

SA123 LC-MS run 1: 123_220709_1a2_01

Protein name	Peptide Rank	Peptide Modification	Peptide Sequence	Peptide sequence start	Peptide sequence Length	Peptide Matched Products	Peptide Score	By Matches	Precursor MH+ (Da)	Retention time (min)	Intensity	z	Precursor m/z	MH+ Error (ppm)
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	1		EMLIADGIDPNELLNSMAAAK	62	21	54	289.3	b2°b2b3°b3b4°b4b5°b5b6°b6b7°b7b8°b8b9°b9b12°b12b13°b13b18b21°b21y1y2y3y4y5y6°y6y7°y7°y7y8°y8y9y10y11°y11y12°y12°y12y13°y13°y13y13y14°y14y15°y15y16°y16y17°y17y21	2216.11	97.465	507100	2	1108.56	8.59
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	8	47.42	y2y7y8y9y10°y10°y10y11	1304.56	33.968	126086	2	652.78	-5.33
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	3	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	12	57.97	b2b7°b7y2°y2y4y5y9y10°y10y11y13	1624.76	93.452	50303	2	812.88	8.64
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	4		EEESAAAAEVEER	41	13	6	26.11	b2°b2y6y7y10y13	1419.62	35.982	12925	2	710.31	-2.24
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	5		REEESAAAAEVEER	40	14	5	38.66	b12y3y8y10y11	1575.73	34.053	7479	2	788.37	2.09
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	6		YSYVDENGETKTWTGQGR	96	18	10	84.09	y3y5°y5y6°y6y13y14y15y16y17	2090.92	47.827	183567	3	697.65	-8.06
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	7		AARPAKYSYVDENGETK	90	17	5	30.53	b3b11y5y6y13	1898.91	107.257	5399	2	949.96	-6.69
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	8	Oxidation+M(17)	EMLIADGIDPNELLNSMAAAK	62	21	5	19.51	b16°b16y7y10y13	2232.11	97.528	23665	2	1116.56	7.44
[P64076]ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	33	215.64	b2°b2b3°b3b4°b4b5°b5b6°b6°b6b12°b12b13°b13b14°b14y1y2y3y4y5y6y7y8y9y10y11y12y13°y13y15°y15	1605.88	86.426	379635	2	803.45	-0.15
[P64076]ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	39	297.33	b2b3°b3b5b7b8°b8b9°b9b10b11b12°b12b14°b14b15b18°b18b22y2y3y4y5y6y7y8°y8y9°y9y10y11y12y13y14°y14y15y16y17y22	2118.07	76.113	247688	2	1059.54	7.49
[P64076]ENO_SALTY Enolase	3		GMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	200	31	29	180.63	b2b4°b4b5°b5b6°b6°b6b12b13b30y1y2y3y4y5y6y7y8y9y10y11y13y14y15y18y25°y25y31	2989.47	95.671	193370	3	997.16	4.00
[P64076]ENO_SALTY Enolase	4		GIANSILIK	333	9	7	51.2	b2y2y3y5y6y7y9	928.57	61.421	189216	2	464.79	-12.16
[P64076]ENO_SALTY Enolase	5		DAGYTAVISHR	360	11	11	76.09	b2°b2b3b7y2y3y4y5y6y7y11	1189.59	42.345	149504	2	595.30	-4.21
[P64076]ENO_SALTY Enolase	6		AVGAVNGPIAQAILGK	66	16	6	38.41	b3b4y3y11y12y16	1478.87	75.914	130339	2	739.94	2.31
[P64076]ENO_SALTY Enolase	7		YSMPVPMMNIIINGGEHADNNVDIQEFMIQPVGAK	143	34	19	50.52	b1b2°b2b3°b3b5°b5b11y2y5y7y9y12°y12y13°y13y14y29y34	3759.78	99.080	114354	3	1253.93	5.32
[P64076]ENO_SALTY Enolase	8		YVLAGEGNK	257	9	10	75.81	b2y3°y3y4y5y6°y6y7y8y9	950.49	34.278	93181	2	475.75	0.64
[P64076]ENO_SALTY Enolase	9		AVGAVNGPIAQAILGKDAK	66	19	6	23.5	b1b2b3y5y6y14	1793.01	69.590	81288	3	598.34	-11.71
[P64076]ENO_SALTY Enolase	10		ILKEGIEK	325	8	5	38.4	y1y2y3y4y5	929.56	30.601	76302	2	465.28	-12.28
[P64076]ENO_SALTY Enolase	11		IQLVGDDLFTNTNK	311	14	19	115.46	b2°b2b3b4y2y4°y4y5y6°y6°y6y8y9y10°y10y11y12y14°y14	1562.85	78.341	64600	2	781.93	3.36
[P64076]ENO_SALTY Enolase	12		IEEALGEK	411	8	6	30.62	b2b5y1y6y7y8	888.45	32.175	34005	2	444.73	-13.95

P64076 ENO_SALTY Enolase	13		QYPIVSIEDGLDESDWDGFAYQTK	282	24	14	34.98	b2*b2b3*b3b9b10b13y2y4*y4y6*y6y9y24	2776.28	94.323	27756	2	1388.64	6.42
P64076 ENO_SALTY Enolase	14		AFTSEEFTHFLEELTK	266	16	3	15.43	b4b11y11	1928.90	107.129	7341	3	643.64	-12.91
P64076 ENO_SALTY Enolase	15		EIIDSR	10	6	2	25.1	b4y3	732.39	29.266	19543	1	732.39	-3.00
P64076 ENO_SALTY Enolase	16		IMIDLDGTENK	92	11	11	76.09	b4b7y4°y4y5*y5y7°y7y8y9*y9	1248.60	64.406	18854	2	624.80	-11.44
P64076 ENO_SALTY Enolase	17		GNPTVEAEVHLEGGFVGMAAAPS GASTGSR	16	30	5	12.81	b3b11°b11y5y8	2856.38	92.720	15651	3	952.80	7.52
P64076 ENO_SALTY Enolase	18		VLGDKIQLVGDDLFVTNTK	306	19	15	84.31	b3b4b7y3°y3y4°y4y5y6°y6y8*y8y10y13*y13	2075.13	80.608	229247	3	692.38	-5.53
P64076 ENO_SALTY Enolase	19		GMPLYEHIAELNGTPGKYSMPVP MMNIINGGEHADNNVDIQEFMIQP VGAK	126	51	7	26.6	b4b5b14b20b22b26y4	5567.61	98.857	112893	5	1114.33	-8.77
P64076 ENO_SALTY Enolase	20		GKGMNTAVGDEGGYAPNLGSNA EALAVIAEAVK	198	33	7	47.16	b4b15y3y4y5y6y15	3174.60	90.632	52612	3	1058.87	9.84
P64076 ENO_SALTY Enolase	21		EIIDSRGNPTVEAEVHLEGGFVGM AAPSGASTGSR	10	36	3	11.01	b4y6y27	3569.73	93.771	16249	4	893.19	-0.14
P64076 ENO_SALTY Enolase	22		IEEALGEKAPYNGR	411	14	4	38.91	y4y5y6y9	1546.77	40.615	14371	3	516.26	-12.31
P64076 ENO_SALTY Enolase	23		EALELRDGDK	46	10	10	80.83	b4b7b8°b8y3y4°y4y6°y6y7	1145.57	65.323	5545	2	573.29	-6.39
P64076 ENO_SALTY Enolase	24	Phohoryl.STY(14)	QYPIVSIEDGLDESDWDGFAYQTK	282	24	3	11.71	b10b12y9	2856.23	110.138	2027	4	714.81	5.13
P64076 ENO_SALTY Enolase	25	Oxidation+M(27)	YSMPVPMMNINGGEHADNNVDI QEFMIPVGAK	143	34	6	26.79	b5b7b14y11*y11y12	3775.79	108.732	3943	4	944.70	7.50
P64076 ENO_SALTY Enolase	26	Oxidation+M(18)	GNPTVEAEVHLEGGFVGMAAAPS GASTGSREALELR	16	36	4	14.07	b6y5y11y14	3583.75	99.907	3544	3	1195.25	1.16
P64076 ENO_SALTY Enolase	27	Carbamidomethyl+C(8); Oxidation+M(6)	DITLAMDCAASEFYKDGK	239	18	4	21.19	y3y8y11°y11	2050.94	80.220	1617	4	513.49	13.09
P64076 ENO_SALTY Enolase	28		GYTAVISHR	362	9	4	17.59	b3°b3b5°b5	1003.53	42.403	60965	2	502.27	-1.89
P64076 ENO_SALTY Enolase	29		LKEGIEK	326	7	0	1.49		816.47	30.596	42927	2	408.74	-13.90
P64076 ENO_SALTY Enolase	30		ANSILIK	335	7	4	21.82	b3°b3b4°b4	758.47	61.435	28050	1	758.47	-3.22
P64076 ENO_SALTY Enolase	31		AGYTAVISHR	361	10	1	7.5	b3	1074.56	42.357	7263	2	537.78	-8.97
P64076 ENO_SALTY Enolase	32		TAVISHR	364	7	1	7.5	b3	783.44	42.335	6556	2	392.22	-7.17
P64076 ENO_SALTY Enolase	33		LAGEGNK	259	7	2	21.82	b3b5	688.36	34.339	5920	1	688.36	-3.64
P64076 ENO_SALTY Enolase	34		YSMPVPMMNINGGEHA	143	17	1	12.08	y8	1860.85	99.085	2845	3	620.96	3.67
P64076 ENO_SALTY Enolase	35		DAGYTAVISHR	360	11	0	2.98		1171.58	42.346	3874	3	391.20	-0.10
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VVGQLGQVLGPR	122	12	17	113.5	b2b4b5°b5b7°b7y2y3y4y6y7*y7y8y9y10*y10y12	1222.72	59.968	209659	2	611.86	-6.09
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VAVFTQGPNAEAAK	74	14	29	225.93	b2b3b4b5b6b9b10b11*b11b12°b12b13y2y3y4°y4y5y7y8°y8y9*y9y10*y10y11°y11*y11y12y14	1402.73	46.212	172164	2	701.87	-0.52
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VGTVTPNVAEAVK	141	13	26	161.45	b1b2b3°b3b5°b5b11°b11b12*b12b13y3y4y5y6y7y8y9*y9y10y11°y11y12°y12*y12y13	1284.72	48.961	171979	2	642.86	0.67
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		QYDINEAIALLK	19	12	7	50.52	b8b12y3y4y5y6y12	1390.76	86.001	63681	2	695.88	-1.23
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		GEMNFDVVIADAMR	106	16	4	21.96	b10b11y3y16	1751.83	63.288	42028	3	584.62	12.96
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		AAGAELVGMEDLADQIK	88	17	9	65.65	b3b4b5b6°b6b7y4y11y17	1730.87	80.591	41032	2	865.94	5.64
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		GATVLPHTGR	60	11	15	106.72	b3°b3b4°b4y2y3y4°y4y5y6°y6y7y8y9y11	1065.57	30.765	36950	2	533.29	-6.76
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		AAGAELVGMEDLADQIKK	88	18	6	40.3	b2b3b4b7b8y10	1858.94	73.945	31268	3	620.32	-8.86

[P0A2A3]RL1_SALTY 50S ribosomal protein L1	9		ELATAK	31	6	1	12.8	b4	632.35	29.271	11460	1	632.35	-13.71
[P0A2A3]RL1_SALTY 50S ribosomal protein L1	10		SDQNVR	54	6	1	12.8	b5	718.34	87.589	5617	1	718.34	-8.67
[P0A2A3]RL1_SALTY 50S ribosomal protein L1	11		VDATKQYDINEAIALLK	14	17	4	24.84	b8b13b14y4	1905.02	80.923	21312	3	635.68	-7.37
[P0A2A3]RL1_SALTY 50S ribosomal protein L1	12		GLMPNPKVGTVTPNVAEAVK	134	20	5	20.34	b3b6*b6b19y5	2022.10	63.645	2838	3	674.71	-1.69
[P0A2A3]RL1_SALTY 50S ribosomal protein L1	13	Phohoryl STY(5)	VAVFTQGPNAEAAK	74	14	3	17.37	b3b11y9	1482.69	50.481	1644	2	741.85	1.98
[P0A2A3]RL1_SALTY 50S ribosomal protein L1	14	Oxidation+M(9)	AAGAELVGMEDLADQIKK	88	18	3	14.03	b3b5y12	1874.95	59.783	4788	2	937.98	-0.85
[P0A2A3]RL1_SALTY 50S ribosomal protein L1	15	Oxidation+M(9)	AAGAELVGMEDLADQIK	88	17	7	48.99	b4b13b15y8*y8y9y10	1746.87	84.699	3203	2	873.94	8.53
[P0A2A3]RL1_SALTY 50S ribosomal protein L1	16		TVLPHGTGR	62	9	0	2.98		937.51	30.762	30653	2	469.26	-11.59
[P0A2H9]DSBA_SALTY Thioldisulfide interchange protein dsbA	1		AAADLQLQGVPMFVNGK	158	18	20	159.3	b2b4b5b6*b6b9b10b12b15y2y3y4y5y7y8y9y10y12y13y18	1829.97	81.544	82835	2	915.49	5.34
[P0A2H9]DSBA_SALTY Thioldisulfide interchange protein dsbA	2		TQTVQSAADIR	116	11	7	22.11	b3°b3*b3y2y7y9y11	1189.61	36.296	24889	2	595.31	-3.80
[P0A2H9]DSBA_SALTY Thioldisulfide interchange protein dsbA	3		YQINPQGMdTSSMDVFVQQYADTVK	176	25	18	76.65	b1b2*b2b4b5b7b13y1y5y6y7°y7*y7y8°y8y9y12y25	2865.32	87.248	23487	2	1433.16	5.28
[P0A2H9]DSBA_SALTY Thioldisulfide interchange protein dsbA	4		YHVEFLGPLGK	77	11	7	47.42	b1b2b3b4b7b8y2	1259.67	71.975	5785	2	630.34	-4.46
[P0A2H9]DSBA_SALTY Thioldisulfide interchange protein dsbA	5		ELTQAWAVAMALGVEDK	88	17	8	66.77	b5b9y4y5y6y7y13y15	1831.93	61.383	6906	2	916.47	3.27
[P0A2H9]DSBA_SALTY Thioldisulfide interchange protein dsbA	6		TQTVQSAADIRK	116	12	3	20.17	b5b11y4	1317.71	67.060	2922	2	659.36	-4.26
[P0A2H9]DSBA_SALTY Thioldisulfide interchange protein dsbA	7		GEDYDAAWNSFVVKSLVAQQEK	136	22	6	22.13	b3y3y4°y4*y4y8	2484.18	136.418	2646	2	1242.59	-8.94
[P0A2H9]DSBA_SALTY Thioldisulfide interchange protein dsbA	8	Oxidation+M(21)	YHVEFLGPLGKELTQAWAVAMALGVEDK	77	28	3	11.08	b8b11y9	3088.57	79.296	8171	4	772.90	-4.35
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTTQETFGNEHWAPK	135	20	22	97.65	b1b2b3b12b13b15*b15y1y2y4y7°y7y8y9y10*y10y12*y12y13°y13y17y20	2199.08	64.403	75756	3	733.70	-1.22
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	18	153.13	b4b5°b5b7b11°b11b12°b12y5y6y7°y7y8y9y10y11y12y13	1425.69	56.183	63006	2	713.35	1.63
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	3		NSDIQPTVASLK	120	12	14	91.11	b1b2°b2b3°b3b4y3y4y7y8*y8y9y10y12	1272.68	49.034	50776	2	636.84	-2.01
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	19	89.57	b2*b2b3°b3b4°b4*b4b8°b8*b8b9y1y2y3y4y5y6y7y20	2273.20	104.484	41179	2	1137.10	4.94
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	5		FGGPAVKDEK	201	10	7	24.62	b6y2°y2y4°y4y6y10	1047.54	27.724	16583	2	524.27	-5.13
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	6		NAQGELVGFIDIDLAK	42	15	5	33.44	b8b9b14y6y8	1589.83	80.422	10156	2	795.42	10.29
[P02910]HISJ_SALTY Histidine-binding periplasmic protein	7		LFGVGTGMGLR	211	11	3	22.11	b10y3y7	1107.59	73.349	8976	2	554.30	-8.71

P02910 HISJ_SALTY Histidine-binding periplasmic protein	8		GIEIVSYQGQDNIYSDLTAGR	155	21	7	19.51	b7°b7b9°b9b11°b11y11	2299.14	80.403	1657	2	1150.07	6.48
P02910 HISJ_SALTY Histidine-binding periplasmic protein	9	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLKAK	62	22	3	12.26	b4b15y20	2472.32	99.361	185883	3	824.78	1.38
P02910 HISJ_SALTY Histidine-binding periplasmic protein	10		IGTDPTYAPFESKNAQGELVGFDI DLAK	29	28	4	23.78	y4y11y15y17	2996.52	96.577	23629	3	999.51	10.35
P02910 HISJ_SALTY Histidine-binding periplasmic protein	11		NSDIQPTVASLKGK	120	14	4	25.94	b4°b4b6b9	1457.79	43.242	10849	3	486.60	-6.62
P02910 HISJ_SALTY Histidine-binding periplasmic protein	12		IDAAFQDEVAASEGFLKQPVGK	176	22	7	27.27	b6b10°b10b12°b12b13°b13	2320.17	64.396	4520	3	774.06	-5.58
P02910 HISJ_SALTY Histidine-binding periplasmic protein	13		EALNKAFAEMR	229	11	8	47.42	y3°y3y4°y4y5°y5y6°y6	1279.63	64.411	4488	2	640.32	-12.69
P02910 HISJ_SALTY Histidine-binding periplasmic protein	14		AFAEMRADGTYEK	234	13	3	18.63	b6y8y11	1488.68	136.458	3803	1	1488.68	-0.82
P02910 HISJ_SALTY Histidine-binding periplasmic protein	15		EDNELREALNK	223	11	6	25.12	b9°b9b10°b10y10*y10	1330.65	136.392	1958	1	1330.65	-8.53
P02910 HISJ_SALTY Histidine-binding periplasmic protein	16	Phohoryl STY(6)	LFGVGTGMGLRK	211	12	3	20.17	b4y8y10	1315.67	63.646	7528	2	658.34	12.53
P02910 HISJ_SALTY Histidine-binding periplasmic protein	17	Oxidation+M(8)	LFGVGTGMGLR	211	11	3	22.11	b4b8y3	1123.58	31.645	4623	3	375.20	-7.93
P02910 HISJ_SALTY Histidine-binding periplasmic protein	18		GGPAVKDEK	202	9	2	19.31	b3b8	900.47	27.699	5187	2	450.74	-4.27
P02910 HISJ_SALTY Histidine-binding periplasmic protein	19		VGVLQGTQTQE	135	10	3	20.59	y3y4°y4	1031.54	64.383	2748	2	516.28	6.39
P02910 HISJ_SALTY Histidine-binding periplasmic protein	20		FGNEHWAPK	146	9	0	7.45		1085.53	64.433	2407	2	543.27	11.25
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		LADVLAAANAR	57	11	18	119.03	b2b3b4°b4y1y3*y3y4*y4y5y6*y6y7*y7y8y9y10y11	1084.60	54.228	235822	2	542.80	-8.10
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGSLGDQVNVK	8	14	21	163.71	b2b3b4b11°b11b12°b12*b12b13y3y4y6y7*y7y8y9y10°y10y11y12y14	1413.77	57.487	122653	2	707.39	-3.19
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		NVEYFEAR	42	8	7	50.7	y2y3y4y5y6y8*y8	1027.47	47.753	117905	2	514.24	-9.86
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		DIADAVTAAGVDVAK	97	15	11	121.06	b3b4b5b6y4y6y7y9y10y11y13	1415.74	67.097	116784	2	708.37	-1.55
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		VIINVVAE	141	8	7	38.4	b1b5°b5b6b7y1y8	856.51	64.407	88800	1	856.51	-5.42
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		INALETVTIASK	71	12	6	24.15	b2°b2b3y10y11y12	1259.72	61.919	64965	2	630.36	-0.19
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		NVEYFEARR	42	9	4	35.89	b9y6y7y8	1183.59	67.194	3517	2	592.30	4.43
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		MQVILLDK	0	8	3	38.4	y3y4y5	959.55	65.136	123640	2	480.28	-11.00
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	9		NFLVPK	27	6	2	25.1	y3y4	717.43	52.000	42550	1	717.43	-3.57
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	10		TTGEHEVNFQVHSEVFAK	123	18	5	22.36	b5y3y6y11°y11	2059.03	65.998	3250	3	687.01	19.80
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	11		NVEYFEARR	42	9	6	42.17	b5y3y7°y7y8°y8	1183.58	64.434	5294	2	592.29	-5.47
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	12		AELEAKLADVLAAANAR	51	17	6	14.67	b3°b3b5°b5y4*y4	1725.96	123.528	2819	2	863.48	6.72
P0A1D5 CH10_SALTY 10 kDa chaperonin	1		ILDNGTVQPLDVK	47	13	37	213.13	b2b3b4°b4*b4b5°b5b6°b6°b6b7°b7°b7b8°b8b10b11°b11°b11b13y1y2y3y5y6°y6°y6y7y8y9y10y11°y11°y11y12y13*y13	1411.77	58.235	348925	2	706.39	-3.89

P0A1D5 CH10_SALTY 10 kDa chaperonin	2		VGDIVIFNDGYGVK	60	14	18	161.95	b3b4b5°b5b9b13y1y3y4y5y6y8y9y10y11y12*y12y14	1495.78	74.326	314352	2	748.39	2.12
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	18	129.56	b3°b3b4b5°b5b10b13°b13y1y2y3y4y6y7y8y9y12y14	1188.65	44.623	162951	2	594.83	-5.75
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIAVGK	37	8	5	58.24	b5y3y4y5y6	786.46	42.535	36180	2	393.73	-15.37
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		IDNEEVLIMSESILAIVEA	77	20	3	19.8	b5b8b11	2203.09	74.615	1732	4	551.53	-4.77
P0A1D5 CH10_SALTY 10 kDa chaperonin	6		VGDIVIFNDGYGVKSEK	60	17	4	14.67	b14°b14y3y8	1839.96	100.283	36136	2	920.48	3.65
P0A1D5 CH10_SALTY 10 kDa chaperonin	7		ILDNGTVQPLDVKVGDIVIFNDGYGVK	47	27	6	23.61	b5b8b12y3y6y14	2888.53	91.576	15877	3	963.52	-2.45
P0A1D5 CH10_SALTY 10 kDa chaperonin	8		SEKIDNEEVLIMSESILAIVEA	74	23	7	34.18	b3b7b9b10*b10b12y3	2547.30	136.382	2962	2	1274.15	8.82
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	1		EAKDLVESAPAALKEGVSK	82	19	7	22.66	b5b7°b7b8°b8y1y19	1942.05	55.787	61863	3	648.02	-0.19
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		DQIIIEAVSAMSVM DVVVELISAMEEK	5	25	23	136.98	b2°b2*b2b3°b3b4b5b6°b6b7b8°b8b10y2°y2y3y4y5y6°y6y7y9y10	2737.34	137.117	47509	3	913.12	2.32
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	3		SLEEAGAEVEVK	109	12	5	31.23	b5b12y3y8y9	1260.63	58.008	5668	2	630.82	-1.26
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	4		MSITKDQIIIEAVSAMSVM DVVELISAMEEK	0	30	4	10.94	b6y7y13y30	3297.60	110.575	1824	3	1099.87	-9.18
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	5		DLVESAPAALK	85	11	4	22.11	b4°b4b6y4	1113.61	55.313	5362	2	557.31	-3.29
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	6		AAGANK	60	6	1	12.8	y5	531.29	31.571	3863	1	531.29	2.41
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	7		SITKDQIIIEAVSAMSVM DVVELISAMEEK	1	29	3	11	b6y11y15	3166.64	136.618	4281	3	1056.22	14.19
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	8	Oxidation+M()	SITKDQIIIEAVSAMSVM DVVELISAMEEK	1	29	4	20.68	b10y3y6y7	3182.58	102.116	30886	3	1061.53	-1.30
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	1		VINDNFGII EGLMTTVHATTATQK	160	24	44	273.17	b2b3b4°b4°b4b5°b5°b5b6°b6°b6b7°b7°b7b8°b8y1y3y4y5y6y7°y7°y7y8°y8°y8y9y10y11y14*y14y15°y15y16y18°y18y19y20y21y22°y22y24*y24	2574.32	98.605	641275	3	858.78	-1.61
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	2		AGIALNDNFVK	296	11	16	118.23	b3b4b5b10y1y2y3y4y5°y5y6°y6y7°y7y8y11	1161.62	62.250	347104	2	581.31	-6.83
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	3		LVSWYDNETGYSNK	307	14	24	165.93	b3°b3b6b7°b7°b7b8b9b11y2y3y4°y4°y4y5°y5y6°y6y9y10°y10y11y12y14	1675.77	59.067	257066	2	838.39	6.99
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	4		GASQNIIPSSTGAAK	198	15	26	188.81	b3°b3b5°b5°b5b6°b6b7°b7°b7b11b14y2y3y4y5y6y7y8°y8y9y10y11y13°y13y15	1401.73	41.800	230953	2	701.37	-3.31
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	5		VLDLIAHISK	321	10	10	69.31	b3°b3y1y2°y2y3y4y5y6y8	1108.66	66.177	202630	2	554.84	-6.94
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phosphate dehydrogenase	6		SDIEIVAINDLLDAEY MAYMLK	24	22	18	94.92	b2b3°b3b4°b4b5b6°b6b8b10y4y6y9y10y11y14*y14y22	2530.24	126.798	174338	3	844.08	-3.28

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		VPTPNVSVVDLTVR	232	14	15	110.02	b2b3b5*b5y2y3y4y5y6y8y10y11y12°y12y14	1495.85	71.856	88129	2	748.43	-1.80
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		TVDGPSHKDWR	184	11	4	29.1	y3y6y7y11	1297.62	29.537	8166	2	649.32	-4.33
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		AATYEQIK	249	8	6	30.62	b3y5*y5y6°y6*y6	923.47	32.013	219877	2	462.24	-17.71
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		VLPELNGK	217	8	10	63.01	y3*y3y4*y4y5°y5*y5y6°y6y7	869.50	45.704	68652	2	435.25	-15.09
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11		VGINGFGR	4	8	3	30.62	b3y4y5	819.46	65.306	3092	2	410.24	19.37
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12	Carbamidomethyl+C(12) ;Carbamidomethyl+C(16))	YEQQDIVSNASCTTNCLAPLAK	138	22	4	27.65	y3y10y13y15	2412.15	72.650	1801	3	804.72	11.64
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEQQDIVSNASCTTNCLAPLAK	132	28	44	322.58	b3b4b5*b5b6b8*b8b10*b10b11°b11*b11b12°b12b13°b13b15b16b18b22b23b24*b24b26b27y3y4y5y6y8y9y10y11°y11*y11y12*y12y13°y13y14y15°y15*y15y21	3044.41	67.593	498941	3	1015.48	0.72
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14		VLPELNGKLTGMAFR	217	15	3	24.39	y6y9y13	1645.89	73.890	19509	3	549.30	-12.31
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15		KHITAGAK	107	8	6	63.01	y3y4y5°y5y6y7	825.49	12.556	11351	2	413.25	-10.94
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		GGRGASQNIPSSTGAAK	195	18	6	36.77	b8b9y3y7y8°y8	1671.88	37.687	8394	2	836.44	1.46
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		VINDNFGIIEGLMTTVHATTATQK TVDGPSHK	160	32	4	14.69	b10y3y12y17	3395.73	79.676	7889	4	849.69	0.00
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		DNTPMFVKGANFDK	124	14	3	17.37	b11b13y10	1583.77	70.968	5428	2	792.39	12.72
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19		AGIALNDNFVKLSWYDNETGYS NK	296	25	4	26.05	b4b5b7b16	2818.39	136.432	3985	2	1409.70	7.71
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20	Phohoryl STY(4)	VVLTGPSK	116	8	5	45.93	b4b5b6°b6y4	880.45	114.791	2047	1	880.45	2.43
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	21	Oxidation+M(13)	VINDNFGIIEGLMTTVHATTATQK	160	24	8	34.05	b4b5*b5y11*y11y12°y12y14	2590.30	67.288	3540	4	648.33	-5.75
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	22		DLIAHISK	323	8	3	19.31	b3°b3b5	896.51	66.161	66062	2	448.76	-11.51
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	23		LDLIAHISK	322	9	2	7.8	b3°b3	1009.60	66.186	57730	2	505.30	-5.68
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	24		LNDNFVK	300	7	2	17.59	b3b5	849.45	62.194	21547	1	849.45	-1.58

P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		AVLEVAGVHNVLAK	112	14	16	132.57	b2b3b4°b4b5b11b13y2y3y6y8y9y10y11y12y14	1419.83	61.394	373563	2	710.42	-0.17
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		VFMQPASEGTGHIAGGAMR	93	19	29	259.85	b2b3b4b6b7b10b11°b11b12b13b14°b14y1y3y4y5y6y7y9y10y11y12y13y15°y15y16*y16y17y19	1892.94	68.994	257205	2	946.98	3.93
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		AYGSTNPINVVR	126	12	23	167.94	b2b3b4b5b6°b6*b6b11*b11y2y3y4*y4y5y6y7y8y9*y9y10*y10y11y12	1290.68	51.984	231210	2	645.84	-2.55
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNEMVAAKR	138	19	18	134.18	b2°b2b8b10y1y3y4y5y8y9°y9y10y11y12*y12y13y16y17	2046.99	59.888	160020	3	683.00	-4.17
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		SVEEILGK	159	8	4	33.63	b4b7y6y8	874.48	51.257	131555	2	437.74	-13.68
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		ATIDGLENMNEMVAAK	138	18	13	113.22	b15b16y2y3y4y5y7y10y11y12y13y15y18	1890.90	64.306	93702	2	945.95	4.52
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		EVPAAIQK	54	8	5	38.4	y3*y3y4y6y8	855.48	30.907	35221	2	428.24	-12.70
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		AREVPAAIQK	52	10	6	36.93	b4b6b7y2y6y10	1082.63	29.754	25638	2	541.82	-5.64
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		NMINVALNNGTLQHPVK	69	17	5	27.36	b1b3b7y9y10	1862.97	63.768	24606	3	621.66	-10.75
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		VGFGYGK	45	7	3	37.9	y3y5y6	727.37	40.781	42213	2	364.19	-15.36
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		LIAVNR	14	6	3	25.1	y4*y4y5	685.43	33.935	36373	1	685.43	-8.37
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12		IFSFTALTTVGDGNGRVGFGYGK	29	23	3	18.37	b4b6b12	2362.22	95.433	11735	3	788.08	0.52
P0A7W4 RS5_SALTY 30S ribosomal protein S5	13		AHIEKQAGELQEK	1	13	5	18.63	b9y3*y3y10°y10	1480.76	40.135	11012	3	494.26	-9.73
P0A7W4 RS5_SALTY 30S ribosomal protein S5	14		GVHTGSRVFMQPASEGTGHIAGGA MR	86	26	3	11.33	b15y15y17	2587.32	136.644	8859	3	863.11	14.06
P0A7W4 RS5_SALTY 30S ribosomal protein S5	15		MAHIEKQAGELQEK	0	14	5	43.06	b3b4b5y7y10	1611.81	60.764	2931	4	403.71	-5.07
P0A7W4 RS5_SALTY 30S ribosomal protein S5	16		NMINVALNNGTLQHPVKGVHTG SR	69	24	8	42.36	b3b5b9*b9b10b11y3y5	2557.37	102.064	2442	4	640.10	10.12
P0A7W4 RS5_SALTY 30S ribosomal protein S5	17		QAGELQEKLIAVNR	6	14	4	25.15	b8b9b13°b13	1568.88	62.469	1867	3	523.63	1.17
P0A7W4 RS5_SALTY 30S ribosomal protein S5	18	Oxidation+M(3)	VFMQPASEGTGHIAGGAMR	93	19	4	13.48	b5y12y15°y15	1908.94	62.504	8692	2	954.98	7.35
P0A7W4 RS5_SALTY 30S ribosomal protein S5	19		LEVAGVHNVLAK	114	12	4	25.94	b3b6b8*b8	1249.71	61.431	86370	2	625.36	-13.87
P0A7W4 RS5_SALTY 30S ribosomal protein S5	20		EVAGVHNVLAK	115	11	3	14.6	b4b8°b8	1136.64	61.396	13429	2	568.82	-5.48
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	1		LGEIEYR	48	7	11	77.83	b2b3b6y2y3°y3y4y5y6°y6y7	879.45	43.101	239489	2	440.23	-12.98
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	2		MITGIQITK	0	9	11	60.49	b1b2b3y2y3y4°y4*y4y6y7y9	1004.57	55.755	227330	2	502.79	-9.84
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	3		SGFAEDEVVAVSK	35	13	15	106.22	b3b4°b4b5b9y1y2°y2y4y6y7y8y9y10y13	1337.65	55.185	226671	2	669.33	-2.83
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	4		EIPMEVKPEVR	55	11	9	76.8	y2y4y5y6y7y8°y8y9y11	1326.71	49.464	111716	2	663.86	-0.83
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	5		FNSLTPEQQR	106	10	15	93.13	b2*b2b3°b3b5b10y3*y3y5y6y7y8*y8y9y10	1219.60	39.013	103513	2	610.30	-6.51

Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	6		FNSLTPEQQRDVIR	106	15	15	68.13	b2°b2b3°b3°b3b7b8y1y3y4y6y10°y10y13y15	1773.90	48.327	90815	3	591.97	-11.29
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	7		VEGGQHNLNVNVL	66	13	7	87.09	y3y4y5y6y7y8y11	1434.76	51.047	136018	3	478.92	-17.61
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	8		TFTESL	121	6	5	40.42	b3°b3b5°b5y4	697.34	56.197	80259	1	697.34	-3.50
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	9		AANDDLLNSFWLLDSEK	9	17	4	27.36	b3b4y10y13	1950.99	101.553	4689	2	976.00	21.59
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	10		AANDDLLNSFWLLDSEKGEAR	9	21	32	277.67	b3b4b5°b5°b5b6°b6°b6b7°b7b9b14y3y4y5y6°y6y7y8°y8y9°y9y10y11y12y13y14y15y16y17y18y19	2364.14	93.271	455838	3	788.72	-2.38
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	11		SGFAEDEVVAVSKLGEIEYR	35	20	3	21.14	b15y5y6	2198.11	116.108	26279	3	733.37	3.67
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	12	Carbamidomethyl+C(1)	CIVAKSGFAEDEVVAVSK	30	18	4	14.03	b8y13°y13y15	1908.97	76.303	4899	2	954.99	-2.69
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	13		DVIARTFTESL	116	11	5	48.48	b7b9y4y6y9	1251.64	63.697	2937	2	626.33	-10.63
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	14		PMEVKPEVR	57	9	3	29.1	b3b4b7	1084.58	49.473	106869	2	542.79	-6.19
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	15		TGIQITK	2	7	2	21.82	b4b5	760.46	55.740	9208	1	760.46	7.62
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	16		EIPMEVKPEVR	55	11	0	2.98		1308.68	49.468	39170	3	436.90	-12.31
P0A1H5 EFTU_SALTY Elongation factor Tu	1		MVVTLIHPIAMDDGLR	358	16	26	193.29	b1b2b3b4°b4b5°b5b6y1y3y4y5°y5y6y7y8y9°y9y10°y10y11°y11y12y13y15y16	1780.92	79.814	694534	3	594.31	-12.75
P0A1H5 EFTU_SALTY Elongation factor Tu	2		AIDKPFLPIEDVFSISGR	205	19	22	141.88	b2b6b7b8b9b12y2y3y4y5y6°y6y7y8°y8y9°y9y11°y11y15°y15y19	2117.14	105.404	499829	3	706.39	-10.15
P0A1H5 EFTU_SALTY Elongation factor Tu	3		ELLSQYDFPGDDTPIVR	155	17	25	177.55	b2°b2b5°b5°b5b6°b6b7b12b16y1y3y4y5y6y8y9y10y11°y11y12°y12y13y14y17	1964.97	77.575	325075	2	982.99	6.27
P0A1H5 EFTU_SALTY Elongation factor Tu	4		AGENVGVLLR	270	10	10	69.31	b4°b4y1y2y3y4y5y6y7°y7	1027.58	57.212	276404	2	514.29	-10.10
P0A1H5 EFTU_SALTY Elongation factor Tu	5		TTLTAAITTVLAK	25	13	15	117.98	b2°b2b4°b4b13y2y3y4y5y6y7y8y9y10y11	1303.78	85.335	242810	2	652.39	-2.34
P0A1H5 EFTU_SALTY Elongation factor Tu	6		TTDVTGTIELPEGVEMVMPGDNIK	334	24	38	234.6	b2°b2b3°b3b4°b4b5°b5b7°b7b8°b8b10°b10b12b13b14°b14b15b16b17°b17b18y3°y3y5y6°y6°y6y7y8y9y10y14°y14y15y16y24	2546.25	87.399	233124	2	1273.63	4.22
P0A1H5 EFTU_SALTY Elongation factor Tu	7		IIELAGFLDSYIPEPER	188	17	26	221.95	b2b3b4b5b6b7b11b12°b12b14y1y2y3y4y5°y5y7y8y9y10y12y13y14°y14y15y17	1962.03	102.544	215536	2	981.52	4.73
P0A1H5 EFTU_SALTY Elongation factor Tu	8		QVGVPYIIVFLNK	124	13	9	70.86	b3b4b13y4y5y6y9y11y13	1489.88	99.744	211817	2	745.44	1.72
P0A1H5 EFTU_SALTY Elongation factor Tu	9	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	10	76.3	b1y2y3y4y5°y5y6y7y8y10	1187.51	53.768	124971	2	594.26	-4.63
P0A1H5 EFTU_SALTY Elongation factor Tu	10	Carbamidomethyl+C(1)	CDMVDDDEELLELVEMEV	137	18	10	54.04	y3°y3y5y6°y6y8°y8y9°y9y11	2224.01	106.495	45139	2	1112.51	10.54

P0A1H5 EFTU_SALTY Elongation factor Tu	11		NMITGAAQMDGAILVVAATDGP MPQTR	90	27	8	36.18	b2b3b13y8y11*y11y12y13	2729.36	127.287	6810	3	910.46	6.17
P0A1H5 EFTU_SALTY Elongation factor Tu	12		GITINTSHVEYDTPTR	59	16	6	25.02	b10y5y8°y8y11°y11	1803.90	60.910	6691	2	902.45	6.56
P0A1H5 EFTU_SALTY Elongation factor Tu	13		VGEEVEIVGIK	238	11	8	38.39	b2b4°b4b7b10y2y3y11	1171.67	45.943	6528	2	586.34	10.11
P0A1H5 EFTU_SALTY Elongation factor Tu	14		ALEGDAEWEAK	177	11	4	33.62	b3b4b10y8	1218.56	47.378	189740	2	609.78	-2.91
P0A1H5 EFTU_SALTY Elongation factor Tu	15		TVGAGVVAK	382	9	6	60.49	b7°b7y3y5y7y8	801.47	29.361	184482	2	401.24	-20.94
P0A1H5 EFTU_SALTY Elongation factor Tu	16		TKPHVNVGTIGHVDH GK	8	17	3	14.67	b3b12y8	1795.93	90.671	50277	3	599.32	-12.37
P0A1H5 EFTU_SALTY Elongation factor Tu	17	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	4	16.31	b3b5y4°y4	1768.75	39.406	17517	4	442.94	-18.70
P0A1H5 EFTU_SALTY Elongation factor Tu	18		LLDEGR	264	6	1	12.8	b5	702.38	27.630	13422	1	702.38	-2.09
P0A1H5 EFTU_SALTY Elongation factor Tu	19		GIHK	234	4	1	11.81	y3	430.30	45.870	4891	1	430.30	-3.48
P0A1H5 EFTU_SALTY Elongation factor Tu	20		LLDEGRAGENVG VLLR	264	16	11	64.51	b7°b7b8b9°b9b10°b10b11° b11*b11b15	1710.93	66.064	13064	3	570.98	-8.63
P0A1H5 EFTU_SALTY Elongation factor Tu	21		GYRPQFYFR TTDVTGTIELPEGVE MVMPGDN IK	325	33	13	31.9	b4b11°b11b28y4°y4y6°y6* y6y10y11°y11y28	3760.87	136.418	3874	3	1254.30	10.32
P0A1H5 EFTU_SALTY Elongation factor Tu	22		HTPFKGYRQFYFR	319	15	6	26.7	b10°b10y3y4y8*y8	1990.99	80.380	3829	2	996.00	-7.11
P0A1H5 EFTU_SALTY Elongation factor Tu	23	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLE LVEMEV R	124	31	4	20.56	b3y3y4y7	3694.82	127.835	3819	3	1232.28	-6.48
P0A1H5 EFTU_SALTY Elongation factor Tu	24		ARGITINTSHVEYDTPTR	57	18	3	21.19	y6y9y12	2031.04	68.194	2287	3	677.69	9.38
P0A1H5 EFTU_SALTY Elongation factor Tu	25		ALEGDAEWEAKIIELAGFLDSYIPE PER	177	28	4	11.08	b5b11°b11y9	3161.58	84.310	1826	3	1054.53	4.86
P0A1H5 EFTU_SALTY Elongation factor Tu	26	Oxidation+M(1)	MVVTLIHPIAMDDGLR	358	16	4	37.19	y5y8y9y10	1796.92	74.486	32293	3	599.65	-8.90
P0A1H5 EFTU_SALTY Elongation factor Tu	27	Oxidation+M(18)	TTDVTGTIELPEGVEMVMPGDNI K	334	24	7	20.78	b6b11°b11y4y8*y8y10	2562.26	87.282	3151	2	1281.63	9.34
P0A1H5 EFTU_SALTY Elongation factor Tu	28		TGTIELPEGVEMVMPGDNIK	338	20	4	22	b5°b5b10b11	2130.03	87.369	20309	2	1065.52	-5.62
P0A1H5 EFTU_SALTY Elongation factor Tu	29		VTLIHPIAMDDGLR	360	14	5	23.13	b3°b3b5°b5b13	1550.83	79.795	20165	2	775.92	-0.87
P0A1H5 EFTU_SALTY Elongation factor Tu	30		TLIHPIAMDDGLR	361	13	1	7.35	b10	1451.77	79.808	1762	2	726.39	-1.35
P0AA28 THIO_SALTY Thioredoxin-1	1		LNIDQNPGTAPK	58	12	27	152.63	b2*b2b3b6°b6°b6b7°b7b10y1y2y3y4y5y6°y6y7y8°y8*y8y9°y9*y9y10°y10y11y12	1267.66	39.511	179353	2	634.33	-6.16
P0AA28 THIO_SALTY Thioredoxin-1	2		MIAPILDEIADEYQGK	37	16	15	127.38	b2b3y2y3*y3y4y5y7y9y10y11y12y13y14y16	1805.91	94.308	145118	2	903.46	4.93
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	9	63.5	b2y1y2y3y4y5y6y7y9	1001.63	91.533	96053	2	501.32	-7.37
P0AA28 THIO_SALTY Thioredoxin-1	4		EFLDANLA	101	8	9	47.69	b2b5°b5b7b8°b8°b8y6y7	892.43	71.103	10423	1	892.43	-11.76
P0AA28 THIO_SALTY Thioredoxin-1	5		VGALSK	91	6	2	25.1	b5y5	574.35	39.427	16657	1	574.35	-7.44
P0AA28 THIO_SALTY Thioredoxin-1	6		IIHLTDDSFDTDV LK	4	15	3	16.31	b8b10y9	1731.85	69.574	1817	2	866.43	-16.14
P0AA28 THIO_SALTY Thioredoxin-1	7		MIAPILDEIADEYQGKLTVAK	37	21	11	79.77	b3b11y4y5y7y11y12*y12y16y18y19	2318.23	95.449	192934	3	773.41	-0.53

P0AA28 THIO_SALTY Thioredoxin-1	8	Oxidation+M(1)	MIAPILDEIADEYQGK	37	16	6	21.61	b8b13°b13y9y13°y13	1821.88	123.554	1916	2	911.44	-7.77
P0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	16	112.24	b2b3°b3b4°b4b7y1y2y4y6y8y9y10y11y12y13	1447.78	65.992	142235	2	724.39	-0.84
P0A297 RL10_SALTY 50S ribosomal protein L10	2		AAAFEGELIPASQIDR	109	16	24	153.91	b1b3b5b7b8°b8b9b11y1y2°y2y5°y5°y5y6°y6y7y8y9y10y11y12°y12y16	1687.87	69.590	91022	2	844.44	5.42
P0A297 RL10_SALTY 50S ribosomal protein L10	3		GALSAVVADSR	20	11	7	48.93	b3y2y3y4y5y7y11	1045.56	49.201	59807	2	523.28	-8.17
P0A297 RL10_SALTY 50S ribosomal protein L10	4		DTFVGPTLIAYSMEHPGAAAR	73	21	7	35.49	b3b4b5°b5b11y14°y14	2204.09	76.893	22053	3	735.37	5.32
P0A297 RL10_SALTY 50S ribosomal protein L10	5	Carbamidomethyl+C(9)	VVEGTQFECLK	62	11	3	22.11	b4b7y5	1309.67	68.350	5435	2	655.34	19.76
P0A297 RL10_SALTY 50S ribosomal protein L10	6		GVTVDKMTCLR	31	11	3	29.1	y4y5y7	1248.65	48.313	8972	2	624.83	-11.83
P0A297 RL10_SALTY 50S ribosomal protein L10	7		FEVKAAAFEGELIPASQIDR	105	20	3	19.8	y5y11y15	2191.12	76.156	6975	4	548.53	-10.03
P0A297 RL10_SALTY 50S ribosomal protein L10	8		AAAFEGELIPASQIDRLATLPTYEEAIAR	109	29	7	29.06	b5b6b11b18b25°b25y4	3116.59	100.856	6301	3	1039.53	-13.16
P0A297 RL10_SALTY 50S ribosomal protein L10	9	Carbamidomethyl+C(10)	RVVEGTQFECLK	61	12	5	52.69	y4°y4y6y9y11	1465.73	65.404	2601	2	733.37	-12.49
P0A297 RL10_SALTY 50S ribosomal protein L10	10		AGREAGVYMR	43	10	7	80.83	b6b9y3y4y5y7y8	1109.55	64.410	1896	2	555.28	-2.75
P0A297 RL10_SALTY 50S ribosomal protein L10	11	Oxidation+M(13)	DTFVGPTLIAYSMEHPGAAAR	73	21	3	12.6	b11y9y12	2220.09	71.040	12663	3	740.70	5.17
P0A297 RL10_SALTY 50S ribosomal protein L10	12	Oxidation+M(9)	AGREAGVYMR	43	10	4	36.13	b4b7y5y9	1125.54	103.747	1633	1	1125.54	-4.66
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		EMLPVLEAVAK	231	11	10	79.81	b2°b2y1y3y4y5y7y8y9y11	1199.67	80.860	190028	2	600.34	-4.27
P0A1D3 CH60_SALTY 60 kDa chaperonin	2		ANDAAGDGTTTATVLAQSIITEGLK	80	25	31	205.08	b2°b2b3°b3b4°b4°b4b5b6b14b15°b15b16b18°b18y1y3y4°y4y5y6y7y8y9°y9y10y11y12y13y18y25	2418.23	92.748	183301	3	806.75	-1.62
P0A1D3 CH60_SALTY 60 kDa chaperonin	3		VVINKDTTTHIDGVGEEAAIQGR	322	23	9	53.18	b2b3y2y3y4y5y6y9y12	2399.27	68.540	150366	3	800.43	-1.93
P0A1D3 CH60_SALTY 60 kDa chaperonin	4		AVAAAVEELK	122	10	11	69.31	b1b2b3y2y3°y3y5y6y7y8y10	1000.56	48.352	149353	2	500.78	-9.82
P0A1D3 CH60_SALTY 60 kDa chaperonin	5	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDLPK	501	25	14	63.1	b1b3b5°b5b9b11y2y3y6°y6y7y8y9y25	2670.32	125.367	125697	3	890.78	0.18
P0A1D3 CH60_SALTY 60 kDa chaperonin	6		SFGAPTITK	42	9	8	49.95	b2b3°b3y1y2y3y5y7	921.49	45.967	124514	2	461.25	-13.05
P0A1D3 CH60_SALTY 60 kDa chaperonin	7		GVNVLADAVK	18	10	9	85.6	b2b3b4b5b7y3y6y8y10	985.56	56.964	116477	2	493.28	-12.70
P0A1D3 CH60_SALTY 60 kDa chaperonin	8	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	16	93.01	b6°b6b7b10b13°b13y5y6y9y12y13°y13y14y15y18°y18	1957.01	62.586	102105	2	979.01	4.55
P0A1D3 CH60_SALTY 60 kDa chaperonin	9		QQIEEATSDYDREK	350	14	11	88.58	b8b14y3y5y6y7y8y9y11y14°y14	1711.75	34.587	100074	3	571.26	-13.69
P0A1D3 CH60_SALTY 60 kDa chaperonin	10	Carbamidomethyl+C(6)	ALSVPSCDSK	132	10	12	81.62	b2b3°b3y2y4y5y6°y6y7y8y9y10	1063.50	36.346	92991	2	532.25	-7.12
P0A1D3 CH60_SALTY 60 kDa chaperonin	11		AIAQVGTISANSDETGVGK	142	18	14	85.98	b4b7b12°b12y2y9y10y11y12y13°y13°y13y14y18	1760.91	49.352	66695	2	880.96	3.60
P0A1D3 CH60_SALTY 60 kDa chaperonin	12		VEDALHATR	395	9	9	83.34	b1b3b4y3y4y6y7y8y9	1011.51	27.336	60505	2	506.26	-6.82

[P0A1D3]CH60_SALTY 60 kDa chaperonin	13		AVAAGMNPMDLK	105	12	10	78.14	b2b3y2y5y6y7y8y9y10y12	1217.60	59.296	47861	2	609.30	-0.80
[P0A1D3]CH60_SALTY 60 kDa chaperonin	14		AVAAGMNPMDLKR	105	13	17	113.79	b2b3b8b13y2y3y5y6*y6y7*y7y8y9y10*y10y11y13	1373.71	51.807	46932	2	687.36	3.11
[P0A1D3]CH60_SALTY 60 kDa chaperonin	15		GGDGNYGYNAAATEEYGNMIDMG ILDPTK	470	28	7	31.03	y2y3y4y9y12y14y28	2966.32	89.089	45513	3	989.44	11.93
[P0A1D3]CH60_SALTY 60 kDa chaperonin	16		LIAEAMDK	160	8	5	38.4	y2y3y5y6y8	890.46	40.244	23856	2	445.73	-10.90
[P0A1D3]CH60_SALTY 60 kDa chaperonin	17		SFGAPTITKDGVSVAR	42	16	5	31.87	b3b4b15y7y10	1605.86	55.930	13823	2	803.43	-1.37
[P0A1D3]CH60_SALTY 60 kDa chaperonin	18		AGKPLIIAEDVEGEALATLVVNT MR	242	26	7	11.33	b2b7y1y2y5y8*y8	2723.54	136.321	12066	3	908.52	13.80
[P0A1D3]CH60_SALTY 60 kDa chaperonin	19		SDAPDLGAAGGMGGMGGMGGM M	526	22	5	18.77	b2b3b6*b6b8	1927.77	81.195	8197	2	964.39	14.06
[P0A1D3]CH60_SALTY 60 kDa chaperonin	20		ATLEDLGQAK	311	10	3	31.61	b4b5b9	1045.55	37.321	228113	2	523.28	1.40
[P0A1D3]CH60_SALTY 60 kDa chaperonin	21		LAGGVAVIK	371	9	6	74.05	b5b6y3y4y7y8	827.52	46.072	126783	2	414.26	-20.06
[P0A1D3]CH60_SALTY 60 kDa chaperonin	22		GQNEDQNVGIK	430	11	3	22.11	b10y3y5	1201.56	38.818	9408	2	601.28	-19.20
[P0A1D3]CH60_SALTY 60 kDa chaperonin	23		VTLGPK	28	6	3	37.41	b3y4y5	614.38	29.296	5844	1	614.38	-4.87
[P0A1D3]CH60_SALTY 60 kDa chaperonin	24		DTTTIIDGVGEEAAIQGR	327	18	7	42.11	b3b4b9*b9b12b15y12	1845.90	122.867	2241	2	923.46	-8.07
[P0A1D3]CH60_SALTY 60 kDa chaperonin	25		EIELEDK	58	7	3	37.9	y3y5y6	875.43	43.207	2070	2	438.22	-2.79
[P0A1D3]CH60_SALTY 60 kDa chaperonin	26		FGNDAR	7	6	2	25.1	b3y5	679.33	74.059	1791	1	679.33	13.66
[P0A1D3]CH60_SALTY 60 kDa chaperonin	27		GYLYFINKPETGAVELEFILLADK K	197	29	14	89.52	b3b4*b4b7y3y4*y4y5y6y7y9y12y25y26	3239.71	96.510	238453	4	810.68	-3.39
[P0A1D3]CH60_SALTY 60 kDa chaperonin	28		IADLKGQNEQNVGIK	425	16	16	130.39	b3*b3y3y4y6y8*y8y9*y9y11y12*y12y13y14y15*y15	1741.89	40.972	143513	3	581.30	-12.33
[P0A1D3]CH60_SALTY 60 kDa chaperonin	29		EIELEDKFENMGAMVK	58	17	5	20.37	b3*b3b9y6y8	2010.94	74.190	141810	3	670.99	-4.86
[P0A1D3]CH60_SALTY 60 kDa chaperonin	30	Carbamidomethyl+C(16)	AVAAAVEELKALSVPSCDSK	122	20	4	29.72	y3y6y10y18	2045.05	72.894	85051	3	682.35	-6.15
[P0A1D3]CH60_SALTY 60 kDa chaperonin	31		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	24	106.77	b3b4b6*b6*b6b8*b8b9b15y4y6*y6y7y9*y9y12*y12y17y21y25*y25y26y27y29	3675.88	122.880	49692	3	1225.96	1.39
[P0A1D3]CH60_SALTY 60 kDa chaperonin	32	Carbamidomethyl+C(13)	AMEAPLRQIVLNCGEEPSVVANT VK	445	25	14	70.71	b3b6b7*b7b9*b9b10b11b19y5y9y12*y12y14	2725.41	74.894	38897	3	909.14	3.05
[P0A1D3]CH60_SALTY 60 kDa chaperonin	33		VGKEGVITVEDGTGLQDELDDVVE GMQFDR	168	29	4	20.68	b11y3y4y12	3135.51	73.765	27427	4	784.63	-2.34
[P0A1D3]CH60_SALTY 60 kDa chaperonin	34		AIAQVGTISANSDETGVGLIAEAM DK	142	26	3	11.33	b5y6y21	2632.35	92.428	17439	3	878.12	-0.37
[P0A1D3]CH60_SALTY 60 kDa chaperonin	35	Carbamidomethyl+C(6)	ALSVPSCDSKAIAQVGTISANSDE TVGK	132	28	3	21.29	b18y13y14	2805.38	100.797	12344	3	935.80	-3.66
[P0A1D3]CH60_SALTY 60 kDa chaperonin	36	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVKGGDGN YGYNAATEEYGNMIDMGILDPTK	452	46	6	22.86	b9b13b14y3y9y13	4904.27	90.202	10406	4	1226.82	0.80
[P0A1D3]CH60_SALTY 60 kDa chaperonin	37		DGVSVAREIELEDK	51	14	3	17.37	b4b6y5	1559.79	60.099	3201	3	520.60	-2.43
[P0A1D3]CH60_SALTY 60 kDa chaperonin	38		ANDAAGDGTTTATVLAQSIIIEGL KAVAAGMNPMDLK	80	37	3	11.08	b16y3y6	3616.85	113.355	3162	3	1206.29	8.84
[P0A1D3]CH60_SALTY 60 kDa chaperonin	39		VGAATEVEMKEK	380	12	5	29.17	b6b11*b11y5y9	1291.64	74.882	2358	2	646.32	-14.84

[P0A1D3]CH60_SALTY 60 kDa chaperonin	40	Phohoryl STY(6)	SFGAPTITKDGVSVAR	42	16	3	21.96	b5y11y12	1685.81	94.483	22560	2	843.41	-2.10
[P0A1D3]CH60_SALTY 60 kDa chaperonin	41	Oxidation+M(21)	AMLQDIATLTGGTVISEEIGMELE K	286	25	3	11.5	b11y5y10	2665.29	93.162	21485	3	889.10	-14.84
[P0A1D3]CH60_SALTY 60 kDa chaperonin	42	Oxidation+M(22)	EGVITVEDGTGLQDELDVVEGMQ FDR	171	26	5	34.55	b9°b9b10b11°b11	2867.36	66.050	13122	3	956.46	12.86
[P0A1D3]CH60_SALTY 60 kDa chaperonin	43	Oxidation+M(9)	AVAAGMNPMDLKR	105	13	7	26.74	b6b8y7°y7*y7y12*y12	1389.70	65.368	10968	2	695.35	3.16
[P0A1D3]CH60_SALTY 60 kDa chaperonin	44	Oxidation+M(9)	VGAATEVEMK	380	10	3	31.61	b4b6b7	1050.51	110.868	2049	1	1050.51	-5.81
[P0A1D3]CH60_SALTY 60 kDa chaperonin	45		AAGMNPMDLKR	107	11	1	7.25	b3	1203.60	51.806	97575	2	602.30	-1.52
[P0A1D3]CH60_SALTY 60 kDa chaperonin	46		EDALHATR	396	8	2	8.27	b3°b3	912.45	27.332	43436	2	456.73	-8.50
[P0A1D3]CH60_SALTY 60 kDa chaperonin	47		AAAVEELK	124	8	2	7.8	b6°b6	830.46	48.359	22430	1	830.46	-7.13
[P0A1D3]CH60_SALTY 60 kDa chaperonin	48		SFGAPTITKDG V	42	12	0	5.46		1192.63	55.891	12855	2	596.82	9.83
[P0A1D3]CH60_SALTY 60 kDa chaperonin	49		NVLADAVK	20	8	0	2.48		829.48	56.946	9659	1	829.48	-3.38
[P0A1D3]CH60_SALTY 60 kDa chaperonin	50		AAVEELK	125	7	3	21.07	b5°b5b6	759.42	48.341	3500	1	759.42	-8.52
[P0A1D3]CH60_SALTY 60 kDa chaperonin	51	Carbamidomethyl+C(4)	SVPCSDSK	134	8	1	7.8	b4	879.39	36.356	2610	1	879.39	-1.25
[P0A1D3]CH60_SALTY 60 kDa chaperonin	52		DVEGEALATLVVNTMR	252	16	4	34.55	b10°b10b11b12	1717.87	136.372	1585	2	859.44	-5.76
[P0A1D3]CH60_SALTY 60 kDa chaperonin	53		EMLPVLEAVAK	231	11	1	7.5	y6	1181.65	80.878	12070	2	591.33	-7.54
[P0A1D3]CH60_SALTY 60 kDa chaperonin	54		QQIEEATSDYDREK	350	14	0	4.47		1693.74	34.566	4187	3	565.25	-14.85
[P0A1E3]CYSK_SALTY Cysteine synthase A	1		IGANMIWDAEKR	44	12	12	54.74	b5°b5b7b12y1y2y5y7°y7y9y10y12	1403.69	60.848	129290	3	468.57	-14.61
[P0A1E3]CYSK_SALTY Cysteine synthase A	2		YLLQQFSNPANPEIHEK	137	18	23	157.66	b2b3b4b9°b9b12°b12y3y4y5y6°y6y8y9°y9*y9y10y11°y11y12y15y16y18	2141.10	74.848	118721	3	714.37	-2.62
[P0A1E3]CYSK_SALTY Cysteine synthase A	3		IQGIGAGFIPGNLDLK	226	16	18	92.14	b2°b2b3b4b8°b8y1y2y3y6y7°y7y10*y10y11y12y14y16	1612.91	84.249	110181	2	806.96	2.57
[P0A1E3]CYSK_SALTY Cysteine synthase A	4		LTLTMPETMSIER	87	13	11	78.6	b5°b5b8b12y1y6y8y9y10y12y13	1521.77	74.708	88714	2	761.39	5.21
[P0A1E3]CYSK_SALTY Cysteine synthase A	5		GVLKPGVELVEPTSGNTGIALAYV AAAR	56	28	4	22.1	y6y7y9y28	2753.53	82.364	82961	3	918.51	3.37
[P0A1E3]CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	9	77.05	b2b3b4y6y7y8y9y10y12	1283.73	64.879	53686	2	642.37	-0.95
[P0A1E3]CYSK_SALTY Cysteine synthase A	7		IYEDNSLTIGHTPLVR	3	16	4	28.14	b7b8y7y14	1827.94	62.530	47747	3	609.98	-12.89
[P0A1E3]CYSK_SALTY Cysteine synthase A	8		AEEIVASDPQK	126	11	10	79.1	b2b3b4y2y3y6y7y8y9y11	1186.59	32.563	39097	2	593.80	-3.81
[P0A1E3]CYSK_SALTY Cysteine synthase A	9		VVGITNEEAISTAR	246	14	7	38.66	b3y4y9y10*y10y12y14	1459.77	50.406	22576	2	730.39	-0.75
[P0A1E3]CYSK_SALTY Cysteine synthase A	10		YLSTALFADLFTEK	305	14	3	17.37	b5b11y9	1618.83	104.012	10012	2	809.92	-2.04
[P0A1E3]CYSK_SALTY Cysteine synthase A	11		IGANMIWDAEK	44	11	13	87.61	b4°b4b5°b5b6°b6b7°b7b9y4y8y9°y9	1247.62	63.673	2616	2	624.31	5.19
[P0A1E3]CYSK_SALTY Cysteine synthase A	12		YLSTALFADLFTEKELQQ	305	18	4	22.36	b16y5y8y13	2117.10	103.060	107615	2	1059.05	7.15
[P0A1E3]CYSK_SALTY Cysteine synthase A	13		LIDKVVGITNEEAISTAR	242	18	7	42.11	b4y3y8y10y11y13*y13	1929.04	60.835	95715	3	643.69	-12.72

[P0A1E3]CYSK_SALTY Cysteine synthase A	14		AEEIVASDPQKYLLQQFSNPANP EIHEK	126	29	12	80.01	b3b5b10b12b13b14y3y6y7y9y10y11	3308.66	77.914	45705	4	827.92	-4.72
[P0A1E3]CYSK_SALTY Cysteine synthase A	15		IGANMIWDAEKR	44	12	4	24.15	b7b8°b8y5	1403.69	64.371	19899	2	702.35	-12.35
[P0A1E3]CYSK_SALTY Cysteine synthase A	16		LQEDESFTNKNIVVILPSSGER	283	22	3	22.13	y5y6y8	2475.29	70.416	19890	3	825.77	8.09
[P0A1E3]CYSK_SALTY Cysteine synthase A	17		GYKLTLTMPETMSIER	84	16	3	15.43	b12y6y8	1869.96	87.170	15712	2	935.49	10.05
[P0A1E3]CYSK_SALTY Cysteine synthase A	18		ILAKVESR	27	8	3	38.4	y3y4y5	915.56	72.427	12501	2	458.28	-5.47
[P0A1E3]CYSK_SALTY Cysteine synthase A	19		MSKIYEDNSLTIGHTPLVR	0	19	4	21.28	b4b7b13y13	2174.16	90.145	9464	2	1087.58	14.26
[P0A1E3]CYSK_SALTY Cysteine synthase A	20		LMEEEGILAGISSGAAVAAALKLQ EDESFTNK	261	32	4	10.89	b8y6y10*y10	3292.68	127.131	4190	3	1098.23	6.23
[P0A1E3]CYSK_SALTY Cysteine synthase A	21	Phohoryl STY(8)	YLLLQQFSNPANPEIHEK	137	18	10	50.56	b8_H3PO4 b8_HPO3 b8y4°y4y7°y7*y7y8y9*y9y10	2221.08	64.399	16065	3	741.03	7.91
[P0A1E3]CYSK_SALTY Cysteine synthase A	22	Phohoryl STY(4)	YLSTALFADLFTEK	305	14	3	17.37	b3b12y12	1698.82	64.363	8466	2	849.91	13.58
[P0A1E3]CYSK_SALTY Cysteine synthase A	23	Phohoryl STY(12)	IYEDNSLTIGHTPLVR	3	16	9	54.84	b4b7°b7b8b9b11°b11y5y9	1907.94	122.843	1817	2	954.47	12.16
[P0A1E3]CYSK_SALTY Cysteine synthase A	24	Oxidation+M(9)	LTLTMPETMSIER	87	13	6	49.8	b7b9b10b12y8y11	1537.78	65.397	2851	2	769.40	14.84
[P0A1E3]CYSK_SALTY Cysteine synthase A	25		ANMIWDAEKR	46	10	1	7.33	b5	1233.61	60.897	70267	2	617.31	7.03
[P0A1E3]CYSK_SALTY Cysteine synthase A	26		NSLTIGHTPLVR	7	12	4	13.54	b4°b4b7*b7	1307.74	62.510	5163	2	654.37	-4.67
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	22	105.43	b2*b2b3*b3b4*b4b9y1y2y3°y3y4*y4y5*y5y6°y6y7°y7*y7y8y10	1129.61	40.000	190803	2	565.31	-7.56
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	17	121.36	b2b3b5°b5b9y2y3y4y5°y5y6y7°y7y8y9y10y14	1452.65	58.349	137023	2	726.83	1.85
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	3		TPPAAVLLKK	72	10	4	34.62	y6y7y8y10	1037.66	45.506	37793	2	519.34	-8.59
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	4		TPPAAVLLK	72	9	6	55.72	b3b6°b6y4y5y7	909.56	55.248	140906	2	455.28	-15.84
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	5		SFTFVTK	65	7	4	37.9	y4y5°y5y6	829.44	54.713	89833	2	415.22	-10.30
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	6		SMGLVVED	134	8	3	33.63	b6y3y5	849.39	59.143	69104	1	849.39	-19.69
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	7		AFNAKTDSIEK	40	11	9	51.94	b4b6°b6b7°b7b10°b10y10°y10	1223.61	65.354	12035	2	612.31	-10.38
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	8		AQLQEIAQTKAADMTGADIEAMT R	103	24	4	11.71	b8*b8y5y10	2563.28	106.170	6704	3	855.10	10.67
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	9	Carbamidomethyl+C(29) ;Oxidation+M(26)	LQVAAGMANPPVGPALGQQGVNI MEFCCK	10	30	3	21.54	b15y7y8	3097.52	132.250	1675	3	1033.18	-2.60
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	10		PAAVLLKK	74	8	1	7.8	b3	839.56	45.513	14665	2	420.29	-9.96
[P0A7K0]RL11_SALTY 50S ribosomal protein L11	11		QLQEIAQTK	104	9	1	7.8	b6	1058.57	40.037	6079	2	529.79	-14.53
[P66038]RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	20	120.55	b3b8b9b10°b10b11°b11b12b13b14°b14b20y2y3y4y9y12y15y16y29	3110.69	99.127	143403	3	1037.57	4.24

P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	23	170.06	b3b4b5b6*b6b11*b11*b11 b13b14y2y3y4y5y6y8y9y1 0y12y14°y14y15y19	2109.08	102.078	98602	2	1055.04	8.57
P66038 RISB_SALTY 6	3		GAEAAALTALEMINVLK	136	16	11	104.7	b4b5b6b7b9b11b12b13y1 4y5	1643.90	103.744	42712	2	822.46	0.45
P66038 RISB_SALTY 6	4		VAITIAI	14	7	4	50.21	y3y4y5y6	743.46	45.157	24174	2	372.24	-18.31
P66038 RISB_SALTY 6	5	Phohoryl STY(10)	IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	7	38.1	b3b7b8b11°b11b12*b12	3190.65	136.438	6913	3	1064.22	4.06
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	34	202.42	b2*b2b3b5°b5b7°b7b9°b9* b9b10*b10b11*b11b12°b1 2b14b16b17y4y5y6*y6y7* y7y8y9*y9y10*y10y11y12 y17y23	2379.24	65.371	213615	3	793.75	0.62
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2		AQAFTLVAK	24	9	9	42.17	b3y1y2y3y6°y6y7y9*y9	948.54	54.184	176270	2	474.77	-12.74
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	16	85.48	b1b2b3b4b5°b5b10y2y3y6 y10y13°y13y14y15y18	1919.02	86.002	104870	2	960.01	5.09
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	9	52.43	b2b3b7y4y5y6y13y15y17	1837.96	86.887	103449	2	919.48	4.91
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		DLSDVSLSQYAGK	33	13	14	90.9	b2b4b5b7b11b12y1y2y3y6 y7*y7y8y13	1382.69	60.114	57735	2	691.85	6.18
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVRK	48	19	5	29.22	b2y8y11y14y15	2047.09	79.189	36961	3	683.03	-6.56
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		DLSDVSLSQYAGKR	33	14	6	38.91	y5y6y7*y7y9y14	1538.78	55.672	28918	2	769.89	0.48
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8		AQAFTLVAKDLSDVSLSQYAGK	24	22	4	12.26	b13y2y6y13	2312.23	84.448	13493	3	771.41	6.34
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9		NYGVEIVDGPLK	116	12	5	33.15	b3b11y8y9y12	1303.69	36.640	7898	2	652.35	2.06
Q8ZP65 TPX_SALTY Probable thiol peroxidase	10		AVIVLDENDNVIFSQLVDEITHEPD YDAALNVLK	133	34	3	10.91	b3b8y11	3811.89	125.618	2910	4	953.73	-11.08
Q8ZP65 TPX_SALTY Probable thiol peroxidase	11		AVIVLDENDNVIFSQLVDEITHEPD YDAALNVLKA	133	35	30	220.64	b3b4b5b6b7b10°b10b11*b 11b14°b14y3y4y5y6y7y8y1 1y12y13°y13*y13y18y19y2 0y22y24y28y30y31	3882.97	120.748	182646	3	1294.99	0.06
Q8ZP65 TPX_SALTY Probable thiol peroxidase	12		DLSDVSLSQYAGKR	33	14	9	52.06	b3b6b10°b10°b10b13*b13 y3y7	1538.80	64.483	4569	3	513.60	10.95
Q8ZP65 TPX_SALTY Probable thiol peroxidase	13	Phohoryl STY(13)	MSQTVHFQGNPVTVANVIPQAGS K	0	24	4	11.71	b4b12°b12y12	2590.21	87.402	55567	3	864.08	-10.65
Q8ZP65 TPX_SALTY Probable thiol peroxidase	14		LSDVSLSQYAGKR	34	13	0	4.47		1423.77	55.725	3307	3	475.26	13.03
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	21	118.14	b2°b2b3°b3b4°b4y2y3y4°y 4y5y11*y11y12°y12*y12y1 3y15y16y17y19	2130.16	93.430	311782	3	710.73	-5.50
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		VGDPVIEFDLPLEEK	115	16	23	166.21	b2b3b4b5b6b7b8°b8b11b1 6y2°y2y3°y3y4y6y8y9y10° y10y11y13y16	1812.98	100.299	166931	2	906.99	7.14
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		MVAPVDGTIGK	59	11	15	115.22	b1b2b3b8b9y2y3y5y6y7°y 7y8y9y10y11	1087.57	47.144	144195	2	544.29	-10.78
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		IVGDGIAIKPTGNK	45	14	11	100.73	b5b7y3y4y5°y5°y5y6y8y10 y12	1382.77	44.475	172606	3	461.59	-21.63

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		STLTPVVISNMDEIK	133	15	10	68.13	b3°b3b4b6y3y4y7y8°y8y11	1646.89	73.949	9023	2	823.95	12.68
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		GEGFK	100	5	3	24.61	b3b4°b4	537.27	64.410	3962	1	537.27	8.75
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		VKVGDPVIEFDLPLLEEK	113	18	9	37.69	b5°b5b11°b11b12y3°y3y6y10	2040.12	96.330	104501	3	680.71	-5.15
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		SLVSDDKK	8	8	3	30.62	b5b6y5	891.48	64.426	1864	2	446.24	1.92
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9		PVDGTIGK	62	8	5	47.42	b4b5b6°b6b7	786.42	47.158	2772	1	786.42	-14.67
P64052 EFTS_SALTY Elongation factor Ts	1		VASLEGDVLGSYQHGAR	134	17	18	152.48	b1b8b9°b9y1y3y4y5y6y7y8°y8y10y11y12y13y16y17	1758.86	59.919	231229	3	586.96	-9.09
P64052 EFTS_SALTY Elongation factor Ts	2		ITDVEVLK	104	8	9	72.3	b2b3b4y2y4y5y6y7y8	916.52	49.560	145514	2	458.77	-10.99
P64052 EFTS_SALTY Elongation factor Ts	3		AEITASLVK	1	9	7	69.79	b3y3y4y5y6y7y9	931.54	49.635	138602	2	466.27	-10.29
P64052 EFTS_SALTY Elongation factor Ts	4		IGENINIR	125	8	10	63.01	y2y3°y3y4y5y6y7°y7°y7y8	928.51	45.605	90423	2	464.76	-12.88
P64052 EFTS_SALTY Elongation factor Ts	5	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	5	48.69	y3y4y5y7y10	1098.48	22.046	41601	2	549.74	2.44
P64052 EFTS_SALTY Elongation factor Ts	6		AGNVAADGVIK	52	11	6	33.62	b9y2y4y6y7y11	1014.55	37.822	39511	2	507.78	-11.31
P64052 EFTS_SALTY Elongation factor Ts	7		EYQVQLDIAMQSGKPKEIAEK	193	21	4	12.6	b3b6°b6y10	2405.24	86.368	18490	3	802.42	0.61
P64052 EFTS_SALTY Elongation factor Ts	8		ALTEANGDIELAIENMRK	25	18	4	22.95	y3y5y6y18	1988.02	67.735	17574	2	994.52	6.63
P64052 EFTS_SALTY Elongation factor Ts	9		ALTEANGDIELAIENMR	25	17	4	24.84	b5y4y6y7	1859.94	81.608	11992	2	930.48	14.90
P64052 EFTS_SALTY Elongation factor Ts	10		FTGEVSLTGQPFVMEPSK	222	18	5	36.77	b7b8y5y7y8	1953.96	68.298	3815	3	651.99	-2.00
P64052 EFTS_SALTY Elongation factor Ts	11		VETDFAAEVAAMSK	267	14	4	17.37	b6b14y3y12	1468.70	107.771	2346	2	734.85	-1.16
P64052 EFTS_SALTY Elongation factor Ts	12		IGVLVAAK	151	8	6	72.3	b3b4y3y4y5y7	770.50	48.162	86876	2	385.75	-21.70
P64052 EFTS_SALTY Elongation factor Ts	13		QLAMHVAASKPEFVKPEDVSADV VEK	167	26	10	53.12	b5b6b9°b9b25y7y8°y8y11y12	2824.50	136.380	15574	3	942.17	17.63
P64052 EFTS_SALTY Elongation factor Ts	14	Carbamidomethyl+C(13)	IDGNVAFILEVNCQTDFVAK	65	20	6	27.44	b4b10y9y13°y13y14	2253.16	107.932	4621	2	1127.08	17.99
P64052 EFTS_SALTY Elongation factor Ts	15		KAGNVAADGVIK	51	12	3	27.38	y7y10y11	1142.64	33.088	64821	2	571.82	-9.83
P64052 EFTS_SALTY Elongation factor Ts	16		DAGFQAFADKVLDAAVAGK	85	19	6	28.34	b5b13b14°b14y3y7	1893.96	98.989	58747	2	947.48	-5.93
P64052 EFTS_SALTY Elongation factor Ts	17		ALTEANGDIELAIENMRK	25	18	3	22.95	y4y5y14	1988.00	75.155	48294	3	663.34	-4.18
P64052 EFTS_SALTY Elongation factor Ts	18		FEVGEGIEK VETDFAAEVAAMSK	258	23	9	40.71	b4b7°b7b9b14b17y5y9°y9	2457.18	107.949	29733	3	819.73	-1.79
P64052 EFTS_SALTY Elongation factor Ts	19		EHNADVTGFIRFEVGEGIEK	247	20	5	27.44	b9b10b15y8y19	2247.08	87.344	18154	3	749.70	-12.28
P64052 EFTS_SALTY Elongation factor Ts	20		KFTGEVSLTGQPFVMEPSK	221	19	12	68.66	b11y4y5y7y8y9°y9°y9y10°y10y12°y12	2082.06	65.406	9436	2	1041.53	-0.70
P64052 EFTS_SALTY Elongation factor Ts	21	Oxidation+M(16)	ALTEANGDIELAIENMR	25	17	6	30.53	b5°b5b15y6y7y11	1875.93	96.346	2891	2	938.47	10.61

P64052 EFTS_SALTY Elongation factor Ts	22	Oxidation+M(14)	FTGEVSLTGQPFVMEPSK	222	18	6	34.09	b10b11°b11y11y12°y12	1969.95	120.757	1593	2	985.48	-6.01
P64052 EFTS_SALTY Elongation factor Ts	23		ITASLVK	3	7	0	1.99		731.46	49.644	15514	1	731.46	-5.34
P64052 EFTS_SALTY Elongation factor Ts	24	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	0	2.48		997.42	22.054	11980	2	499.22	-2.02
P64052 EFTS_SALTY Elongation factor Ts	25		VASLEGDVLGS	134	11	0	5.96		1046.54	59.928	7230	2	523.78	7.82
P64052 EFTS_SALTY Elongation factor Ts	26		TDVEVLK	105	7	4	38.4	b3b4°b4b5	803.44	49.553	6397	1	803.44	-9.12
P64052 EFTS_SALTY Elongation factor Ts	27		SLEGDVLGSYQHGAR	136	15	3	22.08	b3b6b10	1588.79	59.971	6320	2	794.90	9.68
P00499 HIS1_SALTY ATP phohoribosyltransferase	1		LSLATPVDEAWDGPAALDGKR	105	21	21	145.21	b2°b2b3°b3b14y1y3y4y5y7y8y9y10y11°y11y12y16y17y18°y18y21	2182.11	76.891	100038	3	728.04	-0.78
P00499 HIS1_SALTY ATP phohoribosyltransferase	2		LIAMAENMPIDILR	38	14	15	117.26	b3b5b6b8y1y2y3y6y8*y8y9y10y11y12y14	1599.87	91.310	96732	2	800.44	5.04
P00499 HIS1_SALTY ATP phohoribosyltransferase	3		IQGVIQAR	216	8	8	50.7	b2y1y4y5y6y7*y7y8	884.52	36.742	51101	2	442.76	-11.59
P00499 HIS1_SALTY ATP phohoribosyltransferase	4		LEEVIALLPGAERPTILPLAGEQQR	237	25	9	37.87	b2°b2b3b4y5y6*y6y17y21	2713.51	90.749	29516	3	905.18	-5.13
P00499 HIS1_SALTY ATP phohoribosyltransferase	5		LSLATPVDEAWDGPAALDGK	105	20	9	25.61	b1b9°b9b12y2y10°y10y11°y11	2026.02	63.688	3592	2	1013.51	2.83
P00499 HIS1_SALTY ATP phohoribosyltransferase	6		ELLAR	22	5	2	24.61	b3b4	601.36	29.353	95943	1	601.36	-7.10
P00499 HIS1_SALTY ATP phohoribosyltransferase	7		LDNTR	1	5	2	24.61	b4y4	618.31	81.549	15838	1	618.31	-10.76
P00499 HIS1_SALTY ATP phohoribosyltransferase	8		YLTLR	92	5	1	12.3	y4	665.39	45.314	8350	1	665.39	-9.08
P00499 HIS1_SALTY ATP phohoribosyltransferase	9	Carbamidomethyl+C(8)	AGLADAICDLVSTGATLEANGLR	160	23	17	75.21	b3b6°b6b7b8°b8b9°b9b13°b13b15y6°y6*y6y12y13*y13	2288.11	65.341	5942	3	763.37	-20.27
P00499 HIS1_SALTY ATP phohoribosyltransferase	10		YLDQK	137	5	1	12.3	y3	666.35	49.781	4600	1	666.35	8.52
P00499 HIS1_SALTY ATP phohoribosyltransferase	11		DDDIPGLVMDGVVDLGIIGENVLEEELLNR	54	30	4	10.94	b14b16°b16y4	3251.59	98.089	4539	4	813.65	-13.67
P00499 HIS1_SALTY ATP phohoribosyltransferase	12		VAMHMOVSETLFWETMEK	262	18	4	22.36	b8y5y8y10	2156.00	84.581	2614	3	719.34	6.23
P00499 HIS1_SALTY ATP phohoribosyltransferase	13		ALGASSILVLPIEK	282	14	10	85.96	b5b7°b7b10y5y6y7y9y10y12	1410.83	85.292	2406	1	1410.83	-18.43
P00499 HIS1_SALTY ATP phohoribosyltransferase	14		YIMMHAPSERLEEVIALLPGAERTILPLAGEQQR	227	35	4	23.02	y3y5y6°y6	3929.05	97.876	22405	5	786.62	-7.02
P00499 HIS1_SALTY ATP phohoribosyltransferase	15	Carbamidomethyl+C(7)	GVSFKSCLLNGSVEVAPR	142	18	4	22.36	b7b9b16y5	1920.00	60.734	21453	3	640.67	0.64
P00499 HIS1_SALTY ATP phohoribosyltransferase	16	Carbamidomethyl+C(6)	LDFGGCRLSLATPVDEAWDGPAALDGK	98	27	5	24.38	b4b9b12b13y15	2831.37	97.986	8177	3	944.46	1.81
P66593 RS6_SALTY 30S ribosomal protein S6	1		YSAAITGAEGK	24	11	18	133.55	b1b2°b2b3°b3b4b6b9y2y3y4y5y6°y6y7y9y10y11	1067.53	34.447	234096	2	534.27	-10.75
P66593 RS6_SALTY 30S ribosomal protein S6	2		FNDAVIR	79	7	9	59.5	b2b3y1y3y4y5y6*y6y7	834.43	43.147	169574	2	417.72	-14.34
P66593 RS6_SALTY 30S ribosomal protein S6	3		AHYVLMNVEAPQVEIDELETTFR	56	23	10	51.47	b7b11y2y4y5y6y8y10y14y23	2704.33	111.555	107243	3	902.12	0.99
P66593 RS6_SALTY 30S ribosomal protein S6	4		HAVTEAMVK	93	11	8	59.02	b2b7b10y4y8y9y10y11	1169.59	31.943	83034	2	585.30	-5.74
P66593 RS6_SALTY 30S ribosomal protein S6	5		LEDWGR	38	6	2	25.1	b3y5	775.38	39.528	5802	1	775.38	13.85

P66593 RS6_SALTY 30S ribosomal protein S6	6		HYEIVFMVHPDQSEQVPGMIER	2	22	5	27.65	b6y4y8y11y16	2641.24	79.290	3076	3	881.09	-3.70
P66593 RS6_SALTY 30S ribosomal protein S6	7		RQLAYPINK	44	9	4	42.17	b5b7b8y4	1102.63	38.706	53044	2	551.82	-4.10
P66593 RS6_SALTY 30S ribosomal protein S6	8		YSAAITGAEGKIHR	24	14	3	25.94	b3b6b8	1473.76	96.226	9957	2	737.39	-12.18
P66593 RS6_SALTY 30S ribosomal protein S6	9		RHYEIVFMVHPDQSEQVPGMIER	1	23	6	34.35	b3b4y5y6y8°y8	2797.39	106.320	1714	3	933.13	11.69
P66593 RS6_SALTY 30S ribosomal protein S6	10	Phohoryl STY(13)	HYEIVFMVHPDQSEQVPGMIER	2	22	6	50.01	b6b11y5y6y7y8	2721.17	126.500	2157	2	1361.09	-13.82
P66593 RS6_SALTY 30S ribosomal protein S6	11	Oxidation+M(9)	HAVTEAMVK	93	11	6	38.39	b3b5b8°b8y9°y9	1185.61	40.005	2949	2	593.31	10.61
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	17	128.02	b2b3b4b5b10°b10y1y2y3y4y5y7°y7y8y9y10y12	1150.67	54.238	164845	2	575.84	-7.85
P66313 RL6_SALTY 50S ribosomal protein L6	2		INGQVITIK	18	9	12	74.05	b2°b2b3b5°b5y3y4y7y8*y8y9*y9	985.60	49.383	127740	2	493.30	-8.30
P66313 RL6_SALTY 50S ribosomal protein L6	3		TLNDAVEVK	35	9	19	109.71	b1°b1b2°b2b3b4°b4b8y1y2y3°y3y4y5y6y7y8y9*y9	988.52	39.466	119004	2	494.76	-12.97
P66313 RL6_SALTY 50S ribosomal protein L6	4		DGYADGWAQAGTAR	55	14	5	22.81	b3y2y10°y10y11	1438.64	50.786	113893	2	719.83	6.02
P66313 RL6_SALTY 50S ribosomal protein L6	5		YADEVVR	163	7	5	37.9	y3y4°y4y5y7	851.42	31.662	107552	2	426.21	-11.83
P66313 RL6_SALTY 50S ribosomal protein L6	6		ALLNSMVIGVTEGFTKK	69	17	5	23.59	b2b3y7y9y15	1807.99	89.405	82820	3	603.33	-7.49
P66313 RL6_SALTY 50S ribosomal protein L6	7		ALLNSMVIGVTEGFTK	69	16	6	37.19	y2y5y9y10y11y16	1679.91	95.264	76512	2	840.46	4.14
P66313 RL6_SALTY 50S ribosomal protein L6	8		LQLVGVGYS	86	9	6	35.89	b2°b2y2y3y5y6	1004.58	60.648	24211	2	502.79	-6.99
P66313 RL6_SALTY 50S ribosomal protein L6	9		QVIGQVAADLR	138	11	4	47.42	y4y6y8y9	1169.65	58.225	28143	2	585.33	-9.71
P66313 RL6_SALTY 50S ribosomal protein L6	10		RPEPYK	152	6	2	25.1	b3y4	789.42	52.737	14931	2	395.21	-11.75
P66313 RL6_SALTY 50S ribosomal protein L6	11		GADKQVIGQVAADLR	134	15	4	26.7	b4b6b13y4	1540.83	60.079	21099	3	514.28	-11.65
P66313 RL6_SALTY 50S ribosomal protein L6	12		TLNDAVEVKHADNALTGPR	35	20	6	28.47	b6°b6°b6b8b13b14	2168.09	109.480	2136	3	723.37	-8.78
P66313 RL6_SALTY 50S ribosomal protein L6	13		INGQVITIK	18	9	0	1.99		968.58	49.319	26680	2	484.79	6.62
P0A2B1 RS20_SALTY 30S ribosomal protein S20	1		AFNEMQPIVDR	49	11	18	108.94	b2b3b4b9b10°b10y1y2y3y5y6*y6y8°y8y9*y9y11*y11	1319.63	58.013	175940	2	660.32	-5.74
P0A2B1 RS20_SALTY 30S ribosomal protein S20	2		ANLTAQINK	76	9	8	35.89	b2°b2y2y5*y5y6y7y9	972.54	36.452	27249	2	486.77	-7.15
P0A2B1 RS20_SALTY 30S ribosomal protein S20	3		AFNEMQPIVDRQAAK	49	15	5	29.07	b9°b9b10y6y13	1717.86	113.337	3072	2	859.43	-7.96
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	1	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	9	33.1	b2b20y4y5y10y12°y12y18y24	2589.31	83.595	67704	3	863.78	3.39
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	2		SATPAQAQAVHK	176	12	20	114.75	b2b3b5°b5y1y2y3y4y5*y5y6*y6y7*y7y8y9*y9y10°y10y12	1208.63	19.672	58656	2	604.82	-5.15
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	3	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	5	11.96	b1b12y3y10y23	2433.22	88.936	29717	2	1217.11	5.92
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	4		TQGAAAFEGAVIAYEPVWAIGTGK	152	24	24	112.32	b1°b1b2b3°b3b5°b5°b5b8b9b11b12°b12b14b15y1y2y4y7y10y11y12y13y24	2407.24	94.413	21289	2	1204.12	3.35

Q8ZKP7 TPIS_SALTY Triosephohate isomerase	5		AAAGSHIMLGAQNVDLNLSGAFT GETSAEMLK	52	32	7	20.53	b6b14b15°b15y2y14y32	3204.55	102.107	4098	3	1068.86	-4.11
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	6		QIDAVLK	145	7	3	37.9	y3y4y5	786.46	43.769	54729	2	393.73	-17.15
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	7		ADAFIVK	238	9	6	42.17	b4°b4b5°b5b8y5	933.53	63.698	19260	2	467.27	-15.89
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	8	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAEENEAGKTEE VCAR	117	28	23	209.02	b5°b5y3y4y5°y5y6y7y10y11y12*y12y13y14y16y18y19y20y21y23*y23y24y26	3090.45	73.125	171153	3	1030.82	3.16
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	9		MRHPLVMGNWK	0	11	3	22.11	b3b5y7	1368.68	57.324	9813	3	456.90	-13.38
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	10	Oxidation+M(8)	AAAGSHIMLGAQNVDLNLSGAFT GETSAEMLK	52	32	10	32.82	b5°b5b7°b7b13°b13b26y6y7°y7	3220.57	136.443	7365	3	1074.20	3.71
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	11	Carbamidomethyl+C(8); Oxidation+M(17)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	7	25.91	b4°b4b5°b5b10b14y11	2605.31	105.184	1908	3	869.11	5.53
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	12		TPAQQAVHK	178	10	7	57.21	b4°b4b5°b5b7b8b9	1050.56	19.672	23426	2	525.78	-7.55
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	13		PAQAQAVHK	179	9	11	74.29	b3°b3b4°b4b5°b5b6°b6b7°b7b8	949.51	19.673	19960	2	475.26	-7.78
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	14		VAIAPPEMYIDLAK	37	14	1	8.69	b4	1530.84	88.902	10684	2	765.92	9.73
O54297 RS4_SALTY 30S ribosomal protein S4	1		LSDYGVLQR	47	9	11	71.04	b3°b3b7y1y2y5y6y7y8*y8y9	1050.55	51.923	128423	2	525.78	-6.39
O54297 RS4_SALTY 30S ribosomal protein S4	2		VVNIASYQVNDVVSIR	128	18	21	168.05	b3b8b12b14°b14b15°b15b17°b17y1y3y4y5y8y9y10y11y12y13y14y18	1960.06	73.025	116775	2	980.53	3.36
O54297 RS4_SALTY 30S ribosomal protein S4	3		LDNVVYR	97	7	7	37.9	b2y3y5y6°y6*y6y7	878.46	38.884	58535	2	439.73	-13.83
O54297 RS4_SALTY 30S ribosomal protein S4	4		VVNIASYQVNDVVSIREK	128	20	7	42.02	b2y5y10y11y12y16y20	2217.18	66.996	33280	3	739.73	-4.40
O54297 RS4_SALTY 30S ribosomal protein S4	5		IYGVLER	63	7	3	34.89	b3y5y6	849.47	50.548	43901	2	425.24	-16.53
O54297 RS4_SALTY 30S ribosomal protein S4	6		AAELEAEQR	156	9	8	60.49	b3y3y4°y4y6°y6*y6y7	1000.54	44.250	11057	1	1000.54	-2.87
O54297 RS4_SALTY 30S ribosomal protein S4	7		GNTGENLLALLEGR	83	14	3	17.37	b5b7y3	1456.78	72.505	9052	2	728.89	2.85
O54297 RS4_SALTY 30S ribosomal protein S4	8		IEQAPGQHGAR	33	11	3	33.87	y6y7y8	1163.57	16.230	5184	3	388.53	-18.67
O54297 RS4_SALTY 30S ribosomal protein S4	9		SDLSADINEHLIVELYSK	188	18	3	14.03	b9b13y3	2045.99	88.347	3573	2	1023.50	-21.72
O54297 RS4_SALTY 30S ribosomal protein S4	10		EKPTWLEVDAGKMEGTYK	165	18	4	22.36	b10y5y8y13	2082.03	65.994	70013	3	694.68	2.81
O54297 RS4_SALTY 30S ribosomal protein S4	11		MARYLGPK	0	8	3	38.4	b4b6b7	935.52	64.471	4484	2	468.26	8.29
O54297 RS4_SALTY 30S ribosomal protein S4	12	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	9	54.57	b4°b4b12y3y4y6°y6y7*y7	1451.74	100.343	2083	2	726.37	12.78
O54297 RS4_SALTY 30S ribosomal protein S4	13	Phohoryl STY(13)	AAELEAEQREKPTWLEVDAGK	156	21	3	12.6	b13y5y8	2434.17	92.405	3710	4	609.30	-10.93
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	1	Carbamidomethyl+C(10)	VAEVIDIPFCVAGGIR	68	16	9	76.87	b2b3b12b13y8y9y10y11y12	1715.93	91.571	44441	2	858.47	6.54
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	2		VTQWETLDWVQEVQQR	153	16	19	124.83	b1b2b3b11°b11b12b13y1y2y3y4y5y6°y6y8y9y11y12y16	2045.03	85.198	40209	2	1023.02	9.61

[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	3		NHEIIGDIVPLAK	24	13	4	27.87	b3*b3b6b8	1418.79	70.195	5865	2	709.90	-8.86
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	4		GAGEIVLNMMNQDGVR	169	16	3	21.96	b13b14y10	1703.84	78.723	56168	2	852.42	12.25
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	5		VPLIASGGAGTMEHFLEAFR	201	20	5	28.47	y3y6°y6y12y13	2103.06	66.043	21318	4	526.52	-4.41
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	6		DADVDGALAASVFHK	221	15	4	16.31	b9b11°b11y7	1515.74	54.224	2847	2	758.38	0.72
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	7		ILSFGADKISINALADPTLITR	91	24	4	33.54	b12b13y6y7	2513.39	85.351	70387	3	838.47	-1.17
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	8		VTQWETLDWVQEVQQRGAGEIV LNMMNQDGVR	153	32	5	27.16	b6b7y4y9y20	3729.86	115.838	2022	3	1243.96	11.98
[P0A1R2]HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	9	Oxidation+M()	GAGEIVLNMMNQDGVR	169	16	3	15.43	b6b12y12	1719.81	72.590	6388	3	573.94	-4.40
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	10	86.17	b2b3b4y3y7y8y9y10y11y13	1365.68	63.775	55298	2	683.35	0.98
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2		ATFVVDPPQHIAIEVTAEIGIR	120	23	9	38.2	b6b8y2y4y7°y7y8°y8y9	2384.27	129.215	46780	3	795.43	-4.40
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		AWHSSSETIAK	80	11	4	25.12	b3y8y9y11	1216.58	31.174	32124	3	406.20	-14.35
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		NGEFIEVTEK	17	10	3	24.62	b6b8y5	1165.56	89.357	5893	2	583.29	-8.69
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		LGVDVYSVSTDTHFTHK	63	17	4	14.67	b1b3b10y10	1905.96	67.744	1997	2	953.48	13.83
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6	Carbamidomethyl+C(13)	AAQYVAAHGPEVCPAK	153	16	17	118.12	b3b4b5°b5b8°b8b13y3y4y5y8°y8y9°y9y11°y11y12	1668.79	36.371	115032	3	556.93	-16.53
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTLGDVA DHYEELQK	32	31	5	12.58	b8b11°b11y7y12	3757.78	96.458	5217	5	752.36	15.53
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8		DASDLLR	143	7	5	65.52	b3b6y3y4y5	789.40	46.691	4210	1	789.40	-17.63
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9		IKYAMIGDPTGALTR	91	15	11	43.01	b6b8°b8y8°y8y10°y10y13°y13y14°y14	1606.84	64.382	21001	3	536.29	-12.84
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10		NGEFIEVTEKDTEGR	17	15	4	24.39	y6°y6y9y10	1723.83	66.094	14893	3	575.28	10.34
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	11		EGEATLAPSLDLVGKI	171	16	4	36.23	b7b9b12b14	1612.86	77.349	7816	2	806.94	-9.46
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	12	Carbamidomethyl+C(13)	AAQYVAAHGPEVCPAKWK	153	18	3	21.43	b7y9y10	1982.98	47.847	4939	3	661.67	-3.02
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	13		LGVDVYSVSTDTHFTHKAWHSSS ETIAK	63	28	4	20.79	b4y8y10y11	3103.53	133.377	2168	3	1035.18	5.74
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	14	Phohoryl STY(7)	LGVDVYSVSTDTHFTHK	63	17	4	20.37	b6b9_H3PO4 b9y5y9	1985.87	116.698	1605	2	993.44	-9.34
[P0A251]AHPC_SALTY Alkyl hydroperoxide reductase subunit C	15		YAMIGDPTGALTR	93	13	0	3.97		1347.67	63.704	3601	2	674.34	1.54
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1		MIIPALDLIDGTVVR	0	15	9	63.31	b2b3y5y6y7y9y12y13y15	1625.93	103.502	83177	2	813.47	2.70

[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	2		VVIGSTAVK	98	9	5	35.89	y2y3y6y7y9	873.53	38.404	17736	2	437.27	-9.50
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	3		QVAVSGWQENSGVSLEQLVETYL PVGLK	138	28	15	67.43	b3b7°b7*b7b8b11°b11b12 b13b14b17y1y2y3y5	3030.60	118.645	12860	3	1010.87	6.61
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	4	Carbamidomethyl+C(9)	FTVKEAICWQNV	232	13	6	31.15	b10y4*y4y10*y10y12	1622.80	69.505	9360	3	541.61	0.60
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	5		YPQIAFQSSGGIGDIDDIAALR	193	22	6	27.65	b6*b6b9b12°b12b14	2307.19	87.124	6115	3	769.73	12.38
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	6		TEEDVAALLK	83	10	3	34.62	b7b8b9	1088.56	28.748	39898	2	544.78	-21.08
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	7		GWFER	113	5	1	12.3	b3	694.32	51.968	17581	1	694.32	-11.34
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	8	Carbamidomethyl+C(16)	DGTLAGSNVSLYEVCAR	175	18	5	22.36	b4b8°b8b10y3	1940.91	67.288	10267	2	970.96	4.65
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	9		QIPLIK	60	6	3	37.41	b4b5y3	711.48	55.250	5334	1	711.48	3.60
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	10		IDEHGTK	131	7	4	47.2	b3b4b6y4	799.40	122.865	1501	1	799.40	5.80
[Q7CPL6]RL18_SALTY 50S ribosomal protein L18	1		YTG NKDAAAAVGK	63	13	10	49.8	b2b5°b5b7b8b10y2y6y8y1 3	1265.63	24.435	92456	3	422.55	-14.18
[Q7CPL6]RL18_SALTY 50S ribosomal protein L18	2		AIAEQLK	56	7	7	47.2	b2b4°b4y4y5y6y7	772.45	33.241	46292	2	386.73	-13.91
[Q7CPL6]RL18_SALTY 50S ribosomal protein L18	3		GIKDVSFDR	85	9	12	97.4	b4°b4b5b8y2y3y4y5°y5y6y 7y9	1036.54	43.244	44355	2	518.77	-2.00
[Q7CPL6]RL18_SALTY 50S ribosomal protein L18	4		HIYAQVIAPNGSEVLVAASTVEK	33	23	9	47.61	b1b3b4b5b12*b12b13y13y 23	2396.30	64.411	31973	3	799.44	6.42
[Q7CPL6]RL18_SALTY 50S ribosomal protein L18	5		VQALADAAR	102	9	7	69.79	b3*b3y3y4y5y6y7	914.49	32.580	209133	2	457.75	-16.89
[Q7CPL6]RL18_SALTY 50S ribosomal protein L18	6		EAGLQF	111	6	4	40.42	b3b5*b5y5	664.33	62.966	69953	1	664.33	-6.89
[Q7CPL6]RL18_SALTY 50S ribosomal protein L18	7		DVSFDRSGFYHGR	88	14	3	25.15	b4b9b10	1670.76	68.247	5507	3	557.59	-3.58

Q7CPL6 RL18_SALTY 50S ribosomal protein L18	8		SGFQYHGRVQALADAAR	94	17	3	23.33	b3b11b12	1846.95	78.937	5086	3	616.32	9.58
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	9		YAQVIAPNGSEVLVAASTVEK	35	21	3	12.21	b5*b5b9	2146.12	64.419	3915	3	716.04	-10.12
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	10		YTGNDKDAAAVVGK	63	13	0	3.97		1247.62	24.437	3599	3	416.54	-11.55
P65702 PGK_SALTY Phohoglycerate kinase	1		VLPVAMLEER	373	11	5	25.12	b3y2y7y8y11	1227.68	80.872	205107	2	614.34	-0.99
P65702 PGK_SALTY Phohoglycerate kinase	2	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	21	160.96	b2b3b5°b5b6b7b8b12y1y2y3y4y5y6y8y9y12y13y14y15y20	2002.04	99.778	203718	2	1001.52	4.94
P65702 PGK_SALTY Phohoglycerate kinase	3	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	22	151.41	b2b3b6°b6b7°b7b9°b9b12°b12y1y2y3y5y7y8y9y10y11°y11y12y14	1599.85	69.510	185004	2	800.43	2.67
P65702 PGK_SALTY Phohoglycerate kinase	4		SVNDVKEDEQILDIGDASAQQLAEILK	272	27	14	49.67	b1b2°b2b4b5°b5b11y1y2y3y4y5y13y15	2941.52	100.999	183364	3	981.18	5.73
P65702 PGK_SALTY Phohoglycerate kinase	5		VATEFSETAPATLK	258	14	24	146.63	b1b2b3°b3b4°b4b6°b6b7b9y1y2y3y5°y5y6y7y9°y9y10y11°y11y12y14	1464.76	53.463	142773	2	732.88	1.08
P65702 PGK_SALTY Phohoglycerate kinase	6		VMVTSHLGRPTEGEYNNEEFSLLPVVNYLK	53	29	6	15.45	b2b6b13b18y7y29	3321.66	93.118	138995	4	831.17	-7.64
P65702 PGK_SALTY Phohoglycerate kinase	7		TILWNGPVGVFEFPNFR	302	17	10	46.74	b2b6y4y5°y5y7y12y13°y13y17	1993.05	107.048	128193	2	997.03	6.49
P65702 PGK_SALTY Phohoglycerate kinase	8		LTVLDSLK	197	9	6	35.89	b2y2y4y5y6y9	975.56	62.758	102441	2	488.28	-11.57
P65702 PGK_SALTY Phohoglycerate kinase	9		ADLNPVKEGK	19	11	17	102.92	b1b2b3b9°b9b10°b10y2y3y4y6°y6y7y8y9°y9y11	1169.65	37.884	101674	2	585.33	-1.88
P65702 PGK_SALTY Phohoglycerate kinase	10		ASLPTIELALK	38	11	4	44.41	y4y6y7y8	1155.69	78.054	77906	2	578.35	-2.96
P65702 PGK_SALTY Phohoglycerate kinase	11		MTDLDLAGK	5	9	5	28.11	b6b8y2y5y9	963.47	49.301	53755	2	482.24	-8.05
P65702 PGK_SALTY Phohoglycerate kinase	12		LVKDYLDGVDVAEGELVVLENVR	90	23	5	21.8	b14°b14y4y5y12	2544.36	98.092	51174	3	848.79	2.88
P65702 PGK_SALTY Phohoglycerate kinase	13		IADQLIVGGGIANTFVAAQGHSVGK	206	25	7	37.87	b3b4y3y6y7°y7y9	2423.30	78.941	41103	3	808.44	-3.43
P65702 PGK_SALTY Phohoglycerate kinase	14		MTDLDLAGKR	5	10	6	48.69	y3y7y8°y8y9y10	1119.58	43.728	40774	2	560.29	-4.80
P65702 PGK_SALTY Phohoglycerate kinase	15	Carbamidomethyl+C(5)	YAALCDVFVMDAFGTAHR	128	18	5	26.68	b2b3b9y9y10	2043.95	90.843	20526	3	681.99	4.54
P65702 PGK_SALTY Phohoglycerate kinase	16		AQASTHGIGK	146	10	11	69.31	b2°b2b6y1y2y3y4y6y7y8y10	969.50	16.303	16114	2	485.26	-6.74
P65702 PGK_SALTY Phohoglycerate kinase	17		DYLDGVDVAEGELVVLENVR	93	20	3	13.01	b17y4y11	2204.09	83.418	9589	3	735.37	-10.30
P65702 PGK_SALTY Phohoglycerate kinase	18		SLYEADLVDEAKR	231	13	6	26.74	b4b9y5y10°y10y13	1508.75	107.925	3227	2	754.88	-7.36
P65702 PGK_SALTY Phohoglycerate kinase	19		LSNPVR	84	6	1	12.8	y5	685.39	28.831	8110	2	343.20	-13.71
P65702 PGK_SALTY Phohoglycerate kinase	20		SLYEADLVDEAK	231	12	5	34.24	b3b7b10y8°y8	1352.66	136.424	3399	1	1352.66	1.62
P65702 PGK_SALTY Phohoglycerate kinase	21		GTEIVANAIADSEAFSIAGGGDTLAIDLFGIADK	320	35	4	10.95	b7°b7y6y15	3393.72	110.999	2523	3	1131.91	4.96
P65702 PGK_SALTY Phohoglycerate kinase	22		ISYISTGGGAFLEFVEGK	355	18	6	39.14	b9b10°b10b12°b12b13	1874.95	81.473	2003	2	937.98	-1.30
P65702 PGK_SALTY Phohoglycerate kinase	23	Carbamidomethyl+C(6)	RLLTTCDIPVPTDVR	243	15	7	46.99	b6b7°b7b8b10y4y14	1755.93	66.011	2299	2	878.47	-5.07
P65702 PGK_SALTY Phohoglycerate kinase	24	Carbamidomethyl+C(6)	KYAALCDVFVMDAFGTAHR	127	19	3	13.48	b13y9y12	2172.03	86.879	1694	3	724.68	-3.48

P65702 PGK_SALTY Phohoglycerate kinase	25		LNVPVKEGK	21	9	0	2.98		983.58	37.857	18915	2	492.29	-9.56
P65702 PGK_SALTY Phohoglycerate kinase	26		DLNVPVKEGK	20	10	2	7.5	b3°b3	1098.60	37.861	18910	2	549.80	-14.56
P65702 PGK_SALTY Phohoglycerate kinase	27		TDLDLAGKR	6	9	0	2.48		988.54	43.745	13092	2	494.77	-3.70
P65702 PGK_SALTY Phohoglycerate kinase	28		ASTHGIGK	148	8	4	21.07	b4°b4b5°b5	770.41	16.307	3857	2	385.71	-11.17
P65702 PGK_SALTY Phohoglycerate kinase	29		QASTHGIGK	147	9	4	31.61	b3°b3b4b6	898.46	16.306	1723	2	449.74	-11.07
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	21	187.39	b3b4*b4b6b7y3y5y6y7°y7*y7y9y10y11y12y14y15y17y18y19y21	2215.17	75.801	76145	3	739.06	-1.43
Q56073 DNAK_SALTY Chaperone protein dnaK	2		ASSGLNEEEIQK	502	12	13	57.21	b2°b2y1y5*y5y6°y6y7°y7y9y10°y10y12	1304.63	35.772	25127	2	652.82	-5.52
Q56073 DNAK_SALTY Chaperone protein dnaK	3		SLGQFNLDGINPAPR	452	15	4	24.39	y5y7y10y15	1598.84	72.781	24778	2	799.92	4.43
Q56073 DNAK_SALTY Chaperone protein dnaK	4		QAVTNPQNTLFAIK	56	14	9	41.67	b3*b3y1y2y3y9y10y11y14	1544.85	68.298	23970	2	772.93	1.50
Q56073 DNAK_SALTY Chaperone protein dnaK	5		TAEDYLGEVPVTEAVITVPAYFNDAQR	125	26	9	40.67	b2b6b14y5y8y9y11y12y26	2869.40	94.233	23369	3	957.14	2.30
Q56073 DNAK_SALTY Chaperone protein dnaK	6		IELSSAQQTVDVNLPLYITADATGPK	270	24	4	18.02	b2y5y8y13	2532.32	109.457	3592	3	844.78	13.50
Q56073 DNAK_SALTY Chaperone protein dnaK	7		FQDEEVQRDVSIMPYK	76	16	4	25.02	b8y4y8y11	1983.96	73.968	2603	2	992.48	4.55
Q56073 DNAK_SALTY Chaperone protein dnaK	8		LMEIAQQQHAQQAGSADASANNAK	597	25	3	11.5	b5b9y11	2610.23	39.322	1572	3	870.75	-2.34
Q56073 DNAK_SALTY Chaperone protein dnaK	9		TAIESALNALETALK	562	15	5	22.33	b10*b10y12*y12y13	1544.87	66.215	12252	2	772.94	10.67
Q56073 DNAK_SALTY Chaperone protein dnaK	10		EAAEK	263	5	2	24.61	b4y4	547.27	69.540	11435	1	547.27	-2.45
Q56073 DNAK_SALTY Chaperone protein dnaK	11		MPMVQK	345	6	1	12.8	b4	733.37	32.643	10987	1	733.37	0.50
Q56073 DNAK_SALTY Chaperone protein dnaK	12		GMPQIEVTFDIDADGILHVSAK	467	22	4	27.65	b3b6b8b10	2356.20	60.798	8560	3	786.07	7.05
Q56073 DNAK_SALTY Chaperone protein dnaK	13		TIAVYDLGGGTFDISIIEIDVDEGEK	188	26	4	16.56	b10y4y6y11	2769.42	77.015	6734	3	923.81	18.51
Q56073 DNAK_SALTY Chaperone protein dnaK	14		MAPPQISAEVLK	109	12	4	46.67	b4b5b6b7	1283.70	83.470	4388	2	642.35	-1.14
Q56073 DNAK_SALTY Chaperone protein dnaK	15	Carbamidomethyl+C(12)	IIGIDLGTNTSCVAIMDGTQAR	3	22	3	12.26	b14y7y10	2306.14	65.362	2536	2	1153.57	-3.18
Q56073 DNAK_SALTY Chaperone protein dnaK	16		MQELAQVSQK	587	10	4	31.61	y3y6*y6y7	1161.59	38.277	2404	1	1161.59	-4.62
Q56073 DNAK_SALTY Chaperone protein dnaK	17		FQDEEVQR	76	8	3	38.4	y4y5y7	1050.46	25.974	1843	2	525.73	-22.43
Q56073 DNAK_SALTY Chaperone protein dnaK	18		VAEFFGK	352	7	6	53.22	b3°b3b4°b4y3y6	797.41	63.713	1821	2	399.21	-7.65
Q56073 DNAK_SALTY Chaperone protein dnaK	19		SIEPLK	315	6	1	12.8	b3	686.40	40.735	1543	2	343.71	-5.25
Q56073 DNAK_SALTY Chaperone protein dnaK	20	Carbamidomethyl+C(15)	MGKIIIGIDLGTNTSCVAIMDGTQAR	0	25	4	11.5	b15y9*y9y13	2622.29	85.878	192985	3	874.77	-4.28
Q56073 DNAK_SALTY Chaperone protein dnaK	21		FQDEEVQRDVSIMPYK	76	16	3	15.43	b9y4y9	1983.96	61.797	7718	3	661.99	6.77
Q56073 DNAK_SALTY Chaperone protein dnaK	22		GQKMAPPQISAEVLK	106	15	4	24.39	b4b5°b5b14	1596.85	66.074	6877	2	798.93	-14.45
Q56073 DNAK_SALTY Chaperone protein dnaK	23		MQELAQVSQKLMEIAQQQHAQQAGSADASANNAK	587	35	6	26.64	b7b8°b8y5y7y13	3752.81	92.494	5927	4	938.96	0.98

Q56073 DNAK_SALTY Chaperone protein dnaK	24		ASDNKSLGQFNLDGINPAPR	447	20	10	29.01	b3°b3b7°b7b9°b9b10°b10y12*y12	2114.07	66.075	5074	3	705.36	2.66
Q56073 DNAK_SALTY Chaperone protein dnaK	25		TTPSIIAYTQDGETLVGQPAKR	34	22	3	12.26	b10b13y11	2346.22	99.130	4274	2	1173.61	-3.75
Q56073 DNAK_SALTY Chaperone protein dnaK	26	Carbamidomethyl+C(14)	GKIIGIDLTTNSCVAIMDGTQAR	1	24	4	11.71	b14y9y13*y13	2491.23	72.036	4203	3	831.08	-12.64
Q56073 DNAK_SALTY Chaperone protein dnaK	27		VALQDAGLSVSDINDVILVGGQT RMPMVQK	321	30	6	12.81	b11°b11b15°b15y10y18	3154.62	93.625	3508	3	1052.21	-14.01
Q56073 DNAK_SALTY Chaperone protein dnaK	28		QVEEAGDKLPADDK	548	14	3	17.37	b11y3y9	1514.73	72.371	3232	2	757.87	-1.21
Q56073 DNAK_SALTY Chaperone protein dnaK	29		KTAEDYLGEPVTEAVITVPAYFND AQR	124	27	4	20.92	b13y3y8y9	2997.50	100.799	2414	3	999.84	6.76
Q56073 DNAK_SALTY Chaperone protein dnaK	30		DQGIDLRNDPLAMQR	246	15	3	24.39	b4b7b8	1741.89	92.621	1936	3	581.30	13.32
Q56073 DNAK_SALTY Chaperone protein dnaK	31		KDVNPDEAVAIGAAVQGGVLTG DVK	362	25	5	21.98	b4°b4b9°b9b10	2423.25	107.206	1511	3	808.42	-12.19
Q56073 DNAK_SALTY Chaperone protein dnaK	32	Phohoryl STY(15)	TIAVYDLGGGTFDISIIEIDEVDGE K	188	26	3	21.11	b10y10y11	2849.35	89.905	4490	3	950.46	8.23
Q56073 DNAK_SALTY Chaperone protein dnaK	33	Phohoryl STY(16)	TAEDYLGEVPVTEAVITVPAYFNDA QR	125	26	6	36.37	b11b14y8y9*y9y10	2949.38	90.964	2722	3	983.80	11.59
Q56073 DNAK_SALTY Chaperone protein dnaK	34		LMEIAQQQHA	597	10	0	9.93		1168.57	39.261	10052	3	390.20	-4.91
P60446 RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	11	69.31	b2°b2b7y2y3y5y6y7°y7y8y10	1115.63	57.362	135959	2	558.32	-7.66
P60446 RL3_SALTY 50S ribosomal protein L3	2		IFTEDGVSIPTVIEVEANR	13	20	10	41.61	b2b9b10y2y3y4°y4y7y15y20	2188.17	88.936	87990	2	1094.59	8.48
P60446 RL3_SALTY 50S ribosomal protein L3	3		VTQVKDLANDGYR	33	13	12	81.4	b1b2°b2b7b10y3y4°y4y6y7y8y9	1478.74	40.847	23762	3	493.58	-13.46
P60446 RL3_SALTY 50S ribosomal protein L3	4		AVQVTTGAK	46	9	8	57.48	b2b3y3y4y5y7*y7y9	874.49	23.046	7946	2	437.75	-7.89
P60446 RL3_SALTY 50S ribosomal protein L3	5	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	5	43.96	y4y5y6y11y15	1738.92	54.822	35909	3	580.31	-16.64
P60446 RL3_SALTY 50S ribosomal protein L3	6		NLLLVK	184	6	5	62.01	b3b4y3y4y5	699.47	57.368	27016	1	699.47	-2.88
P60446 RL3_SALTY 50S ribosomal protein L3	7		TQDATHGNSLSHR	128	13	5	43.19	y3°y3y4y6y7	1423.64	15.290	17356	3	475.22	-16.12
P60446 RL3_SALTY 50S ribosomal protein L3	8		GLWEFR	77	6	3	25.1	b4y4°y4	807.41	47.716	13688	1	807.41	-2.95
P60446 RL3_SALTY 50S ribosomal protein L3	9		VPGSIGQNQTPGK	141	13	8	26.74	b3b9°b9°b9y5*y5y12*y12	1282.70	57.289	5525	2	641.85	17.42
P60446 RL3_SALTY 50S ribosomal protein L3	10		LAEGEETVVGQISVELFADV K	83	22	4	22.13	b3b10b11y11	2384.21	76.992	2771	3	795.41	9.63
P60446 RL3_SALTY 50S ribosomal protein L3	11		IFTEDGVSIPTVIEVEANRVTQVK	13	25	5	25.34	b9y16y20y21y23	2743.49	95.755	107459	3	915.17	2.31
P60446 RL3_SALTY 50S ribosomal protein L3	12		AGVEAGRGLWEFR	70	13	4	23.4	b3b4°b4y6	1447.75	60.692	18837	2	724.38	0.76
P60446 RL3_SALTY 50S ribosomal protein L3	13		VTQVKDLANDGYR	33	13	6	26.74	b7b12°b12y4°y4y7	1478.76	72.533	16992	2	739.88	-1.65
P60446 RL3_SALTY 50S ribosomal protein L3	14		DLANDGYRAVQVTTGAK	38	17	8	32.67	b4°b4°b4b5°b5b8b10y13	1778.89	65.370	5195	2	889.95	-8.44
P60446 RL3_SALTY 50S ribosomal protein L3	15		WNFRTQDATHGNSLSHR	124	17	6	34.35	b8b9y11°y11*y11y12	2026.97	65.286	2217	4	507.50	7.11
P60446 RL3_SALTY 50S ribosomal protein L3	16		LAEGEETVVGQISVELFADVKK	83	23	8	39.82	b3b4°b4b5b9b13°b13y14	2512.26	123.695	1965	3	838.09	-6.71
P60446 RL3_SALTY 50S ribosomal protein L3	17		KMAGQMGNER	159	10	4	51.7	y4y5y8y9	1121.53	17.872	1584	2	561.27	5.55
P60446 RL3_SALTY 50S ribosomal protein L3	18		IFTEDGVSIPTVIEVEANR	13	20	1	7.99	y11	2170.14	88.965	6306	3	724.05	0.34

P66541 RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAE LNK	45	14	19	129.02	b2°b2b3°b3b5b7b9°b9b12y3y4y9y10°y10y11°y11y12*y12y14	1576.81	85.290	216510	2	788.91	3.17
P66541 RS2_SALTY 30S ribosomal protein S2	2		ILFVGTK	66	7	6	37.9	y2y3°y3y4y6y7	777.48	58.012	65268	2	389.24	-14.37
P66541 RS2_SALTY 30S ribosomal protein S2	3	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	10	51.22	y1y3*y3y4y5*y5y7*y7y10y14	1694.71	48.336	60012	3	565.58	-11.31
P66541 RS2_SALTY 30S ribosomal protein S2	4		EANNLGIPVFAIVDTSNDPDGVDFVIPGNDDAIR	174	34	13	39.25	b2°b2b5°b5°b5b6°b6b7°b7y8y12y16y34	3569.74	105.001	24060	3	1190.58	-0.48
P66541 RS2_SALTY 30S ribosomal protein S2	5		MATVSMR	0	7	4	34.89	b4b7y4y5	795.39	51.870	12873	1	795.39	9.13
P66541 RS2_SALTY 30S ribosomal protein S2	6		SQDLASQAEE SFVEAE	225	16	5	23.13	b1b4°b4b8b10	1739.77	73.942	12539	2	870.39	7.86
P66541 RS2_SALTY 30S ribosomal protein S2	7		MKPFIFGAR	26	9	4	41.66	b6b7y3y4	1066.56	65.398	24259	2	533.79	-21.40
P66541 RS2_SALTY 30S ribosomal protein S2	8		DMGGLPDALFVIDADHEHIAIK	152	22	3	12.26	b10y9y13	2377.23	82.203	3270	2	1189.12	20.54
P66541 RS2_SALTY 30S ribosomal protein S2	9		WLGGMLTNWK	95	10	9	50.2	b3b4b9°b9y6°y6*y6y7°y7	1205.62	63.689	1918	2	603.32	7.90
P66541 RS2_SALTY 30S ribosomal protein S2	10		YWNPKMKPFIFGAR	21	14	4	28.7	b4b7b11y7	1754.94	77.351	25862	2	877.97	8.90
P66541 RS2_SALTY 30S ribosomal protein S2	11		EGRSQDLASQAEE SFVEAE	222	19	7	38.76	b8b9°b9b10°b10y4y6	2081.95	59.936	5004	3	694.66	11.96
P66541 RS2_SALTY 30S ribosomal protein S2	12		LKDLETQSQDGT FEK	113	15	3	22.33	b7b8y10	1738.84	79.536	2519	2	869.92	-7.02
P66541 RS2_SALTY 30S ribosomal protein S2	13	Oxidation+M(11)	LENSLGGIKDMGGLPDALFVIDADHEHIAIK	143	31	3	22.4	b3b13b14	3304.68	103.590	50278	4	826.93	-1.03
P66541 RS2_SALTY 30S ribosomal protein S2	14	Oxidation+M(1)	MATVSMR DMLK	0	11	3	22.11	b7y6y8	1298.62	68.364	6422	2	649.81	-3.20
P66541 RS2_SALTY 30S ribosomal protein S2	15	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	0	4.47		1676.72	48.333	7334	3	559.58	2.04
P66541 RS2_SALTY 30S ribosomal protein S2	16		MATVSMR	0	7	0	0.99		777.38	51.843	2097	1	777.38	9.19
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	1		TGEDIPITAR	66	10	12	82.59	b2b3°b3b4°b4y2y3y4y5y8y9y10	1072.56	43.909	78558	2	536.78	-6.71
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	2		LSGFGNFDLR	45	10	8	48.44	b5b8y1y2y6y8y9y10	1125.57	73.144	24280	2	563.29	-1.95
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	3		ALENGEQVK	36	9	5	41.66	b6b8y6y7*y7	987.50	23.849	17925	2	494.25	-8.47
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	4		RNAKELVELFEEIR	20	15	4	22.33	b11y2y7y8	1894.00	113.429	1525	3	632.01	-2.45
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	5		ELVELFEEIR	24	11	3	22.11	b5b7y9	1423.72	94.298	2234	2	712.36	-21.86
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	6		ELVELFEEIRR	24	12	3	20.17	b5b9y6	1579.83	96.433	9463	3	527.28	-13.68
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	7		MALTKAEMSEYLF DK	0	15	5	29.07	b3b4y3°y3y6	1776.86	77.351	6349	3	592.96	4.67
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	8		ALTKAEMSEYLF DK	1	14	9	52.06	b7°b7b8b10°b10b11y5°y5y11	1645.81	63.679	3963	2	823.41	-5.04
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	9		DAKELVELFEEIR	21	14	3	17.37	b3b10y9	1737.88	65.378	3438	2	869.44	-14.75
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	10		ALENGEQVKLSGFGNFDLR	36	19	5	21.28	b3b6°b6b14y6	2094.06	97.399	2628	2	1047.53	-2.68
P25077 MDH_SALTY Malate dehydrogenase	1		NQLPSGSELSYDIAPVTPGVAVDLSHIPTAVK	21	33	12	34.62	b1b2°b2b3b15y3y5y6y15y18y30y33	3388.80	94.540	75753	3	1130.27	1.37
P25077 MDH_SALTY Malate dehydrogenase	2		VAVLGAAGGIGQALALLK	2	19	13	87.84	b3b9y1y2y3y4y5y6y7y9y11y12y19	1735.09	120.306	58149	2	868.05	2.74
P25077 MDH_SALTY Malate dehydrogenase	3		FFSQPLLLGK	262	10	3	31.61	y3y4y6	1149.66	76.715	56672	2	575.34	-1.49

P25077 MDH_SALTY Malate dehydrogenase	4	Carbamidomethyl+C(2)	ACVGIITNPVNTTVAIAAEVLKK	111	23	7	47.61	b2b3b4b5b6b11y15	2382.33	105.362	42223	3	794.78	-6.76
P25077 MDH_SALTY Malate dehydrogenase	5		IQNAGTEVVEAK	205	12	10	64.08	b2b3y4y6y8y9y10°y10*y10y12	1258.66	35.637	38361	2	629.83	-2.72
P25077 MDH_SALTY Malate dehydrogenase	6		AGGGSATLSMGQAAAR	217	16	9	66.6	b3b13y7y8y9°y9y10y11y16	1405.68	40.961	21877	2	703.35	-1.22
P25077 MDH_SALTY Malate dehydrogenase	7		SDLFNVNAGIVK	87	12	4	30.39	b4b6b11y1	1276.68	70.619	11947	2	638.84	-9.18
P25077 MDH_SALTY Malate dehydrogenase	8		GFSGEDATPALEGADVVLISAGVAR	56	31	3	16.76	b4b15b17	3086.52	98.958	3083	3	1029.51	-13.53
P25077 MDH_SALTY Malate dehydrogenase	9		NGVEER	272	6	3	25.1	y3°y3y4	703.35	76.277	3579	1	703.35	13.19
P25077 MDH_SALTY Malate dehydrogenase	10		IKGFSGEDATPALEGADVVLISAGVAR	54	27	5	25.5	b9b11b12°b12b15	2643.39	88.355	5923	3	881.80	-4.99
P25077 MDH_SALTY Malate dehydrogenase	11		FFSQPLLLGKNGVEER	262	16	4	15.43	b3b6°b6y6	1833.99	108.746	4178	3	612.00	0.80
P25077 MDH_SALTY Malate dehydrogenase	12	Oxidation+M(10)	AGGGSATLSMGQAAAR	217	16	3	15.43	b6b12y11	1421.69	87.331	1831	2	711.35	5.58
P25077 MDH_SALTY Malate dehydrogenase	13	Oxidation+M(29)	GFSGEDATPALEGADVVLISAGVAR	56	31	3	21.69	b3b4y8	3102.54	97.012	1657	3	1034.85	-5.51
P0A1Z2 SKP_SALTY Chaperone protein skp	1		IAIVNMGNLFQQVAQK	23	16	22	137.63	b2b3b5b8b12b13b15y1y2*y2y3y4y5*y5y6*y6y7*y7y12y13*y13y16	1773.98	90.672	99993	2	887.49	7.50
P0A1Z2 SKP_SALTY Chaperone protein skp	2		TGVSNTLENEFK	39	12	8	41.9	y2y6y8*y8y9°y9y11y12	1338.65	58.789	68042	2	669.83	0.91
P0A1Z2 SKP_SALTY Chaperone protein skp	3		VANDQSIDLVDANTVAYNSSDVK	126	24	4	14.96	b6b10y4y15	2537.24	136.369	3270	2	1269.12	2.21
P0A1Z2 SKP_SALTY Chaperone protein skp	4		QTFAQKAQAFEK	91	12	3	30.39	b4b7b11	1396.71	82.768	11983	2	698.86	-5.86
P0A1Z2 SKP_SALTY Chaperone protein skp	5		IAIVNMGNLFQQVAQKTGVSNTLENEFK	23	28	11	46.29	b8y3°y3y6°y6*y6y7y8°y8*y8y9	3093.59	123.569	7718	3	1031.87	-5.45
P0A1Z2 SKP_SALTY Chaperone protein skp	6		MQRLQSMK	67	8	3	33.63	b6y4y7	1021.53	65.369	7642	2	511.27	6.51
P0A1Z2 SKP_SALTY Chaperone protein skp	7		AAELQKMETDLQSK	53	14	4	28.7	b4b7b13y3	1591.81	92.470	6195	2	796.41	8.90
P0A1Z2 SKP_SALTY Chaperone protein skp	8		LEKDVMSQR	82	9	10	77.57	b3°b3b4b7°b7y4*y4y6y8°y8	1105.55	63.701	2122	2	553.28	-10.93
P0A1Z2 SKP_SALTY Chaperone protein skp	9	Oxidation+M(11)	WLLAAGLGLAMVTSQAADK	3	20	4	22.43	y3°y3y6y7	2003.08	104.492	3645	2	1002.04	6.58
P55900 SERC_SALTY Phohoserine aminotransferase	1	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	11	54.87	b3b10y3°y3y4y5°y5y9y10y12°y12	2567.19	74.974	54223	4	642.55	-7.61
P55900 SERC_SALTY Phohoserine aminotransferase	2		AQVFNFSSGPAMLPAEVLK	1	19	17	71.5	b2°b2b5°b5b6°b6b9b13b15°b15y3y6y13y15°y15y16y19	2006.06	92.193	44468	2	1003.53	9.31
P55900 SERC_SALTY Phohoserine aminotransferase	3		YGVIIYAGAQK	188	10	7	51.45	b2b3b7y4y5y6y10	1069.56	44.230	39404	2	535.29	-3.42
P55900 SERC_SALTY Phohoserine aminotransferase	4		ASIYNAMPIEGVK	335	13	12	57.97	b1b3°b3b4b6°b6b7b8y1y2y9y13	1392.71	60.072	29446	3	464.91	-3.51
P55900 SERC_SALTY Phohoserine aminotransferase	5		MNVPFQLADNTLDK	297	14	6	17.37	b2b9°b9b12°b12y6	1605.82	99.086	3968	2	803.41	13.23
P55900 SERC_SALTY Phohoserine aminotransferase	6	Carbamidomethyl+C(5)	AHESCP SILDYTVLNDNDSMFNTPTFAWYLSGLVFK	217	37	4	22.84	b2b12b13y17	4250.03	125.413	3097	3	1417.35	9.88
P55900 SERC_SALTY Phohoserine aminotransferase	7		ALTD FMIDFERR	348	12	3	30.39	y5y7y10	1513.74	82.852	1656	2	757.37	-5.32
P55900 SERC_SALTY Phohoserine aminotransferase	8		ALTD FMIDFER	348	11	9	55.22	b4°b4b5b7°b7y3y4°y4y9	1357.67	63.685	2564	2	679.34	21.58
P55900 SERC_SALTY Phohoserine aminotransferase	9		AELLYGVIDNSDFYRNDVAQANR	272	23	4	11.96	b12°b12y14y18	2643.28	80.158	10065	3	881.77	0.37

[P55900]SERC_SALTY Phohoserine aminotransferase	10		SRMNVPFQLADNTLDK	295	16	5	15.43	b7°b7*b7b9y11	1848.91	60.886	2612	2	924.96	-8.45
[P55900]SERC_SALTY Phohoserine aminotransferase	11	Carbamidomethyl+C(14)	DLLNIPSNYKVLFCGGGR	58	19	4	23.5	b9y8y9y12	2160.11	100.899	2305	4	540.78	5.09
[P55900]SERC_SALTY Phohoserine aminotransferase	12		GKEFIQVAAEAEQDFR	42	16	10	50.76	b4b10°b10b12*b12b13y4°y4y11y12	1895.91	108.537	1904	2	948.46	-1.80
[P55900]SERC_SALTY Phohoserine aminotransferase	13	Oxidation+M(1)	MNVPFQLADNTLDK	297	14	4	30.18	b3b10y4y5	1621.78	69.521	3898	4	406.20	-6.40
[P55900]SERC_SALTY Phohoserine aminotransferase	14	Carbamidomethyl+C(7); Oxidation+M(17)	LAQQELCDWHGLGTSVMEISHR	20	22	4	22.13	y5y6y8°y8	2583.19	92.450	2635	4	646.55	-5.29
[P55900]SERC_SALTY Phohoserine aminotransferase	15	Oxidation+M(8)	AQGGVAAMHK	257	10	3	24.62	b3y6y8	985.50	136.497	1589	1	985.50	11.64
[P0A1H3]EFG_SALTY Elongation factor G	1		VYSGVVNSGDTVLSNVK	337	17	14	85.49	b2b4°b4b5b17y4y5y9y10y11*y11y12y15y17	1737.90	63.086	76441	2	869.46	1.76
[P0A1H3]EFG_SALTY Elongation factor G	2		IATDPFVGNLTFFR	323	14	8	38.66	b2b4y1y4y6y7y10y14	1597.84	93.997	69262	2	799.42	2.98
[P0A1H3]EFG_SALTY Elongation factor G	3		IGEVHDGAATMDWMEQEQR	39	20	6	25.61	b3b12y4°y4y5y20	2331.99	63.275	60724	3	778.00	-3.14
[P0A1H3]EFG_SALTY Elongation factor G	4		SGPLAGYPVVDLGVR	562	15	11	66.95	b3°b3b5b6b7°b7y4y8y10y11y15	1499.83	77.381	54616	2	750.42	4.96
[P0A1H3]EFG_SALTY Elongation factor G	5	Carbamidomethyl+C(11)	VLNNEILVTCGSAFK	255	16	7	15.43	b1b2b4y4°y4y8°y8	1777.97	107.198	44335	3	593.33	10.23
[P0A1H3]EFG_SALTY Elongation factor G	6		LGANPVPLQLAIGAEEGFTGVVDL VK	161	26	4	11.33	b3b6°b6y14	2607.44	120.471	20344	3	869.82	-1.22
[P0A1H3]EFG_SALTY Elongation factor G	7		VWTDEESNQTIAGMGELHLDIIV DR	446	26	9	29.05	b2b4b5b14°b14y3y6°y6y23	2954.42	136.476	18495	2	1477.71	-13.47
[P0A1H3]EFG_SALTY Elongation factor G	8		LHFGSYHDVDSSELAFK	577	17	5	14.67	b8y1y12y16y17	1951.92	92.751	17830	3	651.31	0.38
[P0A1H3]EFG_SALTY Elongation factor G	9		GQYGHVVIDMYPLEPGSNPK	512	20	7	35.57	b6b11b12y9°y9y10°y10	2201.09	90.714	12647	3	734.37	11.31
[P0A1H3]EFG_SALTY Elongation factor G	10		VEVETPEENTGDVIGDL SR	618	19	13	58.61	b2b3b5°b5b6°b6b7b14y1y4y5°y5y13	2058.95	95.540	9333	3	686.99	-13.75
[P0A1H3]EFG_SALTY Elongation factor G	11		AINWNDADQGVTFEYEDIPADMQ DLANEWHQNLIESAASEELME K	189	47	21	93.8	b3b4b8b11b13°b13y2y3°y3y4y5°y5y6y7y8°y8y10y11°y11y13y29	5380.34	126.498	8460	4	1345.84	-8.80
[P0A1H3]EFG_SALTY Elongation factor G	12	Carbamidomethyl+C(9)	DVTTGDTLCDPENPIILER	389	19	5	13.48	b4b8y2y11*y11	2158.05	65.326	5416	3	720.02	7.13
[P0A1H3]EFG_SALTY Elongation factor G	13		MEFPEPVISIAVEPK	408	15	4	24.39	b2b9b11b13	1685.88	64.421	4495	3	562.63	1.01
[P0A1H3]EFG_SALTY Elongation factor G	14		IHAEVPLSEMGYATQLR	653	18	6	21.43	b14°b14y2y8y9*y9	2062.05	96.347	3321	4	516.27	2.60
[P0A1H3]EFG_SALTY Elongation factor G	15		VTDIEGK	497	7	9	74.81	b3°b3b4b6y4°y4y5°y5y6	761.42	57.325	29587	2	381.21	18.76
[P0A1H3]EFG_SALTY Elongation factor G	16		GQSEVTGVK	643	10	4	31.61	y3y4y8°y8	1033.50	26.518	24533	2	517.25	-17.95
[P0A1H3]EFG_SALTY Elongation factor G	17		YDDAPNNVAQAVIEAR	686	16	4	23.13	y3°y3y6y14	1745.86	66.053	20104	2	873.43	7.83
[P0A1H3]EFG_SALTY Elongation factor G	18		VVGQIK	153	6	1	12.8	b4	643.41	46.073	19806	1	643.41	-6.74
[P0A1H3]EFG_SALTY Elongation factor G	19		QANK	128	4	1	11.81	b3	460.25	31.387	8789	1	460.25	-2.92
[P0A1H3]EFG_SALTY Elongation factor G	20		GITITSAATTAFWSGMAK	59	18	7	38.86	b9b14y3y5°y5y7y16	1813.95	69.574	6562	3	605.32	17.90
[P0A1H3]EFG_SALTY Elongation factor G	21		NIGISAHIDAGK	11	12	6	45.75	b4b5b6b10°b10y7	1195.62	46.077	6159	2	598.32	-16.74
[P0A1H3]EFG_SALTY Elongation factor G	22		HASDDEPFSALAFK	309	14	6	35.28	b3b11y3y9y10°y10	1534.74	66.054	2595	2	767.87	16.46

P0A1H3 EFG_SALTY Elongation factor G	23		ASYTMEFLKYDDAPNNVAQAVIE AR	677	25	10	42.59	b9°b9b12b13b14y4°y4y8°y 8y10	2816.36	85.301	50826	3	939.46	3.03
P0A1H3 EFG_SALTY Elongation factor G	24		VYSGVVNSGDTVLNSVKTAR	337	20	3	19.8	b4b8b17	2066.06	102.186	22042	2	1033.53	-13.47
P0A1H3 EFG_SALTY Elongation factor G	25		GYEFINDIKGGVIPGEYIPAVDK	532	23	4	18.12	b11y5y9y14	2494.28	84.255	13609	3	832.10	-2.45
P0A1H3 EFG_SALTY Elongation factor G	26		GGVIPGEYIPAVDKGIQEQLK	541	21	3	12.6	b3b12y12	2211.19	75.137	11964	3	737.74	-3.20
P0A1H3 EFG_SALTY Elongation factor G	27		AKVTDIEGK	495	9	4	35.89	y3y5°y5y6	960.52	26.813	7972	2	480.77	-13.53
P0A1H3 EFG_SALTY Elongation factor G	28		IHAEVPLSEMFYATQLRSLTK	653	22	5	12.26	b11°b11b14y15°y15	2491.29	123.596	2243	3	831.10	-5.00
P0A1H3 EFG_SALTY Elongation factor G	29		VWTDEESNQTHIAGMGELHLDIIV DRMK	446	28	5	25.3	b3b4b11b13°b13	3213.56	122.805	2001	3	1071.86	-8.36
P0A1H3 EFG_SALTY Elongation factor G	30		INIIDTPGHVDFTIEVERSMR	83	21	4	22.26	y6y7°y7y11	2442.25	81.427	1690	3	814.75	1.30
P0A1H3 EFG_SALTY Elongation factor G	31	Phohoryl STY(8)	YLGGEELTEEEIK	236	13	4	31.15	b5b9b11y5	1589.71	54.640	14393	3	530.57	12.29
P0A1H3 EFG_SALTY Elongation factor G	32	Oxidation+M(16)	GITITSAATTAFWSGMAK	59	18	7	36.52	b3°b3b8y3y6y13y14	1829.89	122.854	2366	2	915.45	-8.94
P0A1H3 EFG_SALTY Elongation factor G	33		SNQTHIAGMGELHLDIIVDR	452	20	8	34.79	b7°b7b10°b10b11b12°b12* b12	2195.14	136.408	2504	2	1098.07	-4.12
P66643 RS9_SALTY 30S ribosomal protein S9	1		SLEQYFGR	33	8	10	58.24	b2b4y2y3y4y5*y5y6°y6y8	999.48	61.386	157794	2	500.25	-5.92
P66643 RS9_SALTY 30S ribosomal protein S9	2		GGGISGQAGAIR	68	12	12	90.14	b3b4b5°b5y4y5y6y7y8°y8* y8y12	1043.55	34.477	154172	2	522.28	-11.35
P66643 RS9_SALTY 30S ribosomal protein S9	3		AENQYYGTGR	1	10	7	48.69	y4y5y6y8°y8y10*y10	1158.51	27.895	47086	2	579.76	-4.21
P66643 RS9_SALTY 30S ribosomal protein S9	4		QPLELVDMVEK	49	11	10	81.32	b9°b9b11y4y5y6y7y9y10y 11	1300.69	74.912	22772	2	650.85	3.94
P66643 RS9_SALTY 30S ribosomal protein S9	5		VFIKPGNGK	18	9	4	43.67	y3y5*y5y7	959.55	30.343	35353	2	480.28	-12.91
P66643 RS9_SALTY 30S ribosomal protein S9	6	Phohoryl STY(5)	GGGISGQAGAIR	68	12	4	37.13	b3b4y9y10	1123.53	79.547	2679	2	562.27	9.45
P66643 RS9_SALTY 30S ribosomal protein S9	7		SGQAGAIR	72	8	1	7.33	b3	759.40	34.483	2964	1	759.40	-13.50
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1		VTLEPLER	25	8	8	50.7	y1y4°y4y5°y5y6y7y8	956.53	53.058	50597	2	478.77	-11.10
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2	Carbamidomethyl+C(6)	LLVDACYVER	170	12	11	89.6	b2b12y4y5y6°y6y7y8y9y10 y12	1421.71	60.131	49532	2	711.36	2.32
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3		IAYNVEAAR	182	9	13	83.34	b2b5b8y3y4°y4y6*y6y7*y7 y8y9*y9	1006.52	40.054	34073	2	503.77	-7.64
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4		EGVQEDILEILLNLK	71	15	13	53.4	b2°b2b4b8b10°b10y1y2y3 y4y6y8y15	1725.97	122.821	16128	2	863.49	5.80
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5		LVDIEQVSSTHAK	12	13	4	29.38	b3y4y5y7	1426.73	46.470	81663	3	476.25	-16.43
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		LVIEMETNGTIDPEEAIR	200	18	4	19.28	b5b12y10y12	2030.04	84.489	41407	3	677.35	16.18
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		MQGSVTEFLKPR	0	12	3	27.38	b7b9b10	1392.71	60.709	25863	3	464.91	-17.00

P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8	Carbamidomethyl+C(9)	ILLSSMPGCAVTEVEIDGVLHEYS TK	45	26	3	22	y4y5y7	2848.42	91.690	15129	3	950.14	2.66
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9		AEAIHYGDLVQR	271	13	4	18.63	b8b12*b12y9	1484.81	78.435	13358	2	742.91	18.91
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	10		QPEVKEEKPEFDPILLRPVDDLELT VR	238	27	7	31.56	b3b7*b7b9*b9b10b12	3204.70	114.118	1629	3	1068.91	-3.43
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	11	Carbamidomethyl+C(6)	LLVDACYVERIAYNVEAAR	170	21	4	12.6	b8b12y4°y4	2409.21	80.829	1592	3	803.74	-7.40
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	12	Oxidation+M(5)	LVIEMETNGTIDPEEAIR	200	18	5	19.28	b6°b6b9y4y10	2045.99	99.799	22709	3	682.67	-9.43
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		VALTGLTMAEK	219	11	11	76.8	b2y1y2°y2y3y4y5y6y8y9y11	1133.62	60.076	77110	2	567.31	-2.48
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		QLDPLVVGQEHYDTAR	343	16	10	52.64	b2b3°b3b16y3y4y9y10*y10y11	1840.90	58.776	43102	3	614.30	-12.60
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		TVNMMELIR	156	9	10	55.72	b2°b2b3°b3b4b8y1y5y7y9	1106.57	76.937	36953	2	553.79	-1.32
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	8	60.74	b2b3b8b9y4y7y8y10	1193.60	81.679	36671	2	597.31	-2.15
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		QIASLGIYPAVDPLDSTSR	324	19	11	73.5	b4b9y4y5y7°y7y11y12y13y14y19	2003.06	81.276	31856	2	1002.03	8.41
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		FLSQPFFVAEVFTGGK	399	18	5	21.19	b2y3y5y7y18	1958.02	100.478	31583	2	979.52	9.66
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		MPSAVGYQPTLAEEMGVLQER	261	21	11	52.57	b6b9b12y2y3y6y7y8y11*y11y21	2306.14	82.391	26592	2	1153.57	11.22
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		VYDALEVQNGNEK	25	13	6	31.15	b2b3°b3b8b10y11	1478.72	45.510	19569	2	739.86	5.78
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		NIAIEHSGYSVFAGVGER	165	18	6	14.03	b3b13°b13y2°y2y13	1905.94	67.193	2410	2	953.47	-4.48
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		AAPSYEELSNSQELLETKIK	112	20	7	40.47	b9b15°b15y4y5y6y14	2179.09	74.495	20543	2	1090.05	7.51
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		GLDVK	65	5	1	12.3	b3	531.31	41.748	9452	1	531.31	1.03
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		YQELK	367	5	2	12.3	y4°y4	680.36	32.029	8797	1	680.36	-2.96
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	4	16.15	b5y6y8y11	3057.45	93.315	8446	3	1019.82	20.84
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		TGSITSVQAVYVPADDLTDPATTF AHLDATVVLSR	287	37	4	24.71	b4b5b9b14	3815.97	131.765	3300	4	954.75	9.98
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15	Carbamidomethyl+C(26)	AAPSYEELSNSQELLETKIKVIDLM CPFAK	112	30	8	57.55	b3b6b7b8y4y5y6y28	3353.67	121.223	37511	3	1118.56	1.82
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16		NIAIEHSGYSVFAGVGERTR	165	20	4	13.01	b8*b8b11y9	2163.09	74.855	27425	3	721.70	-3.05
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17		GEIGEEERWAIHR	99	13	3	18.63	b4b12y8	1581.79	61.924	12652	2	791.40	9.72
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18		IMNVLGEPVDMKEIGEEER	87	20	4	22.97	b11y5y7y8	2245.09	110.051	3917	3	749.03	2.61
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19	Phohoryl STY(4)	GVQSILQR	359	8	5	33.63	b3y5°y5*y5y7	980.47	39.966	8147	2	490.74	-8.78
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20	Oxidation+M(4)	TIAMGSSDGLRR	53	12	5	45.75	b5y6y8y9y10	1279.63	63.676	11654	2	640.32	-9.25
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	21	Oxidation+M(4)	TIAMGSSDGLR	53	11	5	32.19	b4°b4b6y3y6	1123.55	98.680	4758	1	1123.55	11.84
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	22		HSGYSVFAGVGER	170	13	0	6.46		1365.67	67.192	10722	2	683.34	9.39

P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	1		TDGLMPAIVQHAVSGEVLMLGY MNPQALDK	14	30	10	23.42	b1b9°b9b11°b11y1y2y9y10y30	3198.64	136.431	28117	4	800.42	13.89
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	2		TADPTSSYTAK	126	11	10	59.99	b2°b2b3b8b10y4y8y9°y9y11	1141.53	27.817	16557	2	571.27	-4.60
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	3		MLTEQQR	0	7	5	34.89	b5°b5y4°y4y5	905.45	60.131	8979	2	453.23	-3.24
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	4	Carbamidomethyl+C(17);Carbamidomethyl+C(33)	GETSGHVLNVSVIAPDCDNDTLL VLANPVGPTCHK	64	35	5	15.18	b3b11b14y7y10	3699.84	115.265	3296	4	925.72	7.52
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	5		VGEEGVETALAATVNDR	149	17	6	32.67	b10y3y6y7°y7y9	1730.88	83.504	17250	2	865.95	16.08
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	6		FELTNEASDLMYHLLVLLQDQDL NLTTVIDNLR	166	33	10	46.37	b5b6°b6°b6b8b9b11y8y13y14	3859.96	114.013	7909	4	965.75	-4.62
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	7	Carbamidomethyl+C(5)	GTSSCFGDASHQWLFLYQLEQLL AER	99	26	3	22	y3y4y7	3056.48	117.865	7375	3	1019.50	6.23
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	8		KTADPTSSYTAK	125	12	4	44.91	y4y5y8y9	1269.63	24.501	7151	2	635.32	1.92
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	9		MLTEQQR	0	8	6	47.69	b3°b3b4y3*y3y5	1061.55	97.508	4941	1	1061.55	-6.32
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	10	Oxidation+M(11)	FELTNEASDLMYHLLVLLQDQDL NLTTVIDNLR	166	33	3	16.67	b6b8b23	3875.93	118.066	10282	4	969.74	-10.90
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	11	Oxidation+M(5)	TDGLMPAIVQHAVSGEVLMLGY MNPQALDK	14	30	4	12.81	b5b15y3y13	3214.58	87.358	3361	3	1072.20	-4.03
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	12		TDGLMPAIVQHAVSGEVLMLGY MNPQA	14	27	3	12.61	y4y12°y12	2842.43	136.473	6117	2	1421.72	11.34
P10367 HIS2_SALTY Histidine biosynthesis bifunctional protein hisIE	13		AIVQHAVSGEVLMLGYMNPQAL DK	20	24	1	10.74	b3	2584.29	136.376	4638	2	1292.65	-13.89
P26976 PHON_SALTY Non-ecific acid phohatase	1		IFVVGAK	85	9	9	69.79	b3y1y3y4y6y7y8°y8y9	917.53	52.082	102546	2	459.27	-14.70
P26976 PHON_SALTY Non-ecific acid phohatase	2		LQTIPAFQK	215	9	4	43.67	y3y5y7y9	1045.59	55.936	96693	2	523.30	-10.86
P26976 PHON_SALTY Non-ecific acid phohatase	3		YVGAVEFAR	206	9	9	88.11	b2b3b4b5y3y5y7y8y9	1011.52	52.323	88516	2	506.26	-7.72
P26976 PHON_SALTY Non-ecific acid phohatase	4		NGSYPSGHTAYGTLLALVLSEARPER	150	26	7	24.79	b2°b2y5y8y11y22y26	2759.38	97.149	70777	4	690.60	-12.48
P26976 PHON_SALTY Non-ecific acid phohatase	5	Carbamidomethyl+C(3)	VICGAHWQSDVDAGR	191	15	11	74.82	b2b6b12y3y5°y5y6y7y9y13y15	1670.75	46.546	50243	3	557.59	-13.15
P26976 PHON_SALTY Non-ecific acid phohatase	6		DTPETWNMLK	98	10	11	64	b10°b10y3y5y6°y6*y6y7°y7y8y10	1234.58	66.116	34693	2	617.79	3.36
P26976 PHON_SALTY Non-ecific acid phohatase	7		NLLTMGGYYATASAK	108	15	3	24.39	y9y11y13	1560.77	59.012	7894	3	520.93	-1.64
P26976 PHON_SALTY Non-ecific acid phohatase	8		QAAEDADVSVENIAR	70	15	3	22.33	b13y12y13	1587.77	51.484	19432	2	794.39	2.77
P26976 PHON_SALTY Non-ecific acid phohatase	9		NLLTMGGYYATASAKK	108	16	10	41.47	b5°b5b8°b8°b8b11°b11y10y11y14	1688.86	65.303	25301	3	563.62	-7.37
P26976 PHON_SALTY Non-ecific acid phohatase	10		WKQAAEDADVSVENIAR	68	17	12	38.36	b9°b9b11°b11°b11y7*y7y9*y9y10*y10y13	1901.92	63.694	17788	4	476.24	-6.23

[P26976]PHON_SALTY Non-ecific acid phohatase	11		INPKDTPETWNMLK	94	14	5	25.94	y7y11°y11y13*y13	1686.85	106.441	16085	2	843.93	-3.04
[P26976]PHON_SALTY Non-ecific acid phohatase	12	Carbamidomethyl+C(11)	GWEFGQSRVICGAHWQSDVDAGR	183	23	3	11.96	b13y4y8	2618.22	60.756	1668	3	873.41	11.19
[P26976]PHON_SALTY Non-ecific acid phohatase	13	Phohoryl STY(4)	NLLTMGGYYATASAKK	108	16	4	15.43	b3*b3y9y11	1768.81	83.460	5283	3	590.27	-9.11
[P26976]PHON_SALTY Non-ecific acid phohatase	14	Phohoryl STY(9)	INPKDTPETWNMLK	94	14	5	27.91	b4b7*b7b8y4	1766.82	38.801	1846	3	589.61	4.15
[P26976]PHON_SALTY Non-ecific acid phohatase	15	Oxidation+M(12)	INPKDTPETWNMLK	94	14	5	28.7	b8b10b12y5*y5	1702.84	73.935	44120	2	851.92	-4.80
[P26976]PHON_SALTY Non-ecific acid phohatase	16	Oxidation+M(5)	NLLTMGGYYATASAK	108	15	7	33.44	b6°b6b11*b11b12y8y12	1576.79	82.646	4415	3	526.27	12.85
[P26976]PHON_SALTY Non-ecific acid phohatase	17		GAVEFAR	208	7	2	21.82	b4b6	749.39	52.308	5099	1	749.39	-3.67
[P26976]PHON_SALTY Non-ecific acid phohatase	18		IFVVGAK	85	9	1	8.27	y5	899.53	52.055	8678	2	450.27	-1.70
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	1		TITSWADLWKPEYK	146	14	8	44.68	b12y1y2y4y5y11y12y14	1737.86	83.786	70095	3	579.96	-12.29
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	2		EGGIFWMDSLAIPANAK	249	17	14	47.28	b3b5b6°b6b12°b12y1y2y5*y5y7y12*y12y17	1819.91	94.407	49983	2	910.46	4.56
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	3		EVAETIGYPTPNLAAR	285	16	7	48.66	b7y7y8y10y11y13y16	1701.89	61.863	41577	2	851.45	5.59
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	4		DGAYDLVVPSTYYVDK	73	16	3	15.43	b9b11y8	1804.89	74.930	6274	2	902.95	13.59
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	5		NSLLLTDDAR	160	10	4	26.38	b2b7y3y4	1117.59	62.369	4312	2	559.30	7.97
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	6		QAGTPLEVWPK	237	12	7	45.75	b4b7b8*b8b10°b10y3	1324.75	57.281	34552	3	442.26	21.65
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	7		EIEAAYEELK	190	10	3	24.62	b5b8y3	1194.61	55.098	25537	2	597.81	14.71
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	8		LTNFHNLDP EMLNKPFPDPNN DYS VPYIWGATAIGVNSDAIDPK	103	43	4	11.75	b26°b26y6y21	4803.23	118.603	8738	4	1201.56	-15.35
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	9		SLYPDAQTISK	312	11	4	33.87	y7y8°y8y9	1222.62	76.333	6363	2	611.81	-8.19
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	10		EGMIQK	92	6	1	12.8	b5	705.36	42.052	4889	1	705.36	-1.64
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	11		EGGIFWMDSLAIPANAKNK	249	19	4	20.44	b5°b5b11b13	2062.02	71.097	4030	3	688.01	-9.71
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	12		DGAYDLVVPSTYYVDKMR	73	18	14	88.54	b3b7b8°b8b10°b10b12y6y7y9y11y12°y12y15	2092.03	122.861	1867	3	698.02	13.77
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	13	Phohoryl STY(15)	TYKDGAYDLVVPSTYYVDK	70	19	3	13.48	b10b13_H3PO4 b13y3	2277.04	60.142	4243	4	570.02	7.61
[P0A2C7]POTD_SALTY ermidine/putrescine-binding periplasmic protein	14	Phohoryl STY(10)	EVAETIGYPTPNLAARK	285	17	3	14.67	b3b8y8	1909.94	117.951	3655	2	955.47	4.99

P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	15		TSWADLWKPEYK	148	12	1	7.23	b10	1523.77	83.818	4229	2	762.39	11.14
P66032 RIBB_SALTY 3	1	Carbamidomethyl+C(4)	APECIAFAGQHNMVVTIEDLVA YR	184	25	6	20	b2b8b13y3y5y7	2775.37	99.707	56347	3	925.80	4.49
P66032 RIBB_SALTY 3	2		MNQTLSSFGTPFER	0	15	12	94.11	b2b5°b5b10y3y4y6y7y9y1 0y12y15	1727.85	85.470	46381	2	864.43	6.99
P66032 RIBB_SALTY 3	3		VELALDALR	15	9	6	14.55	b2b3y2y4°y4y9	999.58	70.099	38140	2	500.29	-5.31
P66032 RIBB_SALTY 3	4	Carbamidomethyl+C(23)	GGHTEATIDLMTLAGFKPAGVLC ELTNDDGTMAR	150	34	13	30.91	b3b7b9°b9b12°b12b30y4°y 4y6y10°y10*y10	3562.77	123.577	26975	3	1188.26	20.28
P66032 RIBB_SALTY 3	5		DGAKPSDLNRPGHVFPPLR	123	18	5	21.43	b14°b14b15°b15y14	1976.01	100.161	2857	2	988.51	-16.43
P66032 RIBB_SALTY 3	6		VELALDALREGR	15	12	5	24.15	b4°b4y9°y9y10	1341.73	64.441	60507	2	671.37	-10.74
P66032 RIBB_SALTY 3	7		NQTLSSFGTPFERVELALDALR	1	23	4	18.12	b5b7b11y4	2577.34	117.201	1686	3	859.78	-11.18
P66032 RIBB_SALTY 3	8	Oxidation+M(1)	MNQTLSSFGTPFER	0	15	4	26.7	b13y3y4y10	1743.85	83.095	2684	2	872.43	6.02
P0A2B3 RS7_SALTY 30S ribosomal protein S7	1		STAESIVYSALETLAQR	36	17	15	67.36	b1b2°b2b7°b7b12b13°b13y 1y3*y3y4y5y6y9	1838.93	107.293	111029	3	613.65	-11.95
P0A2B3 RS7_SALTY 30S ribosomal protein S7	2		SELEAFEVALENVRPTVEVK	56	20	7	13.01	b2b3°b3b8y1y11y20	2259.18	92.630	64543	3	753.73	-2.49
P0A2B3 RS7_SALTY 30S ribosomal protein S7	3		FVNILMVDGK	25	10	8	69.31	b2b3y2y3y4y5y6y8	1135.62	76.550	63251	2	568.31	-1.93
P0A2B3 RS7_SALTY 30S ribosomal protein S7	4		FGSELLAK	17	8	5	61.25	b6y3y4y6y7	864.47	52.429	154201	2	432.74	-18.71
P0A2B3 RS7_SALTY 30S ribosomal protein S7	5		WIVEAAR	102	7	6	74.81	b4b5y3y4y5y6	844.45	51.325	113561	2	422.73	-17.13
P0A2B3 RS7_SALTY 30S ribosomal protein S7	6		NALAMR	96	6	1	12.8	y5	675.36	37.070	5949	1	675.36	0.99
P0A2B3 RS7_SALTY 30S ribosomal protein S7	7		ILPDPK	11	6	2	12.8	y4°y4	682.41	33.396	3061	1	682.41	-6.17
P0A2B3 RS7_SALTY 30S ribosomal protein S7	8		LANELSDAADNKGTAVK	119	17	23	134.11	b3*b3b5b7°b7b9y5°y5y9* y9y10*y10y11°y11*y11y12 °y12*y12y13y14y15*y15y1 6	1716.85	40.106	238959	3	572.96	-12.58
P0A2B3 RS7_SALTY 30S ribosomal protein S7	9		WIVEAARK	102	8	3	38.4	b4b5b6	972.56	56.832	47794	2	486.78	-1.95
P0A2B3 RS7_SALTY 30S ribosomal protein S7	10		EDVHRMAEANK	138	11	14	105.93	b5b6b7b8y5°y5y6y7°y7y8 *y8y10°y10*y10	1299.62	63.660	3507	2	650.31	4.60
P0A2B3 RS7_SALTY 30S ribosomal protein S7	11		SELEAFEVALENVRPTVEVKSR	56	22	5	27.27	b6b8°b8b9b16	2502.33	109.741	1662	3	834.78	3.12
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	1		LAEAGIPTQMER	60	12	8	61.07	b2b3y5y6y8y9y10y12	1315.67	50.857	74131	2	658.34	-0.28
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	2		QSLGGLIEAYEAVHR	215	16	7	37.74	b3b5b10y1y5y6y16	1713.87	85.929	50747	3	571.96	-10.33
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	3		TVYSTENPDLLVLEFR	13	16	10	50.09	b4b11°b11b13y2y3y9y12y 13y16	1895.99	89.314	31845	2	948.50	7.28
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	4		GEVVLGDEFDGSR	184	15	4	16.31	b9y4y6y15	1563.74	95.487	1686	2	782.37	7.18
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	5		LGVEEGMELNPPIFDLFLK	104	19	3	20.44	b3b5b7	2161.08	82.669	14801	2	1081.04	-20.45
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	6		LWDK	199	4	2	11.81	y3°y3	561.31	32.139	12283	1	561.31	9.46

P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	7		IEQFDR	39	6	1	12.8	b4	807.39	110.709	2414	1	807.39	-9.98
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	8	Carbamidomethyl+C(9)	KLEMPVECVVR	82	12	13	101.2	b3°b3b4b9°b9y5y6y7°y7y9 y10y11°y11	1458.78	63.650	19031	2	729.89	-0.08
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	9		TVYSTENPDLLVLEFRNDTSAGD GAR	13	26	7	29.05	b6b12b13y5°y5y12y19	2840.35	110.157	18343	3	947.45	-7.22
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	10		GEVVLGDEFDGSRLWDK	184	19	5	28.34	b10b11b13y7y10	2106.00	59.965	5512	2	1053.50	-6.96
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	11		NDTSAGDGARIEQFDR	29	16	6	40.91	b13b14b15°b15y3y6	1751.78	72.528	4909	3	584.60	-7.11
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	12	Carbamidomethyl+C(8); Oxidation+M(3)	LEMVPVECVVR	83	11	4	33.62	b5y5y6y8	1346.70	82.860	2170	3	449.57	11.87
P0A1P6 GLNA_SALTY Glutamine synthetase	1		AGGVFTDEAIDAYIALR	430	17	7	36.27	b5b7b10y12y13°y13y17	1781.88	77.285	94852	2	891.45	-12.47
P0A1P6 GLNA_SALTY Glutamine synthetase	2		LVPGYEAPVMLAYSAR	322	16	10	75.7	b2b15y4y5y7y9y10y11y14 y16	1736.92	78.372	38014	2	868.96	6.89
P0A1P6 GLNA_SALTY Glutamine synthetase	3		AINALANPTTNSYKR	307	15	5	24.39	y7°y8y10y13y15	1633.87	43.759	35997	3	545.29	2.54
P0A1P6 GLNA_SALTY Glutamine synthetase	4		AINALANPTTNSYK	307	14	9	88.58	b4y7y8y9y10y11y12y13y1 4	1477.76	48.771	35606	2	739.38	-2.23
P0A1P6 GLNA_SALTY Glutamine synthetase	5		GGYFPVPPVDSAQDIR	177	16	8	38.41	b12b13°b13y2y5*y5y6y8	1717.86	58.222	26175	3	573.29	5.68
P0A1P6 GLNA_SALTY Glutamine synthetase	6	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	7	29.16	b3b12b14b15°b15y4y6	2565.32	136.684	17016	3	855.78	11.42
P0A1P6 GLNA_SALTY Glutamine synthetase	7		ATGIADTVLFGPEPEFFLFDDIR	117	23	11	38.2	b2b3°b3b13y12y3y4y5y1 2y23	2570.28	117.770	14671	3	857.43	-1.52
P0A1P6 GLNA_SALTY Glutamine synthetase	8		GINESDMVLPDASTAVIDPFFAD STLIIR	59	30	17	77.37	b2b3b4b5b9°b9*b9b10b13 b24y1y2y3y4y6y11y12	3238.62	114.080	13107	3	1080.21	6.03
P0A1P6 GLNA_SALTY Glutamine synthetase	9		MSAEHVLTMLNEHEVK	0	16	4	15.43	b7b11°b11y4	1867.93	105.172	3384	3	623.31	13.20
P0A1P6 GLNA_SALTY Glutamine synthetase	10	Carbamidomethyl+C(19)	TATFMPKPMFGDNGSGMHCHMS LAK	252	25	10	50.92	b4b5°b5b6b8y3y6°y6y11y1 2	2753.27	65.337	4448	3	918.43	21.37
P0A1P6 GLNA_SALTY Glutamine synthetase	11		EIPQVAGSLEEALNALDLDR	406	20	4	21.14	b13b14°b14y8	2153.07	109.444	3122	3	718.36	-16.10
P0A1P6 GLNA_SALTY Glutamine synthetase	12		SAEHVLTMLNEHEVK	1	15	4	16.31	b3b9y8*y8	1736.87	31.028	2976	4	434.97	1.90
P0A1P6 GLNA_SALTY Glutamine synthetase	13	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK NK	360	26	3	11.33	b3b9y11	2807.42	129.336	27845	3	936.48	-2.26
P0A1P6 GLNA_SALTY Glutamine synthetase	14		FVDLRFTDTK	16	10	6	50.2	b3°b3b7b8y4y5	1241.66	64.413	4405	2	621.33	3.05
P0A1P6 GLNA_SALTY Glutamine synthetase	15		ADEIQIYKYVVHNV AHR	232	17	3	23.33	b6b7b9	2055.06	71.298	2272	2	1028.03	-7.72
P0A1P6 GLNA_SALTY Glutamine synthetase	16		MSAEHVLTMLNEHEVKFVDLR	0	21	4	22.52	b8b12b13y5	2498.22	59.022	1818	3	833.41	-14.76
P0A1P6 GLNA_SALTY Glutamine synthetase	17	Oxidation+M(9)	MSAEHVLTMLNEHEVK	0	16	3	23.8	y5y11y12	1883.89	81.541	1871	3	628.63	-5.90
P0A1P6 GLNA_SALTY Glutamine synthetase	18		NALANPTTNSYKR	309	13	0	4.97		1449.75	43.761	2535	2	725.38	3.62
Q8ZRP4 DAPD_SALTY 2	1		MQQLQNVIAFER	0	14	7	44.68	b13y3y7y10*y10y12y14	1706.86	86.831	93843	2	853.93	2.36
Q8ZRP4 DAPD_SALTY 2	2		EAVNQVISLLDSGALR	28	16	12	99.76	b2b6°b6y2y3y4y5y6y7y8y9 y10	1684.93	92.929	70446	2	842.97	5.58

Q8ZRP4 DAPD_SALTY 2	3		INDNQVIDGAESR	68	13	9	70.01	y3°y3y5y6y7°y7y8y9y13	1430.69	42.202	58454	2	715.85	-0.85
Q8ZRP4 DAPD_SALTY 2	4		IDGQWVTHQWLK	48	12	6	20.17	b5°b5b8°b8y6°y6	1510.77	73.919	10345	2	755.89	-6.95
Q8ZRP4 DAPD_SALTY 2	5		ETGEVHYGR	217	9	6	63.5	b3°b3b4y3y5y8	1047.49	58.084	2901	2	524.25	2.56
Q8ZRP4 DAPD_SALTY 2	6		MQQLQNVIAFERR	0	15	4	24.39	b5b10b12°b12	1862.95	82.711	5433	3	621.65	-2.95
Q8ZRP4 DAPD_SALTY 2	7		YFDKVPKM	81	8	4	44.68	b4b5y3y4	1027.53	83.560	1607	2	514.27	-2.85
Q8ZRP4 DAPD_SALTY 2	8	Phohoryl STY(7)	IDGQWVTHQWLK	48	12	5	27.38	b3°b3b5b6°b6	1590.76	101.968	2782	3	530.93	14.96
Q8ZRP4 DAPD_SALTY 2	9	Carbamidomethyl+C(30) ;Oxidation+M(20)	NTVLMPSYVNIGAYVDEGTMVD TWATVGSQAQIGK	119	35	11	51.09	b3°b3b5°b5b9b14b15y7°y7 y8y9	3763.81	96.466	11303	4	941.71	12.00
Q8ZRP4 DAPD_SALTY 2	10	Oxidation+M(1)	MQQLQNVIAFER	0	14	3	17.37	b5y3y6	1722.87	108.636	1759	2	861.94	12.61
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		AGLGMMEGVLENVPSAR	78	17	9	38.36	b11b13°b13y4y7y12°y12y 13y17	1730.87	82.672	52679	2	865.94	9.31
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		VLVLVAAPEGIAALEK	155	16	8	66.6	b3b4b5b6b7y2y9y11	1592.97	86.769	44019	2	796.99	3.07
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		NEETLEPVVPYFQK	103	13	3	26.11	y5y7y8	1593.79	66.367	18931	2	797.40	5.59
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		LGLMRENDISTK	14	12	8	24.15	b2b9y8°y9°y9y10°y10y12	1376.70	60.782	18080	2	688.85	-13.12
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		ITVVPILR	70	8	4	38.4	y4y5y6y8	910.60	70.803	14619	2	455.80	-10.66
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	6		ELASEVGSLLTYEATADLETEK	29	22	5	22.13	b11°b11b14b15y14	2369.20	99.108	2742	3	790.40	16.49
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	7		ELASEVGSLLTYEATADLETEKVT IEGWNGPVEIDQIK	29	38	4	23.61	b3b4°b4b6	4148.03	112.579	10795	4	1037.76	-11.65
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	8		LGLMRENDISTK	14	12	4	30.39	b6b8°b8b10	1376.74	67.273	7444	2	688.87	12.24
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	9		NEETLEPVVPYFQKLVSNIDER	103	21	4	21.05	b11b12°b12y8	2520.24	81.454	3918	3	840.75	-6.68
P63411 ACKA_SALTY Acetate kinase	1	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPE AR	17	26	17	76.68	b2b3b10b15b22y2y3°y3y4 y8y10y13y14°y14y19y23y2 6	2907.39	105.196	42295	3	969.80	-2.44
P63411 ACKA_SALTY Acetate kinase	2		EGTRPAVVIPTNEELVIAQDASR	374	23	13	86.77	b7b8b9b14b15y1y2y5y6y7 y8y14y23	2465.30	69.988	36925	3	822.44	-1.09
P63411 ACKA_SALTY Acetate kinase	3	Carbamidomethyl+C(14)	ESGLLGLTEVTSDCR	272	15	5	24.39	b4b6b12y2y15	1636.79	72.711	26633	2	818.90	5.67
P63411 ACKA_SALTY Acetate kinase	4		SGDIDPAIFHLHDTLGMSVDQINK	243	25	3	11.5	b6y7y9	2736.36	91.628	4439	3	912.79	-2.77
P63411 ACKA_SALTY Acetate kinase	5	Carbamidomethyl+C(14)	MLNKPVEELNIITCHLGNGGSVSA IR	195	26	4	11.33	b8b16y1y13	2822.46	125.607	4162	3	941.49	-0.43
P63411 ACKA_SALTY Acetate kinase	6		DSASFAPLHNPAHLIGIAEALK	114	22	3	18.77	b3b9b14	2272.23	87.276	31631	3	758.08	9.67
P63411 ACKA_SALTY Acetate kinase	7		YTSSVVIDESVIQGIK	98	16	5	32.42	b3b6°b6b7b12	1737.91	34.151	17853	4	435.23	-11.73
P63411 ACKA_SALTY Acetate kinase	8	Carbamidomethyl+C(1)	CVDTSMGLTPLEGLVMGTR	224	19	14	107.44	b3b11b12b14y3°y3y5°y5y8 y10y11y13y14y16	2036.97	95.544	2847	3	679.66	-5.03
P63411 ACKA_SALTY Acetate kinase	9		LDAVVFTGGIGENAAMVR	324	18	5	22.95	y7°y7y8°y8y14	1819.92	83.608	2803	2	910.46	-11.40
P63411 ACKA_SALTY Acetate kinase	10	Carbamidomethyl+C(14)	ESGLLGLTEVTSDCRYVEDNYAT K	272	24	3	21.01	b14y5y6	2720.30	112.592	4442	3	907.44	9.42
P63411 ACKA_SALTY Acetate kinase	11		SGFINKEGTRPAVVIPTNEELVIAQ DASR	368	29	11	36.57	b3°b3b5°b5b9°b9b20y3y6y 7y14	3111.61	71.104	4426	4	778.66	-9.26
P63411 ACKA_SALTY Acetate kinase	12		IVHGGEKYTSSVVIDESVIQGIK	91	23	3	18.37	b5b8b11	2458.31	62.513	3619	3	820.11	-3.87
P63411 ACKA_SALTY Acetate kinase	13		LAKYIGSYTALMDGR	309	15	3	24.39	y5y6y14	1658.84	60.083	2725	3	553.62	-11.63
P63411 ACKA_SALTY Acetate kinase	14	Carbamidomethyl+C(4)	NGKCVDTSMGLTPLEGLVMGTR	221	22	8	44.44	b3b5b13b14°b14b15y3y8	2336.15	82.150	2601	3	779.39	3.55

P63411 ACKA_SALTY Acetate kinase	15	Carbamidomethyl+C(18)	MLTKESGLLGLTEVTSDCR	268	19	7	36.14	b4b5b7°b7y6y9y12	2110.02	92.534	2512	2	1055.52	-13.19
P63411 ACKA_SALTY Acetate kinase	16	Phohoryl STY(7)	LDVVFTGGIGENAAMVR	324	18	4	14.03	b5y7y11*y11	1899.89	108.679	6553	2	950.45	-3.02
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	1		MIQEQTMLNVADNSGAR	0	17	13	66.77	b2b3b13y6y7y8y9*y9y12y14°y14*y14y17	1877.90	59.972	91705	2	939.45	8.78
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	2	Carbamidomethyl+C(6)	FDGNACVILNNNSEQPIGTR	78	20	6	19.8	b2y3y7°y7y10y20	2219.08	60.114	14405	2	1110.04	12.65
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	3		IISLAPEVL	114	9	3	35.89	y4y5y7	954.58	86.263	77719	1	954.58	-9.02
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	4		IQEQTMLNVADNSGAR	1	16	10	48.66	b6°b6*b6y5y6°y6y10y12y13°y13	1746.86	64.402	12750	3	582.96	8.25
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	5		IQEQTMLNVADNSGARR	1	17	15	47.28	b5°b5*b5b7°b7b9°b9y3y6°y6y9*y9y10°y10*y10	1902.93	64.444	20283	4	476.49	-7.44
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	6		MIQEQTMLNVADNSGARR	0	18	8	44.84	b4b6b12y8y11y13*y13y14	2034.00	105.330	2041	2	1017.51	8.76
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	1		AAPNTIPTAAK	149	11	7	33.62	b4y2y5y8y9*y9y11	1054.58	33.183	27259	2	527.79	-7.52
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	2		SVDGIQVGEGR	266	11	9	32.19	b2°b2b3b10y6*y6y9*y9y11	1116.56	42.333	25552	2	558.79	0.44
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	3		AGGNYLSSSLVGSEARR	160	17	5	38.11	b5b7b8b9y6	1749.90	73.947	20590	3	583.97	-11.79
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	4		IQQAFFGLFTGETEDK	284	16	13	86.65	b2*b2b6b12y4y6y8y9°y9y10y11y13°y13	1830.89	94.414	17861	2	915.95	-1.87
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	5		ESLYLADEVFMSGTAAEITPVR	244	22	5	18.77	b2b8b12°b12b15	2399.18	118.728	9140	3	800.40	-0.81
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	6		VHVMShALHYGTSVFEGIR	22	19	4	22.66	b1y4y13y14	2140.09	86.018	1798	3	714.03	6.27
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	7		ADYIWFNGEMVR	5	12	5	33.15	b3b4y5°y5y7	1500.72	69.496	5089	3	500.91	17.16
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	8		WEDAKVHVMShALHYGTSVFEGIR	17	24	3	21.01	b8y11y12	2769.32	119.885	59972	3	923.78	-12.78
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	9		AGGNYLSSSLVGSEARR	160	17	4	27.36	b3b6y5y6	1749.92	114.116	22827	2	875.46	-1.60
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	10		RHGYQEGIALDVNGYISEGAGENLFEVK	176	28	4	15.78	b4b8b10y10	3065.50	136.489	6009	2	1533.25	0.08
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	11	Carbamidomethyl+C(12)	SVDGIQVGEGRCPVTK	266	17	6	30.53	b3b15y3y10y11°y11	1758.89	77.468	4515	2	879.95	3.05
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	12	Carbamidomethyl+C(20)	VHVMShALHYGTSVFEGIRCYDSHK	22	25	3	17.73	b4b9b12	2930.40	88.480	2422	4	733.36	5.67
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	13	Oxidation+M(4)	VHVMShALHYGTSVFEGIR	22	19	4	23.5	b4b12b13y14	2156.06	76.128	82273	3	719.36	-3.74
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	14	Oxidation+M(11)	ESLYLADEVFMSGTAAEITPVR	244	22	6	27.27	b6°b6b9b11b12°b12	2415.19	63.673	2659	4	604.55	6.97
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	1		QTMLINEK	45	8	6	45.93	b7y3y4y5y8*y8	976.51	42.239	21879	2	488.76	-2.00
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	2	Carbamidomethyl+C(4)	TIFCTYLQRDAEGQDFQLYPGELGK	3	25	5	24.67	b4b7b11b13y11	2949.45	122.736	2494	3	983.82	14.07
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	3	Carbamidomethyl+C(4)	TIFCTYLQR	3	9	8	74.05	b4b7°b7y3y5°y5y7y8	1201.61	65.362	49773	2	601.31	1.42
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	4		DVHIEGYTPEDK	78	12	8	65.8	b4°b4b6b7y3y5y8y9	1402.67	136.408	7378	1	1402.67	15.75
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	5		LLEQEMVVSFLFEGK	64	14	4	22.81	b7b8y9°y9	1669.85	79.401	3008	2	835.43	-2.19
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	6		IYNEISKDAWQWQHK	29	16	22	123.86	b3*b3b4b5b8b9°b9°b9b10°b10°b10b11y4*y4y5y6*y6y8*y8y9°y9*y9	2017.02	63.680	3070	2	1009.01	13.98

P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	7		QTMLINEK	45	8	0	1.49		958.49	42.233	2100	2	479.75	-4.01
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	1		LFNELGPR	78	8	6	53.71	b2y3y4y6y7y8	945.50	56.027	217071	2	473.26	-13.04
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	2		NMAGSLVR	22	8	12	58.24	b2*b2b7*b7y2y3y5y6*y6y7y8*y8	847.43	41.766	79454	2	424.22	-12.82
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	3		VVEPLITLAK	46	10	7	36.93	b2b3y1y4y7y8y10	1082.68	70.108	42140	2	541.84	-4.28
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	4		TRDNEIVAK	69	9	7	35.89	b1b2*b2b4b5b6y1	1045.55	20.642	5916	2	523.28	-9.11
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	5		AGGYTR	90	6	1	12.8	b3	624.31	89.762	12775	1	624.31	-3.32
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	6		AGDNAPMAYIELVDR	103	15	4	29.07	b12b13y5y9	1634.81	54.694	2225	3	545.61	17.77
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	7		RVVEPLITLAK	45	11	4	38.21	b3b4y4y5	1238.78	63.175	158407	2	619.89	-2.76
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	8		AGDNAPMAYIELVDRSEK	103	18	3	21.19	y3y5y13	1978.95	73.978	12314	3	660.32	-4.38
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	9		NMAGSLVR	22	8	0	1.49		830.41	41.766	5890	2	415.71	-5.81
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	1		TFDSESSAAR	62	10	11	81.62	b2b3y1y3y5y6y7y8*y8y9y10	1070.47	25.895	77068	2	535.74	-6.39
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	2		EIELDGVITYPYVTIDVSSK	33	19	3	21.26	b7y11y12	2128.08	85.695	10217	2	1064.55	6.77
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	3		TVVFHDTSANEYVK	10	14	24	187.52	b3*b3b5b6b10b11b12y3y4*y4y5*y5y6y7y8*y8y9*y9*y9y10*y10*y10y11y12	1609.76	47.836	385612	3	537.26	-16.46
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	4		MKPDHPVYR	0	10	4	24.62	b6*b6y6y9	1255.65	43.300	1556	2	628.33	-8.26
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	5		VGSTIKTER	24	9	4	54.21	y3y4y6y8	990.55	19.142	38379	2	495.78	-6.90
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	6		EIELDGVITYPYVTIDVSSKSHPFYTG	33	27	12	62.17	b7b8*b8b9*b9b10b16y3y6y8y9*y9	3073.54	122.792	3577	3	1025.18	7.63
P65692 K6PF_SALTY 6-phohofructokinase	1		IGVLTSGGDAPGMNAAIR	4	18	11	72.22	b3b10y2y8*y8y9y10y12y13y14y18	1699.88	63.129	36544	2	850.45	2.44
P65692 K6PF_SALTY 6-phohofructokinase	2		GGTFLGSAR	64	9	3	28.11	b3b4y5	865.46	48.467	23209	2	433.23	6.77
P65692 K6PF_SALTY 6-phohofructokinase	3	Carbamidomethyl+C(11)	HAIVAITEHMCVDDELAHFIEK	215	22	4	12.26	b12*b12b19y12	2578.22	87.300	5107	2	1289.61	-8.33
P65692 K6PF_SALTY 6-phohofructokinase	4	Carbamidomethyl+C(8)	LTEMGFPCIGLPGTIDNDIK	112	20	3	13.01	b12b14y13	2191.08	82.706	8553	3	731.03	0.33
P65692 K6PF_SALTY 6-phohofructokinase	5		MVQLDR	49	6	1	12.8	b4	761.39	96.517	4965	1	761.39	-4.41
P65692 K6PF_SALTY 6-phohofructokinase	6	Carbamidomethyl+C(1)	CVGIQNEQLVHHDIIDAENMK	283	22	3	12.26	b8y5y13	2576.22	93.494	4956	2	1288.61	-15.73
P65692 K6PF_SALTY 6-phohofructokinase	7		MGAYAIDLLLEGHGGR	267	16	4	37.19	y3y4y5y8	1672.81	84.267	4813	3	558.28	-21.16
P65692 K6PF_SALTY 6-phohofructokinase	8		GIDALVVIGGDGSYMGAK	93	18	3	14.03	b13y4y12	1722.88	92.980	4552	2	861.94	3.40
P65692 K6PF_SALTY 6-phohofructokinase	9		DTSSSHQRISIVEVMGR	155	17	3	14.67	b4b9y4	1901.97	87.293	8649	2	951.49	10.27
P65692 K6PF_SALTY 6-phohofructokinase	10		GGTFLGSARFPEFR	64	14	5	48.66	b4b5b6b7y5	1541.77	43.176	4640	2	771.39	-8.63
P65692 K6PF_SALTY 6-phohofructokinase	11		GVVRAALTEGLEVMGIYDGYLGLYEDR	22	27	4	34.8	y6y12y13y14	2959.46	135.424	1697	2	1480.23	-9.65
P65692 K6PF_SALTY 6-phohofructokinase	12	Carbamidomethyl+C(11);Oxidation+M(10)	HAIVAITEHMCVDDELAHFIEKETGR	215	26	5	14.07	b3b13y6*y6y12	3037.43	98.927	2802	2	1519.22	-5.87

Q7CQC4 CMOA_SALTY tRNA (cmo5U34)-methyltransferase	1		DITIENASMVVLNFTLQFLEPAER	119	24	15	30.59	b2b3°b3b6°b6b7°b7y2°y2y4°y4y6y7°y8°y8	2750.38	136.390	7281	2	1375.69	-10.03
Q7CQC4 CMOA_SALTY tRNA (cmo5U34)-methyltransferase	2	Carbamidomethyl+C(13)	FVQPNTQVYDLGCSLGAATLSVR	52	23	4	21.8	b9y12y14y15	2496.29	98.093	4686	3	832.77	14.77
Q7CQC4 CMOA_SALTY tRNA (cmo5U34)-methyltransferase	3		DTLFSAPIAR	4	10	3	26.38	b6b7y5	1090.58	46.470	2091	3	364.20	-5.93
Q7CQC4 CMOA_SALTY tRNA (cmo5U34)-methyltransferase	4		APTPVEVVEGDIR	106	13	3	18.63	b4b9y6	1381.73	72.473	6178	3	461.25	-0.18
Q7CQC4 CMOA_SALTY tRNA (cmo5U34)-methyltransferase	5		IIAVDNAMIER	84	13	4	38.42	b7b9b11b12	1428.77	66.030	4169	2	714.89	15.38
Q7CQC4 CMOA_SALTY tRNA (cmo5U34)-methyltransferase	6		HIDAYK	100	6	2	12.8	y4°y4	746.37	34.256	1885	2	373.69	-13.33
Q7CQC4 CMOA_SALTY tRNA (cmo5U34)-methyltransferase	7		MSHRDTLFSAPIAR	0	14	5	25.94	b4b10°b10b12°b12	1601.84	64.407	2718	2	801.42	13.03
Q7CQC4 CMOA_SALTY tRNA (cmo5U34)-methyltransferase	8	Oxidation+M(8)	VAEVFPDMIQR	23	11	6	25.12	b6y7°y7y8°y8°y8	1320.68	74.886	4641	3	440.90	13.03
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(6)	AALIDCLAPDR	321	11	11	59.99	b1b2b3b8°b8b10y1y3y7y8y11	1214.62	62.803	57033	2	607.81	0.70
P02936 OMPA_SALTY Outer membrane protein A	2	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	14	79.06	b3b4y1y2y5y8°y8y10y11*y11y13y14y17y19	2032.90	38.687	46411	3	678.31	-7.15
P02936 OMPA_SALTY Outer membrane protein A	3		SNVPGGPSTKDHD TG VVFAGGIE YAITPEIATR	128	35	4	10.95	b7b16°b16y11	3540.77	96.501	13027	4	885.95	1.38
P02936 OMPA_SALTY Outer membrane protein A	4		AQGVQLTAK	94	9	3	28.11	b3y5y6	915.52	26.903	30985	2	458.26	-5.40
P02936 OMPA_SALTY Outer membrane protein A	5		GIPSDK	292	6	1	12.8	y4	616.34	32.500	12652	1	616.34	9.41
P02936 OMPA_SALTY Outer membrane protein A	6		DNTWYAGAK	24	9	4	49.95	b3y3y5y7	1025.48	64.412	4706	2	513.24	11.43
P02936 OMPA_SALTY Outer membrane protein A	7		SNVPGGPSTK	128	10	6	44.71	b4b6°b6b8°b8y6	943.47	63.727	2663	1	943.47	-13.46
P02936 OMPA_SALTY Outer membrane protein A	8		DVVTQPQA	342	8	7	38.4	y3*y3y4*y4y5°y5*y5	857.43	122.857	2266	1	857.43	-12.17
P02936 OMPA_SALTY Outer membrane protein A	9		FGQQEAAPVVAPAPAPEVQTK	194	23	3	11.96	b7y10y12	2303.21	54.683	2044	2	1152.11	2.23
P02936 OMPA_SALTY Outer membrane protein A	10		DHD TG VVFAGGIE YAITPEIATR	138	25	3	21.04	b13y5y6	2616.28	107.217	1502	2	1308.64	-5.60
P02936 OMPA_SALTY Outer membrane protein A	11		AQGVQLTAKLGYPITDDLDVYTR	94	23	4	20.99	b3b4°b4y3	2537.30	125.728	12344	3	846.44	-8.56
P02936 OMPA_SALTY Outer membrane protein A	12	Carbamidomethyl+C(17)	ISARGMGESNPVTGNTCDNVKPR	298	23	3	11.96	b8y8y15	2460.20	70.698	11226	3	820.74	10.52
P02936 OMPA_SALTY Outer membrane protein A	13		DGSVVVLGFTDRIGSDAYNQGLS EK	255	25	3	11.5	b13b23y10	2627.28	67.312	9644	4	657.58	-5.48
P02936 OMPA_SALTY Outer membrane protein A	14		LGYPITDDLDVYTRLGGMVWR	103	21	13	91.99	b8b9b10b11°b11b12°b12y5y6y9y10y12°y12	2440.24	64.425	5498	3	814.08	1.60
P02936 OMPA_SALTY Outer membrane protein A	15		ADTKSNVPGGPSTK	124	14	4	24.74	b8b10y9y13	1358.69	68.369	2047	2	679.85	-3.14
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		VTDIEPGLVGGTEFSSVR	171	18	11	55.81	b2b3°b3b5y7y8y9y13y14°y14y18	1862.96	70.138	29607	2	931.98	5.96
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		GHIINIGSTAGSWPYAGGNVYGAT K	126	25	18	67.08	b2b13°b13b14°b14y2y3y4y5y8y9°y9*y9y11*y11y13°y13*y13	2491.27	66.082	18549	4	623.57	14.11
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		ASVEDWETMIDTNNK	93	15	3	24.39	y7y8y10	1752.78	79.521	4400	3	584.93	1.32
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4		AVLPGMVER	115	9	3	35.89	y4y6y7	971.53	53.970	30651	2	486.27	-8.67

[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5		TYENTTALTPEDITEAVWWVATL PAHVNINTVEMMPVTQSFAGLSV HR	199	48	7	23.67	b3b8b13°b13b14b27y6	5340.69	136.509	10240	4	1335.93	10.24
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		TDLHGTA VR	162	9	3	35.89	y4y5y6	969.50	24.221	9339	2	485.25	-10.14
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		DIDVLVNNAGLALGLEPAHK	73	20	8	42.78	b4b6b7°b7b9b11y3y7	2059.08	90.774	6582	3	687.03	-19.56
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	8	Carbamidomethyl+C(15)	MIVLVTGATAGFGECIAR	0	18	3	14.03	b14y5y16	1865.97	95.502	6285	2	933.49	5.43
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	9		NRAAIEEMMASLPAQWR	56	17	3	14.67	b6b12y8	1973.94	82.165	1785	4	494.24	-12.68
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	10	Carbamidomethyl+C(15) ;Phohoryl STY(9)	MIVLVTGATAGFGECIARR	0	19	5	29.22	y7_HPO3 y6y7y9°y9y12	2102.04	66.041	8021	5	421.21	9.87
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	11	Carbamidomethyl+C(15) ;Oxidation+M(1)	MIVLVTGATAGFGECIAR	0	18	6	42.11	b16y3y6y8y9y11	1881.96	120.684	21037	2	941.48	3.18
[Q7CPP7 RL21_SALTY 50S ribosomal protein L21	1		MYAVFQSGGK	0	10	8	57.01	b2b3y3y4°y4y7y8y10	1087.52	53.369	68841	2	544.26	-5.28
[Q7CPP7 RL21_SALTY 50S ribosomal protein L21	2		VSEGTQTVR	13	8	3	38.4	y5y6y7	875.46	16.986	1854	2	438.23	-3.21
[Q7CPP7 RL21_SALTY 50S ribosomal protein L21	3		IGVPFVDGGVIK	48	12	3	27.38	y5y6y9	1200.69	77.704	42395	2	600.85	-3.97
[Q7CPP7 RL21_SALTY 50S ribosomal protein L21	4		LDIATGETIEFAEVLMIANGEEVK	24	24	8	28.81	b3b14y4°y4y8*y8y10y14	2592.26	117.775	26262	3	864.76	-17.99
[Q7CPP7 RL21_SALTY 50S ribosomal protein L21	5		YAVFQSGGK	1	9	3	28.11	b5y3y6	956.46	90.752	4038	1	956.46	-21.31
[Q7CPP7 RL21_SALTY 50S ribosomal protein L21	6		QWFTDVK	90	7	3	37.9	y3y5y6	923.44	114.154	1578	1	923.44	-19.89
[Q7CPP7 RL21_SALTY 50S ribosomal protein L21	7		MYAVFQSGGKQHR	0	13	4	26.11	b3b4b10*b10	1508.72	41.817	3112	3	503.58	-13.67
[Q7CPP7 RL21_SALTY 50S ribosomal protein L21	8	Oxidation+M(16)	LDIATGETIEFAEVLMIANGEEVK	24	24	5	24.25	b10°b10b11y6y12	2608.31	77.072	6948	4	652.83	-0.19
[P67904 RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAK	16	14	18	131.32	b2b3b7°b7b9b10y2y3y4y5 y6y8y9y10y12°y12*y12y14	1517.80	56.296	159798	2	759.41	-1.45
[P67904 RS10_SALTY 30S ribosomal protein S10	2		LVDIVEPTEK	72	10	12	76.3	b2y2°y2y3y4y5°y5y6°y6y8 y9y10	1142.62	52.723	76820	2	571.81	-6.84
[P67904 RS10_SALTY 30S ribosomal protein S10	3		GPIPLPTRK	37	9	6	42.17	b2b3y4y5y6y9	978.60	44.150	55017	2	489.80	-7.67
[P67904 RS10_SALTY 30S ribosomal protein S10	4		DARDQYEIR	59	9	5	28.11	b8y4°y4y8y9	1165.56	45.957	10160	2	583.28	1.05
[P67904 RS10_SALTY 30S ribosomal protein S10	5		FTVLIHVNKDAR	48	14	4	32.93	y2y6y7y8	1596.88	54.756	5756	2	798.94	-3.29
[P67904 RS10_SALTY 30S ribosomal protein S10	6		FTVLIHV N K	48	11	3	29.1	y4y6y7	1254.70	59.331	52376	3	418.90	-17.90
[P67904 RS10_SALTY 30S ribosomal protein S10	7		MQNQ R	0	5	1	12.3	y4	676.32	107.124	1733	1	676.32	5.60
[P67904 RS10_SALTY 30S ribosomal protein S10	8		RLVDIVEPTEK	71	11	5	61.49	b3b4b5b6b7	1298.73	52.353	79682	2	649.87	-0.85
[P67904 RS10_SALTY 30S ribosomal protein S10	9		LIDQSTAEIVETAKR	16	15	5	26.7	b6b10b12y13*y13	1673.90	113.359	1801	2	837.45	-5.32
[P67904 RS10_SALTY 30S ribosomal protein S10	10		IPLPTRK	39	7	0	1.99		824.53	44.155	10335	2	412.77	-9.40

[P67904]RS10_SALTY 30S ribosomal protein S10	11		DIVEPTEK	74	8	2	19.31	b5b7	930.47	52.764	3035	1	930.47	-7.87
[P65882]PURA_SALTY Adenylosuccinate synthetase	1	Carbamidomethyl+C(19)	VGAGPFPTELFDETGEFLCK	273	20	11	42.78	b1b4b6b9b11°b11b12y2y5y10y20	2214.07	100.837	24229	2	1107.54	12.24
[P65882]PURA_SALTY Adenylosuccinate synthetase	2		VLDDTMAVADILTSMVVDVSDLLDQAR	186	27	17	113.97	b2b5b6b7b8b11b13°b13y1y3y4y5y6y8y9y10y27	2905.45	138.435	16511	3	969.16	0.00
[P65882]PURA_SALTY Adenylosuccinate synthetase	3		GVEPIYETMPGWSESTFGVKDR	367	22	6	25.95	b3b4b8y9y12°y12	2485.17	70.188	13639	3	829.06	-0.20
[P65882]PURA_SALTY Adenylosuccinate synthetase	4		VGDLFDKETFAEK	148	13	9	43.45	b5°b5y2°y2y7y9y10y11°y11	1498.73	60.075	13347	3	500.25	-11.08
[P65882]PURA_SALTY Adenylosuccinate synthetase	5	Carbamidomethyl+C(11)	AVQLNSLSGFCLTK	318	14	6	36.07	b3b11y6y8°y8y10	1537.78	74.849	5809	2	769.40	-13.26
[P65882]PURA_SALTY Adenylosuccinate synthetase	6	Carbamidomethyl+C(7)	LLLSEACPLILDYHVALDNAR	97	21	9	48.39	b3y3y6*y6y8*y8y11y12y14	2396.26	92.414	29816	3	799.42	-2.45
[P65882]PURA_SALTY Adenylosuccinate synthetase	7		EVTTTPLAADDWK	354	13	3	18.63	b3b8y12	1446.70	81.395	5971	3	482.90	-7.59
[P65882]PURA_SALTY Adenylosuccinate synthetase	8		ETFAEK	155	6	2	12.8	y3°y3	724.35	37.312	4921	1	724.35	-8.43
[P65882]PURA_SALTY Adenylosuccinate synthetase	9		MPDGR	349	5	3	24.61	b3y4°y4	575.27	63.640	3276	1	575.27	12.10
[P65882]PURA_SALTY Adenylosuccinate synthetase	10		MGNNVVVLGTQWGDEGK	0	17	6	23.59	b11°b11y4°y4y8y11	1803.89	63.616	3041	2	902.45	13.67
[P65882]PURA_SALTY Adenylosuccinate synthetase	11		ENVTSIIGNGVLSALMK	62	20	4	22.97	b4b5b11y6	2029.06	117.213	2267	3	677.03	-18.83
[P65882]PURA_SALTY Adenylosuccinate synthetase	12	Carbamidomethyl+C(2)	LCVAYR	343	6	1	12.8	b5	781.41	35.905	1907	2	391.21	4.06
[P65882]PURA_SALTY Adenylosuccinate synthetase	13		MPDGREVTTTPLAADDWK	349	18	4	14.03	b5°b5b15y14	2002.97	103.676	25952	2	1001.99	10.48
[P65882]PURA_SALTY Adenylosuccinate synthetase	14	Carbamidomethyl+C(12)	RAVQLNSLSGFCLTK	317	15	3	16.31	b11y5y8	1693.90	79.493	24641	2	847.46	-0.65
[P65882]PURA_SALTY Adenylosuccinate synthetase	15		EVMMEYHNFLVNYKAEAVDYQK	163	23	4	18.12	b3y4y7y10	2881.34	114.188	8921	3	961.12	-5.00
[P65882]PURA_SALTY Adenylosuccinate synthetase	16		VGDLFDKETFAEK	148	13	4	31.15	b9y6y9y11	1498.74	57.893	6033	3	500.25	1.14
[P65882]PURA_SALTY Adenylosuccinate synthetase	17		EVTTTPLAADDWKVGVEPIYETMPGWSESTFGVK	354	33	9	24.86	b3b6°b6b10b14y8y10y13°y13	3641.76	122.899	5169	3	1214.59	6.23
[P65882]PURA_SALTY Adenylosuccinate synthetase	18	Carbamidomethyl+C(2)	LCVAYRMPDGR	343	11	10	102.92	b5b7b8b9y5y6y7y8y9°y9	1337.64	63.692	3499	2	669.32	-3.74
[P65882]PURA_SALTY Adenylosuccinate synthetase	19		VLDDTMAVADILTSMVVDVSDLLDQARQR	186	29	7	22.76	b5b14y6y7y12°y12*y12	3189.62	136.498	2385	4	798.16	1.91
[P65882]PURA_SALTY Adenylosuccinate synthetase	20		GNNVVVLGTQWGDEGKGK	1	18	6	22.95	b12b13°b13°b13b15°b15	1857.93	79.395	2172	2	929.47	-10.51
[P65882]PURA_SALTY Adenylosuccinate synthetase	21		EMKELEDR	82	8	3	30.62	b5b6y5	1049.49	71.052	1920	2	525.25	-4.30
[P65882]PURA_SALTY Adenylosuccinate synthetase	22	Oxidation+M()	ENVTSIIGNGVLSALMKEMKELEDR	62	28	7	36.99	b16y3y4y8y10y11°y11	3075.56	115.019	4269	3	1025.86	-4.29
[P65882]PURA_SALTY Adenylosuccinate synthetase	23	Oxidation+M(9)	GVEPIYETMPGWSESTFGVKDR	367	22	3	12.26	b4b15y11	2501.17	88.959	3655	2	1251.09	2.05
[P65882]PURA_SALTY Adenylosuccinate synthetase	24	Oxidation+M(9)	GVEPIYETMPGWSESTFGVK	367	20	3	13.01	b3y9y12	2230.06	106.167	3436	3	744.03	10.29
[P00924]ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	8	45.75	b2b5y2y5y7y8y10*y10	1286.71	67.011	86652	2	643.86	-3.13
[P00924]ENO1_YEAST Enolase 1	2		VNQIGTLSSEIK	346	12	17	101.2	b2b3b6b8y1y2y3y4°y4y6°y6y7y8°y8y9°y9y12	1288.71	55.238	72373	2	644.86	1.14
[P00924]ENO1_YEAST Enolase 1	3		SIVPSGASTGVHEALEMR	32	18	6	22.36	b2°b2b5y3y6y15	1840.91	62.640	53827	3	614.31	-9.22
[P00924]ENO1_YEAST Enolase 1	4		TFAEALR	178	7	7	50.21	b1y1y3y4y5y6y7	807.42	46.585	48117	2	404.22	-14.66
[P00924]ENO1_YEAST Enolase 1	5		IATAIEK	330	7	5	19.58	b2b4y5°y5y7	745.45	48.377	20095	1	745.45	7.70

[P00924]ENO1_YEAST Enolase 1	6		AVDDFLISLDGTANK	88	15	6	33.44	b7b13y6y7y13y15	1578.81	83.101	16296	2	789.91	7.04
[P00924]ENO1_YEAST Enolase 1	7		AADALLLK	338	8	6	70.54	b3y3y4y5y6y7	814.49	54.691	105398	2	407.75	-16.56
[P00924]ENO1_YEAST Enolase 1	8		IGSEVYHNLK	185	10	4	37.9	b4b9y4y5	1159.59	39.417	56421	3	387.20	-17.90
[P00924]ENO1_YEAST Enolase 1	9		GNPTVEVELTTEK	15	13	10	50.01	b4b5°b5°b5b8y4°y4y6y12° y12	1416.71	63.741	55586	2	708.86	-6.89
[P00924]ENO1_YEAST Enolase 1	10		LNQLLR	409	6	3	37.41	y3y4y5	756.46	43.694	35288	2	378.73	-13.55
[P00924]ENO1_YEAST Enolase 1	11		NVPLYK	126	6	2	25.1	b3y4	733.42	37.987	13348	1	733.42	-5.33
[P00924]ENO1_YEAST Enolase 1	12		AAQDSFAAGWGVMSHR	358	17	4	23.33	y3y4y7°y7	1789.87	51.763	12686	3	597.29	11.87
[P00924]ENO1_YEAST Enolase 1	13		TFAEALRGSEVYHNLK	178	17	3	14.67	b10b16y9	1948.03	89.336	3077	3	650.02	2.44
[P00924]ENO1_YEAST Enolase 1	14		SVYDSRGNPTVEVELTTEK	9	19	3	20.44	y3y6y10	2124.05	69.638	3032	2	1062.53	1.03
[P00924]ENO1_YEAST Enolase 1	15		AVDDFLISLDGTANKSK	88	17	3	22.08	b11b13b16	1793.91	74.626	1839	3	598.64	-7.69
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	1		VITDVHEASQAQPVADVVDVIQL PAFLAR	91	29	10	29.06	b7b8b10°b10°b10b12°b12° b18y2y6	3101.66	105.227	23902	3	1034.56	-0.16
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	2		AGMAVGLAGLFLESHDPANAK	226	22	9	57.28	b3b4b8b9y2y5y7y12y18	2166.09	89.090	20491	3	722.70	-6.65
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	3	Carbamidomethyl+C(17)	VSGNVIFDVTHALQCR	189	18	8	37.69	b1b7b9b13y6°y6y7y11	2000.00	80.395	8674	3	667.34	-3.17
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	4		VANDLPFVFLGGMNVLERS	12	19	8	33.93	b5b7°b7b14y9y11y13°y13	2078.05	96.398	5024	3	693.35	-12.69
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	5		GPGLEEGMK	70	9	6	51.2	y3y4°y4y5y7y9	917.44	48.329	2304	1	917.44	4.59
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	6	Carbamidomethyl+C(2)	ICEHYVTVTQK	36	11	5	22.11	b3°b3b9°b9y9	1377.67	37.459	10920	3	459.89	-11.78
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	7		QTDLVEAMAK	120	10	6	36.93	b4°b4b6°b6b7y3	1105.55	103.674	7653	1	1105.55	-2.65
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	8		SSIHSYR	63	7	5	34.89	b4°b4b5y3°y3	849.44	33.401	1623	2	425.22	21.13
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	9		GANFGYDNLVVDMLGFSVMKK	168	21	3	21.05	b10b11y10	2305.16	79.452	28456	3	769.06	12.71
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	10		VVNIGDIKVANDLPFVFLGGMNVLERS	4	27	5	17.27	y7y9°y9°y9y20	2916.58	92.557	11734	3	972.86	3.60
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	11	Carbamidomethyl+C(4)	VILCDRGANFGYDNLVVDMLGFS VMK	162	26	3	21.11	b4y4y5	2933.42	56.737	4004	5	587.49	-5.08
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	12		SSIHSYRGPGLLEEGMK	63	16	6	37.74	b7b9b12y6°y6y7	1747.83	69.550	2159	3	583.28	-9.99
[P65215]KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	13	Oxidation+M(3)	AGMAVGLAGLFLESHDPANAK	226	22	8	22.13	b11y8°y8°y8y9°y9y11°y11	2182.10	116.960	2512	2	1091.56	3.80
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	1		LAEVAGEYLR	63	10	7	54	b2b3y5y6y7y8y10	1120.59	55.331	40665	2	560.80	-6.43
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	2		VILVGNLGQDPEVR	8	14	9	51.48	b3b4y1y2y4y8y11y12y14	1508.84	66.710	31316	2	754.93	1.05
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	3		YTTEINVPQIGGVMQMLGGR	97	20	8	25.61	b9°b9°b9b12°b12y7y8°y8	2164.07	115.948	10464	2	1082.54	-9.70
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	4		QTGEMK	44	6	1	12.8	y5	693.33	50.387	15987	1	693.33	9.24
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	5		VVMFGK	57	6	1	12.8	b5	680.37	46.470	8339	2	340.69	-8.79
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	6		GSQVYIEGQLR	74	11	3	33.87	b4b6b8	1249.63	80.901	3419	3	417.22	-15.92
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	7		VVMFGKLAEVAGEYLR	57	16	3	21.96	b13y4y5	1781.94	76.287	12909	3	594.65	-13.56
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	8		QTGEMKEQTEWHR	44	13	3	18.63	b6b12y9	1659.75	80.259	4834	3	553.92	-0.59
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	9		YMPSSGAVANLTLATSESWRDK	22	22	16	98.41	b9b10b11°b11b12°b12b13° b13y4°y4y5y7y8°y8y9°y9	2354.13	114.081	3402	3	785.38	-4.87
[P0A2F6]SSB_SALTY Single-stranded DNA-binding protein	10	Oxidation+M(5)	QTGEMKEQTEWHR	44	13	3	18.63	b3b9y8	1675.75	47.809	2679	2	838.38	3.28

P0A1V4 KAD_SALTY Adenylate kinase	1		LVEYHQMTAPLIGYYQK	167	17	6	38.11	b11y3y4y5y8y17	2054.03	70.247	55142	3	685.35	-5.82
P0A1V4 KAD_SALTY Adenylate kinase	2		VDGTQAVADV R	195	11	5	25.12	b3y2y9y10y11	1130.57	37.614	43898	2	565.79	-4.97
P0A1V4 KAD_SALTY Adenylate kinase	3		YGIPQISTGDMLR	23	13	6	38.42	b2y3y7y8y10y13	1450.74	73.651	41992	2	725.87	1.51
P0A1V4 KAD_SALTY Adenylate kinase	4		NGFLLDGFPR	78	10	6	54	b3y1y4y5y6y7	1135.59	81.717	37381	2	568.30	-3.98
P0A1V4 KAD_SALTY Adenylate kinase	5		GTQAQFIMEK	13	10	4	31.61	y2y3y4y7	1152.58	49.536	27307	2	576.79	7.73
P0A1V4 KAD_SALTY Adenylate kinase	6		IILLGAPGAGK	2	11	8	62.74	b2b3y2y3y5y7y9y11	1009.63	61.978	25991	2	505.32	-5.80
P0A1V4 KAD_SALTY Adenylate kinase	7		VEGKDDVTGEDLTTR	141	15	4	16.31	b9y10y12y15	1634.81	72.434	19741	2	817.91	12.92
P0A1V4 KAD_SALTY Adenylate kinase	8		FNPPK	136	5	1	12.3	b3	602.32	56.749	15087	1	602.32	-9.02
P0A1V4 KAD_SALTY Adenylate kinase	9	Carbamidomethyl+C(6)	IAQEDCRNGFLLDGFPR	71	17	3	23.33	y5y9y10	2007.99	89.619	36677	2	1004.50	9.30
P0A1V4 KAD_SALTY Adenylate kinase	10		IILLGAPGAGKGTQAQFIMEK	2	21	4	25.19	b3b4y17y19	2143.18	73.638	33615	3	715.07	-4.44
P0A1V4 KAD_SALTY Adenylate kinase	11		AAVKS GSELGK	36	11	4	25.12	b8y6°y6y7	1046.60	68.264	18551	2	523.80	11.20
P0A1V4 KAD_SALTY Adenylate kinase	12		EAEAGNTKYAK	184	11	4	33.62	b4b7b8y9	1181.59	47.837	8328	3	394.53	4.65
P0A1V4 KAD_SALTY Adenylate kinase	13		GTQAQFIMEKYGIPQISTGDMLR	13	23	15	85.31	b5°b5b8b9b10°b10b11°b11y6y7y8°y8y9°y9*y9	2584.26	64.421	5050	4	646.82	-9.83
P0A1V4 KAD_SALTY Adenylate kinase	14		NGFLLDGFPR TIPQADAMK	78	19	3	13.48	b13y6y9	2091.06	82.217	1514	3	697.69	-2.57
P0A1V4 KAD_SALTY Adenylate kinase	15	Oxidation+M(11)	YGIPQISTGDMLR	23	13	4	31.51	b3b5y4y5	1466.75	103.521	2469	3	489.59	11.40
P0A1V4 KAD_SALTY Adenylate kinase	16	Oxidation+M(7)	LVEYHQMTAPLIGYYQK	167	17	8	40.07	b7°b7b8°b8b9y4y6*y6	2070.01	122.879	2272	3	690.68	-12.38
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	1		TLFEPGEMVR	125	10	9	24.62	b2°b2b6°b6b9y1y2y5y10	1178.59	66.008	38934	2	589.80	-0.21
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	2		VMGFIGGTS DRPAPISDKEVDAIMNR	88	26	7	37.93	b2b3b4b8b9b13y5	2776.35	74.024	25263	4	694.84	-10.02
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	3		EVDAIMNR	106	8	5	30.62	b4b5°b5b8y3	947.46	34.183	14997	2	474.23	-0.71
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	4		WYVVQAFSGFEGR	8	13	7	31.15	b6y3y6°y6y11°y11y13	1545.73	71.872	4213	2	773.37	-11.69
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	5		VMGFIGGTS DRPAPISDK	88	18	6	19.28	b4b9°b9y3y13°y13	1847.91	70.197	3590	3	616.64	-14.53
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	6		VNDGPFADFN GVVEEVDYEK	135	20	5	24.81	b3b8b15y3y8	2243.03	87.104	21153	2	1122.02	7.62
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	7		FFPGYVLVQMVMNDASWHLVR	63	21	3	22.26	y5y9y10	2509.25	130.047	3033	3	837.09	-1.46
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	8		ATPVELDFSQVEKA	167	14	8	53.98	b10y3y4°y4y9*y9y10y12	1533.78	70.650	23673	2	767.39	-0.40

P0AA02 NUSG_SALTY Transcription antitermination protein nusG	9		VNDGPFADFNGVVEVDYEKSR	135	22	4	18.77	y5°y5y10y13	2486.18	95.494	4689	2	1243.59	12.96
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	10		WYVVQAFSGFEGRVATSLR	8	19	4	20.44	b7*b7b9b11	2173.15	107.943	1730	2	1087.08	14.49
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	11		TLFEPGE	125	7	0	2.48		792.39	66.035	5299	1	792.39	14.10
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	12		VMGFIGGTSDRPAPISDKE	88	19	1	9.51	y3	1976.97	74.051	4774	3	659.66	0.12
P0AA02 NUSG_SALTY Transcription antitermination protein nusG	13		FEPGEMVR	127	8	0	2.48		964.46	66.018	1960	1	964.46	4.56
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	1		TFVYPIAGYSK	108	11	9	33.87	b2b3°b3b6b10b11y2°y2y11	1245.64	65.274	34425	2	623.32	-8.23
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	2		IVELEAPQLPR	178	11	4	33.62	b3y5y6y9	1264.72	67.123	30576	2	632.86	-6.47
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	3		SLDELKDGSQVAVPNDPTNLGR	122	22	7	31.47	b7°b7b10b13b15y6y9	2325.16	58.745	18641	3	775.73	-2.10
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	4		FVQAYQSDEVYEAANK	245	16	3	15.43	b3b10y12	1861.88	51.887	7352	2	931.45	12.33
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	5		DGIFVEDKDYVNLIVTREDNKDA ENVK	215	29	5	11	b7y8y12°y12y29	3322.69	111.521	7016	3	1108.24	14.92
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	6	Carbamidomethyl+C(17)	TFAAVGALIGSLALAGCGQDEKD PNHK	6	28	5	17.09	y9*y9y13y15y28	2853.44	94.331	5866	3	951.82	-4.11
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	7		DGSQVAVPNDPTNLGR	128	16	8	54.84	b5b8b9*b9b14b15y11y14	1639.80	66.036	12743	3	547.27	-2.38
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	8		DGVGLLPTSLDIVENPK	158	17	7	24.84	b10y7y10°y10*y10y11°y11	1766.99	82.159	8528	3	589.67	19.90
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	9	Carbamidomethyl+C(17)	TFAAVGALIGSLALAGCGQDEK	6	22	6	34.7	b5b7b8y3y4°y4	2149.06	102.067	4239	2	1075.03	-18.63
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	10		FVQAYQSDEVYEAANKVFNGGA VK	245	24	5	14.96	b7°b7b20y14y22	2634.29	78.405	23548	3	878.77	1.30
P0A2A9 RS16_SALTY 30S ribosomal protein S16	1		IAHWVGQGATISDR	56	14	8	46.04	b4b8b10°y5y7y10y11y14	1510.78	49.007	65512	2	755.89	0.97
P0A2A9 RS16_SALTY 30S ribosomal protein S16	2		VGFFNPIASEKEEGTR	35	16	9	31.21	b1b2b3b7y6y9y11°y11y16	1780.87	59.912	29205	2	890.94	-6.65
P0A2A9 RS16_SALTY 30S ribosomal protein S16	3		VGFFNPIASEK	35	11	8	51.94	b5b7*b7b9*b9b10y7*y7	1208.62	47.716	23707	2	604.81	-12.02
P0A2A9 RS16_SALTY 30S ribosomal protein S16	4		VGFFNPIASEKEEGTR	35	16	3	21.96	b10y13y14	1780.91	82.305	7805	2	890.96	13.30
Q7CPZ4 GRPE_SALTY Protein grpE	1		FVNELLPVIDSLDR	90	14	3	22.81	b4b5y8	1629.89	97.694	38967	2	815.45	5.47
Q7CPZ4 GRPE_SALTY Protein grpE	2		IANLEVQLAEAQTR	43	14	14	63.11	b2b3b10*b10y4y5*y5y6°y6y7*y7y10*y10y14	1555.84	64.390	21646	2	778.42	-2.67

Q7CPZ4 GRPE_SALTY Protein grpE	3		DEKIANLEVQLAEAQTR	40	17	5	14.67	b6*b6b16y5°y5	1928.01	65.433	8234	3	643.34	-1.27
Q7CPZ4 GRPE_SALTY Protein grpE	4		TPEGQAPEEIMDQHEEVEAVEPN DSAEQVDPREK	7	36	5	22.07	b6y4y5y7y12	4060.82	64.334	6789	4	1015.96	-0.66
Q7CPZ4 GRPE_SALTY Protein grpE	5		ALEVADKANPDMAAMVEGIELTL K	104	24	9	57.16	b4b5b11b12*b12b15b16°b 16y16	2529.27	122.798	2248	3	843.76	-8.20
Q7CPZ4 GRPE_SALTY Protein grpE	6		RTEQDIEK	74	8	7	50.7	b4b6°b6*b6y5y7*y7	1018.52	82.819	1588	1	1018.52	2.58
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	1		FDGFFVHSIGFAPGDQLDGDYVNA VTR	84	26	13	43.73	b11°b11b12b18y1y2y4y5* y5y8y10y14y26	2797.34	83.417	29451	3	933.12	5.50
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	2		TMLNPGSALLTLSYLGAER	132	19	15	64.63	b1°b1b2b7b8b10y1y4y5y6° y6y7°y7y15y19	2007.07	101.900	24019	2	1004.04	4.26
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	3		MGFLSGKR	0	8	4	38.4	b3b5°b5b6	895.47	53.450	3558	2	448.24	-13.43
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	4		VAHDISSYSFVAMAK	114	15	11	100.8	b3b4b6b9b12b14y3y6y8°y 8y9	1625.80	63.668	28958	3	542.60	-2.25
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	5		MGFLSGK	0	7	3	34.89	b3b4y3	739.40	35.706	28515	1	739.40	19.81
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	6		AIPNYNVMLAK	151	12	3	30.39	y6y8y10	1290.69	67.304	24195	2	645.85	-1.61
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	7		VNAISAGPIR	183	10	4	36.93	b3y5y6y8	997.57	45.218	16446	2	499.29	-10.52
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	8		EGAELAFYQNDK	30	13	5	44.03	b6b7y5y8y11	1485.71	66.009	14069	3	495.91	18.16
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	9		ASLEANVRYMANAMGPEGVR	163	20	9	32.14	b4°b4b6°b6b9*b9y5y9y11	2136.05	71.143	3412	4	534.77	8.12
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	10	Oxidation+M(8)	AIPNYNVMLAK	151	12	6	56.54	b3b6b9b11y10*y10	1306.69	48.952	14386	2	653.85	7.10
P16657 FABI_SALTY Enoyl-[acyl-carrier- protein] reductase [NADH]	11	Oxidation+M(13)	VAHDISSYSFVAMAK	114	15	5	39.46	b8b9y7y8y12	1641.78	47.795	3555	2	821.39	-7.51
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	1		SSDVSLPVLVLTAR	68	14	7	41.67	b3°b3y4y8y9y10y14	1456.84	87.502	62618	2	728.92	0.67
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	2		VLVVEDNALLR	3	11	6	44.41	b2y5y7y8*y8y9	1240.72	68.501	44360	2	620.86	-5.90
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	3		VQLQDSGHQVDAEDAR	18	17	11	45.22	b2*b2y2y3y9*y9y10y11°y1 1y15y17	1838.84	37.246	16512	3	613.62	-10.75
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	4		DSLMLQLYPDAELR	172	14	7	36.07	b6°b6b13*b13y7y9y11	1663.81	94.483	14136	2	832.41	-14.16
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	5		VEVLSSGADDYVTKPFHIEVMA R	88	24	4	11.71	b8°b8y3y11	2692.30	125.351	88694	3	898.11	-9.16
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	6		IQAQYPHDVITTVR	201	14	7	70.51	y4y6y7y9°y9y10y12	1640.85	52.454	61962	3	547.62	-15.77
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	7		GQGYLFELR	215	9	4	42.17	b7y4y6y7	1082.55	72.683	3184	1	1082.55	-9.81
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	8	Oxidation+M(8)	VVSKDSLMLQLYPDAELR	168	18	3	14.03	b6y12y14	2093.07	92.527	21304	3	698.36	-10.15
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	9	Oxidation+M(4)	DSLMLQLYPDAELR	172	14	4	27.91	b5b12b13y6	1679.84	98.096	3541	2	840.42	4.51

[P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	10	Oxidation+M(22)	VEVLSSGADDYVTKPFHIEEVMA R	88	24	11	60.3	b3b4b7°b7b8°b8b9y4y5°y5y11	2708.29	136.445	2543	2	1354.65	-13.34
[P58661 AAT_SALTY Aartate aminotransferase	1		QLFVNTLQEK	322	10	7	36.93	b7y3*y3y4*y4y6*y6	1219.65	64.410	32223	2	610.33	-12.91
[P58661 AAT_SALTY Aartate aminotransferase	2		GSALINDK	85	8	7	45.93	b2°b2b5b6b7y7y8	817.44	39.444	31693	2	409.22	-2.24
[P58661 AAT_SALTY Aartate aminotransferase	3		TAQTPGGTGALR	96	12	4	24.15	b4y8y9y12	1129.59	30.629	14541	2	565.30	-9.62
[P58661 AAT_SALTY Aartate aminotransferase	4		MFENITAAPADPILGLADLFR	0	21	12	55.11	b2b3b4b6b14y1y2y3y4y5y13y21	2275.19	121.093	13248	2	1138.10	5.26
[P58661 AAT_SALTY Aartate aminotransferase	5		VWVSNPSWPNHK	122	12	5	33.15	b5°b5b9y7y8	1450.71	60.810	9664	2	725.86	-10.27
[P58661 AAT_SALTY Aartate aminotransferase	6		FENITAAPADPILGLADLFR	1	20	4	19.8	b7b11°b11b13	2144.16	100.860	8764	3	715.39	8.77
[P58661 AAT_SALTY Aartate aminotransferase	7		DQVLR	355	5	1	12.3	b4	630.35	42.284	8319	1	630.35	-14.81
[P58661 AAT_SALTY Aartate aminotransferase	8		AIWEQELTDMR	304	11	6	35.2	b6b7°b7y5°y5y9	1391.67	73.991	4874	2	696.34	5.35
[P58661 AAT_SALTY Aartate aminotransferase	9		GWLPLFD FayQGfAR	204	15	3	16.31	b3b7y4	1787.89	116.850	3339	2	894.45	-2.59
[P58661 AAT_SALTY Aartate aminotransferase	10	Carbamidomethyl+C(4)	VGACTLVAADAETVDR	254	16	4	21.96	b6y11°y11y12	1647.80	65.297	3191	2	824.41	1.41
[P58661 AAT_SALTY Aartate aminotransferase	11		GLEEDAEGLR	219	10	3	24.62	b4y7y9	1088.53	90.865	1678	2	544.77	7.85
[P58661 AAT_SALTY Aartate aminotransferase	12		DETGK	37	5	1	12.3	b3	549.25	105.346	1588	1	549.25	0.11
[P58661 AAT_SALTY Aartate aminotransferase	13		NFGLYNER	246	8	5	45.93	b3b4b5y7*y7	1012.50	114.155	1519	1	1012.50	19.35
[P58661 AAT_SALTY Aartate aminotransferase	14		NYLGIDGIPEFAR	63	13	4	31.15	b4y5y8y10	1464.76	81.670	1510	3	488.92	4.75
[P58661 AAT_SALTY Aartate aminotransferase	15	Carbamidomethyl+C(4)	VGACTLVAADAETVDRAFSQMK	254	22	3	12.26	b14y5y7	2340.13	86.635	8069	3	780.71	-2.92
[P58661 AAT_SALTY Aartate aminotransferase	16	Carbamidomethyl+C(14)	NYLGIDGIPEFARCTQELLFGK	63	22	5	33.59	b7b8°b8b9y3	2541.29	108.075	5984	3	847.77	2.69
[P58661 AAT_SALTY Aartate aminotransferase	17		RVWVSNPSWPNHK	121	13	4	18.63	b3y5y8*y8	1606.82	63.746	4487	3	536.28	-3.27
[P58661 AAT_SALTY Aartate aminotransferase	18		DFSFIKQNGMFsfSGLTK	336	19	6	39.61	b10y9y10y13°y13y14	2167.12	105.379	3896	3	723.04	11.83
[P58661 AAT_SALTY Aartate aminotransferase	19		SALINDK	86	7	1	9.02	b3	760.42	39.420	37234	1	760.42	-4.74
[P40732 ARGD_SALTY Acetylornithine/succinyl diaminopimelate aminotransferase	1		TGDLFAymHYGVTPDILTSak	234	21	5	12.6	b1b3b6y8y21	2300.13	88.959	49895	3	767.38	1.06
[P40732 ARGD_SALTY Acetylornithine/succinyl diaminopimelate aminotransferase	2		FAPSLVVEEADIHEGMQR	377	18	3	22.95	y5y6y9	2027.97	69.302	47105	3	676.66	-6.50
[P40732 ARGD_SALTY Acetylornithine/succinyl diaminopimelate aminotransferase	3		SQGETLWHTSNVFTNEPALR	68	20	14	42.78	b1b2°b2b3°b3b11°b11y4y6y8°y8y12y13y20	2287.12	72.521	37822	3	763.05	6.08
[P40732 ARGD_SALTY Acetylornithine/succinyl diaminopimelate aminotransferase	4		VLFMNSGTEANETAFK	101	16	9	78.58	y6y9y10y11y12*y12y13y14y16	1758.85	68.788	37797	2	879.93	6.94
[P40732 ARGD_SALTY Acetylornithine/succinyl diaminopimelate aminotransferase	5		ATFDEVILPVYAPADFIpVK	10	20	9	33.48	b3°b3b5b7°b7b8y1y3y12	2205.19	103.804	23523	2	1103.10	4.32
[P40732 ARGD_SALTY Acetylornithine/succinyl diaminopimelate aminotransferase	6	Carbamidomethyl+C(8)	AVMDDHTCAVVVEIQGEGGVQ AATPEFLK	180	30	11	47.79	b10b11b13y1y2y5y9y13y14y15y30	3168.55	76.161	21844	3	1056.85	4.55

[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	7		YSDGFGPKPADIIHVPFNDLHAVK	156	24	6	21.52	b1b8b9b12°b12y3	2637.33	85.803	3761	3	879.78	-6.02
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	8	Carbamidomethyl+C(3); Carbamidomethyl+C(17)	DLCDEHQALLVFDEVQCGMGR	213	21	5	19.51	b11°b11y5y8y12	2492.11	86.048	16945	3	831.38	4.41
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	9		DFLYAGAEAGVMVLNAGADVMR	355	22	4	21.01	b11y9°y9y10	2270.14	112.603	8589	2	1135.57	18.28
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	10		MATEQTAITR	0	10	3	24.62	b4b8y7	1121.56	63.583	4213	2	561.28	-2.18
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	11		QQFVQHLQAIDEQFDIFSDIR	315	21	5	16.74	b3b5y7y10°y10	2577.25	80.290	1914	3	859.75	-10.04
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	12		ATEQTAITR	1	9	4	28.11	b3b5y8*y8	990.51	57.228	1832	2	495.76	-11.15
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	13		ATEQTAITRATFDEVILPVYAPADF IPVK	1	29	8	29.06	b3b5b10b11°b11*b11b21y 9	3176.68	136.441	96629	3	1059.56	-3.46
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	14		ATFDEVILPVYAPADFIPVKGK	10	22	4	16.07	b4b6y5y14	2390.30	95.408	27852	3	797.44	0.00
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	15	Carbamidomethyl+C(17)	EYIDFAGGIAVTALGHCHPALVEA LKSQGETLWHTSNVFTNEPALR	42	46	4	12.22	b3°b3b9y21	5020.43	88.558	25045	5	1004.89	-14.49
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	16		LIDATFAERVLFMNSGTEANETAF K	92	25	3	11.5	b3y5y11	2775.38	106.274	2049	3	925.80	4.75
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	17	Oxidation+M(16)	FAPSLVVEEADIHEGMQR	377	18	3	14.03	b11b13y12	2043.98	92.192	13546	3	682.00	-2.57
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	18	Oxidation+M(4)	VLFMNSGTEANETAFK	101	16	4	21.61	b4b11y9y11	1774.83	78.383	3718	3	592.28	1.58
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	19	Oxidation+M(12)	DFLYAGAEAGVMVLNAGADVMR	355	22	3	18.77	y5y7y12	2286.11	77.940	3679	3	762.71	7.90
[P40732]ARGD_SALTY Acetylornithine/succinyldiaminopimelate aminotransferase	20		TSNVFTNEPALR	76	12	6	38.47	b5*b5b6*b6b10b11	1348.69	72.542	12970	2	674.85	1.36
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	16	112.71	b2b3b4b7b10b12y2y3y5y6 °y6y8y9y10°y10y12	1377.65	79.108	259876	2	689.33	-0.18
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	2		AAVTMPSSK	22	9	12	69.79	b2b4°b4y2y3y4°y4y5y6y7° y7y9	891.45	32.415	107124	2	446.23	-11.37
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	3		AVVESIQR	69	8	5	45.93	b3y4y5y6*y6	901.50	33.851	117248	2	451.25	-15.77
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	4	Carbamidomethyl+C(10)	QAGLGGEIICYVA	117	13	3	18.63	b7b12y5	1350.65	58.187	6084	2	675.83	-15.18
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	5		VTMPSSK	24	7	0	1.99		749.38	32.400	13615	1	749.38	-3.01
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	6		AVTMPSSK	23	8	0	1.99		820.42	32.381	3275	2	410.71	-3.94
[P60626]RL24_SALTY 50S ribosomal protein L24	1		VIVEGINLVK	33	10	8	54	b2b3y4y6y7°y7y8y10	1083.67	66.414	123272	2	542.34	-6.65
[P60626]RL24_SALTY 50S ribosomal protein L24	2		RDDEVIVLTGKDK	6	13	4	29.38	b3b4b9y8	1487.79	43.883	4161	3	496.60	-13.21

P60626 RL24_SALTY 50S ribosomal protein L24	3		SNSETIK	97	7	3	37.9	b3b5y3	778.40	104.540	5457	1	778.40	10.27
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		MQLNSTEISELIK	0	13	8	49.8	b2b3b8y3y5y10y11y13	1505.80	77.674	56845	2	753.40	5.03
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	7	26.12	b2b3b6b9y3y10y19	2098.98	70.277	45006	3	700.33	-2.56
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3		ILEVPVGR	93	8	6	58.24	b3y3y4y5y6y8	882.53	53.396	40765	2	441.77	-14.32
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4		DSVGAVVMGPYADLAEGMK	68	19	5	26.11	b5°b5b13y11y12	1909.93	84.412	38169	2	955.47	11.76
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		GYLADVELAK	453	10	7	37.9	b2b3b8y2y6y7y10	1078.57	61.450	30392	2	539.79	-4.75
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6		TALAIDAIINQR	175	12	5	27.38	y4*y4y7y8y12	1298.74	74.918	24731	2	649.87	-3.67
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		QSVDQPQVTGYK	139	12	13	101.9	b12y1y2y3y4y6y7y8*y8y9y10y11y12	1349.66	35.100	20063	2	675.34	-4.16
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		ELAAFSQFASDLDDATRK	401	18	8	39.45	b7b8b15y1y5y6°y6y11	1984.94	84.298	16895	3	662.32	-8.30
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9		DHAPLMQEINQSGGYNDEIEGK	477	22	5	18.77	b4b9b11y2y3	2445.11	107.243	2703	3	815.71	3.69
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		AVDSMIPIGR	151	10	5	50.2	b3b4y4y5y7	1058.56	60.773	39449	2	529.79	-2.77
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		QYAPMSVAQQLVLFAAER	434	19	3	13.48	b3y5y10	2109.10	93.924	26264	2	1055.05	8.80
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12		GLLGR	101	5	3	36.91	b3y3y4	515.33	74.673	12811	1	515.33	-3.91
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		IAQFNVVSEAHNEGATIVSVSDGVI R	15	25	3	17.73	b4b6b12	2641.31	75.896	5914	3	881.11	-17.56
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		VGGAAQTK	376	8	3	33.63	b4y3y6	731.39	43.302	3498	1	731.39	-16.69
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		VVNTLGAPIDGKGPVDNDGFSAV EAIAPGVIDR	106	33	15	65.99	b4°b4b5°b5°b5b27y3y5y6°y6y7y10y15y24y28	3263.71	84.960	47808	3	1088.57	5.39
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16		VNADYVEAFTKGEVK	303	15	6	33.44	b4b9y8y9°y9y12	1669.82	64.377	42393	3	557.28	-11.84
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17		GEDALIYDDLKQAVAYR	252	19	4	13.48	b6b11°b11y13	2140.09	78.827	2351	2	1070.55	-1.37
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18	Phohoryl STY(20)	YAIALNLERDSVGAVVMGPYADL AEGMK	59	28	5	22.1	y4y7°y7y8°y8	3033.44	95.641	22754	3	1011.82	-0.40
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	19	Phohoryl STY(29)	IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	3	22.62	b5y6y7	4030.87	103.605	3710	3	1344.30	6.84
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	20	Oxidation+M(18)	DSVGAVVMGPYADLAEGMK	68	19	5	26.12	b4b8y4y6y11	1925.90	43.261	1502	3	642.64	-1.01
P66932 TIG_SALTY Trigger factor	1		NVALEEQAVEAVLAK	399	15	11	84.69	b2b3b5b6b7y3y4y11y12y13y15	1583.87	81.043	112089	2	792.44	2.39
P66932 TIG_SALTY Trigger factor	2		SQAIEGLVK	287	9	4	28.11	b3b5y4y9	944.53	48.379	52666	2	472.77	-10.21
P66932 TIG_SALTY Trigger factor	3		ANDIDVPSALIDSEIDVLRR	296	20	10	24.81	b2°b2b3b5b13y1y2y14y16y20	2211.16	91.361	45168	3	737.72	-2.32
P66932 TIG_SALTY Trigger factor	4		ANDIDVPSALIDSEIDVLR	296	19	4	13.48	b4y2y3y13	2055.08	95.429	18747	2	1028.04	8.55
P66932 TIG_SALTY Trigger factor	5		VTIDFTGSVDGEEFEGGK	163	18	8	27.6	b2b4b7b10y1y2y3y5	1886.88	121.713	15463	2	943.94	5.05
P66932 TIG_SALTY Trigger factor	6		GLIEEMASAYEDPKEVIEFYK	368	22	5	22.13	b2b3y3y4y6	2548.19	82.535	9765	3	850.07	-9.29
P66932 TIG_SALTY Trigger factor	7		INPAGAPNYVPGEYK	83	15	6	51.01	b13y6y8y9y11y12	1589.81	69.637	2111	2	795.41	6.53
P66932 TIG_SALTY Trigger factor	8		FGVEDGSVAGLR	255	12	5	43.23	b3b5b11y4y8	1206.61	58.164	33798	2	603.81	-2.12

P66932 TIG_SALTY Trigger factor	9		QVSVETTQGLGR	1	12	5	41.9	y5y8y9y10°y10	1274.65	44.122	20970	3	425.56	-15.04
P66932 TIG_SALTY Trigger factor	10		QDVLGDLMSR	63	10	3	24.62	b5b8y5	1133.58	71.040	9572	2	567.29	16.37
P66932 TIG_SALTY Trigger factor	11		VEER	239	4	1	11.81	y3	532.28	65.393	8564	1	532.28	7.11
P66932 TIG_SALTY Trigger factor	12		VTITIAADSIETAVK	14	15	4	29.07	b8b12y9y10	1531.84	90.849	6155	3	511.28	-11.48
P66932 TIG_SALTY Trigger factor	13		MQVSVETTQGLGR	0	13	3	23.4	b4y10y11	1405.70	50.449	4636	2	703.35	-6.69
P66932 TIG_SALTY Trigger factor	14		AGEEFTIDVTFPEEYHAENLK	206	21	3	12.6	b8y7y9	2439.09	75.135	2390	4	610.53	-20.42
P66932 TIG_SALTY Trigger factor	15		ELPELTEEFIK	243	11	8	92.38	b3b4b5b6b8y3y7y10	1347.68	79.528	2119	2	674.35	-15.49
P66932 TIG_SALTY Trigger factor	16		QAAQRFGGNEK	316	11	3	25.12	b3b4y8	1205.59	49.343	177369	2	603.30	-12.45
P66932 TIG_SALTY Trigger factor	17		VSEKATSFNELMNQQA	416	16	6	38.41	b4b8b9°b9y4y5	1796.85	67.303	3037	3	599.62	1.09
P66932 TIG_SALTY Trigger factor	18		AGEEFTIDVTFPEEYHAENLK GK	206	23	5	11.96	b11b13°b13y13°y13	2624.26	77.079	2778	5	525.66	3.07
P66932 TIG_SALTY Trigger factor	19	Phohoryl STY(8)	MQVSVETTQGLGRR	0	14	9	56.04	b4b7y7°y7y8°y8*y8y9y10	1641.79	114.097	2287	2	821.40	11.90
P66932 TIG_SALTY Trigger factor	20	Oxidation+M(8)	QDVLGDLMSR	63	10	3	31.61	b5b6b9	1149.54	56.332	2180	2	575.28	-11.57
O54296 RS11_SALTY 30S ribosomal protein S11	1		ALNAAGFR	98	8	8	75.31	b4b7y3y4y5y6*y6y8	819.44	42.906	63723	2	410.22	-10.06
O54296 RS11_SALTY 30S ribosomal protein S11	2		QGNALGWATAGGSGFR	37	16	7	47.41	b5y5y7y8y11y14y16	1549.76	66.950	58939	2	775.38	5.12
O54296 RS11_SALTY 30S ribosomal protein S11	3		NLEVMVK	80	7	5	34.89	b5y4y5°y5y7	832.45	49.193	51318	2	416.73	-10.26
O54296 RS11_SALTY 30S ribosomal protein S11	4		QVSDGVAHIHASFNNITVITIDR	14	23	5	22.05	b9b10°b10*b10b12	2495.24	113.336	2802	3	832.42	-8.90
O54296 RS11_SALTY 30S ribosomal protein S11	5		STPFAAQVAAER	57	12	15	143.34	b4b5b6°b6b7b9y4y5y6y7y8*y8y9y10°y10	1247.66	50.493	124011	2	624.33	15.17
O54296 RS11_SALTY 30S ribosomal protein S11	6		QGNALGWATAGGSGFRGSR	37	19	4	18.32	b10b12y12y14	1849.89	58.741	20182	3	617.30	-10.49
O54296 RS11_SALTY 30S ribosomal protein S11	7	Carbamidomethyl+C(13)	STPFAAQVAAERCADAVK	57	18	4	14.03	b7b17y17*y17	1891.91	136.809	2236	1	1891.91	-13.16
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	8	22.36	b1b2b13°b13y3y12y16y18	1970.01	64.317	55899	3	657.34	-8.12
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		AVAFMMDDALLAGER	198	15	7	43.01	b3b11y1y3y4y8y11	1609.78	85.288	46860	2	805.39	6.22
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		ESSVPFSYYDNQOK	47	14	10	35.28	b1b2°b2b9b11y5y6y10°y10y14	1691.76	56.255	46817	2	846.39	5.20
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		VVGYSQDYSNAIVEAVK	61	17	7	36.6	y2y3y11y12*y12y13y17	1841.94	68.774	39966	2	921.47	5.10
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTTNLER	98	22	4	33.57	b11b12y9y10	2526.22	111.951	1763	3	842.74	8.79
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(19)	KPDNWEIVGKPKSQEAYGCMLR	217	22	4	12.26	b3°b3y3y5	2606.31	136.441	21780	3	869.44	22.20
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7		WFDK	264	4	1	11.81	b3	595.29	34.037	2157	1	595.29	3.59

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8		NGVIVVGHR	38	9	4	28.11	b3*b3y4y5	950.57	12.444	1905	2	475.79	13.93
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTTNNLER	89	31	5	24.87	y6°y6y7y10y14	3548.80	87.646	113127	3	1183.60	4.88
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		NPIPPKNLNMNFELSDEMK	271	19	6	35.75	y6°y6y7y8°y8y17	2231.07	97.500	8939	3	744.36	-5.47
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11		ALFKAPNDK	290	9	5	28.11	b8°b8y3y5*y5	1003.56	65.358	4843	2	502.29	7.36
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12	Carbamidomethyl+C(21)	AKKPDNWEIVGKPQSQEAYGCMRL	215	24	3	11.71	b7b11y5	2805.39	91.024	2505	3	935.80	2.18
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	13		AVAFMMDDALLAGERAK	198	17	3	14.67	b10b13y11	1808.91	64.389	1538	2	904.96	5.87
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	14	Phohoryl STY(27)	LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	3	10.94	b26y3y8_HPO3 y8	2949.43	138.426	3298	3	983.81	8.94
P0AA07 PTHP_SALTY Phohocarrier protein HPr	1		MFQQEVTITAPNGLHTRPAAQFVK	0	24	25	140.36	b2b3*b3b4b6b7°b7b10°b10°b10b11°b11°b11b12b13y1y3y10y13y14y15y16y18y19y24	2684.38	64.471	504139	4	671.85	-6.37
P0AA07 PTHP_SALTY Phohocarrier protein HPr	2		GFTSEITVTSNGK	27	13	5	27.87	b2y4y8y11y13	1340.67	51.542	25038	2	670.84	3.10
P0AA07 PTHP_SALTY Phohocarrier protein HPr	3		LMAELE	79	6	7	62.01	b3b4b5y3°y3y4°y4	705.35	55.240	286478	1	705.35	-5.37
P0AA07 PTHP_SALTY Phohocarrier protein HPr	4		LQTLGLTQGTVVTTISAEGEDEQK	49	23	5	11.96	b7y6y11°y11*y11	2417.19	65.370	85850	3	806.40	-19.90
P0AA07 PTHP_SALTY Phohocarrier protein HPr	5		LQTLGLTQGTVVTTISAEGEDEQKA VEHLVK	49	30	32	223.28	b3°b3*b3b4°b4b5b6°b6°b6b10°b10b11°b11y3y5y10y11°y11y13°y13y14°y14y15y16y17y18y19y20y22y24y26y28	3193.67	82.254	430704	4	799.17	-6.50
P0AA07 PTHP_SALTY Phohocarrier protein HPr	6		EAKGFTSEITVTSNGK	24	16	3	23.13	y6y9y11	1668.85	60.862	2153	2	834.93	2.27
P0AA07 PTHP_SALTY Phohocarrier protein HPr	7		MFQQEVTITAPNGLHTRPAAQF	0	22	9	39.6	y5*y5y7°y7y8*y8y12y13°y13	2457.21	64.403	7631	3	819.74	-11.53
P0AA07 PTHP_SALTY Phohocarrier protein HPr	8		MFQQEVT	0	7	1	8.95	y4	882.40	64.433	2902	1	882.40	-5.33
P10370 HISX_SALTY Histidinol dehydrogenase	1		AGFSALASTIETLAAER	397	18	13	70.62	b7b8b12°b12b14b16y2y3y4y5°y5y7y18	1778.93	103.699	111815	2	889.97	3.23
P10370 HISX_SALTY Histidinol dehydrogenase	2		VTPEEIAAAGAR	67	12	8	78.14	b8y5y6y7y8y9y10y12	1184.62	50.275	82655	2	592.82	-3.09
P10370 HISX_SALTY Histidinol dehydrogenase	3		NIETFHSAQTLPPVDVETQPGVR	93	23	4	20.99	b11y11y12y23	2535.29	63.231	57994	3	845.77	0.77
P10370 HISX_SALTY Histidinol dehydrogenase	4	Carbamidomethyl+C(5)	DLAQCVAINSQYGEHLIIQTR	311	22	8	25.95	b2b4b8b9°b9y11y14y22	2526.29	76.186	47311	3	842.77	6.86
P10370 HISX_SALTY Histidinol dehydrogenase	5	Carbamidomethyl+C(1)	CQQVTRPVSSVGLYPGGSAPLFS TVLMLATPAR	116	34	21	90.1	b2b4°b4b6°b6b7b8°b8b9°b9b12°b12°b12b14y1y2y3y4y5y6°y6	3573.90	113.324	29349	3	1191.97	3.42
P10370 HISX_SALTY Histidinol dehydrogenase	6	Carbamidomethyl+C(11)	SFNTLIDWNSCEQQR	1	17	11	44.52	b6°b6°b6y2y3y5°y5y6y10y12y17	2081.96	75.398	28481	2	1041.48	12.55
P10370 HISX_SALTY Histidinol dehydrogenase	7		QLAELPR	287	7	5	37.9	b3°b3y3y5y7	826.47	44.968	15380	2	413.74	-11.08

[P10370]HISX_SALTY Histidinol dehydrogenase	8		QVSQR	219	5	3	24.61	b4°b4y4	617.34	44.072	17725	1	617.34	11.07
[P10370]HISX_SALTY Histidinol dehydrogenase	9		VAEAVER	280	7	5	37.9	y4°y4y5y6°y6	773.41	54.652	16983	1	773.41	-10.89
[P10370]HISX_SALTY Histidinol dehydrogenase	10		LDGAAIDMPAGPSEVLVIADSGAT PDFVASDLLSQAHEGPDQSQVILLT PDADIAR	224	55	7	47.09	b4b7y3y4y5y7y8	5541.79	113.814	7302	4	1386.20	4.85
[P10370]HISX_SALTY Histidinol dehydrogenase	11		MTVQELSK	389	8	3	30.62	b4y5y6	935.50	56.879	5707	2	468.25	16.31
[P10370]HISX_SALTY Histidinol dehydrogenase	12		LSDELK	79	6	1	12.8	b5	704.38	23.062	2214	1	704.38	2.08
[P10370]HISX_SALTY Histidinol dehydrogenase	13		VDKIFGPGNAFVTEAK	202	16	7	38.12	b14y6y8y11°y11y13*y13	1692.91	65.417	16488	2	846.96	9.30
[P10370]HISX_SALTY Histidinol dehydrogenase	14		LSDELKQAMTAAVK	79	14	3	22.81	b5b6y6	1504.79	60.802	14166	2	752.90	-9.98
[P10370]HISX_SALTY Histidinol dehydrogenase	15		GDDALREYSAK	46	11	9	48.48	b5°b5b6°b6b7°b7y6°y6y9	1224.59	63.657	8028	2	612.80	-0.10
[P10370]HISX_SALTY Histidinol dehydrogenase	16		FDKTEVTALR	57	10	3	24.62	b4b8y7	1179.63	43.941	2058	2	590.32	-5.80
[P10370]HISX_SALTY Histidinol dehydrogenase	17	Phohoryl STY(4)	ALLTRPAISASDSITR	18	16	3	15.43	b4b8y11	1751.91	118.129	2845	2	876.46	10.45
[Q9L9I8]THIE_SALTY Thiamine-phohate pyrophohorylase	1		QMPSAPQGLAQLASHIER	137	18	8	33.61	b2b5y2y6y11*y11y13y16	1933.98	76.140	32989	3	645.33	-8.21
[Q9L9I8]THIE_SALTY Thiamine-phohate pyrophohorylase	2		LGLYPVVDSVEWIER	12	15	7	36.27	b13y2y4y7y8y11y15	1774.95	95.875	28870	2	887.98	7.63
[Q9L9I8]THIE_SALTY Thiamine-phohate pyrophohorylase	3		MYQPDPFPTVPFR	0	12	8	56.54	b2b3y3y6y9°y9y11y12	1497.74	78.816	20456	2	749.37	11.33
[Q9L9I8]THIE_SALTY Thiamine-phohate pyrophohorylase	4		LADYPTVAIGGISLER	155	16	6	25.69	b6b8°b8b9y12y16	1674.92	78.945	18334	2	837.96	5.32
[Q9L9I8]THIE_SALTY Thiamine-phohate pyrophohorylase	5		LFINDYWR	65	8	5	45.93	b7y4y5y6y8	1126.57	78.750	15619	2	563.79	-0.54
[Q9L9I8]THIE_SALTY Thiamine-phohate pyrophohorylase	6		APAVLATGVGSIJVVSAITQAAD WR	171	25	3	21.98	y6y7y11	2424.29	112.205	2888	2	1212.65	-15.41
[Q9L9I8]THIE_SALTY Thiamine-phohate pyrophohorylase	7		QMPSAPQGLAQLASHIERLADYPT VAIGGISLER	137	34	6	22.85	b8b9°b9b12°b12*b12	3589.90	113.326	2015	3	1197.31	6.19
[Q8ZQS2]GPMA_SALTY 2	1		VIPYWNDITLPR	160	12	7	54.74	b3b8y5y7y8y9y12	1486.81	82.462	67560	2	743.91	3.28
[Q8ZQS2]GPMA_SALTY 2	2		VIIAAHGNSLR	178	11	10	76.8	y4*y4y5y6°y6*y6y7y8y9y11	1150.66	38.646	39375	2	575.84	-5.52
[Q8ZQS2]GPMA_SALTY 2	3		AAAVANQGK	239	9	3	28.11	b7b8y5	829.47	61.958	13120	1	829.47	21.41
[Q8ZQS2]GPMA_SALTY 2	4		EEGFSFDFAYTSVLK	46	15	4	16.31	b4b14y13°y13	1739.82	71.013	8878	3	580.61	3.37
[Q8ZQS2]GPMA_SALTY 2	5		GVSEAK	33	6	2	12.8	b5°b5	590.32	29.327	8382	1	590.32	1.03
[Q8ZQS2]GPMA_SALTY 2	6		FTGWYDVDLSEK	21	12	3	24.15	b4y7y8	1459.69	31.972	7441	3	487.24	14.05
[Q8ZQS2]GPMA_SALTY 2	7		LVLVR	5	5	1	12.3	y4	599.43	45.469	6499	1	599.43	8.04
[Q8ZQS2]GPMA_SALTY 2	8		YLDNMSDEILELNIPITGVPLVYEF DENFKPLK	193	33	6	21.84	b4b6y8°y8y9y13	3884.96	95.527	4301	5	777.80	11.44
[Q8ZQS2]GPMA_SALTY 2	9		AETAKEYGDEQVK	100	13	3	18.63	b3b10y5	1467.72	58.242	5944	3	489.91	14.80
[Q8ZQS2]GPMA_SALTY 2	10		FTGWYDVDLSEKGVSEAK	21	18	4	14.03	b4b13°b13y3	2030.97	103.658	5420	2	1015.99	0.18
[Q8ZQS2]GPMA_SALTY 2	11		HYGALQGLNKAETAEK	90	16	12	41.47	b5b6°b6b8°b8y6°y6y8°y8*y8y10°y10	1729.86	63.643	5289	2	865.43	-14.61
[Q8ZQS2]GPMA_SALTY 2	12	Phohoryl STY(14)	LLKEEGFSDFAYTSVLK	43	18	7	26.68	b10°b10b12°b12y5y6°y6	2174.04	122.797	2258	3	725.35	3.26
[Q8ZQS2]GPMA_SALTY 2	13		IAAHGNSLR	180	9	0	2.98		938.51	38.626	38719	2	469.76	-8.58
[P0A2C9]FABG_SALTY 3-oxoacyl-[acyl-carrier-protein] reductase	1		IITIGSVVGTMGNAGQANYAAAK	132	23	9	43.35	b2b3b16y9y10y14y15y20y23	2207.13	101.367	31315	3	736.38	-7.52
[P0A2C9]FABG_SALTY 3-oxoacyl-[acyl-carrier-protein] reductase	2		AGILAQVPAGR	197	11	7	51.94	b3y2y4y5y6y7y11	1052.61	52.778	21395	2	526.81	-12.18
[P0A2C9]FABG_SALTY 3-oxoacyl-[acyl-carrier-protein] reductase	3		IALVTGASR	6	9	6	35.89	b2y6°y6y7°y7y8	887.52	43.306	14638	2	444.26	-12.72

[P0A2C9]FABG_SALTY 3-oxoacyl-[acyl-carrier-protein] reductase	4		GLMLNVTDPASIESVLENIR	54	20	5	20.34	b6y7y10y14*y14	2171.09	84.604	4660	3	724.37	-20.24
[P0A2C9]FABG_SALTY 3-oxoacyl-[acyl-carrier-protein] reductase	5		DNLLMR	91	6	3	25.1	b3b4*b4	761.39	64.433	2684	1	761.39	-14.11
[P0A2C9]FABG_SALTY 3-oxoacyl-[acyl-carrier-protein] reductase	6		VIGTATSENGAKNISDYLGANGK	31	23	3	11.96	b3b12y9	2280.17	91.181	6695	3	760.73	10.17
[P0A2C9]FABG_SALTY 3-oxoacyl-[acyl-carrier-protein] reductase	7		GLMLNVTDPASIESVLENIRAIEFG EVDILVNNAGITR	54	37	14	63.39	b3b7b9*b9b11*b11*b11b1 2b13*b13y7°y7y8y9	3970.02	136.426	5862	4	993.26	-10.45
[P0A2C9]FABG_SALTY 3-oxoacyl-[acyl-carrier-protein] reductase	8	Oxidation+M(16)	GITVNVVAPGFIETDMTR	172	18	8	45.12	b3°b3y3y7y9°y9y10y11	1936.01	122.889	1675	2	968.51	12.23
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	1		LNSAVFPSAQGGPLMHVIAGK	251	21	11	42.63	b2*b2b4°b4b10*b10y3y4y 14y15y21	2094.11	79.219	67010	3	698.71	-4.90
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	2		VMQAQGSQLTNK	42	12	16	125.81	b2b3b9b10y2y3y4y5y6y7y 8*y8y9y10*y10y12	1304.66	30.843	46852	2	652.83	-4.49
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	3		FVTSGIR	354	9	6	55.72	b3b5y5y6y7y9	963.52	50.101	38072	2	482.26	-5.70
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	4		EMNIADYDAELWQAMEQEK	4	19	4	22.66	y4y6y7y19	2314.02	93.334	17654	2	1157.52	10.45
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	5		YAEGYPGK	54	8	3	33.63	b3b7y5	884.43	61.459	24941	2	442.72	17.12
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	6		LYNIVPYGIDESGK	138	14	6	35.28	b9b11°b11y5y8y9	1567.83	69.599	8999	2	784.42	20.56
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	7		NSVPNDPKFVTSGIR	346	17	8	47.28	b3°b3b5b13y8y9y11y14	1814.92	53.255	36960	3	605.65	-10.09
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	8	Carbamidomethyl+C(5)	VLDICARFPVYA	405	12	4	20.17	b8°b8y5y11	1423.76	60.801	23661	3	475.26	13.38
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	9		GYKVVSOGGTENHLFLDLVDK	305	21	4	12.6	b10y11*y11y13	2304.21	102.017	20337	2	1152.61	-5.30
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	10		MIIGGFSAYSGVVDWAKMR	168	19	4	21.28	b3b5b13y6	2088.03	102.156	13149	3	696.68	-3.39
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	11		ANITVNKNSVPNDPK	339	15	4	16.31	b5y5*y5y7	1610.83	35.060	5902	3	537.61	-14.63
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	12		LYNIVPYGIDESGKIDYDEMAK	138	22	5	22.13	y4y5°y5y11°y11	2533.24	138.143	3636	3	845.09	10.70
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	13		EHKPKMIIGGFSAYSGVVDWAK	163	22	3	12.26	b4y8y10	2420.25	105.322	1689	4	605.82	4.34
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	14	Oxidation+M(15)	LNSAVFPSAQGGPLMHVIAGK	251	21	4	21.05	b3°b3b4y3	2110.09	85.639	35027	3	704.03	-10.88
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	15	Carbamidomethyl+C(12) ;Oxidation+M(11)	EAEVKELAGWMCDVLDNINDEAT IER	375	26	8	23.84	b6°b6b7°b7y3°y3y10*y10	3036.40	80.384	8674	4	759.86	3.86
[P0A2E1]GLYA_SALTY Serine hydroxymethyltransferase	16	Oxidation+M(8)	AVALKEAMEPEFK	272	13	5	26.74	b3b12y3°y3y12	1478.75	66.035	3436	2	739.88	-3.38
[Q8ZLJ2]GREB_SALTY Transcription elongation factor greB	1		KDYISIDMAR	114	12	6	46.24	b9b10b11y5°y5y8	1395.69	51.803	8932	2	698.35	-4.90
[Q8ZLJ2]GREB_SALTY Transcription elongation factor greB	2		QELNYLWREERPEVTK	15	16	3	13.54	b7°b7b9	2090.09	89.376	5152	2	1045.55	10.40
[Q8ZLJ2]GREB_SALTY Transcription elongation factor greB	3		IVGYDEIFGR	104	10	6	37.9	b3b5y6°y6y7°y7	1168.58	65.299	5179	2	584.79	-16.30
[Q8ZLJ2]GREB_SALTY Transcription elongation factor greB	4		DYISIDMAR	115	11	7	43.71	b7°b7b9y4y5°y5y7	1267.62	63.678	2572	2	634.31	13.58

Q8ZLJ2 GREB_SALTY Transcription elongation factor greB	5		VTWAASLGDR	32	10	5	36.13	b5b7y3y5°y5	1075.54	105.397	1638	1	1075.54	-15.55
Q8ZLJ2 GREB_SALTY Transcription elongation factor greB	6		KDYISIDMAR	114	12	4	41.9	y4y7y8y10	1395.68	136.481	2722	1	1395.68	-10.93
Q8ZLJ2 GREB_SALTY Transcription elongation factor greB	7	Carbamidomethyl+C(1)	CMENLKIVDYQQEGK	67	17	12	52.43	b9°b9b12°b12y5y6°y6y7*y7y9°y9y13	2038.97	124.371	1646	3	680.33	5.93
Q8ZLJ2 GREB_SALTY Transcription elongation factor greB	8	Phohoryl STY(7)	EERPEVTKK	23	9	5	55.72	b3_H3PO4 b3b6y4y6y7	1195.58	64.431	82056	2	598.29	13.38
Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTEPTWFPDSQTLAFTSDQAGRPQVYK	287	29	9	27.94	b2*b2b4b5°b5y12y20y24y29	3285.56	78.471	35365	3	1095.86	5.80
Q8ZQT5 TOLB_SALTY Protein tolB	2		WAGPGAAPEDIGGIVAADLR	43	20	7	22.97	b13y2y5°y5y13y14y20	1936.00	86.323	30147	2	968.51	6.05
Q8ZQT5 TOLB_SALTY Protein tolB	3		SALVIQTLANGAVR	223	14	8	44.68	b3°b3y2y5y6°y6y8y9	1412.82	71.829	15400	2	706.91	-1.04
Q8ZQT5 TOLB_SALTY Protein tolB	4		MNINGGAAQR	316	10	4	36.93	b4y6y7y9	1031.50	28.917	15326	2	516.25	-4.62
Q8ZQT5 TOLB_SALTY Protein tolB	5		YAGHTASDEVFEK	142	13	6	43.45	b2b3y6y8y9y10	1453.68	63.694	6431	2	727.34	12.76
Q8ZQT5 TOLB_SALTY Protein tolB	6		IAYVVQTNGGQFPYELR	166	17	3	14.67	b14y6y14	1954.99	82.602	4047	2	978.00	-6.43
Q8ZQT5 TOLB_SALTY Protein tolB	7		TGSLNLYVMDLASGQIR	264	17	4	14.67	b8b14*b14y14	1837.92	80.295	1747	2	919.47	-12.35
Q8ZQT5 TOLB_SALTY Protein tolB	8		QVASFPR	237	7	7	62.51	b5b6°b6°b6y3y4y5	804.42	39.460	9073	2	402.72	-16.16
Q8ZQT5 TOLB_SALTY Protein tolB	9		HNGAPAFDGTK	244	13	4	29.38	b4b5b11y8	1298.59	44.291	5935	3	433.53	-20.30
Q8ZQT5 TOLB_SALTY Protein tolB	10		QWLR	138	4	1	11.81	b3	602.35	31.105	3967	1	602.35	12.16
Q8ZQT5 TOLB_SALTY Protein tolB	11		QPLMAWDGSK	197	16	8	66.57	b4b6y4y5y6y9y12y13	1684.81	73.947	2329	3	562.28	6.96
Q8ZQT5 TOLB_SALTY Protein tolB	12		LPATDGQVKAWYL	413	17	4	23.59	b10y5y7y9	1829.95	90.804	8859	2	915.48	2.74
Q8ZQT5 TOLB_SALTY Protein tolB	13		IAYVVQTNGGQFPYELRVSDYDGYNQFVVHR	166	31	5	20.56	b9°b9y8y9y19	3634.79	113.320	8183	3	1212.27	5.17
Q8ZQT5 TOLB_SALTY Protein tolB	14		ARLPATDGQVK	411	11	3	33.87	b3b7b9	1155.63	30.604	5991	2	578.32	-14.26
Q8ZQT5 TOLB_SALTY Protein tolB	15		TGSLNLYVMDLASGQIRQITDGR	264	23	3	11.96	b5b11y3	2508.32	74.971	2794	2	1254.66	12.26
Q8ZQT5 TOLB_SALTY Protein tolB	16		VIQTLANGAVR	226	11	0	4.47		1141.66	71.894	29643	2	571.33	-10.91
Q8ZQT5 TOLB_SALTY Protein tolB	17		WAGPGAAPEDIGGIVAAD	43	18	2	12.47	y13y16	1666.81	86.329	2911	3	556.28	2.71
P61179 RL22_SALTY 50S ribosomal protein L22	1		IFVDEGPSMK	73	10	10	69.31	b2b4y2y4y5y6°y6y8y9y10	1122.55	51.936	91737	2	561.78	-1.85
P61179 RL22_SALTY 50S ribosomal protein L22	2		VLESAIANAEHNDGADIDDLK	49	21	3	22.26	y3y6y7	2210.05	88.954	4855	4	553.27	-4.86
P61179 RL22_SALTY 50S ribosomal protein L22	3		LVADLIR	18	7	6	59.5	b4°b4y3y4y5y6	799.49	58.192	105751	2	400.25	-21.15
P61179 RL22_SALTY 50S ribosomal protein L22	4		ETIAK	1	5	2	24.61	b3b4	561.32	29.287	12641	1	561.32	0.43
P61179 RL22_SALTY 50S ribosomal protein L22	5		VLESAIANAEHNDGADIDDLKVT K	49	24	3	11.71	b6y3y11	2538.24	62.157	75382	4	635.32	-11.83
P61179 RL22_SALTY 50S ribosomal protein L22	6		VSQALDILTYTNKK	28	14	3	17.37	b3b11y3	1593.89	67.285	68054	2	797.45	3.60

P61179 RL22_SALTY 50S ribosomal protein L22	7	Phohoryl STY(9)	VSQALDILTYTNKK	28	14	6	44.68	b9y5*y5y7y10y13	1673.86	85.284	6986	2	837.43	11.16
P22107 TRAT_SALTY TraT complement resistance protein	1		ATVTTDNVAALR	177	12	7	37.25	b8y2y8y9y10*y10y12	1231.66	46.476	26820	2	616.33	-5.75
P22107 TRAT_SALTY TraT complement resistance protein	2		IQTSTETGNQHK	196	12	5	41.9	y2y5y6y7y10	1343.64	14.758	9152	3	448.55	-12.99
P22107 TRAT_SALTY TraT complement resistance protein	3		AYYWIQANVLK	89	11	5	33.87	b6b7b8y2y11	1368.73	57.879	7262	2	684.87	-0.09
P22107 TRAT_SALTY TraT complement resistance protein	4		DIQAKGYTVVTDK	74	15	4	26.7	b6y4y5y13	1621.83	69.517	29267	2	811.42	-10.01
P22107 TRAT_SALTY TraT complement resistance protein	5		MDLRESQGWLNR	103	12	10	80.32	b3b4b9b11°b11y4y7y8°y8y11	1504.74	63.703	8263	3	502.25	2.51
P22107 TRAT_SALTY TraT complement resistance protein	6		NLEVKTQMSQTYWHPVSER	31	20	6	22.97	b12y9y11y12°y12*y12	2448.14	98.967	3888	2	1224.57	-8.88
P22107 TRAT_SALTY TraT complement resistance protein	7		IQTSTETGNQHXYQTR	196	16	6	23.13	y8°y8*y8y11y13°y13	1891.90	87.133	3467	3	631.31	-11.03
P22107 TRAT_SALTY TraT complement resistance protein	8	Carbamidomethyl+C(16) ;Phohoryl STY(10)	LMMVTLVSSTLALSGCGAMSTAI KK	5	25	14	75.3	b4b5°b5b8°b8b12b24_H3P O4 b24y9y10°y10y11y12y14y23	2650.32	136.430	4345	3	884.11	6.54
P22107 TRAT_SALTY TraT complement resistance protein	9		TDNVAALR	181	8	0	3.48		859.46	46.489	5204	2	430.23	-1.28
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	1		VLSESDFQVNQLLDILR	49	17	12	61.34	b1b2b8b11b13y1y3y4y5y11y13y17	1989.07	105.345	38907	2	995.04	2.15
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	2		GIEGASLDVPDEFVHSGK	72	18	4	22.36	b6y3y5y9	1856.89	67.932	28075	3	619.64	-6.44
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	3		QGIESAVQK	99	9	5	28.11	b3y6y8*y8y9	959.52	31.162	6741	2	480.26	2.86
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	4		TWYVEAK	90	7	3	37.9	b6y3y5	896.46	100.250	4842	1	896.46	6.13
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	5		MPSFDIVSEVDLQEAR	0	16	6	39.08	b11y3y4y5y9*y9	1835.86	50.472	2245	3	612.62	-14.10
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	6		GGDLGQPFQFK	148	11	4	29.1	b7b9b10°b10	1193.57	94.457	1679	2	597.29	-22.19
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	7		PSFDIVSEVDLQEARNGVDNAVR	1	23	5	33.54	b8b9y7*y7y8	2530.27	74.969	6531	3	844.10	7.24
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	8		EVESRFDFR	24	9	3	28.11	b4b8y5	1184.56	33.382	3996	2	592.78	-11.85
Q8ZRC9 YAJQ_SALTY UPF0234 protein yajQ	9		GIEGASLDVPDEFVHSGK	72	18	0	6.46		1838.88	67.964	13720	3	613.63	-2.39
Q56026 SIPD_SALTY Cell invasion protein sipD	1		SAFSAPTSALFSAMAQPR	106	20	18	74.92	b1b3°b3b7b16y1y3*y3y5*y5y6y8°y8*y8y11y13y14y20	2023.97	66.091	28294	2	1012.49	-8.08
Q56026 SIPD_SALTY Cell invasion protein sipD	2		YNQINSNTVLFPAQSGSGVK	204	20	4	17.48	b5b9y4y10	2124.09	79.062	3063	3	708.70	9.88
Q56026 SIPD_SALTY Cell invasion protein sipD	3		NDLNSLVNK	195	9	9	57.48	b3b6°b6°b6b7°b7b8°b8y8	1016.55	65.356	8737	2	508.78	12.31
Q56026 SIPD_SALTY Cell invasion protein sipD	4		IHQAAQTLQSTPPISEENNDER	54	22	3	22.13	b4b10b11	2535.16	61.821	5072	3	845.72	-19.07
Q56026 SIPD_SALTY Cell invasion protein sipD	5		YSNANSLYDNLVK	311	13	3	23.4	b7b8y10	1500.75	70.618	3033	2	750.88	8.46
Q56026 SIPD_SALTY Cell invasion protein sipD	6		MVQDIDGLGAPGKDSK	263	16	6	15.43	b5°b5°b5b9°b9y10	1630.80	67.268	7733	2	815.90	-6.06
Q56026 SIPD_SALTY Cell invasion protein sipD	7		SGVSLSAEQNENLRSAFSAPTSALFSAMAQPR	92	34	6	21.68	b8b13b14°b14y10y14	3508.68	84.599	4545	4	877.92	-10.37
Q56026 SIPD_SALTY Cell invasion protein sipD	8	Carbamidomethyl+C(20)	VATEAEARQWLSELNLPNSCLK	224	22	3	12.26	b4b7y3	2529.31	108.593	2080	3	843.78	14.48
Q56026 SIPD_SALTY Cell invasion protein sipD	9	Phohoryl STY(8)	GTDIISLSQAATK	41	13	6	36.37	b5°b5b6°b6b7y10	1384.67	136.459	2054	1	1384.67	7.32

IQ56026 SIPD_SALTY Cell invasion protein sipD	10	Oxidation+M(16)	SAFSAPTSALFSAMAQPR	106	20	8	53.45	b3b4b7b8y8y11*y11y12	2039.97	60.797	6624	2	1020.49	-6.52
Q56026 SIPD_SALTY Cell invasion protein sipD	11	Oxidation+M(1)	MGGWLLPGKDGNTVK	173	15	3	16.31	b6b10y6	1588.80	81.731	2178	2	794.90	-11.76
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	1	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLALASGAK	257	25	19	124.61	b2b3*b3b4b5*b5b6*b6y2y3y4y5y7y8y19y20y22y23y25	2684.45	128.391	108314	3	895.49	-0.36
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	2		SALLVLEDGTQFHGR	3	15	7	29.07	b7b13*b13y7y8*y8y15	1642.87	125.713	23046	2	821.94	6.76
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	3		DLPLIASNFR	83	10	4	34.62	y1y4y5y6	1145.63	76.831	20302	2	573.32	0.21
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	4	Carbamidomethyl+C(18)	MNPDGIFLSNGPGDPAPCDYAITAIQK	230	27	10	36.21	b2b8b14*b14y1y11y12y13*y13y27	2862.36	83.750	11384	3	954.79	5.37
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	5		NVVMITAQNHGFAVDEDSL PANLR	302	24	7	17.54	b2b4b13*b13b15y2y10	2611.28	83.600	10280	4	653.58	-5.33
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	6		AFPGLNGMDLAKEVTTAETYR	148	21	5	22.52	b14y5*y5y8y9	2284.11	110.319	3274	2	1142.56	-5.77
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	7		SEDDLPHFHV VAYDFGAK	185	17	4	24.84	b14y4y7y8	1909.91	82.735	4877	3	637.31	8.82
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	8		AIGATGSAVGEEVFN TSMTGYQEILTDPSYSR	18	32	10	47.42	b3b4b10b12b14b17y3y4y7y9	3321.58	96.373	3056	4	831.15	-4.85
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	9	Carbamidomethyl+C(6)	GAQNGCIIAGDDAK	125	16	7	25.02	b9*b9y7y9y13*y13*y13	1573.76	101.960	2470	3	525.26	20.94
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	10		MLVDR	207	5	1	12.3	b3	633.33	118.698	2066	1	633.33	-12.72
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	11		EVTTAETYR	160	9	7	41.66	b3*b3b4*b4y4y7*y7	1069.53	57.276	1997	2	535.27	17.46
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	12		MKFGHHGGNHPVK	285	13	4	23.4	b5b6y10*y10	1445.74	65.271	3889	3	482.59	13.68
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	13		DGLPEAKSEDDLPHFHV VAYDFGAK	178	24	5	24.76	b9b12b13y5y7	2620.27	111.896	2867	3	874.10	6.34
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	14	Carbamidomethyl+C(7)	MLVDRGCR	207	8	3	38.4	y3y4y7	1006.49	88.706	2692	1	1006.49	-2.00
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	15		NVVMITAQNHGFAVDEDSL PANLRVTHK	302	28	4	22.1	b5b11b12*b12	3076.60	120.676	2370	3	1026.20	11.98
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	16		RHNIVAIADIDTR	103	13	4	38.42	y3y5y7y8	1493.80	63.702	2106	2	747.40	-13.40
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	17	Phohoryl STY(9)	LTVVPAQTSAAEVLK	215	15	4	23.05	b9b11y5y11	1664.86	101.868	66108	3	555.62	10.41
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	18	Phohoryl STY(5)	WTQGSWTLKDG LPEAK	169	16	4	15.43	b3*b3y3y13	1896.91	89.337	1803	3	632.97	13.39
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	19	Oxidation+M(18)	AIGATGSAVGEEVFN TSMTGYQEILTDPSYSR	18	32	10	33.74	b5*b5b11b17b30y4y8*y8y9y11	3337.63	129.427	6619	3	1113.22	12.58
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	20	Oxidation+M(8)	AFPGLNGMDLAK	148	12	8	51.28	b3b7b8y7*y7y9y10*y10	1249.62	63.690	3140	2	625.31	-1.95
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	1	Carbamidomethyl+C(19)	LQDGLPVELVDVVEGLDGCHSANITPDNR	110	29	12	60.14	b2b3y2*y2y3y4y5y7y10y12y24y27	3132.55	103.179	42091	3	1044.85	7.56
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	2	Carbamidomethyl+C(2)	ICLFTLSDDGHLVAQEPAE VNTVEGAGPR	150	29	8	34.9	b2y6*y6y7*y7y8*y8y10	3095.52	80.405	13688	3	1032.51	4.57
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	3		TASLITVFSVSEDGSVLSVEGFQPT EAQPR	248	30	3	16.84	y9y13y20	3151.58	105.187	3008	3	1051.20	0.62
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	4		SHHIAVYEITGTQGLLTEK	295	19	7	36.14	b3b5b8*b8y8y9y13	2097.06	85.315	12213	2	1049.03	-17.46
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	5		YAVGQGPMWVVVNAY	316	15	4	26.7	b4b9b12y13	1653.83	94.534	1837	2	827.42	9.89
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	6		WAADIHITPDGR	229	12	4	20.17	b5*b5b8y3	1351.66	39.359	1724	2	676.33	-12.10
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	7		GRYAVGQGPMWVVVNAY	314	17	6	40.07	b7b8b9y8*y8y13	1866.92	105.241	55641	2	933.97	-4.58

Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	8		GFNIDNSGKYLIAAGQK	278	17	4	22.08	b3b5b10*b10	1795.92	63.698	6840	3	599.31	-10.06
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	9	Phohoryl STY(10)	SHHIAVYEITGTQGLLTEK	295	19	6	26.11	b8°b8b12y10y11*y11	2177.05	116.668	4696	2	1089.03	-0.34
Q8ZQR4 6PGL_SALTY 6-phohogluconolactonase	10	Phohoryl STY(14)	IAPDDGALTFAAESALPGTHISTD HHGR	64	30	6	35.79	b13b14y6y7y9y16	3121.44	72.640	2449	3	1041.15	4.85
P66491 RS19_SALTY 30S ribosomal protein S19	1		LGEFAPTR	70	8	5	50.7	y4y5y6y7y8	890.46	42.962	101093	2	445.74	-9.12
P66491 RS19_SALTY 30S ribosomal protein S19	2		QHVPVFVSDEMVGHK	55	15	5	23.05	b6b10°b10y9y11	1708.83	56.273	22696	3	570.28	-12.57
P66491 RS19_SALTY 30S ribosomal protein S19	3		STIFPNMIGLTIAVHNGR	37	18	9	52.95	b7b8°b8b11b12*b12y4*y4y5	1941.01	65.375	3010	2	971.01	-15.28
P66491 RS19_SALTY 30S ribosomal protein S19	4		LGEFAPTRTYR	70	11	3	33.87	b3b5b10	1310.67	55.219	18315	2	655.84	-13.13
P66491 RS19_SALTY 30S ribosomal protein S19	5		VEKAVESGDK	18	10	6	26.38	b8°b8b9°b9y9°y9	1061.54	63.708	2503	2	531.27	-7.36
P66491 RS19_SALTY 30S ribosomal protein S19	6	Oxidation+M(11)	QHVPVFVSDEMVGHK	55	15	5	40.25	b3b11b12b13y6	1724.82	73.941	9727	2	862.91	-14.79
P65226 KHSE_SALTY Homoserine kinase	1	Carbamidomethyl+C(13) ;Carbamidomethyl+C(26))	NMPIGSLGSSACSVVAALVAMN EHCGKPLNDTR	88	34	8	19.55	b2b17y2y6y9y15y32y34	3513.67	96.042	34970	4	879.17	-0.42
P65226 KHSE_SALTY Homoserine kinase	2	Carbamidomethyl+C(24)	QAVSEIGALASGISGPTLFALCD KPETAQR	246	32	9	28.92	b8b17y6y7y9y12°y12*y12y16	3231.63	90.038	19434	4	808.66	-1.81
P65226 KHSE_SALTY Homoserine kinase	3		TIPVAMTLEK	78	10	5	36.13	b7b9y6y8y10	1102.61	60.857	19267	2	551.81	-5.42
P65226 KHSE_SALTY Homoserine kinase	4		DVIAEPYR	227	8	4	38.4	y4y5y7y8	962.49	38.690	3160	2	481.75	-5.64
P65226 KHSE_SALTY Homoserine kinase	5	Carbamidomethyl+C(13)	HYLQNQEGFVHICR	285	14	8	52.06	b7b9b11°b11b13y4y8°y8	1800.89	103.639	38813	3	600.97	14.71
P65226 KHSE_SALTY Homoserine kinase	6	Carbamidomethyl+C(7)	ENIVYQCWER	61	10	4	39.94	b8y6y7y8	1396.65	59.265	12760	2	698.83	15.73
P65226 KHSE_SALTY Homoserine kinase	7		VYAPASSANMSVGFVDLGAAVTP VDGTL LGDVVSVEAADHFR	3	42	6	36.72	b14y5y6°y6y8y9	4205.04	81.227	2666	4	1052.02	-9.75
P65226 KHSE_SALTY Homoserine kinase	8	Carbamidomethyl+C(9)	HLAGFIHACYSR	205	12	9	65.8	b4b5b7b11°b11y4y10y11°y11	1431.70	63.690	2432	2	716.35	3.07
P65226 KHSE_SALTY Homoserine kinase	9	Carbamidomethyl+C(2)	FCQALGKTIPVAMTLEK	71	17	6	20.37	b9°b9b12°b12y3y8	1907.01	64.390	3757	2	954.01	0.70
P65226 KHSE_SALTY Homoserine kinase	10		DVIAEPYRAR	227	10	5	36.93	b3b6b7°b7y7	1189.62	107.194	3629	2	595.31	-8.52
P65226 KHSE_SALTY Homoserine kinase	11	Carbamidomethyl+C(13) ;Carbamidomethyl+C(26));Oxidation+M(22)	NMPIGSLGSSACSVVAALVAMN EHCGKPLNDTR	88	34	5	12.07	b9°b9b13y4y10	3529.68	91.008	11174	4	883.18	5.12
P05989 ILVC_SALTY Ketol-acid reductoisomerase	1		GFGVPTLIAPHENDPQGEGMAIA K	167	25	7	29.54	b2b3b4y10y14y21y25	2548.29	78.119	42270	3	850.10	-0.38
P05989 ILVC_SALTY Ketol-acid reductoisomerase	2		ANYFNTLNL	1	10	7	48.44	b3b7b8y1y3y7y10	1225.63	68.979	24274	2	613.32	1.20
P05989 ILVC_SALTY Ketol-acid reductoisomerase	3		LIQFGWETITEALK	252	14	4	17.37	b11b13y2y13	1648.90	106.456	20833	2	824.95	0.37
P05989 ILVC_SALTY Ketol-acid reductoisomerase	4	Carbamidomethyl+C(6)	VVIVGCGAQGLNQGLNMR	39	18	6	35.93	b6b9b11y5y10y12	1886.00	105.423	11702	2	943.50	13.27
P05989 ILVC_SALTY Ketol-acid reductoisomerase	5		DGAALGYSHGFNIVEVGEQIR	123	21	7	23.64	b2b3b5°b5b7y8y13	2232.11	136.411	3662	2	1116.56	0.66
P05989 ILVC_SALTY Ketol-acid reductoisomerase	6		LVAEGTDPAYAEK	239	13	11	76.84	b7°b7b8°b8b12y4y5y6y8°y8y11	1363.70	64.430	15534	2	682.35	20.50
P05989 ILVC_SALTY Ketol-acid reductoisomerase	7		TAFETAPQYEGK	336	12	5	33.15	b3b5°b5y4y5	1341.60	79.816	2765	3	447.87	-20.74

P05989 ILVC_SALTY Ketol-acid reductoisomerase	8		GYMTDMK	478	7	4	37.9	b4y3°y3y5	845.36	71.172	2279	2	423.18	4.48
P05989 ILVC_SALTY Ketol-acid reductoisomerase	9		IGEQEYFDK	348	9	3	28.11	b6y3y6	1128.54	78.036	1546	1	1128.54	15.90
P05989 ILVC_SALTY Ketol-acid reductoisomerase	10		AGVLESSFVAEVK	202	13	5	18.63	b6b11°b11y9°y9	1335.70	69.631	1534	2	668.36	-9.14
P05989 ILVC_SALTY Ketol-acid reductoisomerase	11		LLTWREETGK	326	10	3	26.38	b9y4y5	1232.68	81.631	85216	2	616.84	14.85
P05989 ILVC_SALTY Ketol-acid reductoisomerase	12		FMGRDEFADGASYLQGK	21	17	8	50.79	b3b4y7y10°y10y11°y11y12	1891.86	64.410	17375	3	631.29	-3.03
P05989 ILVC_SALTY Ketol-acid reductoisomerase	13	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21))	SDLMGEQTILCGMLQAGSLLCFD KLVAEGTDPAYAEK	215	37	5	14.65	b3b7y3y6y9	4031.92	118.470	13646	3	1344.65	2.79
P05989 ILVC_SALTY Ketol-acid reductoisomerase	14		LIQFGWETITEALKQGGITLMMDR	252	24	3	11.71	b13y8y14	2751.45	90.765	6229	4	688.62	11.98
P05989 ILVC_SALTY Ketol-acid reductoisomerase	15		TAFETAPQYEGKIGEQEYFDK	336	21	5	12.6	b9y4°y4y10°y10	2451.14	93.266	5311	3	817.72	0.30
P05989 ILVC_SALTY Ketol-acid reductoisomerase	16	Phohoryl STY(3)	LLTWREETGK	326	10	3	24.62	b4y4y7	1312.62	66.030	2469	2	656.82	2.32
P05989 ILVC_SALTY Ketol-acid reductoisomerase	17	Oxidation+M(21)	GFGVPTLIAVHPENDPQGEGMAIA K	167	25	3	21.04	b6y11y12	2564.27	109.763	1648	3	855.43	-6.00
Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	7	25.69	b2°b2b3b4°b4b15y12	1686.94	90.743	34384	2	843.97	-1.23
Q7CR87 SURA_SALTY Chaperone surA	2		LNAGQAGQQLPDDATLR	50	17	11	63.76	b6b8y4y5y7°y7y9y11°y11y12y17	1767.90	51.796	21043	2	884.46	3.38
Q7CR87 SURA_SALTY Chaperone surA	3		ITDEQLDQAIANIAK	90	15	10	63.77	b12°b12b13°b13y5y10y12°y12y13y14	1642.87	81.234	19883	2	821.94	5.05
Q7CR87 SURA_SALTY Chaperone surA	4		GDIVGPIR	252	8	3	38.4	b3b5b6	826.49	37.681	7618	2	413.75	15.21
Q7CR87 SURA_SALTY Chaperone surA	5		GQSQSISVTEVHAR	274	14	5	38.66	b8y5y6y8y10	1498.75	37.992	7322	3	500.26	-5.70
Q7CR87 SURA_SALTY Chaperone surA	6		QAESIVEEAR	197	10	3	24.62	b7y3y6	1131.54	60.034	2821	2	566.27	-19.31
Q7CR87 SURA_SALTY Chaperone surA	7		QIGTQNDASTELNLSHILIALPENP TSEQVNDAQR	162	35	6	11.94	b7b10y8°y8y11°y11	3816.96	131.745	2686	3	1272.99	15.48
Q7CR87 SURA_SALTY Chaperone surA	8		GQISAPVHSSFGWHLELDTR	362	22	5	18.77	b3°b3y3y11y13	2463.26	88.453	1740	3	821.76	-9.12
Q7CR87 SURA_SALTY Chaperone surA	9		LAITYSADQQALKGGQMGWGR	214	21	9	49.54	b8°b8b15b16y3y4y5y12°y12	2251.14	66.115	14191	3	751.05	3.47
Q7CR87 SURA_SALTY Chaperone surA	10		LAYDGLNYSTYRNQIR	117	16	9	45.27	b6°b6b7°b7b8°b8b14y9y13	1946.96	66.023	6012	3	649.66	-5.14
Q7CR87 SURA_SALTY Chaperone surA	11		SRLAYDGLNYSTYR	115	14	5	30.18	b3b7y3y4°y4	1678.81	45.948	5018	2	839.91	-3.20
Q7CR87 SURA_SALTY Chaperone surA	12		EMIISEVRNNEVR	134	13	4	26.11	b7b8b10°b10	1588.80	41.775	3233	2	794.90	-9.68
Q7CR87 SURA_SALTY Chaperone surA	13		NGADFGKLAITYSADQQALK	207	20	5	13.01	b9b13°b13y9°y9	2111.05	105.146	2547	2	1056.03	-13.99
Q7CR87 SURA_SALTY Chaperone surA	14	Oxidation+M(10)	LIMDQIILQMGQK	73	13	7	42.27	b5b6°b6y4y5°y5y12	1546.81	89.872	16186	2	773.91	-12.71
Q7CR87 SURA_SALTY Chaperone surA	15	Oxidation+M(19)	VAAVVNNGVVLESVDGLMQSV K	27	23	7	18.12	b8°b8y5°y5y8y12°y12	2359.23	114.158	2780	2	1180.12	4.97
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	1		LGSVFSSTGTGGGQEQTITSTWTT LAHHGMVIVPIGYAAQELFDVSQ VR	106	49	13	43.2	b7b8b12y2y5y6°y6y9°y9y10°y10y22y49	5134.55	116.929	9791	4	1284.39	-2.09
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	2		TQNAPVATPQELADYDAIIFGTPT R	54	25	12	50.25	b1b2°b2b4b7b11b13y6y11y12y13y25	2689.35	90.672	9259	3	897.12	1.63
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	3		TFLDQTGGLWASGSLYGK	88	18	4	14.03	b4°b4y3y7	1900.94	73.916	6194	3	634.32	-2.83

Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	4		GGTPYGATTIAGGDGSR	155	17	6	37.52	b4b5b11y4°y4y5	1537.76	77.373	10497	3	513.26	21.27
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	5		ILVLYYSMYGHETMAHAVAEGA K	3	24	4	11.71	b10y4°y4y12	2667.37	84.359	2476	3	889.79	13.55
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	6		TQNAPVATPQELADYDAIIFGTPT RFGNMSGQMR	54	34	15	36.13	b3b6°b6°b6b8°b8°b8b10°b 10y3y5y8y10y12*y12	3697.83	122.869	61644	4	925.21	14.66
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	7		MAKILVLYYSMYGHETMAHAVA EGAK	0	27	4	34.8	y5y8y9y10	2997.55	89.872	7529	3	999.85	14.42
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	8		AKILVLYYSMYGHETMAHAVA EGAK	1	26	4	11.33	b12y4y13°y13	2866.50	65.304	2612	6	478.59	12.09
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA	9	Oxidation+M(15)	ILVLYYSMYGHETMAHAVAEGA K	3	24	5	18.02	y8y11°y11y15°y15	2683.36	100.212	4275	3	895.12	12.01
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	1		ITAVIPYFGYAR	84	12	4	41.9	y5y7y8y10	1370.74	81.552	26030	2	685.88	-2.85
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	2		LFAGNATPELAQR	5	13	5	26.11	y6y10°y10y11y13	1387.73	54.810	23683	2	694.37	-2.81
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	3	Carbamidomethyl+C(11)	GGDIFIQSTCAPTNDNLMEVLVM VDALR	49	29	5	11	b11b13*b13y7y29	3192.60	121.706	1902	4	798.91	8.56
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	4		AAEALK	231	6	2	25.1	b4y3	602.35	33.052	14694	1	602.35	-5.98
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	5	Carbamidomethyl+C(10)	NSVIDEVVVCDTIPLTDEIK	262	20	5	22.97	b15y4y11y12°y12	2259.17	89.060	8997	2	1130.09	14.05
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	6		LLNDTDMAIIDK	182	12	4	34.24	b4b6b10y9	1361.67	65.453	6114	2	681.34	-20.44
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	7		FSDGEVSVQINENVR	34	15	12	77.7	b3b9b10°b10b13°b13y4y5 *y5y6y8y14	1692.84	64.385	2324	2	846.92	13.99
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	8		MPDMKLFAGNATPELAQR	0	18	3	14.03	b9b14y13	1989.96	77.403	29417	2	995.49	-12.70
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	9		LLNDTDMAIIDKR	182	13	3	27.87	b5b9b11	1517.80	71.867	26476	3	506.61	3.38
P0A1V6 KPRS_SALTY Ribose-phohate pyrophohokinase	10	Carbamidomethyl+C(11)	GGDIFIQSTCAPTNDNLME	49	20	2	12.49	y4y16	2196.02	121.703	8897	3	732.68	9.89
P67605 YEEX_SALTY UPF0265 protein yeeX	1		METTKPSFQDVLEFVR	0	16	6	25.69	b8y2y8y10y11y16	1926.95	85.986	67659	3	642.99	-7.48
P67605 YEEX_SALTY UPF0265 protein yeeX	2		EIQDIEKK	26	8	7	60	b4b6b7°b7y5y6y8	1002.53	26.463	16807	2	501.77	-13.82
P67605 YEEX_SALTY UPF0265 protein yeeX	3		ETTKPSFQDVLEFVR	1	15	7	26.7	b4b6°b6b7°b7y2y14	1795.90	72.536	14715	2	898.46	-10.67
P67605 YEEX_SALTY UPF0265 protein yeeX	4		NAEISK	82	6	4	37.41	b3°b3b4y3	661.35	29.286	40246	1	661.35	-8.12
P67605 YEEX_SALTY UPF0265 protein yeeX	5		VLLLDNLSDYIKPGMSVEAIQGIIA SMK	41	28	3	17.09	b3b10b15	3018.63	119.640	9817	3	1006.88	2.43
P67605 YEEX_SALTY UPF0265 protein yeeX	6		VLLLDNLSDYIKPGMSVEAIQGIIA SMKSDYEDR	41	34	4	23.37	b6b7y7y11	3783.93	107.263	4071	5	757.59	3.55
Q8ZL96 SYGB_SALTY Glycyl-tRNA synthetase beta subunit	1		SLAESFAANFTAELDNAGLAHGN VEWFAPR	21	31	18	77.83	b3b5b7b8°b8b9°b9b11b12 °b12b13°b13b14°b14y1y2y 8y10	3276.55	114.086	21111	3	1092.85	-6.78
Q8ZL96 SYGB_SALTY Glycyl-tRNA synthetase beta subunit	2		VANLAESQPDREVEK	57	15	5	24.39	b2y4°y4y6y7	1684.85	60.723	10664	3	562.29	0.87
Q8ZL96 SYGB_SALTY Glycyl-tRNA synthetase beta subunit	3		LADAEFFNTDRK	326	13	4	29.38	b6b7b11y11	1573.74	71.848	1674	2	787.38	-13.26
Q8ZL96 SYGB_SALTY Glycyl-tRNA synthetase beta subunit	4		FLAVPAEALVYTMK	268	14	6	52.98	y6y9°y9y10y11y12	1552.86	101.973	31062	2	776.93	9.91
Q8ZL96 SYGB_SALTY Glycyl-tRNA synthetase beta subunit	5		DPTQIISGNEK	310	11	7	48.48	b6b8y3°y3*y3y4y5	1201.60	35.740	22744	2	601.31	-1.83
Q8ZL96 SYGB_SALTY Glycyl-tRNA synthetase beta subunit	6		TLEEASALAAANK	571	13	4	18.63	b7b12°b12y7	1288.70	60.108	7532	2	644.85	17.05

[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	7		RPTRPADFDAR	552	11	6	48.48	b7b10y4y7y10°y10	1301.64	65.332	6205	2	651.33	-20.54
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	8		GEWLLYR	112	7	4	47.2	b4b5b6y5	936.49	66.048	2797	2	468.75	-4.69
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	9		GESTEALVPNMVATSLAK	123	18	5	33.61	b4b8b10b15y10	1817.93	81.237	2568	2	909.47	1.68
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	10	Carbamidomethyl+C(13)	FAGDDLPSNPVACALAIADK	437	20	3	13.01	b10y11y13	2044.97	102.563	1632	2	1022.99	-13.79
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	11		APVDEFFENVMVNAEEK	645	17	7	40.7	b4b7b8°b8y5y6y8	1967.93	73.990	1613	2	984.47	12.22
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	12	Carbamidomethyl+C(2)	GCGITVDQAER	96	11	5	48.93	b6y4y6y7y8	1205.58	103.831	1543	1	1205.58	17.01
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	13		LQPYFADGR	624	9	5	42.17	b4b7°b7b8y6	1066.51	114.123	1511	1	1066.51	-16.48
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	14		SLAESFAANFTAELDNAGLAHGN VEWF AAPRR	21	32	5	16.7	b5b10°b10°b10b12	3432.72	105.334	7063	3	1144.91	13.44
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	15		FEEKFLAVPAEALVYTMK	264	18	6	31.27	b6b10b11b13y4°y4	2086.07	76.312	5371	2	1043.54	-9.25
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	16		GPAIAQAFDAEGKPSKAAEGWAR	73	23	6	20.99	b9°b9°b9b10°b10y13	2328.16	136.371	3156	2	1164.59	-4.09
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	17	Phohoryl STY(5)	VIPATILGIQSDR	171	13	3	23.4	b3y9y10	1462.76	60.184	7262	2	731.88	-1.34
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	18	Phohoryl STY(8)	NLALDLQTLTEEAVR	494	15	10	71.14	b3°b3b8b9°b9b10b11y7y8 y10	1765.89	114.108	5788	2	883.45	12.79
[Q8ZL96]SYGB_SALTY Glycyl-tRNA synthetase beta subunit	19	Oxidation+M(14)	LTNANVVDDVIDFMLGR	514	17	9	39.45	b3°b3b6°b6b14°b14y7y8y1 1	1907.95	65.332	3971	2	954.48	-2.24
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	1		AALESTLAAITESLKEGDAVQLVG FGTFK	22	29	26	191.05	b2b3b4b5°b5b7b9°b9b12b 13b19b23y2y3y4y5y6y7y8 y13y14y21y22y24y25y26	2966.57	115.442	418408	3	989.53	-1.73
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLK	22	15	3	22.33	b3b4y7	1517.85	97.819	25683	2	759.43	1.85
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	3		ALKDAVK	83	7	6	34.89	b4y1y4°y4y5y7	744.45	21.052	25059	2	372.73	-13.20
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	4		IAAANVPAFVSGK	70	13	12	114	b4b5°b5b6°b6b10y4y5y6y 8y10y12	1244.69	60.212	15765	1	1244.69	-6.96
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	5		EGDAVQLVGFGTFK	37	14	9	36.07	b6b8°b8b12°b12°b12y6°y6 y13	1467.77	63.671	5516	2	734.39	14.55
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	6		VNHRAER	51	7	4	37.9	b5y3°y3y5	881.46	12.433	4291	2	441.24	-6.02
[P0A1R6]DBHA_SALTY DNA-binding protein HU-alpha	7	Phohoryl STY(11)	IAAANVPAFVSGK	70	13	4	27.87	b4b9°b9b11	1324.65	136.391	2652	1	1324.65	-1.38
[P26982]DEGP_SALTY Protease do	1		GAFVSQVMPNSSAAK	313	15	9	57.38	b3b5b12y2y8y9y10y12y15	1493.75	54.232	15770	2	747.38	5.48
[P26982]DEGP_SALTY Protease do	2		VGDYTVAIGNPFLGETVTSGIVS ALGR	186	28	11	48.71	b3b6b7b8°b8y3y5°y5y6y14 y28	2750.41	117.094	13907	3	917.47	-9.59
[P26982]DEGP_SALTY Protease do	3		LADSDALR	178	8	4	33.63	b3°b3b5y3	860.43	32.535	87089	2	430.72	-15.61
[P26982]DEGP_SALTY Protease do	4		SGLNVENYENFIQTDAAINR	214	20	4	22.43	y5y11°y11y12	2268.12	78.401	7382	2	1134.56	12.59
[P26982]DEGP_SALTY Protease do	5		NLTSQMVEYGQVK	275	13	8	43.45	b7b8b9°b9b11°b11y6°y6	1496.74	63.692	4568	2	748.87	-2.61
[P26982]DEGP_SALTY Protease do	6		NIAELR	443	6	1	12.8	y4	715.40	30.341	4357	2	358.20	-13.05
[P26982]DEGP_SALTY Protease do	7		FMALGSGVIIDAAK	110	14	4	25.15	b5b12°b12b13	1392.73	81.557	4094	2	696.87	-17.79
[P26982]DEGP_SALTY Protease do	8		VMPSVVSINVEGSTTVNTPR	48	20	8	51.61	b9b10°b10b13b14y10y11° y11	2087.11	65.357	2646	2	1044.06	13.45
[P26982]DEGP_SALTY Protease do	9		GELGIMGTELNSELAKE	289	16	7	58.49	y5y7y8y9y11°y11y12	1661.81	63.696	2211	3	554.61	-16.75
[P26982]DEGP_SALTY Protease do	10		AQVGTMPVGSKE	352	11	8	46.72	b3b6b7°b7y6°y6y7°y7	1074.54	108.607	1970	1	1074.54	-18.40
[P26982]DEGP_SALTY Protease do	11		RGELGIMGTELNSELAKE	288	17	7	24.84	b3b13°b13b14°b14°b14y1 3	1817.97	87.208	4021	2	909.49	14.91

P26982 DEGP_SALTY Protease do	12	Phohoryl STY(17)	VGDYTV AIGNPFG LGETVTS GIVS ALGR	186	28	5	25.3	b9b11b15b16°b16	2830.40	105.406	4783	2	1415.70	3.45
P26982 DEGP_SALTY Protease do	13	Phohoryl STY(7)	VMPSVV SINVEGSTTVNTPR	48	20	9	34.78	b4°b4b5b10*b10y11*y11y 13y15	2167.05	96.417	1672	2	1084.03	6.87
P26982 DEGP_SALTY Protease do	14	Oxidation+M(2)	VMPSVV SINVEGSTTVNTPR	48	20	4	13.01	b5b7°b7y15	2103.06	65.361	10565	3	701.69	-5.11
P26982 DEGP_SALTY Protease do	15	Oxidation+M(6)	AQVGTMPVGSK	352	11	3	22.11	b4b6y9	1090.57	55.255	8827	2	545.79	12.20
P26982 DEGP_SALTY Protease do	16	Oxidation+M(8)	GAFVSQVMPNSSAAK	313	15	5	33.44	b5b10y8y9y11	1509.74	42.776	1941	2	755.37	2.18
P77983 KPYK1_SALTY Pyruvate kinase I	1		GDLGVEIPVEEVIFAQK	244	17	6	41.12	b3b4b7b8y1y14	1843.00	95.532	39996	2	922.00	9.47
P77983 KPYK1_SALTY Pyruvate kinase I	2		MLDAGMNVMR	22	10	6	48.69	b2y5y7y8y9y10	1137.52	58.216	19449	2	569.26	-2.68
P77983 KPYK1_SALTY Pyruvate kinase I	3	Carbamidomethyl+C(13)	YPLEAVSIMATICER	319	15	7	16.31	b1b4°b4b6°b6y2y4	1752.87	83.471	19153	2	876.94	-0.49
P77983 KPYK1_SALTY Pyruvate kinase I	4		IENQEGLNNFDEILEASDGIMVAR	220	24	8	21.52	b2b12y1y2y3y4y8y24	2677.29	97.091	17147	3	893.10	4.01
P77983 KPYK1_SALTY Pyruvate kinase I	5	Carbamidomethyl+C(6)	ITEAVCR	353	7	5	50.21	y3y4y5y6y7	848.42	26.005	10742	2	424.71	-9.78
P77983 KPYK1_SALTY Pyruvate kinase I	6		AGQTFTFITDK	86	11	6	32.19	b6b8b11y2y5y8	1216.59	51.852	7006	2	608.80	3.51
P77983 KPYK1_SALTY Pyruvate kinase I	7		AEAGDVANAILDGTDAVMLSGES AK	292	25	6	14.49	b1b7b15y2y11y15	2405.16	93.124	6590	2	1203.09	5.38
P77983 KPYK1_SALTY Pyruvate kinase I	8		IQNLR	46	5	1	12.3	y4	643.38	41.533	6701	1	643.38	-10.62
P77983 KPYK1_SALTY Pyruvate kinase I	9		MMIEK	261	5	1	12.3	y3	651.31	55.920	3466	1	651.31	-12.37
P77983 KPYK1_SALTY Pyruvate kinase I	10		DVALQSGLAQK	434	11	3	29.1	b3b6b7	1129.60	31.605	2591	3	377.21	-15.99
P77983 KPYK1_SALTY Pyruvate kinase I	11		VMNSR	337	5	1	12.3	y4	606.30	83.532	2266	1	606.30	-2.92
P77983 KPYK1_SALTY Pyruvate kinase I	12		GAVETA EKLEAPLIVVATQGGK	360	22	3	22.13	b10b11b13	2181.20	82.303	26438	3	727.74	-3.81
P77983 KPYK1_SALTY Pyruvate kinase I	13		LEGGNDVSLKAGQTFITDK	76	21	5	35.23	y6y10y11°y11y12	2229.13	79.595	14498	3	743.71	9.97
P77983 KPYK1_SALTY Pyruvate kinase I	14	Carbamidomethyl+C(3)	IVCTIGPKTESEEMLSK	5	17	3	14.67	b12y3y15	1921.95	51.897	14297	3	641.32	-5.72
P77983 KPYK1_SALTY Pyruvate kinase I	15		VLNNGDLGENKGVNLPGVSIALP ALAEK	145	28	5	11.08	b5°b5b11°b11y5	2802.55	136.372	11111	3	934.85	3.57
P77983 KPYK1_SALTY Pyruvate kinase I	16	Carbamidomethyl+C(6)	MMIEKCIR	261	8	3	46.18	b3b5b7	1080.53	63.654	2363	1	1080.53	-9.94
P77983 KPYK1_SALTY Pyruvate kinase I	17		TESEEMLSKMLDAGMNVMR	13	19	5	23.5	b4y5y6y12*y12	2171.99	76.183	1649	3	724.67	6.63
P77983 KPYK1_SALTY Pyruvate kinase I	18		AGQTFITFTD	86	10	0	2.98		1088.48	51.915	3967	3	363.50	-6.84
P77983 KPYK1_SALTY Pyruvate kinase I	19		AGQTFITFTDK	86	11	1	7.5	b9	1199.56	51.880	1789	2	600.29	8.96
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	1		TFDTPTYPNSLALSADGK	308	18	7	33.61	b3y2y3y5y11y14y18	1897.93	66.538	27155	2	949.47	6.05
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	2		QAGQVSVIDAK	291	11	5	12.02	b9°b9y2y4y11	1115.60	38.658	17416	2	558.30	-5.58
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	3		EQEATQPDDVIR	338	12	5	30.39	y2y6y8y10y12	1400.66	40.488	16774	2	700.83	-2.18
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	4		LLDDGKEHFFINLSLDTAGHR	223	21	7	48.07	b8b10b11b12y10*y10y11	2398.25	76.859	5368	3	800.09	14.56
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	5		LYTTNADGEFTIDTASNK	198	19	4	13.48	b8y10y14y19	2074.01	77.490	4479	2	1037.51	8.12
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	6		TTIENTGK	177	8	5	33.63	b6y5°y5y7°y7	863.44	61.356	13504	1	863.44	-8.13
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	7		ELVADAATNTIYISGVGK	144	18	6	24.12	b7b11°b11b12°b12y11	1821.94	82.849	10499	3	607.98	-13.13

Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	8		LLDDGK	223	6	1	12.8	b3	660.37	35.039	10191	1	660.37	14.42
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	9		EHFFINLSLDTAGHR	229	15	9	39.46	b10b11°b11*b11y4y6°y6y8°y8	1756.90	65.378	6906	3	586.31	14.59
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	10		ESAIWVVDGETIK	162	13	4	18.63	b8°b8b11y8	1446.72	44.197	2116	2	723.86	-20.50
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	11		IAAPASLAVLFNPNTRNEAYVTHR	268	23	4	26.8	y3y16y20y22	2511.32	83.360	48183	4	628.58	-12.25
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	12		NEAYVTHRQAGQVSVIDAK	283	19	10	36.67	b8°b8b10°b10°b10b16b18y3°y3y8	2086.08	65.346	20070	3	696.03	7.61
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	13		AQRLYTTNADGEFITIDTASNK	195	22	4	12.26	b5b9°b9y13	2429.21	94.474	7034	2	1215.11	6.73
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	14		LLDDGKEHFFINLSLDTAGHR	223	21	3	12.6	b6b12y6	2398.24	96.576	1673	3	800.09	12.22
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	15	Phohoryl STY(14)	LLDDGKEHFFINLSLDTAGHR	223	21	5	19.51	b10°b10y6y9y11_H3PO4y11	2478.17	107.175	1905	4	620.30	-1.77
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	16		LLDDGKEHFFINLSLDTAGH	223	20	0	7.95		2242.10	76.815	16412	2	1121.55	-6.21
P66738 RRF_SALTY Ribosome-recycling factor	1		ASLLDGIVVEYYGTPTPLR	31	21	5	16.74	b8b15y5y14y21	2248.20	94.084	55278	2	1124.61	7.38
P66738 RRF_SALTY Ribosome-recycling factor	2		SMGPAVEK	72	8	8	38.4	b8y2°y2y5y6y7°y7y8	818.40	27.734	25148	2	409.70	-7.91
P66738 RRF_SALTY Ribosome-recycling factor	3		QLASVTVEDSR	52	11	5	29.1	y2y5y6y8y11	1204.62	40.891	24587	2	602.82	5.67
P66738 RRF_SALTY Ribosome-recycling factor	4		AIMASDLGLNPSSAGTDIR	80	19	10	36.14	b1b4b10b13y2y5°y5y6y9y19	1888.96	68.375	10121	2	944.98	6.40
P66738 RRF_SALTY Ribosome-recycling factor	5		ALLK	140	4	1	11.81	y3	444.32	38.479	20263	1	444.32	-3.92
P66738 RRF_SALTY Ribosome-recycling factor	6		INVFDR	66	6	4	40.42	b5°b5y3y5	763.41	50.413	15376	2	382.21	-6.16
P66738 RRF_SALTY Ribosome-recycling factor	7		VPLPLTEER	99	10	5	39.39	y3°y3y5y7°y7	1150.64	59.024	12988	2	575.82	-7.96
P66738 RRF_SALTY Ribosome-recycling factor	8		AIMASDLGLNPSSAGTDIRVPLPLTEER	80	29	12	48.36	b5°b5b7°b7b8°b8y7y12y19y21y22y25	3020.58	87.165	83724	3	1007.53	4.20
P66738 RRF_SALTY Ribosome-recycling factor	9		IVRGAEQAR	115	10	3	24.62	b5b7y7	1128.61	16.733	15021	2	564.81	0.00
P0A2C1 RNH2_SALTY Ribonuclease HII	1		AEAHEIDELNILHATMLAMQR	72	21	13	32.09	b4b6b12*b12y1y2*y2y6*y9*y9y10°y10y21	2406.17	107.230	11634	3	802.73	-9.03
P0A2C1 RNH2_SALTY Ribonuclease HII	2		MIEFVYPHTLVAGVDEVGR	0	20	5	25.61	b3b8y8y9y20	2269.13	70.122	10377	3	757.05	-4.41
P0A2C1 RNH2_SALTY Ribonuclease HII	3		GYPTAFHLEK	163	10	3	24.62	b3b8y9	1162.58	41.876	22891	2	581.80	-4.09
P0A2C1 RNH2_SALTY Ribonuclease HII	4		LAQYGATAHHR	173	11	7	55.22	b3b8°b8b9y4y5y10	1224.61	64.444	4132	3	408.88	-10.17
P0A2C1 RNH2_SALTY Ribonuclease HII	5		AVAGLHIAPEYVLIDGNR	93	18	8	37.29	b17y4°y4y5°y5y6*y6y8	1908.03	64.391	4000	3	636.68	-3.52
P0A2C1 RNH2_SALTY Ribonuclease HII	6		GYPTAFHLEKLAQYGATAHHR	163	21	4	22.52	b5b6b10y6	2368.23	79.310	11662	3	790.08	13.30
P0A2C1 RNH2_SALTY Ribonuclease HII	7		EKALSWSLGR	62	10	4	36.93	b4b6b7y5	1146.61	66.100	5245	2	573.81	-14.80
P0A2C1 RNH2_SALTY Ribonuclease HII	8	Phohoryl STY(15)	AEAHEIDELNILHATMLAMQR	72	21	8	12.6	b13°b13°b13y6°y6y11°y11°y11	2486.16	83.538	9119	3	829.39	4.62
P0A2C1 RNH2_SALTY Ribonuclease HII	9	Oxidation+M()	AEAHEIDELNILHATMLAMQR	72	21	5	16.74	b4b6y8y10°y10	2422.15	86.973	147671	3	808.05	-14.51
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	1		AGDIVGEHTAMFADIGER	212	18	10	37.69	b6°b6b7b14y6°y6y10°y10y13°y13	1888.88	105.223	25883	3	630.30	-4.52
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	2		VMGDYSDIEIEAHR	145	16	4	21.96	b2b12b13y5	1884.91	70.135	14148	3	628.98	10.82

Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	3		NGLFDMR	258	7	3	19.58	b4y4°y4	852.40	51.934	9138	2	426.70	-6.73
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	4	Carbamidomethyl+C(22)	DDFDVFDTRPEGTLTHLAFCR	70	23	6	26.55	b4y4y6y7y11°y11	2772.32	111.976	5625	3	924.78	4.58
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	5		VDAPSGTALAMGEAIAIGALDK	163	21	4	25.19	b14b15y10y12	1957.99	82.161	7164	3	653.34	0.69
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	6		QLIQAAMAMEGVQLGAALER	19	20	3	19.8	b5b8b13	2100.05	96.313	3150	3	700.69	-19.88
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	7		VAGTIGFATVR	201	11	3	22.11	b4b8y6	1091.61	57.341	2306	2	546.31	-12.08
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	8		AAKVMGDYSIEIEAHHR	142	19	3	13.48	b7b13y12	2155.09	105.388	72810	3	719.04	14.05
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	9		VAGTIGFATVRAGDIVGEHTAMFADIGER	201	29	3	16.95	b5b9b19	2961.46	66.199	31245	4	741.12	-11.29
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	10		ASSRMTFANGALR	236	13	4	23.4	b11°b11b12y10	1381.70	58.261	5217	2	691.35	-2.30
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	11	Phohoryl STY(7)	QAIREASQEIAIVFAANFSGVNV MLK	111	27	3	22.04	b5b6b12	2985.49	79.423	3276	3	995.83	-10.47
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	12	Oxidation+M()	QLIQAAMAMEGVQLGAALEREGRS SLLGSDAGELAGAGK	19	38	6	33.17	b12b13y3y12y13°y13	3715.84	103.893	8230	4	929.72	-6.44
Q8ZRX8 DAPB_SALTY Dihydrodipicolinate reductase	13	Oxidation+M(11)	AGDIVGEHTAMFADIGER	212	18	4	21.43	b8°b8b9y3	1904.91	120.627	2601	3	635.64	13.71
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		LADPNTAYASYLQYGHIANIDIIA GKKPATDLGVK	125	38	9	36.59	b3b6b7b8°b8y4y8y30y38	4001.03	83.971	65437	5	801.01	-8.60
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		AEQQLDKDSAIVPVYYYVNAR	494	21	9	23.64	b2b4b7°b7b12y1y6y9y21	2442.23	73.887	29991	3	814.75	1.00
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3	Carbamidomethyl+C(4)	AGWCADYNEPTSFLNTMLSDSSN NTAHYK	439	29	4	16.95	y3y7y13y29	3294.43	90.898	17972	3	1098.81	5.56
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4		NQGDLPAYSYTPPYTDGAK	333	19	10	33.93	b7°b7b11b13°b13y2y9y11y14y19	2057.97	59.984	16805	2	1029.49	10.56
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		TVINQVTYLPISSEVTDVNR	241	20	9	49.1	b1b4°b4y5y6y7y11y12y20	2248.20	77.916	11715	2	1124.60	5.86
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		LVEPEWFK	352	8	3	30.62	b5y5y6	1047.54	72.046	24270	2	524.28	-6.29
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7		WSDGTPVTAHDFVYSWQR	107	18	3	22.95	y5y9y10	2152.02	73.411	24019	3	718.01	15.09
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		NLGVNVNLENQEWK	410	14	5	25.94	b4b7b12°b12°b12	1656.84	67.693	8178	2	828.92	4.79
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9	Carbamidomethyl+C(6)	VDPYLCTYYEINNQK	291	16	3	21.96	b7b8y9	2082.99	117.738	6320	3	695.00	22.39
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		LLAEAGFTADKPLTFDLLYNTSDL HK	372	26	5	16.56	b8°b8b10b12y4	2893.44	116.761	3841	3	965.15	-21.26
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		ALDDHTFEVTLSEPVPHYFK	163	20	3	13.01	b11y6y10	2371.13	91.201	3090	3	791.05	-6.69
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		LVKPWVGGYTGK	515	12	4	27.38	y3y6y7°y7	1304.71	72.539	2968	1	1304.71	-21.52

[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	13		DSAIVPVYYYVNAR	501	14	4	17.37	b3°b3y7y12	1629.84	63.682	2935	2	815.42	6.82
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	14		VADDTQR	481	7	4	37.9	b5y4*y4y6	804.39	98.630	2616	1	804.39	10.40
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	15		SLIAAGILTALIAASAATAADVPAG VQLADK	7	31	7	34.92	b13b29y15y19y20y21°y21	2863.63	136.880	2509	3	955.22	7.08
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	16		DLFEGLLISDVEGHPGVAEK	67	22	5	27.27	b3y7y8y12y14	2309.17	89.948	1801	3	770.39	0.74
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	17		APFNDVRVR	307	9	5	35.89	b3b4*b4b8°b8	1073.60	26.872	52743	2	537.30	11.37
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	18		NQGDLPAYSYTPPYTDGAKLVEP EWFK	333	27	4	34.83	b5°b5b6b7	3086.44	72.533	11442	4	772.37	-12.66
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	19		SELYAKAEQQLDK	488	13	5	18.63	b10°b10y5y7*y7	1522.77	58.965	7655	2	761.89	-2.08
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	20		FGDKWTQPANIVTNGAYK	200	18	16	89.51	b4°b4b5b6b8b9b13y3y6°y6 y7*y7y10°y10*y10y12	2009.99	64.413	6104	3	670.67	-9.96
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	21		TFLDTRHQGTDFVAR	424	15	6	26.7	b5b6b11°b11*b11y11	1763.88	69.513	3369	2	882.45	0.42
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	22		DPLDNIYVKNLYIIK	527	15	4	24.39	b3b9b10°b10	1821.03	101.305	3215	2	911.02	6.44
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	23		AEQQLDKDSAIVPVYYYVNAR	494	21	7	40.67	b5b6b11b15y6*y6y7	2442.26	97.361	3161	4	611.32	12.70
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	24		ASYLQYGHIANIDDIAGKKPATDL GVK	135	28	0	16.39		2971.61	84.030	2317	4	743.66	8.46
[P41031]CY_SALTY Thiosulfate-binding protein	1		VNNPEIMGK	286	9	7	49.95	b1b2b6y4y6y8y9	1001.50	37.198	46700	2	501.25	-8.59
[P41031]CY_SALTY Thiosulfate-binding protein	2		TEQFMTQFLK	179	10	4	26.38	b3b4y9y10	1272.63	76.351	41496	2	636.82	3.84
[P41031]CY_SALTY Thiosulfate-binding protein	3		LPNNSFYSTMGFLVR	110	17	7	30.53	b6b7b10°b10y5y13y17	1929.97	92.754	41357	2	965.49	7.46
[P41031]CY_SALTY Thiosulfate-binding protein	4		NVEVFDTGGR	189	10	5	36.93	b5y4y7y8y10	1093.52	48.203	36207	2	547.27	-3.91
[P41031]CY_SALTY Thiosulfate-binding protein	5		QALAILQLK	71	10	5	36.93	b1b3y5y6y8	1054.66	75.839	33071	2	527.83	-3.01
[P41031]CY_SALTY Thiosulfate-binding protein	6		LIFPNPK	146	7	7	37.9	y1y2y3y4y5*y5y7	828.49	56.767	33060	2	414.75	-11.35
[P41031]CY_SALTY Thiosulfate-binding protein	7		FGSWPEVMK	311	9	7	35.89	b2y2y4y5°y5y7y9	1080.51	69.624	27832	2	540.76	-5.99
[P41031]CY_SALTY Thiosulfate-binding protein	8		NIHDWSDLVR	132	10	13	70.28	b1b2b3*b3b4°b4*b4y2y4y 6y7y9y10	1254.62	64.474	22088	2	627.81	-4.28
[P41031]CY_SALTY Thiosulfate-binding protein	9		GLGDVLISFESEVNNIRK	208	18	3	21.43	b13b14y11	1990.09	75.033	5215	2	995.55	14.35
[P41031]CY_SALTY Thiosulfate-binding protein	10		ELFAALNPPFEQQWAK	37	16	6	31.21	b6b12y9y11y13°y13	1888.97	90.676	46904	2	944.99	7.69
[P41031]CY_SALTY Thiosulfate-binding protein	11		GLGDVLISFESEVNNIR	208	17	5	32.67	b11y6y8y10y11	1861.94	60.828	3550	3	621.32	-11.74

[P41031 CY_SALTY Thiosulfate-binding protein	12		FPQTELFRR	299	8	9	63.01	b4*b4b5b7°b7*b7y4°y4y6	1037.56	66.081	2441	2	519.29	21.41
[P41031 CY_SALTY Thiosulfate-binding protein	13		QYEAQGFEVVIPK	226	13	4	26.11	b7b8b11*b11	1507.75	64.443	2288	2	754.38	-20.40
[P41031 CY_SALTY Thiosulfate-binding protein	14		THFASGGELDK	320	11	4	32.19	b4b6y4y10	1161.55	91.828	2109	1	1161.55	-1.37
[P41031 CY_SALTY Thiosulfate-binding protein	15		NVQANGTEK	253	9	9	71.04	b4b5b6b7°b7*b7y4y6*y6	960.47	113.378	1713	1	960.47	-7.50
[P41031 CY_SALTY Thiosulfate-binding protein	16		TNLAEPVAVWDKNVQANGTEK	239	23	12	47.95	b3°b3b8y6°y6y9*y9y10y13*y13y18y20	2544.32	91.448	79203	3	848.78	3.26
[P41031 CY_SALTY Thiosulfate-binding protein	17		GNPKNIHDWSDLVR	128	14	5	44.68	b3b5b7b9y12	1650.83	84.241	23044	3	550.95	-2.00
[P41031 CY_SALTY Thiosulfate-binding protein	18		TSGNARYTYLAAWGAADNADGGDK	153	24	9	44.99	b5b8b9*b9b12b14°b14b15y6	2445.14	94.425	8383	4	612.04	13.98
[P41031 CY_SALTY Thiosulfate-binding protein	19		LIFPNPKTSGNAR	146	13	5	29.38	b3y3y4y6°y6	1414.80	72.560	6493	2	707.90	13.55
[P41031 CY_SALTY Thiosulfate-binding protein	20		TEQFMTQFLKNVEVFDTGGR	179	20	4	21.14	b11*b11y4y5	2347.14	58.756	5343	3	783.05	1.14
[P41031 CY_SALTY Thiosulfate-binding protein	21		QADKFPQTELFRR	295	12	3	20.17	b5b8y7	1479.75	60.028	5093	2	740.38	-6.02
[P41031 CY_SALTY Thiosulfate-binding protein	22		ELFAALNPPFEQQWAKDNGGDK	37	22	9	29.1	b5b7b12*b12y7y9*y9y14*y14	2475.22	87.143	3346	3	825.75	10.95
[P41031 CY_SALTY Thiosulfate-binding protein	23		NVEVFDTGGRGATTTFAER	189	19	11	48.59	b4*b4b9y3y5°y5y6°y6y7y13°y13	2027.99	64.464	2683	3	676.67	7.89
[P41031 CY_SALTY Thiosulfate-binding protein	24		VEEKFGSWPEVMK	307	13	3	18.63	b4b11y11	1565.76	74.811	1730	2	783.38	-4.37
[P41031 CY_SALTY Thiosulfate-binding protein	25		VNNPEIMGKQADK	286	13	12	73.29	b3*b3b4b5b7°b7*b7b10°b10b11°b11y8	1443.71	63.682	1653	2	722.36	-11.33
[P41031 CY_SALTY Thiosulfate-binding protein	26	Phohoryl STY(8)	AYLNWLYQAQTIITHYYR	265	21	5	35.1	b6b7y5y6y10	2744.29	106.195	2866	3	915.44	4.45