP0446 RL3_SALTY 50S ribosomal protein L3	15		DLANDGYRAVQVTTGAK	38	17	3	24.32	b4b8b10	1778.88	50.583	2356	3	593.63	-10.50
IP0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	12	80.9	b2b3°b3b13y2y4y5y8y9y10y11y13	1447.78	64.924	98548	2	724.39	-2.87
IP0A297 RL10_SALTY 50S ribosomal protein L10	2		AAAFEGELIPASQIDR	109	16	15	137.23	b4b5b6b8°b8b9y2y5y6y7y8y9y11y12y16	1687.87	68.431	75453	2	844.44	1.08
IP0A297 RL10_SALTY 50S ribosomal protein L10	3		QAIVAEVSEVAK	8	12	6	33.22	b2b12y5y8y10y12	1243.68	56.992	40507	2	622.35	-3.73
IP0A297 RL10_SALTY 50S ribosomal protein L10	4		DTFVGPTLIAYSMHEPGAAAR	73	21	7	27.85	b3°b3b8b10y6y12y21	2204.07	82.424	13874	3	735.36	-4.87
IP0A297 RL10_SALTY 50S ribosomal protein L10	5		EAGVYMR	46	7	4	38.33	b3y4y5y7	825.39	31.179	5931	2	413.20	-8.65
IP0A297 RL10_SALTY 50S ribosomal protein L10	6		GALSAVVADSR	20	11	4	25.06	b3b10°b10y5	1045.55	35.915	179108	2	523.28	-8.52
IP0A297 RL10_SALTY 50S ribosomal protein L10	7		LMATMK	138	6	1	13.9	b5	694.37	40.545	12488	1	694.37	9.67
IP0A297 RL10_SALTY 50S ribosomal protein L10	8		TLA AVR	153	6	3	27.43	b3°b3y5	630.40	50.490	7318	1	630.40	12.97
IP0A297 RL10_SALTY 50S ribosomal protein L10	9		GVTVDK	31	6	1	13.9	b5	618.35	71.054	3149	1	618.35	13.62
IP0A297 RL10_SALTY 50S ribosomal protein L10	10	Carbamidomethyl+C(9)	VVEGTQFECLKDTFVGPTLIAYSM EHPGAAAR	62	32	4	16.36	b10y7y10y17	3494.70	92.108	63807	4	874.43	-3.07
IP0A297 RL10_SALTY 50S ribosomal protein L10	11		ALNLQDKQAIVA EVSEVAK	1	19	4	24.66	y3y8°y8y9	2026.09	71.079	14260	3	676.04	-13.07
IP0A297 RL10_SALTY 50S ribosomal protein L10	12		MALNLQDKQAIVA EVSEVAK	0	20	3	24.31	b6b7b19	2157.14	57.584	8756	3	719.72	-7.24
IP0A297 RL10_SALTY 50S ribosomal protein L10	13		AAAFEGELIPASQIDRLATLPTYEE AIAR	109	29	3	11.8	b11y6y12	3116.60	99.885	7120	3	1039.54	-9.64
IP0A297 RL10_SALTY 50S ribosomal protein L10	14		DTFVGPTLIAYSMHEPGAAARL FK	73	24	3	23.4	b5b7b8	2592.29	59.630	2198	3	864.77	-14.50

P0A297 RL10_SALTY 50S ribosomal protein L10	15	Carbamidomethyl+C(9); Phosphoryl STY(13)	VVEGTQFECLKDTFVGPTLIAYSMEHPGAAAR	62	32	6	28.4	b4b8b11b12_H3PO4 b12y5y17	3574.66	109.941	4785	5	715.74	-1.98
P0A297 RL10_SALTY 50S ribosomal protein L10	16	Phosphoryl STY(3)	LATLPTYEEAIAR	125	13	6	35.09	b5°b5y7y9y11°y11	1527.71	136.535	1509	1	1527.71	-14.30
P0A297 RL10_SALTY 50S ribosomal protein L10	17	Oxidation+M(13)	DTFVGPTLIAYSMEHPGAAAR	73	21	6	30.86	b4°b4b8y6y7y12	2220.09	115.284	6674	3	740.70	7.59
P0A297 RL10_SALTY 50S ribosomal protein L10	18	Oxidation+M(2)	LMATMKEASAGK	138	12	4	37.21	b6b7y8y11	1253.63	45.439	5162	2	627.32	6.82
Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	12	45.71	b1b2*b2b3*b3b4*b15y2y12y13y14y16	1686.95	89.740	58105	2	843.98	3.84
Q7CR87 SURA_SALTY Chaperone surA	2		ITVLPQEVDALAK	149	13	9	62.72	b3°b3b4y2y5y9y10y11y13	1396.80	70.399	51589	2	698.90	-3.58
Q7CR87 SURA_SALTY Chaperone surA	3		LNAGQAGQQLPDDATLR	50	17	8	62.47	b2y4y7y8y9y11y12y17	1767.90	50.768	49064	2	884.45	2.07
Q7CR87 SURA_SALTY Chaperone surA	4		ITDEQLDQAIANIAK	90	15	8	41.2	b10°b10*b10y4y5y10y13y15	1642.87	80.202	47938	2	821.94	3.57
Q7CR87 SURA_SALTY Chaperone surA	5		LAYDGLNYSTYR	117	12	10	75.35	b10°b10y3y6y8°y8*y8y10y11y12	1435.69	58.189	43112	2	718.35	4.08
Q7CR87 SURA_SALTY Chaperone surA	6		QIGTQNDASTELNLSHILIALPENPTSEQVNDAQR	162	35	12	28.41	b2*b2b3b12b21y3*y3y5y9°y9y14y35	3816.94	88.651	39279	3	1272.99	11.39
Q7CR87 SURA_SALTY Chaperone surA	7		HILLKPSPIMNDQQAR	288	16	8	50.33	b3b5y4y7y9y11°y11*y11	1860.99	48.421	33495	3	621.00	-13.58
Q7CR87 SURA_SALTY Chaperone surA	8		QAESIVEEAR	197	10	10	88.8	b4b8b10y2y4y5y6y8y9y10	1131.56	37.837	25945	2	566.28	-7.66
Q7CR87 SURA_SALTY Chaperone surA	9		VAAVVNNGVVLESDDVGLMQSVK	27	23	8	34.64	b2b3b4y3y8y10°y10y23	2343.20	90.933	22480	3	781.74	-8.54
Q7CR87 SURA_SALTY Chaperone surA	10		GQSQSISVTEVHAR	274	14	6	56.26	y3y5y6y8y9y14	1498.74	36.535	19184	3	500.25	-14.09
Q7CR87 SURA_SALTY Chaperone surA	11		LAITYSADQQALK	214	13	4	21.35	b9y5y10y13	1421.76	54.438	10941	2	711.38	-5.67
Q7CR87 SURA_SALTY Chaperone surA	12		GQISAPVHSSFGWHLIELLDTR	362	22	4	27.69	b4b10y10y11	2463.27	87.678	5973	3	821.76	-4.56
Q7CR87 SURA_SALTY Chaperone surA	13		TTFAAAAKEYSQDPGSANQGGDLGWATPDIFDPAFR	318	36	3	10.98	b12y10y12	3772.77	90.915	2080	3	1258.26	4.72
Q7CR87 SURA_SALTY Chaperone surA	14		HQILER	67	6	2	27.43	y4y5	795.45	24.706	15103	2	398.23	-2.53
Q7CR87 SURA_SALTY Chaperone surA	15		EYSQDPGSANQGGDLGWATPDIFDPAFR	326	28	4	36.99	y3y4y5y8	3011.38	93.561	10607	3	1004.46	10.38
Q7CR87 SURA_SALTY Chaperone surA	16		LEEIAADIK	306	9	3	31.3	b5b8y8	1001.55	39.291	1571	2	501.28	-2.32
Q7CR87 SURA_SALTY Chaperone surA	17		LAITYSADQQALKGGQMGWGR	214	21	11	147.05	y3y4y6y8y9y11y12y15y16y18y19	2251.12	64.776	30415	3	751.05	-3.69
Q7CR87 SURA_SALTY Chaperone surA	18		KGDIVGPIR	251	9	6	76.65	b4y4y5y6y7y8	954.56	37.261	21943	2	477.79	-10.10
Q7CR87 SURA_SALTY Chaperone surA	19		GGQMGWGRIQELPGIFAQALSTAK	227	24	3	23.4	b4b9b10	2516.34	84.360	8047	4	629.84	10.87
Q7CR87 SURA_SALTY Chaperone surA	20		LNAGQAGQQLPDDATLRHQILER	50	23	3	19.89	b3b5b11	2544.34	75.815	4787	3	848.78	4.03
Q7CR87 SURA_SALTY Chaperone surA	21		KFSEEATWMQEQR	404	14	3	27.74	b5b6b9	1740.80	76.869	2879	2	870.90	-1.75
Q7CR87 SURA_SALTY Chaperone surA	22		LNAGQAGQQLPDDATL	50	16	0	4.53		1611.78	50.751	6214	2	806.40	-8.56
Q7CR87 SURA_SALTY Chaperone surA	23		GQSQSISVTEVHAR	274	14	0	3.4		1481.72	36.522	2026	3	494.58	-6.76
Q8ZRP4 DAPD_SALTY 2	1		MQQLQNVIAFER	0	14	9	68.84	b3b10y3y7y9y10*y10y11y14	1706.85	85.735	70530	2	853.93	0.29
Q8ZRP4 DAPD_SALTY 2	2		EAVNQVISLLDSGALR	28	16	13	66.08	b4°b4*b4b6°b6°b6y4y5y6°y6y9y10y16	1684.92	91.845	43339	2	842.97	0.14

Q8ZRP4 DAPD_SALTY 2	3		INDNQVIDGAESR	68	13	12	83.91	b2b3y1y5y6y7°y7y8y9°y9y10y13	1430.69	40.954	22477	2	715.85	0.34
Q8ZRP4 DAPD_SALTY 2	4		FADYDEAR	89	8	6	68.77	y2y3y4y5y6y7	986.41	34.061	13829	2	493.71	-8.48
Q8ZRP4 DAPD_SALTY 2	5		QQLQNVIAFER	1	13	3	30.59	y4y8y11	1575.79	66.966	8777	3	525.94	-12.47
Q8ZRP4 DAPD_SALTY 2	6		VPAGSVVVSGNLPSKDGK	226	18	5	16.15	b5y2y10y17y18	1710.95	43.485	5885	2	855.98	4.99
Q8ZRP4 DAPD_SALTY 2	7		IDGQWVTHQWLK	48	12	5	30.21	b4b5b9b12*b12	1510.79	98.629	3354	3	504.27	9.13
Q8ZRP4 DAPD_SALTY 2	8	Carbamidomethyl+C(30)	NTVLMPSYVVGAYVDEGTMVD TWATVGSQAQIGK	119	35	3	11.04	b6y10y18	3747.80	110.650	3862	4	937.71	8.73
Q8ZRP4 DAPD_SALTY 2	9		SEVVEGVIVEEGSVISMGVYLGQS TK	187	26	4	28.14	b4b10b12b13	2696.40	100.796	2936	3	899.47	12.40
Q8ZRP4 DAPD_SALTY 2	10	Carbamidomethyl+C(28)	NVHLSGGVGIGGVLEPLQANPTIIE DNCFIGAR	154	33	6	29.74	b5b9b12*b12y6y7	3417.70	119.947	1699	4	855.18	-17.50
Q8ZRP4 DAPD_SALTY 2	11		RADITPANVDTVTR	14	14	5	28.56	b3°b3b7y12	1528.80	56.587	49069	3	510.27	-6.47
Q8ZRP4 DAPD_SALTY 2	12		MQQLQNVIAFER	0	15	6	26.87	b4*b4b5b12°b12*b12	1862.94	64.901	20562	3	621.65	-6.42
Q8ZRP4 DAPD_SALTY 2	13		YFDKVPKM	81	8	4	52.23	b6b7y3y6	1027.52	42.391	17389	2	514.26	-10.69
Q8ZRP4 DAPD_SALTY 2	14		IYDRETGEVHYGR	213	13	5	44.42	b4b6b12y3y9	1594.77	57.041	10734	3	532.26	5.28
Q8ZRP4 DAPD_SALTY 2	15		ETGEVHYGRVPAGSVVVSGNLPS K	217	24	3	13.11	b5b13y23	2439.27	110.541	4540	3	813.76	1.60
Q8ZRP4 DAPD_SALTY 2	16	Phosphoryl STY(5)	VPAGSVVVSGNLPSK	226	15	4	32.78	b3b4y11y13_H3PO4 y13	1490.76	72.301	11399	2	745.88	3.60
Q8ZRP4 DAPD_SALTY 2	17		VPAGSVVVS	226	9	0	4.9		814.47	43.498	9941	2	407.74	0.45
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	22	156.32	b2b3b5b9*b9b11°b11b12° b12*b12b13b14y4y6y7y8y 9y10y11y12*y12y23	2379.23	64.353	113785	3	793.75	-3.39
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2	Carbamidomethyl+C(13)	VLNIFPSIDTGVCASVR	48	18	12	54.37	b2b3b5b18y2y3y6y11y13° y13y14y18	1919.01	85.136	79529	2	960.01	4.77
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	15	131.59	b2b3b4b7b10b11b13b16y4 y6y9y12y15°y15y17	1837.95	85.857	54613	2	919.48	3.59
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4		DLSDVLSQYAGK	33	13	11	86.92	b2b4°b4y1y3y4y6y9y11y12 y13	1382.68	59.237	45338	2	691.84	0.71
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		NYGVEIVDGPLK	116	12	11	75.35	b2b3*b3b12y1y3y4y6y8y1 0y12	1303.69	64.581	41459	2	652.35	-0.94
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		DLSDVLSQYAGKR	33	14	6	25.4	b12°b12y1y7y8y14	1538.78	54.701	11928	2	769.89	-2.06
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		AVIVLDENDNVIFSQLVDEITHEPD YDAALNVLK	133	34	7	49.79	b2b3b4y10y11y12y34	3811.97	118.141	10526	3	1271.33	12.17
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8	Carbamidomethyl+C(15)	FNQLATEVENTVLCVSADLPFA QSR	67	26	6	28.14	y8*y8y9°y9y13y19	2908.44	109.889	7737	3	970.15	-5.37
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9		AQAFTLVAK	24	9	6	76.65	b3y3y4y5y6y7	948.54	52.964	5343	1	948.54	-7.34
Q8ZP65 TPX_SALTY Probable thiol peroxidase	10		AVIVLDENDNVIFSQLVDEITHEPD YDAALNVLKA	133	35	30	279.46	b3b4b5b6b7b9b10°b10*b1 0b11b12b13y3y4y5y6y7y8 y9y12°y12*y12y14y16y19y 20y22y24y30y31	3882.99	119.949	80095	3	1295.00	6.92
Q8ZP65 TPX_SALTY Probable thiol peroxidase	11		NNEFLKNYGVEIVDGPLK	110	18	8	38.18	b3b6b8°b8b12°b12*b12y4	2049.05	75.905	14262	3	683.69	-5.72
Q8ZP65 TPX_SALTY Probable thiol peroxidase	12	Phosphoryl STY(13)	MSQTVHFQGNPVTVANVIPQAGS K	0	24	8	53.05	b3b5°b5b6_H3PO4 b6b7b12b19y12	2590.21	97.609	13115	4	648.31	-10.09
Q8ZP65 TPX_SALTY Probable thiol peroxidase	13		SDVLSQYAGKR	35	12	1	7.38	b10	1310.66	54.723	2959	2	655.83	-9.22
Q7CPE5 ATPD_SALTY ATP synthase subunit delta	1		LNALPDVLEQFIHLR	85	15	19	156.56	b2*b2b3*b3b4*b4y1y2y3y 4y5y6y7y8y9y10y11y13y1 5	1777.97	105.658	63617	3	593.33	-14.62
Q7CPE5 ATPD_SALTY ATP synthase subunit delta	2		AAFDFAVEHQSVVER	13	14	12	45.77	b1b2b5b6y1y2y4y5*y5y7°y 7y14	1605.74	57.017	41226	3	535.92	-14.37

Q7CPE5 ATPD_SALTY ATP synthase subunit delta	3		AGDMVIDGSVR	154	11	4	36.37	b3b5y7y9	1119.55	45.839	15709	2	560.28	1.85
Q7CPE5 ATPD_SALTY ATP synthase subunit delta	4		SEFVTVARPYAK	1	12	7	72.04	b3b5°b5y4y6y8y10	1367.71	47.048	37871	3	456.57	-18.03
Q7CPE5 ATPD_SALTY ATP synthase subunit delta	5		ISAAMEK	124	7	4	38.33	b6°b6y3y4	749.39	50.400	3774	2	375.20	-1.63
Q7CPE5 ATPD_SALTY ATP synthase subunit delta	6		AASEATSEVEVTSATALSEEQLSK	100	24	8	33.88	b12b15y6y8y11°y11y13°y13	2438.21	89.208	1728	3	813.41	13.72
Q7CPE5 ATPD_SALTY ATP synthase subunit delta	7		MSEFVTVARPYAKAAFDFAVEHQSVR	0	27	5	15.96	b6b11y3°y3y8	3085.48	132.851	3303	3	1029.16	-14.48
Q7CPE5 ATPD_SALTY ATP synthase subunit delta	8		AAFDFAVEHQSVRWQDMLAFAAEVTK	13	27	3	12.23	b11b22y4	3096.53	83.388	1797	3	1032.85	13.17
Q7CPE5 ATPD_SALTY ATP synthase subunit delta	9		ALPDVLEQFIHLR	87	13	0	3.77		1550.86	105.642	1640	2	775.93	-8.34
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	1		LAEAGIPTQMER	60	12	22	145.42	b1b2b3°b3b4°b4b5°b5b6y3y5y6°y6y7*y7y8*y8y9y10°y10*y10y12	1315.66	49.802	57905	2	658.34	-3.06
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	2	Carbamidomethyl+C(7)	LLSDTECLVK	72	10	7	41.22	b1b8°b8y3y7y8y10	1177.61	53.004	41045	2	589.31	-2.49
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	3		TVYSTENPDLLVLEFR	13	16	11	81.06	b4b13y2y3y4y10y11y12y13y16*y16	1895.98	88.338	31299	2	948.50	4.64
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	4		LFDDAGLILVDFK	164	13	4	21.35	b5b8y3°y3	1465.79	97.577	1894	2	733.40	-3.25
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	5		QSLGGLIEAYEAVHR	215	16	8	87.18	b13y3y4y5y6y7y11y13	1713.86	84.510	45710	3	571.96	-16.03
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	6	Carbamidomethyl+C(8)	LEMVPVECVVR	83	11	3	25.06	b4b10y6	1330.71	39.746	15125	3	444.24	14.40
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	7		IEQFDR	39	6	1	13.9	y3	807.40	26.240	8980	2	404.20	1.97
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	8		ANDVLK	157	6	2	13.9	b4*b4	659.37	31.165	4555	1	659.37	1.57
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	9	Carbamidomethyl+C(19)	LAEAGIPTQMERLLSDTECLVK	60	22	3	13.9	b3b11y12	2474.29	92.088	44527	3	825.43	9.28
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	10		FRQSLGGLIEAYEAVHR	213	18	3	16.15	b13y7y9	2017.05	79.087	37139	3	673.02	-7.75
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	11	Carbamidomethyl+C(9)	KLEMVPVECVVR	82	12	5	51.03	b5y3y7y10y11	1458.78	61.694	32371	2	729.89	0.08
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	12		TVYSTENPDLLVLEFRNDTSAGD GAR	13	26	8	47.39	b5b6b12b15y3y11y13y23	2840.37	80.588	6906	3	947.46	1.81
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	13		GEVVLGDEFSPDGSRLWDK	184	19	8	55.49	b4b7b8b10b11y8y11°y11	2106.03	75.933	3378	3	702.68	9.16
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	14		LEFGLYKGEVVLGDEFSPDGSR	177	22	3	13.9	b14y6y13	2414.16	94.650	2969	2	1207.59	-10.21
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	15	Phosphoryl STY(5)	TVYSTENPDLLVLEFR	13	16	7	36.01	b4b10b13*b13y3y12*y12	1975.91	73.757	1834	4	494.73	-12.36

Q7CPL4 RL16_SALTY 50S ribosomal protein L16	1		VLYEMDGVPEELAR	100	14	17	147.94	b1b6b7b8b10°b10y2y3y5y6y8°y8y9y10y11y12y14	1620.80	69.584	71780	2	810.90	1.81
Q7CPL4 RL16_SALTY 50S ribosomal protein L16	2		GNVEYWVALIQPGK	86	14	5	39.51	b9b10°b10b11y13	1573.83	84.414	5567	2	787.42	-7.14
Q7CPL4 RL16_SALTY 50S ribosomal protein L16	3		TTFVTK	127	6	1	13.9	b5	696.40	22.807	2504	1	696.40	9.29
Q7CPL4 RL16_SALTY 50S ribosomal protein L16	4		GLAAGADVSGSFGLK	18	16	5	28.6	b5b7°b7b11y10	1496.80	44.036	2254	3	499.61	18.76
Q7CPL4 RL16_SALTY 50S ribosomal protein L16	5		GNVEYWVALIQPGKVLYEMDGVPEELAR	86	28	3	18.02	b3b5b7	3175.62	136.200	2736	3	1059.21	2.84
Q7CPL4 RL16_SALTY 50S ribosomal protein L16	6	Phosphoryl STY(9)	GLAAGADVSGSFGLK	18	16	3	17.79	b3y6y9	1576.74	43.307	7896	3	526.25	4.80
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	1		QQYGEGLAR	170	9	14	63.12	b2°b2b3°b3b9y1y2y4y5°y5y6°y6y7y9	1021.50	32.512	116187	2	511.25	-8.90
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	2		QGNANIVFFDGITAGEKDFSALIA R	186	25	14	79.95	b2°b2b6°b6b25y4y5y6y13y15y18y19y20y25	2654.36	104.252	58590	3	885.46	0.09
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	3		TAGLDSQQGPTAAK	139	14	14	126.63	b3°b3b4y5y6y7°y7y8y9y10°y10y11y12y14	1303.64	28.663	52413	2	652.33	-4.31
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	4		TQFMGPEGVGNASLSNIAGGAEE GMLVTMPK	242	31	14	82.32	b2°b2b3b4b7y2y3y4y5y8y11y12y13y31	3035.47	92.533	49958	3	1012.49	1.53
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	5		SASHAPLDLVK	316	11	7	56.89	b4b5y1y3y7y10y11	1137.62	47.012	40022	2	569.32	-2.79
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	6		VAIVGAMSGPVAQWGDMEFNGA R	27	23	8	49.76	b3b14y4y5y6y9y15y23	2363.14	87.291	37675	3	788.38	4.65
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	7		LQKENIDFVYYGGYYPEMGMLR	211	23	10	63.39	y1y5y6y8°y8y9°y9y11y12y23	2814.34	84.606	34348	3	938.78	3.99
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	8	Carbamidomethyl+C(10)	LVGVEYDDACDPK	66	13	7	33.32	b2b11y2y3y8y9y13	1480.66	46.885	31808	2	740.84	1.57
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	9		IAIIHDK	163	7	6	41.34	y2y3°y3y5y6y7	809.48	32.088	27832	2	405.24	-11.46
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	10		DPSGPYVWITYAAVQSLATAMTR	293	23	5	20.86	b8°b8b10b13y3	2498.21	126.776	3278	3	833.41	-12.41
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	11		YILETVKPKQR	153	10	9	69.52	y3°y3y4y6°y6y7°y7y8°y8	1246.69	44.861	44652	3	416.24	-18.70
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	12		GYQYIMR	132	7	4	41.34	y3y4y5°y5	930.45	46.948	28710	2	465.73	-4.72
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	13		ANGADTVIGPLK	330	12	4	35.29	b4b5b7y4	1155.63	51.761	6031	2	578.32	-5.70
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	14		GFEFGVFQWHADGSSTVAK	350	19	6	34.51	b5b8b9°b9b12y6	2070.00	78.133	1773	3	690.67	15.57
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	15		GYQYIMRTAGLDSQGPPTAAK	132	21	6	22.49	b3b9°b9b12°b12y11	2215.06	85.508	4123	3	739.03	-9.26
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	16		SVQDGLKQGNANIVFFDGITAGE K	179	24	4	17.58	b5b11y7y15	2508.24	107.701	3222	3	836.75	-13.53
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	17		GDCLKGFEFGVFQWHADGSSTVA K	346	23	4	19.89	b7b12°b12b14	2483.17	92.047	2877	2	1242.09	-11.31
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	18	Oxidation+M(22)	KDPSGPYVWITYAAVQSLATAMT R	292	24	3	13.11	b12y3y6	2642.35	87.573	3799	3	881.46	8.50
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	19	Oxidation+M()	TQFMGPEGVGNASLSNIAGGAEE GMLVTMPKR	242	32	4	16.36	b7b9b14y26	3207.54	114.093	2916	3	1069.85	-5.40
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	20		SHAPLDLVK	318	9	0	2.26		979.54	47.023	4062	2	490.28	-13.52
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	8	42.66	b2b3b11y7y8y10°y10y13	1365.68	62.750	105499	2	683.34	-0.63
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2		NFDNMREDEGLADR	106	14	8	57.75	b2b8b9y3y5y6y12y14	1681.70	46.689	64232	3	561.24	-13.28

P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		ATFVVDPQGIIQAEIVTAEGIGR	120	23	25	197.34	b2°b2b3°b3b4°b4b5b6b8b9y1y2y3y4y5°y5y6y7y8y9y10y11y12y17y23	2384.26	128.413	51644	3	795.43	-7.37
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		LGVDVYSVSTDTHFTHK	63	17	13	108.64	b3b4b7b9°b9b12y3°y3y6y8y9y11y15	1905.92	57.033	42056	3	635.98	-5.70
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTELGDVA DHYEELQK	32	31	13	90.72	b3b4°b4b6b7b9b10y3y8y9y24y25y31	3757.77	119.198	22005	3	1253.26	12.41
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6		NGEFIEVTEKDTEGR	17	15	7	30.4	b1b2b9y3y4y9°y9	1723.81	49.614	5574	2	862.41	-1.70
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7		ATFVVDPQGIIQAEIVTAEGIGRDA SDLLR	120	30	5	11.62	b2b6y9°y9y16	3154.67	137.188	2122	3	1052.23	-1.39
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8		AWHSSSETIAK	80	11	8	83.94	b3b9y3y4y5y8°y8y9	1216.57	29.105	59148	3	406.20	-19.87
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9		NGEFIEVTEK	17	10	4	27.7	b4b7°b7y7	1165.56	88.565	2718	2	583.28	-11.31
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10		EGEATLAPSLDLVGKI	171	16	4	29.27	b3b4b7y4	1612.88	84.896	23665	2	806.94	-0.61
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	11		IKYAMIGDPTGALTR	91	15	4	30.4	b13y3y5y6	1606.84	62.318	19902	3	536.29	-12.23
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	12		NQAFKNGEFIEVTEK	12	15	3	26.87	y8y9y14	1753.89	82.747	7599	2	877.45	7.80
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	13		NGEFIEVTEKDTEGR	17	15	3	18.79	b10y7y10	1723.81	93.986	3187	3	575.28	-0.57
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	14		STDTHFTHK	71	9	0	4.53		1073.51	57.046	14062	2	537.26	11.71
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	15		SVSTDTHFTHK	69	11	2	7.26	b8°b8	1259.61	57.045	7622	2	630.31	7.37
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	16		LGVDVYSVSTDTHFTHK	63	17	1	7.26	y10	1887.91	57.077	6719	4	472.73	-6.72
P66932 TIG_SALTY Trigger factor	1		NVALEEQAWEAVLAK	399	15	17	155.82	b2b3b4b5b6b7°b7b9b14°b14y3y4y10y11y12y13y15	1583.87	79.957	68493	2	792.44	0.77
P66932 TIG_SALTY Trigger factor	2		ANDIDVPSALIDSEIDVLR	296	20	7	23.44	b2°b2b3°b3y4y14y16	2211.15	90.360	41554	3	737.72	-5.52
P66932 TIG_SALTY Trigger factor	3		FGVEDGSVAGLR	255	12	12	76.54	b2b3b4°b4b11y1y2y3y4y7y8y12	1206.61	56.991	41541	2	603.81	-0.40
P66932 TIG_SALTY Trigger factor	4		INPAGAPNYVPGEYK	83	15	6	26.87	b2y2y5y9y13y15	1589.79	50.754	33679	2	795.40	-0.69
P66932 TIG_SALTY Trigger factor	5		SQAIEGLVK	287	9	9	58.63	b2°b2y1y4y5y7y8°y8y9	944.53	46.980	28559	2	472.77	-12.08
P66932 TIG_SALTY Trigger factor	6		GLIEEMASAYEDPKEVIEFYK	368	22	5	26.68	b3b6y5y7y13	2548.22	97.378	26662	3	850.08	0.77
P66932 TIG_SALTY Trigger factor	7		VEERELPELTEEFIK	239	15	6	42.44	b2b4b6b8°b8b12	1860.94	95.790	24402	2	930.97	-11.61
P66932 TIG_SALTY Trigger factor	8		ANDIDVPSALIDSEIDVLR	296	19	5	24.5	b14y3y13y15y19	2055.07	94.419	22337	2	1028.04	2.73
P66932 TIG_SALTY Trigger factor	9		MIPGFEDGVK	193	10	5	14.96	b2b8y3y8°y10	1092.54	58.000	16976	2	546.77	-2.23
P66932 TIG_SALTY Trigger factor	10		VPMNIVAQR	48	9	3	46.86	y4y6y8	1027.56	46.838	15962	2	514.29	-7.13
P66932 TIG_SALTY Trigger factor	11		NKELMDNMR	390	9	5	55.62	y3y4y5y7y9	1150.53	34.629	9755	2	575.77	-3.08
P66932 TIG_SALTY Trigger factor	12		MQVSVETTQGLGR	0	13	3	21.35	b7y3y9	1405.72	58.369	5929	2	703.36	3.99
P66932 TIG_SALTY Trigger factor	13		ATSFNELMNQQA	420	12	4	23.01	b1b3b5y11	1353.59	49.806	5546	3	451.87	-13.89
P66932 TIG_SALTY Trigger factor	14		SELVNVAKK	29	9	5	31.3	b2b4b5°b5y7	987.57	29.997	3835	2	494.29	-10.14

P66932 TIG_SALTY Trigger factor	15		AGEEFTIDVTFPEEYHAENLK	206	21	3	24.02	b10b12b13	2439.11	71.740	2908	4	610.53	-11.61
P66932 TIG_SALTY Trigger factor	16		QDVLGDLMSR	63	10	6	59.52	b3b5b6*b6b7y9	1133.57	49.827	2573	2	567.29	6.78
P66932 TIG_SALTY Trigger factor	17		ATDFVLAMGQGR	181	12	3	36.23	y4y5y6	1265.63	65.633	21073	2	633.32	-1.45
P66932 TIG_SALTY Trigger factor	18		SELVNVAK	29	8	3	41.71	y4y5y6	859.47	37.057	19608	2	430.24	-17.61
P66932 TIG_SALTY Trigger factor	19		NFVDIAIK	73	8	3	33.93	b4y3y4	919.52	53.287	15036	2	460.27	-1.19
P66932 TIG_SALTY Trigger factor	20		VTIDFTGSVDGEEFEGGK	163	18	5	32.17	b11b13y4y6y11	1886.83	121.175	5478	3	629.61	-18.83
P66932 TIG_SALTY Trigger factor	21		YGASVR	57	6	1	13.9	b3	652.33	26.717	5008	1	652.33	-11.32
P66932 TIG_SALTY Trigger factor	22		VTITIAADSIETAVK	14	15	6	67.15	b8b9b10b11b12y9	1531.82	76.016	3666	2	766.42	-21.83
P66932 TIG_SALTY Trigger factor	23		QAAQRFGGNEK	316	11	4	37.8	b3b4b8y8	1205.59	48.138	97047	2	603.30	-14.07
P66932 TIG_SALTY Trigger factor	24		MQVSVETQGLGRR	0	14	6	42.73	b3b4°b4b5°b5b13	1561.82	88.130	38497	2	781.41	2.97
P66932 TIG_SALTY Trigger factor	25		ANDIDVPSALIDSEIDLRR	296	20	3	21.68	b5b7b13	2211.14	90.258	17502	2	1106.08	-7.73
P66932 TIG_SALTY Trigger factor	26		GKVPMNIVAGR	46	11	9	94.92	b3b5b6*b6b7y4y6y7y8	1212.68	43.355	9548	2	606.84	-10.27
P66932 TIG_SALTY Trigger factor	27		AGEEFTIDVTFPEEYHAENLK GK	206	23	4	22.51	b10b11°b11y20	2624.23	73.709	7379	4	656.81	-9.68
P66932 TIG_SALTY Trigger factor	28		GLIEEMASAYEDPKEVIEFYSK	368	22	3	13.9	b7y4y12	2548.23	82.515	5424	4	637.81	4.98
P66932 TIG_SALTY Trigger factor	29		QDVLGDLMSRNFVDIAIK	63	18	5	22.62	b8°b8b10y3y10	2034.08	100.752	2308	3	678.70	7.56
P66932 TIG_SALTY Trigger factor	30		VEERELPEL TEEFIK	239	15	3	18.79	b3b12y13	1860.95	97.139	1794	2	930.98	-4.26
P66932 TIG_SALTY Trigger factor	31	Phosphoryl STY(10)	GLIEEMASAYEDPKEVIEFYSK	368	22	3	13.9	b8y7y12	2628.19	86.585	2678	2	1314.60	5.02
P66932 TIG_SALTY Trigger factor	32	Oxidation+M(8)	ATDFVLAMGQGR	181	12	3	23.01	b3b9y5	1281.64	63.369	24553	2	641.33	14.48
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	1		AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	8	35	32	247.65	b2b3b4b5b6b9b10*b10b11b17y2y3y4y5y6y11°y11y12°y12y14y15y17y19y20y24y26y27y28*y28y29y30y35	3487.81	107.343	74796	3	1163.28	2.80
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	2	Carbamidomethyl+C(3)	FICIADASK	112	9	8	69.14	b2y3y4°y4y5y6y7y9	1024.51	50.826	31257	2	512.76	-6.31
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	3		GADVALIGTPDGVK	201	14	9	31.73	b5°b5y1y2y5°y5y7y8y14	1312.71	57.171	24626	2	656.86	-1.49
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	4		GLGIHVFDLNEVDSLGIYVDGADEINGHMQMIK	61	33	4	36.99	y7y8y9*y9	3599.74	107.749	10947	5	720.75	-3.59
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	5		GQIEGAVSSSDASTEK	43	16	11	51.57	b2*b2b6°b6*b6b8*b8b11b12b13y16	1565.74	50.878	10691	2	783.38	9.12
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	6		GQIEGAVSSSDASTEKLK	43	18	6	25.07	b3b4°b4b7°b7*b7	1806.90	38.775	3083	2	903.95	-3.18
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	7	Phosphoryl STY(14)	GLGIHVFDLNEVDSLGIYVDGADEINGHMQMIK	61	33	6	22.36	b12°b12b13°b13y14_H3PO4 y14°y14	3679.68	84.316	2105	4	920.67	-8.82
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	8	Oxidation+M(31)	GLGIHVFDLNEVDSLGIYVDGADEINGHMQMIK	61	33	5	16.05	b13°b13y3y7y24	3615.77	86.780	2821	3	1205.93	7.22
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	9		GQIEGAVSSSDAST	43	14	1	7.26	y4	1308.61	50.925	2968	2	654.81	13.71
P66692 RPIA_SALTY Ribose-5-phohate isomerase A	10		SLGIYVDGADEINGHMQMIK	74	20	2	9.62	b3°b3	2191.08	107.747	1853	3	731.03	14.15

P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	12	76.06	b2*b2b3y2y3y5y6y7°y7y8y10	1129.61	38.722	75625	2	565.31	-11.24
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	10	112.59	b3y3y4y5y6y7y8y9y12y14	1452.65	57.111	59094	2	726.83	3.78
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3		GLPIPVVITVYADR	51	14	7	46.56	b3b4y2y8y10y12y14	1512.88	91.130	57464	2	756.94	0.56
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4		TPPAAVLLK	72	9	6	58.63	b2y3y5y7y8y9	909.57	54.035	50066	2	455.29	-11.41
P0A7K0 RL11_SALTY 50S ribosomal protein L11	5	Carbamidomethyl+C(29)	LQVAAGMANPSPVGPALGQQG VNIMEFCK	10	30	4	11.62	b12y9°y9y16	3081.59	110.248	11995	4	771.15	18.94
P0A7K0 RL11_SALTY 50S ribosomal protein L11	6	Carbamidomethyl+C(29)	LQVAAGMANPSPVGPALGQQG VNIMEFCKAFNAK	10	35	3	22.5	b10y7y8	3612.79	130.757	35370	4	903.95	-7.03
P0A7K0 RL11_SALTY 50S ribosomal protein L11	7		SIEGTARSMGLVVED	127	15	3	18.79	b8y9y14	1563.78	55.693	2290	2	782.40	9.37
P0A7K0 RL11_SALTY 50S ribosomal protein L11	8	Carbamidomethyl+C(29) ;Oxidation+M(26)	LQVAAGMANPSPVGPALGQQG VNIMEFCK	10	30	4	22.23	b7y8y9°y9	3097.57	126.648	2551	3	1033.19	12.45
P0A1P6 GLNA_SALTY Glutamine synthetase	1	Carbamidomethyl+C(1)	CDILEPGTLQGYDRDPR	89	17	12	70.74	b2b3b9b11b15y1y2y6y9*y9y11y13	2004.94	59.748	43894	3	668.98	-3.17
P0A1P6 GLNA_SALTY Glutamine synthetase	2		LVPGYEAPVMLAYSAR	322	16	8	68.88	b14y4y5y9y11y13y14y16	1736.91	77.391	39212	2	868.96	5.06
P0A1P6 GLNA_SALTY Glutamine synthetase	3		ATGIADTVLFGPEPEFFLFDDIR	117	23	24	132.3	b2°b2b3°b3b4b6b8°b8b9b10°b10b13b18y1y2y3y4y5°y5y8y10y11y13y23	2570.27	117.004	28324	3	857.43	-4.46
P0A1P6 GLNA_SALTY Glutamine synthetase	4		EIPQVAGSLEEALNALDLDR	406	20	18	82.98	b4°b4b8°b8b11°b11°b11b14y1y6°y6y7°y7y10y11y13y19y20	2153.09	95.678	27328	3	718.37	-10.77
P0A1P6 GLNA_SALTY Glutamine synthetase	5		AINALANPTTNSYKR	307	15	12	59.16	b2b3b4°b4y8*y8y9°y9y10°y10y13y15	1633.85	42.420	26853	3	545.29	-12.10
P0A1P6 GLNA_SALTY Glutamine synthetase	6		GGYFVPPVDSAQDIR	177	16	8	17.79	b5y1y2y8°y8*y8y14*y14	1717.87	56.990	24709	3	573.30	11.16
P0A1P6 GLNA_SALTY Glutamine synthetase	7		GINESDMVLPMDASTAVIDPFFAD STLIR	59	30	16	112.75	b3b9b10°b10b16y2y3y4y6y8y9y11y12y13y20y21	3238.61	113.318	17953	3	1080.21	3.17
P0A1P6 GLNA_SALTY Glutamine synthetase	8	Carbamidomethyl+C(1)	CDILEPGTLQGYDR	89	14	7	49.73	b10y5y8*y8y11y13y14	1636.79	71.658	17322	2	818.90	14.54
P0A1P6 GLNA_SALTY Glutamine synthetase	9	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	9	45.26	b3b14b15°b15y3y6y7y11y24	2565.30	136.628	14110	3	855.77	3.24
P0A1P6 GLNA_SALTY Glutamine synthetase	10		FGASISGSHVAIDDIEGAWNSSTK	140	24	8	50.18	b6b9b11b14y6y9y12y15	2449.17	75.902	13210	3	817.06	4.29
P0A1P6 GLNA_SALTY Glutamine synthetase	11		YVVHNVahr	240	9	5	55.62	b2y3y4y5y7	1094.58	21.974	12381	2	547.80	-1.45
P0A1P6 GLNA_SALTY Glutamine synthetase	12		NGTNLFSGDK	277	10	5	27.7	b3b9y2y8y10	1052.52	48.426	7267	2	526.76	14.27
P0A1P6 GLNA_SALTY Glutamine synthetase	13		SAEHLVTMLNEHEVK	1	15	4	18.79	b5°b5y6y9	1736.84	54.493	41244	3	579.62	-15.67
P0A1P6 GLNA_SALTY Glutamine synthetase	14		NLYDLPPEEAK	395	11	3	28.07	b6y3y4	1288.64	43.995	19416	3	430.22	1.89
P0A1P6 GLNA_SALTY Glutamine synthetase	15		ADEIQIYK	232	8	4	33.93	b5°b5b6y6	979.50	48.111	8811	2	490.26	-5.86
P0A1P6 GLNA_SALTY Glutamine synthetase	16		MTPHPVEFELYYSV	455	14	4	39.44	b6b7y4y5	1711.84	85.658	4831	2	856.42	21.46
P0A1P6 GLNA_SALTY Glutamine synthetase	17		EQHVTIPAHQVNAEFFEEGK	28	20	10	51.47	b5b7°b7b9°b9b11°b11y6y7y9	2310.13	112.732	4696	3	770.71	5.81
P0A1P6 GLNA_SALTY Glutamine synthetase	18		AGGVFTDEAIDAYIALR	430	17	6	30.82	b10°b10b13y11°y11y12	1781.87	99.452	3374	2	891.44	-20.21
P0A1P6 GLNA_SALTY Glutamine synthetase	19		AINALANPTTNSYK	307	14	4	28.56	b10b12y4y9	1477.73	78.142	2995	3	493.25	-21.56

P0A1P6 GLNA_SALTY Glutamine synthetase	20		YAGLSEQALYYIGGVK	287	17	3	23.9	b5b6y4	1844.96	33.972	2453	3	615.66	-11.05
P0A1P6 GLNA_SALTY Glutamine synthetase	21		MSAEHVLTMLNEHEVK	0	16	3	17.79	b3b8y11	1867.89	91.673	2006	2	934.45	-5.16
P0A1P6 GLNA_SALTY Glutamine synthetase	22		NGTNLFSGDKYAGLSEQALYYIGGVK	277	27	3	12.23	b5b19y5	2878.47	99.039	30390	3	960.16	1.87
P0A1P6 GLNA_SALTY Glutamine synthetase	23		LVPGYEAPVMLAYSARNR	322	18	3	16.15	b8b13y5	2007.07	100.894	13654	2	1004.04	10.46
P0A1P6 GLNA_SALTY Glutamine synthetase	24	Carbamidomethyl+C(1)	CDILEPGTLQGYDRDPR	89	17	4	28.3	b3y5y6y8	2004.96	32.434	11134	3	668.99	6.33
P0A1P6 GLNA_SALTY Glutamine synthetase	25		FGASISGSHVAID DIEGAWNSSTK YEGGNK	140	30	5	11.62	b7y10°y10y13*y13	3097.48	75.930	9349	4	775.13	11.11
P0A1P6 GLNA_SALTY Glutamine synthetase	26		AEDYLRATGIADTVLFGPEPEFFLFD DIR	111	29	6	22.71	b6b7°b7b13°b13y9	3317.62	97.133	7704	4	830.16	-4.42
P0A1P6 GLNA_SALTY Glutamine synthetase	27		NKIHPGEAMDK	384	11	3	28.07	b8b9y9	1239.62	68.307	2668	2	620.32	7.19
P0A1P6 GLNA_SALTY Glutamine synthetase	28		VRMTPHPVEFELYYSV	453	16	3	17.79	b5y3y6	1966.99	59.188	1746	4	492.50	6.21
P0A1P6 GLNA_SALTY Glutamine synthetase	29	Carbamidomethyl+C(4); Oxidation+M()	SEMCLVMEQMGLVVEAHHHEVA TAGQNEVATR	193	32	6	11.33	b6y11°y11y13°y13*y13	3579.68	117.064	23862	3	1193.90	10.37
P0A1P6 GLNA_SALTY Glutamine synthetase	30	Oxidation+M(4)	FNTMTKK	225	7	3	41.34	b3b6y6	885.44	57.668	2255	2	443.22	-14.06
P0A1P6 GLNA_SALTY Glutamine synthetase	31		ID DIEGAWNSSTK	151	13	0	7.17		1435.65	75.907	5691	2	718.33	-11.22
P0A1P6 GLNA_SALTY Glutamine synthetase	32		NALANPTTNSYKR	309	13	0	3.77		1449.75	42.429	3663	2	725.38	0.93
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	1		GVDVVAYANQDLIYSDLTAGR	155	21	7	27.85	b6b13y7°y7y13y16y21	2240.12	72.343	100538	3	747.38	0.76
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	2	Carbamidomethyl+C(1)	CTWVASDFDALIPSLK	66	16	9	62.78	b3°b3b4b5b12y3y4y13y16	1822.92	97.920	40706	2	911.96	7.10
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	3		HVGVLQGSTQEAYANDNWR	134	19	14	95.03	b2b3b4b10b13y2y3*y3y5y6y7y8y9y19	2144.99	53.171	40527	3	715.67	-8.65
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	4		IGTDTTYAPFSSK	29	13	8	59.86	b1y5y8y9y10y11°y11y13	1387.67	52.993	39041	2	694.34	-0.79
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	5		YFGDGTGVGLR	211	11	4	32.05	y7y9y10y11	1141.56	55.597	36573	2	571.28	-3.10
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	6		GSPIQPTLESLK	120	12	3	23.01	b11y6y10	1269.72	55.103	93056	3	423.91	13.65
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	7	Carbamidomethyl+C(15)	GEFIGFDIDLGNEMCK	45	16	4	31.73	b3b4y3y14	1844.85	78.894	38008	3	615.62	17.87
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	8		QQEIAFS DK	99	9	6	31.3	b3°b3y4°y4y5°y5	1065.53	38.790	3152	2	533.27	9.05
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	9		DDTELK	223	6	1	13.9	y3	720.34	61.467	2322	1	720.34	0.00
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	10		GVDVVAYANQDLIYSDLTAGRLD AALQDEVAASEGFLK	155	38	6	24.55	b13°b13b14y5y13*y13	3997.99	102.619	27724	4	1000.25	-2.44
P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	11		ALTEL RQDGTYDK	234	13	4	26.12	b8y9°y9y10	1509.74	57.490	7581	2	755.37	-11.72

[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	12		LDAALQDEVAASEGFLKQPAGK	176	22	3	23.77	b5b6b15	2258.17	99.748	3316	3	753.39	0.00
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	13		IGTDTTYAPFSSKDAK	29	16	3	24.32	b5y9y10	1701.82	47.457	3087	3	567.94	-9.18
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	14		QQEIAFSDKLYAADSR	99	16	3	17.79	b8b12y6	1841.90	68.217	2475	3	614.64	-2.92
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	15		TKGVDDVVAYANQDLIYSDLTAGR	153	23	4	18.23	b10b12y4y12	2469.26	77.437	2062	3	823.76	-2.18
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	16	Phosphoryl STY(14)	GVDVVAYANQDLIYSDLTAGR	155	21	8	45.06	b9b12°b12y7y10y11°y11y12	2320.05	81.534	3673	4	580.77	-12.31
[P66451]RS17_SALTY 30S ribosomal protein S17	1	Carbamidomethyl+C(10)	MHVHDENNECGIGDVVEIR	43	19	13	76.58	b2b3b5b9y2y3y4y5y7°y7y9y10y19	2222.98	55.093	42221	3	741.66	-7.14
[P66451]RS17_SALTY 30S ribosomal protein S17	2		SIVVAIER	19	8	4	41.71	y4y5y6y8	886.53	51.635	40672	2	443.77	-11.91
[P66451]RS17_SALTY 30S ribosomal protein S17	3		SWTLVR	71	6	2	27.43	y3y4	761.42	55.536	36051	2	381.21	-14.75
[P26976]PHON_SALTY Non-ecific acid phohatase	1		NGSYPSGHTAYGTLLALVLSEARPER	150	26	7	27.17	b2*b2y3y5y7y10y26	2759.38	95.978	36915	4	690.60	-12.48
[P26976]PHON_SALTY Non-ecific acid phohatase	2		NLLTMGGYYATASAK	108	15	6	60.92	b3b5y10y11y12y13	1560.78	69.476	34818	2	780.89	2.89
[P26976]PHON_SALTY Non-ecific acid phohatase	3		IFSPVVGAK	85	9	6	31.3	b2b3y1y3y4y9	917.54	50.917	30386	2	459.27	-9.58
[P26976]PHON_SALTY Non-ecific acid phohatase	4	Carbamidomethyl+C(3)	VICGAHWQSDVDAGR	191	15	6	30.4	b9y3y5y9*y9y15	1670.75	44.873	19366	3	557.59	-13.01
[P26976]PHON_SALTY Non-ecific acid phohatase	5		YVGAVEFAR	206	9	4	31.3	b3b5y7y9	1011.51	51.030	17282	2	506.26	-13.15
[P26976]PHON_SALTY Non-ecific acid phohatase	6		QAAEDADVSVENIAR	70	15	17	97.52	b2*b2b4b10°b10b11b13°b13y9°y9y10y11°y11*y11y12y13y15	1587.76	50.505	10009	2	794.38	-0.08
[P26976]PHON_SALTY Non-ecific acid phohatase	7		NLLTMGGYYATASAKK	108	16	3	17.79	b10y10y12	1688.84	63.595	8579	3	563.62	-14.24
[P26976]PHON_SALTY Non-ecific acid phohatase	8		INPKDTPETWNMLK	94	14	4	19.96	b1b8b11y10	1686.87	82.748	1709	3	562.96	12.52
[P26976]PHON_SALTY Non-ecific acid phohatase	9		AQELAR	176	6	1	13.9	b5	687.37	27.552	4251	1	687.37	-10.21
[P26976]PHON_SALTY Non-ecific acid phohatase	10	Carbamidomethyl+C(12)	TRPFVLFNHSTCRPEDENTLR	128	21	5	27.85	b4b8b10y8y13	2589.32	49.890	1994	4	648.08	20.56
[P26976]PHON_SALTY Non-ecific acid phohatase	11		DTPETWNMLKNLLTMGGYYATASAK	98	25	3	12.79	b12y7y9	2776.33	92.125	3438	3	926.11	-0.70
[P26976]PHON_SALTY Non-ecific acid phohatase	12	Carbamidomethyl+C(16)	YYMRTRPFVLFNHSTCRPEDENTLR	124	25	5	22.33	b9y9°y9y10°y10	3202.54	84.999	2968	3	1068.18	1.52
[P26976]PHON_SALTY Non-ecific acid phohatase	13		EELNDKNLLSK	230	12	3	23.01	b6y6y9	1416.72	54.797	1772	2	708.86	-10.60
[P26976]PHON_SALTY Non-ecific acid phohatase	14	Oxidation+M(5)	NLLTMGGYYATASAKK	108	16	7	39.12	b3b4°b4b6°b6b8y13	1704.87	84.122	6405	2	852.94	2.22
[P26976]PHON_SALTY Non-ecific acid phohatase	15		LTMGGYYATASAKK	110	14	0	4.15		1461.75	63.579	1568	2	731.38	4.59
[P26976]PHON_SALTY Non-ecific acid phohatase	16		IFSPVVGAK	85	9	0	1.51		899.53	50.907	1899	2	450.27	0.68
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	1		TMNTPHGDAITVFDLR	23	16	12	83.43	b2b3b4b6b11y2y4y5y6y10y12y16	1787.85	70.795	41335	3	596.62	-12.56
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	2	Carbamidomethyl+C(2)	FCIPNKEVMPEK	39	12	9	35.29	b2b7y3y4°y4y9*y9y12*y12	1491.71	51.892	35516	3	497.91	-12.77

Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	3		TGFYMSLIGTPDEQR	84	15	4	32.78	b3b14y7y8	1714.82	78.233	24551	2	857.91	4.56
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	4	Carbamidomethyl+C(15)	VQDQNQIPELNVYQCGTYQMHSLS SEAQDIAR	113	31	7	32.16	b10y4y10y11y21y24y31	3635.72	74.952	20312	3	1212.58	8.80
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	5		PLLDSDFAVDHTR	1	12	4	38.3	b4y3y5y10	1370.68	61.656	62288	3	457.56	-19.15
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	6		MPLLDSDFAVDHTR	0	13	3	30.59	y3y5y9	1501.77	49.862	14120	3	501.26	12.19
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	7		EVMPEK	45	6	1	13.9	b3	732.35	57.626	2997	1	732.35	-14.17
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	8		GIHTLEHLFAGFMR	51	14	3	19.96	b5y8y10	1628.80	122.407	1935	2	814.90	-21.13
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	9	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCR	65	19	3	23.26	b10b11y9	2097.03	63.663	1855	2	1049.02	22.00
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	10		VADAWKAAMADV LK	99	14	3	27.74	b3b4b13	1488.78	90.226	350190	2	744.90	-3.36
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	11		TGFYMSLIGTPDEQRVADAWK	84	21	3	14.36	b3y5y12	2385.17	108.997	3735	3	795.73	6.55
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	12		EVMPEKGIHTLEHLFAGFMR	45	20	7	54.11	b10b13y3y5y8y11y14	2342.16	98.679	3204	3	781.39	-5.94
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	13	Phosphoryl STY(4)	GIHTLEHLFAGFMR	51	14	3	19.96	b3y7y10	1708.81	66.650	65317	2	854.91	11.00
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	14	Oxidation+M(1)	MPLLDSDFAVDHTR	0	13	3	30.59	y6y8y11	1517.74	81.973	2724	3	506.58	-2.49
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	15	Oxidation+M(5)	TGFYMSLIGTPDEQR	84	15	6	30.4	b9y4°y4y5°y5y9	1730.81	59.736	1583	3	577.61	3.81
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	16	Oxidation+M(13)	GIHTLEHLFAGFMR	51	14	7	52.31	b4°b4b12y4y5y8y10	1644.81	91.422	1505	2	822.91	-12.39
Q7CQ71 RL25_SALTY 50S ribosomal protein L25	1		AEFYSEVLT LVVDGK	53	15	18	137.53	b2b3b4b7°b7b8b13y2y3°y3y4°y4y5y6y7y8y11y15	1669.87	100.857	61578	2	835.44	-0.51
Q7CQ71 RL25_SALTY 50S ribosomal protein L25	2		LTHIDFVR	85	8	7	50.47	b2°b2b5y3y4y5y8	1000.55	50.437	11951	2	500.78	-4.82
Q7CQ71 RL25_SALTY 50S ribosomal protein L25	3		FP AIYGGSEAPIAIELDHDQVMNM QAK	25	28	3	22.22	b12b13y10	3058.50	111.382	2752	4	765.38	-0.72
Q7CQ71 RL25_SALTY 50S ribosomal protein L25	4		MFTINAEVR	0	9	3	31.3	b6b7y4	1080.55	42.502	20175	2	540.78	2.94
Q7CQ71 RL25_SALTY 50S ribosomal protein L25	5		AANKFP AIYGGSEAPIAIELDHDQ VMNMQAK	21	32	19	125.58	b4°b4b5b7°b7b8°b8b9y5y7y9y12y13°y13y17y18y20y22y23	3442.70	83.517	132173	4	861.43	-5.04
Q7CQ71 RL25_SALTY 50S ribosomal protein L25	6		LTHIDFVRA	85	9	4	55.62	y4y5y6y7	1071.59	53.259	44556	2	536.30	-8.09
Q7CQ71 RL25_SALTY 50S ribosomal protein L25	7		THIDFVR	86	7	0	1.13		887.46	50.433	9596	2	444.24	-10.45
Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTEPTWFPDSQTLAFTSDQAG RPQVYK	287	29	12	41.09	b2b4°b4b5°b5b8y2y13y14y21y24y29	3285.56	77.473	84261	3	1095.86	5.72
Q8ZQT5 TOLB_SALTY Protein tolB	2		WAGPGAAPEDIGGIVAADLR	43	20	9	60.22	b6b7b13b14y2y4y5y13y20	1936.00	85.323	79525	2	968.50	3.22
Q8ZQT5 TOLB_SALTY Protein tolB	3		VSDYDGYNQFVVHR	183	14	5	43.71	b10y4y10y12y13	1698.77	53.494	68794	3	566.93	-11.57
Q8ZQT5 TOLB_SALTY Protein tolB	4		IEITQGVSARPIGVVPFK	24	19	9	50.97	b2b11y2y3y12y14y16y18y19	2026.11	70.202	66130	3	676.04	-10.66
Q8ZQT5 TOLB_SALTY Protein tolB	5		LAYVTFESGR	213	10	7	62.53	b2b3y5y6y8y9y10	1142.58	57.241	45759	2	571.79	-1.92
Q8ZQT5 TOLB_SALTY Protein tolB	6		IAYVVQTNGGQFPYELR	166	17	8	16.91	b12°b12y2y5°y5y12°y12°y12	1955.01	73.103	37441	2	978.01	1.56
Q8ZQT5 TOLB_SALTY Protein tolB	7		MNINGGAAQR	316	10	9	59.52	b2°b2b3y6y7°y7y8y9y10	1031.50	27.733	35875	2	516.25	-5.80

Q8ZQT5 TOLB_SALTY Protein tolB	8		SALVIQTLANGAVR	223	14	9	70.09	b1b3b4b11y3y7y9y11y14	1412.82	70.594	21936	2	706.91	-1.12
Q8ZQT5 TOLB_SALTY Protein tolB	9		SPQPLMSPAWSPDGSK	197	16	7	29.27	b3°b3y1y6y7°y7y11	1684.80	59.200	15010	3	562.27	1.52
Q8ZQT5 TOLB_SALTY Protein tolB	10		HNGAPAFSPDGTK	244	13	13	147.05	b2b3*b3b4b7b8b10y3y5y7y9y11y12	1298.63	32.105	14102	2	649.82	13.16
Q8ZQT5 TOLB_SALTY Protein tolB	11		LAFALSK	257	7	4	41.34	b3y2y3y5	749.45	56.019	13211	2	375.23	-14.17
Q8ZQT5 TOLB_SALTY Protein tolB	12		TGSLNLNVMDLASGQIR	264	17	5	16.91	b6b10y11°y11y17	1837.95	89.266	12324	2	919.48	3.65
Q8ZQT5 TOLB_SALTY Protein tolB	13		ITWEGSQNQDADVSSDGK	326	18	4	27.46	b10y5y6y12	1936.84	55.915	2204	2	968.93	-4.41
Q8ZQT5 TOLB_SALTY Protein tolB	14		YAGHTASDEVFEK	142	13	3	30.59	y6y9y11	1453.64	36.711	44844	3	485.22	-13.02
Q8ZQT5 TOLB_SALTY Protein tolB	15		FMVMVSSNNGQQHIAK	344	16	4	17.79	b8y7y11*y11	1790.84	50.188	22065	3	597.62	-14.04
Q8ZQT5 TOLB_SALTY Protein tolB	16		FNPLDR	67	6	3	40.96	y3y4y5	761.39	45.065	7193	2	381.20	-11.78
Q8ZQT5 TOLB_SALTY Protein tolB	17		QVASFPR	237	7	5	41.34	b3*b3b6*b6y5	804.42	67.366	6934	1	804.42	-15.17
Q8ZQT5 TOLB_SALTY Protein tolB	18		LPATDGQVK	413	9	3	31.3	b3b6y8	928.50	49.301	5284	2	464.76	-7.43
Q8ZQT5 TOLB_SALTY Protein tolB	19		LPATDGQVKSPAWSPYL	413	17	4	16.91	b14°b14y9y13	1829.95	89.811	29287	2	915.48	5.80
Q8ZQT5 TOLB_SALTY Protein tolB	20		ITWEGSQNQDADVSSDGKFMVMVSSNNGQQHIAK	326	34	5	21.96	b6b8b9°b9y9	3708.72	96.147	25489	3	1236.91	3.95
Q8ZQT5 TOLB_SALTY Protein tolB	21		ARLPATDGQVK	411	11	5	68.14	b3b5b7b9y6	1155.64	28.920	11164	2	578.33	-4.33
Q8ZQT5 TOLB_SALTY Protein tolB	22		QWLRYAGHTASDEVFEK	138	17	3	16.91	b3y5y13	2037.00	106.048	3587	2	1019.00	9.05
Q8ZQT5 TOLB_SALTY Protein tolB	23		QVASFPRHNGAPAFSPDGTK	237	20	4	14.89	b4°b4y6y9	2084.02	70.575	2252	4	521.76	-5.86
Q8ZQT5 TOLB_SALTY Protein tolB	24		VIQTLANGAVR	226	11	0	3.4		1141.66	70.557	19290	2	571.33	-10.80
Q8ZQT5 TOLB_SALTY Protein tolB	25		DYDGYNQFVVHR	185	12	1	7.38	b5	1512.71	53.536	1935	2	756.86	13.56
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	18	142.62	b2b3y2y3y5y7°y7y8y9y10*y10y11*y11y13°y13y15y17y19	2032.90	37.318	94414	3	678.30	-10.69
P02936 OMPA_SALTY Outer membrane protein A	2		STLKPEGQQALDQLYSQSLNDPK	231	24	9	48.66	b4b13y2y3y6y9y10y11y24	2673.38	89.227	80992	3	891.80	1.19
P02936 OMPA_SALTY Outer membrane protein A	3	Carbamidomethyl+C(6)	AALIDCLAPDR	321	11	9	71.67	b2b3b4y3y4y7y8°y8y11	1214.62	61.756	59869	2	607.81	-2.81
P02936 OMPA_SALTY Outer membrane protein A	4		SDVLFNFNK	222	9	7	39.08	b1b2y2y4y5y6y9	1083.54	68.288	48972	2	542.27	-9.01
P02936 OMPA_SALTY Outer membrane protein A	5		GVKDVVTQPQA	339	11	11	66.61	b2b5b6b8°b8y1y3*y3y4y5y11	1141.61	36.918	32580	2	571.31	-8.55
P02936 OMPA_SALTY Outer membrane protein A	6		LGYPITDDLVDYTR	103	14	5	27.74	y7y9y10°y10y14	1640.81	75.891	13982	2	820.91	-1.41
P02936 OMPA_SALTY Outer membrane protein A	7		IGSDAYNQLSEK	267	13	8	35.45	b4b5°b5b13y2y8y10y13	1381.65	37.829	13412	2	691.33	-3.53
P02936 OMPA_SALTY Outer membrane protein A	8		FGQQEAAPVVAPAPAPEVQTK	194	23	7	48.43	b9b10b11y6y10y12y23	2303.19	54.011	10039	3	768.40	-5.72
P02936 OMPA_SALTY Outer membrane protein A	9		DVVTQPQA	342	8	7	33.93	b5°b5y6y7°y7*y7y8	857.45	32.431	4020	2	429.23	10.25
P02936 OMPA_SALTY Outer membrane protein A	10		LEYQWTNNIGDANTIGTRPDNGLLSVGVSYSR	163	31	4	11.47	b10y7y12*y12	3423.76	80.624	3055	4	856.70	20.82
P02936 OMPA_SALTY Outer membrane protein A	11		MPYKGDNINGAYK	81	13	3	21.35	b9b11y8	1470.71	83.187	7650	3	490.91	3.82

P02936 OMPA_SALTY Outer membrane protein A	12	Carbamidomethyl+C(17)	ISARGMGESNPVTGNTCDNVKPR	298	23	3	23.57	b3b7b8	2460.18	69.763	4421	3	820.73	1.39
P02936 OMPA_SALTY Outer membrane protein A	13	Phosphoryl STY(7)	GVKDVVTQPQA	339	11	3	25.06	b5b9y4	1221.59	30.636	152413	2	611.30	7.49
P0A6B1 ACP_SALTY Acyl carrier protein	1		IIGQLGVK	10	9	11	76.65	b2b8y1y3y4y5*y5y7*y7y8y9	956.57	48.730	180043	2	478.79	-11.93
P0A6B1 ACP_SALTY Acyl carrier protein	2		ITTVQAAIDYINGHA	62	16	8	50.32	y1y4y5y8y10y12y13°y16	1714.85	82.154	9103	3	572.29	-13.38
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	1		VDQLSNDVNAMR	40	12	6	51.03	b3y3y4y7y9y12	1361.65	48.463	31729	2	681.33	0.18
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	2		SDVQAAKDDAAR	52	12	14	77.79	b1b2°b2b4b6y1y2y3y4y7y8y9*y9y12	1246.59	17.677	21080	2	623.80	-6.27
Q7CQN4 LPP1_SALTY Major outer membrane lipoprotein 1	3		IDQLSSDVQTLNAK	26	14	6	11.36	b7°b12*b12y2y8y14	1531.82	66.124	14799	2	766.41	12.35
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	12	124.9	b2b3b4b6y3y4y5y6y8y9y10y12	1377.65	77.922	105711	2	689.33	0.00
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AVVESIQR	69	8	12	68.77	b2b5°b5b7y1y4*y4y5°y5y6*y6y8	901.50	32.498	75728	2	451.25	-12.93
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3		VSRPGLR	77	7	5	41.34	y1y3y4y6y7	784.47	21.917	13707	2	392.74	-14.16
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4		VEGDTKPELELTk	50	14	5	32.52	b7b9b12y12°y12	1571.84	64.570	7943	2	786.42	-9.94
P0A7X0 RS8_SALTY 30S ribosomal protein S8	5		YFQgK	64	5	2	27.05	b4y3	642.33	32.421	2902	1	642.33	6.08
P0A7X0 RS8_SALTY 30S ribosomal protein S8	6		VMAGLGIAVVSTSK	94	14	4	27.74	y3y4°y4y9	1332.76	68.664	2153	2	666.88	0.37
P0A7X0 RS8_SALTY 30S ribosomal protein S8	7		GVMtDR	108	6	2	27.43	b5y5	678.33	111.449	2072	1	678.33	7.02
P0A7X0 RS8_SALTY 30S ribosomal protein S8	8		MSMQDPIADMLTR	0	13	4	26.12	b12y10°y10y11	1508.71	68.923	1716	2	754.86	11.49
P0A7X0 RS8_SALTY 30S ribosomal protein S8	9	Carbamidomethyl+C(13)	AARQAGLGGEIIcYVA	114	16	4	17.79	b10b13y10°y10	1648.85	56.547	3268	3	550.29	-0.37
P0A7X0 RS8_SALTY 30S ribosomal protein S8	10		NGQAANKAAVTMPSSK	15	16	3	17.79	b3b5y9	1574.81	104.350	1937	2	787.91	6.74
Q8ZP20 TREA_SALTY Periplasmic trehalase	1		VAAAAQAHLQPGGLATTSVK	428	21	7	28.17	b1b2b10b11y8y10y21	2004.11	57.393	35851	3	668.71	-5.66
Q8ZP20 TREA_SALTY Periplasmic trehalase	2		TFADAIPNSDPLMILADYR	68	19	14	64.51	b6°b6b14*b14b16y2y4y5°y5y9y13°y13y14y19	2123.07	101.221	34969	2	1062.04	9.20
Q8ZP20 TREA_SALTY Periplasmic trehalase	3	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPK	534	29	8	38.83	b2b3b4y3y10y25y27y29	3199.56	63.793	21845	4	800.65	-5.88
Q8ZP20 TREA_SALTY Periplasmic trehalase	4		SQPPFFAFMVELLAQHEGDDALK EYLPQLQK	212	31	4	17.33	b5b8b12*b12	3589.78	119.144	15582	4	898.20	-5.17
Q8ZP20 TREA_SALTY Periplasmic trehalase	5		VADMVANFGYEIDAWGHIPNGNR	183	23	4	23.57	b3b5b6y23	2546.16	100.864	11962	3	849.39	-11.60
Q8ZP20 TREA_SALTY Periplasmic trehalase	6		WDSLLPLPESYVVPgGR	142	17	3	16.91	b13y4y9	1884.99	91.416	9615	2	943.00	3.95
Q8ZP20 TREA_SALTY Periplasmic trehalase	7		SNPNRPATEIYR	296	12	6	33.22	b2y2y3y7y10y12	1417.72	32.178	6346	2	709.36	-0.60
Q8ZP20 TREA_SALTY Periplasmic trehalase	8		LEDGSVLNR	266	9	3	31.3	b6b7y7	1002.54	25.066	3779	2	501.77	14.73
Q8ZP20 TREA_SALTY Periplasmic trehalase	9		FLTNVQHTYDR	486	11	5	25.06	b7b9°b9y6°y6	1393.67	42.383	10182	3	465.23	-14.01
Q8ZP20 TREA_SALTY Periplasmic trehalase	10		SQPPFFAFMVELLAQHEGDDALK	212	23	3	13.48	b7b13y11	2590.26	90.275	9687	3	864.09	-3.20
Q8ZP20 TREA_SALTY Periplasmic trehalase	11		DTPRPESWVEDIATAK	280	16	4	31.73	b8b12y10y11	1814.86	62.269	4369	3	605.63	-16.21

Q8ZP20 TREA_SALTY Periplasmic trehalase	12		TYYLSR	206	6	1	13.9	y4	802.41	37.254	2778	2	401.71	2.89
Q8ZP20 TREA_SALTY Periplasmic trehalase	13		LFPDQK	62	6	1	13.9	b5	747.39	46.971	2138	1	747.39	-12.17
Q8ZP20 TREA_SALTY Periplasmic trehalase	14		NVEKWDSLLPLPESYVVPGGR	138	21	4	22.49	b6y5y10y12	2355.23	87.667	35966	3	785.75	-3.01
Q8ZP20 TREA_SALTY Periplasmic trehalase	15	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPTKTPSAATQ	534	36	3	16.65	y8y11y21	3855.89	63.763	29492	4	964.73	-0.63
Q8ZP20 TREA_SALTY Periplasmic trehalase	16		TYYLSRSQPPFFAFMVELLAQHEG DDALK	206	29	9	45.25	b6b8°b8b9b22y5y7y12y13	3373.65	114.055	3321	5	675.54	-0.87
Q8ZP20 TREA_SALTY Periplasmic trehalase	17		TFADAIPNSDPLMILADYRMQR	68	22	7	37.77	b6°b6b7b13y4y6y12	2538.23	116.125	3021	3	846.75	-5.87
Q8ZP20 TREA_SALTY Periplasmic trehalase	18	Oxidation+M(4)	VADMVANFGYEIDAWGHIPNGNR	183	23	3	13.48	b10b22y11	2562.17	56.857	40161	3	854.73	-5.53
Q8ZP20 TREA_SALTY Periplasmic trehalase	19	Oxidation+M(4)	AIEMHLWNNKEGWYADYDLK	380	20	3	21.68	y6y8y12	2512.19	92.070	3807	4	628.80	12.54
Q8ZP20 TREA_SALTY Periplasmic trehalase	20	Oxidation+M(9)	SQPPFFAFMVELLAQHEGDDALK	212	23	3	13.48	b7b14y12	2606.23	102.393	3607	3	869.41	-12.37
Q8ZP20 TREA_SALTY Periplasmic trehalase	21	Oxidation+M(13)	TFADAIPNSDPLMILADYR	68	19	4	29.33	b6b16y3y4	2139.03	66.649	1633	2	1070.02	-5.25
Q8ZP20 TREA_SALTY Periplasmic trehalase	22		PNRPATEIYR	298	10	0	2.64		1216.64	32.168	6405	2	608.82	-5.72
Q8ZP20 TREA_SALTY Periplasmic trehalase	23		SNPNRPATEIYR	296	12	0	2.64		1400.67	32.194	1684	3	467.56	-11.77
P26982 DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	12	85.26	b1b3b4b5y1y2y4y7y9y11y12y15	2017.09	74.653	74201	3	673.03	-9.92
P26982 DEGP_SALTY Protease do	2		GAFVSQVMPNSSAAK	313	15	8	44.38	b3b4y8y10°y10°y10y11y15	1493.74	53.135	49601	2	747.38	1.63
P26982 DEGP_SALTY Protease do	3		GYVVTTNNHVVDNASVIK	124	17	17	145.57	b2b3b7b9b11y1y2y3y6y7y8y9y10y13y14y15y17	1828.93	49.865	48247	3	610.32	-11.95
P26982 DEGP_SALTY Protease do	4		SDIALIQIQNPK	160	12	10	76.54	b3b5b11°b11y2y4y6y7y9y12	1339.75	63.769	42129	2	670.38	-6.83
P26982 DEGP_SALTY Protease do	5		VGDYTVAINPFGLGGETVTSGIVS ALGR	186	28	24	168.27	b2b3b4b5°b5b6°b6b7b8°b8b12y1y2y3y4y5y6y8y9y10y12y14y20y28	2750.43	116.391	34732	3	917.48	-2.13
P26982 DEGP_SALTY Protease do	6		SGLNVENYENFIQTDAAINR	214	20	7	26.08	b4y7°y7y8y12*y12y20	2268.11	77.402	33841	2	1134.56	10.98
P26982 DEGP_SALTY Protease do	7		AQVGTMPVGSK	352	11	8	48.59	b2°b2y5y7y8°y8y9y11	1074.55	34.593	32817	2	537.78	-10.91
P26982 DEGP_SALTY Protease do	8		GELGIMGTELNSELAK	289	16	7	66.08	b4b5b7b8b9y11y13	1661.85	74.809	9088	2	831.43	4.33
P26982 DEGP_SALTY Protease do	9		ISLGLLR	363	7	3	41.34	y4y5y6	771.50	67.925	19306	2	386.25	-16.14
P26982 DEGP_SALTY Protease do	10		NIAELR	443	6	1	13.9	b5	715.41	55.652	7248	1	715.41	-6.06
P26982 DEGP_SALTY Protease do	11	Carbamidomethyl+C(13);Carbamidomethyl+C(25))	NFQQFFGDDSPFCQDGSFPQNSPF CQGGGNGGNGGQQQK	71	39	4	10.87	b3b5y3*y3	4240.81	90.715	4192	3	1414.28	14.39
P26982 DEGP_SALTY Protease do	12		GDSSIYLLMQ	465	10	3	29.46	b7b8y5	1126.57	36.855	3704	2	563.79	21.13
P26982 DEGP_SALTY Protease do	13		FMALGSGVIIDAAK	110	14	3	25.4	b5b6y4	1392.75	32.080	1553	2	696.88	-2.72
P26982 DEGP_SALTY Protease do	14		RGELGIMGTELNSELAK	288	17	12	115.41	b3°b3b5b6b7b8b10b12b14y3y6*y6	1817.92	68.207	45539	3	606.64	-13.90
P26982 DEGP_SALTY Protease do	15		GELGIMGTELNSELAKAMK	289	19	3	15.48	b3b13y18	1991.99	63.025	19103	3	664.67	-9.99
P26982 DEGP_SALTY Protease do	16		VDAQRGAFVSQVMPNSSAAK	308	20	7	42.56	b5b6°b6b7y7*y7y13	2063.03	47.899	8356	4	516.51	-2.60
P26982 DEGP_SALTY Protease do	17	Oxidation+M(6)	NLTSQMVEYGQVK	275	13	10	69.93	b5b7°b7b8b9y5y6*y6y8°y8	1512.76	38.361	24598	3	504.92	14.69
P26982 DEGP_SALTY Protease do	18		VVTNNHVVDNASVIK	126	15	5	40.06	b5b6°b6b7b10	1608.86	49.849	2146	2	804.93	-8.65
P26982 DEGP_SALTY Protease do	19		VTNNHVVDNASVIK	127	14	8	49.09	b4°b4b5°b5°b5b6°b6b7	1509.78	49.865	1835	2	755.39	-14.15

P26982 DEGP_SALTY Protease do	20		GAFVSQVMPNSSAAK	313	15	1	7.3	b7	1476.72	53.181	8250	2	738.86	5.46
P0A1V4 KAD_SALTY Adenylate kinase	1		VDGTQAVADVR	195	11	10	39.38	b1b2b3°b3b6°b6y2y4y5y11	1130.57	36.344	61603	2	565.79	-5.83
P0A1V4 KAD_SALTY Adenylate kinase	2		LVEYHQMTAPLIGYYQK	167	17	16	100.06	b2b6b7b8°b8b9°b9b11°b11y5y6y10y11*y11y15y17	2054.03	68.805	57272	3	685.35	-7.25
P0A1V4 KAD_SALTY Adenylate kinase	3		YGIPQISTGDMLR	23	13	10	64.63	b2y3y5y7°y7y8°y8y10°y10y13	1450.73	72.353	54265	2	725.87	-1.51
P0A1V4 KAD_SALTY Adenylate kinase	4		IILLGAPGAGK	2	11	8	54.34	b2b3y2y5y7y8y9y11	1009.63	60.883	35113	2	505.32	-8.89
P0A1V4 KAD_SALTY Adenylate kinase	5		GTQAQFIMEK	13	10	5	41.22	b7y3y4y7y10	1152.57	48.328	34014	2	576.79	-4.34
P0A1V4 KAD_SALTY Adenylate kinase	6		FNPPK	136	5	2	27.05	b3y4	602.32	55.565	44996	1	602.32	-10.23
P0A1V4 KAD_SALTY Adenylate kinase	7		NGFLLDGFPR	78	10	3	29.46	b3y4y5	1135.57	69.838	8848	2	568.29	-13.33
P0A1V4 KAD_SALTY Adenylate kinase	8		AAVKSGSELGK	36	11	4	28.07	b6°b6y6y7	1046.58	48.729	21416	2	523.80	-1.28
P0A1V4 KAD_SALTY Adenylate kinase	9		IILLGAPGAGKGTQAQFIMEK	2	21	5	22.49	b3y4y9°y9y16	2143.18	72.298	17787	3	715.06	-8.66
P0A1V4 KAD_SALTY Adenylate kinase	10		DIMDAGKLVTDDELVIALVK	50	19	5	43.2	b8b11y4y5y6	2043.13	115.796	10980	3	681.71	-7.23
P0A1V4 KAD_SALTY Adenylate kinase	11		VEGKDDVTGEDLTTR	141	15	6	38.36	b3b7y5y7y8°y8	1634.79	82.504	1792	3	545.60	1.34
P0A1V4 KAD_SALTY Adenylate kinase	12	Oxidation+M(11)	YGIPQISTGDMLR	23	13	3	21.35	b3b6y4	1466.75	61.750	7413	3	489.59	11.73
P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	22	154.18	b2b3b4b6°b6b11b12y3°y3y4y5°y5y6°y6y7°y7y8°y8y9y10°y10y12	1196.59	63.923	412056	2	598.80	-7.65
P0A9Y9 CC_SALTY Cold shock-like protein cC	2		GFGFITPADGSKDVFVHFSAIQGN GFK	15	27	6	27.77	b4b9b10b24y1y27	2843.38	112.932	6925	3	948.47	-10.65
P0A9Y9 CC_SALTY Cold shock-like protein cC	3		DVVFHFSAIQGNNGFK	27	15	3	18.79	b6y8y13	1665.84	56.542	4341	3	555.95	-1.25
P0A9Y9 CC_SALTY Cold shock-like protein cC	4		WFNESK	9	6	5	57.5	b3b4y3°y3y5	810.38	39.830	38148	1	810.38	1.43
P0A9Y9 CC_SALTY Cold shock-like protein cC	5		GQVK	5	4	1	13.15	b3	431.26	73.931	4549	1	431.26	-9.91
P0A9Y9 CC_SALTY Cold shock-like protein cC	6		TLAEGQNVEFEIQDGQK	42	17	4	23.9	b4°b4b5y10	1905.95	72.378	2621	2	953.48	17.23
P0A9Y9 CC_SALTY Cold shock-like protein cC	7		TLAEGQNVEFEIQDGQKGPAAVN VTAI	42	27	3	35.87	b6b7b8	2799.41	84.388	1815	4	700.61	-0.70
P0A9Y9 CC_SALTY Cold shock-like protein cC	8		VFVHFSAIQGNNGFK	28	14	1	7.3	b4	1550.81	56.587	3223	2	775.91	0.63
Q7CQV9 DPS_SALTY DNA protection during starvation protein	1		ASNLLYTR	10	8	5	55.24	y3y4y5y6y8	937.51	43.742	38740	2	469.26	-5.14
Q7CQV9 DPS_SALTY DNA protection during starvation protein	2		AIGEAKDEDTADIFTAASR	134	19	10	76.58	b4b8b12y3y5y6y8y9°y9y10	1980.94	58.104	28315	3	660.98	-5.61
Q7CQV9 DPS_SALTY DNA protection during starvation protein	3		AVQLGGVALGTTQVINSK	83	18	8	38.18	b15y3°y3y9°y9y11y13y18	1756.00	67.217	22624	2	878.50	1.60
Q7CQV9 DPS_SALTY DNA protection during starvation protein	4		SYPLDIHNVQDHLK	105	14	9	40.33	b2°b2b5b8°b8b9°b9y10y12	1678.84	57.054	20736	3	560.29	-6.91
Q7CQV9 DPS_SALTY DNA protection during starvation protein	5		GANFIADVHEMLDGFR	55	15	4	24.81	b5y10y11y15	1676.81	65.252	13341	2	838.91	-6.04
Q7CQV9 DPS_SALTY DNA protection during starvation protein	6		SYPLDIHNVQDHLKELADR	105	19	4	15.48	b7b10°b10y5	2263.16	71.565	2278	2	1132.08	4.75
Q7CQV9 DPS_SALTY DNA protection during starvation protein	7		TALTDHLDTMAER	70	13	10	103.97	b3b5°b5b11y3y4y5y7y8y11	1473.67	51.888	59932	3	491.90	-18.39
Q7CQV9 DPS_SALTY DNA protection during starvation protein	8		AIGEAK	134	6	2	27.43	b4y4	588.33	31.570	19789	1	588.33	-9.96

[Q7CQV9]DPS_SALTY DNA protection during starvation protein	9		DLDK	153	4	2	13.15	y3°y3	490.26	38.323	6649	1	490.26	8.65
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	10		QVIQFIDLSLITK	35	13	5	35.45	b3*b3b8y10y11	1517.91	34.802	2038	3	506.64	7.88
[Q7CQV9]DPS_SALTY DNA protection during starvation protein	11		QAHWNMR	48	7	4	41.34	b5y3*y3y5	942.45	109.515	1749	1	942.45	10.56
[P66541]RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAE LNK	45	14	9	43.71	b8y1y3y9*y9y10y12y14*y14	1576.81	84.307	76364	2	788.91	2.40
[P66541]RS2_SALTY 30S ribosomal protein S2	2		EANNLGIPVFAIVDTSNDPDGVDF VIPGNDDAIR	174	34	17	91.22	b5°b5*b5b6b7°b7*b7y3y4y7y8*y8y11y13y14y16y34	3569.76	104.447	28010	3	1190.59	6.02
[P66541]RS2_SALTY 30S ribosomal protein S2	3	Carbamidomethyl+C(13)	AASEAVKEAANS CDQFFVNHR	74	21	6	14.36	b2b3°b3b6y3y21	2351.08	53.960	9844	3	784.37	0.62
[P66541]RS2_SALTY 30S ribosomal protein S2	4		LENSLGGIK	143	9	8	46.08	b2b6b7y2y3y7*y7y9	930.52	37.810	7065	2	465.76	-6.17
[P66541]RS2_SALTY 30S ribosomal protein S2	5		DMGGLPDALFVIDADHEHIAIK	152	22	5	13.9	b6b12°b12y8y22	2377.19	83.483	2958	2	1189.10	1.95
[P66541]RS2_SALTY 30S ribosomal protein S2	6		YWNPK	21	5	1	13.53	y4	707.34	46.526	12177	1	707.34	-9.23
[P66541]RS2_SALTY 30S ribosomal protein S2	7	Carbamidomethyl+C(6)	EAANS CDQFFVNHRWLG GMLTNWK	81	24	4	22.41	b5y7°y7y8	2881.36	93.600	5637	3	961.12	10.00
[P66541]RS2_SALTY 30S ribosomal protein S2	8		DLETQSQDGTFEKLTK	115	16	4	17.79	b11b13°b13y14	1839.92	136.571	1501	2	920.47	14.46
[P66541]RS2_SALTY 30S ribosomal protein S2	9	Oxidation+M(6)	MATVSMR DMLK	0	11	5	42.57	b4b7b10°b10y7	1298.62	66.744	15303	2	649.81	-8.55
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTDSDAVGNAVK	84	17	20	142.39	b2b3b4b5b10b11b13y2y7y10y11y12*y12y13°y13*y13y14*y14y15y17	1739.96	70.608	97748	2	870.48	1.40
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	2		LAATIAQLPDQIGAK	253	15	10	87.67	y1y2y3y4y5y7y8y10y11y15	1509.86	66.163	81691	2	755.43	-4.29
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	3		IPVITLDR	107	8	7	64	b3y1y4y5y6y7y8	926.55	61.613	53435	2	463.78	-13.90
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	4		GLNVMQNLLTAHPDVQAVFAQN DEMALGALR	193	31	13	79.76	b4y2y3y4y5y6y9y10y11*y11y13°y13y31	3336.71	102.574	41744	3	1112.91	7.61
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	5		FNVLASQPADFDR	178	13	7	48.61	b7y3°y3y8y9y10y13	1479.72	66.081	32835	2	740.37	0.74
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	6		VIELQGIAGTSAAR	150	14	6	43.71	b1b4y6y9y10y12	1385.78	58.892	30107	2	693.39	0.26
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	7		ADVMVVGFDGTPDGEK	231	16	5	29.27	b2b8y5y10y11	1636.76	63.561	27809	2	818.88	3.95
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	8		ELANVQDLTVR	70	11	5	25.06	b10y2y3y6y11	1257.68	57.413	25350	2	629.34	-1.07
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	9		YPVDLK	285	6	2	27.43	y4y5	734.40	42.061	13562	2	367.70	-14.71
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	10		LVIK	291	4	1	13.15	y3	472.35	55.804	10603	1	472.35	-6.01
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	11		QATKGDVVSHIASDNVLGGK	115	20	15	92.84	b6°b6*b6b9°b9*b9b14°b14y7y8y9y10y11*y11y12	1996.03	50.906	42618	3	666.01	-7.83
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	12		EADKLGYNLVVLDSQNNPAK	50	20	3	14.89	b10y3y5	2188.12	65.868	19238	3	730.04	-2.45
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	13		ERGEFQQAVAAHK	164	14	3	19.96	b6b13y9	1527.74	73.351	10916	2	764.38	-14.06
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	14		GEGFQQAVAAHKFNVLASQPADFDR	166	25	4	12.79	b7y3°y3y11	2703.36	84.479	4923	3	901.79	11.47
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	15		FNVLASQPADFDR TK	178	15	5	38.36	b5b9b12y6y9	1708.86	83.474	4139	2	854.93	-6.00

P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	16	Oxidation+M(5)	GLNVMQNLLTAHPDVQAVFAQN DEMALGALR	193	31	4	25.17	b6b14y9y10	3352.64	98.152	2077	5	671.33	-11.29
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	1		VILVGNLGDPEVR	8	14	13	91.79	b2b3b4y2y4y8y9y10°y10y11°y11y12y14	1508.84	65.622	28660	2	754.92	-0.73
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	2		YTTEINVQIGGVMQMLGGR	97	20	6	21.68	y5y6*y10y13*y13y20	2164.10	96.402	20318	2	1082.56	7.33
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	3		YMPSGGAVANLTLATSESWRDK	22	22	7	31.36	b11°b11y3y4y8°y8y11	2354.12	113.543	4042	3	785.38	-12.13
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	4		YMPSGGAVANLTLATSESWR	22	20	5	23.02	b13°b13b14y12°y12	2111.06	84.398	13234	4	528.52	15.50
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		VFMQPASEGTGIIAGGAMR	93	19	23	181.68	b2b3b4b11b12°b12b13b16°b16y4y5y6y7y11y12y13°y13y14y15°y15y16*y16y19	1892.94	67.761	107857	2	946.97	2.45
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		AYGSTNPINVVR	126	12	16	130.92	b2b3b4b5y1y2y3y4*y4y5y6y7y8y10*y10y12	1290.68	50.852	102962	2	645.84	-1.89
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		ATIDGLENMNSPEMVA AK	138	18	10	77.44	b4b15b18y3y4y11y12y14y15y18	1890.91	63.144	69184	2	945.96	6.33
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVA AKR	138	19	10	104.47	b2y3y4y5y8y10y12y13y15y16	2046.98	58.890	44217	3	683.00	-8.35
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		IFSFTALT VVG DGNR	29	16	5	39.12	b3y4y6y7y14	1653.86	86.300	39204	2	827.43	-0.52
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		NMINVALNNGTLQHPVK	69	17	8	37.36	b2b3b9°b9b10b16y12y17	1862.98	62.316	16716	3	621.66	-7.27
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		SVEEILGK	159	8	4	55.24	b4b7y3y6	874.48	49.804	71048	2	437.74	-14.94
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		LIAVNR	14	6	2	27.43	y4y5	685.43	32.254	9254	1	685.43	-4.99
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		AHIEK	1	5	3	40.58	b3b4y4	597.33	22.812	2966	1	597.33	-11.75
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		RNMINVALNNGTLQHPVK	68	18	7	55.73	b3b4b5b11y10*y10y11	2019.08	55.707	29900	3	673.70	-6.47
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		GVHTGSRVFMQPASEGTGIIAGGA MR	86	26	5	12.49	b7°b7y13°y13y15	2587.33	100.727	11752	2	1294.17	14.81
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12		NMINVALNNGTLQHPVKGVHTG SR	69	24	4	26.88	b10b12y10y11	2557.31	55.851	5985	4	640.08	-11.46
P0A7W4 RS5_SALTY 30S ribosomal protein S5	13		IFSFTALT VVG DGNR VGF GYGK	29	23	3	22.51	b5y5y6	2362.25	127.715	3232	2	1181.63	12.61
P0A7W4 RS5_SALTY 30S ribosomal protein S5	14	Phosphoryl STY(7)	VFMQPASEGTGIIAGGAMR	93	19	4	23.26	b5b6°b6y6	1972.92	102.439	2129	3	658.31	12.87
P0A7W4 RS5_SALTY 30S ribosomal protein S5	15	Oxidation+M(18)	VFMQPASEGTGIIAGGAMR	93	19	3	15.48	b6b12y15	1908.91	75.184	3269	4	477.98	-10.74
P0A7W4 RS5_SALTY 30S ribosomal protein S5	16	Oxidation+M()	ATIDGLENMNSPEMVA AK	138	18	4	22.62	b5b8y8y10	1906.87	68.807	1605	3	636.30	-7.43
P0A7W4 RS5_SALTY 30S ribosomal protein S5	17		MINVALNNGTLQHPVK	70	16	1	7.26	b11	1748.93	62.351	2097	3	583.65	-12.70
P0A7W4 RS5_SALTY 30S ribosomal protein S5	18		AYGSTNPINVVR	126	12	0	2.64		1273.65	50.803	1502	2	637.33	1.73
P58661 AAT_SALTY Aartate aminotransferase	1		MFENITAAPADPILGLADLFR	0	21	11	80.15	b4b5b6b11°b11b17y3y5y7y13y14	2275.20	120.465	15822	2	1138.10	8.48
P58661 AAT_SALTY Aartate aminotransferase	2		TAQTPGGTGALR	96	12	5	26.99	b10y1y8y9y12	1129.59	29.359	11353	2	565.30	-3.67
P58661 AAT_SALTY Aartate aminotransferase	3		GWLPLFDFA YQG FAR	204	15	6	41.2	b3y4y5y8y12y15	1787.89	115.427	8952	2	894.45	-0.68
P58661 AAT_SALTY Aartate aminotransferase	4		AIWEQELTDMR	304	11	5	28.07	b2b7b8y3y11	1391.66	82.811	6913	2	696.33	-4.03
P58661 AAT_SALTY Aartate aminotransferase	5	Carbamidomethyl+C(4)	VGACTLVAADAETVDR	254	16	5	25.19	b8b11y4y8°y8	1647.82	78.209	3155	2	824.41	11.26

P58661 AAT_SALTY Aartate aminotransferase	6	Carbamidomethyl+C(15)	VNVAGMTPDNMAPLCEAIVAVL	374	22	3	20.41	b3b7b9	2285.15	118.212	2861	2	1143.08	9.08
P58661 AAT_SALTY Aartate aminotransferase	7		QNGMFSFSGLTK	343	12	3	26.99	b4b5y11	1316.62	54.979	12646	2	658.81	-9.92
P58661 AAT_SALTY Aartate aminotransferase	8		NYLGIDGIPFAR	63	13	11	81.69	b3b4*b4b6°b6b8°b8y6y8y10y11	1464.75	80.542	12554	2	732.88	-0.92
P58661 AAT_SALTY Aartate aminotransferase	9		VWVSNPSWPNHK	122	12	4	26.99	b8y4*y4y5	1450.70	53.270	11686	3	484.24	-17.25
P58661 AAT_SALTY Aartate aminotransferase	10		NFGLYNER	246	8	3	33.93	b3b4y7	1012.50	28.974	4626	2	506.75	11.76
P58661 AAT_SALTY Aartate aminotransferase	11		ANYSNPPAHGASIVATILSNDALR	280	24	3	22.41	b13b14y21	2452.30	84.990	2812	2	1226.66	18.52
P58661 AAT_SALTY Aartate aminotransferase	12		ELIVASSYSKNFGLYNER	236	18	3	25.07	y7y10y11	2090.05	85.530	23280	3	697.36	-0.70
P58661 AAT_SALTY Aartate aminotransferase	13	Carbamidomethyl+C(12)	NFGLYNERVGACTLVAADAETVDR	246	24	5	20.16	b6b8b10°b10y10	2641.29	79.983	12424	3	881.10	10.26
P58661 AAT_SALTY Aartate aminotransferase	14	Carbamidomethyl+C(1)	CTQELLFKGKSALINDK	76	17	6	35.22	b8°b8b9b12y4y11	1893.95	69.662	2086	4	474.24	-11.15
P58661 AAT_SALTY Aartate aminotransferase	15		GWLPLFDFAyQGFARGLEEDAEGLR	204	25	3	12.79	b3y4y9	2857.38	92.959	2025	2	1429.19	-5.98
P58661 AAT_SALTY Aartate aminotransferase	16	Carbamidomethyl+C(4)	VGACTLVAADAETVDRAFSQMK	254	22	8	47.88	b6°b6b10b13b15y9y11y12	2340.14	78.095	1795	3	780.72	3.23
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	1		TGYLPITTAAYELTR	343	15	7	49.97	b3b4b11y6y9y11y15	1669.89	84.701	59385	2	835.45	3.80
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	2		NNGFDGTDAVLEFNKPEQVK	212	20	6	21.68	b1*b1y10y16y18y20	2222.05	65.195	56286	3	741.35	-11.76
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	3		AIKPVYEVFKDAGINFDESQFVPTVAGYYTDAK	99	33	7	63.45	b6y7y8y9°y9y10y11	3682.82	93.158	36335	4	921.46	-4.44
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	4		TIVDEELESVWTGKK	397	15	7	37.67	b2y2y3y7y8y13y15	1733.87	75.248	34242	3	578.63	-12.32
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	5		LGNMPQIR	389	8	5	64	b6y4y5y6y7	928.50	47.448	28627	2	464.75	-8.74
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	6		FLDFLAKPENAAEWHQK	326	17	6	28.3	b3y5y6y10*y10y17	2044.00	72.763	28325	3	682.01	-11.65
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	7		SGHLLSQPFNSSTPVLYYNK	132	20	10	87.04	b3b5b6b7b12y3y5y6y7y10	2252.12	67.864	22710	3	751.38	-6.18
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	8		GAPQNAIIGGASLWVMQGKDKETYTGVAK	297	29	4	17.76	y10y15y18y29	2990.56	104.075	20010	4	748.39	4.98
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	9		FNQANPDYK	47	9	4	39.08	y2y4y6y7	1096.50	28.340	16125	2	548.76	-2.34
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	10		FNYGVGMMPYDADIK	282	15	7	60.16	b5y7y8y10y11y12y15	1720.78	74.349	15773	2	860.89	3.76
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	11	Carbamidomethyl+C(6)	FYNGDCAMTTASSGSLANIR	258	20	6	41.57	y10y11*y11y13y14y20	2135.96	60.912	12722	2	1068.48	6.52
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	12		TIVDEELESVWTGK	397	14	5	25.4	b1b8y11y12y14	1605.81	82.091	11352	2	803.41	6.99

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	13		GAPQNAIIGGASLWVMQGKDK	297	21	5	19.72	b3b6y8y14*y14	2141.10	92.071	1855	2	1071.06	-5.93
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	14		AGLDPEQPPK	157	10	6	29.46	b5°b5b6°b6y6*y6	1051.56	57.132	33201	2	526.28	12.77
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	15		EVDSLAQR	39	8	6	36.94	b4y5°y5*y5y7*y7	917.49	43.908	6213	2	459.25	21.29
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	16		HIALLEEMNK	232	10	5	49.01	b4y3y6y8°y8	1197.61	57.704	4028	2	599.31	-17.63
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	17		IVPVYK	56	6	1	13.9	y4	718.44	36.930	2723	2	359.72	-13.59
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	18		TWQELADYTAK	167	11	3	28.07	b6y4y5	1325.61	97.721	2189	2	663.31	-22.10
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	19		AGLDPEQPPKTWQELADYTAK	157	21	4	22.49	b4y8y14y17	2358.15	72.475	37317	3	786.72	-4.35
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	20		EQGYDKNPGADIATR	358	16	5	29.27	b8°b8y4y5y8	1797.82	39.965	24093	3	599.94	-12.70
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	21		TIVDEELESVWTGKK	397	15	3	26.87	b6b7b14	1733.88	93.727	9939	2	867.44	-10.98
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	22		GAPQNAIIGGASLWVMQGKDK	297	21	4	19.72	b5b14y6y8	2141.14	68.871	2563	3	714.39	11.97
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	23		KAGLDPEQPPK	156	11	5	36.37	b5b10y7y10°y10	1179.63	42.357	1778	2	590.32	-2.79
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	24	Phosphoryl STY(5)	GDFSYYVGRK	243	9	4	31.3	b3°b3y5y6	1108.47	37.785	3247	1	1108.47	0.88
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	25	Phosphoryl STY(12)	GAPQNAIIGGASLWVMQGKDK	297	21	3	21.01	b4b11b13	2221.07	68.268	2150	4	556.02	-1.87
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	26	Oxidation+M(16)	GAPQNAIIGGASLWVMQGK	297	19	9	30.57	b6*b6b10y3*y3y6*y6y11*y11	1913.96	81.041	3289	3	638.66	-14.67
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	27	Oxidation+M(19)	TGNAPAILQVYEVGTATMMASK	77	22	5	30.04	b3b16y4y5y11	2269.12	96.644	2933	2	1135.06	0.86
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB	28		AIKPVYEVFKDAGINFDESQ	99	20	0	10.56		2270.15	93.199	32666	3	757.39	7.53
P05989 ILVC_SALTY Ketol-acid reductoisomerase	1		LIQFGWETITEALK	252	14	9	64.86	b3b7b13y3y8y9y11°y11y14	1648.90	101.134	60594	2	824.95	1.85
P05989 ILVC_SALTY Ketol-acid reductoisomerase	2		GFGVPTLIIVHPENDPQGEGMAIAK	167	25	12	60.66	b2b3b4b7b8y1y2y6y8y14y21y25	2548.28	77.014	47756	3	850.10	-1.34
P05989 ILVC_SALTY Ketol-acid reductoisomerase	3		AYALSEQLKEIMAPLFQK	284	18	12	88.38	b2b3b4b6b10b13b14y5y6y10y16y18	2080.10	102.836	40331	3	694.04	-6.10
P05989 ILVC_SALTY Ketol-acid reductoisomerase	4		DGAALGYSHGFNIVEVGEQIRK	123	22	10	44.52	b2b3b5°b5b7b13y6y8y17y22	2360.18	72.020	38791	3	787.40	-6.93
P05989 ILVC_SALTY Ketol-acid reductoisomerase	5		ANYFNTLNL	1	10	10	55.72	b2*b2b3b4y3*y3y6y7y10*y10	1225.63	67.462	30943	2	613.32	-5.28

[P05989]ILVC_SALTY Ketol-acid reductoisomerase	6		TAFETAPQYEGK	336	12	4	30.21	y6y7y9y12	1341.63	41.730	16796	2	671.32	-2.55
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	7		FMGRDEFADGASYLQGK	21	17	13	70.95	b3b4b6y2y5y6y8°y8y9*y9y11°y11y17	1891.88	62.262	14850	2	946.44	7.42
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	8		LVAEGTDPAYAEK	239	13	3	28.83	y6y7y11	1363.66	37.700	5879	2	682.34	-7.52
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	9		DSGLDISYALRK	57	12	5	35.29	b7b10b11°b11y3	1337.69	51.865	2618	3	446.57	-9.31
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	10		DSGLDISYALR	57	11	6	42.57	b5b8°b8b10°b10y4	1209.61	53.233	2387	2	605.31	1.72
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	11		QGGITLMMDR	266	10	4	27.7	b5y3°y3y7	1121.57	63.346	1896	2	561.29	19.48
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	12		DGAALGYSHGFNIVEVGEQIR	123	21	4	31.6	b3b8b13b15	2232.11	88.095	1669	3	744.71	0.98
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	13		AGVLESSFVAEVK	202	13	4	33.32	b6b7b10y9	1335.69	49.583	1611	2	668.35	-17.36
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	14		VGTYEELIPQADLVVNLTDPKQHS DVVR	88	28	8	27.36	b4°b4b7°b7b16y6y10y14	3135.61	81.457	58190	4	784.66	-7.63
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	15		DGAALGYSHGFNIVEVGEQIRK	123	22	3	20.41	b3b5b21	2360.18	93.684	36055	3	787.40	-6.10
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	16	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21))	SDLMGEQTILCGMLQAGSLLCFD KLVAEGTDPAYAEK	215	37	11	89.79	b3b4b5b12y6°y6y7y8y9y10y22	4031.95	117.784	14366	3	1344.66	10.17
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	17		ANYFNTLNLRQQLAQLGK	1	18	3	16.15	b4b9y3	2092.14	89.641	10102	2	1046.57	3.03
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	18		LIQFGWETITEALKQGGITLMMDR	252	24	5	43.45	y4y5y6y9y13	2751.41	118.596	4908	3	917.81	-3.19
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	19		AGVELAFETMVDSGIIEESAYYES LHELPLIANTIARK	366	38	6	14.85	b3b11°b11b15°b15y21	4180.10	114.094	3550	4	1045.78	-4.21
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	20	Carbamidomethyl+C(7)	KVVIVGCGAQLNQLGNMR	38	19	3	15.48	b5y10y12	2014.07	58.532	2364	2	1007.54	2.67
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	21		EETGKTAFETAPQYEGK	331	17	3	25.57	y4y7y8	1885.89	40.778	1988	2	943.45	4.47
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	22		QGGITLMMDRLSNPAK	266	16	4	17.79	b5°b5b8y9	1731.88	35.911	1564	2	866.44	-3.38
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	23	Phosphoryl STY(6)	ANYFNTLNLR	1	10	5	42.19	b4b5y5_H3PO4 y5°y5y7	1305.59	38.299	23521	3	435.87	2.71
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	24	Phosphoryl STY(8)	LIQFGWETITEALK	252	14	3	19.96	b9_HPO3 b9y5y11	1728.84	64.908	5664	2	864.92	-8.54
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	25	Oxidation+M(6)	SVQPLMKDGAALGYSHGFNIVEVGEQIR	116	28	8	37.83	b3b7°b7y4y5y12y21y24	3031.56	132.850	109807	3	1011.19	10.95
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	26	Oxidation+M(6)	DITVVMVAPK	145	10	4	29.46	b3°b3b4y3	1088.60	28.665	14058	2	544.80	-3.03
[P05989]ILVC_SALTY Ketol-acid reductoisomerase	27		LVAEGTDPAY	239	10	0	3.02		1035.51	37.667	5566	2	518.26	6.25
[Q7CPH8]SECB_SALTY Protein-export protein secB	1	Carbamidomethyl+C(2)	ECITSLVSR	111	9	5	39.08	y1y5y6y7y9	1064.53	53.644	44422	2	532.77	-7.68
[Q7CPH8]SECB_SALTY Protein-export protein secB	2		LDLDTASSQLADDVYEVVLR	41	20	15	89.34	b2b4b6b14y2y3y4y5y6y9y10°y10y14y20*y20	2222.14	109.008	33479	2	1111.57	9.12
[Q7CPH8]SECB_SALTY Protein-export protein secB	3		DVSFEAPNAPHVFQKDWQPEVK	19	22	6	20.41	b2y2y4y7y16y22	2568.21	67.998	18830	4	642.81	-14.54
[Q7CPH8]SECB_SALTY Protein-export protein secB	4		GTFPQLNLAPVNFDAFMNYLQQ QAGEGTEEHQDA	120	35	11	41	b4°b4b7°b7b8°b8b9b21y2y8y10	3893.83	116.102	16211	3	1298.62	6.77
[Q7CPH8]SECB_SALTY Protein-export protein secB	5		DVSFEAPNAPHVFQK	19	15	5	30.4	b3°b3y6y9y11	1685.80	60.270	28372	3	562.61	-16.44
[Q7CPH8]SECB_SALTY Protein-export protein secB	6		MSEQNNTMAFQIQR	0	15	6	30.4	b3y6y7*y7y9*y9	1826.78	71.568	2748	4	457.45	-18.98

[P66643]RS9_SALTY 30S ribosomal protein S9	1		SLEQYFGR	33	8	4	50.47	b4y4y5y6	999.48	59.808	60148	2	500.24	-9.53
[P66643]RS9_SALTY 30S ribosomal protein S9	2		GGGSGQAGAIR	68	12	7	55.81	b5y5y6y7*y7y8y12	1043.55	33.078	25184	2	522.28	-6.67
[P66643]RS9_SALTY 30S ribosomal protein S9	3		AENQYYGTGR	1	10	3	29.46	b4y4y5	1158.52	25.912	1845	2	579.76	-1.48
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	1		GANFGYDNLVVDMLGFSVMKK	168	21	5	21.01	b6b10b12y1y21	2305.15	78.082	36505	3	769.05	4.55
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	2		AGMAVGLAGLFLESHDPANAK	226	22	11	95.19	b3b4b5y2y3y4y5*y5y6y7y ₉	2166.09	88.003	23016	3	722.70	-4.51
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	3		VANDLPFVFLGGMNVLESR	12	19	8	32.79	b4b5b13*b13*b13y2y10y1 ₄	2078.09	110.079	13703	2	1039.55	5.64
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	4		GANFGYDNLVVDMLGFSVMK	168	20	6	42.56	b10b15y8y9*y9y10	2177.04	101.907	3501	3	726.35	0.22
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	5		TGAVINVK	130	8	4	52.23	b5b6y4y7	801.47	28.201	175572	2	401.24	-20.64
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	6		DLAMR	31	5	2	27.05	y3y4	605.31	41.713	32644	1	605.31	-3.93
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	7	Carbamidomethyl+C(17)	VSGNSPVIFDVTHALQCR	189	18	4	16.15	b4b7*b7y3	2000.02	69.749	8729	2	1000.51	9.16
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	8	Carbamidomethyl+C(2)	ICEHYVTVTQK	36	11	4	32.05	b7*b7b8b10	1377.68	63.763	7494	3	459.90	-5.85
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	9		QTDLVEAMAK	120	10	3	37.7	b7b8b9	1105.56	48.857	5501	2	553.29	7.18
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	10		VITDVHEASQAQPVADVVDVIQL PAFLAR	91	29	13	81.83	b6b12b13*b13b18b21b23y _{4y6y7y8y12y24}	3101.64	104.541	5012	4	776.16	-8.89
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	11		IFQELK	79	6	1	13.9	y5	777.44	44.754	4771	2	389.23	-9.81
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	12		ASFDK	55	5	1	13.53	y3	567.28	44.513	4701	1	567.28	12.70
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	13		GPGLEEGMK	70	9	3	31.3	b3b7y5	917.45	52.289	4581	2	459.23	15.23
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	14		VVNIGDIK	4	8	4	33.93	b3*b3y4y5	857.49	39.738	1890	2	429.25	-17.58
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	15		AIDDLVKSFDELDTEN	268	16	3	25.49	b3b11b13	1823.86	68.307	5258	2	912.43	1.67
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	16		SSHSYRGPGLLEEGMK	63	16	3	17.79	b8y4y9	1747.83	40.537	4655	3	583.28	-9.36
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	17	Carbamidomethyl+C(12)	FHEGGNDKVLCDR	154	14	3	19.96	b4y5y13	1659.81	64.811	2987	2	830.41	11.25
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	18	Carbamidomethyl+C(18)	KVSGNSPVIFDVTHALQCR	188	19	6	24.5	b11y4*y4y8y11*y11	2128.08	85.010	2394	2	1064.54	-6.77
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	19	Oxidation+M(23)	VANDLPFVFLGGMNVLESRDLAM R	12	24	7	29.42	b13*b13y4y6y11*y11y14	2680.40	95.634	16385	3	894.14	14.48
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	20	Oxidation+M(19)	GANFGYDNLVVDMLGFSVMK	168	20	4	20.59	b10b15y5y8	2193.02	103.647	9520	4	549.01	-8.91
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	21	Oxidation+M(19)	GANFGYDNLVVDMLGFSVMKK	168	21	3	21.01	b5b10b14	2321.16	77.360	8611	3	774.39	12.52
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	22	Oxidation+M(8)	GPGLEEGMK	70	9	3	31.3	b4b7y8	933.43	70.448	6406	2	467.22	-5.23
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphohooctonate aldolase	23	Oxidation+M(3)	AGMAVGLAGLFLESHDPANAK	226	22	3	13.9	b5b7y8	2182.07	84.861	2419	2	1091.54	-13.43
[P63727]C562_SALTY Soluble cytochrome b562	1		HGFDILVGQIDGALK	84	15	10	83.33	b3b4b7b11y2y3y4y5y6y15	1582.86	83.102	50457	2	791.94	2.85
[P63727]C562_SALTY Soluble cytochrome b562	2		TDSAPELK	41	8	6	41.71	y1y3*y3y4y6y8	860.43	27.485	6024	2	430.72	-9.72
[P63727]C562_SALTY Soluble cytochrome b562	3		AAALDAQK	56	8	5	36.94	b3y3y6y8*y8	787.42	43.987	3829	1	787.42	-8.60

P63727 C562_SALTY Soluble cytochrome b562	4		ATPPK	64	5	1	13.53	y4	513.31	30.167	3944	1	513.31	10.11
P63727 C562_SALTY Soluble cytochrome b562	5		MRAALDAQK	54	10	11	67.49	b4b7°b7b8°b8y3*y3y4°y4y7*y7	1074.58	38.356	10158	2	537.79	5.11
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		AVLPGMVER	115	9	5	46.59	b6y2y4y6y7	971.53	52.702	20823	2	486.27	-4.90
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		AAIEEMMASLPAQWR	58	15	7	38.36	b4b10b14y5y9*y9y15	1703.85	90.263	15663	2	852.43	13.18
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		GHIINIGSTAGSWPYAGGNVYGATK	126	25	9	23.73	b2b3b11°b11b13°b13*b13y9y12	2491.22	69.909	11140	3	831.08	-5.59
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4	Carbamidomethyl+C(15)	MIVLVTGATAGFGECIAR	0	18	4	25.7	b8y5y8y13	1865.94	88.555	6177	2	933.47	-10.47
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		VTDIEPLVGGETESSVR	171	18	3	23.31	y5y9y13	1862.95	68.990	23924	2	931.98	1.83
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		LQALK	36	5	2	27.05	y3y4	572.37	39.786	3963	1	572.37	-11.09
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		AGKTYENTTALTPEDITEAVWWVATLPAHVNINTVEMMPVTQSFAGLSVHR	196	51	5	13.61	b4b9b11°b11y4	5596.83	101.356	11336	5	1120.17	7.50
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	1	Carbamidomethyl+C(11)	YGLPAPVGYACTTPR	14	15	5	26.87	b2y9y10y12y15	1622.80	61.331	48310	2	811.91	2.33
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	2		VALDPLTGMPYQGR	146	15	8	57.15	b10y2y5y7y8y9y13y15	1614.84	70.739	31858	2	807.92	3.48
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	3		IFMGLATIFLER	179	12	10	80.8	b2b3b5y2°y2y3y6y7y9y10	1410.77	108.396	28329	2	705.89	-5.36
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	4		LVTYQTDANGQPVNQILVEAATDIGKELYLGAUVDR	80	36	11	66.61	b2b8y3y4y5°y5y6y7y12y25y36	3874.04	121.302	28030	3	1292.02	4.60
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	5		DLALIEINPLVITK	191	14	6	43.71	b4y3y6y9y10y14	1551.93	97.455	22982	2	776.47	-0.47
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	6		LHGGEPANFLDVGGGATK	277	18	5	33.93	b4b7b8y7y11	1739.85	58.808	21321	3	580.62	-11.65
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	7		LEGNNAELGAK	348	11	5	32.05	b2y4y9y10y11	1115.56	28.912	17864	2	558.28	-7.44
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	8		LHGGEPANFLDVGGGATKER	277	20	7	31.57	b4b8b13°b13*b13b14b20	2025.01	80.476	15751	3	675.67	-2.95
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	9		MNLHEYQAK	0	9	7	39.08	b2y2y4*y4y5y6y9	1133.54	33.566	13082	2	567.27	-5.06
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	10		AFAENWLGK	70	9	3	31.3	b4b5y7	1035.52	64.764	11091	2	518.26	-4.36
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	11		VALDPLTGMPYQGRELAFK	146	20	3	23.02	b4b5y11	2203.17	80.530	7928	3	735.06	4.77

P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	12		VVFMASTEGGVEIEK	120	15	5	18.79	b10°b10b12y9y15	1595.82	112.664	4612	2	798.41	13.77
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	13		VAEETPHLIHK	135	11	4	25.06	b6b9°b9y8	1273.67	32.932	12546	3	425.23	-17.92
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	14		LGADGNALFR	215	10	3	27.7	b3b7y5	1033.53	51.243	11229	2	517.27	-15.94
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	15		EAEAAASK	29	8	3	41.71	y3y5y6	834.39	94.063	3291	1	834.39	11.56
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	16		SLTDAAQQVVAAVEGK	372	16	4	36.01	b6b11b13b14	1586.83	76.338	2822	3	529.62	-2.46
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	17		IILSDDNVK	303	9	3	31.3	b8y7y8	1016.57	58.927	2421	2	508.79	6.12
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	18	Carbamidomethyl+C(6)	QGDLICLDGKLGADGNALFR	205	20	3	23.02	b12y8y9	2133.10	93.042	3185	2	1067.05	10.42
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	19	Oxidation+M(4)	VVFMASTEGGVEIEK	120	15	5	30.4	b10°b10y7y10y12	1611.77	79.055	4846	3	537.93	-14.09
P66869 SUCC_SALTY Succinyl-CoA ligase [ADP-forming] subunit beta	20	Carbamidomethyl+C(20) ;Oxidation+M()	EAQAAQWELNYVALDGNIGCMV NGAGLAMGTMDIVK	241	36	4	10.98	b4b11°b11y14	3826.77	98.161	1907	3	1276.26	-4.98
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	1		ITDAYAENADIANLLLAPYFK	373	21	4	35.16	b5b6b7y21	2326.21	91.076	57191	2	1163.61	4.41
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	2		ELSAEGFNFIGTGVSGGEEGALK	113	23	7	24.54	b11y1y2y6y7y10y23	2269.13	68.898	51700	3	757.05	11.94
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	3	Carbamidomethyl+C(11)	IAAVAEDGEPCVTYIGADGAGHY VK	158	25	11	80.48	b2b3b4y3y10y12y18y19y2 0y21y25	2563.21	60.243	33764	3	855.07	-1.52
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	4		IVSYAQGFSQLR	329	12	5	36.23	b2y6y7y8y12	1368.72	62.225	21090	2	684.87	-1.96
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	5		MVHNGIEYGDMQLIAEAYSLLK	183	22	6	52.59	b3b12b13y7y8y9	2495.23	106.358	17230	3	832.42	0.98
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	6		AAVLPANLIQAQR	432	13	5	21.35	b2b3y5y9y13	1364.79	64.446	16832	2	682.90	-4.74
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	7		WTSQSALDLGEPLSLITESVFAR	264	23	21	105.22	b7°b7b8°b8b9°b9°b9b11° b11b13°b13b22y1y3y5y6° y6y7y8y14y23	2520.28	117.047	14905	3	840.77	-6.78
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	8		ITDAYAENADIANLLLAPYFKK	373	22	4	23.77	b5b13b14y22	2454.32	97.552	6129	3	818.78	10.54
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	9		DEDGNYLVDVILDEAANK	242	18	4	16.15	b8y6°y6y8	1992.92	79.105	5119	2	996.96	-12.13
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	10		DVVAYAVQNGIPVPTFSAAVAYY DSYR	405	27	7	35.06	b3b7°b7b8°b8b11b16	2936.44	124.046	4441	3	979.48	-3.82
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	11		GYTVSVFNR	25	9	4	31.3	b2b3b5y3	1042.52	27.873	1592	2	521.77	-6.79
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	12	Carbamidomethyl+C(3)	AGCIIR	361	6	1	13.9	b3	689.37	36.336	7627	1	689.37	-3.28
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	13		AEFIEK	314	6	1	13.9	y5	736.38	55.295	5852	1	736.38	-4.31
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	14		IADEYQQALR	395	10	3	27.7	b4b9y7	1206.59	42.894	3805	2	603.80	-17.30
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	15		SKQQIGVVGMAMVGR	1	15	4	18.79	b4b11°b11y9	1560.85	122.768	12012	2	780.93	11.50

P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	16		MSKQQIGVVGMAMVGR	0	16	3	17.79	b12b15y12	1691.85	100.843	6204	2	846.43	-13.78
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	17		AASDEYHWDLNYGEIAKIFR	341	20	3	23.02	b5y16y17	2398.17	95.700	5071	3	800.06	9.37
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	18		QQIGVVGMAMVGRNLALNIESR	3	22	3	13.9	b8b14y5	2356.23	68.017	2464	3	786.08	-14.30
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	19	Phosphoryl STY(12)	ELSAEGFNFIGTGVSGGEEGALK	113	23	8	58.09	b4_H3PO4 b4b5b8b10°b10y8y9y10	2349.07	111.457	2357	3	783.70	6.65
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	20	Phosphoryl STY(11)	DAYELVAPILTK	146	12	3	33.22	b6b9b11	1412.71	84.949	2258	3	471.57	5.10
P14062 6PGD_SALTY 6-phohogluconate dehydrogenase	21	Phosphoryl STY(8)	EFVESLETPR	58	10	3	27.7	b7b9y8	1286.54	63.365	1755	3	429.52	-12.43
P0A2T6 CRP_SALTY Catabolite gene activator	1		QLIQVNPDILMR	104	12	7	55.81	b3y6y7y8*y8y9*y9	1439.79	79.872	8604	2	720.40	-7.29
P0A2T6 CRP_SALTY Catabolite gene activator	2		VGNLAFLDVTGR	131	12	4	30.21	y2y5y6y11	1261.69	65.886	6690	2	631.35	-3.77
P0A2T6 CRP_SALTY Catabolite gene activator	3		DEEGKEMILSYLNQGDFIGELGLF EEGQER	53	30	3	12.08	y5°y5y12	3445.59	95.708	3983	3	1149.20	-4.61
P0A2T6 CRP_SALTY Catabolite gene activator	4	Carbamidomethyl+C(18)	VLGKPQTDPTLEWFLSHCHHK	1	22	6	52.85	y3y5y7y8y10y11	2643.29	85.854	21392	3	881.77	-22.07
P0A2T6 CRP_SALTY Catabolite gene activator	5	Carbamidomethyl+C(9)	QEIGQIVGCSR	170	11	4	25.06	b9y8y10*y10	1246.65	63.803	6127	2	623.83	21.74
P0A2T6 CRP_SALTY Catabolite gene activator	6		MLEDQNLISAHGK	189	13	4	35.82	b10b11b12°b12	1455.75	83.226	3503	2	728.38	19.20
P0A2T6 CRP_SALTY Catabolite gene activator	7		EMILSYLNQGDFIGELGLFEEGQER	58	25	6	19.53	b8°b8b11b16y13*y13	2887.34	91.925	1963	3	963.12	-15.56
P0A2T6 CRP_SALTY Catabolite gene activator	8	Carbamidomethyl+C(12)	ITRQEIGQIVGCSR	167	14	3	28.54	y3y5y11	1616.84	51.828	3950	3	539.62	-9.44
P0A2T6 CRP_SALTY Catabolite gene activator	9	Oxidation+M(1)	MLEDQNLISAHGK	189	13	4	21.35	b10°b10y3y5	1471.72	57.120	7647	2	736.36	-2.32
P0A2T6 CRP_SALTY Catabolite gene activator	10	Carbamidomethyl+C(19) ;Oxidation+M(1)	MVLGKPQTDPTLEWFLSHCHHK	0	23	3	13.48	b13y11y20	2790.39	100.356	2985	3	930.80	1.57
P0A2T6 CRP_SALTY Catabolite gene activator	11		DEEGKEMILSYLNQGDFIGEL	53	21	3	12.08	y6y12*y12	2400.11	95.658	2019	4	600.78	-8.04
P0A2T6 CRP_SALTY Catabolite gene activator	12		DEEGKEMILSYLNQGDFIGELGLF EEGQER	53	30	1	8.98	y13	3427.64	95.716	2688	3	1143.22	13.68
P0A7V6 RS3_SALTY 30S ribosomal protein S3	1		LVADSITSQLER	114	12	10	70.58	b2b5y1y3y6y8y9*y9y10y12	1331.71	60.431	45501	2	666.36	-1.92
P0A7V6 RS3_SALTY 30S ribosomal protein S3	2		ADIDYNTSEAHTTYGVIGVK	179	20	6	42.09	y3y10y11y15y17y20	2154.02	56.097	35157	3	718.68	-5.21
P0A7V6 RS3_SALTY 30S ribosomal protein S3	3		VVADIAGVPAQINIAEVR	89	18	7	42.31	b3b8y4°y4y10y12y13	1835.04	76.609	26130	2	918.02	-1.00
P0A7V6 RS3_SALTY 30S ribosomal protein S3	4		LGGAEIAR	156	8	7	36.94	b2b5°b5y2y3y7y8	786.44	30.725	22206	2	393.72	-9.31
P0A7V6 RS3_SALTY 30S ribosomal protein S3	5		LGIVKPWNSTWFANTKEFADNLD SDFK	11	27	5	18.31	b2y2y5y10y13	3143.52	94.416	13350	4	786.64	-8.08
P0A7V6 RS3_SALTY 30S ribosomal protein S3	6		LGIVKPWNSTWFANTK	11	16	3	17.79	b13y6y10	1861.96	82.581	5018	2	931.48	-18.16
P0A7V6 RS3_SALTY 30S ribosomal protein S3	7		GEILGGMAAVEQPEKPAAQPK	204	21	4	14.36	b20y4*y4y11	2121.06	54.613	4865	4	531.02	-19.45
P0A7V6 RS3_SALTY 30S ribosomal protein S3	8		VMFR	127	4	1	13.15	y3	552.29	75.756	3023	1	552.29	-14.04
P0A7V6 RS3_SALTY 30S ribosomal protein S3	9		AVQNAMR	136	7	4	57.87	b5b6y3y6	789.40	94.956	2499	1	789.40	0.15
P0A7V6 RS3_SALTY 30S ribosomal protein S3	10		LVADSITSQL	114	10	0	2.64		1046.58	60.471	6070	2	523.80	10.15

O68883 CISY_SALTY Citrate synthase	1	Carbamidomethyl+C(12)	TAGSSGANPFACIAAGIASLWGPA HGGANEAAALK	240	34	24	112.81	b2°b2b6°b6b8°b8b9b13°b13y1y2y3y9y12y13y14y16y17y25y26°y26y27y29y34	3195.58	116.120	47760	3	1065.86	4.66
O68883 CISY_SALTY Citrate synthase	2		TVGWIAHWNEMHTDGMK	388	17	11	35.22	b1b2°b2b3°b3b6°b6b7y2y11y15	2012.89	66.041	31482	3	671.64	-8.91
O68883 CISY_SALTY Citrate synthase	3		ILILHADHEQNASTSTVR	222	18	8	41.86	b2b3y2y4y5y6y8y18	2005.03	43.502	28325	3	669.02	-6.82
O68883 CISY_SALTY Citrate synthase	4	Carbamidomethyl+C(15)	GVFTFDPGFTSTASCESK	38	18	5	37.46	b12y11y12y13y18	1937.87	75.557	23150	2	969.44	8.00
O68883 CISY_SALTY Citrate synthase	5	Carbamidomethyl+C(18)	NDLSYAGNFLNMMFSTPCETYEV NPVLER	189	29	10	42.3	b4°b4y2°y2y3y5y7y10y13y14	3411.56	111.151	18548	3	1137.86	8.02
O68883 CISY_SALTY Citrate synthase	6	Carbamidomethyl+C(9)	DSHPMAVMCGITGALAAFYHDSL DVNNPR	127	29	20	170.66	b3°b3b4b5b6b7b8b12b15y2y4y5y6y9y10y11y12y13y17y29	3159.42	108.183	16941	4	790.61	-8.35
O68883 CISY_SALTY Citrate synthase	7		AMGIPSSMFTVIFAMAR	371	17	4	28.3	b3y3y4y6	1829.93	119.405	15859	2	915.47	8.81
O68883 CISY_SALTY Citrate synthase	8		ELGTKDDLLEVAAMELEHIALNDP YFIEK	328	28	12	65.73	b3b4b6°b6b8b21y1y5y6y8y9y28	3245.61	119.513	12885	4	812.16	-5.57
O68883 CISY_SALTY Citrate synthase	9		DDLLEVAAMELEHIALNDPYFIEK	333	23	3	19.89	b5b8b12	2717.34	107.387	4886	4	680.09	2.16
O68883 CISY_SALTY Citrate synthase	10	Carbamidomethyl+C(10)	RDSHPMAVMCGITGALAAFYHDS LDVNNPR	126	30	3	22.23	b13y11y12	3315.58	93.549	2997	3	1105.87	10.46
O68883 CISY_SALTY Citrate synthase	11	Carbamidomethyl+C(8)	ATVMRETCHVEVLK	315	13	3	30.59	y6y8y10	1573.76	63.894	1518	2	787.39	-11.79
O68883 CISY_SALTY Citrate synthase	12		ITFIDGDEGILLHR	56	14	7	55.32	b5b13y4y10y11°y11y12	1598.83	74.544	35314	3	533.61	-16.72
O68883 CISY_SALTY Citrate synthase	13		YSIGQPFVYPR	178	11	3	32.05	y5y6y9	1326.68	68.259	28506	2	663.84	-5.24
O68883 CISY_SALTY Citrate synthase	14		LMGFGHR	300	7	3	38.33	b5y4y5	817.41	41.526	18442	2	409.21	-0.82
O68883 CISY_SALTY Citrate synthase	15		NYDPR	310	5	1	13.53	y4	664.30	87.714	3124	1	664.30	-9.83
O68883 CISY_SALTY Citrate synthase	16		TTVTRHTMIHEQITR	105	15	5	44.38	b6b8b14y9y10	1823.96	99.445	303317	2	912.48	2.68
O68883 CISY_SALTY Citrate synthase	17		ELGTKDDLLEVAAMELEHIALNDP YFIEK	328	28	4	22.22	b19y8y9°y9	3245.62	104.504	1867	4	812.16	-3.91
O68883 CISY_SALTY Citrate synthase	18	Oxidation+M(15)	AMGIPSSMFTVIFAMAR	371	17	3	16.91	b8b16y4	1845.89	43.987	50574	3	615.97	-6.81
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1		WFENTNYHYIVPEFSK	117	15	6	42.44	b2y3y5y10y13y15	1944.91	77.613	54516	3	648.98	-8.54
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2	Carbamidomethyl+C(7)	LWVNPDCGLK	719	10	10	88.8	b2b7b9y4y6y7y8°y8y9y10	1201.60	60.295	46991	2	601.30	-5.89
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	3		TILTHTLGFPR	1	11	6	36.82	y2y5y6y7°y7y11	1255.72	63.992	37574	2	628.36	1.94
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	4		QAGIDLLPVGDFAWYDHVLTSSL LLGNVPAR	52	31	16	96.47	b5°b5°b5b6°b6b31y1y3y4y5y6y7y8y24y27y31	3351.80	119.164	35705	3	1117.94	9.03
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	5		LTWTQLLEEVDEALALGHK	137	19	18	129.61	b2°b2b5°b5b19y2y3y5y6y7y8y9y12y13y15y17°y17y19	2166.13	118.619	30683	3	722.72	-5.30
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	6	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	8	36.68	b6b12b13y1y2y7y9y16	1834.95	99.366	25592	2	917.98	9.98

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	7		SWFAFALQK	343	9	7	46.08	b2b5b6y3y7*y7y9	1097.57	84.876	25515	2	549.29	-5.67
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8		LAAITAQDSQRENPYEV	395	18	7	37.46	b2b3y2y14y15y16y18	2061.02	47.249	24422	3	687.68	-6.40
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	9		LPVDWLLSAGLINGR	279	15	7	32.78	b2b3b4y2y8y13y15	1623.93	101.214	23468	2	812.47	3.61
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	10	Carbamidomethyl+C(1)	CVKPPVVIGDISRPAPITVEWAK	515	23	10	46.33	b2b4b6b7y2y5y6y15y20y23	2532.40	75.444	19991	3	844.80	-1.45
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	11		LAAITAQDSQR	395	11	10	89.17	b2b3y3y4*y4y5y6y9y10y11	1173.62	33.894	18491	2	587.31	-5.10
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	12	Carbamidomethyl+C(1)	CGELALLR	352	8	5	36.94	b2b3b6y5y8	931.49	60.169	17692	2	466.25	-11.14
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	13	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETR	315	22	3	13.9	b3b14y7	2441.23	87.690	12022	3	814.42	-5.90
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	14		DALNSGETAALKEWSAPIQAR	360	21	5	24.02	b2b4b5b11°b11	2229.08	60.903	9767	3	743.70	1.42
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	15		YAQSLTDKPVK	538	11	7	49.11	b4b6b7°b7°b7y3y8	1249.65	30.722	32317	3	417.22	-19.24
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	16		AQESYWAGNTTR	21	12	4	23.01	b6b10y8°y8	1383.64	29.251	28544	2	692.32	5.38
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	17		HQNNDGSDIDTLFR	83	15	8	67.76	b3b9b10y4y5y7°y7y8	1730.78	69.275	15159	3	577.60	-15.94
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	18		GQQFR	132	5	1	13.53	b3	635.32	41.376	6965	1	635.32	-7.69
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	19		DEVADLEAAGIGIIQIDEPALR	582	22	4	30.14	b4b5b11b15	2308.16	92.146	6665	3	770.06	-19.88
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	20		VHNAAVEK	386	8	4	36.94	b3b7y4°y4	867.46	37.288	2872	2	434.23	-6.61
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	21		NDMVEYFGEHLDFGVFTQNGWVQSYGSR	487	28	4	12	b11y5y12*y12	3282.53	94.552	2643	3	1094.85	22.16
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	22		AEAQR	413	5	2	13.53	y4*y4	574.29	87.614	1617	1	574.29	-12.86
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	23		GWPETR	731	6	1	13.9	b5	745.36	59.024	1527	1	745.36	-5.00
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	24		GNLDANHYRTGIAEHK	449	17	5	40.37	b5b8b13b15y5	1908.97	120.417	22217	2	954.99	3.52
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	25		GRAPTGEPAAAAEMTK	101	16	4	28.6	b3b5b7y7	1557.75	35.385	19971	3	519.92	-9.17

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	26	Carbamidomethyl+C(22)	YAQSLTDKPVKGMLTGPVTILCW SFPR	538	27	6	37.07	b5b6*b6b7°b7b13	3065.58	99.378	14558	4	767.15	-5.65
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	27		ADLTEKYAQINAIVGK	298	16	5	28.6	b4°b4b9b11y10	1733.95	58.754	4086	3	578.65	1.41
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	28		KAQESYWAGNTTR	20	13	9	58.16	b4°b4b6°b6*b6b8y4y6y8	1511.72	34.942	3409	2	756.36	-3.31
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	29		KGNLDANHYR	448	10	5	40.43	b7b9y4y7°y7	1187.60	55.948	3040	3	396.54	3.39
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	30	Carbamidomethyl+C(12)	IPAQRLWVNPDCGLK	714	15	3	18.79	b4y3y10	1766.95	73.513	2605	3	589.65	4.77
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	31		NVWRADLTEK	294	10	3	27.7	b4b6y6	1231.64	49.771	2106	2	616.32	-6.44
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	32	Carbamidomethyl+C(7)	LWVNPDCGLKTR	719	12	7	35.29	b3b8b9°b9*b9y7°y7	1458.77	56.450	1623	2	729.89	9.62
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	33	Phosphoryl STY(5)	AQESYWAGNTTR	21	12	3	23.01	b4y3y6	1463.60	66.343	1864	3	488.54	11.84
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	34	Oxidation+M(12)	APTGEPA AAAEMTK	103	14	3	19.96	b7b10y4	1360.63	25.562	37990	3	454.21	-8.70
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	35	Carbamidomethyl+C(11) ;Oxidation+M(2)	GMLTGPVTILCWSFPR	549	16	4	17.79	b4°b4b8y7	1850.94	49.861	2186	2	925.98	7.45
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	36		WFNTNYHYIV	117	10	2	7.3	y9°y9	1356.65	77.635	10687	2	678.83	10.26
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	1		TFDTPTYPNSLALSADGK	308	18	8	35.84	b4y2y4°y4y5y11y14y18	1897.93	65.518	28080	2	949.47	5.40
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	2		MSTGLALDSK	185	10	6	59.52	b3y3y7y8y9y10	1022.53	47.007	12732	2	511.77	10.80
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	3		LDPVTLEITQAIHNDLKPFGATINA ATQTLWFGNTINS AVTAIDAK	73	46	4	16.44	y2y3y6y15	4894.52	127.580	10649	4	1224.38	-9.68
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	4		IAAPASLAVLFNPTR	268	15	6	18.79	b1b3y5*y5y12y15	1540.89	89.744	10321	2	770.95	1.58
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	5		LLDDGKEHFFINLSLDTAGHR	223	21	3	14.36	b8b11y6	2398.23	75.813	9938	3	800.08	6.62
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	6		LYTTNADGEFTIDTASNK	198	19	6	24.5	b8y5°y5y8y11y19	2074.01	65.467	9571	2	1037.51	8.36
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	7		GAYEMAWSQQENALWLATSQSR	41	22	5	25	b3y4y10*y10y11	2527.19	84.331	5175	2	1264.10	8.60
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	8		ELVADAATNTIYISGVGK	144	18	3	16.15	b6b12y14	1821.96	81.903	42663	2	911.49	2.48
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	9		LVL DAR	126	6	1	13.9	b3	686.41	51.631	14943	1	686.41	-8.98
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	10		EHFFINLSLDTAGHR	229	15	3	18.79	b4y8y11	1756.88	56.540	11002	2	878.94	0.35
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	11		TGDVK	119	5	1	13.53	b4	519.27	64.686	5532	1	519.27	-7.52
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	12		LLDDGK	223	6	1	13.9	b3	660.36	33.569	3928	1	660.36	8.97

Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	13		EQEATQPDDVIR	338	12	4	26.99	b7b8y8*y8	1400.66	27.783	3406	2	700.83	-3.83
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	14		IAAPASLAVLFNPNTRNEAYVTHR	268	23	8	54.36	b3y6y10y11*y11y12y18y20	2511.31	82.072	42391	4	628.58	-12.74
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	15		TTIENTGKMSTGLALDSK	177	18	5	25.07	b5b6*b6b12*b12	1866.95	50.482	7522	4	467.49	1.77
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	16		AQRLYTTNADGEFITIDTASNK	195	22	3	13.9	b3b11y11	2429.19	87.531	5394	3	810.40	-2.61
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	17		LLDDGKEHFFINLSLDTAGHR	223	21	3	21.01	b3b10b12	2398.24	76.724	2694	3	800.09	12.22
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	18	Phosphoryl STY(20)	TEEVRLQPRLVADAATNTIYISG VGKESAIWVVDGETIK	134	41	4	14.36	b8b17b19y20	4535.36	108.391	31675	5	907.88	13.46
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	19	Phosphoryl STY(7)	GSLLGSLLVASSFSTLAAEDMLR K	12	25	3	23.27	b5b6b14	2659.35	88.967	7791	3	887.12	-6.70
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	20		LLDDGKEHFFINLSLDTAGH	223	20	2	12.88	y7y13	2242.11	75.829	28193	2	1121.56	-2.07
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	21		LYTTNADGEFITIDT	198	15	0	5.28		1673.77	65.430	5043	2	837.39	-9.48
P65882 PURA_SALTY Adenylosuccinate synthetase	1	Carbamidomethyl+C(7)	LLLSEACPLILDYHVALDNAR	97	21	13	81.73	b2b3y3y6*y6y10y11y12y1 4y15*y15y17y21	2396.25	91.435	34364	3	799.42	-5.20
P65882 PURA_SALTY Adenylosuccinate synthetase	2		IEELTGVPIDIISTGPDR	402	18	5	16.15	b2b4*b4b6y3	1925.04	102.498	25302	2	963.02	8.81
P65882 PURA_SALTY Adenylosuccinate synthetase	3		VLDDTMAVADILTSMVVDVSDLL DQAR	186	27	19	61.52	b2b4b7*b7b10*b10b11y1y 5y7*y7y8*y8*y8y10*y10y1 1*y11*y11	2905.45	138.232	6714	3	969.15	-1.09
P65882 PURA_SALTY Adenylosuccinate synthetase	4	Carbamidomethyl+C(11)	AVQLNSLSGFCLTK	318	14	4	25.4	b11*b11y9y10	1537.80	73.889	3454	2	769.40	-4.84
P65882 PURA_SALTY Adenylosuccinate synthetase	5		YVDYVLGILK	258	10	5	66.79	b3b5*b5b7b9	1182.69	33.036	113617	3	394.90	9.29
P65882 PURA_SALTY Adenylosuccinate synthetase	6		TVLHLIPSGILR	50	12	3	26.99	b9y5y6	1318.82	76.609	11970	2	659.91	-2.50
P65882 PURA_SALTY Adenylosuccinate synthetase	7	Carbamidomethyl+C(2)	LCVAYR	343	6	2	27.43	y4y5	781.39	37.539	5030	2	391.20	-10.31
P65882 PURA_SALTY Adenylosuccinate synthetase	8		GIGPAYEDK	132	9	3	31.3	b6b7y6	949.45	23.418	3080	2	475.23	-10.03
P65882 PURA_SALTY Adenylosuccinate synthetase	9		AEAVDYQK	178	8	3	33.93	b5y6y7	923.45	90.742	2394	1	923.45	2.05
P65882 PURA_SALTY Adenylosuccinate synthetase	10		LKEVMEYHNFQLVNYYK	161	17	6	35.22	b7b10y4y9y10*y10	2218.12	72.345	656842	3	740.05	9.69
P65882 PURA_SALTY Adenylosuccinate synthetase	11		VLDDTMAVADILTSMVVDVSDLL DQARQR	186	29	4	15.1	b4b9y11y23	3189.61	109.121	12260	3	1063.88	0.31
P65882 PURA_SALTY Adenylosuccinate synthetase	12		EVTTPLAADDWKGVPIYETMP GWSESTFGVK	354	33	6	18.6	b3*b3b10b14y10y14	3641.76	93.017	9409	3	1214.59	7.24
P65882 PURA_SALTY Adenylosuccinate synthetase	13		MGNVVVLGTQWGDEGKGK	0	19	4	15.48	b4b6y7*y7	1988.98	72.345	6697	3	663.66	-3.13
P65882 PURA_SALTY Adenylosuccinate synthetase	14		MPDGREVTTTPLAADDWK	349	18	3	25.07	b6b7b11	2002.96	92.170	5440	3	668.32	2.19
P65882 PURA_SALTY Adenylosuccinate synthetase	15	Phosphoryl STY(9)	GNNVVVLGTQWGDEGK	1	16	4	17.79	b9*b9y7y11	1752.80	71.670	10888	2	876.90	5.29
P65882 PURA_SALTY Adenylosuccinate synthetase	16	Oxidation+M(9)	GVEPIYETMPGWSESTFGVK	367	20	3	14.89	b11y11y13	2230.07	86.439	16509	2	1115.54	12.48
P65882 PURA_SALTY Adenylosuccinate synthetase	17	Oxidation+M()	ENVTSIIGNGVVLSPSALMKEMKE LEDR	62	28	5	27.36	b4y4y5y12y21	3075.55	81.550	3886	3	1025.86	-6.35
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	1		SPFVTSGIR	354	9	8	76.65	b3y1y3y4y5y6y7y9	963.52	48.592	45256	2	482.26	-5.00
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	2		EMNIADYDAELWQAMEQEK	4	19	12	59.73	b2*b2b3*b3y4y8*y8y9y12y 13y15y19	2314.02	92.459	41989	2	1157.52	10.55
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	3		VMQAQGSQLTNK	42	12	10	70.58	b2b3y2y3y4y7y9y10*y10y 12	1304.66	29.555	40703	2	652.83	-2.90

P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	4		AMVEVFLNR	296	9	6	46.59	b2b3y4y5y6y9	1078.56	67.844	32832	2	539.78	-8.49
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	5	Carbamidomethyl+C(7)	ELAGWMCDVLDNINDEATIER	380	21	8	25.5	b5°b5y1y2y4y5y8y21	2464.14	101.004	28783	2	1232.57	11.39
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	6		YAEGYPGKR	54	9	8	69.14	b2y1y2y3y4y6y7y8	1040.51	23.368	18165	2	520.76	-1.29
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	7		ELFGADYANVQPHSGSQANFAVY TALLQPGDTVLGMNLAQGGHLT HGSPVNFSGK	83	55	5	11.56	b13b15°b15y3y27	5683.81	96.440	13968	5	1137.57	6.87
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	8		LNSAVFPSAQGGPLMHVIAGK	251	21	6	36.64	b3°b3*b3y14y15y16	2094.11	78.075	79705	3	698.71	-5.25
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	9	Carbamidomethyl+C(5)	VLDICAR	405	7	4	54.86	y3y4y5y6	846.44	44.176	47280	2	423.72	-16.73
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	10		IGSPAVTR	363	8	6	68.77	y3°y3y4y5y6y7	800.45	27.535	27244	2	400.73	-15.94
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	11		QEEHIELIASENYTSR	25	17	4	23.9	b5y6°y6y7	2015.95	95.718	2868	3	672.65	-8.72
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	12		MIIGGFSAYSGVVDWAK	168	17	3	25.57	y3y12y13	1800.89	90.601	2663	2	900.95	-5.29
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	13		LYNIVPYGIDESGKIDYDEMAK	138	22	5	30.04	b3b4b10y17y20	2533.22	76.184	72130	3	845.08	0.19
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	14		NSVPNDPKSPFTSGIR	346	17	9	54.41	b3°b3b5b9y8°y8y9y11y14	1814.92	51.916	22305	3	605.64	-11.43
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	15		GFKEAEVK	372	8	4	50.47	b4b6b7y5	907.48	60.998	3698	1	907.48	-9.89
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	16		EHKPKMIIGGFSAYSGVVDWAK	163	22	6	44.71	y9°y9y11y12y13y20	2420.24	84.363	2073	4	605.81	-3.13
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	17	Oxidation+M(15)	LNSAVFPSAQGGPLMHVIAGK	251	21	7	30.86	b3°b3b4°b4b10y3y18	2110.09	84.395	47927	3	704.04	-9.49
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	18	Oxidation+M()	REMNIADYDAELWQAMEQEK	3	20	3	14.89	b7y3y8	2486.13	100.945	13548	3	829.38	12.28
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	19		AEGYPGKR	55	8	0	1.51		877.45	23.370	5631	2	439.23	-6.68
P00929 TRPA_SALTY Tryptophan synthase alpha chain	1	Carbamidomethyl+C(9)	HNIAPIFICPPNADDDLRL	145	19	4	24.66	y6y7y12y19	2191.12	96.179	18325	2	1096.06	9.25
P00929 TRPA_SALTY Tryptophan synthase alpha chain	2		HPTIPIGLLMYANLVFNNGIDAFY AR	91	26	5	23.16	y1y5y6y10y26	2920.53	105.096	17844	3	974.18	5.18
P00929 TRPA_SALTY Tryptophan synthase alpha chain	3		IIDLIDAGADALELGVPFSDPLAD GPTIQNANLR	35	35	5	17.71	b14b21b25y5y18	3605.83	111.249	16128	4	902.21	-10.63
P00929 TRPA_SALTY Tryptophan synthase alpha chain	4	Carbamidomethyl+C(11)	AFAAGVTPAQCFEMLALIR	70	19	7	21.55	b2b3b5y2y12y14y19	2066.07	101.191	16021	2	1033.54	4.49
P00929 TRPA_SALTY Tryptophan synthase alpha chain	5		EGAFVPFVTLGDPGIEQSLK	15	20	10	43.86	b2b5°b5b8°b8b9b12b16y1 5y20	2104.11	94.035	15408	2	1052.56	8.70
P00929 TRPA_SALTY Tryptophan synthase alpha chain	6	Carbamidomethyl+C(1)	CEQVGVDSVLVADVPVEESAPFR	117	23	4	22.51	b11b12°b12y11	2502.22	83.189	1744	3	834.74	0.39
P00929 TRPA_SALTY Tryptophan synthase alpha chain	7		EYHAAPALQGFGISSPEQVSAAVR	201	24	3	22.41	b18y14y15	2485.24	99.416	4450	3	829.08	-3.05
P00929 TRPA_SALTY Tryptophan synthase alpha chain	8		YENLFAQLNDR	3	11	5	25.06	b6°b6b10°b10y5	1382.67	54.552	3871	2	691.84	-2.56
P00929 TRPA_SALTY Tryptophan synthase alpha chain	9		AGAAGAISGSAIVK	225	14	3	27.74	b5b7b8	1172.69	27.487	3234	3	391.57	21.44
P00929 TRPA_SALTY Tryptophan synthase alpha chain	10		GYTYLLSRSGVTGAENR	171	17	3	16.91	b10b16y7	1843.94	86.775	6029	2	922.47	3.71
P00929 TRPA_SALTY Tryptophan synthase alpha chain	11	Carbamidomethyl+C(1)	CEQVGVDSVLVADVPVEESAPFR QAALR	117	28	3	12	b10b18y5	3041.51	85.455	2346	3	1014.51	-7.87
P00929 TRPA_SALTY Tryptophan synthase alpha chain	12		ERYENLFAQLNDR	1	13	5	35.45	b3b4y4°y4y6	1667.81	60.961	1520	2	834.41	-1.39

IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	1		LTANQTQYHFLSGFTAK	371	17	18	85.45	b2°b2b5*b5b7°b7b8°b8b9y 1y2y10y12°y12y14y15y16y 17	1926.95	67.447	39806	3	642.99	-13.05
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	2		MQAAGAQAYL VNTGWNGTGKR	426	21	5	14.36	b2b8y12y14y21	2194.08	59.585	34026	3	732.03	-0.22
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	3	Carbamidomethyl+C(21)	LIGDDEHGWDDDG VFNFEGGCY AK	263	24	5	22.41	b14y1y6y7y24	2716.15	79.079	25719	3	906.05	7.37
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	4		NMFIRPTDEELVGFKPDFIVMNGA K	148	25	8	38.99	b2b3b5b6y9y10y23y25	2868.41	86.092	20727	4	717.86	-13.02
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	5		GVLTNLGAVAVDTGIFTGR	45	19	9	47.35	y1y2y4y8y9y10°y10y13y19	1861.02	93.507	19783	2	931.02	2.75
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	6		GMFSVMNYLLPLK	212	13	5	26.12	b2b4y3y4y13	1512.79	108.554	17394	2	756.90	-0.48
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	7		AYGINDVQDIVNPSYDTLYQEEL NPGLEGYER	12	33	13	56.09	b2b6°b6b10b12*b12b13y5 y7y8y9y11y33	3837.80	90.822	12176	3	1279.94	5.15
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	8		IQLIGGTWYGGEMK	197	14	4	39.72	y5y10y12y13	1552.78	76.043	5888	2	776.89	-2.75
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	9	Carbamidomethyl+C(12)	GVTEPTPTFSACFGAAFLTLHPTQ YAEVLVKR	394	32	6	17.15	b2b10°b10b12°b12b14	3508.74	96.491	4877	4	877.94	-13.92
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	10		MQAAGAQAYL VNTGWNGTGK	426	20	5	26.08	b2b10y7y11y12	2037.99	64.438	3213	2	1019.50	5.45
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	11		TTLSTDPK	253	8	4	36.94	b5°b5y4y6	862.45	35.489	6687	2	431.73	2.05
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	12	Carbamidomethyl+C(8)	LFIVDAFCGANADTR	116	15	4	26.87	y4y13y14*y14	1669.81	97.161	6083	2	835.41	8.77
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	13		EQGLNSEN FVAFNLTER	180	17	5	35.22	b8b9b15y6y10	1967.95	84.184	3312	3	656.65	0.68
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	14		EQGLNSEN FVAFNLTERIQ LIGGT WYGGEMK	180	31	5	19.61	b5b13y7y11y13	3501.71	109.129	16707	3	1167.91	-1.26
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	15		YTDTPAGEALVSAGPKL	521	17	4	34.62	b5b10b11b15	1689.88	81.503	7154	2	845.44	4.12
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	16		KGMFSVMNYLLPLK	211	14	3	27.74	b7b8b10	1640.88	73.778	3686	2	820.94	-6.10
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	17		GDVAVFFGLSGTGK TTLSTDPK	239	22	4	21.64	b13y4y6y13	2198.12	116.138	2338	3	733.38	-8.00
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	18	Oxidation+M(1)	MQAAGAQAYL VNTGWNGTGK	426	20	3	14.89	b4b9y10	2053.98	83.841	21653	2	1027.49	0.24
IP41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP]	19	Oxidation+M(2)	NMFIRPTDEELVGFKPDFIVMNGA K	148	25	6	34.73	b5b13b14y5y13y15	2884.47	62.789	10399	5	577.70	10.41
IP0A1G5 DKSA_SALTY DnaK suppressor protein	1		TVTHMQDEAANFPDPVDR	57	18	13	92.36	b6b7b10b12y1y4y5°y5y6y 7y12y14y18	2042.91	55.397	33685	3	681.64	-8.78

[P0A1G5]DKSA_SALTY DnaK suppressor protein	2		TSSLSILAAGVEPYQEKPGEEYM NEAQLSHFKR	8	34	4	37.21	y10y11y12y34	3822.89	80.523	22656	4	956.48	-2.11
[P0A1G5]DKSA_SALTY DnaK suppressor protein	3		NQLRDEVDR	48	9	7	31.3	b1b8y1y3y4°y4y9	1144.56	28.070	15956	2	572.79	-5.33
[P0A1G5]DKSA_SALTY DnaK suppressor protein	4		ILEAWR	42	6	2	27.43	y3y4	787.44	53.199	27582	2	394.22	-13.56
[P0A1G5]DKSA_SALTY DnaK suppressor protein	5		TSSLSILAAGVEPYQEKPGEEYM NEAQLSHFKR	8	34	3	11.12	b14b18y11	3822.87	98.722	96220	3	1274.96	-8.88
[P0A1G5]DKSA_SALTY DnaK suppressor protein	6		AAQEEEFSLRLNR	75	14	3	19.96	b10b13y10	1691.82	92.463	7130	2	846.41	-7.86
[P0A1G5]DKSA_SALTY DnaK suppressor protein	7	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14)	RLEARPTADLCIDCK	124	15	5	26.76	b4°b4b11y6y9	1817.88	103.607	3443	2	909.45	-8.19
[P0A1G5]DKSA_SALTY DnaK suppressor protein	8		MQDEAANFPDPVDR	61	14	0	4.9		1604.70	55.373	2914	2	802.86	1.90
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	1		THLVSPAMAAAAVTGHFADIR	441	22	9	45.94	b1b2b3y2y5y6y7y10y12	2207.13	84.272	19083	3	736.38	-4.09
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	2		AGLVAPDETTFNYYVK	229	15	7	58.42	b3b4b5y4y10y11y15	1624.83	65.402	18298	2	812.92	2.25
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	3		HLVHEVTSPQAFDGLR	29	16	10	66.08	b2b8b11*b11y4°y4y5y8y9 y10	1805.95	83.295	17122	4	452.24	9.19
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	4		LFDAHVVFEPNETPLLYIDR	8	21	3	14.36	b10b14y4	2459.24	92.401	9726	3	820.42	-9.03
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	5		IEVTGNAAPGITAK	167	14	3	11.36	b4°b9y8	1341.73	36.397	4857	3	447.91	-7.64
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	6		IQMQELIK	80	8	3	36.94	b4b6y6	1002.55	59.260	11096	2	501.78	-15.22
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	7		VAPGVQALVVPGSGPVK	366	17	4	24.32	y7y12y15°y15	1574.93	64.418	9430	2	787.97	1.01
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	8		TFATMDHNVSTQTK	56	14	6	19.96	b6b10°b10y5°y5*y5	1580.73	37.351	4958	2	790.87	-2.63
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	9		ALAYMGLQPGVPLTDVAIDK	321	20	5	23.44	b3b7b14*b14y10	2072.11	84.921	4695	2	1036.56	-1.06
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	10		AEEIAPQVTWGTNPGQVISVTDIIP DPASFSDPVER	280	36	7	23.85	b4°b4b12*b12y4y5y7	3835.96	102.522	3381	3	1279.32	14.70
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	11		IFIEAGFEWR	393	10	3	27.7	b7b9y4	1267.64	81.997	2180	2	634.32	-8.96
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	12		TLYEK	3	5	1	13.53	b4	653.35	27.824	1968	1	653.35	2.34
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	13	Carbamidomethyl+C(14)	TGSAGGTGHVVEFCGDAIR	190	19	4	29.33	b8b12y9y10	1890.88	47.846	1618	4	473.47	0.77
[P15717]LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	14	Carbamidomethyl+C(26)	ALAYMGLQPGVPLTDVAIDKVFI GSCTNSR	321	30	8	35.92	b6b10y4y7y8°y8y10y22	3193.65	95.239	9053	3	1065.22	2.29

P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	15	Carbamidomethyl+C(7)	LNPGERCASTSNR	417	13	7	64.36	b7y5°y5y8y9y10y11	1461.70	71.640	4323	2	731.35	6.35
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	16		DINASGEMARIQMQELIK	70	18	5	27.46	b5*b5b6b10y12	2047.03	80.491	3455	2	1024.02	-2.39
P15717 LEUC1_SALTY 3-isopropylmalate dehydratase large subunit 1	17	Carbamidomethyl+C(14)	TGSAGGTGHVVEFCDAIRALSM EGR	190	26	8	31.44	b6b8b10°b10b12y6°y6y16	2635.23	128.571	1557	3	879.08	-2.78
P63411 ACKA_SALTY Acetate kinase	1	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPE AR	17	26	14	104.38	b2b3b4y2y3y4y5y10y18y19y21y22y23y26	2907.41	104.388	45338	3	969.81	3.78
P63411 ACKA_SALTY Acetate kinase	2	Carbamidomethyl+C(14)	MLNKPVEELNIITCHLGNNGSVSA IR	195	26	7	22.27	b2b10y2y12y13*y13y26	2822.44	77.362	35052	4	706.36	-10.12
P63411 ACKA_SALTY Acetate kinase	3		LDVVFTGGIGENAAMVR	324	18	6	16.15	b3y1y9*y9y16y18	1819.92	93.534	33986	2	910.46	-12.14
P63411 ACKA_SALTY Acetate kinase	4		LGVLGFEVDHER	348	12	9	48.52	b2b3b9y1y3y5°y5y9y12	1370.69	55.892	33927	3	457.57	-9.53
P63411 ACKA_SALTY Acetate kinase	5		EGTRPAVVIPTNEELVIAQDASR	374	23	13	75.99	b9b14y2y4y5*y5y6y7y12°y12y14y15y23	2465.29	68.763	31068	3	822.43	-4.06
P63411 ACKA_SALTY Acetate kinase	6	Carbamidomethyl+C(7)	LVLVLNCGSSSLK	4	13	11	82.94	b2b3b4b5y8°y8y9°y9y10y11y13	1389.77	66.693	28919	2	695.39	-4.22
P63411 ACKA_SALTY Acetate kinase	7		NVAVFDATAFHQTMPEESYLYALP YSLYK	144	28	4	12	b13y6y9y28	3297.61	98.484	16360	3	1099.88	9.92
P63411 ACKA_SALTY Acetate kinase	8	Carbamidomethyl+C(1)	CVDTSMGLTPLEGLVMGTR	224	19	3	15.48	b10b12y15	2036.96	81.500	1856	3	679.66	-11.87
P63411 ACKA_SALTY Acetate kinase	9		YGAHGTSHFYVTQEAAK	178	17	4	23.83	b6b8y3y8	1866.84	37.176	8952	4	467.47	-19.49
P63411 ACKA_SALTY Acetate kinase	10	Carbamidomethyl+C(14)	ESGLGLTEVTSDCR	272	15	5	32.78	b3b8°b8y10y11	1636.79	59.084	2951	2	818.90	0.67
P63411 ACKA_SALTY Acetate kinase	11	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPE ARIK	17	28	4	12	b10°b10b15y15	3148.61	98.134	26152	4	787.91	11.71
P63411 ACKA_SALTY Acetate kinase	12	Phosphoryl STY(11)	EGTRPAVVIPTNEELVIAQDASR	374	23	6	30.52	b3°b3b5b6b12y12	2545.29	91.418	33916	3	849.10	11.61
P63411 ACKA_SALTY Acetate kinase	13		TMPEESYLYALPYSLYK	155	17	0	8.68		2068.00	98.514	2714	3	690.00	-0.47
P66955 TALB_SALTY Transaldolase B	1		QFTTVVADTG DIAAMK	9	16	8	46.83	b3b6b11b16y7y12y14y16	1667.84	67.295	25655	2	834.42	3.66
P66955 TALB_SALTY Transaldolase B	2		LSYDTEASIAK	100	11	7	49.11	b5b9y5y8y9°y9y11	1197.59	44.084	21965	2	599.30	-4.89
P66955 TALB_SALTY Transaldolase B	3		LYQPQDATNP SILNAAQIPEYR	25	24	9	41.28	b3b7b12b13y2y4y6y9y24	2716.40	81.435	14244	3	906.14	1.26
P66955 TALB_SALTY Transaldolase B	4		LTIA PALLK	241	9	4	39.08	y5y6y7y9	939.61	68.762	12034	2	470.31	-11.76
P66955 TALB_SALTY Transaldolase B	5		ELAESEGAIER	250	11	7	48.59	y2y3°y3y7y8y9y11	1203.59	36.318	11825	2	602.30	0.10
P66955 TALB_SALTY Transaldolase B	6		LYNDAGISNDR	117	11	4	32.05	y4y9y10y11	1237.58	35.639	10565	2	619.29	-2.47
P66955 TALB_SALTY Transaldolase B	7		DYAPAE DPGVSVSTEIYEYYK	193	21	5	14.36	b2b4b13y10°y10	2408.09	78.008	8861	3	803.37	-12.88
P66955 TALB_SALTY Transaldolase B	8		MIGDLL	311	6	3	30.44	b3b5°b5	661.35	78.426	10216	1	661.35	-14.58
P66955 TALB_SALTY Transaldolase B	9		LTSLR	4	5	1	13.53	y4	589.37	63.464	7417	1	589.37	6.84
P66955 TALB_SALTY Transaldolase B	10	Carbamidomethyl+C(11)	NVGEILELAGCDR	228	13	4	21.35	b6°b6y6y12	1445.73	52.692	4218	2	723.37	18.49
P66955 TALB_SALTY Transaldolase B	11		QQSSDR	60	6	1	13.9	b3	720.34	62.647	1685	1	720.34	12.20
P66955 TALB_SALTY Transaldolase B	12		ITEAEFLWQH HQDPM AVDKLADG IR	275	25	3	19.01	y3y5y13	2920.40	73.904	10642	4	730.86	-12.71

P66955 TALB_SALTY Transaldolase B	13		LYQPQDATTNPSLILNAAQIPEYR K	25	25	7	43.44	b8°b8b10b11b13b14y10	2844.48	99.380	10176	3	948.83	-3.35
P66955 TALB_SALTY Transaldolase B	14		QQSSDRAQQVV DATDK	60	16	6	46.9	b10y5y6y9*y9y10	1775.86	62.346	2624	3	592.63	7.01
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	1		TVVADGIGQGYKEVQEISPNLR	55	22	7	25	b2b5°b5y7y9y10y22	2373.23	71.515	25686	3	791.75	-5.35
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	2		SELDLKR	91	7	3	38.33	b5y4y5	860.48	28.994	11083	2	430.74	-6.17
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	3		SLGITNPEEIDR	6	12	6	23.01	b3°b3b5y2y6°y6	1343.68	54.645	9642	2	672.34	-0.91
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	4		TVVADGIGQGYK	55	12	7	37.21	b6°b6b8y8°y8y9°y9	1207.63	43.938	3220	2	604.32	-4.95
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	5	Carbamidomethyl+C(10)	YVIDELDQICQR	77	12	4	23.01	b10y5y10°y10	1551.77	63.898	30270	2	776.39	13.77
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	6		ILDDLRL	99	6	1	13.9	b5	744.42	51.641	12840	1	744.42	-7.87
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	7		TVVADGIGQGYKEVQEISPNLR	55	22	3	13.9	b10b13y18	2373.25	78.119	29398	3	791.76	5.56
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	8		SLGITNPEEIDRYSLR	6	16	4	26.16	b3°b3b11b12	1862.94	56.515	22227	3	621.65	-9.83
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	9		YSLRQEANNDILK	18	13	4	21.35	b7y4y10°y10	1563.81	62.882	5075	2	782.41	-2.50
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	10		MYDNLKSLGITNPEEIDR	0	18	3	23.55	b11b12y7	2108.04	75.430	4277	3	703.35	1.16
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	11		YDNLKSLGITNPEEIDR	1	17	3	16.91	b5y6y8	1977.01	109.951	3412	3	659.67	8.95
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	12		HLESVVANKISEI EADLDK	105	19	3	24.66	y10y11y13	2110.07	64.939	2690	3	704.03	-14.69
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	13	87.75	b2b3b4*y5y9y10°y10y11y 12y14y17y19y21	2215.15	74.823	53447	3	739.06	-8.60
Q56073 DNAK_SALTY Chaperone protein dnaK	2		MQELAQVSQK	587	10	10	75.27	b2b3b7°b7°b7y3y4y6y8y1 0	1161.59	36.866	42127	2	581.30	0.95
Q56073 DNAK_SALTY Chaperone protein dnaK	3		TAEDYLGEVPTEAVITVPAYFNDA QR	125	26	13	42.42	b1b2b4b8b13b16°b16y1y5 *y5y8y9y26	2869.39	93.490	34275	3	957.14	1.45
Q56073 DNAK_SALTY Chaperone protein dnaK	4		ASSGLNEEEIQK	502	12	14	100.07	b4b5y3y4°y4*y4y7°y7*y7y 8°y8y9y10y12	1304.62	34.467	27991	2	652.81	-8.33
Q56073 DNAK_SALTY Chaperone protein dnaK	5		NDPLAMQR	253	8	12	68.77	b2b4b6b8°b8y2*y2y3*y3y 4y6y8	944.45	38.778	13975	2	472.73	-10.40
Q56073 DNAK_SALTY Chaperone protein dnaK	6		TFEVLATNGDTHLGGEDFDTR	214	21	4	14.36	b3b17y4y21	2295.04	64.756	12623	4	574.52	-3.40
Q56073 DNAK_SALTY Chaperone protein dnaK	7		HSQVFSTAEDNQSAVTIHVLQGE R	421	24	7	13.11	b1b2b11y3°y3y5y24	2653.27	59.722	5210	3	885.10	-8.56
Q56073 DNAK_SALTY Chaperone protein dnaK	8		IAGLEVK	159	7	3	38.33	b3y5y6	729.44	44.056	3297	2	365.22	-13.56
Q56073 DNAK_SALTY Chaperone protein dnaK	9		QAVTNPQNTLFAIK	56	14	3	19.96	b5y3y10	1544.86	65.184	15567	2	772.94	14.07
Q56073 DNAK_SALTY Chaperone protein dnaK	10		NQGDHLLHSTR	536	11	4	51.6	y3y4y5y6	1277.61	24.221	12467	3	426.54	-17.58
Q56073 DNAK_SALTY Chaperone protein dnaK	11		FQDEEVQR	76	8	3	33.93	b6b7y7	1050.47	89.039	5406	2	525.74	-13.48
Q56073 DNAK_SALTY Chaperone protein dnaK	12	Carbamidomethyl+C(12)	IIGIDLGTTNSCVAIMDGTQAR	3	22	3	13.9	b12y7y10	2306.18	79.185	5272	2	1153.59	13.87
Q56073 DNAK_SALTY Chaperone protein dnaK	13		GMPQIEVTFDIDADGILHVS AK	467	22	4	13.9	b11°b11y10y16	2356.21	96.420	2586	3	786.08	10.88
Q56073 DNAK_SALTY Chaperone protein dnaK	14		AKLES LVEDLVNR	302	13	3	26.12	b6y4y5	1485.82	80.282	23250	2	743.41	-3.70
Q56073 DNAK_SALTY Chaperone protein dnaK	15		SIEPLKVALQDAGLSVSDINDVILV GGQTR	315	30	7	36.22	b3b4°b4y4y5*y5y7	3107.70	106.440	22146	3	1036.57	1.73

Q56073 DNAK_SALTY Chaperone protein dnaK	16		TTPSIIAYTQDGETLVGQPAKR	34	22	3	13.9	b7y4y20	2346.22	68.079	16391	3	782.75	-3.02
Q56073 DNAK_SALTY Chaperone protein dnaK	17		TAEDYLGEPVTEAVITVPAYFNDAQRQATK	125	30	3	17.53	b12b16b22	3297.62	95.287	12206	4	825.16	-1.70
Q56073 DNAK_SALTY Chaperone protein dnaK	18		NDPLAMQRLK	253	10	4	34.69	b3°b3b4b9	1185.65	39.749	11096	2	593.33	8.65
Q56073 DNAK_SALTY Chaperone protein dnaK	19		DQGIDLRNDPLAMQR	246	15	4	26.87	b4°b4b5b11	1741.86	49.139	4228	3	581.29	-1.40
Q56073 DNAK_SALTY Chaperone protein dnaK	20	Carbamidomethyl+C(12)	IIGIDLGTNTNSCVAIMDGTQARVLENAEGDR	3	31	5	26.04	b21y4y5y12y18	3289.62	117.135	1823	4	823.16	0.52
Q56073 DNAK_SALTY Chaperone protein dnaK	21	Phosphoryl STY(15)	IELSSAQQTVDNLPYITADATGPK	270	24	11	39.64	b8°b8*b8b9°b9b11°b11*b11y6y9y10	2612.22	50.497	22192	3	871.41	-8.22
Q56073 DNAK_SALTY Chaperone protein dnaK	22	Phosphoryl STY(9)	QAVTNPQNTLFAIKR	56	15	5	42.44	b3b8b10_H3PO4b10b13*b13	1780.92	81.500	12217	2	890.96	11.58
Q56073 DNAK_SALTY Chaperone protein dnaK	23		HSQVFSTAEDNQSAVTIHVLQGE	421	23	2	12.38	y13y17	2497.20	59.748	241810	3	833.07	1.47
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1	Carbamidomethyl+C(27)	SGIGPVTAAADITHDGDVEIVKPQH VICHLTDENASISMR	104	39	11	29.89	b2°b2b3b12y3y8y10y11°y11*y11y35	4183.00	72.492	71109	5	837.41	-12.02
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2		SLTEIKDVLASR	298	12	7	51.03	b4y2y3y5y6y7y12	1331.74	62.634	57709	2	666.37	-8.71
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3		VTLEPLER	25	8	8	50.47	b1b7y1y2y4y5y6y8	956.53	51.855	38981	2	478.77	-10.08
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4	Carbamidomethyl+C(6)	LLVDACYSPVER	170	12	10	96.09	b2b3b6y4y5y7y9y10y11y12	1421.71	59.215	37183	2	711.36	-1.89
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5	Carbamidomethyl+C(9)	ILLSSMPGCAVTEVEIDGVLHEYS TK	45	26	10	54.32	b2b3b6y5y8y12y15y20y24y26	2848.41	90.744	30686	3	950.14	1.11
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		EGVQEDILEILLNLK	71	15	21	130.81	b2°b2b3b4°b4b8*b8b9*b9b10°b10*b10y1y2y3y4y5y6y7y8y15	1725.96	121.877	26564	2	863.48	-0.42
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		LVIEMETNGTIDPEEAIR	200	18	4	16.15	b9*b9b12y10	2030.04	83.348	23939	3	677.35	14.07
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8		MQGSVTEFLKPR	0	12	4	45.96	y3y4y5y7	1392.70	58.692	43408	3	464.91	-18.93
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9		LVDIEQVSSTHAK	12	13	4	42.36	y4y7y11y12	1426.73	45.158	39664	3	476.25	-15.14
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	10		AEAIHYIGDLVQR	271	13	5	33.32	b5y4*y4y8y9	1484.76	62.402	36819	3	495.59	-16.03
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	11		IHSEEDERPIGR	158	12	3	33.22	y4y6y10	1437.68	24.083	24605	3	479.90	-16.81
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	12		EEKPEFDPILLRPVDDLELTVR	243	22	6	30.14	b5°b5b6°b6b10b19	2623.35	90.210	13961	4	656.59	-17.96
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	13		QPEVK	238	5	1	13.53	b3	600.34	30.710	12620	1	600.34	6.71
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	14		GYVPASTR	150	8	3	36.94	b3b7y6	850.46	46.513	6172	2	425.73	19.52

P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	15		GFGHTLGNALR	33	11	3	25.06	b6b9y9	1142.60	47.788	2579	2	571.80	-7.05
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	16	Carbamidomethyl+C(10)	RILLSSMPGCAVTEVEIDGVLHEY STK	44	27	10	61.75	b10b11y4y6y7y9°y9y10°y10y14	3004.49	114.058	131746	4	751.88	-6.09
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	17		VEQRTDLDK	191	9	4	31.3	b3b8°b8y8	1103.58	41.137	6287	2	552.29	5.64
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	18		GRGYVPASTR	148	10	4	44.23	b3b4b5y5	1063.56	23.866	3640	2	532.29	-0.11
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	19		GLSLGMRLNWPPASIADE	310	19	4	24.5	b11b13b17y11	2056.03	112.012	1696	2	1028.52	7.24
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	20	Phosphoryl STY(10)	LVIEMETNGTIDPEEAI RR	200	19	3	15.48	b8b11y10	2266.07	67.383	5206	3	756.03	2.05
P55900 SERC_SALTY Phohoserine aminotransferase	1		GKEFIQVAEEAEQDFRDL LNIPSN YK	42	26	9	42.19	b2b5b6y3y5*y5y6y12y26	3053.50	113.291	37317	4	764.13	-7.84
P55900 SERC_SALTY Phohoserine aminotransferase	2		ASIYNAMPIEGVK	335	13	6	33.32	b5y1y7y9y10y13	1392.72	64.622	36904	2	696.86	0.09
P55900 SERC_SALTY Phohoserine aminotransferase	3		AQVFNFSSGPAMLPAEVLK	1	19	11	72.6	b3b5*b5b9b13y3y6y13y15 y16y19	2006.05	91.358	35596	2	1003.53	5.35
P55900 SERC_SALTY Phohoserine aminotransferase	4		TTADYVDAGYWAASAIKEAK	91	20	3	14.89	b4y12y15	2131.05	93.078	20289	3	711.02	5.50
P55900 SERC_SALTY Phohoserine aminotransferase	5		ALTD F MIDFER	348	11	7	42.39	b2b5b6°b6y4°y4y5	1357.65	90.246	14908	2	679.33	1.35
P55900 SERC_SALTY Phohoserine aminotransferase	6		GKEFIQVAEEAEQDFR	42	16	4	17.79	b13y3y7y16	1895.93	52.317	9296	3	632.65	9.98
P55900 SERC_SALTY Phohoserine aminotransferase	7		EFIQVAEEAEQDFRDL LNIPSNYK	44	24	5	19.42	b2°b2y5y13y19	2868.43	117.936	6674	3	956.81	7.06
P55900 SERC_SALTY Phohoserine aminotransferase	8	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	3	13.9	b9y3y5	2567.18	118.585	5854	3	856.40	-13.41
P55900 SERC_SALTY Phohoserine aminotransferase	9	Carbamidomethyl+C(5)	AHESCPSILDYTVLNDNDSMFNT P PTFAWYLSGLVFK	217	37	5	10.93	b2b3b8y2y6	4250.04	124.056	3576	3	1417.35	11.95
P55900 SERC_SALTY Phohoserine aminotransferase	10		YGVIIYAGA QK	188	10	3	27.7	b3y4y6	1069.56	43.039	25089	2	535.28	-6.39
P55900 SERC_SALTY Phohoserine aminotransferase	11		MAQVFNFSSGPAMLPAEVLK	0	20	5	38.56	b4b5b6b10°b10	2137.12	90.135	4799	2	1069.07	19.88
P55900 SERC_SALTY Phohoserine aminotransferase	12		AVKPMR	129	6	1	13.9	y3	701.42	54.633	4777	1	701.42	10.09
P55900 SERC_SALTY Phohoserine aminotransferase	13		EFIQVAEEAEQDFR	44	14	4	31.73	b3y3y4y6	1710.80	37.886	2725	3	570.94	0.50
P55900 SERC_SALTY Phohoserine aminotransferase	14		VFLEESFAAGLHALK	311	15	4	30.4	b5b6b14y13	1631.85	62.846	2631	3	544.62	-19.82
P55900 SERC_SALTY Phohoserine aminotransferase	15		AELLYGVIDNSDFYR	272	15	3	18.79	b3b11y3	1774.85	53.244	2250	3	592.29	-6.67
P55900 SERC_SALTY Phohoserine aminotransferase	16	Carbamidomethyl+C(3)	KYCAPQIIDAK	111	11	3	32.05	b7b8b10	1306.67	66.396	77825	2	653.84	-9.53
P55900 SERC_SALTY Phohoserine aminotransferase	17		TTADYVDAGYWAASAIKEAK	91	20	3	14.89	b6b8y4	2131.03	100.872	41699	3	711.01	-2.29
P55900 SERC_SALTY Phohoserine aminotransferase	18		GQFAGVPLNLLGDKTTADYVDA GYWAASAIK	77	31	4	16.71	b25y14y16y25	3212.64	96.882	34242	3	1071.55	3.50
P55900 SERC_SALTY Phohoserine aminotransferase	19		SRMNVFPQLADNTLDK	295	16	4	17.79	b8*b8y7y10	1848.91	121.179	30490	2	924.96	-6.93
P55900 SERC_SALTY Phohoserine aminotransferase	20		MNVFPQLADNTLDKV FLEESFAA GLHALK	297	29	6	20.78	b3b12*b12y3y12y26	3218.63	108.266	30327	4	805.41	-9.25

P55900 SERC_SALTY Phohoserine aminotransferase	21		AELLYGVIDNSDFYRNDVAQANR	272	23	8	44.04	y6y7y10y13°y13y14°y14*y14	2643.28	79.053	19754	3	881.77	1.75
P55900 SERC_SALTY Phohoserine aminotransferase	22	Carbamidomethyl+C(7)	LAQQLCDWHGLGTSVMEISHRGK	20	24	3	13.11	b3y12y14	2752.33	92.875	12534	3	918.12	0.89
P55900 SERC_SALTY Phohoserine aminotransferase	23		INQQKAELLYGVIDNSDFYR	267	20	3	23.02	b3b4y8	2386.20	114.048	4643	3	796.07	-2.66
Q8ZL56 GPMI_SALTY 2	1		TFFANPVLTNADVQAK	91	16	11	47.5	b1°b1b3°b3b5b9y2y7y8y11y16	1735.90	76.445	27479	2	868.46	1.20
Q8ZL56 GPMI_SALTY 2	2		LSDIAPTMLSLMGMEIPQEMTGKPLFIVE	485	29	13	41.07	b2b3°b3b4b5°b5b10°b10b12y1y2y13y29	3191.62	121.070	17261	3	1064.55	4.05
Q8ZL56 GPMI_SALTY 2	3	Carbamidomethyl+C(8)	AVEALDNCIEQVTK	416	14	7	21.42	b2y1y9*y9y10*y10y14	1589.79	61.078	16555	2	795.40	4.84
Q8ZL56 GPMI_SALTY 2	4		TPVMDALWAK	31	10	7	42.47	b2y2y3y6°y6y8y10	1131.58	71.259	14880	2	566.29	-4.32
Q8ZL56 GPMI_SALTY 2	5		QMGNSEVGHVNLGAGR	59	16	3	17.79	b3y6y9	1625.76	41.704	7147	3	542.59	-12.09
Q8ZL56 GPMI_SALTY 2	6		VATYDLQPEMSSAELTEK	364	18	4	16.15	b10y8°y8y11	2011.97	90.252	3500	2	1006.49	9.95
Q8ZL56 GPMI_SALTY 2	7		YAHVTFFFNGGVVEPFAGEER	336	21	7	52.47	y2y3y5°y5y6y7y8	2403.12	95.252	2790	3	801.71	6.81
Q8ZL56 GPMI_SALTY 2	8	Carbamidomethyl+C(6)	YDTIICNYPNGDMVGHTGVMEAAIK	391	25	3	19.01	b3b7b9	2769.28	109.555	4641	3	923.76	2.64
Q8ZL56 GPMI_SALTY 2	9		IYLHAFLDGR	145	10	3	34.69	y3y5y6	1204.63	52.318	4167	3	402.21	-17.33
Q8ZL56 GPMI_SALTY 2	10		RPHTLIDASGLEVGLPDR	41	18	3	16.15	b10y3y5	1946.03	113.185	4066	2	973.52	-9.66
Q8ZL56 GPMI_SALTY 2	11		VVNLNFVMLTEYAADIK	286	17	4	23.9	b8y5y6°y6	1939.99	92.074	3394	2	970.50	-15.04
Q8ZL56 GPMI_SALTY 2	12		DPATGQAHTAHTNLPVPLIYVGEK	452	24	3	13.11	b3b6y5	2529.30	108.444	1910	3	843.77	-3.47
Q8ZL56 GPMI_SALTY 2	13		TAVAYPPASLANTFGEWMAKN DK	303	23	4	18.23	b7b11y7y12	2482.22	68.780	60419	3	828.08	3.64
Q8ZL56 GPMI_SALTY 2	14		ERTFFANPVLTNADVQAK	89	18	5	22.62	b6b8y4y8*y8	2021.06	103.544	9837	2	1011.04	9.66
Q8ZL56 GPMI_SALTY 2	15		EEQQDNAILNAKTPVMDALWAK	19	22	5	35.43	b9b11b13y6y7	2485.25	81.537	7584	2	1243.13	5.21
Q8ZL56 GPMI_SALTY 2	16		TFFANPVLTNADVQAKNAGK	91	20	3	23.02	b4b5y11	2106.09	62.902	6992	4	527.28	-3.13
Q8ZL56 GPMI_SALTY 2	17		DTPPRSAAESLK	155	12	5	37.21	b9°b9b11y6y7	1271.65	38.333	2636	3	424.55	-9.89
Q8ZL56 GPMI_SALTY 2	18		EITRAFVNADFDGFAR	268	16	4	24.32	b3°b3b4y8	1828.91	39.181	2002	3	610.31	6.54
Q8ZL56 GPMI_SALTY 2	19	Phosphoryl STY(20)	DPATGQAHTAHTNLPVPLIYVGEK	452	24	6	43.53	b15_H3PO4 b15b16y3y4y9y12	2609.26	101.258	2585	3	870.42	-2.62
P65692 K6PF_SALTY 6-phohofructokinase	1	Carbamidomethyl+C(1)	CVGIQNEQLVHHDIIDA IENMK	283	22	13	71.38	b1b2b3b4y3y4y5y7°y7*y7y11y12y22	2576.23	80.848	30532	4	644.81	-12.98
P65692 K6PF_SALTY 6-phohofructokinase	2		IGVLTSGGDAPGMNAAIR	4	18	6	41.86	b3y8y12y13y14y18	1699.88	61.995	21379	2	850.44	1.51
P65692 K6PF_SALTY 6-phohofructokinase	3		ISIVEVMGR	163	9	3	39.08	y5y6y7	1003.55	67.845	20143	2	502.28	-8.33
P65692 K6PF_SALTY 6-phohofructokinase	4	Carbamidomethyl+C(11)	HAIVAITEHMCDDVDELAHFIEK	215	22	5	30.14	y1y6y9y10y12	2578.21	81.446	11779	4	645.31	-14.39
P65692 K6PF_SALTY 6-phohofructokinase	5		AALTEGLEVMGIYDGYLGLYEDR	26	23	9	49.76	b6b15y5°y5y6y7y11°y11y15	2548.17	81.545	46170	3	850.06	-20.89
P65692 K6PF_SALTY 6-phohofructokinase	6		MGAYAIDL LLEGHGGR	267	16	5	43.89	b3y4y5y6y10	1672.82	81.645	14140	3	558.28	-15.83
P65692 K6PF_SALTY 6-phohofructokinase	7		ATVLGHIQR	244	9	3	39.08	y3y5y6	994.58	35.975	6129	2	497.79	-4.05
P65692 K6PF_SALTY 6-phohofructokinase	8		GIDALVVIGGDGSYMGAK	93	18	3	16.15	b3y6y8	1722.84	107.306	4478	3	574.95	-18.63
P65692 K6PF_SALTY 6-phohofructokinase	9	Carbamidomethyl+C(8)	LTEMGFPCIGLPGTIDNDIK	112	20	7	23.44	b12°b12y4*y4y8y11*y11	2191.03	85.694	1699	2	1096.02	-21.06
P65692 K6PF_SALTY 6-phohofructokinase	10	Carbamidomethyl+C(12)	KHAIVAITEHMCDDVDELAHFIEK	214	23	5	20.86	b3y3y6y10°y10	2706.38	62.895	50031	3	902.80	14.25
P65692 K6PF_SALTY 6-phohofructokinase	11		DENIRAVAIENLK	78	13	4	28.83	b4b9b10°b10	1484.81	57.561	8168	2	742.91	0.74
P65692 K6PF_SALTY 6-phohofructokinase	12	Phosphoryl STY(5)	IGVLTSGGDAPGMNAAIR	4	18	4	27.46	b3y8y15y16	1779.84	72.938	3747	3	593.95	3.43
P65692 K6PF_SALTY 6-phohofructokinase	13	Oxidation+M(13)	IGVLTSGGDAPGMNAAIR	4	18	7	51.34	b10b13°b13y7y8y13y14	1715.87	56.491	4712	2	858.44	-0.64

P65692 K6PF_SALTY 6-phosphofructokinase	14	Oxidation+M(10)	AALTEGLEVMGIYDGYLGLYEDR	26	23	4	18.23	b6b10y6y9	2564.24	117.043	4206	3	855.42	4.95
P0A2A7 RL30_SALTY 50S ribosomal protein L30	1		GMVNAVSEFMVK	45	11	7	42.39	b2b5b6y5°y5y6y11	1182.60	72.429	97689	2	591.80	-3.30
P0A2A7 RL30_SALTY 50S ribosomal protein L30	2		ATLLGLGLR	21	9	5	39.08	y1y4y6y7y9	913.57	73.217	22838	2	457.29	-14.63
P0A2A7 RL30_SALTY 50S ribosomal protein L30	3		SAIGRLPK	11	8	3	33.93	b4y5y6	841.51	32.961	20974	2	421.26	-12.69
P0A2A7 RL30_SALTY 50S ribosomal protein L30	4		IGHTVEREDTPAVR	31	14	4	19.96	b4y7°y7y9	1579.81	84.391	11649	2	790.41	-5.18
P0A2A7 RL30_SALTY 50S ribosomal protein L30	5		GMVNAVSEFMVK	45	11	0	2.26		1165.56	72.415	1824	2	583.28	-12.15
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	1		NLTGFWIMPDTGFSFDDADLK	491	21	11	33.09	b1b2b6°b6y1y2y6y8y11y13y21	2390.11	106.524	23949	2	1195.56	5.21
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	2		DIGFHPVGTGPYQLETWNQTDFV K	176	24	11	65.71	b5b10b13b14b20y8y9y10°y10*y10y24	2749.34	83.032	23206	3	917.12	4.88
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	3		FQDGADFNAAVK	97	13	5	35.82	b2y9y10y11y13	1353.64	49.420	20368	2	677.33	0.18
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	4		AAMLQTGEAQFAFPIPYEAALLA K	229	25	12	75.48	b3b6°b6b8b9b11b15b20b23°b23y20y25	2679.40	97.028	15581	3	893.81	6.01
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	5		ITAMDAGQR	379	9	4	39.08	y4y5*y5y7	962.46	28.887	14875	2	481.74	-9.39
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	6		ELLKEAGYPDGFSTTLWSSHNHSTAQK	335	27	6	23.19	b2b6b8b9°b9y9	3004.40	65.490	14506	4	751.86	-13.41
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	7		NLELVASPSIMQR	256	13	7	44.42	b3b9y3y8*y8y10y13	1457.77	68.338	12608	2	729.39	-2.76
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	8		SFYQGLFGLDKDMK	56	14	7	43.71	b3b8°b8b11b12°b12y13	1648.80	68.875	5784	2	824.90	-4.37
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	9		EAQDIWKESPWIVLVEK	465	19	4	15.48	b5b11y2y6	2280.21	92.132	1606	3	760.74	-8.67
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	10		YISMNVTQKPFDNPK	269	15	6	71.93	y4y6y8y9y10y13	1781.86	55.403	26531	3	594.63	-15.89
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	11		EALNYAINR	286	9	3	39.08	y3y6y7	1063.54	44.879	18002	2	532.27	-15.38
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	12		LDSITWRPVTDNNTR	214	15	8	70.16	y4°y4y7y10°y10y11y13y14	1787.92	56.544	6998	2	894.46	8.06
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	13		NVLAEGYTVSDDGLTYTITLR	72	21	6	25.5	b13°b13b14b20y11°y11	2301.16	87.237	5609	4	576.05	1.49
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	14		EAGYPDGFSTTLWSSHNHSTAQK	339	23	8	35.27	b3b12y7°y7y9°y9y10y19	2521.13	60.190	4486	3	841.05	-2.03
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	15		NKNLELVASPSIMQR	254	15	3	26.87	b3b4b11	1699.92	66.188	75472	4	425.73	1.08
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	16		ITLKQPFSAFINILAHPATAMISPPA LEK	144	29	6	17.49	b10*b10y6*y6y11y13	3150.71	109.402	29512	4	788.43	-8.21
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	17		AAEVEGKGQK	388	10	3	27.7	b3b9y3	1016.53	38.318	23970	2	508.77	-10.03
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	18		QALVKVAFAGYATPATGTVVPPSIAYAQSYQPWPYPDAK	295	38	4	16.5	y5y8°y8y12	4023.03	82.895	17599	4	1006.51	-9.71
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	19		VAFAGYATPATGTVVPPSIAYAQSYQPWPYPDAKAR	300	35	5	24.72	b8°b8b9y8y11	3710.86	125.985	9777	4	928.47	-1.38
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	20		SFYQGLFGLDKDMK	56	14	4	28.56	b4b6y5y8	1648.79	77.322	4484	3	550.27	-7.03
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	21	Oxidation+M(11)	NLELVASPSIMQR	256	13	4	40.31	b3y6y7y8	1473.76	95.238	5876	2	737.38	-8.37
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	22		NQTDFVK	193	7	0	7.17		851.43	83.017	8104	1	851.43	3.87
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	23		FYQGLFGLDKDMK	57	13	1	7.38	b9	1561.77	68.910	3515	2	781.39	-0.08

P51066 ACEA_SALTY Isocitrate lyase	1	Carbamidomethyl+C(13)	GLAYAPYADLVWCETSTPDLELA R	275	24	5	20.16	b3b7b9°b9y12	2711.29	89.231	19679	4	678.58	-2.97
P51066 ACEA_SALTY Isocitrate lyase	2		VLVPTQEAIQK	201	11	4	28.07	b2b3y8y9	1225.71	47.673	16919	2	613.36	-6.47
P51066 ACEA_SALTY Isocitrate lyase	3	Carbamidomethyl+C(7)	GSVNPECTLAQLGAAK	36	16	4	17.79	b2b6y10y12	1615.83	65.751	13038	2	808.42	9.90
P51066 ACEA_SALTY Isocitrate lyase	4	Carbamidomethyl+C(6)	LLAYNCSPSFNWQK	312	14	11	64.86	b3b6b11°b12y3y7y8°y8y1 0°y11y14	1727.84	68.791	10930	2	864.42	8.05
P51066 ACEA_SALTY Isocitrate lyase	5		LAADVMSGVPTLVIAR	217	15	6	49.16	b4b7y3y7y9y10	1525.88	83.275	10278	2	763.44	3.12
P51066 ACEA_SALTY Isocitrate lyase	6		VTTIIQGGASSVTALTGSTEEAQF	410	24	3	23.4	y3y4y10	2368.21	72.067	7983	3	790.08	10.62
P51066 ACEA_SALTY Isocitrate lyase	7		TIASFQQQLSDMGYK	331	15	4	30.4	b7y5y11y12	1716.83	89.088	5758	2	858.92	-0.21
P51066 ACEA_SALTY Isocitrate lyase	8		SMIEAGAAAVHFEDQLASVKK	173	21	3	21.01	b8b10b13	2202.13	128.462	2216	3	734.72	4.66
P51066 ACEA_SALTY Isocitrate lyase	9		ADQIQWASGIEPNDR	130	16	3	26.16	b4b5b12	1796.86	61.478	2067	2	898.94	3.80
P51066 ACEA_SALTY Isocitrate lyase	10		YVDYFLPIVADAEAGFGGVLNAF ELMK	146	27	3	18.31	y6y13y15	2949.50	137.068	1663	3	983.84	8.44
P51066 ACEA_SALTY Isocitrate lyase	11		INNTR	123	6	1	13.9	b3	764.40	36.252	8118	2	382.70	-5.19
P51066 ACEA_SALTY Isocitrate lyase	12		DGYTFVSHQQEVGTGYFDK	391	19	4	22.44	b5b7b10°b10	2177.94	59.690	6550	4	545.24	-19.06
P51066 ACEA_SALTY Isocitrate lyase	13		EWTPR	13	6	2	30.44	y3y5	816.39	62.348	4016	1	816.39	-9.35
P51066 ACEA_SALTY Isocitrate lyase	14		WEGITRYPYSAEEVVK	19	15	4	24.81	b3°b3b4y9	1763.89	121.875	3718	3	588.63	-5.81
P51066 ACEA_SALTY Isocitrate lyase	15		SMIEAGAAAVHFEDQLASVK	173	20	6	20.59	b3°b3b8°b8y8y12	2073.98	118.222	3421	3	692.00	-21.89
P51066 ACEA_SALTY Isocitrate lyase	16		KGYINSLGALTGGQALQQAQK	62	20	4	20.59	b3b15y9y13	2018.09	64.185	16297	3	673.37	-4.23
P51066 ACEA_SALTY Isocitrate lyase	17	Carbamidomethyl+C(6)	LLAYNCSPSFNWQKNLDDK	312	19	6	30.57	b3b8°b8b11y5y7	2313.12	120.458	9086	3	771.71	10.34
P51066 ACEA_SALTY Isocitrate lyase	18	Carbamidomethyl+C(7)	GSVNPECTLAQLGAQMWR	36	19	3	15.48	b11y13y18	2089.04	104.561	7714	3	697.02	5.03
P51066 ACEA_SALTY Isocitrate lyase	19		TRTQQIEELQK	2	11	4	25.06	b4°b4b8y4	1373.72	125.133	2181	2	687.36	-14.22
P51066 ACEA_SALTY Isocitrate lyase	20	Phosphoryl STY(12)	TQQIEELQKEWTQPR	4	15	3	18.79	b10y3y8	1993.92	82.444	2575	3	665.31	-2.27
P51066 ACEA_SALTY Isocitrate lyase	21		VLVPTQEAIQ	201	10	0	2.26		1097.62	47.626	14873	2	549.32	3.34
P11003 METF_SALTY 5	1	Carbamidomethyl+C(11)	TGLEAAPHLTCIDATRDEL	80	20	5	23.02	b3y2y16y17y20	2239.10	58.839	27401	3	747.04	-5.02
P11003 METF_SALTY 5	2		LVGANIAMDMVK	250	12	6	26.99	b5°b5y4°y8°y8y9	1261.65	70.655	14387	2	631.33	-10.93
P11003 METF_SALTY 5	3		SAQADLLNLKR	160	11	6	39.38	b1b3°b3b4y4y7	1228.70	50.869	11102	2	614.85	-2.48
P11003 METF_SALTY 5	4		IPSWMSLMFEGLDNDNAETRK	230	20	6	26.08	b8y1y8y11°y11y12	2340.11	103.472	10607	3	780.71	2.71
P11003 METF_SALTY 5	5		TSEMEQTLWNSIDR	33	14	5	19.96	b2b12y2y4y10	1709.80	77.072	8332	2	855.40	10.57
P11003 METF_SALTY 5	6		FVSVTYGANSGER	54	13	4	21.35	b10°b10y3y9	1386.67	45.185	2631	2	693.84	2.99
P11003 METF_SALTY 5	7		AITQFFFDVESYLR	179	14	5	40.33	b9b12b13y8y10	1735.86	96.959	1600	2	868.43	-8.02
P11003 METF_SALTY 5	8		EVADFDISVAAYPEVHPEAK	140	20	4	26.08	b5y4y5y15	2187.02	81.105	84173	3	729.68	-16.63
P11003 METF_SALTY 5	9		FADMTNVR	222	8	4	36.94	b3y4y7°y7	953.47	57.036	8811	2	477.24	18.76
P11003 METF_SALTY 5	10		IPSWMSLMFEGLDNDNAETR	230	19	6	30.57	b5°b5b7b13y4y7	2212.05	110.624	7173	2	1106.53	20.09
P11003 METF_SALTY 5	11		MSFFHANQR	0	9	3	31.3	b5y7y8	1137.51	67.377	7138	2	569.26	-9.98
P11003 METF_SALTY 5	12		GDLPPGSGKPEMYAADLVGLLK	118	22	4	20.41	b5b8°b8b15	2228.14	98.554	3505	3	743.38	-12.60
P11003 METF_SALTY 5	13	Carbamidomethyl+C(11)	TGLEAAPHLTCIDATR	80	16	3	24.32	b4b5y3	1725.86	46.512	1960	3	575.96	-0.42
P11003 METF_SALTY 5	14		DFHFYTLNR	270	9	3	39.08	b5b6b8	1212.57	59.131	1945	2	606.79	-7.05

P11003 METF_SALTY 5	15		TIARDYWNNGIR	100	12	3	23.01	b3b9y3	1478.77	62.767	5624	2	739.89	13.70
P11003 METF_SALTY 5	16		DRTHSVIK	67	8	5	41.71	b3°b3b4b5°b5	955.54	72.329	3328	2	478.27	10.28
P11003 METF_SALTY 5	17		VDAGANRAITQFFFDVESYLR	172	21	5	27.85	b4b7b14y7y10	2419.21	91.427	2206	4	605.56	4.24
P11003 METF_SALTY 5	18	Carbamidomethyl+C(13)	ERTGLEAAPHLTICIDATR	78	18	3	16.15	b7b10y7	2010.99	52.718	2098	3	671.00	-8.26
P11003 METF_SALTY 5	19	Oxidation+M(12)	GDLPPGSGKPEMYAADLVGLLKE VADFDISVAAYPEVHPEAK	118	42	7	22.85	b7°b7b8°b8b22y5y10	4412.21	112.713	11356	4	1103.81	1.11
P11003 METF_SALTY 5	20	Oxidation+M(10)	LVGANIAMDMVK	250	12	4	33.23	b8b10y3y6	1277.64	87.281	7121	2	639.33	-11.47
P11003 METF_SALTY 5	21	Carbamidomethyl+C(1)	CIDATRDELRL	90	10	0	5.66		1248.61	58.868	24483	2	624.81	7.92
P11003 METF_SALTY 5	22		SAQADLLNL	160	9	1	8.01	y5	944.51	50.843	6744	1	944.51	5.11
P11003 METF_SALTY 5	23		IPSWMSLMFEGLDND	230	15	3	21.68	y3y6y14	1754.80	103.467	2032	2	877.90	12.73
P11003 METF_SALTY 5	24		QADLLNLKR	162	9	0	2.26		1070.63	50.840	1719	2	535.82	2.17
P0A1S4 STPA_SALTY DNA-binding protein stpA	1		ADGINPEELFAMDSAMPR	66	18	9	32.17	b3b5°b5°b5b11°b11y4y8y1 8	1963.91	88.802	18440	2	982.46	8.64
P0A1S4 STPA_SALTY DNA-binding protein stpA	2		MNLMLQNLNNIR	0	12	8	64.26	b2b3b6y3y4y8y9y12	1473.77	75.997	16841	2	737.39	0.41
P0A1S4 STPA_SALTY DNA-binding protein stpA	3		TPKPIAQALAAGK	113	13	5	21.35	b3y1y4y10y13	1265.75	45.867	16419	2	633.38	-8.87
P0A1S4 STPA_SALTY DNA-binding protein stpA	4		SLDDFLI	126	7	5	51.85	b3b4b6y6°y6	822.42	35.510	84026	2	411.71	-3.12
P0A1S4 STPA_SALTY DNA-binding protein stpA	5		TWTGQGR	106	7	3	38.33	b5y5y6	805.40	35.517	6695	2	403.21	11.37
P0A1S4 STPA_SALTY DNA-binding protein stpA	6	Oxidation+M(14)	AMAREFSIDVLEEMLEK	15	17	5	27.05	b5b7b10°b10y11	2026.99	74.167	2362	3	676.33	1.69
Q7CQ70 YEJL_SALTY UPF0352 protein yejL	1		QAIANSFAR	54	9	8	46.08	b2°b2b6°b7b8y5°y5y7	977.51	39.730	9183	2	489.26	-10.12
Q7CQ70 YEJL_SALTY UPF0352 protein yejL	2		YSDEHVEQLLSELLSVLEK	6	19	5	23.26	b11°b11y1y3y4	2231.13	124.558	6137	3	744.38	-7.99
Q7CQ70 YEJL_SALTY UPF0352 protein yejL	3		ALQSSISEDNAH	63	12	9	45.51	b4b6°b6y1y3°y3y8y9°y9	1271.59	32.059	6094	2	636.30	2.11
Q7CQ70 YEJL_SALTY UPF0352 protein yejL	4		YSDEHVEQLLSELLSVLEKHK	6	21	3	21.01	b3b12b18	2496.30	89.049	12359	3	832.77	2.74
Q7CQ70 YEJL_SALTY UPF0352 protein yejL	5		QAIANSFARALQSSISEDNAH	54	21	8	38.99	b6°b6b9b14°b14y10y11y1 3	2230.11	73.405	2550	3	744.04	10.29
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	1		ALSIVTSDTPVQRETQETGAMLM R	148	24	6	13.11	b3y1y4y7°y7y24	2634.29	77.357	26313	3	878.77	-13.72
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	2		YQDALLTHYGQR	318	12	8	23.01	b1b10°b10y2y3°y3y5y12	1464.71	47.486	13895	2	732.86	-12.33
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	3		TEAVDDALR	403	9	9	76.65	b3b9y4y5°y5y6y7y8y9	989.50	36.825	5232	2	495.25	7.90
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	4		MLSHTEQQSASSPLRDTFIDR	367	21	5	19.72	b4b9y2y6y16	2419.19	62.295	4948	3	807.07	11.00
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	5		DDNVLLNELFSLMAREGSDYTR	342	22	6	30.04	b5b10°b10y4y9y10	2558.24	118.039	3438	3	853.42	7.73
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	6		QQQMQR	412	6	1	13.9	y4	818.40	31.991	17498	2	409.71	13.28
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	7		MLSHTEQQSASSPLR	367	15	4	26.76	b4b7y9y11	1671.81	108.937	14325	3	557.94	-3.07
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	8		AIDAAEQGDMAELHR	432	15	3	24.81	b5b6y10	1626.72	62.985	9971	3	542.91	-18.16
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	9		FDNQPSVALWNLQR	284	14	4	19.96	b12y3y11°y11	1687.89	71.294	5890	2	844.45	20.18
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	10		ETQETGAMLMR	161	11	5	37.8	b7y4y5y9°y9	1266.61	54.620	2692	3	422.87	20.53
Q8ZPS5 YDIU_SALTY UPF0061 protein ydiU	11		NWLAQR	426	6	1	13.9	y5	787.43	39.782	2253	2	394.22	12.25

[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	12		LAQSHMRFGHFHFYYR	172	17	5	28.3	b9y4y5y8°y8	2226.04	88.091	17491	4	557.26	-3.73
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	13		DDNVLLNELFSLMAREGSDYTR	342	22	4	13.9	b5°b5b8y4	2558.24	117.033	9293	3	853.42	7.73
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	14		ALDRYQDALLTHYGQR	314	16	3	17.79	b3y9y11	1919.99	77.124	6500	3	640.67	9.09
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	15		YQDALLTHYGQRM	318	14	4	31.73	b6b8b9y7	1751.86	92.106	3617	3	584.62	-3.55
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	16		VQQLADFAIRHYWPQWQDVPEK	194	22	6	18.94	b5b7°b7*b7y4y10	2754.35	107.665	3020	2	1377.68	-8.86
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	17		TFRMLSHTEQQSASSPLR	364	18	5	30.03	b8b10°b10y9y10	2076.03	68.805	2655	2	1038.52	0.00
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	18		HYWPQWQDVPEKYALWFEEVAA R	204	23	3	13.48	b4b12y8	2948.45	105.091	1976	4	737.87	10.93
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	19		AIDAAEQGDMAELHRLHEVLR	432	21	4	25.5	b4b7b8y6	2374.22	111.437	1622	2	1187.62	13.37
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	20	Phosphoryl STY(9)	STIRESLASEAMHYLGIPTR	127	21	6	36.64	b11y11°y11y12°y12y13	2413.16	62.314	37435	4	604.05	4.65
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	21	Oxidation+M(13)	DDNVLLNELFSLMAREGSDYTR	342	22	5	37.92	b6b7b8°b8b10	2574.21	125.421	10419	3	858.74	-0.95
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	22	Oxidation+M(21)	LGFFTEQKDDNVLLNELFSLMAR	334	23	3	13.48	b5y5y12	2716.34	107.842	6705	3	906.12	-9.53
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	23	Oxidation+M(21)	LGFFTEQKDDNVLLNELFSLMAR EGSDYTR	334	30	4	26.89	y3y5y11y12	3524.69	108.213	1729	3	1175.57	-4.23
[Q8ZPS5]YDIU_SALTY UPF0061 protein ydiU	24	Oxidation+M(13)	DDNVLLNELFSLMAR	342	15	3	18.79	b8b13y9	1765.86	104.144	1631	2	883.43	-11.48
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	1		GIEGASLDVPDEFVHSGK	72	18	7	25.7	b2b9y2y3y6y10y18	1856.89	66.577	34617	3	619.63	-8.87
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	2		VLSESDFQVNQLLDILR	49	17	8	51.83	b2b8y2y3y4y5y6y17	1989.08	104.598	30900	2	995.04	6.01
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	3		SRDDLQSVMAVLR	135	13	13	92.66	b1b3b4°b4b6b7°b7*b7b12 y2y3y4y5	1489.77	75.166	24468	2	745.39	-3.20
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	4		GGDLGQPFQFK	148	11	7	39.38	b2b5b6b11y5y7y11	1193.59	63.250	22744	2	597.30	-1.94
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	5		VQAQIQGEEIR	120	11	10	72.63	b1b2*b2b3y2y4y6y7y8y9	1270.67	39.253	12007	2	635.84	-5.67
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	6		GVEATIELNDANK	33	13	4	33.32	b7b11b12y5	1373.71	56.603	15693	3	458.58	16.35
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	7		QGIESAVQK	99	9	3	39.08	b3b5b6	959.53	72.205	5509	1	959.53	17.49
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	8		DDLQSVMAVLR	137	11	4	25.06	b6°b6y4y6	1246.63	39.800	2016	2	623.82	-16.16
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	9		DDLQSVMAVLRGGDLGQPFQFK	137	22	4	20.41	b6b11b14°b14	2421.21	93.155	34098	3	807.74	-6.25
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	10		MPSFDIVSEVDLQEARNGVDNAV R	0	24	4	22.41	b7b8°b8y12	2661.29	112.285	8614	3	887.77	0.09
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	11		RGIEGASLDVPDEFVHSGK	71	19	4	15.48	b12y11y15°y15	2013.01	70.738	1881	3	671.68	4.00
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	12	Oxidation+M(1)	MPSFDIVSEVDLQEAR	0	16	3	24.32	b3b4y8	1851.88	46.508	4081	3	617.96	-0.40
[Q8ZRC9]YAJQ_SALTY UPF0234 protein yajQ	13		EGASLDVPDEFVHSGK	74	16	1	7.29	b9	1686.81	66.579	2818	2	843.91	7.09
[P61179]RL22_SALTY 50S ribosomal protein L22	1		IFVDEGPSMK	73	10	7	62.53	b2b3y5y6y8y9y10	1122.54	50.821	52226	2	561.78	-6.42
[P61179]RL22_SALTY 50S ribosomal protein L22	2		LVADLIR	18	7	6	51.85	b2b3y3y5y6y7	799.49	56.848	26340	2	400.25	-11.91
[P61179]RL22_SALTY 50S ribosomal protein L22	3		VLESAIANAEHNDGADIDDLK	49	21	5	25.5	b5b11°b11b12y4	2210.02	60.940	4889	3	737.34	-18.01

P61179 RL22_SALTY 50S ribosomal protein L22	4		VSQALDILTYTNK	28	13	4	28.83	b3°b3b5b6	1465.80	39.721	2043	2	733.40	5.83
P61179 RL22_SALTY 50S ribosomal protein L22	5		KVLESAIANAEHNDGADIDDLK	48	22	3	13.9	b9y4y9	2338.15	57.565	2793	3	780.06	0.00
P61179 RL22_SALTY 50S ribosomal protein L22	6		IFVDEGPSMKR	73	11	4	37.8	b5b6b8y7	1278.66	69.814	1911	2	639.83	5.44
P61179 RL22_SALTY 50S ribosomal protein L22	7		RTSHITVVVSDR	98	12	4	36.23	y3y4°y4y5	1369.74	34.924	1550	3	457.25	-11.76
P61179 RL22_SALTY 50S ribosomal protein L22	8	Oxidation+M(9)	IFVDEGPSMKR	73	11	3	28.07	b5y5y6	1294.66	47.955	13353	2	647.83	7.64
P24900 RECF_SALTY DNA replication and repair protein recF	1		NIENADLALSPGFNFLVGANGSGK	12	24	12	71.17	b2°b2b4b5b7b10b11b12y7y8°y8y15	2405.19	100.385	19911	3	802.40	-8.83
P24900 RECF_SALTY DNA replication and repair protein recF	2		ADGAPVEDTLR	259	12	3	23.01	b3b10y5	1230.61	48.424	6158	2	615.81	11.90
P24900 RECF_SALTY DNA replication and repair protein recF	3		LQSEER	73	6	1	13.9	b3	761.38	36.855	7310	2	381.19	3.05
P24900 RECF_SALTY DNA replication and repair protein recF	4		HEQEAFVLHGR	62	11	7	42.57	b3°b3b6b10°b10y10°y10	1322.68	69.798	3096	2	661.84	15.32
P24900 RECF_SALTY DNA replication and repair protein recF	5		MLTYTAHGPHK	242	11	4	25.06	b8°b8y3y5	1255.64	36.246	2773	3	419.22	15.56
P24900 RECF_SALTY DNA replication and repair protein recF	6		QGDSK	89	5	1	13.53	b4	534.26	37.863	1807	1	534.26	9.14
P24900 RECF_SALTY DNA replication and repair protein recF	7	Carbamidomethyl+C(2)	RCLYLIDDFASELDDAR	295	17	3	23.9	b5y7y8	2071.98	101.158	16869	2	1036.50	4.48
P24900 RECF_SALTY DNA replication and repair protein recF	8	Carbamidomethyl+C(15)	AEYSSAIAQDMADTCQQFLPEFSLTFSFQRGWEK	192	34	5	11.12	b3°b3b7°b7y7	3988.79	95.001	12701	5	798.56	-6.92
P24900 RECF_SALTY DNA replication and repair protein recF	9		LAQGEFLTRESGR	282	13	4	33.32	b6y5y6y9	1463.78	105.601	6731	2	732.39	13.59
P24900 RECF_SALTY DNA replication and repair protein recF	10	Carbamidomethyl+C(8)	RAFLDWGCFHNEAGFFTAWSNLK	132	23	3	19.89	b4b11b18	2774.33	80.509	2584	3	925.45	13.82
P24900 RECF_SALTY DNA replication and repair protein recF	11		MLTYTAHGPHKADFR	242	15	4	18.79	b12°b12y4y9	1744.87	83.927	1952	2	872.94	9.16
P24900 RECF_SALTY DNA replication and repair protein recF	12		DFRNIENADLALSPGFNFLVGANGSGK	9	27	8	28.32	b3°b3b6b13y7y9y11°y11	2823.44	89.700	1663	3	941.82	13.58
P24900 RECF_SALTY DNA replication and repair protein recF	13	Phosphoryl STY(8)	GWEKETDYADVLER	222	14	3	28.54	y4y6y8	1790.77	29.899	3714	2	895.89	10.16
P24900 RECF_SALTY DNA replication and repair protein recF	14	Phosphoryl STY(8)	LQSEERETSIGLTK	73	14	4	25.4	b6°b6y7y8	1670.81	72.341	3088	2	835.91	14.83
P24900 RECF_SALTY DNA replication and repair protein recF	15	Oxidation+M(19)	ATQSQVFVSAISAEHVIDMSDENSK	321	25	5	16.99	b7b13°b13y5y22	2709.31	75.941	21373	4	678.08	14.87
P0A2B3 RS7_SALTY 30S ribosomal protein S7	1		STAESIVYSALETLAQR	36	17	21	104.24	b2°b2b5°b5b8b14y1y2°y2y3°y3y4°y4y5°y5y6°y6y7y10y11y17	1838.96	105.966	67530	2	919.98	7.04
P0A2B3 RS7_SALTY 30S ribosomal protein S7	2		SELEAFEVALENVRPTEVK	56	20	12	37.27	b1b2°b2b3°b3b5°b5b13y2y15y16y20	2259.18	91.496	47156	3	753.73	-3.67
P0A2B3 RS7_SALTY 30S ribosomal protein S7	3		FVNILMVDGK	25	10	5	41.22	b2b3y3y4y8	1135.61	75.344	25014	2	568.31	-3.98
P0A2B3 RS7_SALTY 30S ribosomal protein S7	4		WIVEAAR	102	7	4	41.34	b5y3y5°y5	844.46	49.779	53495	2	422.73	-13.73
P0A2B3 RS7_SALTY 30S ribosomal protein S7	5		FGSELLAK	17	8	3	41.71	y3y4y7	864.47	51.061	52967	2	432.74	-16.80
P0A2B3 RS7_SALTY 30S ribosomal protein S7	6		NALAMR	96	6	2	27.43	b5y5	675.36	35.561	7439	1	675.36	-6.33
P0A2B3 RS7_SALTY 30S ribosomal protein S7	7		ILPDPK	11	6	1	13.9	y4	682.41	31.720	3471	1	682.41	-3.76
P0A2B3 RS7_SALTY 30S ribosomal protein S7	8		EDVHRMAEANK	138	11	7	39.38	b3b10°b10y3°y3y4°y4	1299.60	29.356	117594	2	650.30	-10.24
P0A2B3 RS7_SALTY 30S ribosomal protein S7	9		RVGGSTYQVPVEVRPVR	78	17	11	84.17	b5°b5b6°b6b7b8b9°b9y5y8y9	1899.04	48.728	48038	3	633.69	-8.03

[P0A2B3]RS7_SALTY 30S ribosomal protein S7	10		KSTAESIVYSALETLAQR	35	18	5	41.33	b7b8b11y5y6	1967.02	96.969	18971	3	656.35	-11.48
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	11		AFAHYRW	149	7	4	57.87	b3b5y4y5	950.46	50.916	3980	2	475.73	-7.83
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	1		FLFDEYVR	144	8	7	82.29	b4b7y4y5y6y7y8	1088.54	76.855	10347	2	544.77	-4.60
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	2		TVAEGVTEYMAWLN RDA	293	17	9	35.22	b1°b1b3b5y8°y8y9°y9y16	1925.92	97.150	9447	2	963.47	9.70
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	3		SGIFNLGTGR	229	10	7	59.52	b3°b3y3y5y6y7y10	1021.54	64.000	8580	2	511.27	-6.33
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	4	Carbamidomethyl+C(6)	ELLHYCLEREIPFLYASSAATYGG R	98	25	5	28.4	b8y6y8y11y13	2916.46	110.834	2554	3	972.82	7.37
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	5		AESFQAVADATLAYHK	239	16	4	17.79	b3°b3b14y8	1721.82	90.645	14317	3	574.61	-17.51
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	6		YQAFTQADLTNLR	271	13	3	26.12	b3y9y10	1540.78	65.110	12739	2	770.89	4.12
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	7		QILPEANSQIVGFR	152	14	4	27.74	y4y11y12*y12	1571.86	68.875	8296	2	786.43	2.95
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	8		DFVYVGDVAAVNLWFLESGK	209	20	3	24.31	b4b5b7	2229.13	86.857	1837	2	1115.07	4.27
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	9		EYEKPLNVYGYSK	131	13	3	21.35	b3b10y11	1589.78	73.616	1740	3	530.60	-0.69
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	10		EIPFLYASSAATYGG R	107	16	3	24.32	b12b13y14	1702.87	110.915	1574	2	851.94	15.91
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	11		DFVYVGDVAAVNLWFLESGKSGI FNLGTGR	209	30	7	33.28	b3b4°b4b7°b7b9b11	3231.67	94.518	4480	3	1077.89	5.67
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	12		AESFQAVADATLAYHKK	239	17	3	25.57	b3b13b14	1849.95	89.734	2607	3	617.32	1.58
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	13		TVAEGVTEYMAWLN RDA	293	17	5	23.83	b7b14y7*y7y13	1925.92	98.668	1880	3	642.64	4.56
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	14		RDFVYVGDVAAVNLWFLESGK	208	21	7	37.65	b5b7b9b10°b10y7y11	2385.21	111.370	1558	2	1193.11	-7.37
[P67912]HLDD_SALTY ADP-L-glycero-D-manno-heptose-6-epimerase	15	Oxidation+M(3)	GSMASVAFHLNTQLNNGESPK	178	21	4	31.6	y5y7y14y17	2218.09	105.546	2273	2	1109.55	13.32
[Q8ZLM1]RS13_SALTY 30S ribosomal protein S13	1		ISELSEEQIDTLRDE VAK	44	18	12	77.56	b3°b3b11b15b16y1y14y15 y16*y16y17y18	2075.04	66.095	55709	3	692.35	-6.82
[Q8ZLM1]RS13_SALTY 30S ribosomal protein S13	2		ISELSEEQIDTLR	44	13	5	21.35	b6y9y12*y12y13	1532.79	78.046	11797	2	766.90	6.77
[Q8ZLM1]RS13_SALTY 30S ribosomal protein S13	3		ISELSEEQIDTLRDE VAK	44	18	4	30.03	b8b9y6y12	2075.04	53.073	1636	3	692.35	-6.59
[Q7CQ01]CLPB_SALTY Chaperone protein clpB	1		VFVAEPSVEDTIAILR	335	16	7	36.68	b2b3b5y4y12°y12y13	1758.98	88.214	15521	2	879.99	7.01
[Q7CQ01]CLPB_SALTY Chaperone protein clpB	2		LVGAPPGYVG YEEGGYLTEAVR	645	22	5	13.9	b3b14y2y10y22	2297.14	120.464	11574	3	766.38	-2.66

Q7CQ01 CLPB_SALTY Chaperone protein clpB	3		QYSELEEEWK	453	10	4	29.46	b5y6y7y10	1340.59	78.935	8260	3	447.54	-6.74
Q7CQ01 CLPB_SALTY Chaperone protein clpB	4		LPQVEGTGGDVQPSSSELVR	70	19	5	15.48	b11*b11y7y14y19	1968.02	56.241	6010	2	984.51	9.49
Q7CQ01 CLPB_SALTY Chaperone protein clpB	5		AGLSDPNRPIGSFLFLGPTGVGK	588	23	4	23.57	b3b4b8y23	2300.22	86.905	5319	3	767.41	-7.32
Q7CQ01 CLPB_SALTY Chaperone protein clpB	6		AIQQQIENPLAQQLSGELVPGK	819	23	6	38.65	b2b3b4b5b12y3	2474.33	90.258	5023	3	825.45	-11.15
Q7CQ01 CLPB_SALTY Chaperone protein clpB	7		MLEGEREK	550	8	6	36.94	b3*b3b8y4y7y8	991.48	39.239	4168	2	496.24	-8.93
Q7CQ01 CLPB_SALTY Chaperone protein clpB	8		LEQQALMKESDEASK	423	15	8	86.73	b3b5b7b11b14y9y13y14	1706.84	81.587	3211	2	853.92	8.15
Q7CQ01 CLPB_SALTY Chaperone protein clpB	9	Carbamidomethyl+C(5)	GELHCVGATTLDEYR	305	15	6	38.36	b4b8b9*b9y5y7	1720.78	41.984	1971	2	860.90	-6.60
Q7CQ01 CLPB_SALTY Chaperone protein clpB	10		GDNFISSELFVLAALESR	101	18	4	25.07	b6b7b9*b9	1967.99	121.279	1649	2	984.50	-8.31
Q7CQ01 CLPB_SALTY Chaperone protein clpB	11		QEGNVILFIDELHTMVGAGK	268	20	3	23.02	b4y8y9	2171.13	91.937	45767	3	724.38	7.53
Q7CQ01 CLPB_SALTY Chaperone protein clpB	12		VIGQNEAVEAVSNAIR	569	16	4	17.79	b3y5*y5y12	1669.88	101.221	27086	2	835.44	-6.51
Q7CQ01 CLPB_SALTY Chaperone protein clpB	13		GVLNDLAK	260	8	3	41.71	b3b6b7	829.48	42.056	10228	2	415.24	1.69
Q7CQ01 CLPB_SALTY Chaperone protein clpB	14		AHPDVFNILLQVLDDGR	681	17	3	25.57	b3b6b7	1921.98	94.064	8660	3	641.33	-15.12
Q7CQ01 CLPB_SALTY Chaperone protein clpB	15		IDEVVVFHPLGEQHIASIAQIQLQR	756	25	5	40.84	b3b4b8b9y7	2840.53	70.284	5452	4	710.89	-3.35
Q7CQ01 CLPB_SALTY Chaperone protein clpB	16		GYEIHISDEALK	789	12	4	26.99	b4*b4b5y5	1374.70	88.124	4036	2	687.85	5.42
Q7CQ01 CLPB_SALTY Chaperone protein clpB	17		ASLSGTQTIK	466	10	3	42.47	b3b5b8	1005.54	61.525	2679	2	503.27	-17.42
Q7CQ01 CLPB_SALTY Chaperone protein clpB	18		DAALER	325	6	1	13.9	b4	674.34	38.310	2359	1	674.34	-2.81
Q7CQ01 CLPB_SALTY Chaperone protein clpB	19		YRGEFEER	250	8	5	36.94	b4y4°y4y7°y7	1085.49	59.730	9638	2	543.25	-7.87
Q7CQ01 CLPB_SALTY Chaperone protein clpB	20		VGDLARMSELQYGK	491	14	4	19.96	b4b6y6*y6	1566.79	56.551	8125	3	522.94	-2.26
Q7CQ01 CLPB_SALTY Chaperone protein clpB	21	Carbamidomethyl+C(27)	AGLSDPNRPIGSFLFLGPTGVGKT ELCK	588	28	3	12	b5y7y11	2931.56	114.847	5853	3	977.86	6.25
Q7CQ01 CLPB_SALTY Chaperone protein clpB	22		QLEAATQSEGKTMR	511	14	4	31.73	b9y3y4y7	1549.77	73.293	4841	2	775.39	1.58
Q7CQ01 CLPB_SALTY Chaperone protein clpB	23		GTLTDLKSAGATTANITQAIEQM R	119	25	3	19.01	y3y5y11	2604.37	73.364	3719	3	868.79	0.38
Q7CQ01 CLPB_SALTY Chaperone protein clpB	24		TVDFRNTVVIMTSNLGSDLIQER	705	23	5	27.26	b5b6y8y12°y12	2608.31	96.530	1752	2	1304.66	-12.92
Q7CQ01 CLPB_SALTY Chaperone protein clpB	25		RGDNFISSELFVLAALESR	100	19	7	24.5	b3*b3b6°b6*b6b10y5	2124.13	105.032	1662	3	708.71	8.85
Q7CQ01 CLPB_SALTY Chaperone protein clpB	26	Phosphoryl STY(10)	MKEMVLGVVSQNFRPEFINR	736	20	4	28.72	b3b11_H3PO4 b11y10y11_H3PO4 y11	2474.16	102.029	10740	3	825.39	-13.91
Q7CQ01 CLPB_SALTY Chaperone protein clpB	27	Phosphoryl STY(18)	LVGAPPGYVGYEEGGYLTEAVR	645	22	6	18.94	b13b16°b16y6°y6y13	2377.12	88.209	10684	4	595.04	8.01
Q7CQ01 CLPB_SALTY Chaperone protein clpB	28	Phosphoryl STY(7)	NTVVIMTSNLGSDLIQER	710	18	3	16.15	b6y9y11	2069.96	74.365	9939	4	518.25	-11.20
Q7CQ01 CLPB_SALTY Chaperone protein clpB	29	Phosphoryl STY(12)	VIGQNEAVEAVSNAIRR	569	17	4	28.3	b4b5b10y6	1905.96	59.264	6782	3	635.99	8.26
Q7CQ01 CLPB_SALTY Chaperone protein clpB	30	Phosphoryl STY(8)	QLEAATQSEGK	511	11	6	37.8	b3*b3b4b7_H3PO4 b7y3°y3	1241.52	65.044	2391	3	414.51	-8.16
Q7CQ01 CLPB_SALTY Chaperone protein clpB	31	Oxidation+M(1)	MQIDSKPEELDR	402	12	3	23.01	b3b11y9	1476.69	42.905	271284	3	492.90	-5.54

Q7CQ01 CLPB_SALTY Chaperone protein clpB	32	Oxidation+M(16)	SAGATTANITQAIEQMR	127	17	6	35.22	b3b4°b4b9y4y6	1778.88	34.367	27498	4	445.48	6.59
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	1		EVAETIGYPTPNLAAR	285	16	6	38.26	b7b8y1y8y9*y9	1701.88	60.888	21187	2	851.44	-0.72
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	2		LTNFHNLDP EMLNKPFDPNNDYS VPYIWGATAIGVNSDAIDPK	103	43	4	10.88	b8b21y2y11	4803.33	94.652	12565	4	1201.59	6.00
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	3		TYKDGAYDLVVPSTYYVDK	70	19	4	21.55	b4b11y5y8	2197.07	68.357	6679	2	1099.04	1.44
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	4		TITSWADLWKPEYK	146	14	9	96.56	b6b7y4y6y8°y8y10y11y12	1737.85	82.079	52384	3	579.96	-17.77
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	5		NSLLLTDDAR	160	10	3	29.46	b3y5y6	1117.58	52.488	4148	2	559.30	-0.87
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	6		LGYSGNTTDPK	179	11	6	39.38	b3b8°b8y9°y9y10	1152.56	30.200	3901	2	576.78	8.26
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	7		KLMPNVA AFNSDNPANPYMEGE VNLGMVWNGSAFVAR	200	37	3	10.93	b12b14y13	4010.88	94.503	99902	4	1003.48	-5.11
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	8		VIYSTYESNETMYAKLK	53	17	6	23.83	b11°b11b14y9*y9y11	2040.02	79.111	2677	3	680.68	9.51
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	1		YLSLLPYTDR	63	10	8	62.53	b2b3y1y5y6y8y9y10	1240.66	74.651	46669	2	620.83	-0.79
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	2		NYITESGK	30	8	6	41.71	b1b2y3y4y6y8	911.46	28.068	13518	2	456.23	11.72
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	3		FTAEGVQEIDYK	12	12	5	33.23	b3b10y3°y3y6	1399.65	45.164	1784	2	700.33	-15.52
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	4		DIATLKNYITESGK	24	14	4	25.4	b3b4°b4y12	1552.80	71.339	10636	3	518.27	-12.18
O68926 BFR_SALTY Bacterioferritin	1		LLGNELVAINQYFLHAR	13	17	5	10	b3y2y8*y8y17	1971.06	95.603	10945	3	657.69	-11.70
O68926 BFR_SALTY Bacterioferritin	2		ILFLEGIPNLQDLGK	61	15	8	49.16	b1b2b3b6y3y4y6y8	1669.97	100.473	8583	2	835.49	9.50
O68926 BFR_SALTY Bacterioferritin	3		EAIAYADSVHDYVSR	102	15	3	24.81	b8b9y7	1695.82	48.759	5203	3	565.95	14.83
O68926 BFR_SALTY Bacterioferritin	4		NWGLTR	33	6	1	13.9	y5	746.40	28.149	2179	1	746.40	14.07
O68926 BFR_SALTY Bacterioferritin	5		NWGLTRLNDVEYHESIDEMK	33	20	3	14.89	b3b10y9	2449.12	76.630	6858	3	817.05	-9.77
O68926 BFR_SALTY Bacterioferritin	6		DLREAIYADSVHDYVSR	99	18	3	23.55	b7y5y6	2080.01	82.809	3798	2	1040.51	-2.11
O68926 BFR_SALTY Bacterioferritin	7	Oxidation+M(10)	LGIGEDVEEMLR	76	12	4	23.01	b9°b9y4y8	1376.68	59.722	3887	2	688.85	7.98
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	1		RPPSSDVDAIEAENFESGGALKEIS NPENLMLSEELR	91	37	13	54.18	b6°b6b7b8b9°b9b12b14y1 y10*y11y15*y15	4043.93	95.676	49219	4	1011.74	-5.61
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	2		MSEQLTDQVLVER	0	13	7	35.82	b2b9b10°b10°b10b11y13	1547.79	66.157	10402	3	516.60	7.57
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	3		RPPSSDVDAIEAENFESGGALK	91	22	3	13.9	b4b6y9	2289.10	98.545	2288	3	763.70	-1.81
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	4		EISNPENLMLSEELR	113	15	8	38.36	b3°b3b9y5y6°y6y10°y10	1773.87	114.032	1962	2	887.44	3.17
P0A2F0 RPOE_SALTY RNA polymerase sigma-E factor	5		ALDSFRGDSAFYTWLYR	59	17	4	25.57	b6°b6b7b11	2067.99	83.350	2441	3	690.00	-2.95

[P0A2F0]RPOE_SALTY RNA polymerase sigma-E factor	6	Phosphoryl STY(14)	YVPSGDVPDVVQESFIK	39	17	4	28.3	b5b12b13_H3PO4 b13y9	1958.91	84.005	2512	3	653.64	4.42
[P0A2F0]RPOE_SALTY RNA polymerase sigma-E factor	7	Carbamidomethyl+C(16) ;Oxidation+M(14)	ELDGLSYEEIAAIMDCPVGTVR	149	22	5	13.9	b3°b3b5°b5y12	2454.17	66.359	59066	4	614.30	7.86
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	1		LKDGVGLLPTSLDIVENPK	156	19	10	48.36	b4b5y1y2y4y5y7°y7y11y19	2008.12	79.013	43257	3	670.04	-8.15
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	2		SLLLLQK	144	7	4	21.79	b3°b3y5y7	814.53	63.127	16399	2	407.77	-11.54
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	3		FVQAYQSDEVYEAANK	245	16	8	43.89	b7y2y6*y6y10y11y12y16	1861.86	50.829	14969	2	931.43	0.72
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	4		DGIFVEDKDSPYVNLIVTREDNK	215	23	3	19.89	b4b8b12	2666.29	92.280	12652	3	889.44	-14.47
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	5		VGIVVGAEQQVAEVAQK	34	17	4	16.91	b2b3b13y12	1724.95	67.366	5917	2	862.98	-4.53
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	6		DGIFVEDKDSPYVNLIVTREDNKD AENVK	215	29	4	15.1	b10b13y6y11	3322.61	89.106	1592	3	1108.21	-8.82
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	7	Carbamidomethyl+C(17)	TFAAVGALIGSLALAGCGQDEK	6	22	3	13.9	b4b12y3	2149.06	42.027	30943	4	538.02	-18.52
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	8		DGSQVAVPNDPTNLGR	128	16	6	36.01	b12b14y7*y7y10y12	1639.80	80.083	13067	2	820.40	-3.13
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	9		DPNHIK	28	6	2	27.43	b3b4	723.37	69.335	5965	1	723.37	-11.39
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	10		DGVGLLPTSLDIVENPK	158	17	5	30.82	b6b14y10y11°y11	1766.95	85.082	3340	2	883.98	-1.04
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	11		DSPYVNLIVTREDNK	223	15	4	30.4	b4y3y4y14	1762.91	91.930	100259	2	881.96	7.48
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	12		SLDELKDGSQVAVPNDPTNLGR	122	22	7	36.4	b4b5b9b13y6y9*y9	2325.19	57.745	5109	2	1163.10	9.66
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	13	Phosphoryl STY(10)	LKDGVGLLPTSLDIVENPK	156	19	3	22.44	y7y9y11	2088.11	84.391	266660	3	696.71	10.76
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	14	Carbamidomethyl+C(17) ;Phosphoryl STY(11)	TFAAVGALIGSLALAGCGQDEKD PNHIK	6	28	4	17.93	b12y12_H3PO4 y12y14_H3PO4 y14y16	2933.41	52.556	164409	5	587.49	-0.58
[Q8ZRN1]METQ_SALTY D-methionine-binding lipoprotein metQ	15	Phosphoryl STY(10)	DGIFVEDKDSPYVNLIVTREDNKD AENVK	215	29	5	31.2	b8b9y4y8y12	3402.64	98.695	18424	4	851.42	12.27
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	1		WENLPPEQPER	80	12	8	26.99	b10y1y6*y6y7°y7*y7y12	1481.69	63.019	58142	3	494.57	-5.19
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	2		ITTSHYDVGGAIDNHHGHLPK	37	22	10	31.74	b5°b5b7b9°b9b11y1y2y9°y 9	2342.16	50.916	27643	4	586.29	-13.86
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	3	Carbamidomethyl+C(9)	LYQGLEAFCPLR	112	12	7	52.5	b3b7b9y2y8y9y12	1466.76	77.412	9412	2	733.88	8.16
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	4		YSLDANDAATAIEQAINR	310	18	6	16.15	b2°b2b12y5y11y18	1935.96	83.969	8719	2	968.48	9.46

[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	5		NIANPIAQLSLALLR	293	17	11	75.72	b1b2b3b4b5b6b8y5y7y8y17	1833.15	137.361	8396	2	917.08	7.72
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	6		GAAAVSTDEMGDIIAR	341	16	3	25.49	b3b9b15	1576.78	71.669	4019	2	788.89	8.83
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	7	Carbamidomethyl+C(12)	ADIAANGFDILCVR	124	14	6	27.74	b2°b2y9y12*y12y13	1534.75	88.220	3574	2	767.88	-11.45
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	8	Carbamidomethyl+C(12)	ADIAANGFDILCVRELTTGGIYFGQPK	124	26	3	22.27	b13b14y13	2825.40	81.988	2289	2	1413.20	-9.42
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	9		EIVNDVAK	206	8	5	33.93	b4y5°y5y6*y6	887.48	32.531	8898	2	444.24	-3.37
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	10		NYHIAVLPGDGIGPEVMAQALK	3	22	5	38.79	b13b14y9y13y14	2293.17	85.117	6914	3	765.06	-13.95
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	11		ELTGGIYFGQPK	138	12	4	23.01	b4b6°b6y11	1309.68	46.537	2625	2	655.34	-1.96
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	12		TGDLAR	335	6	1	13.9	b5	632.33	29.851	2616	1	632.33	-2.80
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	13		EGSGQYЕК	152	8	6	33.93	b4y4°y4y5°y5*y5	897.41	59.131	1863	2	449.21	19.59
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	14		ALEEGVR	328	7	6	38.33	b4°b4b5°b5y4°y4	773.42	37.856	1855	2	387.22	11.60
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	15	Carbamidomethyl+C(6)	ATVEGCEQADAILFGSVGGPK	59	21	4	24.02	b3°b3b4b15	2106.00	82.831	1744	2	1053.50	-8.81
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	16		EIVNDVAKTYPDVELAHMYIDNATMQLIK	206	29	3	22.99	b12b13b23	3334.68	84.200	21915	5	667.74	4.54
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	17		EGSGQYЕКAFDTEVYHR	152	17	3	23.9	b11y4y5	2015.91	71.943	13402	2	1008.46	-0.61
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	18		GAAAVSTDEMGDIIARYVAEGV	341	22	6	25	b3b6°b6b7°b7y5	2195.07	60.998	3437	3	732.36	1.00
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	19		AFDTEVYHRFEIER	160	14	4	19.96	b4°b4y3y7	1811.86	71.190	3378	2	906.43	-5.66
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	20	Carbamidomethyl+C(6)	ATVEGCEQADAILFGSVGGPKWENLPPESQPER	59	33	3	22.36	b10y4y5	3568.75	116.345	3137	4	892.94	12.86
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	21		ALEEGVRTGDLAR	328	13	4	42.36	b3b4b8b12	1386.74	64.419	2668	3	462.92	2.90
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	22		FDMRITTSHYDVGGIAIDNHGHLPK	33	26	3	23.16	b4b5b7	2891.41	100.813	2584	3	964.48	-4.81
[P37412]LEU3_SALTY 3-isopropylmalate dehydrogenase	23	Oxidation+M(10)	GAAAVSTDEMGDIIAR	341	16	3	26.16	y3y7y8	1592.74	51.917	3810	2	796.88	-8.97
[P0A9Z4]GLNB_SALTY Nitrogen regulatory protein P-II 1	1		IFVFDVAR	90	8	9	68.77	b2y1y3y4y5y6°y6y7y8	966.53	74.631	18963	2	483.77	-9.85
[P0A9Z4]GLNB_SALTY Nitrogen regulatory protein P-II 1	2		LDDVREALAEVGITGMTVTEVK	12	22	4	23.77	b7b10b11y1	2346.25	136.479	1698	3	782.75	10.20
[P0A9Z4]GLNB_SALTY Nitrogen regulatory protein P-II 1	3		GAEYMVDFLPK	47	11	5	42.39	b5°b5b6y6y7	1269.62	79.119	12281	2	635.31	-1.06
[P0A9Z4]GLNB_SALTY Nitrogen regulatory protein P-II 1	4		EALAEVGITGMTVTEVK	17	17	5	33.97	b4b10b14y7y11	1747.91	121.882	11338	3	583.31	-3.21
[P0A9Z4]GLNB_SALTY Nitrogen regulatory protein P-II 1	5		GHTELYRGAEYMVDFLPK	40	18	6	33.45	b5b6°b6b10°b10b13	2126.06	94.049	7789	3	709.36	10.68
[P40720]FUMA_SALTY Fumarate hydratase class I	1	Carbamidomethyl+C(5); Carbamidomethyl+C(13)	HGASCPVGMGVSCSADR	305	17	9	44.11	b3b5b7y6y8°y8y10°y10y17	1747.73	35.895	12553	3	583.25	-1.26
[P40720]FUMA_SALTY Fumarate hydratase class I	2		VWTGGGDEAALAR	120	13	4	28.83	b1y6y11y12	1302.65	47.792	10605	2	651.83	4.40
[P40720]FUMA_SALTY Fumarate hydratase class I	3		TYLYQETK	192	8	7	50.47	b1b5y2y5y6y7y8	1045.52	38.745	9869	2	523.26	2.34
[P40720]FUMA_SALTY Fumarate hydratase class I	4		TPEGYASGSLGPTTAGR	426	17	5	25.57	b2y3y4y10y17	1621.79	42.836	9201	2	811.40	2.41
[P40720]FUMA_SALTY Fumarate hydratase class I	5		QAFHDASFMLRPAHQQQVADILR	52	23	4	27.26	b7b16y10y11	2679.37	78.948	4272	3	893.80	5.38

P40720 FUMA_SALTY Fumarate hydratase class I	6	Carbamidomethyl+C(3)	LECVEYPELGMEAIWK	499	16	6	36.68	b4°b4b5b9y4y9	1966.95	111.485	2921	3	656.32	9.31
P40720 FUMA_SALTY Fumarate hydratase class I	7		NYLVDK	209	6	2	13.9	b5°b5	751.41	26.697	5846	2	376.21	9.02
P40720 FUMA_SALTY Fumarate hydratase class I	8	Carbamidomethyl+C(8)	SQQVTDACK	466	9	4	31.3	b3*b3b7y6	1036.48	66.079	5777	1	1036.48	4.59
P40720 FUMA_SALTY Fumarate hydratase class I	9		DIAHAK	393	6	1	13.9	b3	654.35	75.087	5638	1	654.35	-4.48
P40720 FUMA_SALTY Fumarate hydratase class I	10		YSQNAALDMYK	145	11	3	25.06	b10y4y7	1303.59	22.763	5537	3	435.20	-7.49
P40720 FUMA_SALTY Fumarate hydratase class I	11		SNKPFFYQDPFPLK	1	14	3	19.96	b4b9y9	1727.85	84.401	5400	2	864.43	-16.04
P40720 FUMA_SALTY Fumarate hydratase class I	12		EVNTGTNLPAQIDLYSVDGDEYK	156	23	3	13.48	b5b8y8	2541.17	86.782	3983	3	847.73	-10.28
P40720 FUMA_SALTY Fumarate hydratase class I	13		GGNMIR	554	6	1	13.9	y5	647.32	28.909	2666	1	647.32	-10.09
P40720 FUMA_SALTY Fumarate hydratase class I	14		HGGFYLGSIGGPAAVLAQGSIK	476	22	3	20.41	b6b13b16	2100.09	97.604	2646	2	1050.55	-18.02
P40720 FUMA_SALTY Fumarate hydratase class I	15		VWTGGGDEAALARGVYNTYIED NLR	120	25	5	12.79	b23y5°y5*y5y7	2740.32	93.590	83995	3	914.11	-3.65
P40720 FUMA_SALTY Fumarate hydratase class I	16		GGNMIRYFAGER	554	12	6	49.48	b10b11°b11y3y4y7	1370.68	66.913	28101	3	457.57	14.69
P40720 FUMA_SALTY Fumarate hydratase class I	17		DHPIYYAGPAKTPEGYASGSLGPT TAGR	415	28	3	12	b5y12y25	2834.39	91.959	25058	3	945.47	6.98
P40720 FUMA_SALTY Fumarate hydratase class I	18	Carbamidomethyl+C(4)	RLECVEYPELGMEAIWK	498	17	4	28.3	b3b4b9y11	2123.05	76.877	20382	3	708.36	10.92
P40720 FUMA_SALTY Fumarate hydratase class I	19		QAFHDASFMLRPAHQQQVADILR DPQASENDK	52	32	4	11.33	b11*b11y11y14	3663.77	92.991	12974	4	916.70	-0.67
P40720 FUMA_SALTY Fumarate hydratase class I	20		GQRVWTTGGGDEAALAR	117	16	4	24.32	b9°b9b10y12	1643.80	66.873	4560	2	822.40	-13.66
P40720 FUMA_SALTY Fumarate hydratase class I	21		NYLVDKMR	209	8	3	41.71	b5b6b7	1038.53	46.520	2964	2	519.77	-13.40
P40720 FUMA_SALTY Fumarate hydratase class I	22	Phosphoryl STY(5)	HGGFYLGSIGGPAAVLAQGSIK	476	22	4	40.93	b3b4b11_HPO3 b11b12_HPO3 b12	2180.10	78.937	6146	3	727.37	10.41
P40720 FUMA_SALTY Fumarate hydratase class I	23	Oxidation+M(9)	QAFHDASFMLRPAHQQQVADILR	52	23	3	13.48	b4y11y13	2695.35	89.206	28439	3	899.12	0.54
P40720 FUMA_SALTY Fumarate hydratase class I	24	Oxidation+M(1)	MSNKPFFYQDPFPLK	0	15	4	38.85	b6b7b8y9	1874.91	69.786	3313	2	937.96	-1.24
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	1	Carbamidomethyl+C(18) ;Carbamidomethyl+C(32))	ANVSQVMHIIGDVAGRDCVLVDD MIDTGGTLCK	198	33	8	25.34	b2b4b5b20b24y2y8y33	3559.68	104.948	35753	4	890.68	-5.21
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	2		LYTSLGDAAVGR	22	12	4	30.21	y5y6y10y12	1222.64	52.224	21941	2	611.82	-5.59
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	3		ITAVIPYFGYAR	84	12	3	23.01	b4y5y7	1370.74	80.399	18459	2	685.88	-1.78
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	4		LFAGNATPELAQR	5	13	5	28.83	b1y6y10y11y13	1387.74	53.706	17694	2	694.37	2.29
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	5	Carbamidomethyl+C(10)	NSVIDEVVVCDTIPTLDEIK	262	20	7	23.44	b2b15y1y5y7y10y20	2259.17	88.150	14095	2	1130.09	9.94
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	6		VFAYATHPIFSGNAANNLR	243	19	6	35.07	b1y10°y10*y10y11y12	2063.03	64.837	12675	3	688.35	-7.81
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	7		FSDGEVSVQINENVR	34	15	4	32.78	b10b11y4y12	1692.82	86.772	1650	2	846.91	2.02
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	8		AAEALK	231	6	1	13.9	b4	602.34	31.032	17812	1	602.34	-13.38
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	9		ANVSQVMHIIGDVAGR	198	16	3	25.49	y5y7y10	1666.83	78.710	9164	3	556.28	-21.09

P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	10	Carbamidomethyl+C(2); Carbamidomethyl+C(16)	DCVLVDDMIDTGGTLCK	214	17	4	16.91	b4°b4b11y9	1911.89	76.448	3392	2	956.45	19.28
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	11		LLNDTDMAIIDK	182	12	4	33.23	b4b6y3y9	1361.70	97.542	2457	2	681.35	3.05
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	12		RVFAYATHPIFSGNAANNLR	242	20	3	23.02	b7y11y12	2219.12	73.370	17071	4	555.54	-11.77
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	13		ITAVIPYFGYARQDR	84	15	5	26.87	y4°y4*y4y6y10	1769.95	84.327	16061	2	885.48	10.62
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	14		PDMKLFAGNATPELAQR	1	17	4	16.91	b9y7*y7y12	1858.95	83.453	10096	2	929.98	-0.53
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	15	Carbamidomethyl+C(18);Carbamidomethyl+C(32)	ANVSQVMHIIGDVAGRDCVLVDD MIDTGGTLCK	198	33	4	23.65	y3y5y9y12	3559.68	89.669	3287	4	890.68	-5.28
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	16		AIALLNDTDMAIIDK	178	16	3	26.16	b3b4b11	1744.93	74.584	1722	2	872.97	-10.56
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	17	Oxidation+M(7)	ANVSQVMHIIGDVAGR	198	16	3	25.49	b5b10b14	1682.84	62.271	2096	3	561.62	-12.91
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	18	Carbamidomethyl+C(11);Oxidation+M()	GGDIFIQSTCAPTNDNLMELVVM VDALLR	49	30	4	17.53	b6b9*b9b11	3364.72	102.774	1941	3	1122.24	14.44
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1	Carbamidomethyl+C(3)	FACGVIEK	169	8	9	55.24	b2y1y2°y2y3y5y6y7y8	923.45	40.576	126432	2	462.23	-13.48
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2		EVPALMAGGHLDPEK	84	15	9	30.4	b2b11y2y3y8°y8y9°y13y15	1563.77	57.028	40140	3	521.93	-10.77
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3	Carbamidomethyl+C(49)	MNDALSSGTGENIGEITVSETPYG LLFTPHLNLTPGIHGFHVHTNPS CMPGMK	27	54	5	11.55	b5°b5b16y5y10	5733.69	91.937	32125	6	956.45	-6.47
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	4		GGDNYSDKPAPLGGGGAR	151	18	21	197.84	b4*b4b5*b5b7b8*b8b9b10°b10*b10y3y4y5y6y7y8y9y10y11y12	1688.77	32.952	124321	3	563.59	-18.29
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	5		HLGPYNDKGHLGDLPLVVNAD GTATYPLLAPR	102	33	19	138.03	b3b6b8b10°b10b11b13°b13b17b18b19b22b23y3y4y5y6y8y12	3441.77	80.555	186596	4	861.20	-5.75
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	6		EVPALMAGGHLDPEKTGK	84	18	6	42.31	b3b10y8y12y13y16	1849.93	52.352	23387	3	617.31	-11.09
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	7		DGKEVPALMAGGHLDPEK	81	18	4	22.62	b7b13y4y11	1863.92	67.467	18868	2	932.46	-5.37
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	8		PALMAGGHLDPEK	86	13	1	7.3	b3	1335.68	57.048	8543	2	668.34	2.65
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	9		EVPALMAGGHLDPEK	84	15	1	7.3	y13	1545.75	57.023	8355	3	515.92	-9.87
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	1	Carbamidomethyl+C(5)	VNAICPGYVR	179	10	6	56	y2y5y6y8y9y10	1148.59	44.768	9257	2	574.80	4.14
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	2		LGNFLDMSEEDRDFHIDINIK	94	21	5	25.5	b8°b8b9b13y9	2521.21	101.373	7607	4	631.06	3.29
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	3		DFHIDINIK	106	9	4	46.59	b5b6b8y4	1114.59	75.122	18675	2	557.80	3.50
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	4		DFASVQAAVAR	64	11	3	25.06	b6b8y3	1134.57	107.333	1723	1	1134.57	-15.06
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	5	Carbamidomethyl+C(5)	VNAICPGYVRTPMAESIR	179	19	6	44.03	b9b10b14y5y7y8	2105.05	75.898	6362	3	702.35	-8.35
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	6	Carbamidomethyl+C(17)	SLAVEYAQSGIRVNAICPGYVR	167	22	3	22.65	b15y6y7	2423.23	97.642	5941	3	808.41	-8.16
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	7		ADVRDFASVQAAVAR	60	15	4	26.87	b5b9b10°b10	1575.83	86.968	4968	2	788.42	1.47
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	8		LADELGGRGHR	44	11	4	25.06	b6b8°b8y9	1180.62	70.626	4618	2	590.81	-0.41
P0A2D1 UCPA_SALTY Oxidoreductase ucpA	9		LGNFLDMSEEDRDFHIDINIK	94	21	4	21.01	b3*b3b6b20	2521.18	68.778	1570	3	841.07	-7.75

P63601 AROK_SALTY Shikimate kinase 1	1		VVANQIIHMLESN	160	13	6	35.09	b11y2y5y8y10y13	1467.76	83.984	18155	2	734.38	-0.75
P63601 AROK_SALTY Shikimate kinase 1	2		QGIVLATGGGSVK	73	13	6	46.85	b3y5y7y8y10y13	1186.68	46.984	7877	2	593.84	-2.47
P63601 AROK_SALTY Shikimate kinase 1	3		NPLYEEIADVTIR	140	13	3	21.35	b9b11y9	1532.80	74.632	3955	2	766.90	1.11
P63601 AROK_SALTY Shikimate kinase 1	4		NIFLVGPMGAGK	5	12	3	23.01	b10y8y10	1203.65	74.918	9996	2	602.33	-5.07
P63601 AROK_SALTY Shikimate kinase 1	5		TGADVGVWVDFVEGEDGFR	42	18	3	16.15	b14y6y10	1955.91	72.247	2195	2	978.46	17.60
P63601 AROK_SALTY Shikimate kinase 1	6		TGADVGWVDFVEGEDGFRNR	42	20	3	21.68	b3b8b13	2226.04	106.822	2045	3	742.68	7.46
P63601 AROK_SALTY Shikimate kinase 1	7	Oxidation+M(8)	QLAQQLNMEFYDSDQEIEKR	22	20	4	14.89	b9*b9y7y10	2501.17	105.468	4701	3	834.40	3.81
P63601 AROK_SALTY Shikimate kinase 1	8		ATGGGSVK	78	8	2	7.51	b3*b3	676.36	46.999	6898	1	676.36	1.99
P58627 YCEF_SALTY Maf-like protein yceF	1		ASGNIVTFYTGLALYNSASGHLQTEVEPFDVHFR	94	34	12	35.67	b3b5b8*b8*b8b10*b10y1y6y11y13y16	3740.78	95.733	13856	4	935.95	-13.97
P58627 YCEF_SALTY Maf-like protein yceF	2	Carbamidomethyl+C(7)	LTIPFECAAPDVDETPMPGEAPR	19	23	4	13.48	b1b9y6y21	2513.17	73.312	13384	4	629.05	-1.07
P58627 YCEF_SALTY Maf-like protein yceF	3	Carbamidomethyl+C(6)	EHPLHCAGSFK	141	11	3	28.07	b3b4y7	1282.59	27.478	1505	3	428.20	-8.57
P58627 YCEF_SALTY Maf-like protein yceF	4		QLVLR	42	5	2	27.05	b3b4	628.41	70.604	11158	1	628.41	-11.07
P58627 YCEF_SALTY Maf-like protein yceF	5		AQSLAAR	52	7	7	38.33	b3*b3b4*b4*b4y6*y6	716.39	36.363	10842	1	716.39	-16.87
P58627 YCEF_SALTY Maf-like protein yceF	6		QQLAK	89	5	1	13.53	b4	587.34	51.634	5304	1	587.34	-14.55
P58627 YCEF_SALTY Maf-like protein yceF	7	Carbamidomethyl+C(14)	DPNTLIGLPLIALCQMLRR	167	19	6	37.14	b5*b5b6b7*b7y8	2194.20	105.114	2306	4	549.31	-9.68
P58627 YCEF_SALTY Maf-like protein yceF	8		PMPGEAPR	34	8	0	6.79		854.41	73.348	1591	1	854.41	-6.29
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	1		ALTEETGTTIEEDDGTVK	577	19	6	21.55	b7b14y1y3y7y19	2022.01	69.757	15312	2	1011.51	14.37
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	2		VTDYLMGQEVVPK	661	14	4	25.4	b10b11y1y3	1606.82	63.880	12565	2	803.92	5.09
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	3		SETIEQLIAEDETLDANELGEILHAI EK	274	28	7	15.51	b2b4b7*b7y3y5y28	3123.56	125.747	6568	3	1041.86	1.49
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	4		QATAAVMVSMDDTAVFVTVVGQ KK	25	24	4	12.38	b3*b3*b4b10	2496.29	97.215	6006	2	1248.65	0.98
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	5		TDSFLFHYNFPPYSVGETGMVGSP K	372	25	6	22.33	b11*b11b12*b12y1y7	2777.32	136.546	4754	2	1389.16	9.49
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	6	Carbamidomethyl+C(18)	VVSEITESNGSSSMASVCGASLAL MDAGVPIK	426	32	4	11.33	b1b4b11y3	3167.52	87.700	4177	3	1056.51	-1.70
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	7		VGYINDQYVLNPTQDELK	153	18	4	16.15	b6b11y2y7	2109.05	70.315	2179	2	1055.03	-1.39
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	8		IAATDGEK	596	8	3	33.93	b5y4y5	804.43	37.843	13387	2	402.72	20.64
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	9		IEEITAEIEVGR	611	12	4	23.01	b4b10y11*y11	1358.75	68.233	9465	2	679.88	21.65

Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	10		FQYGQHTVTLETGMMAR	8	17	5	27.05	b7*b7b10b16y10	1969.96	79.590	6288	2	985.49	18.90
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	11		GVLAVMPPMDK	409	11	3	36.82	y4y8y10	1175.56	61.499	4936	2	588.28	-19.00
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	12		AKPGQDFFPLTVNYQER	49	17	5	28.3	b11*b11y3y4y10	2010.00	89.651	3132	4	503.25	-6.38
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	13		GDISEFAPR	545	9	6	46.59	b3b4°b4b7°b7y5	991.46	97.138	3071	1	991.46	-21.30
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	14		YAQVDVIK	266	8	4	49.22	b4b5y6y7	935.51	55.793	3060	2	468.26	-9.66
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	15		QATAAVMVSMDDTAVFVTVVGQ K	25	23	4	37.68	b4b5b6b13	2368.23	75.810	2327	2	1184.62	18.45
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	16		WDWQPEAVNDALNAR	230	15	6	44.38	b5b6y10y12y13*y13	1784.87	72.313	2227	2	892.94	18.81
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	17		EGDNYVVLSDILGDEHLGDMDF K	470	24	3	13.11	b4y6y13	2696.23	94.452	1523	2	1348.62	10.87
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	18		IEGITKEIMQVALNQAK	510	17	7	35.22	b5b11y4y5*y5y9*y9	1886.05	103.651	19138	2	943.53	4.98
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	19		THGSALFTRGETQALVTATLGTA R	336	24	3	13.11	b3b9y14	2459.31	77.785	17789	4	615.58	5.26
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	20		GGSVIRALTEETGTTIEIEDDGTVK	571	25	3	12.79	b21y7y10	2591.33	85.114	8579	2	1296.17	7.82
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	21		GVLAVMPPMDKFPYTVR	409	17	5	23.83	b3b9y6y11°y11	1938.97	82.013	4023	3	646.99	-6.42
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	22		EGDNYVVLSDILGDEHLGDMDF KVAGSR	470	29	3	22.22	b5y12y13	3166.50	94.481	1899	4	792.38	11.03
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	23	Phosphoryl STY(9)	ALTEETGTTIEIEDDGTVK	577	19	3	23.26	b8y8y9	2101.96	75.219	6078	3	701.32	11.85
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	24	Oxidation+M(10)	QATAAVMVSMDDTAVFVTVVGQ K	25	23	4	13.48	b7°b7b10y14	2384.16	98.191	4304	3	795.39	-10.96
Q8ZLT3 PNP_SALTY Polyribonucleotide nucleotidyltransferase	25	Oxidation+M(7)	QATAAVMVSMDDTAVFVTVVGQ KK	25	24	6	19.42	b5°b5b8°b8°b8b15	2512.27	101.936	2273	3	838.09	-5.05
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	1	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLASGAK	257	25	16	87.38	b2b3b4°b4b6b25y1y4y7y8 y14y19y20y21y23y25	2684.44	127.531	52225	3	895.49	-1.18
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	2		AFPGLNGMDLAKEVTTAETYR	148	21	7	28.17	b10°b10b11y4°y4y7y21	2284.16	80.518	40603	3	762.06	12.08
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	3		TDKPAFSFQGHPEASPGPHDAAPL FDHFIELIEQYR	342	36	9	65.99	b4b5b9b10y1y3y4y5y36	4064.92	105.974	25521	5	813.79	-9.67
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	4		DLPLIASNFR	83	10	4	29.46	b3y5y6y10	1145.62	75.827	15906	2	573.31	-8.31
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	5		SEDDLPPFHVVAYDFGAK	185	17	7	10	b1b2b11°b11y1y9y17	1909.88	81.437	7989	3	637.30	-6.90

P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	6	Carbamidomethyl+C(18)	MNPDGIFLSNGPGDPAPCDYAITA IQK	230	27	4	12.23	b2b4y11y13	2862.37	82.959	2585	2	1431.69	8.87
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	7		QIVTLTYPHIGNVGTNK	50	17	4	30.82	b3b4y8y10	1854.97	52.782	51938	3	618.99	-19.94
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	8		SALLVLEDGTQFHGR	3	15	4	18.79	b3y5y10*y10	1642.83	66.802	9597	3	548.28	-16.42
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	9		SLFDGTLQGIHR	330	12	5	38.3	b11*b11y4y6y10	1343.68	64.446	5740	3	448.57	-17.53
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	10		EVTTAETYR	160	9	5	31.3	b5*b5b7*b7y4	1069.52	70.601	5265	2	535.27	6.85
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	11		NVVMITAQNHGFAVDEDSL PANL R	302	24	3	22.41	b12b13y5	2611.24	101.208	3064	4	653.57	-20.38
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	12		FGHHGGNHPVK	287	11	5	37.8	b4y5*y5y6y8	1186.57	80.490	2314	1	1186.57	-16.25
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	13		DGLPEAK	178	7	3	41.34	b6y3y5	729.37	44.463	1880	1	729.37	-16.90
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	14		MKFGHHGGNHPVK	285	13	3	21.35	b5y5y11	1445.73	57.721	490009	3	482.58	4.05
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	15		AFPGLNGMDLAKEVTTAETYR	148	21	3	22.82	b7y6y7	2284.13	83.314	11701	2	1142.57	0.75
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	16		RHNIVAIADIDTR	103	13	3	21.35	b3b9y7	1493.82	98.610	4789	3	498.61	0.00
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	17		DGLPEAKSEDDLPHFVVAYDFGA K	178	24	5	24.63	b6b10b13y6y17	2620.22	69.772	3200	4	655.81	-12.21
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	18		AKAFPLNGMDLAK	146	14	4	28.56	b10b12y4y7	1432.78	59.618	3013	2	716.89	13.21
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain	19	Carbamidomethyl+C(6)	GAQNGCIIAGDSPDAKLALEK	125	21	5	32.3	b7b8b12b15y13	2128.06	97.536	1832	2	1064.53	-6.65
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	1		GGTPYGATTIAGGDGSR	155	17	5	34.62	y5y6y8y12y17	1537.73	34.012	31924	3	513.25	5.95
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	2		LGSVFSSTGTGGGQEQTITSTWTT LAHHGMVIVPIGYAAQELFDVSQ VR	106	49	13	78.23	b9y1y2y3y4y5y6y7y8y10y12*y12y49	5134.59	116.100	29333	4	1284.40	5.71
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	3		TQNAPVATPQELADYDAIIFGTPT R	54	25	7	34.73	b3b11b14y4y6y7y25	2689.35	89.925	17473	3	897.12	1.82
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	4		FGNMSGQMR	79	9	4	46.86	y3y5y7y9	1027.44	37.767	11861	2	514.22	-5.35
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	5		YQGEYVAGLAVK	183	12	4	35.29	b4b7b8y10	1297.67	55.319	4645	2	649.34	-9.88
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	6		TFLDQTGGLWASGSLYGK	88	18	5	45.52	b4b6b7b9b14	1900.95	66.198	3377	2	950.98	3.72
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	7		ILVLYYSMYGHETMAHAVAEGA K	3	24	4	24.14	b11y8y9y17	2667.35	89.143	2940	3	889.79	7.05
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	8		MAKILVLYYSMYGHETMAHAVA EGAK	0	27	3	12.23	b13y5y14	2997.50	85.408	6023	3	999.84	-2.20
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	9		LGSVFSSTGTGGGQEQTITSTWTT LA	106	26	1	13.69	y15	2587.25	116.095	3544	3	863.09	-1.32
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	10		TQNAPVATPQELADYDAI	54	18	1	8.06	y9	1916.92	89.964	3467	3	639.64	-4.20
Q7CPB2 YJBJ_SALTY UPF0337 protein yjbJ	1		LTDDDMTVIEGKR	24	13	3	26.12	b3b4y11	1492.72	76.061	15319	2	746.86	-9.40
Q7CPB2 YJBJ_SALTY UPF0337 protein yjbJ	2		DQAEKEVVDWETR	52	13	3	28.83	y3y4y8	1604.77	73.631	8337	2	802.89	10.12
Q7CPB2 YJBJ_SALTY UPF0337 protein yjbJ	3		YGYQKDQAEK	47	10	6	42.19	b1b3b6y5y6y10	1229.59	30.679	5621	2	615.30	8.64
Q7CPB2 YJBJ_SALTY UPF0337 protein yjbJ	4		MNKDEAGGNWK	1	11	3	32.05	y5y7y8	1249.55	25.885	2038	3	417.19	-8.60
Q7CPB2 YJBJ_SALTY UPF0337 protein yjbJ	5		DQAEKEVVDWETR	52	13	3	26.12	b8b9y8	1604.77	51.278	6775	2	802.89	6.31

[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	1		TEDIDLINEINKETILQQPEAR	218	22	6	21.64	b4b9°b9b11*b11y10	2582.29	69.747	8783	3	861.44	-14.37
[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	2		TEDIDLINEINK	218	12	6	26.99	b9°b9*b9b10*b10y8	1416.74	61.510	5289	2	708.87	12.06
[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	3		LFEGTPSQMYQSLMK	136	15	3	21.28	y11*y11y12	1759.83	96.113	3623	2	880.42	-5.34
[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	4		WMPEAIFLTHHHHDHVGGVK	43	20	4	14.89	b1b9y11y13	2348.14	75.951	3529	3	783.38	-4.57
[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	5		MNLNSIPAFQDNYIWVLTNDEGR	0	23	3	13.48	b6y3y5	2710.25	92.779	1803	4	678.32	-14.86
[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	6		NLNSIPAFQDNYIWVLTNDEGR	1	22	6	37.77	b3b4b21y4y7y10	2579.30	116.100	5387	2	1290.15	17.32
[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	7		ELLQHFPQMTVYGPAETQDKGAT HLVGDGDTIR	63	33	4	16.05	b10y6y10y27	3624.83	97.122	12503	3	1208.95	14.75
[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	8		AIAEHKWMPEAIFLTHHHHDHVG GVK	37	26	3	12.49	b7b18y10	2997.49	88.783	11126	3	999.84	-4.48
[Q8ZRM2 GLO2_SALTY Hydroxyacylglutathione hydrolase	9	Oxidation+M(1)	MNLNSIPAFQDNYIWVLTNDEGR	0	23	8	30.52	b9*b9y3y7*y7y9°y9y11	2726.27	98.140	3698	4	682.32	-6.81
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	1	Carbamidomethyl+C(9)	NTLLHEQWCDLLEANSVDAVK	860	21	6	21.01	b1y1y4y7y13*y13	2455.19	88.211	19496	3	819.07	-0.89
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	2		IALASPD MIR	21	10	5	69.52	y5y6y7y8y9	1086.59	60.836	11057	2	543.80	-8.54
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	3		YIVNEVQDVYR	1231	11	5	37.8	b5°b5y4y5y8	1397.71	59.662	7070	2	699.36	0.09
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	4		AAAESSIQVK	943	10	6	29.46	b2b3b4y2y6y10	1003.55	38.775	5811	2	502.28	10.52
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	5		MLQEAVDALLDNRR	297	15	5	18.79	b2b3b12y5*y5	1700.85	76.026	5416	3	567.62	-14.07
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	6		HEIIEAEAEVAEIQEQFSGLVTA GER	650	28	6	25.84	b3b6b10b14y12*y12	3070.52	106.528	3567	3	1024.18	7.71
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	7	Carbamidomethyl+C(36)	ALMMSTNNILSPANGEPHIPSQD VVLGLYYMTRDCVNAK	481	40	3	38.6	b4b5b6	4395.17	107.713	3541	5	879.84	-4.00
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	8		LVITPVDGSDPYEEMIPK	1174	18	3	16.15	b3b14y13	2003.00	73.082	3203	3	668.34	-1.10
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	9		ASLATESFISAASFQETTR	1311	19	7	32.79	b4°b4b13b14y8°y8y13	2017.00	81.952	2855	4	505.01	8.29
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	10		LIPAGTGYAYHQDR	1355	14	3	28.54	y3y8y10	1561.78	42.201	2014	2	781.39	3.20
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	11		SGASVGIDDMVIEK	634	15	3	24.81	b4b5y9	1517.78	46.537	52027	2	759.39	19.14
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	12		GLMAKPDGSIHETPITANFR	744	20	10	40.33	b4b7°b7b8y4*y4y10°y10*y 10y17	2131.12	95.676	38288	3	711.04	-0.69
[P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	13		AAGEQPATPQVTAEDASASLAELL NAGLGGSDNE	1373	34	6	22.78	b6b12b15y9y11y21	3254.59	82.813	17060	3	1085.53	17.25

P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	14		LVITSR	972	6	1	13.9	y5	688.43	53.553	13712	2	344.72	-9.31
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	15		EGLNVLQYFISTHGAR	764	16	5	40.78	y3y4y5°y5y9	1804.90	90.142	13175	3	602.31	-16.23
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	16		VTAEDVLKPGTADILVPR	842	18	5	41.86	b6y3y4y5y9	1894.03	71.964	12045	3	632.02	-15.60
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	17		FATSDLNDLYR	259	11	3	28.07	b9b10y9	1314.61	69.257	11416	3	438.88	-16.44
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	18		GDVISDGPEAPHDILR	1206	16	4	17.79	b6°b6y6y13	1690.81	34.981	7128	2	845.91	-16.24
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	19		DLAR	901	4	1	13.15	b3	474.26	29.836	6302	1	474.26	-4.95
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	20		MGHIELASPTAHIWFLK	101	17	4	28.3	b5b6b10y8	1951.06	59.205	5635	2	976.03	17.02
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	21		TFHIGGAASR	933	10	7	69.52	b3b4°b4b5°b5b6b9	1016.53	35.004	5287	2	508.77	3.30
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	22		QTDELTLGLSSLVVLSAER	1048	19	6	26.72	b6°b6b7b14°b14y6	2033.06	86.636	4953	2	1017.03	7.87
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	23	Carbamidomethyl+C(4)	GVICEK	81	6	1	13.9	b3	705.35	40.579	4281	1	705.35	-7.87
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	24		VIDIWAAANDR	681	11	4	25.06	b3y5°y5y7	1243.62	47.458	4207	2	622.31	-19.14
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	25		ALMMSTNNILSPANGEPHIVPSQDVVLGLYYMTR	481	34	5	18.14	b4b13y3y7y12	3707.87	115.210	3557	3	1236.63	-3.62
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	26		AMMDNLQTETVINR	695	14	3	19.96	b3b13y5	1635.77	46.872	3415	3	545.93	-7.76
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	27		EEAVVWDILDEVIR	403	14	4	25.4	b4°b4b5y3	1685.86	39.210	2892	3	562.62	-11.51
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	28		ATIESAGSSDFLEGEQVEYSR	1263	21	5	28.17	b9b14y3y4°y4	2275.04	72.341	2853	4	569.52	2.04
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	29		QLNVFEGER	1194	9	3	31.3	b3b6y4	1091.53	27.425	2719	2	546.27	-17.56
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	30		AIVQLEDGVQISSGDTLAR	1104	19	3	15.48	b3b7y8	1972.03	73.276	2542	3	658.01	-4.58
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	31		VLTEAAVAGK	1330	10	6	62.53	b4y3y4y8°y8y9	958.54	35.516	2444	2	479.77	-15.60
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	32	Carbamidomethyl+C(1)	CGVEVTQTK	87	9	3	31.3	b3b4y6	1021.50	25.461	2020	2	511.25	-0.18

P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	33		YNKVIDIWAANDR	678	14	3	25.4	b12y7y8	1648.82	59.648	238924	2	824.91	-14.66
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	34		AQTKTEEFDAIK	9	12	3	23.01	b8b11y10	1380.71	76.548	7805	2	690.86	4.60
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	35		DLARGHIINK	901	10	3	37.7	y6y7y8	1136.64	60.015	4739	2	568.82	-13.64
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	36		KGLADTALK	780	9	3	31.3	b5b6y6	916.54	33.112	4102	2	458.78	-1.73
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	37		VPYGAVMAKGDGEQVAGGETVA NWDPHTMPVITEVSGFIR	996	40	5	21.75	b4b6b13b15*b15	4186.06	114.093	3767	4	1047.27	5.48
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	38		QTDELTLGLSSLVLDsaERTTGG K	1048	24	5	13.11	b9°b9y9°y9y11	2477.29	110.880	2701	3	826.44	8.48
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	39		GEaIGVIAaQSIGEPGTQlTMRTF HIGGAASR	911	32	4	14.06	b3b21y12y15	3196.67	113.225	2318	4	799.92	5.04
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	40		AAAESSIQVKNK	943	12	6	61.83	b4b6b8*b8b11y5	1245.68	34.965	1880	2	623.34	-3.33
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	41	Phosphoryl STY(12)	AIVQLEDGVQISSGDTLAR	1104	19	3	15.48	b12y7y11	2052.02	83.317	4003	3	684.68	14.16
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	42	Phosphoryl STY(11)	MALELFKPFiyGK	371	13	5	30.68	b9b11y4y10°y10	1636.81	81.033	3425	2	818.91	-2.61
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	43	Phosphoryl STY(7)	GEGMVLtGPKEaER	521	14	4	31.73	b5y3y7y8	1553.71	39.257	2010	3	518.58	11.08
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	44	Oxidation+M(10)	SGASVGIDDMVIEK	634	15	7	44.38	b3°b3b4b6°b6y7y8	1533.73	76.518	4980	3	511.92	-8.04
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	45	Oxidation+M(10)	SGASVGIDDMVIEKK	634	16	3	26.16	b3b4b14	1661.85	101.212	2926	3	554.62	7.20
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	46		PAGtGYaYHQDR	1357	12	1	7.38	b10	1335.62	42.202	5003	2	668.32	12.25
P0A2R4 RPOC_SALTY DNA-directed RNA polymerase subunit beta'	47		DPYEEMIPK	1183	9	0	4.9		1121.53	73.043	1671	2	561.27	10.01
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	1	Carbamidomethyl+C(18)	TFaHVDpKVEIPiVPTCHyMMG GIPTK	335	28	9	31.65	b5b6°b6y2y3°y3y5y13y28	3135.55	73.207	39351	4	784.64	-10.20
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	2		LGgNSLLDLVVFGR	399	14	4	19.96	b3y4y8y14	1459.83	103.383	26635	2	730.42	1.34
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	3	Carbamidomethyl+C(5)	ALQECMQHNFSVFR	461	14	4	28.54	y5y7y10y14	1766.79	63.254	25447	3	589.60	-8.84
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	4	Carbamidomethyl+C(12)	AALQISQSGQTcALLSK	21	17	6	43.07	b2y8y9y11y12y17	1775.94	71.531	15287	2	888.47	1.99
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	5		NHTTIFSEWYALDLVK	155	16	5	36.01	b2b5b7b8b10	1936.99	94.050	10712	2	969.00	4.60
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	6		DaSESDVEGSLER	430	13	3	26.12	b4y5y6	1393.62	41.442	8085	2	697.31	10.16
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	7	Carbamidomethyl+C(29)	AGVPVQdMEMWQFHTGIAGAG VLVTEGCR	228	30	3	11.62	b7b28y15	3213.57	92.897	3953	5	643.52	13.90

Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	8		AAGLHLQESIAEQGVLRDASESDV EGSRLER	413	30	8	24.45	b3y2y4°y4y9y12°y12y20	3166.59	93.109	3809	4	792.40	9.71
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	9		IYQSTTNAHINTGDGVGMALR	207	21	3	14.36	b8y5y9	2219.07	59.226	3510	2	1110.04	-6.82
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	10		TGPEAILELEHMGLPFSR	90	18	7	63.98	b6y4y6y7y8y10y16	1996.99	93.550	52865	3	666.33	-15.16
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	11		GLEQLK	482	6	2	27.43	b3y3	687.40	43.671	9666	1	687.40	-6.48
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	12		LPVR	2	4	1	13.15	b3	484.32	76.529	9463	1	484.32	-7.18
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	13		NGEDPVAIR	451	9	3	31.3	b6b7y8	970.51	30.696	6093	2	485.76	20.25
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	14		TAAAADR	133	7	9	81.92	b4°b4b5b6°b6y3°y3y4y5	675.34	111.418	3835	1	675.34	-9.40
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	15		EFDVAVVIGAGGAGMR	6	15	4	18.79	b9b12°b12y7	1449.73	61.657	3254	2	725.37	8.76
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	16	Carbamidomethyl+C(3)	VECLELDNLMETAYATAVSANFR	510	23	4	22.51	b7y3y4*y4	2617.23	109.497	2712	3	873.08	-0.56
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	17		HGER	267	4	1	13.15	b3	498.24	31.201	1520	1	498.24	-5.45
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	18	Carbamidomethyl+C(18)	TFAHVDPVKEPIPVITCHYMMG GIPTK	335	28	3	12	b8b21y3	3135.59	98.616	31786	3	1045.87	0.78
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	19	Carbamidomethyl+C(15)	LDDTSSEFNTQRVECLELDNLME TAYATAVSANFR	498	35	9	56.54	b9b12b20y4*y4y5*y5y6y7	4010.87	109.994	6303	3	1337.63	8.03
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	20	Carbamidomethyl+C(29) ;Oxidation+M(8)	AGVPVQDMEMWQFHPTGIAGAG VLVTEGCR	228	30	4	11.62	b3b8°b8y11	3229.51	121.068	16991	4	808.13	-3.70
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	21		AEQGVLRDASESDVEGSRLER	423	20	2	12.08	b9b15	2147.01	93.062	9044	3	716.34	-6.37
Q8ZQU3 DHSA_SALTY Succinate dehydrogenase flavoprotein subunit	22		AGVPVQDMEMWQFHPTGIAGAG VL	228	24	0	9.43		2511.21	92.924	4374	3	837.74	-2.53
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	1		VLAEQALAQPTTDELMTLVNK	546	21	7	25.5	b6y9°y9y12*y12y13y21	2285.19	86.288	32986	3	762.40	-7.69
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	2		TMDIGGDKELPYMNFPEENPFL GWR	332	26	7	22.27	b2b3b4y1y2y11y26	3084.47	89.620	31464	4	771.87	3.01
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	3		HMTADAAAHEVIEGQATALEELD DEYLK	96	28	8	35.66	y2y7y10°y10y12y15y17y28	3070.42	100.687	21674	3	1024.14	-4.69
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	4		MISGILASPGIAFGK	0	15	7	30.4	b2b4y1y3y4y8y15	1461.79	81.066	17964	2	731.40	-13.61
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	5		TEFLFMDRDALPTEEEQFAAYK	296	22	11	41.13	b1°b1b2°b2b5°b5b10b11y6y7y9	2651.24	84.209	14282	3	884.42	2.49
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	6		NGDYLLDAVNNQVYNPTNDVI EQLR	213	27	10	51.18	b14y2y3y4°y4y5y10y11°y11y27	3089.57	94.540	6156	3	1030.53	6.64
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	7		VLGFITDAGGR	175	11	5	32.05	y5y6°y6y9°y9	1105.62	50.432	3866	2	553.32	21.42
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	8		VDQEVER	35	7	8	68.39	b5b6°b6y4y5y6°y6*y6	874.43	29.912	3560	2	437.72	7.75
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	9		QVIDASHAEGK	486	11	4	36.82	b6°b6b8b10	1154.60	42.896	2992	3	385.54	21.46

P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	10		GNDMISHLYQPMSPSVLNLIK	465	21	3	14.36	b6b9y12	2357.16	98.673	2239	3	786.39	-18.13
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	11		ELPYMNFPK	340	9	4	46.08	b3b6y5y7	1138.54	81.535	2144	1	1138.54	-21.12
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	12		AFDESIEIGVMVETPAAATIAR	418	22	6	52.12	b4b5b6b9°b9b10	2291.17	117.032	1652	2	1146.09	6.71
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	13		NTNFEDAKVLAEQALAQPTTDEL MTLVNK	538	29	4	11.8	b10y15y18*y18	3204.65	85.826	38483	5	641.74	12.11
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	14		EIEIYKQELR	404	10	3	29.46	b3b4y8	1320.70	34.025	4945	3	440.91	-10.35
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	15	Oxidation+M(5)	ELPYMNFPKEENPFLGWR	340	18	3	16.15	b14y11y13	2283.12	81.597	59465	3	761.71	13.47
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	16	Oxidation+M(5)	IMFPMIISVEEVR	387	13	3	28.83	b4b6b7	1579.80	42.496	7238	3	527.27	-11.59
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	17	Oxidation+M(9)	EAI FEGHIMLLEDEELEQEIIALIKD K	69	27	5	36.61	b5b10b12b14b21	3184.63	105.514	2852	3	1062.21	-2.61
P0A249 PT1_SALTY Phohoenolpyruvate-protein phohotransferase	18	Oxidation+M(13)	TMDIGGDKELPYMNFPKEENPFL GWR	332	26	3	23.16	b6b9b10	3100.42	109.592	2577	2	1550.71	-11.26
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	1		IQVTGSEGELGIYPGHAPLLTAIKP GMIR	23	29	11	54.79	b2*b2b3b4y2y5y12y13y26 y27y29	3018.60	81.726	119670	4	755.41	-14.48
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	2		AMTYHLDVVSAEQQMFSGLVEK	1	22	9	37.77	b2b3b8b9y2y3y8y10y22	2483.19	90.128	35437	3	828.40	-1.77
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	3		SSHGDVDYAQASAE LAK	107	17	4	37.84	b7y6y7y8	1748.79	44.985	33330	3	583.60	-9.28
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	4		MAMTYHLDVVSAEQQMFSGLVE K	0	23	4	13.48	b3b9y1y5	2614.25	110.877	2375	3	872.09	7.56
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	5		AEEHIK	101	6	1	13.9	b5	726.37	68.683	1996	1	726.37	-5.88
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	6		AEEHIKSSHGDVDYAQASAE LAK	101	23	3	13.48	b6y7y11	2456.18	65.237	20860	4	614.80	4.17
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	7	Oxidation+M(16)	MAMTYHLDVVSAEQQMFSGLVE K	0	23	3	13.48	b5b13y13	2630.22	117.015	6766	3	877.41	-3.99
P0A1B7 ATPE_SALTY ATP synthase epsilon chain	8	Oxidation+M(2)	AMTYHLDVVSAEQQMFSGLVEK	1	22	3	13.9	b11b16y12	2499.19	99.466	6446	3	833.74	2.05
P0A269 PPX_SALTY Exopolyphohatase	1		LSDGALR	291	7	7	51.85	b3°b3b4b6y5°y5y7	731.40	32.498	18373	1	731.40	-9.68
P0A269 PPX_SALTY Exopolyphohatase	2		SPRPQEFAAVDLGSNSFHMVIAR	6	23	3	22.51	b10b11y6	2529.29	84.284	13325	3	843.77	10.42
P0A269 PPX_SALTY Exopolyphohatase	3	Carbamidomethyl+C(4)	GLSCLSLFAER	64	11	4	42.57	b3b4b5y10	1252.62	59.932	2546	3	418.21	-9.36
P0A269 PPX_SALTY Exopolyphohatase	4	Carbamidomethyl+C(10)	LQGFSPSSVCIVGTHTLR	75	18	3	35.07	b10b11b12	1959.00	66.892	1940	2	980.00	-8.23
P0A269 PPX_SALTY Exopolyphohatase	5		LSDGALREGVLYEMEGR	291	17	5	16.91	b5°b5b8y2y7	1894.92	91.356	1775	3	632.31	-6.06
P0A269 PPX_SALTY Exopolyphohatase	6		LSEEAMER	56	8	4	41.71	y4y5y6°y6	964.46	30.393	39252	2	482.73	20.00
P0A269 PPX_SALTY Exopolyphohatase	7		LDDMPR	417	6	1	13.9	b3	746.34	45.097	13080	1	746.34	-7.03
P0A269 PPX_SALTY Exopolyphohatase	8		VIPYPIIISGNEEAR	107	16	3	24.32	b6b7y6	1799.98	78.947	11922	2	900.49	12.48

P0A269 PPX_SALTY Exopolyphohatase	9		VVDGAMQIIGR	29	11	3	25.06	b10y3y10	1158.65	83.439	5190	2	579.83	15.49
P0A269 PPX_SALTY Exopolyphohatase	10		LNIEEESPEIAA	500	13	3	26.12	b6y3y4	1401.68	60.416	2357	2	701.34	4.62
P0A269 PPX_SALTY Exopolyphohatase	11		VLETTMQMYEQWQAQQPK	335	18	4	16.15	b4b9y9*y9	2239.07	74.822	1857	4	560.52	7.41
P0A269 PPX_SALTY Exopolyphohatase	12	Carbamidomethyl+C(11)	LTTDDSHWTLCFPHDWFSQNALV LLDLEK	459	29	4	22.22	b5y3°y3y4	3501.71	100.228	1806	4	876.18	7.88
P0A269 PPX_SALTY Exopolyphohatase	13		HRSFNALSLPGLSEER	251	16	6	25.19	b7°b7b14y7y12*y12	1812.94	84.349	12516	2	906.97	3.77
P0A269 PPX_SALTY Exopolyphohatase	14		LIFMGVEHTQPEKGR	123	15	5	49.43	y9y10y11y12*y12	1741.89	81.507	3454	2	871.45	-9.60
P0A269 PPX_SALTY Exopolyphohatase	15		LSDGALREGVLYEMEGR	291	17	6	23.83	b8°b8b14y12y14°y14	1894.94	136.616	2124	2	947.97	4.70
P0A269 PPX_SALTY Exopolyphohatase	16		SLANQYNIDREQAR	320	14	3	19.96	b13y3y10	1677.85	87.825	1959	2	839.43	9.31
P0A269 PPX_SALTY Exopolyphohatase	17		QAQNAADFLKR	93	11	4	32.05	b3*b3b4b9	1261.66	52.260	1628	2	631.33	-7.06
P0A269 PPX_SALTY Exopolyphohatase	18	Phosphoryl STY(9)	LVIDIGGGSTELVIGENFEPR	139	21	4	22.49	b16_H3PO4 b16y10y12y14	2295.14	93.733	1972	3	765.72	10.85
P0A269 PPX_SALTY Exopolyphohatase	19	Oxidation+M(6)	VVDGAMQIIGR	29	11	3	25.06	b5b8y8	1174.63	38.874	5856	2	587.82	8.31
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	1		NFVDYVNSGFYNNTTFHR	54	18	8	41.72	b2b3b6b10y10y12y16y18	2194.98	74.237	59516	3	732.33	-8.01
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	2		TADKDSATSQFFINVADNAFLDH GQR	116	26	15	78.31	b2b3b8b10b11b13y4*y4y7 y9°y9y10y11y13y26	2868.31	85.671	55730	4	717.83	-14.47
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	3		VIPGFMIQGGGFNEQMQQK	72	19	6	34.21	b2y4y11y13y17y19	2109.04	76.388	44609	2	1055.03	8.80
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	4		ISQVPTHDVGPYQNVPTKPVVILS AK	161	26	5	18.64	y2y3y8y11y26	2787.51	61.873	22132	4	697.63	-11.65
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	5		TADKDSATSQFFINVADNAFLDH GQRDFGYAVFGK	116	35	8	21.87	b2b13y1y3y10y11°y11*y1 1	3852.84	106.587	4939	5	771.37	3.68
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	6		GMDVADKISQVPTHDVGPYQNV PTKPVVILSAK	154	33	9	58.69	b3b9b10y4y5y6y8y11y22	3503.83	68.111	89674	4	876.71	-6.97
P20753 PPIA_SALTY Peptidyl-prolyl cis-trans isomerase A	7		KPNPPIKNEADNGLR	91	15	3	26.87	y6y8y12	1662.87	30.031	39805	3	554.96	-13.14