

SA123 LC-MS run 2: 123_220709_1a2_02

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	60	384.93	b2°b2b3°b3b4°b4b5°b5b6°b6b7°b7b8°b8b9b10°b10b11°b11b12°b12b13°b13b14°b14b15b17°b17b18b21y1y2y3y4y5y6°y6y7°y7°y7y8y9y10y11°y11y12°y12y13°y13°y13y14°y14y15°y15y16°y16y17°y17°y17y21	2216.10	96.924	623133	2	1108.55	1.10
P0A1S2 HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	11	97.24	b6y2y3y4y6y7y8y9°y9y10y11	1304.56	33.613	96616	2	652.78	-2.15
P0A1S2 HNS_SALTY DNA-binding protein H-NS	3	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	9	56.74	y1y5y6y8°y8y9°y9y10y13	1624.75	92.946	75391	2	812.88	5.94
P0A1S2 HNS_SALTY DNA-binding protein H-NS	4		REEESAAAAEVEER	40	14	6	26.24	b2°b2b6b8y9y11	1575.73	33.410	24733	2	788.37	3.18
P0A1S2 HNS_SALTY DNA-binding protein H-NS	5		LEVVVNER	32	8	10	39.72	y2°y2y3°y3°y3y6y7°y7°y7y8	957.53	42.971	15522	2	479.27	-8.67
P0A1S2 HNS_SALTY DNA-binding protein H-NS	6		MSEALK	0	6	1	13.24	y4	678.35	49.190	10583	1	678.35	-4.23
P0A1S2 HNS_SALTY DNA-binding protein H-NS	7		EEESAAAAEVEER	41	13	9	57.1	b8b10y3°y3y4°y4y9°y9y10	1419.63	35.237	7522	2	710.32	4.82
P0A1S2 HNS_SALTY DNA-binding protein H-NS	8		TPAVIK	114	6	2	29.04	y3y5	628.39	27.654	3061	2	314.70	-13.60
P0A1S2 HNS_SALTY DNA-binding protein H-NS	9		YSYVDENGETKTWTGQGR	96	18	5	51.18	y6y13y14y15y16	2090.93	47.700	191422	3	697.65	-6.07
P0A1S2 HNS_SALTY DNA-binding protein H-NS	10	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEVVVNER	19	21	3	21.7	b12y3y4	2563.28	125.550	1773	2	1282.14	7.62
P0A1H5 EFTU_SALTY Elongation factor Tu	1		AIDKPFLLPIDVFSISGR	205	19	17	127.83	b3b7b8b12y2y3y4y5y6y7y8y9°y9y11y15°y15y19	2117.14	105.632	488503	3	706.39	-9.23
P0A1H5 EFTU_SALTY Elongation factor Tu	2		ELLSQYDFPGDDTPIVR	155	17	32	274.02	b2°b2b3°b3b5°b5b6°b6b8°b8b9b12b13°b13b15b16y1y2y3y4y5y6y8y9°y9y10y11y12y13y14y15y17	1964.96	76.780	342338	2	982.98	1.12
P0A1H5 EFTU_SALTY Elongation factor Tu	3		GITINTSHVEYDTPTR	59	16	29	200.94	b2b3°b3b7b8°b8°b8b10b12b16y3y4y5°y5y6°y6y7°y7y8°y8y9y10y11y12°y12y13y14°y14y16	1803.87	50.218	299637	3	601.96	-11.03
P0A1H5 EFTU_SALTY Elongation factor Tu	4		TTLTAAITTVLAK	25	13	10	65.27	b2°b2b5°b5y1y3y5y6y8y11	1303.78	84.605	292891	2	652.39	-5.99
P0A1H5 EFTU_SALTY Elongation factor Tu	5		IIELAGFLDSYIPEPER	188	17	28	251.23	b2b3b4b5b7b9b11°b11b12°b12b14y2y3y4°y4y5y6y7y8°y8y10°y10y11y12y13y14y15y17	1962.03	102.156	288007	2	981.52	2.80
P0A1H5 EFTU_SALTY Elongation factor Tu	6		AGENVGVLLR	270	10	12	85.76	b4°b4b5°b5y1y2y3y4y5y6y7y10	1027.58	56.842	264393	2	514.29	-13.42

P0A1H5 EFTU_SALTY Elongation factor Tu	7		TTDVTGTIELPEGVEMVMPGDNI K	334	24	40	246.46	b2°b2b3°b3b4°b4b5°b5b10° b10b11b12b13b14b15b17 b18y3y4y5y6°y6°y6y7°y7* y7y8y9°y9y10°y10°y10y12 *y12y14y15°y15y20y24*y2 4	2546.25	86.594	252735	2	1273.63	5.37
P0A1H5 EFTU_SALTY Elongation factor Tu	8		QVGVPIIVFLNK	124	13	10	57.1	b3b4°b4b13y14y5y9y11y 13	1489.88	99.304	227090	2	745.44	0.00
P0A1H5 EFTU_SALTY Elongation factor Tu	9	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	9	66.2	b2°b2b10y3y4y6y7y8y10	1187.51	53.501	113367	2	594.26	-3.50
P0A1H5 EFTU_SALTY Elongation factor Tu	10		ALEGDAEWEAK	177	11	12	84.45	b1b2b3y1y3°y3y4y5y6y8y9 y11	1218.56	47.123	86621	2	609.79	-0.40
P0A1H5 EFTU_SALTY Elongation factor Tu	11	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEV	137	18	16	93.1	b2b3b12b13y2y3°y3y4y5y 7°y7y8°y8y9y14y18	2224.00	106.327	52995	2	1112.50	9.11
P0A1H5 EFTU_SALTY Elongation factor Tu	12		MVVTLIHPIAMDDGLR	358	16	18	174.47	b3b4°b4b5°b5y3y4y5y7y8y 9y10°y10y11y12°y12y13y1 4	1780.92	79.266	740413	3	594.31	-16.52
P0A1H5 EFTU_SALTY Elongation factor Tu	13		TVGAGVVAK	382	9	11	110.16	b3°b3b4b6°b6b7°b7y3y5y7 y8	801.47	29.035	187663	2	401.24	-19.95
P0A1H5 EFTU_SALTY Elongation factor Tu	14		TKPHVNVGTIGHVDHGK	8	17	5	26.18	b6y3y5°y5y6	1795.92	42.971	23404	4	449.74	-20.87
P0A1H5 EFTU_SALTY Elongation factor Tu	15	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	3	17.27	b6b11y7	1768.82	94.896	20382	2	884.91	20.29
P0A1H5 EFTU_SALTY Elongation factor Tu	16		LLDEGR	264	6	4	38.83	b5y3°y3y4	702.38	27.270	15090	1	702.38	-2.78
P0A1H5 EFTU_SALTY Elongation factor Tu	17		NMITGAAQMDGAILVVAATDGP MPQTR	90	27	3	11.52	b9b15y5	2729.29	105.978	10377	3	910.44	-18.25
P0A1H5 EFTU_SALTY Elongation factor Tu	18		GIHK	234	4	1	12.35	y3	430.30	45.735	8641	1	430.30	2.34
P0A1H5 EFTU_SALTY Elongation factor Tu	19		EEIER	284	5	2	25.59	b3y4	675.33	64.776	7224	1	675.33	0.72
P0A1H5 EFTU_SALTY Elongation factor Tu	20		VGEEVEIVGIK	238	11	7	35.27	b3°b3b4°b4b10°b10y4	1171.66	45.671	6585	2	586.34	5.63
P0A1H5 EFTU_SALTY Elongation factor Tu	21		HTPFFK	319	6	2	13.24	y5°y5	776.42	34.410	3503	1	776.42	10.93
P0A1H5 EFTU_SALTY Elongation factor Tu	22		GSALKALEGDAEWEAK	172	16	4	33.82	y7y12y13y15	1674.83	82.435	6384	3	558.95	-2.33
P0A1H5 EFTU_SALTY Elongation factor Tu	23	Oxidation+M(23)	NMITGAAQMDGAILVVAATDGP MPQTREHILLGR	90	34	4	16.62	b3b15°b15b17	3563.76	92.962	2824	3	1188.59	-14.93
P0A1H5 EFTU_SALTY Elongation factor Tu	24	Oxidation+M()	TTDVTGTIELPEGVEMVMPGDNI K	334	24	4	22.5	b3b5b6y13	2562.24	77.616	2423	2	1281.63	4.95
P0A1H5 EFTU_SALTY Elongation factor Tu	25	Oxidation+M(9)	NMITGAAQMDGAILVVAATDGP MPQTR	90	27	6	14.52	b7b15°b15y8°y8y13	2745.37	128.473	2360	3	915.80	13.70
P0A1H5 EFTU_SALTY Elongation factor Tu	26		TGTIELPEGVEMVMPGDNIK	338	20	4	27.38	b8b10b11b18	2130.04	86.555	14869	2	1065.52	-4.93
P0A1H5 EFTU_SALTY Elongation factor Tu	27		TINTSHVEYDTPTR	61	14	6	24.7	b4°b4b10°b10b11°b11	1633.79	50.198	10651	2	817.40	4.48
P0A1H5 EFTU_SALTY Elongation factor Tu	28		TTDVTGTIELPEGVEM	334	16	4	22.49	y3°y3y4y14	1691.78	86.501	5675	3	564.60	-13.85
P0A1H5 EFTU_SALTY Elongation factor Tu	29		TTDVTGTIELPEGVEMVMPGD	334	21	2	8.46	y3°y3	2191.02	86.584	5460	2	1096.01	1.45
P0A1H5 EFTU_SALTY Elongation factor Tu	30		GITINTSHVEYDTPTR	59	16	1	7.27	b13	1785.88	50.183	16301	3	595.96	3.55

P64076 ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	34	239.76	b2*b2b3*b3b4*b4b5b6*b6*b6b7*b7b12b13*b13b14*b14y1y2y3y4y5y6y7y8y9y10y11*y11y12y13*y13y15*y15	1605.88	85.723	533935	2	803.45	-0.30
P64076 ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	40	324.44	b2b3b4b5b8*b8b9*b9b11b12*b12b13*b13b14b15b16°b16b17b18*b18b22y1y2y3y4y5*y5y6y7y8y9y10y11y12y13y14*y14y16y17y22	2118.06	75.285	275171	2	1059.54	3.34
P64076 ENO_SALTY Enolase	3		GMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	200	31	27	172.63	b2b3b4b5*b5b6*b6*b6b13b30y1y2y3y4y5°y5y6y7y8y10y11y14y15y18y19y25y31	2989.46	95.031	200355	3	997.16	2.37
P64076 ENO_SALTY Enolase	4		YSMPVPMMNININGGEHADNNVDIQEFMIQPVGAK	143	34	22	104.21	b2°b2b3°b3b13b14b23y2y3y5y6*y6y7y8y9y10°y10*y10y13y29y31y34	3759.78	98.694	148421	3	1253.93	3.31
P64076 ENO_SALTY Enolase	5		AVGAVNGPIAQAILGK	66	16	10	77.49	b2b3b4b5y3y5y6y7y12y16	1478.87	75.138	147793	2	739.94	-0.58
P64076 ENO_SALTY Enolase	6		GIANSILIK	333	9	5	37.15	y2y3y4y7y9	928.57	61.155	135100	2	464.79	-13.87
P64076 ENO_SALTY Enolase	7		DAGYTAVISHR	360	11	14	98.04	b2°b2b3b4y2y3°y3y4y5y6y7y9°y9y11	1189.59	42.052	121891	2	595.30	-5.03
P64076 ENO_SALTY Enolase	8		IQLVGDDLFVTNTK	311	14	16	102.34	b2b3b4y1y2y4y5y6°y6*y6y9y10y11y12*y12y14	1562.84	77.602	97227	2	781.92	-0.39
P64076 ENO_SALTY Enolase	9		GMPLYEHIAELNGTPGK	126	17	5	26.18	b2b8y3y4y10	1826.90	67.602	81559	3	609.64	-8.42
P64076 ENO_SALTY Enolase	10		QYPIVSIEDGLDESDWDGFAYQTK	282	24	11	37.43	b2b4*b4b9°b9b10b16y6y8y10y24	2776.28	93.746	70553	3	926.10	6.07
P64076 ENO_SALTY Enolase	11		IEEALGEK	411	8	5	39.72	y3y6°y6y7y8	888.46	31.767	35371	2	444.73	-9.07
P64076 ENO_SALTY Enolase	12	Carbamidomethyl+C(16)	AAGYELGKIDITLAMDCAASEFYKDGK	231	26	7	11.72	b2b9b11°b11y1y8y26	2824.32	138.215	9429	3	942.11	1.04
P64076 ENO_SALTY Enolase	13		AAGYELGK	231	8	4	23.91	b1y5y6°y6	808.43	47.079	8613	2	404.72	6.42
P64076 ENO_SALTY Enolase	14		EIDSR	10	6	2	26.03	y3y4	732.40	27.119	36019	1	732.40	8.67
P64076 ENO_SALTY Enolase	15		IMIDLDGTENK	92	11	3	23.27	b6y4y7	1248.62	110.834	15935	2	624.81	2.35
P64076 ENO_SALTY Enolase	16		VIGR	6	4	1	12.35	y3	444.30	50.852	9058	1	444.30	11.26
P64076 ENO_SALTY Enolase	17		EALELR	46	6	1	13.24	b5	730.41	23.394	4161	1	730.41	-4.85
P64076 ENO_SALTY Enolase	18		VLGDKIQLVGDDLFVTNTK	306	19	6	48.32	b4y3y4*y4y5y6	2075.12	80.033	213603	3	692.38	-8.71
P64076 ENO_SALTY Enolase	19		GKGMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	198	33	5	23.57	b7b8b15b17y4	3174.58	90.020	39808	3	1058.86	0.92
P64076 ENO_SALTY Enolase	20		EALELRDGDK	46	10	3	25.84	b3b9y9	1145.57	54.890	8988	2	573.29	-7.57
P64076 ENO_SALTY Enolase	21		QYPIVSIEDGLDESDWDGFAYQTKVLGDK	282	29	3	11.23	b9y6y14	3288.57	58.642	6250	4	822.90	3.04
P64076 ENO_SALTY Enolase	22		GVTKAVGAVNGPIAQAILGK	62	20	3	13.7	b13b17y19	1864.08	136.771	2022	1	1864.08	-13.49
P64076 ENO_SALTY Enolase	23	Oxidation+M(18)	GNPTVEAEVHLEGGFVGMAAAPSGASTGSREALELR	16	36	3	16.55	b4b6b8	3583.78	101.720	4953	3	1195.26	9.95
P64076 ENO_SALTY Enolase	24		GYTAVISHR	362	9	2	18.26	b3b8	1003.53	42.073	65761	2	502.27	-1.95
P64076 ENO_SALTY Enolase	25		ANSILIK	335	7	2	8.55	b4°b4	758.47	61.143	19573	1	758.47	-5.63
P64076 ENO_SALTY Enolase	26		AGYTAVISHR	361	10	2	18.26	b3b6	1074.56	42.025	9562	2	537.79	-5.91
P64076 ENO_SALTY Enolase	27		GMNTAVGDEGGYAPNLGSNAEALAVI	200	26	0	11.57		2491.20	94.993	2349	3	831.07	7.55
P64076 ENO_SALTY Enolase	28		YSMPVPMMNININGGEHA	143	17	3	12.71	y9°y9y13	1860.87	98.745	2115	3	620.96	13.32
P64076 ENO_SALTY Enolase	29		DAGYTAVISHR	360	11	1	7.68	b9	1171.58	42.029	4176	3	391.20	-0.94
POA297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	16	123.05	b2b3°b3b4b13y1y4y6y7y8y9°y9y10y11y12y13	1447.78	65.330	137919	2	724.39	-1.26

P0A297 RL10_SALTY 50S ribosomal protein L10	2		AAAFEGELIPASQIDR	109	16	17	144.99	b4b5°b5b8b9b12y5°y5y6y7y8y9y10y11y12°y12y16	1687.87	68.847	92979	2	844.44	3.11
P0A297 RL10_SALTY 50S ribosomal protein L10	3		GALSAVVADSR	20	11	7	68.64	b10y2y3y4y5y6y8	1045.56	49.257	68933	2	523.28	-3.85
P0A297 RL10_SALTY 50S ribosomal protein L10	4		TLAAVRDAKEAA	153	12	7	25.26	b6y1y8°y8y9°y9y12	1215.66	33.537	10142	2	608.33	-7.73
P0A297 RL10_SALTY 50S ribosomal protein L10	5		DTFVGPTLIAYSMEHPGAAAR	73	21	6	28.28	b4b5°b5b8y10y12	2204.10	82.608	9432	3	735.37	9.19
P0A297 RL10_SALTY 50S ribosomal protein L10	6		TLAAVR	153	6	1	13.24	b4	630.38	27.409	4423	1	630.38	-15.10
P0A297 RL10_SALTY 50S ribosomal protein L10	7	Carbamidomethyl+C(9)	VVEGTQFECLKDFTVGPTLIAYSM EHPGAAAR	62	32	4	21.09	b8y12y13y16	3494.68	92.397	51895	4	874.43	-7.54
P0A297 RL10_SALTY 50S ribosomal protein L10	8		AAAFEGELIPASQIDRLATLPTYEE AIAR	109	29	6	23.08	b10°b10y4y6y9y11	3116.62	93.017	44195	3	1039.55	-1.80
P0A297 RL10_SALTY 50S ribosomal protein L10	9		GVTVDKMTCLR	31	11	3	23.27	b5b9y5	1248.64	59.552	19975	2	624.83	-13.49
P0A297 RL10_SALTY 50S ribosomal protein L10	10		FEVKAAAFEGELIPASQIDR	105	20	5	21.53	b10°b10y7y9y13	2191.12	85.003	14954	3	731.05	-8.36
P0A297 RL10_SALTY 50S ribosomal protein L10	11		EFAKANAK	97	8	4	47.74	b5b6b7y5	878.48	36.901	8475	2	439.74	3.96
P0A1D5 CH10_SALTY 10 kDa chaperonin	1		ILDNGTVQPLDVK	47	13	32	221.06	b2b3b5°b5b6b7°b7°b7b8°b8b10b11°b11°b11b12°b12b13y1y2y3y4y5y7y8y9y10y11°y11°y11y12°y12y13	1411.78	57.723	343160	2	706.39	-2.85
P0A1D5 CH10_SALTY 10 kDa chaperonin	2		VGDIVIFNDGYGVK	60	14	24	181.15	b3b4°b4b5°b5b11°b11°b11b13°b13y1y2y3y4y5y6°y6y7y8y9y10y11y12y14	1495.78	73.542	305745	2	748.39	-0.73
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	20	149.76	b2°b2b3°b3b4b5°b5b6b14y2y3y4y6y7y8°y8y9y11y12y14	1188.65	44.201	202581	2	594.83	-6.06
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIAVGK	37	8	8	60.54	b2b3y2y3y4y5y6y8	786.47	42.124	43393	1	786.47	-5.98
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		IDNEEVLIMSESILAIVEA	77	20	8	44.73	b4°b4b9°b9b10b11b15y11	2203.08	70.643	12484	3	735.03	-10.75
P0A1D5 CH10_SALTY 10 kDa chaperonin	6		SEKIDNEEVLIMSESILAIVEA	74	23	5	19.15	b9y4y10y12°y12	2547.24	136.279	5136	2	1274.12	-14.66
P0A1D5 CH10_SALTY 10 kDa chaperonin	7		SAGGIVLTGSAAGK	20	14	0	4		1170.64	44.193	29305	2	585.82	-3.65
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		VFMQPASEGTHIAGGAMR	93	19	24	246.34	b2b3b4b6b10b11b12b13b14b15b18y4y5y6y7y9y10y11y12y13y15°y15y17y19	1892.94	68.230	272976	2	946.97	2.58
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		AYGSTNPINVVR	126	12	19	130.84	b2b3b4°b4b6°b6y2y3y4°y4y5y6y7y8y9°y9°y9y10y12	1290.68	51.706	265280	2	645.84	-2.84
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		ATIDGLENMNSPEMVAAGR	138	19	17	153.31	b2b13y3y4y5y6y8y9y10y11°y11°y11y12°y12y13y16y17	2046.98	59.378	147952	3	683.00	-9.24
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVAAG	138	18	22	172.22	b2b4b8b11b14b15b16y2y3y4y5y7y10y11y12°y12°y12y13y14y15y18°y18	1890.90	63.501	135820	2	945.95	3.62
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		SVEEILGK	159	8	4	34.95	b4y3y6y8	874.48	50.996	94063	2	437.74	-12.14
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		VGFGYGK	45	7	6	39.27	b1y2y3y4y6y7	727.37	40.645	59236	2	364.19	-14.10

P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		IFSFTALTVVGDGNR	29	16	5	38.59	y6y7y8y12y16	1653.86	86.433	49276	2	827.43	-1.48
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		AVLEVAGVHNVLAK	112	14	9	76.82	b3b4°b4b5b11y6y8y9y10	1419.80	61.025	259126	3	473.94	-21.92
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		LIAVNR	14	6	5	38.83	y3*y3y4y5*y5	685.43	33.557	27616	1	685.43	-2.40
P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		NMINVALNNGTLQHPVK	69	17	3	15.53	b7b10y10	1862.97	63.382	24696	3	621.66	-9.44
P0A7W4 RS5_SALTY 30S ribosomal protein S5	11		IFSFTALTVVGDGNRGVFGYGK	29	23	5	16.51	b6b15°b15y3y5	2362.20	94.919	2271	2	1181.60	-8.68
P0A7W4 RS5_SALTY 30S ribosomal protein S5	12	Oxidation+M(18)	VFMQPASEGTGIIAGGAMR	93	19	3	14.23	b4b6y15	1908.94	61.861	4635	2	954.97	2.81
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VVGQLGQVLGPR	122	12	12	110.48	b2b4b5y3y4y6y7y8y9y10*y10y12	1222.72	59.490	188334	2	611.86	-6.39
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VAVFTQGPNAEAAK	74	14	17	106.6	b3y2y3y4y7y8°y8y9°y9*y9y10*y10y11°y11*y11y12y14	1402.73	45.816	178013	2	701.87	0.00
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VGTVTPNVAEAVK	141	13	20	142.32	b2b3°b3b4°b4b12y3y4°y4y5y7y8y9y10y11°y11y12°y12*y12y13	1284.71	48.554	171341	2	642.86	-3.52
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		QYDINEAIALLK	19	12	6	48.27	b12y3y4y5y6y12	1390.76	85.361	65339	2	695.88	0.88
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		GATVLPHTGR	60	11	5	49.08	y4y5y6y7y11	1065.57	30.545	39665	2	533.29	-5.73
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		AAGAELVGMEDLADQIK	88	17	10	65.11	b3b6b7b9y4y9y10°y10y11y17	1730.87	79.757	36925	2	865.94	2.47
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		GEMNFDVVIASPDAMR	106	16	12	83.69	b2b3b10b12°b12b13b14b15y4y12y13°y13	1751.80	71.872	15047	3	584.60	-7.46
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		VSISTTMGAGVAVDQAGLSASAN	211	23	3	18.91	b11b13b17	2107.01	74.693	3638	3	703.01	-12.98
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9		FNESVDVAVNLGIDAR	37	16	5	33.76	b7b8b12y4y7	1718.88	136.280	2057	2	859.94	3.34
P0A2A3 RL1_SALTY 50S ribosomal protein L1	10		KVSISTTMGAGVAVDQAGLSASAN	210	24	6	54.84	y5y11y13y14y15y16	2235.13	70.470	2024	3	745.72	2.40
P0A2A3 RL1_SALTY 50S ribosomal protein L1	11		TVLPHGTGR	62	9	0	2.67		937.51	30.543	32200	2	469.26	-7.75
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	1		SGFAEDEVVAVSK	35	13	11	54.09	b2b3b5y1y2°y2y3y8y9y10y13	1337.65	54.839	220468	2	669.33	-5.29
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	2		MITGIQITK	0	9	10	76.79	b1b3b4y2y3y4*y4y6y7y9	1004.57	55.443	219103	2	502.79	-11.85
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	3		FNSLTPEQQR	106	10	16	84.8	b2*b2b3°b3b10y3*y3y4y5*y5y6y7y8°y8y10*y10	1219.60	38.686	151403	2	610.30	-5.50
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	4		EIPMEVKPEVR	55	11	13	76.67	b2°b2b4b9b10y1y2y4y6y8°y8y9y11	1326.71	49.292	148498	2	663.86	-1.93
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	5		LGEIEYR	48	7	10	49.06	b2b3y1y2y3°y3y5y6°y6y7	879.45	42.918	141756	2	440.23	-12.77
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	6		FNSLTPEQQRDVIIAR	106	15	14	76.47	b2*b2b3°b3b5y1y3y4y6y7y10*y10y13y15	1773.90	48.087	82310	3	591.97	-11.29
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	7		VSGYAVR	99	7	4	36.26	b4b5y2y4	751.40	27.329	22847	2	376.20	-13.73
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	8		VEGGQHNLNVNLRR	66	14	7	40.41	b1b5b7b8b9°b9y2	1590.88	47.171	13296	2	795.95	0.46
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	9		VEGGQHNLNVNLRLR	66	13	8	69.11	b4b7y3y4*y4y6y7y8	1434.76	50.931	125968	3	478.92	-15.48
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor	10		TFTESL	121	6	7	51.62	b3°b3b4°b4b5y4°y4	697.34	55.874	82893	1	697.34	-3.15

Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	11		AANDDLLNSFWLLDSEKGEAR	9	21	29	265.01	b3b4b5°b5°b5b6°b6°b6b7°b7y3y4y5y7y8°y8y9°y9y10y11y12y13y14y15y16y17y18y19°y19	2364.13	92.760	495123	3	788.72	-5.99
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	12	Carbamidomethyl+C(1)	CIVAKSGFAEDEVVAVSK	30	18	4	27.97	b8b11y12y13	1908.96	64.679	1817	2	954.98	-6.91
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	13		PMEVKPEVR	57	9	3	30.26	b3b4b7	1084.58	49.317	137108	2	542.79	-5.63
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	14		EGGQHLNVNVLRR	67	13	3	15.12	b3b11°b11	1491.79	47.178	18786	3	497.94	-14.24
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	15		EIPMEVKPEVR	55	11	0	2.67		1308.68	49.336	40296	3	436.90	-10.63
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	16		MITGIQITK	0	9	0	1.78		986.55	55.373	2715	2	493.78	-15.10
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		LADVLAANAR	57	11	17	124.59	b2b3b4b5y1y3°y3y4°y4y5°y5y6°y6y7y8y9y11	1084.60	53.847	206214	2	542.80	-12.27
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGS LGDQVNVK	8	14	18	152.55	b2b3b4b10b13y3y4y6y7°y7y8y9°y9y10°y10y11y12y14	1413.76	56.967	193678	2	707.39	-3.54
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		DIADAVTAAGVDVAK	97	15	13	151.75	b3b4b5b6b9b10y4y6y7y8y9y11y13	1415.74	66.351	118189	2	708.37	1.72
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		LFGSIGTRDIADAVTAAGVDVAK	89	23	3	8.49	b17°b17y18	2247.19	95.037	4185	3	749.74	-3.26
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		INALETVTIASK	71	12	3	25.26	b3y10y11	1259.71	61.390	64635	2	630.36	-5.04
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		TTGEHEVNFQVHSEVFAK	123	18	6	14.83	b10°b10b13°b13y6°y6	2058.97	72.068	3907	4	515.50	-10.32
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		AGDEGKLFGSIGTR	83	14	3	23.81	b9y7y8	1407.70	55.469	93108	3	469.91	-13.70
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	8		IGTRDIADAVTAAGVDVAK	93	19	2	21.29	b4b5	1842.99	94.936	40397	2	922.00	1.52
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	1		IAAANVPAFVSGK	70	13	24	175.69	b2b3b4b5°b5b6°b6y1y2y3°y3y4y5y6y7°y7y8y9y10y11°y11y12°y12y13	1244.69	59.797	1106778	2	622.85	-6.87
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVG FGTFK	22	29	15	92.76	b2b3b4°b4b5b7b9b10b13y3y4y6°y6y7y8	2966.57	115.951	338055	3	989.53	-1.98
P00499 HIS1_SALTY ATP phohoribosyltransferase	1		LIAMAENMPIDILR	38	14	15	136.75	b3b8b11b12y2y3y4y6y8y9y10y11y12°y12y14	1599.86	90.645	105090	2	800.43	1.07
P00499 HIS1_SALTY ATP phohoribosyltransferase	2		LSLATPVDEAWDGPAALDGKR	105	21	10	51.67	b14y2y3y4°y4y10y11y13y16y21	2182.10	76.219	101479	3	728.04	-5.26
P00499 HIS1_SALTY ATP phohoribosyltransferase	3	Carbamidomethyl+C(8)	AGLADAICDLVSTGATLEANGLRE VEVYR	160	30	25	167.53	b3b4b5°b5b6°b6b7°b7b9b10°b10b11y3y5y12°y12y13y14y15y17y19y23y26y30°y30	3176.63	136.526	84662	3	1059.55	1.54
P00499 HIS1_SALTY ATP phohoribosyltransferase	4		ALGASSILVLPIEK	282	14	14	109.4	b2b3b5°b5b7°b7b9y4y5y6y7y8y12y14	1410.86	84.495	71099	2	705.93	0.43
P00499 HIS1_SALTY ATP phohoribosyltransferase	5		IQGVIQAR	216	8	5	31.94	b2b3°b3b4y6	884.52	45.743	52678	2	442.77	-9.66
P00499 HIS1_SALTY ATP phohoribosyltransferase	6		YIMMHAPSER	227	10	4	27.6	b3y5y6y10	1234.58	65.547	34307	2	617.79	9.39
P00499 HIS1_SALTY ATP phohoribosyltransferase	7		LEEVIALLPGAERPTILPLAGEQQR	237	25	11	39.78	b1b2°b2b3b4°b4y5y6y17y19y25	2713.50	90.048	30895	3	905.17	-7.29
P00499 HIS1_SALTY ATP phohoribosyltransferase	8		LSLATPVDEAWDGPAALDGK	105	20	4	20.49	b2y8y11y14	2026.02	85.480	4735	3	676.01	4.22

P00499 HIS1_SALTY ATP phohoribosyltransferase	9		ELLAR	22	5	2	25.59	b3b4	601.36	29.024	87945	1	601.36	-8.93
P00499 HIS1_SALTY ATP phohoribosyltransferase	10		VAMHMOVSETLFWETMEK	262	18	5	36.79	b4b6b10y7y8	2156.03	75.304	87159	3	719.35	22.31
P00499 HIS1_SALTY ATP phohoribosyltransferase	11	Carbamidomethyl+C(2)	SCLLNGSVEVAPR	147	13	4	19.69	b10°b10y4y10	1401.70	37.381	5773	2	701.35	-11.58
P00499 HIS1_SALTY ATP phohoribosyltransferase	12	Carbamidomethyl+C(2)	ACLIQR	192	6	1	13.24	b3	760.41	30.250	4862	1	760.41	-0.96
P00499 HIS1_SALTY ATP phohoribosyltransferase	13		AQGEDPR	85	7	4	36.26	b3b4y5°y5	772.37	64.703	3332	1	772.37	12.01
P00499 HIS1_SALTY ATP phohoribosyltransferase	14	Carbamidomethyl+C(6)	LDFGGCRLSLATPVDEAWDGPAALDGK	98	27	7	34.96	b7b10b11°b11y10y12y13	2831.38	76.272	41480	3	944.47	4.83
P00499 HIS1_SALTY ATP phohoribosyltransferase	15		ESKYIMMHAPSER	224	13	7	39.54	b5b11y5°y5y9y10°y10	1578.75	90.115	5100	3	526.92	3.71
P00499 HIS1_SALTY ATP phohoribosyltransferase	16	Carbamidomethyl+C(2); Carbamidomethyl+C(21)	SCLLNGSVEVAPRAGLADAICDLVSTGATLEANGLR	147	36	3	10.87	b12b14y6	3670.89	137.668	2706	3	1224.30	11.31
P00499 HIS1_SALTY ATP phohoribosyltransferase	17	Carbamidomethyl+C(2); Oxidation+M(10)	ACLIQRDGEMAQSK	192	14	3	26.15	b3b12b13	1622.76	136.662	10690	1	1622.76	-3.61
P00499 HIS1_SALTY ATP phohoribosyltransferase	18		PLAGEQQR	254	8	0	8.9		898.46	90.006	8547	1	898.46	-13.25
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	47	316.55	b2b3°b3b4°b4°b4b5°b5b6°b6b7°b7°b7y1y3y4y5y6y7°y7°y7y8°y8°y8y9°y9y10°y10y11y12°y12y13y14y15°y15°y15y16°y16y17y18y19y20y21y22°y22y24°y24	2574.32	98.194	937740	3	858.78	-0.09
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	2		AGIALNDNFVK	296	11	18	107.03	b3b4b10°b10y1y2y3y4°y4y5°y5y6°y6y7°y7y8y11°y11	1161.62	61.719	444969	2	581.31	-9.14
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	3		LVSWYDNETGYSNK	307	14	12	96.9	b9b11y2y3°y3y5y6y9y10y11y12y14	1675.77	58.719	238883	2	838.39	3.06
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		AATYEQIK	249	8	12	62.3	b6b7°b7b8y2y4°y4y5y6°y6y8°y8	923.47	31.627	179980	2	462.24	-11.10
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		SDIEIVAINDLLDAEYMAYMLK	24	22	19	129.1	b2b3b4°b4b5b6b7°b7b8y1y2y3y4y5y6y7y12°y12y22	2530.24	127.092	164833	3	844.08	-2.99
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		GASQNIIPSSTGAAK	198	15	12	99.26	b6b7°b7y2y4y5y7y8y9y10y11y15	1401.73	41.375	128082	2	701.37	-3.22
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		VPTPNVSVVDLTVR	232	14	12	114.47	b3b5y2y4y5y6y7y8y9y11y12y14	1495.85	71.024	113214	2	748.43	1.06
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		VVLTGPSKDNTPMFVK	116	16	7	36.2	b2b3y5y7y13y14y16	1732.91	58.024	90076	3	578.31	-14.51
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		VLPELNGK	217	8	7	39.72	b2y3°y3y4°y4y6y8	869.50	45.365	65174	2	435.25	-12.21
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		TVDGPSHKDWR	184	11	6	50.62	b3b7b9y4y9°y9	1297.61	30.209	31590	3	433.21	-14.77

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11		IVFR	15	4	1	12.35	y3	534.34	38.299	11453	1	534.34	-8.00
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12		LTGMAFR	225	7	8	77.66	b3b5b6°b6y4y5y6°y6	795.40	101.639	5150	1	795.40	-18.95
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13	Carbamidomethyl+C(20)	GVLGYTEDDVVSTDFNGEVCTSV FDAK	269	27	3	22.37	b8b12b13	2924.35	94.752	4220	4	731.84	11.60
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEGQDIVSNASCTTNCL APLAK	132	28	39	306.27	b3b4b5°b5b8°b8b10°b10b11°b11°b11b12°b12b13°b13b15b16b17b23b24°b24b26b27y3y4y5y6y8y9y10y11y12°y12y13°y13y14y15°y15y16	3044.41	66.948	400967	3	1015.47	-0.56
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15		LTGMAFRVPTPNVSVVDLTVR	225	21	3	19.89	b4b7b16	2272.22	86.678	43621	3	758.08	-10.85
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		GGRGASQNIIPSSTGAAK	195	18	6	48.62	b6b7b8b9y8°y8	1671.89	37.370	17428	2	836.45	5.62
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		TVDGPSHKDWR	184	11	3	23.27	b9y4y9	1297.62	71.852	12344	2	649.32	-2.82
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		DGPSHKDWR	186	9	0	2.67		1097.52	30.244	9439	2	549.26	9.01
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19		LTGPSKDNTPMFVK	118	14	2	7.27	b9°b9	1534.78	58.031	7233	2	767.89	-9.62
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20		AATYEQIK	249	8	0	1.33		905.46	31.619	65740	2	453.23	-8.43
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	21		VVLTGPSKDNTPMFVK	116	16	0	4.89		1715.89	57.966	3488	3	572.63	-6.54
P0AA28 THIO_SALTY Thioredoxin-1	1		LNIDQNPGTAPK	58	12	29	158.65	b2°b2b4°b4°b4b6°b6°b6b7b10y1y2y3y4y5y6°y6y7y8°y8°y8y9°y9y10°y10°y10y11°y11y12	1267.66	39.119	204468	2	634.34	-0.96
P0AA28 THIO_SALTY Thioredoxin-1	2		MIAPILDEIADEYQGK	37	16	21	165.44	b2b3b12b13y2y3°y3y4y5y6°y6y7y8°y8y10y11°y11y12y13y14y16	1805.90	93.680	158401	2	903.46	2.10
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLFK	74	9	9	65.75	b2y1y2y3y4y5y6y7y9	1001.63	91.037	140409	2	501.32	-12.49
P0AA28 THIO_SALTY Thioredoxin-1	4		MIAPILDEIADEYQGKLTVAK	37	21	13	105.8	b3b4b11y4y5y7y11y12°y12y13y16y18y19	2318.22	94.870	221135	3	773.41	-3.90
P0AA28 THIO_SALTY Thioredoxin-1	5		GQLKEFLDANLA	97	12	4	21.29	b5b10°b10y7	1318.69	49.337	4618	2	659.85	-11.11
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	42	243.13	b2°b2b3°b3b4°b4b5b7°b7b8°b8b9°b9°b9b10°b10b11°b11b12°b12b13°b13b14b16°b16b17y1y2°y2y4y6°y6°y6y7y8y9y10y11y12y17°y17y23	2379.23	64.722	220979	3	793.75	-4.31

Q8ZP65 TPX_SALTY Probable thiol peroxidase	2		AQAFTLVAK	24	9	11	76.79	b2*b2b3b5y1y2y3y4y6y7y9	948.54	53.835	118427	2	474.77	-13.58
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	10	71.13	b2b3b4b14b15y4y6y13y15y17	1837.96	86.156	116083	2	919.48	4.18
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	13	77.38	b3b4b5*b5b15y2y3y10y12y13*y13y14y18	1919.01	85.234	112877	2	960.01	3.63
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		DLSDVSLSQYAGK	33	13	15	94.91	b4b5b6b8y3y5*y5y6*y6y7*y7y11*y11*y11y13	1382.68	59.553	74612	2	691.84	-0.44
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		NYGVEIVDGPLK	116	12	6	35.84	b2b3y4y8y10y12	1303.69	65.145	44180	2	652.35	-2.53
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7		DLSDVSLSQYAGKR	33	14	9	64.32	b7b12*b12y5y6y7y9*y9y12	1538.76	55.283	16229	3	513.59	-12.38
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8	Carbamidomethyl+C(15)	FNQLATEVENTVVL CVSADLPFAQSR	67	26	8	25.19	b9*b9b13y10y13*y13y14*y14	2908.43	104.939	3124	4	727.86	-5.79
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9		AVIVLDENDNVIFS QLVDEITHEPDYDAALNVLKA	133	35	21	137.12	b3b4b5b10*b10b11*b11b14y3y4y5*y5y6y12y13y18y22y24y29y30y31	3882.96	120.707	153490	3	1294.99	-0.57
Q8ZP65 TPX_SALTY Probable thiol peroxidase	10	Carbamidomethyl+C(16)	KFNQLATEVENTVVL CVSADLPFAQSR	66	27	11	51.27	b4b8*b8y5y8*y8y9*y9*y9y10y11	3036.59	136.264	41203	4	759.90	12.94
Q8ZP65 TPX_SALTY Probable thiol peroxidase	11		DLSDVSLSQYAGKR	33	14	3	18.37	b4b9y4	1538.77	47.282	9594	2	769.89	-3.97
Q8ZP65 TPX_SALTY Probable thiol peroxidase	12	Phosphoryl STY(13)	MSQTVHFQGNPVTVANVIPQAGSK	0	24	9	41.41	b11b12_H3PO4b12b15y5*y5y12*y12y16y17	2590.21	86.618	55472	3	864.08	-9.71
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	9	78.65	b2b3b4y7y8y9y10y11y13	1365.68	63.351	97181	2	683.35	-0.18
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2	Carbamidomethyl+C(13)	AAQYVAAHGPEVCPAK	153	16	17	138.97	b3b4b8b10*b10b13y2y3y4y6y7y8y9*y9y11y12y16	1668.79	35.971	83839	3	556.94	-13.68
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		ATFVVDPPQGIQAEIVTAEGIGR	120	23	18	100.23	b2b3*b3b5*b5b7b9y2y3y4y5*y5y7y8y9*y9y10y12	2384.28	129.220	52539	3	795.43	-2.25
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		NFDNMREDEGLADR	106	14	4	43.42	y4y5y7y8	1681.71	48.633	42962	3	561.24	-7.84
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		LGVDVYSVSTDTHTFHK	63	17	7	40.69	b2b3b8y7y9y10y12	1905.92	58.397	9966	3	635.98	-7.94
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6	Carbamidomethyl+C(15)	WSVFFFPADFTFVCPTELGDVA DHYEELQK	32	31	3	11.03	b11y7y13	3757.76	95.824	7972	5	752.36	11.30
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7		EGEATLAPSLDLVGK	171	15	3	25.35	b4b6b13	1499.77	48.423	5288	2	750.39	-16.69
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8		NGEFIEVTEK	17	10	3	27.6	b8b9y9	1165.59	33.609	3865	2	583.30	10.79
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9	Carbamidomethyl+C(10)	YVAAHPGEVCPAK	156	13	3	24.03	b3b5b12	1398.69	36.009	2866	2	699.85	4.97
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10	Carbamidomethyl+C(11)	QYVAAHPGEVCPAK	155	14	3	13.95	b9b11*b11	1526.75	35.997	1587	2	763.88	7.92
P65702 PGK_SALTY Phohoglycerate kinase	1		VLPAVAMLEER	373	11	12	84.45	b2b3y1y2*y2y3y5y6y7y8y9y11	1227.67	80.170	229359	2	614.34	-6.16
P65702 PGK_SALTY Phohoglycerate kinase	2	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	20	161.14	b2b3b4b5b7b8b9b12y1y2y3y4y5y6y8y9y12y13y15y20	2002.04	99.276	198660	2	1001.52	5.12
P65702 PGK_SALTY Phohoglycerate kinase	3		SVNDVKEDEQILDIGDASAQQLAE ILK	272	27	11	51.27	b1b11b15y1y2y3y4y12y13y14y27	2941.50	100.977	164038	3	981.17	-0.42
P65702 PGK_SALTY Phohoglycerate kinase	4	Carbamidomethyl+C(5)	LLTTCIDIPVPTDVR	244	14	20	155.56	b2b5*b5b6*b6b7*b7b9b12y1y2y3y5y7y8y9y10y11y12y14	1599.84	68.697	151118	2	800.42	0.15

P65702 PGK_SALTY Phohoglycerate kinase	5		VATEFSETAPATLK	258	14	19	125.5	b1b2b3°b3b4°b4b9y5°y5y6y7y9°y9y10y11°y11y12y13y14	1464.76	53.052	125274	2	732.88	0.08
P65702 PGK_SALTY Phohoglycerate kinase	6		VMVTSHLGRPTEGEYNEEFSLLPV VNYLK	53	29	8	21.41	b1b2b12b13b22y1y2y7	3321.65	92.915	105862	4	831.17	-10.14
P65702 PGK_SALTY Phohoglycerate kinase	7		ADLNVPVKEGK	19	11	8	50.62	b5b9y2y4°y4y6y8y11	1169.65	37.541	104138	2	585.33	-3.24
P65702 PGK_SALTY Phohoglycerate kinase	8		TILWNGPVGVFEPNFR	302	17	15	99.7	b2b13y4*y4y5y6°y6*y6y7y11y12°y12y13y14y17	1993.04	106.792	100968	2	997.02	4.10
P65702 PGK_SALTY Phohoglycerate kinase	9		IADQLIVGGGIANTFVAAQGHSVG K	206	25	4	11.94	b2b3b5y19	2423.29	78.188	49279	3	808.43	-5.74
P65702 PGK_SALTY Phohoglycerate kinase	10		MTDLDLAGKR	5	10	6	59.21	b4y4y5y7y9y10	1119.57	43.594	41239	2	560.29	-7.85
P65702 PGK_SALTY Phohoglycerate kinase	11		AQASTHGIGK	146	10	12	84	b2*b2b3b7y1y2y3y4y5y7y8y10	969.50	16.299	25704	2	485.25	-9.82
P65702 PGK_SALTY Phohoglycerate kinase	12	Carbamidomethyl+C(5)	YAALCDVFVMDAFGTAHR	128	18	6	20.57	b2b9b13°b13y9y11	2043.94	90.216	16205	3	681.99	0.66
P65702 PGK_SALTY Phohoglycerate kinase	13		SLYEADLVDEAKR	231	13	9	28.29	b2b8b12b13°b13y5y12°y12y13	1508.75	81.680	10161	3	503.59	-4.85
P65702 PGK_SALTY Phohoglycerate kinase	14		LVKDYLDGVDVAEGELVVLENV R	90	23	4	25.55	b14b16y4y5	2544.35	98.179	3383	2	1272.68	-0.38
P65702 PGK_SALTY Phohoglycerate kinase	15		ISYISTGGGAFLEFVEGK	355	18	3	21.99	b3b5b10	1874.93	80.615	2223	2	937.97	-12.57
P65702 PGK_SALTY Phohoglycerate kinase	16		LTVLDSLK	197	9	3	37.15	y4y5y6	975.56	62.306	98324	2	488.28	-12.39
P65702 PGK_SALTY Phohoglycerate kinase	17		DYLDGVDVAEGELVVLENVR	93	20	4	13.7	b6°b6y5y12	2204.12	100.550	4096	2	1102.56	4.98
P65702 PGK_SALTY Phohoglycerate kinase	18		SLYEADLVDEAK	231	12	4	25.26	b3°b3y3y4	1352.63	60.895	2170	3	451.55	-18.86
P65702 PGK_SALTY Phohoglycerate kinase	19		EGKVTSDAR	27	9	7	59.73	b3°b3y3°y3y4y5y8	962.48	136.302	2192	1	962.48	-13.19
P65702 PGK_SALTY Phohoglycerate kinase	20	Carbamidomethyl+C(6)	KYAALCDVFVMDAFGTAHR	127	19	3	22.01	b13y8y9	2172.05	78.563	1711	3	724.69	6.74
P65702 PGK_SALTY Phohoglycerate kinase	21		ISYISTGGGAFLEFV	355	15	1	7.44	y10	1560.81	80.696	19572	2	780.91	7.43
P65702 PGK_SALTY Phohoglycerate kinase	22		TDLDLAGKR	6	9	0	2.22		988.54	43.565	15803	2	494.77	-6.73
P65702 PGK_SALTY Phohoglycerate kinase	23		DLNVPVKEGK	20	10	2	18.26	b3b6	1098.60	37.482	15329	2	549.81	-9.56
P65702 PGK_SALTY Phohoglycerate kinase	24		PAVAMLEER	375	9	2	18.26	b3b5	1015.51	80.202	12457	2	508.26	-10.76
P65702 PGK_SALTY Phohoglycerate kinase	25		LNVPVKEGK	21	9	0	2.67		983.58	37.460	11589	2	492.30	-4.78
P65702 PGK_SALTY Phohoglycerate kinase	26		ISYISTGG	355	8	0	5.78		797.40	80.715	7017	1	797.40	-9.72
P65702 PGK_SALTY Phohoglycerate kinase	27		SLYEADL	231	7	1	7.32	y4	810.39	81.590	2493	1	810.39	6.18
P65702 PGK_SALTY Phohoglycerate kinase	28		QASTHGIGK	147	9	5	50.39	b4b5b6b8*b8	898.46	16.314	2260	2	449.74	-12.02
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	1		AESFTTTNR	1	9	11	72.53	b2b3b4b7b9y5y6y7°y7*y7y9	1026.48	28.251	18586	2	513.75	-2.02
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	2		HGHAFNDLDLKG	37	12	4	25.26	b1b5b6y6	1323.66	27.320	3080	2	662.33	10.61
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	3		GEREPVTD AER	65	11	3	26.28	b3y4y5	1258.60	23.089	1982	2	629.80	-5.04
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	4		EPVTD AER	68	8	3	39.72	b3b4b7	916.43	65.268	4506	1	916.43	-8.13

Q7CPD8 YIFE_SALTY UPF0438 protein yifE	5		GFSR	19	4	1	12.35	y3	466.25	19.349	3357	1	466.25	10.21
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	6		YFDNKHYP	10	9	4	29.37	b5y4y7°y7	1239.61	35.158	7329	3	413.87	13.79
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	7		HYPRGFSR	15	8	5	46.49	b5b6y3y4°y4	1019.51	35.181	2330	2	510.26	-2.33
Q7CPD8 YIFE_SALTY UPF0438 protein yifE	8		GHAFNDLGLK	38	11	0	3.11		1186.60	27.236	5868	3	396.21	13.89
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	14	62.64	b2°b2b4°b4b13°b13y1y3y1l*y1l1y12y13y15y17	2130.15	93.020	402408	3	710.72	-10.54
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	2		VGDVPVIEFDLPLEEK	115	16	17	155.44	b2b3b4b5b6b7b8b10°b10b11y4y6y9y10y11y13y16	1812.97	99.775	142685	2	906.99	3.70
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	3		MVAPVDGTIGK	59	11	9	79.44	b2y2y3y5y6y8y9y10y11	1087.57	46.815	129217	2	544.29	-9.54
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	4		LSGSVTVGETPVIR	152	14	4	23.81	b4y7y8y14	1414.79	55.818	20257	2	707.90	-0.52
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	5		IFETNHAFSIESDSGIELFVHFGIDTVELK	70	30	5	15.84	b3b6b13°b13y6	3394.74	126.244	3926	3	1132.25	16.04
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	6		IAEEGQR	106	7	5	36.26	b4°b4y3y4*y4	802.40	71.981	2194	1	802.40	-0.91
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	7		VKVGDPVIEFDLPLEEK	113	18	4	20.57	b5b11y6y14	2040.11	96.018	143577	3	680.71	-6.46
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	8		IVGDGIAIKPTGNKMVAPVDGTIGK	45	25	3	11.94	b3b12y15	2451.33	84.829	2419	3	817.78	-11.95
P0A1E3 CYSK_SALTY Cysteine synthase A	1		IQGIGAGFIPGNLDLK	226	16	16	86.7	b2*b2b3b4b8y1y2y3y6y7°y7*y7y10y12y14y16	1612.91	83.462	118307	2	806.96	2.88
P0A1E3 CYSK_SALTY Cysteine synthase A	2		YLSTALFADLFTEKELQQ	305	18	10	41.72	b2b6b16b17y2*y2y7y8y11y18	2117.09	102.728	114730	2	1059.05	3.46
P0A1E3 CYSK_SALTY Cysteine synthase A	3		LTLTMPETMSIER	87	13	12	92.69	b8°b8b9°b9y4y5y6y8y9°y9y10y13	1521.76	73.942	103634	2	761.39	-1.28
P0A1E3 CYSK_SALTY Cysteine synthase A	4		YLLQQFSNPANPEIHEK	137	18	11	71.11	b2b3b4y3y4y7°y7y9y11y12y18	2141.09	74.188	102108	3	714.37	-5.13
P0A1E3 CYSK_SALTY Cysteine synthase A	5		GVLKPGVELVEPTSGNTGIALAYVAAAR	56	28	6	26.07	b2y1y4y6y7y9	2753.52	81.676	88394	3	918.51	0.18
P0A1E3 CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	10	80.12	b2b3b4y6y7°y7y8y9y10y12	1283.73	64.277	47257	2	642.37	-4.56
P0A1E3 CYSK_SALTY Cysteine synthase A	7		AEEIVASDPQK	126	11	13	91.22	b2°b2b3b4°b4b6y2y3y5y6y7y8y11	1186.59	32.053	39810	2	593.80	-1.85
P0A1E3 CYSK_SALTY Cysteine synthase A	8		VVGITNEEAISTAR	246	14	3	18.37	b7b10y4	1459.78	49.942	22947	2	730.40	6.44
P0A1E3 CYSK_SALTY Cysteine synthase A	9		YLSTALFADLFTEK	305	14	3	18.37	b13y6y12	1618.84	103.745	11798	2	809.92	2.94
P0A1E3 CYSK_SALTY Cysteine synthase A	10		IYEDNSLTIGHTPLVR	3	16	3	16.33	b12y4y7	1827.94	61.974	42541	3	609.98	-13.36
P0A1E3 CYSK_SALTY Cysteine synthase A	11		VESR	31	4	2	12.35	y3°y3	490.26	27.249	14028	1	490.26	-4.30
P0A1E3 CYSK_SALTY Cysteine synthase A	12		IGNGR	22	5	2	25.59	y3y4	516.29	34.334	6842	1	516.29	-4.97
P0A1E3 CYSK_SALTY Cysteine synthase A	13		AEEIVASDPQKYLLQQFSNPANPEIHEK	126	29	12	99.71	b3b6b11b12b13b14y3y4y6y7y9y10	3308.65	77.212	62524	4	827.92	-8.56

[P0A1E3]CYSK_SALTY Cysteine synthase A	14		GYKLTLTMPETMSIER	84	16	3	22.86	b12b13y10	1869.93	77.389	41988	2	935.47	-10.58
[P0A1E3]CYSK_SALTY Cysteine synthase A	15		LQEDSFNTKNIVILPSSGER	283	22	5	36.27	b3b4y5y6y9	2475.28	69.598	23790	3	825.77	3.55
[P0A1E3]CYSK_SALTY Cysteine synthase A	16		GKTDLITVAVEPTDSPVIAQALAGEEIKPGPHK	193	33	4	35.01	b5y3y4y5	3381.83	79.931	10742	3	1127.95	0.58
[P0A1E3]CYSK_SALTY Cysteine synthase A	17	Carbamidomethyl+C(8)	NPSFSVKCR	35	9	9	57.97	b4b7*b7b8°b8y5°y5y6°y6	1094.53	136.314	1521	1	1094.53	-8.36
[P0A1E3]CYSK_SALTY Cysteine synthase A	18	Oxidation+M(5)	LTLTMPETMSIERR	87	14	3	18.37	b10y9y12	1693.87	78.674	32344	3	565.29	4.32
[P0A1E3]CYSK_SALTY Cysteine synthase A	19	Oxidation+M(5)	IGANMIWDAEK	44	11	3	30.26	y3y4y10	1263.60	70.005	2737	2	632.30	-1.16
[P0A1E3]CYSK_SALTY Cysteine synthase A	20		QFSNPANPEIHEK	142	13	2	13.18	b3b5	1510.71	74.099	13274	3	504.24	-10.02
[O54297]RS4_SALTY 30S ribosomal protein S4	1		LSDYGVQLR	47	9	9	73.77	b3°b3b7y2y5y6y7y8y9	1050.55	51.744	140517	2	525.78	-6.86
[O54297]RS4_SALTY 30S ribosomal protein S4	2		VVNIASYQVSPNDVVSIR	128	18	20	153.69	b1b3b8b9b14b15b17*b17y3y4y5y8y9y11*y11y12y13y14y18*y18	1960.06	72.197	104980	2	980.53	3.49
[O54297]RS4_SALTY 30S ribosomal protein S4	3		LDNVVYR	97	7	5	52.07	y3y4y5y6y7	878.46	38.665	79022	2	439.74	-10.98
[O54297]RS4_SALTY 30S ribosomal protein S4	4		VVNIASYQVSPNDVVSIREK	128	20	6	50.23	b1y5y9y10y11y12	2217.18	66.278	35341	3	739.73	-2.09
[O54297]RS4_SALTY 30S ribosomal protein S4	5		MGFGATR	104	7	4	39.27	y3y4y5y7	739.34	36.869	24166	2	370.18	-14.61
[O54297]RS4_SALTY 30S ribosomal protein S4	6		GNTGENLLALLEGR	83	14	6	40.65	b2b3b5b8b9y11	1456.77	94.944	12677	2	728.89	-4.36
[O54297]RS4_SALTY 30S ribosomal protein S4	7		AALELAEQR	156	9	10	72.53	b3y3*y3y4*y4y6°y6*y6y7y8	1000.54	43.973	11479	1	1000.54	-1.59
[O54297]RS4_SALTY 30S ribosomal protein S4	8		SDLSADINEHLIVELYSK	188	18	3	22.24	b9b10y12	2046.05	80.411	3535	2	1023.53	5.19
[O54297]RS4_SALTY 30S ribosomal protein S4	9		LDNVVYRMGFGATR	97	14	3	23.81	b11y6y7	1598.82	84.689	27667	2	799.91	2.83
[O54297]RS4_SALTY 30S ribosomal protein S4	10	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	4	19.69	b6b12*b12y9	1451.73	85.392	2372	2	726.37	10.59
[O54297]RS4_SALTY 30S ribosomal protein S4	11	Phosphoryl STY(10)	VVNIASYQVSPNDVVSIREK	128	20	4	29.65	b8b11_H3PO4 b10b11b13	2297.14	120.882	8435	3	766.38	-2.02
[O54297]RS4_SALTY 30S ribosomal protein S4	12		VVNIASYQVSPN	128	12	1	7.71	y4	1290.65	66.184	2758	3	430.89	-14.66
[P0A1P8]GLRX1_SALTY Glutaredoxin-1	1		TVGKPVETVPQIFVDQK	50	17	11	67	b8b9y2y5y6°y6y7*y7y8y11y17	1885.02	65.246	43148	3	629.01	-10.62
[P0A1P8]GLRX1_SALTY Glutaredoxin-1	2	Carbamidomethyl+C(11);Carbamidomethyl+C(14)	MFTVIFGRPGCPYCVR	0	16	7	33.09	b4°b4b7b12°b12y10y14	1959.93	77.706	43021	3	653.98	-4.73
[P0A1P8]GLRX1_SALTY Glutaredoxin-1	3	Carbamidomethyl+C(11);Carbamidomethyl+C(14)	MFTVIFGRPGCPYCVRAK	0	18	3	21.99	b6b9b13	2159.09	90.163	5442	3	720.37	6.78
[P0A1P8]GLRX1_SALTY Glutaredoxin-1	4		PQIFVDQK	59	8	0	5.34		974.54	65.186	17972	1	974.54	6.51
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	1	Carbamidomethyl+C(2)	FCIPNKEVMPEK	39	12	7	50.85	b2b9y3y4°y4y8y9	1491.72	53.092	25900	3	497.91	-10.31
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	2		TGFYMSLIGTPDEQR	84	15	9	73.46	b3b12y3*y3y4y5y7y9y10	1714.83	78.727	25541	2	857.92	9.40
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	3	Carbamidomethyl+C(15)	VQDQNQIPELNVYQCGTYQMHSLSAQDIAR	113	31	18	44.8	b2*b2b5b7°b7°b7b11b12°b12y1y3y4°y4y7°y7y12y24y31	3635.69	75.078	24461	3	1212.57	0.94
[Q9L4T0]LUXS_SALTY S-ribosylhomocysteine lyase	4		MQAPAVR	13	7	6	39.27	b2y2y4y5y6y7	772.40	31.165	21248	2	386.71	-11.93

Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	5		PLLDsFAVDHTR	1	12	7	81.21	b10y3y4y6y9y10y11	1370.69	62.839	72494	3	457.57	-15.32
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	6		TMNTPHGDAITVFDLR	23	16	5	36.2	b13y4y6y11y12	1787.86	71.702	51871	3	596.62	-9.90
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	7	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCR	65	19	6	24.74	b9°b9*b9y5y10y11	2097.01	66.687	16463	3	699.68	13.04
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	8		LQELHI	165	6	1	13.24	b4	752.42	57.983	13984	2	376.71	-14.11
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	9		GIHTLEHLFAGFMR	51	14	5	31.68	b7b8°b8y3y10	1628.86	76.299	5293	2	814.93	14.16
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	10		MPLLDsFAVDHTR	0	13	6	41.3	b5b9y3y7°y7y11	1501.75	47.133	2365	2	751.38	0.89
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	11		DVRVNSNK	149	8	5	31.94	b6°b6b7°b7y4	931.49	47.129	2562	2	466.25	-7.01
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	12		VAKTMNTPHGDAITVFDLR	20	19	5	19.56	b7°b7b11y10y12	2086.07	56.147	2147	3	696.03	-3.51
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	13		TGFYMSLIGTPDEQRVADAWK	84	21	3	13.25	b3b11y6	2385.17	109.293	1776	3	795.73	6.24
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	14	Oxidation+M(1)	MPLLDsFAVDHTR	0	13	4	32.7	b5b7b12y5	1517.76	73.548	58905	2	759.38	13.67
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	15	Carbamidomethyl+C(15) ;Oxidation+M(20)	VQDQNQIPELNVYQCGTYQMHSLSAQDIAR	113	31	4	11.03	b4b7y11°y11	3651.67	104.636	9599	3	1217.89	-3.68
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		GYLSPYFINKPETGAVELESPFILLADKK	197	29	9	36.05	b2b3b4y2y4y6y13y26y29	3239.71	96.393	258335	4	810.68	-5.65
P0A1D3 CH60_SALTY 60 kDa chaperonin	2		ANDAAGDGTTTATVLAQSIITEGLK	80	25	26	155.66	b2*b2b3*b3b4*b4b5°b5b14b15°b15b17°b17b25y1y3y4°y4y5y6y7y8y9y10y11y25	2418.22	92.064	251484	3	806.75	-5.45
P0A1D3 CH60_SALTY 60 kDa chaperonin	3		EMLPVLEAVAK	231	11	13	84.45	b2°b2b3°b3y1y2y3y4y5y6y7y8y11	1199.66	80.141	196039	2	600.34	-6.11
P0A1D3 CH60_SALTY 60 kDa chaperonin	4		QQIEEATSDYDREK	350	14	15	92.05	b9b14y1y3y4°y4y5y6y7°y7y8°y8y9y14*y14	1711.76	34.324	104220	3	571.26	-10.27
P0A1D3 CH60_SALTY 60 kDa chaperonin	5	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	20	162.89	b3*b3b6b7b12°b12b13y3y5*y5y6°y6y9y11y12y13y14y15y16y18	1957.01	61.887	103111	2	979.01	1.37
P0A1D3 CH60_SALTY 60 kDa chaperonin	6		GVNVLADAVK	18	10	8	78.99	b2y3y4y5y6y7y8y10	985.56	56.668	99250	2	493.28	-10.22
P0A1D3 CH60_SALTY 60 kDa chaperonin	7		AVAAAVEELK	122	10	8	59.21	b2b3y2y3y5y6y8y10	1000.56	48.045	91768	2	500.78	-7.81
P0A1D3 CH60_SALTY 60 kDa chaperonin	8		VEDALHATR	395	9	11	73.77	b2b3b8y1y2°y2y3y4y5y7y9	1011.52	27.198	75131	2	506.26	-5.01
P0A1D3 CH60_SALTY 60 kDa chaperonin	9	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	9	56.2	b2b3°b3y2y4y6y7y8y10	1063.50	35.948	68301	2	532.26	-3.90
P0A1D3 CH60_SALTY 60 kDa chaperonin	10		SFGAPTITK	42	9	7	29.37	b2b3°b3y1y2y5y7	921.49	45.624	66165	2	461.25	-10.00
P0A1D3 CH60_SALTY 60 kDa chaperonin	11		AVAAGMNPMDLK	105	12	6	47.84	b3y5y8y9y10y12	1217.60	58.910	54063	2	609.30	-3.21
P0A1D3 CH60_SALTY 60 kDa chaperonin	12		AIAQVGTISANSDETVGK	142	18	11	58.58	b4b16y2y9y10y12y13*y13y14*y14y18	1760.91	48.904	51560	2	880.96	2.91
P0A1D3 CH60_SALTY 60 kDa chaperonin	13		GGDGNYGYNAAATEEYGNMIDMGILDPTK	470	28	9	32.3	b2y1y2y3y4y10y12y14y28	2966.29	88.335	40972	3	989.43	2.80
P0A1D3 CH60_SALTY 60 kDa chaperonin	14		AGKPLLIIAEDVEGEALATLVVNTMR	242	26	11	61.01	b3b6b7y1y3y4°y4*y4y5y6*y6	2723.50	136.263	22682	3	908.51	0.00
P0A1D3 CH60_SALTY 60 kDa chaperonin	15		GQNEQNVGIK	430	11	7	51.08	b2b8y2y3y4y5y7	1201.59	27.474	12971	2	601.30	4.06
P0A1D3 CH60_SALTY 60 kDa chaperonin	16		MAAKDVK	0	7	4	39.27	b6y4y6y7	762.41	35.221	7858	2	381.71	-7.77

[P0A1D3]CH60_SALTY 60 kDa chaperonin	17		SFGAPTITKDGVSVAREIELEDK	42	23	4	27.83	b3b7b12b17	2462.24	87.587	5781	3	821.42	-14.38
[P0A1D3]CH60_SALTY 60 kDa chaperonin	18	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDL PK	501	25	6	21.42	b5b9*b9y5y7y12	2670.31	125.826	120105	3	890.78	-2.93
[P0A1D3]CH60_SALTY 60 kDa chaperonin	19		DTTTHIDGVGEEAAIQGR	327	18	8	59.73	b3b5b7*b7b9b10b15y9	1845.91	99.779	79461	3	615.97	-6.81
[P0A1D3]CH60_SALTY 60 kDa chaperonin	20		EIELEDK	58	7	3	36.26	b4b5y5	875.43	59.451	8275	2	438.22	-1.26
[P0A1D3]CH60_SALTY 60 kDa chaperonin	21		NVVLDK	36	6	1	13.24	y3	687.41	24.334	4602	2	344.21	7.46
[P0A1D3]CH60_SALTY 60 kDa chaperonin	22		EIELEDKFENMGAMVK	58	17	5	24.93	b12y6y8y10*y10	2010.94	73.664	186875	3	670.98	-7.35
[P0A1D3]CH60_SALTY 60 kDa chaperonin	23		IADLKGQNEQNVGIK	425	16	14	90.5	b3b10*b10y3y4y8y9*y9y10*y10y11*y11y12*y12	1741.89	40.800	177602	3	581.30	-9.18
[P0A1D3]CH60_SALTY 60 kDa chaperonin	24	Carbamidomethyl+C(16)	AVAAAVEELKALSVPSCDSK	122	20	7	69.21	y3y4y6y8y10y14y18	2045.04	72.154	74997	3	682.35	-7.40
[P0A1D3]CH60_SALTY 60 kDa chaperonin	25		GGDGNYGYNAAATEEYGNMIDMG ILDPTKVTR	470	31	4	15.53	b3y6y13y16	3322.51	86.655	67225	3	1108.18	3.82
[P0A1D3]CH60_SALTY 60 kDa chaperonin	26		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	8	60.15	b3b4b5b6*b6b8y20y21	3675.87	123.126	61364	3	1225.96	-0.13
[P0A1D3]CH60_SALTY 60 kDa chaperonin	27	Carbamidomethyl+C(13)	AMEAPLRQIVLNCGEESV VANT VK	445	25	6	29.57	b3b5y5y9y11y14	2725.40	74.159	44899	3	909.14	-1.16
[P0A1D3]CH60_SALTY 60 kDa chaperonin	28		VGKEGVITVEDGTGLQDEL DVVE GMQFDR	168	29	5	17.18	y4y9*y9y12*y12	3135.51	73.082	25962	4	784.63	-0.62
[P0A1D3]CH60_SALTY 60 kDa chaperonin	29		AIAQVGTISANSDET VGKLIAEAM DK	142	26	6	29.43	b4b14y4y6y20y21	2632.34	91.890	15563	3	878.12	-3.62
[P0A1D3]CH60_SALTY 60 kDa chaperonin	30		VVINKDTTTHIDGVGEEAAIQGR	322	23	7	69.37	y3y4y5y6y7y11y14	2399.25	67.932	10005	4	600.57	-13.02
[P0A1D3]CH60_SALTY 60 kDa chaperonin	31		VAQIRQQIEATSDYDR	345	17	3	22.52	b3b4y13	2022.00	81.472	7501	2	1011.51	7.18
[P0A1D3]CH60_SALTY 60 kDa chaperonin	32		ANDAAGDGTTTATVLQSIITEGL KAVAAGMNPMDLK	80	37	3	37.85	y7y8y9	3616.81	132.214	3788	4	904.96	-1.82
[P0A1D3]CH60_SALTY 60 kDa chaperonin	33		DGVSVAREIELEDK	51	14	3	18.37	b7b11y7	1559.80	36.077	1841	3	520.61	7.51
[P0A1D3]CH60_SALTY 60 kDa chaperonin	34	Phosphoryl STY(13)	SFGAPTITKDGVSVAREIELEDK	42	23	4	12.5	b8b14y9*y9	2542.24	117.607	4426	3	848.08	2.02
[P0A1D3]CH60_SALTY 60 kDa chaperonin	35	Phosphoryl STY(9)	VVINKDTTTHIDGVGEEAAIQGR	322	23	3	12.5	b9b12_HPO3 b12y13	2479.20	108.845	4406	3	827.07	-13.88
[P0A1D3]CH60_SALTY 60 kDa chaperonin	36	Oxidation+M(9)	AVAAGMNPMDLK	105	12	4	25.26	b6y4*y4y5	1233.60	62.670	5879	3	411.87	0.89
[P0A1D3]CH60_SALTY 60 kDa chaperonin	37	Carbamidomethyl+C(18);Oxidation+M()	SALQYAASVAGLMITTECMVTDL PK	501	25	5	40.62	b3b5b6b7b11	2686.34	136.136	5060	3	896.12	8.91
[P0A1D3]CH60_SALTY 60 kDa chaperonin	38		EDALHATR	396	8	1	8.55	b6	912.45	27.211	54134	2	456.73	-6.76
[P0A1D3]CH60_SALTY 60 kDa chaperonin	39		AAAVEELK	124	8	0	2.22		830.46	48.050	9588	1	830.46	-7.13
[P0A1D3]CH60_SALTY 60 kDa chaperonin	40	Carbamidomethyl+C(4)	SVPCSDSK	134	8	0	2.22		879.40	36.021	3769	1	879.40	8.33
[P0A1D3]CH60_SALTY 60 kDa chaperonin	41		EMLPVLEAVAK	231	11	0	2.67		1181.64	80.119	13925	2	591.32	-12.19
[P0A1D3]CH60_SALTY 60 kDa chaperonin	42		QQIEEATSDYDREK	350	14	0	4		1693.75	34.312	5797	3	565.26	-6.34
[P66032]RIBB_SALTY 3	1		MNQTLSSFGTPFER	0	15	16	139.99	b2b5b6b10b11y2y4y5*y5y6y7y8y9y10y11y15	1727.85	84.770	66215	2	864.43	5.09
[P66032]RIBB_SALTY 3	2		VELALDALR	15	9	8	57.97	b2b3b7y1y3y4y7y9	999.57	69.426	50785	2	500.29	-8.49
[P66032]RIBB_SALTY 3	3	Carbamidomethyl+C(23)	GGHTEATIDLMTLAGFKPAGVLC ELTNDGDTMAR	150	34	5	35.95	b3b8b9b10y1	3562.73	123.587	29483	4	891.44	10.07

P66032 RIBB_SALTY 3	4	Carbamidomethyl+C(4)	APECIAFAGQHNMVVTIEDLVAYR	184	25	3	12.16	y4y7°y7	2775.33	99.821	14055	4	694.59	-9.15
P66032 RIBB_SALTY 3	5		AQAGGVLTR	141	9	3	29.37	b5b8y5	872.49	30.061	57802	2	436.75	-8.95
P66032 RIBB_SALTY 3	6	Carbamidomethyl+C(7); Carbamidomethyl+C(9)	HGSGIVCLCITEDR	60	14	3	18.37	b6y6y9	1616.73	82.293	2841	3	539.58	-12.84
P66032 RIBB_SALTY 3	7		DGAKPSDLNRPGHVFPLR	123	18	5	33.05	b6b9b11b12y5	1976.08	36.072	1549	3	659.36	16.06
P66032 RIBB_SALTY 3	8		MNQTLSSFGTPFERVELALDALR	0	24	4	21.5	b10°b10b11y3	2708.40	118.489	14798	3	903.47	-3.34
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	15	124.07	b2b3b4b5y1y2y3y4y5°y5y7 y8y9y10y12	1150.68	53.783	154684	2	575.84	-5.62
P66313 RL6_SALTY 50S ribosomal protein L6	2		TLNDAVEVK	35	9	13	73.77	b2°b2b3b4y1y2y3°y3y6°y6 y7y8y9	988.52	39.113	134375	2	494.77	-7.35
P66313 RL6_SALTY 50S ribosomal protein L6	3		ALLNSMVIGVTEGFTK	69	16	9	63.88	y3y6°y6y8°y8y11y12y13y1 6	1679.91	94.780	93436	2	840.46	2.54
P66313 RL6_SALTY 50S ribosomal protein L6	4		INGQVITIK	18	9	8	55.97	b2°b2y3y5y7y8°y8y9	985.60	49.088	93246	2	493.30	-9.10
P66313 RL6_SALTY 50S ribosomal protein L6	5		DGYADGWAQAGTAR	55	14	3	26.95	y7y9y11	1438.64	50.478	65069	2	719.82	1.95
P66313 RL6_SALTY 50S ribosomal protein L6	6		LQLVGVGYYR	86	9	5	37.15	b2y3y5y6y9	1004.58	60.138	56945	2	502.79	-10.69
P66313 RL6_SALTY 50S ribosomal protein L6	7		TLNDAVEVKHADNALTFGPR	35	20	3	13.7	b4y10y13	2168.10	92.977	35549	3	723.37	-6.19
P66313 RL6_SALTY 50S ribosomal protein L6	8		INGQVITIK	18	9	0	1.78		968.58	48.987	18282	2	484.79	2.71
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	1		ISELSEEQIDTLRDEVAK	44	18	15	110.54	b3°b3b11y4y8y9y10y13°y 13y14y15y16y17°y17y18	2075.03	66.636	164145	3	692.35	-7.65
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	2		IAGINIPDQK	3	10	10	59.21	b2b4y2°y2y4°y4y5y8y9y10	1068.60	54.917	111098	2	534.80	-8.57
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	3		ISELSEEQIDTLR	44	13	3	19.69	b3b10y9	1532.80	61.805	13369	2	766.90	13.62
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	4		EISMSIK	71	7	7	49.06	b2b4b5b6y5°y5y7	807.43	47.153	9899	1	807.43	-3.78
Q8ZLM1 RS13_SALTY 30S ribosomal protein S13	5		AILAAAGIAENVK	31	13	6	43.73	b3y5y7y9y10°y10	1240.71	61.558	12668	2	620.86	-10.33
P67093 UG_SALTY Universal stress protein G	1		TIIMPVDVFEMELSDK	3	16	11	82.06	b2°b2b3y3y5y6y7y12y13y1 4y16	1866.94	104.912	75697	2	933.97	8.83
P67093 UG_SALTY Universal stress protein G	2		LQTMVGHFSDPSR	69	14	9	64.32	b2b4b7y3y4y6y7°y7y11	1587.77	64.719	45107	3	529.93	-13.53
P67093 UG_SALTY Universal stress protein G	3		RFEHLQHEAETR	56	13	3	19.69	b6b9y6	1681.83	45.974	3184	2	841.42	14.81
P67093 UG_SALTY Universal stress protein G	4		FEEHLQHEAETRLQTMVGHFSIDP SR	57	26	5	21.96	b6y6y7°y7y12	3094.47	103.521	2920	2	1547.74	-2.37
P67093 UG_SALTY Universal stress protein G	5	Oxidation+M(6)	DVVNEMGEELDADV VVIGSR	94	20	4	18.67	b5b11y4y15	2162.02	75.315	13251	3	721.34	-5.53
P67093 UG_SALTY Universal stress protein G	6	Oxidation+M(4)	TIIMPVDVFEMELSDK	3	16	5	26.41	b9°b9y9y12y14	1882.94	88.718	6779	2	941.98	14.07
P66643 RS9_SALTY 30S ribosomal protein S9	1		GGGISQAGAIR	68	12	10	91.67	b2b3b4b5b6y4y5y7y8y12	1043.55	34.114	121002	2	522.28	-6.67
P66643 RS9_SALTY 30S ribosomal protein S9	2		SLEQYFGR	33	8	10	60.54	b2b3°b3y2y3y4y5°y5y6y8	999.48	61.029	102006	2	500.24	-8.67
P66643 RS9_SALTY 30S ribosomal protein S9	3		QPLELVDMVEK	49	11	6	26.28	b8°b8y6°y6y7y11	1300.68	74.201	28486	2	650.85	1.31
P66643 RS9_SALTY 30S ribosomal protein S9	4		VFIKPGNGK	18	9	3	37.15	y4y5y7	959.56	30.269	44083	2	480.28	-12.15
P66643 RS9_SALTY 30S ribosomal protein S9	5		AENQYYGTGR	1	10	5	25.84	b5°b5y4y6°y6	1158.52	27.411	32306	2	579.76	-0.63

P66643 RS9_SALTY 30S ribosomal protein S9	6		AGFVTRDAR	100	9	3	29.37	b4y7y8	992.52	85.423	24594	2	496.76	-4.86
P66643 RS9_SALTY 30S ribosomal protein S9	7		ALMEYDESLRGELR	85	14	3	26.15	b9b10b12	1681.82	84.066	1678	2	841.41	-0.15
P0A7X0 RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	12	94.68	b2b3b4y2y3y4y6y8y9°y9y10y12	1377.65	78.415	205292	2	689.33	-0.27
P0A7X0 RS8_SALTY 30S ribosomal protein S8	2		AVVESIQR	69	8	18	87.89	b1b2b3b4y1y2*y2y3*y3y4y5°y5y6°y6*y6y7y8*y8	901.50	33.453	155617	2	451.25	-12.46
P0A7X0 RS8_SALTY 30S ribosomal protein S8	3		AAVTMPSSK	22	9	10	65.75	b2y2y3°y3y4°y4y5y6y7y9	891.45	31.948	118918	2	446.23	-8.22
P0A7X0 RS8_SALTY 30S ribosomal protein S8	4		MSMQDPIADMLTR	0	13	4	19.69	b6b8*b8y6	1508.72	42.985	3916	3	503.58	22.41
P0A7X0 RS8_SALTY 30S ribosomal protein S8	5	Oxidation+M(2)	SMQDPIADMLTR	1	12	3	21.29	b11y6y9	1393.66	70.703	9328	2	697.33	11.47
P0A7X0 RS8_SALTY 30S ribosomal protein S8	6		VTMPSSK	24	7	0	1.78		749.38	31.939	21931	1	749.38	-5.38
P0A7X0 RS8_SALTY 30S ribosomal protein S8	7		AVTMPSSK	23	8	1	8.55	b5	820.42	31.894	4210	2	410.71	-4.91
P66541 RS2_SALTY 30S ribosomal protein S2	1		TVPMFNEALAE LNK	45	14	14	109.4	b3b7b8b9y1y3*y3y5y6y9*y9y11y12y14	1576.81	84.526	224917	2	788.91	1.70
P66541 RS2_SALTY 30S ribosomal protein S2	2		WLGGMLTNWK	95	10	9	50.63	b4b7y1y3*y3y4°y4y8y10	1205.61	86.434	174061	2	603.31	-5.37
P66541 RS2_SALTY 30S ribosomal protein S2	3	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	8	56.46	b4y1y3y4y8y9y11y14	1694.72	48.124	43057	3	565.58	-9.80
P66541 RS2_SALTY 30S ribosomal protein S2	4		EANNLGIPVFAIVDTNSDPDGVDFVIPGNDDAIR	174	34	15	64.67	b5°b5*b5b6b7*b7b26y3y4y7y8*y8y14y16*y16	3569.75	104.616	35565	3	1190.59	2.94
P66541 RS2_SALTY 30S ribosomal protein S2	5		SQDLASQAEESFVEAE	225	16	5	16.33	b4b13°b13y4y16	1739.77	73.289	32232	2	870.39	7.58
P66541 RS2_SALTY 30S ribosomal protein S2	6		LKDLETQSQDGTFEK	113	15	9	35.41	b2y2°y2y3°y3y4y6y9y15	1738.86	41.906	15344	2	869.94	8.00
P66541 RS2_SALTY 30S ribosomal protein S2	7		ILFVGTK	66	7	4	52.07	y3y4y5y6	777.47	57.686	46312	2	389.24	-16.41
P66541 RS2_SALTY 30S ribosomal protein S2	8		YWNPK	21	5	1	12.79	b4	707.35	22.975	20186	1	707.35	4.31
P66541 RS2_SALTY 30S ribosomal protein S2	9		DLETQSQDGTFEK	115	13	3	34.16	b3b4b5	1497.68	41.082	8576	2	749.35	9.29
P66541 RS2_SALTY 30S ribosomal protein S2	10		AGVHFHGQTR	11	10	5	25.84	b6y5*y5y7°y7	1109.54	29.249	2336	3	370.52	-19.91
P66541 RS2_SALTY 30S ribosomal protein S2	11		YWNPKMKPFIFGAR	21	14	3	26.95	b3b5b9	1754.93	76.573	27954	2	877.97	4.87
P66541 RS2_SALTY 30S ribosomal protein S2	12	Oxidation+M(11)	LENSLGGIKDMGGLPDALFVIDADHEHIAIK	143	31	3	11.03	b3b11y11	3304.68	103.280	34929	4	826.93	-1.40
P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	12	72	b2*b2b3y2y3y4*y4y5y6y8*y8y10	1129.62	39.579	321366	2	565.31	-4.11
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	17	142.1	b2b3b7b11y2y3y4y5y6y7y8y9y10°y10y11°y11y14	1452.65	57.915	150336	2	726.83	-0.17
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3	Carbamidomethyl+C(29)	LQVAAGMANPSPVGPALGQQGVNIMEFCK	10	30	6	28.36	b6b7b10y9y20y22	3081.57	136.224	4340	3	1027.86	13.39
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4	Carbamidomethyl+C(29);Oxidation+M()	LQVAAGMANPSPVGPALGQQGVNIMEFCK	10	30	3	17.02	b3b10b12	3097.52	133.189	5002	3	1033.18	-0.87
P0A7K0 RL11_SALTY 50S ribosomal protein L11	5	Oxidation+M(2)	SMGLVVED	134	8	5	49.5	b6°b6b7y4y7	865.41	91.130	1598	1	865.41	10.65
P0A7K0 RL11_SALTY 50S ribosomal protein L11	6		QLQEIAQTK	104	9	0	2.22		1058.57	39.542	9172	2	529.79	-8.88

[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	1		FAPSLVVEADIHEGMQR	377	18	13	118.33	b10b11b12y1y5°y5y6y7y8y9y10y12y16	2027.97	68.619	51178	3	676.66	-6.50
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	2		VLFMNSGTEANETAFK	101	16	12	68.46	b6b7b15y5°y5y10y11y12*y12y14*y14y16	1758.84	68.086	41713	2	879.93	4.16
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	3		SQGETLWHTSNVFTNEPALR	68	20	9	31.94	b1b7y4y6y11°y11y14*y14y20	2287.12	71.984	40952	3	763.04	2.78
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	4	Carbamidomethyl+C(8)	AVMDDHTCAVVVEPIQGEGGVQ AATPEFLK	180	30	7	21.28	b10b12b13y1y2y5y30	3168.55	75.338	26452	3	1056.85	3.93
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	5		ATEQTAITR	1	9	3	37.15	y5y6y7	990.51	23.533	18131	2	495.76	-9.49
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	6	Carbamidomethyl+C(6); Carbamidomethyl+C(20)	GLRDLCEHQALLVFDEVQCGM GR	210	24	3	12.2	b4b6y12	2818.33	138.155	3199	3	940.11	8.23
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	7		MATEQTAITR	0	10	5	38.63	b9y3°y3y7y8	1121.54	19.177	22074	2	561.27	-20.46
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	8		YSDGFGPKPADIIHVPFNDLHAVK	156	24	3	12.2	b10b12y14	2637.41	86.485	15424	3	879.81	22.40
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	9		DFLYAGAEAGVMVLNAGADV MR	355	22	7	37.46	b3°b3b4b13b15b17y8	2270.05	96.943	10164	3	757.36	-17.42
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	10		SLFTVSVGGQPK	144	12	3	31.5	y3y5y8	1219.66	59.718	8366	2	610.33	-10.61
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	11		ATFDEVILPVYAPADFIPVK	10	20	7	36.94	b5b6°b6b17y3y8y14	2205.16	103.409	1623	3	735.72	-11.51
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	12		LIDATFAERVLFMNSGTEANETAF K	92	25	3	21.48	b7y8y9	2775.37	99.607	73967	3	925.80	1.76
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	13	Carbamidomethyl+C(17)	EYIDFAGGIATV ALGHCHPALVEA LKSQGETLWHTSNVFTNEPALR	42	46	5	13.68	b3°b3y8y21y23	5020.46	87.822	54054	4	1255.87	-8.95
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	14		ATFDEVILPVYAPADFIPVK GK	10	22	3	12.85	b7y5y14	2390.29	94.827	29945	3	797.43	-4.39
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	15	Carbamidomethyl+C(8)	AVMDDHTCAVVVEPIQGEGGVQ AATPEFLKGLR	180	33	7	21.03	b15b17°b17°b17b18y18*y18	3494.69	136.737	8573	2	1747.85	-14.60
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	16	Oxidation+M(23)	ARDFLYAGAEAGVMVLNAGADV MR	353	24	3	12.2	b9b13y5	2513.20	79.408	3329	2	1257.10	-11.85
[P40732]ARGD_SALTY Acetylornithine/succinyl-diaminopimelate aminotransferase	17		PSLVVEADIHEGMQR	379	16	1	7.44	b13	1809.88	68.533	2291	2	905.44	-2.50
[Q7CR46]IRAP_SALTY Anti-adaptor protein iraP	1		QVEGALEGV KPDASVPDHDTELL R	50	24	10	51.17	b6b9y2y3y6y7y9y10y14y24	2575.26	60.145	67695	4	644.57	-13.56
[Q7CR46]IRAP_SALTY Anti-adaptor protein iraP	2		NMAQNEQEMLIR	38	12	9	66.66	b3y6y7y8y9°y9y10°y10y12	1476.70	56.536	60429	2	738.85	1.90
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	1		DQIIEAVSAMSVM DVVELISAMEE K	5	25	22	148.88	b2°b2°b2b3b4b5b6b7b8b10b13y2°y2y3y4y5°y5y6y7y9y10y25	2737.33	137.107	83447	3	913.12	0.09

P0A299 RL7_SALTY 50S ribosomal protein L7/L12	2		SLEEAGAEVEVK	109	12	4	11.8	b1b3°b3y9	1260.64	59.478	15412	3	420.89	8.13
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	3		SITKDKIIEAVSAMSVMDEVVELISA MEEK	1	29	4	11.23	b14y3°y3y5	3166.62	89.727	3316	3	1056.21	8.17
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	4		FGVSAAAAVAVAAGPAEAAEEK	30	22	8	47	b7b11b13°b13b14b15y6y14	1987.02	70.622	1845	2	994.01	1.84
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	5		AAGANKVAVIK	60	11	3	26.28	b3b4y5	1041.63	30.117	22544	2	521.32	-13.59
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	6		FGVSAAAAVAVAAGPAEAAEEKT EFDVILK	30	30	6	15.84	b6°b6b8b10°b10y14	2932.52	136.282	9074	3	978.18	-2.00
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	7		EGVSKDDAEALK	96	12	6	49.3	b3b4y5y7y10°y10	1261.65	36.059	4622	2	631.33	15.00
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	8		MSITKDKIIEAVSAMSVMDEVVELI SAMEEK	0	30	9	29.56	b7°b7b9b14y7y9°y9y12y14	3297.62	103.625	2919	3	1099.88	-5.11
P0A299 RL7_SALTY 50S ribosomal protein L7/L12	9	Phosphoryl.STY(8)	EAKDLVESAPAALK	82	14	4	26.24	b7b13y8y12	1521.73	66.672	78716	2	761.37	-12.59
P66038 RISB_SALTY 6	1		IGQVKDDNITVVVWPGAYELPLA TEALAK	40	29	20	117.19	b3b4b8b9°b9b10°b10°b10b11°b11b12b13°b13b14y2y4y9y14y15y29	3110.68	98.704	216206	3	1037.57	2.28
P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	17	126.78	b3b4b5°b5b12b14°b14y2y4y5y6y8y9y10y13y14y19	2109.08	101.808	108005	2	1055.04	7.29
P66038 RISB_SALTY 6	3		GAEAALTALEMINVLK	136	16	10	76.67	b3b5b6b7b8b13b14°b14°b14y1	1643.90	103.526	42946	2	822.45	-4.23
P66038 RISB_SALTY 6	4		VAITIAI	14	7	3	39.27	y4y5y6	743.46	44.855	27121	2	372.24	-18.96
P66038 RISB_SALTY 6	5		MNIHK	0	5	1	12.79	b4	618.37	49.353	6258	1	618.37	4.05
P66038 RISB_SALTY 6	6		ANVAAPDAR	5	9	9	73.77	b4°b4b7°b7y3y4y5°y5y7	884.45	23.116	3358	1	884.45	-4.21
P0A2A1 RL19_SALTY 50S ribosomal protein L19	1		VFQTHSPVVDIAVK	72	15	13	103.94	b2b6°b6b8b11b13y4y5y6y7y11y12y15	1626.86	56.385	118927	3	542.96	-13.43
P0A2A1 RL19_SALTY 50S ribosomal protein L19	2		QLEQEQMK	6	8	8	39.72	b8y4y5°y5y7°y7y8°y8	1033.50	26.144	34575	2	517.25	-0.35
P0A2A1 RL19_SALTY 50S ribosomal protein L19	3		QNVPSFRPGDTVEVK	14	15	6	24.5	b4°b4b6y8°y8y11	1672.85	41.946	7909	2	836.93	-7.66
P0A2A1 RL19_SALTY 50S ribosomal protein L19	4		VWVVEGTK	29	8	4	34.95	b3b6°b6y7	917.49	35.220	1741	1	917.49	-19.82
P0A2A1 RL19_SALTY 50S ribosomal protein L19	5		QLEQEQMKQNVPSFRPGDTVEVK	6	23	4	12.5	b3°b3b6y12	2687.32	55.051	60930	4	672.59	-9.54
P0A2A1 RL19_SALTY 50S ribosomal protein L19	6		VFQTHSPVVDIAVK	72	15	0	4.45		1609.84	56.391	2137	3	537.29	-6.90
P66932 TIG_SALTY Trigger factor	1		NVALEEQAWEVLAK	399	15	11	91.61	b2b3b4b11b12y3y4y11y12y13y15	1583.86	80.310	97772	2	792.43	-2.85
P66932 TIG_SALTY Trigger factor	2		ANDIDVPSALIDSEIDVLR	296	20	8	29.12	b2°b2b3b4b13y1y14y16	2211.16	90.807	46839	3	737.72	-2.21
P66932 TIG_SALTY Trigger factor	3		FGVEDGSVAGLR	255	12	8	56.87	b2b4b8b9y7y9y11y12	1206.61	57.801	25197	2	603.81	-4.05
P66932 TIG_SALTY Trigger factor	4		ANDIDVPSALIDSEIDVLR	296	19	10	54.96	b6b7°b7b10°b10b11y3y8y13y19	2055.08	94.780	22590	2	1028.04	7.60
P66932 TIG_SALTY Trigger factor	5		INPAGAPNYVPGEYK	83	15	8	53.43	b6y4°y4y5y7y9y13y15	1589.80	51.428	16471	2	795.40	2.00
P66932 TIG_SALTY Trigger factor	6		SELVNVAK	29	8	4	31.94	b3b4°b4y3	859.49	41.995	9019	2	430.25	-1.21
P66932 TIG_SALTY Trigger factor	7		GLIEEMASAYEDPKEVIEFYK	368	22	3	12.85	b3y4y8	2548.19	81.670	7853	3	850.07	-11.78
P66932 TIG_SALTY Trigger factor	8		ATDFVLAMGQGR	181	12	5	35.84	b4b7b9y7y12	1265.64	69.832	2007	2	633.32	6.85
P66932 TIG_SALTY Trigger factor	9		YGASVR	57	6	2	26.03	b3b4	652.34	27.324	15482	1	652.34	-3.84

P66932 TIG_SALTY Trigger factor	10		GLIEEMASAYEDPK	368	14	4	29.41	b6y5y6y10	1552.69	118.562	6977	1	1552.69	-16.90
P66932 TIG_SALTY Trigger factor	11		AGEEFTIDVTFPEEYHAENLK	206	21	3	21.7	b8y8y9	2439.09	74.273	4914	4	610.53	-18.62
P66932 TIG_SALTY Trigger factor	12		QQATWK	146	6	1	13.24	b4	761.38	38.130	4321	2	381.20	-14.35
P66932 TIG_SALTY Trigger factor	13		ELPELTEEFIK	243	11	6	50.62	b4b6°b6b9y5y7	1347.73	85.422	3011	2	674.37	20.02
P66932 TIG_SALTY Trigger factor	14		QVSVETTQGLGR	1	12	4	21.29	b5*b5b8y10	1274.64	114.584	1865	2	637.83	-20.78
P66932 TIG_SALTY Trigger factor	15		QDVLGDLMSRNFVDIIK	63	18	4	22.24	b7b8°b8y3	2034.07	80.586	6726	3	678.69	0.54
P66932 TIG_SALTY Trigger factor	16		AGEEFTIDVTFPEEYHAENLK GK	206	23	4	34.59	b11b12b13y10	2624.25	76.283	3342	5	525.66	-0.37
P66932 TIG_SALTY Trigger factor	17		VSEKATSFNELMNQQA	416	16	3	24.03	y4y10y12	1796.87	84.812	2538	2	898.94	10.12
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	18	125.28	b3b4*b4b7b8y1y5°y5y6*y6y7y9y10y11y12y17y19y21	2215.16	74.999	57967	3	739.06	-6.06
Q56073 DNAK_SALTY Chaperone protein dnaK	2		SLGQFNLDGINPAPR	452	15	12	38.21	b1b2°b2b4*b4y1y4y5y7y10*y10y15	1598.84	72.041	34123	2	799.92	5.57
Q56073 DNAK_SALTY Chaperone protein dnaK	3		MQELAQVSQK	587	10	8	38.63	b2*b2b3y5*y5y6y8y10	1161.59	37.834	33980	2	581.30	-1.26
Q56073 DNAK_SALTY Chaperone protein dnaK	4	Carbamidomethyl+C(12)	IIGIDLGTNSCVAIMDGTQAR	3	22	8	19.37	b1y10°y10*y10y13y15°y15y22	2306.13	81.539	27689	2	1153.57	-8.05
Q56073 DNAK_SALTY Chaperone protein dnaK	5		QAVTNPQNTLFAIK	56	14	8	46.67	b6°b6b7b12°b12b13y10y14	1544.84	67.597	24668	2	772.92	-0.95
Q56073 DNAK_SALTY Chaperone protein dnaK	6		ASSGLNEEEIQK	502	12	16	92.68	b1b2y2*y2y4°y4y5y6°y6y7y8y9y10°y10*y10y12	1304.63	35.247	20915	2	652.82	-4.30
Q56073 DNAK_SALTY Chaperone protein dnaK	7		TAEDYLGEVPTEAVITVPAYFNDAQR	125	26	7	62.31	y5y6y7y8y9y12y26	2869.39	93.566	18026	3	957.13	-0.43
Q56073 DNAK_SALTY Chaperone protein dnaK	8		VAEFGKEPR	352	10	6	46.41	b1b3b5b8°b8y8	1179.63	44.564	16011	2	590.32	11.69
Q56073 DNAK_SALTY Chaperone protein dnaK	9		FEELVQTR	528	8	4	49.5	b3b7y3y4	1021.54	49.062	10326	2	511.28	13.20
Q56073 DNAK_SALTY Chaperone protein dnaK	10		FQDEEVQR	76	8	4	34.95	b4y2y4y6	1050.47	29.137	8954	2	525.74	-11.39
Q56073 DNAK_SALTY Chaperone protein dnaK	11		VLENAEGDR	25	9	8	51.71	b1b2b3b5b8y5y9*y9	1002.49	35.150	4870	2	501.75	5.05
Q56073 DNAK_SALTY Chaperone protein dnaK	12		LMEIAQQQHAQQAGSADASANNAK	597	25	3	21.48	b5y10y11	2610.23	38.968	2367	3	870.75	0.56
Q56073 DNAK_SALTY Chaperone protein dnaK	13		TIAVYDLGGGTFDISIIIDEVDGEK	188	26	4	14.94	b10b16y8y13	2769.32	119.797	53838	3	923.78	-20.36
Q56073 DNAK_SALTY Chaperone protein dnaK	14		IIGADNGDAWLDDVK	92	14	4	26.95	y6y8y12°y12	1486.76	70.551	16514	2	743.88	3.37
Q56073 DNAK_SALTY Chaperone protein dnaK	15		DVSIMPYK	84	8	3	34.95	b5b7y5	952.48	70.914	3027	2	476.74	-2.24
Q56073 DNAK_SALTY Chaperone protein dnaK	16		IELSSAQQTQDVNLPYITADATGPK	270	24	3	18.51	y4y7y11	2532.33	109.110	2769	3	844.78	17.84
Q56073 DNAK_SALTY Chaperone protein dnaK	17		AAIEAK	581	6	1	13.24	y3	602.35	30.542	2490	1	602.35	-6.69
Q56073 DNAK_SALTY Chaperone protein dnaK	18		SIEPLKVALQDAGLSVSDINDVILVGGQTR	315	30	3	11.12	b3y3y5	3107.69	104.984	33051	3	1036.57	0.00
Q56073 DNAK_SALTY Chaperone protein dnaK	19		VLENAEGDRTPSIIAYTQDGETLVGQPAK	25	30	4	17.02	b13°b13b16b24	3173.58	99.702	12143	4	794.15	-4.46
Q56073 DNAK_SALTY Chaperone protein dnaK	20		EVGNRTIAVYDLGGGTFDISIIIDEVDGEK	183	31	3	11.03	b3y6y11	3324.69	88.909	8538	4	831.93	13.14

Q56073 DNAK_SALTY Chaperone protein dnaK	21		FEELVQTRNQGDHLLHSTR	528	19	3	21.19	b7b9b12	2280.16	90.433	5795	3	760.73	6.85
Q56073 DNAK_SALTY Chaperone protein dnaK	22		IIGADNGDAWL DVKGQK	92	17	4	15.53	b3b5y10*y10	1799.92	136.221	5269	2	900.47	-3.26
Q56073 DNAK_SALTY Chaperone protein dnaK	23		RFQDEEVQR	75	9	5	29.37	b5°b5b7y7°y7	1206.58	118.526	3957	1	1206.58	-9.00
Q56073 DNAK_SALTY Chaperone protein dnaK	24		AKIELSSAQQT DVNLPYITADATG PK	268	26	6	14.94	b4b14°b14y7°y7y11	2731.39	118.455	2752	3	911.14	-7.42
Q56073 DNAK_SALTY Chaperone protein dnaK	25		NDPLAMQRLK	253	10	4	32.83	b3b4°b4b8	1185.65	28.337	2657	3	395.89	11.63
Q56073 DNAK_SALTY Chaperone protein dnaK	26		DVSIMPYKIIGADNGDAWL DVK	84	22	9	36.63	b5b6°b6b7b15°b15y9°y9*y9	2420.24	93.828	2366	3	807.42	10.19
Q56073 DNAK_SALTY Chaperone protein dnaK	27		VALQDAGLSVSDINDVILVGGQT RMPMVQK	321	30	9	34.47	b7°b7°b7b9°b9b10b11y10°y10	3154.66	137.227	2173	3	1052.23	1.39
Q56073 DNAK_SALTY Chaperone protein dnaK	28		TAEDYLGEVPTEAVITVPAYFNDA QRQATK	125	30	4	25.65	b3b6b7b11	3297.58	110.315	2116	3	1099.87	-13.03
Q56073 DNAK_SALTY Chaperone protein dnaK	29	Phosphoryl STY(17)	IELSSAQQT DVNLPYITADATGPK	270	24	7	35.53	b6b7°b7y6y7°y7y12_H3PO4 y12	2612.21	86.644	6665	3	871.41	-11.31
Q56073 DNAK_SALTY Chaperone protein dnaK	30	Phosphoryl STY(9)	TTPSIIAYTQDGETLVGQPAK	34	21	3	21.7	b12y12y13	2270.11	86.694	6519	3	757.37	10.43
Q56073 DNAK_SALTY Chaperone protein dnaK	31	Phosphoryl STY(11)	FQDEEVQR DVSIMPYK	76	16	3	22.86	b12y3y4	2063.90	88.852	1588	3	688.64	-0.47
Q56073 DNAK_SALTY Chaperone protein dnaK	32	Oxidation+M(2)	LMEIAQQQHAQQAGSADASAN NAK	597	25	6	25.68	b11b13y6°y6y8y9	2626.23	92.964	6832	2	1313.62	-0.09
Q56073 DNAK_SALTY Chaperone protein dnaK	33	Oxidation+M(2)	GMPQIEVTFDIDADGILHVS AK	467	22	4	12.85	b9b11°b11y11	2372.19	116.192	2080	2	1186.60	3.29
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	1		YLSLLPYTDR	63	10	7	66.2	b2y4y5y6y7y8y10	1240.65	75.264	125454	2	620.83	-6.10
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	2		NYITESGK	30	8	7	52.51	b1y3y4°y4y5y6y8	911.45	30.043	45364	2	456.23	-1.54
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	3		IVPSR	38	5	2	12.79	y3°y3	571.36	46.283	23921	1	571.36	-1.07
Q8ZK81 RS18_SALTY 30S ribosomal protein S18	4		FTAEGVQEIDYK	12	12	9	71.88	b4b6°b6b7b8y3y8*y8y11	1399.69	40.971	12370	2	700.35	14.56
P64052 EFTS_SALTY Elongation factor Ts	1		ITDVEVLK	104	8	10	73.33	b2°b2b3y2y3y4y5y6y7y8	916.53	49.282	193665	2	458.77	-10.52
P64052 EFTS_SALTY Elongation factor Ts	2		AEITASLVK	1	9	10	88.33	b3°b3b4b7y1y4y5y6y7y9	931.54	49.366	128952	2	466.27	-9.04
P64052 EFTS_SALTY Elongation factor Ts	3		FTGEVSLTGQPFVMEPSK	222	18	7	44.39	b5b7b10b14b15y3y18	1953.97	74.767	107116	2	977.49	4.75
P64052 EFTS_SALTY Elongation factor Ts	4		IGENINIR	125	8	6	52.51	y3y4y5y7*y7y8	928.51	45.265	94526	2	464.76	-11.17
P64052 EFTS_SALTY Elongation factor Ts	5	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	5	40.61	b2y3y5y7y10	1098.47	21.646	49057	2	549.74	-3.44
P64052 EFTS_SALTY Elongation factor Ts	6		ALTEANGDIELAIENMRK	25	18	5	14.83	b2b16y5*y5y11	1987.99	74.384	45321	3	663.33	-11.30
P64052 EFTS_SALTY Elongation factor Ts	7		VLDAAVAGK	95	9	9	91.34	b2b5b6b8y3y4y6y7y9	843.48	34.311	32648	2	422.24	-14.40
P64052 EFTS_SALTY Elongation factor Ts	8		AGNVAADGVIK	52	11	6	46.07	y2y4y6y7y8y11	1014.55	37.385	27253	2	507.78	-5.78
P64052 EFTS_SALTY Elongation factor Ts	9		AQFEEER	112	7	7	39.27	b2°b2b5y3°y3y5y7	908.40	25.327	13902	2	454.70	-10.28
P64052 EFTS_SALTY Elongation factor Ts	10		ALTEANGDIELAIENMR	25	17	5	34.5	b5y7y9y11y12	1859.93	80.754	11542	2	930.47	7.74
P64052 EFTS_SALTY Elongation factor Ts	11		VASLEGDVLGSYQHGAR	134	17	6	40.52	b3b6b13y4y8y10	1758.85	59.526	175797	3	586.95	-16.03
P64052 EFTS_SALTY Elongation factor Ts	12		IGVLVAAK	151	8	3	34.95	b3y5y7	770.50	47.882	76237	2	385.75	-16.56

[P64052 EFTS_SALTY Elongation factor Ts	13		QLAMHVAASKPEFVKPEDVSADV VEK	167	26	10	38.46	b5b11°b11y5y6°y6y7°y7y10°y10	2824.48	136.356	6685	3	942.16	7.87
[P64052 EFTS_SALTY Elongation factor Ts	14		FEVGEGIEK	258	9	4	29.37	b8y6y7°y7	1007.49	116.077	4565	1	1007.49	-13.39
[P64052 EFTS_SALTY Elongation factor Ts	15		KALTEANGDIELAIENMR	24	18	5	21.99	y9°y9y12y14°y14	1988.02	67.005	19123	2	994.51	4.05
[P64052 EFTS_SALTY Elongation factor Ts	16	Phosphoryl STY(5)	MAEITASLVKELRER	0	15	4	28.14	b4b11b12_H3PO4 b12y12	1825.90	112.280	2912	2	913.46	-6.35
[P64052 EFTS_SALTY Elongation factor Ts	17	Oxidation+M(16)	ALTEANGDIELAIENMRK	25	18	5	31.15	b8b12y4y5y13	2004.02	85.417	2218	3	668.68	6.70
[P64052 EFTS_SALTY Elongation factor Ts	18		ITASLVK	3	7	0	1.78		731.46	49.364	16976	1	731.46	-7.93
[P64052 EFTS_SALTY Elongation factor Ts	19		TDVEVLK	105	7	5	39.72	b3°b3b4b5°b5	803.44	49.277	7100	1	803.44	-13.60
[P64052 EFTS_SALTY Elongation factor Ts	20	Carbamidomethyl+C(7)	GAGMMDCKK	16	9	1	8.03	b3	997.42	21.572	6146	2	499.22	-3.30
[P64052 EFTS_SALTY Elongation factor Ts	21		LDAAVAGK	96	8	1	8.55	b3	744.42	34.288	2330	1	744.42	-7.05
[P66593 RS6_SALTY 30S ribosomal protein S6	1		YSAAITGAEGK	24	11	13	94.23	b2°b2b3b4b9y2y3°y3y5y6y9y10y11	1067.53	34.079	183566	2	534.27	-8.23
[P66593 RS6_SALTY 30S ribosomal protein S6	2		HAVTEASPMVK	93	11	8	64.66	b2b5b10y4y5y7y9y11	1169.59	31.849	87767	2	585.30	-4.38
[P66593 RS6_SALTY 30S ribosomal protein S6	3		RDDFANETADDAEAGDSEE	112	19	5	33.82	b9b10b11y1y19	2056.80	42.968	7804	2	1028.91	9.50
[P66593 RS6_SALTY 30S ribosomal protein S6	4		FNDAVIR	79	7	8	80.67	b3°b3b5y3y4y5°y5y6	834.43	43.008	121065	2	417.72	-16.60
[P66593 RS6_SALTY 30S ribosomal protein S6	5		HYEIVFMVHPDQSEQVPGMIER	2	22	4	12.85	b8y4y9°y9	2641.20	37.243	15152	3	881.07	-20.52
[P66593 RS6_SALTY 30S ribosomal protein S6	6		LEDWGR	38	6	2	13.24	y4°y4	775.38	39.263	7386	1	775.38	11.97
[P66593 RS6_SALTY 30S ribosomal protein S6	7	Oxidation+M(6)	AHYVLMNVEAPQEVIDELETTFR	56	23	4	19.15	b3b8b12y10	2720.35	112.394	7006	2	1360.68	8.97
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	1		MKPDIHVPYR	0	10	6	37.84	b3b6y2y4y8y10	1255.68	43.021	73532	3	419.23	11.18
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	2		TFDSESSAAR	62	10	7	50.39	b1y5y6y7y8°y8y10	1070.47	25.386	71536	2	535.74	-6.39
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	3		SHPFYTGR	52	8	10	47.74	b2b7y1y2y4°y4y5y6°y6y8	964.46	34.339	52892	2	482.73	-1.20
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	4		TEREIELDGVTYPYVTIDVSSK	30	22	4	17.16	b5b7y6y11	2514.25	114.038	2368	3	838.75	-4.27
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	5		TVVFHDTSANEYVK	10	14	10	86.54	b11b12y3y8y9°y9°y9y10y11y12	1609.76	47.758	358414	3	537.26	-16.83
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	6		VGSTIKTER	24	9	5	52.96	y3°y3y4y5y8	990.55	18.987	38963	2	495.78	-8.13
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	7		TVVFHDTSANEYVKVGSTIK	10	20	3	23.12	b7b8b13	2195.14	103.669	26516	3	732.39	4.67
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	8		QKTFDSESSAAR	60	12	7	74.89	b6b8b11y4y5y7y8	1326.62	35.254	2989	2	663.81	-10.12
[P66193 RL31B_SALTY 50S ribosomal protein L31 type B	9		SHPFYTGR	52	8	0	1.33		946.44	34.353	2124	3	316.15	-10.51
[P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	1		AAADLQLQGVPMFVNGK	158	18	14	68.35	b2b5b6b8b10b15b18y2y3°y3y4y8y10y18	1829.96	80.659	69821	2	915.48	2.00
[P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	2		YQINPQGMDTSSMDVVFVQQYAD TVK	176	25	15	29.57	b2°b2b4°b4b6°b6b8b11y1y7°y7°y7y9°y9y25	2865.31	86.434	24620	2	1433.16	2.04
[P0A2H9 DSBA_SALTY Thioldisulfide interchange protein dsbA	3		TQTVQSAADIR	116	11	8	23.27	b2°b2b3y2y5y7°y9y11	1189.61	35.960	23121	2	595.31	-3.90

P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		TQTVQSAADIRK	116	12	3	21.29	b8b10y6	1317.70	51.305	14742	3	439.90	-11.49
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	5		ELTQAWAVAMALGVEDK	88	17	4	35.69	b13b14y6y7	1831.91	53.682	4234	4	458.73	-11.13
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	6	Oxidation+M(21)	YHVEFLGPLGKELTQAWAVAMALGVEDK	77	28	7	24.33	b4°b4b6y9y11y12°y12	3088.56	78.598	6806	4	772.89	-8.14
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA	7	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	3	22.52	b8b9y11	1847.92	136.223	2238	2	924.46	0.79
P67537 YBED_SALTY UPF0250 protein ybeD	1		LNELLEFPPTPTYK	4	14	8	37.27	b2b3b12°b12y5y7y8y14	1711.89	94.814	13864	2	856.45	0.21
P67537 YBED_SALTY UPF0250 protein ybeD	2		VMGQALPELVDQVVEVVQR	18	19	4	14.23	b11y1y6y13	2109.12	109.074	10699	3	703.71	-5.90
P67537 YBED_SALTY UPF0250 protein ybeD	3		GNYHSVSITINATHIEQVETLYEELGNIDIVR	52	32	3	16.78	b9b12b24	3627.86	112.282	7159	3	1209.96	7.94
P67537 YBED_SALTY UPF0250 protein ybeD	4		HAPGDYSPTVKPSSK	37	15	6	35.38	b4b10y4y13y14°y14	1570.77	76.298	10578	2	785.89	-12.98
P02910 HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTQTETFGNEHWAPK	135	20	11	66.56	b2b3b4y2y4y7y9y11y12y17y20	2199.08	63.865	68531	3	733.70	-3.33
P02910 HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	14	129.53	b2b4b5b10y3y5y6y7y8y9°y9y11y12y13	1425.69	55.770	65362	2	713.35	0.17
P02910 HISJ_SALTY Histidine-binding periplasmic protein	3	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	6	18.67	b9b16y2y4y6y20	2273.20	104.052	54664	2	1137.10	6.66
P02910 HISJ_SALTY Histidine-binding periplasmic protein	4		NSDIQPTVASLK	120	12	15	84.68	b2°b2*b2b3°b3*b3b4b10y3y7y8*y8y9y10y12	1272.68	48.676	51783	2	636.84	-2.49
P02910 HISJ_SALTY Histidine-binding periplasmic protein	5		FGGPAVKDEK	201	10	8	52.39	b2b5b8b9y4y5°y5y10	1047.54	27.426	9373	2	524.27	-9.79
P02910 HISJ_SALTY Histidine-binding periplasmic protein	6		IDAAFQDEVAASEGFLK	176	17	3	15.53	b6b15y16	1810.90	86.570	2364	2	905.95	5.93
P02910 HISJ_SALTY Histidine-binding periplasmic protein	7		LFGVGTGMGLR	211	11	7	45.85	b4b6°b6b7y5y7°y7	1107.60	41.998	6511	2	554.30	-1.21
P02910 HISJ_SALTY Histidine-binding periplasmic protein	8		AFAEMR	234	6	2	26.03	b3y5	724.35	37.045	5387	1	724.35	3.12
P02910 HISJ_SALTY Histidine-binding periplasmic protein	9		ADGTYEK	240	7	5	61.85	b4y3y4y5y6	783.37	34.185	4401	2	392.19	20.88
P02910 HISJ_SALTY Histidine-binding periplasmic protein	10		IGTDPTYAPFESKNAQGELVGFDIDLAK	29	28	3	11.36	b9b13y4	2996.50	129.906	2158	3	999.51	4.16
P02910 HISJ_SALTY Histidine-binding periplasmic protein	11		IRIGTDPTYAPFESK	27	15	4	36.6	b10b11b12y10	1694.90	55.956	1715	3	565.64	12.46
P02910 HISJ_SALTY Histidine-binding periplasmic protein	12		EALNKAFEMR	229	11	3	30.26	y5y6y9	1279.66	107.766	1602	2	640.33	10.40
P02910 HISJ_SALTY Histidine-binding periplasmic protein	13		GGPAVKDEK	202	9	0	2.22		900.49	27.388	4298	2	450.75	12.95
P67904 RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAK	16	14	17	130.27	b2b3b10y3y4°y4y5y7y8y9y10y11*y11y12°y12*y12y14	1517.81	55.845	152973	2	759.41	0.88
P67904 RS10_SALTY 30S ribosomal protein S10	2		GPIPLPTRK	37	9	5	29.37	b2b3y4y6y9	978.60	44.002	88576	2	489.80	-9.79
P67904 RS10_SALTY 30S ribosomal protein S10	3		LVDIVEPTEK	72	10	9	66.2	b2y2y3y4y5°y5y6y8y10	1142.62	52.294	48732	2	571.82	-6.41
P67904 RS10_SALTY 30S ribosomal protein S10	4		FTVLISPHVNKDAR	48	14	4	15.12	y4°y5°y5y9	1596.88	55.406	10193	2	798.94	-5.73
P67904 RS10_SALTY 30S ribosomal protein S10	5		DQYEIR	62	6	1	13.24	y4	823.40	71.977	11074	2	412.20	8.90

P67904 RS10_SALTY 30S ribosomal protein S10	6	Phosphoryl STY(6)	FTVLISPHVNKDARDQYEIR	48	20	3	13.7	b6y4y14	2481.25	98.224	2037	3	827.76	13.58
P67904 RS10_SALTY 30S ribosomal protein S10	7		IPLPTRK	39	7	0	1.78		824.52	44.011	11350	2	412.77	-13.92
P0A1P6 GLNA_SALTY Glutamine synthetase	1		LVPGYEAPVMLAYSAR	322	16	11	79.05	b2b15y4y5y8°y8y9y10y11y14y16	1736.92	77.616	51928	2	868.96	6.82
P0A1P6 GLNA_SALTY Glutamine synthetase	2		GGYFPVPPVDSAQDIR	177	16	6	26.41	b6y2y6y10y12y16	1717.87	70.228	39700	2	859.44	7.11
P0A1P6 GLNA_SALTY Glutamine synthetase	3		AINALANPTTNSYK	307	14	11	93.56	y3°y3y5y7y8°y8y9y10y12°y12y14	1477.76	48.460	35024	2	739.39	-0.74
P0A1P6 GLNA_SALTY Glutamine synthetase	4		EIPQVAGSLEEALNALDLDR	406	20	6	18.67	b7b14*b14y4y10y20	2153.10	96.022	27944	3	718.37	-3.63
P0A1P6 GLNA_SALTY Glutamine synthetase	5		ATGIADTVLFGPEPEFFLFDDIR	117	23	16	72.26	b2b3°b3b6b8b12y2y3y5y6y8°y8y9y10°y10y23	2570.28	117.624	21528	3	857.43	0.57
P0A1P6 GLNA_SALTY Glutamine synthetase	6		GINESDMVLPDASTAVIDPFFADSTLIIR	59	30	8	50	b4b9b10y2y3y4y11y12	3238.61	113.823	19095	3	1080.21	3.54
P0A1P6 GLNA_SALTY Glutamine synthetase	7	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK	360	24	7	22.25	b3b11°b11b14y6y15°y15	2565.29	136.644	17751	3	855.77	1.24
P0A1P6 GLNA_SALTY Glutamine synthetase	8		NLYDLPPEEAK EIPQVAGSLEEALNALDLDR	395	31	5	13.2	b7°b7b11y7y11	3422.78	80.774	7780	3	1141.60	12.55
P0A1P6 GLNA_SALTY Glutamine synthetase	9		NLYDLPPEEAK	395	11	3	23.27	b5b8y6	1288.62	80.529	2321	2	644.82	-14.02
P0A1P6 GLNA_SALTY Glutamine synthetase	10		MSAEHVLTMLNEHEVK	0	16	4	16.33	b13°b13y8y10	1867.89	99.770	8151	3	623.30	-7.52
P0A1P6 GLNA_SALTY Glutamine synthetase	11		AGGVFTDEAIDAYIALR	430	17	4	22.52	b15b16°b16y12	1781.89	92.580	6486	2	891.45	-10.34
P0A1P6 GLNA_SALTY Glutamine synthetase	12		YVVHNV AHR	240	9	3	29.37	b3y3y7	1094.57	27.338	4146	3	365.53	-16.51
P0A1P6 GLNA_SALTY Glutamine synthetase	13		YAGLSEQALYYIGGV I K	287	17	5	35.51	b3b6b8°b8b10	1844.94	35.215	3770	3	615.65	-21.30
P0A1P6 GLNA_SALTY Glutamine synthetase	14		EQHVTIPAHQVNAEFFE EGK	28	20	9	43.47	b4b5°b5b7°b7b9y5y9y12	2310.09	114.593	3138	3	770.70	-11.20
P0A1P6 GLNA_SALTY Glutamine synthetase	15		SAEHVLTMLNEHEVK	1	15	7	35.38	b3b6b9°b9y5y8°y8	1736.90	33.533	2533	4	434.98	18.77
P0A1P6 GLNA_SALTY Glutamine synthetase	16		MTPHPVEFELYYSV	455	14	3	23.81	b4b5y12	1711.83	83.459	1507	3	571.28	14.76
P0A1P6 GLNA_SALTY Glutamine synthetase	17	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK NK	360	26	3	17.86	b3b6b14	2807.41	129.309	30900	3	936.48	-4.00
P0A1P6 GLNA_SALTY Glutamine synthetase	18		AEDYL RATGIADTVLFGPEPEFFLFDDIR	111	29	6	24.84	b7°b7b10b11b20y5	3317.60	47.026	13704	5	664.33	-10.89
P0A1P6 GLNA_SALTY Glutamine synthetase	19		RAEDYLR	110	7	3	36.26	b5b6y5	922.47	34.422	10396	2	461.74	-5.03
P0A1P6 GLNA_SALTY Glutamine synthetase	20		MSAEHVLTMLNEHEVKFVDLR	0	21	5	21.7	b10°b10b11°b11y17	2498.25	134.823	1602	3	833.42	-0.78
P0A1P6 GLNA_SALTY Glutamine synthetase	21	Phosphoryl STY(7)	GKEQHVTIPAHQVNAEFFE EGK	26	22	5	19.86	b6°b6b8b10y5	2575.22	127.230	8024	3	859.08	11.09
P0A1P6 GLNA_SALTY Glutamine synthetase	22		ALANPTTNSYK	310	11	0	4		1179.59	48.540	18188	3	393.87	-8.59
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	1		DGIFVEDKDSPYVNLIVTREDNKDAENVK	215	29	9	23.97	b3°b3b4b12y1y8°y8y12y29	3322.61	70.593	29110	4	831.41	-10.73
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	2		SLDELKDGSQVAVPNDPTNLGR	122	22	9	43.52	b5b9b12b13y2y6y7°y7y9	2325.17	58.322	21594	3	775.73	-0.11
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	3		TFVYPIAGYSK	108	11	7	23.27	b4°b4b10y2°y2y10y11	1245.64	64.641	15553	2	623.33	-5.68

Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	4		YGLDVELVTFNDYVLPNEALSK	56	22	3	12.85	b5y11y13	2499.23	108.889	1801	3	833.75	-12.31
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	5		DGIFVEDK	215	8	3	34.95	b4b7y4	922.45	124.686	13424	1	922.45	1.92
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	6		IVELEAPQLPR	178	11	3	26.28	b3y5y6	1264.73	66.407	12099	2	632.87	2.32
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	7		DGVGLLPTSLDIVENPK	158	17	4	21.71	b9b12y4y7	1766.98	81.694	8561	3	589.67	17.55
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	8		FVQAYQSDEVYEAANK	245	16	4	27.08	b6y5y6y9	1861.87	51.454	7618	2	931.44	3.67
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	9		GDIDANAFQHKKPYLDQQIK	78	19	3	22.01	b11b12y6	2201.10	90.285	5847	3	734.37	1.44
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	10		VGLIK	151	5	1	12.79	b3	529.37	26.891	3439	1	529.37	-10.38
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	11		DGSQVAVPNDPTNLGR	128	16	3	16.33	b7y6y12	1639.80	65.884	2167	3	547.27	-1.79
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	12	Carbamidomethyl+C(17)	TFAAVGALIGSLALAGCGQDEK	6	22	4	12.85	b7°b7y6y9	2149.07	136.322	2013	2	1075.04	-10.91
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ	13		KFVQAYQSDEVYEAANK	244	17	4	33.72	b11°b11b12b13	1989.96	94.742	4906	2	995.48	2.94
P00924 ENO1_YEAST Enolase 1	1		VNQIGTLESSEIK	346	12	10	90.7	b2b3b9y3y5y6y8y9y10y12	1288.71	54.901	86462	2	644.86	-3.41
P00924 ENO1_YEAST Enolase 1	2		NVNDVIAPAFVK	67	12	16	112.24	b2b4°b4b5°b5°b5b6°b6b7y3y5y7y9y10°y10y12	1286.71	66.346	85824	2	643.86	-2.37
P00924 ENO1_YEAST Enolase 1	3		SIVPSGASTGVHEALEMR	32	18	5	41.15	b13b17y10y11y12	1840.91	74.197	34326	3	614.31	-4.04
P00924 ENO1_YEAST Enolase 1	4		WLTGPQLADLYHSLMK	272	16	3	16.33	b11b14y6	1872.95	82.648	5969	2	936.98	-8.86
P00924 ENO1_YEAST Enolase 1	5		AVDDFLISLDGTANK	88	15	3	25.35	y8y12y13	1578.79	63.732	2977	3	526.94	-5.57
P00924 ENO1_YEAST Enolase 1	6		AADALLK	338	8	3	39.72	y4y6y7	814.49	54.416	67686	2	407.75	-16.19
P00924 ENO1_YEAST Enolase 1	7		IEEELGDNAVFAGENFHHGDK	415	21	4	13.25	b9°b9b11y9	2328.09	81.535	44960	3	776.70	16.15
P00924 ENO1_YEAST Enolase 1	8		TAGIQIVADDLTVTNPK	312	17	3	33.72	y11y12y13	1755.95	72.460	32950	2	878.48	1.88
P00924 ENO1_YEAST Enolase 1	9		NVPLYK	126	6	1	13.24	y4	733.42	37.776	19987	1	733.42	-4.66
P00924 ENO1_YEAST Enolase 1	10		TFAEALR	178	7	6	67.87	b4b5°b5b6y4y6	807.44	36.073	4065	2	404.22	1.74
P00924 ENO1_YEAST Enolase 1	11		AAGHDGK	234	7	3	39.27	b4y4y6	655.32	46.113	3309	1	655.32	8.10
P00924 ENO1_YEAST Enolase 1	12		YDLDFK	258	6	1	13.24	y3	800.38	43.623	2120	2	400.69	-0.92
P00924 ENO1_YEAST Enolase 1	13		AVDDFLISLDGTANKSK	88	17	3	15.53	b13y9y15	1793.91	65.248	94695	2	897.46	-7.55
P00924 ENO1_YEAST Enolase 1	14		GNPTVEVELTTEKGVFR	15	17	4	24.18	b10b11b14°b14	1875.97	105.257	13712	2	938.49	-5.53
P00924 ENO1_YEAST Enolase 1	15		TFAEALRIGSEVYHNLK	178	17	3	22.52	b3b4y9	1948.01	68.720	7141	2	974.51	-8.08
P00924 ENO1_YEAST Enolase 1	16		SIVPSGASTGVHEALEMRDGDK	32	22	8	37.46	b5y5y8°y8y12y13y15°y15	2256.07	87.817	3294	3	752.69	-10.39
P00924 ENO1_YEAST Enolase 1	17	Phosphoryl STY(13)	WLTGPQLADLYHSLMKR	272	17	4	26.18	b12y5y6y11	2109.01	91.927	5190	4	528.01	-9.49
P00924 ENO1_YEAST Enolase 1	18	Phosphoryl STY(15)	AAQDSFAAGWGVMSHR	358	17	3	15.53	b14b16y12	1869.77	136.776	1630	1	1869.77	-14.49
P00924 ENO1_YEAST Enolase 1	19	Oxidation+M(15)	WLTGPQLADLYHSLMK	272	16	4	23.01	b4b8y5y9	1888.98	85.606	12274	2	944.99	8.01
P00924 ENO1_YEAST Enolase 1	20	Oxidation+M(17)	SIVPSGASTGVHEALEMR	32	18	4	20.57	b8b14y4y14	1856.91	99.757	2927	3	619.64	-5.65
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	1		EGGIFWMDSLAIPANAK	249	17	10	40.69	b3b6°b6b7b11y12y5y12y17	1819.91	93.783	48468	2	910.46	4.90

P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	2		QAGTPLEVVPWK	237	12	7	21.29	b2*b2b3b10*b10b12y8	1324.72	75.232	41918	2	662.87	-1.29
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	3		EVAETIGYPTPNLAAR	285	16	7	40	b3*b3y5y8y10y13y16	1701.88	61.176	28509	2	851.44	0.14
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	4		EVFQMALR	170	8	6	65.31	b5b7y2y3y4y6	993.51	63.786	18687	2	497.26	-4.98
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	5		NSLLLTDDAR	160	10	3	27.6	b3y5y6	1117.57	53.453	9823	2	559.29	-13.11
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	6		QAGTPLEVVPWKEGGIFWMDSLA IPANAK	237	29	3	21.64	b5y3y4	3125.65	123.302	5501	4	782.17	12.11
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	7		LGYSGNTTDPKEIEAAYEELK	179	21	3	21.7	b6b7y5	2328.11	78.935	3926	3	776.71	-5.35
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	8		SLYPDAQTISK	312	11	3	30.26	b5b6b9	1222.66	72.357	18307	2	611.83	21.67
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	9		LTNFHNLDPEMLNKPFDPNNDYS VPYIWGATAIGVNSDAIDPK	103	43	4	11.25	b5*b5y9y15	4803.29	95.752	14399	4	1201.58	-2.54
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	10		DGAYDLVVPSTYYVDK	73	16	3	16.33	b10y6y11	1804.83	68.617	4645	3	602.28	-20.63
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	11		EIEAAYEELK	190	10	5	32.83	b3b5*b5b6*b6	1194.57	104.551	2043	1	1194.57	-15.84
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	12		EVAETIGYPTPNLAARK	285	17	3	22.93	b7b9b12	1829.96	88.839	94276	3	610.66	-9.81
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	13		KLMPNVAAFNSDNPANPYMEGE VNLGMVWNGSAFVAR	200	37	3	37.85	y11y12y13	4010.88	95.014	49665	4	1003.48	-4.69
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	14		VIYSTYESNETMYAKLK	53	17	4	15.53	b4y11*y11y13	2039.97	99.274	38554	3	680.66	-15.08
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	15	Oxidation+M(15)	NSLLLTDDAREVFQMALR	160	18	4	22.24	b3*b3y4y5	2108.11	127.906	2030	3	703.38	15.06
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	16		NSLLLTDD	160	8	0	2.22		890.43	53.469	59847	2	445.72	-14.39
P0A2C7 POTD_SALTY ermidine/putrescine-binding periplasmic protein	17		QAGTPLEVVPWKEGGIFWM	237	19	2	12.23	y4y10	2145.09	123.293	4955	3	715.70	0.68
Q8ZRP4 DAPD_SALTY 2	1		EAVNQVISLLDSGALR	28	16	7	55.01	b6*b6y5y6y7y9y10	1684.93	92.399	70807	2	842.97	4.85
Q8ZRP4 DAPD_SALTY 2	2		MQQLQNVIETAFER	0	14	6	18.37	b2b3y6y12*y12y14	1706.86	86.179	65391	2	853.93	2.29
Q8ZRP4 DAPD_SALTY 2	3		INDNQVIDGAESR	68	13	10	92.69	b8b9y5y7y8y9*y9y10y12y13	1430.69	41.888	41102	2	715.85	0.51
Q8ZRP4 DAPD_SALTY 2	4		FADYDEAR	89	8	8	47.74	b2b3*b3y2y5y6y7*y7	986.42	35.211	19502	2	493.71	0.62
Q8ZRP4 DAPD_SALTY 2	5		IDGQVWTHQWLK	48	12	5	48.34	b7b8b9y7y11	1510.76	73.322	22033	2	755.88	-13.17
Q8ZRP4 DAPD_SALTY 2	6		ADITPANVDTVTR	15	13	4	19.69	b10*b10b12y5	1372.71	49.093	10247	2	686.86	1.96
Q8ZRP4 DAPD_SALTY 2	7		QQLQNVIETAFER	1	13	3	19.69	b5b8y6	1575.82	68.567	8411	2	788.41	2.25
Q8ZRP4 DAPD_SALTY 2	8		IYDR	213	4	1	12.35	b3	566.29	36.038	8177	1	566.29	-9.27
Q8ZRP4 DAPD_SALTY 2	9		IYDRETGEVHYGR	213	13	6	33.06	b11*b11b12y10*y10y12	1594.76	136.637	14716	1	1594.76	-1.38

Q8ZRP4 DAPD_SALTY 2	10		AVLLSFRINDNQVIDGAESR	61	20	5	29.65	y4y6y8y9*y9	2217.15	104.860	1533	2	1109.08	-5.95
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		QLDPLVVGQEHYDTAR	343	16	8	63.25	b13y3y5y6y9°y9y10y11	1840.90	58.398	63243	3	614.30	-10.15
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	9	71.21	b1b3b6b8y4y7y8°y8y10	1193.59	80.991	52192	2	597.30	-14.11
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		TVNMMELIR	156	9	8	43.93	b3b9y3y6°y6y7y9*y9	1106.56	76.329	37142	2	553.79	-4.30
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4		TIAMGSSDGLRR	53	12	4	21.29	b11y3y10y12	1263.64	38.327	31539	2	632.32	-6.38
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5		QIASLGIYPAVDPLDSTSR	324	19	9	55.54	b4y2y4y5y7y11y12y14y19	2003.05	80.421	28938	2	1002.03	3.84
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		VGLFGGAGVGK	145	11	4	35.27	b3y4y7y8	961.53	59.524	27432	2	481.27	-13.58
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		VALTGLTMAEK	219	11	9	82.45	b2y3y4y5y7°y8y9y10y11	1133.61	59.600	23636	2	567.31	-7.86
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		AAPSYEELSNSQELLETKIK	112	20	4	13.7	b13b15y1y12	2179.09	73.676	23630	2	1090.05	5.49
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		VYDALEVQNGNEK	25	13	3	19.69	b5y7y12	1478.74	71.706	21246	2	739.88	21.63
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		VSLVYGQMNEPPGNR	202	15	3	17.27	b6y11y13	1660.79	79.448	3298	2	830.90	-13.60
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		NIAIEHSGYSVFAGVGER	165	18	8	29.38	b9b11°b11b14°b14y5y15°y15	1905.93	105.208	1997	2	953.47	-8.84
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12	Carbamidomethyl+C(26)	AAPSYEELSNSQELLETKIKVIDLMCPFAK	112	30	5	18.2	b6b9y4y6y10	3353.67	121.182	31501	3	1118.56	0.80
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		IMNVLGEPVDMKGEIGEEER	87	20	4	13.7	b11°b11b13y4	2245.07	69.843	6889	3	749.03	-4.24
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		TIAMGSSDGLRR	53	12	3	21.29	b6b11y11	1263.63	75.257	5433	2	632.32	-12.17
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15	Phosphoryl STY(8)	QIASLGIYPAVDPLDSTSR	324	19	5	40.49	b3b11_H3PO4 b11y9y10y11	2083.00	117.374	5732	3	695.00	-2.93
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16	Oxidation+M(1)	MPSAVGYQPTLAEEMGVLQER	261	21	3	13.25	b7b14y14	2322.13	88.462	11804	3	774.72	9.25
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17	Oxidation+M(2)	IMNVLGEPVDMK	87	12	5	30.77	b8°b8b11y7y11	1361.70	91.130	11388	2	681.35	10.94
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18	Oxidation+M(4)	TIAMGSSDGLR	53	11	4	35.27	b6y4y5y7	1123.55	74.955	4823	2	562.28	8.37
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19		AMGSSDGLRR	55	10	0	3.11		1049.51	38.276	18740	2	525.26	-5.70
P0A1H3 EFG_SALTY Elongation factor G	1		IATDPFVGNLTFFR	323	14	12	76.82	b2b4b5b7b12y4y7y10y12° y12*y12y14	1597.84	93.436	90833	2	799.42	0.23
P0A1H3 EFG_SALTY Elongation factor G	2		VYSGVVNSGDTVLSNVK	337	17	13	89.28	b2b4°b4b5b17y4y9y10y11 y12y14y15y17	1737.90	62.461	71112	2	869.45	-0.84
P0A1H3 EFG_SALTY Elongation factor G	3		SGPLAGYPVVDLGVR	562	15	14	70.36	b2b3b5°b5b6b7°b7y1y2y4y8y10y11y15	1499.82	76.633	66912	2	750.42	1.14
P0A1H3 EFG_SALTY Elongation factor G	4		IGEVHDGAATMDWMEQEQR	39	20	5	21.53	b3b5b11y6y20	2331.99	62.817	43417	3	778.00	-2.30
P0A1H3 EFG_SALTY Elongation factor G	5		YDDAPNNVAQAVIEAR	686	16	5	16.33	b12y8y12*y12y16	1745.85	65.340	22366	2	873.43	4.06
P0A1H3 EFG_SALTY Elongation factor G	6		GQYGHVVIDMYPLEPGSNPK	512	20	6	26.8	b2b11b12y6*y6y9	2201.07	70.697	12201	3	734.36	0.22
P0A1H3 EFG_SALTY Elongation factor G	7		AINWNDADQGVTFEYEDIPADMQLANEWHQNLIESAASEELMEK	189	47	8	45.33	b11y2y3y7y8y9y12y13	5380.39	126.344	9273	4	1345.85	0.18
P0A1H3 EFG_SALTY Elongation factor G	8		VVGQIK	153	6	1	13.24	b4	643.41	45.744	19993	1	643.41	-0.09
P0A1H3 EFG_SALTY Elongation factor G	9		LGANPVPLQLAIGAEEGFTGVVDLVK	161	26	3	11.72	b6y4y14	2607.43	120.235	19806	3	869.82	-3.37

P0A1H3 EFG_SALTY Elongation factor G	10		VEVETPEENTGDVIGDL SR	618	19	7	27.85	b3b13b15°b15y8y12*y12	2058.95	94.912	15366	3	686.99	-16.13
P0A1H3 EFG_SALTY Elongation factor G	11		TTTTTER	23	6	1	13.24	y4	708.35	47.199	9594	1	708.35	-6.72
P0A1H3 EFG_SALTY Elongation factor G	12		QSGGR	507	5	2	25.59	b4y4	504.26	35.155	7861	1	504.26	11.56
P0A1H3 EFG_SALTY Elongation factor G	13		NIGISAHIDAGK	11	12	9	57.33	b7b10°b10y3y7°y7y10y11°y11	1195.62	47.142	6700	2	598.32	-16.34
P0A1H3 EFG_SALTY Elongation factor G	14		AGDIAAAIGLK	378	11	3	26.28	b3b4y3	999.57	35.142	6440	2	500.29	-18.32
P0A1H3 EFG_SALTY Elongation factor G	15		IHAEVPLSEMFYATQLR	653	18	4	21.99	b3b7b12°b12	2062.04	91.494	3674	2	1031.52	-3.55
P0A1H3 EFG_SALTY Elongation factor G	16		GITITSAATTAFWSGMAK	59	18	3	14.83	b9b12y7	1813.92	88.022	2800	2	907.46	1.08
P0A1H3 EFG_SALTY Elongation factor G	17		QANK	128	4	1	12.35	b3	460.25	20.730	1742	1	460.25	-12.86
P0A1H3 EFG_SALTY Elongation factor G	18		ASYTMEFLK	677	9	4	37.15	y5°y5y6y7	1089.53	110.240	1644	1	1089.53	-2.69
P0A1H3 EFG_SALTY Elongation factor G	19		NIGISAHIDAGKTTTTTER	11	18	4	14.83	b14*b14b17y16	1884.98	136.786	3071	1	1884.98	3.43
P0A1H3 EFG_SALTY Elongation factor G	20	Carbamidomethyl+C(10) ;Oxidation+M(7)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	8	31.12	b4b16y6°y6y7°y7y12y21	2637.27	94.963	102341	3	879.76	-3.33
P0A1H3 EFG_SALTY Elongation factor G	21		GQYGHVVID	512	9	0	6.67		987.48	70.623	2713	2	494.24	-14.03
P60446 RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	9	66.2	b9°y1y2y3y5y6y7y8y10	1115.63	56.914	169765	2	558.32	-7.44
P60446 RL3_SALTY 50S ribosomal protein L3	2		IFTEDGV SIPVTVIEVEANR	13	20	8	60.23	b2y2y3y4y5y6y7y20	2188.16	88.185	125362	2	1094.58	5.91
P60446 RL3_SALTY 50S ribosomal protein L3	3		VTQVKDLANDGYR	33	13	6	30.93	b4*b4y3y4°y4y7	1478.74	40.830	27940	3	493.59	-11.47
P60446 RL3_SALTY 50S ribosomal protein L3	4	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	6	51.18	y4y5y6y14y15y18	1738.93	54.520	25499	3	580.32	-11.65
P60446 RL3_SALTY 50S ribosomal protein L3	5		AVQVTTGAK	46	9	9	65.75	b2y1y3y4y5y6y7*y7y9	874.49	22.465	16783	2	437.75	-14.80
P60446 RL3_SALTY 50S ribosomal protein L3	6		LAEGEETYVGQ SISVELFADV K	83	22	3	22.72	b3b4b9	2384.18	118.455	2194	4	596.80	-1.84
P60446 RL3_SALTY 50S ribosomal protein L3	7		VTKPEAGHFAK	59	11	5	46.07	y3y5y6y7°y7	1184.62	26.286	39947	3	395.54	-19.99
P60446 RL3_SALTY 50S ribosomal protein L3	8		NLLLVK	184	6	4	51.62	b4y3y4y5	699.48	57.240	38111	1	699.48	-0.70
P60446 RL3_SALTY 50S ribosomal protein L3	9		GLWEFR	77	6	1	13.24	y5	807.40	49.444	1929	1	807.40	-15.12
P60446 RL3_SALTY 50S ribosomal protein L3	10	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	8	82.35	y5y6y7y8y10y12y15y16	1809.97	56.611	146383	3	603.99	-11.53
P60446 RL3_SALTY 50S ribosomal protein L3	11		DLANDGYRAVQVTTGAK	38	17	3	15.53	b3b12y13	1778.93	103.498	97299	2	889.97	13.93
P60446 RL3_SALTY 50S ribosomal protein L3	12		AGVEAGRGLWEFR	70	13	3	19.69	b5b7y11	1447.75	82.852	3418	2	724.38	6.75
P60446 RL3_SALTY 50S ribosomal protein L3	13	Phosphoryl STY(14)	LAEGEETYVGQ SISVELFADV KK	83	23	5	28.08	b4b9b12b13y10	2592.26	117.626	21599	3	864.76	8.38
P60446 RL3_SALTY 50S ribosomal protein L3	14	Phosphoryl STY(12)	IFTEDGV SIPVTVIEVEANR	13	20	7	48.04	b10°b10b11b12y12y13*y13 3	2268.14	78.745	3202	2	1134.57	14.21
P60446 RL3_SALTY 50S ribosomal protein L3	15		QVTTGAK	48	7	0	1.78		704.39	22.479	5321	1	704.39	-11.96
P25077 MDH_SALTY Malate dehydrogenase	1		NQLPSGSELSLYDIAPVTPGVAVD LSHIPTAVK	21	33	12	30.28	b1b2*b2b3b13y1y3y5y15y 18y30y33	3388.80	93.912	84879	3	1130.27	0.65
P25077 MDH_SALTY Malate dehydrogenase	2		VAVLGAAGGIGQALALLK	2	19	8	57.3	b3y3y4y5y9y11y12y19	1735.09	120.182	57741	2	868.05	2.25

P25077 MDH_SALTY Malate dehydrogenase	3		FFSQPLLLGK	262	10	5	25.84	b2b6y2y4y6	1149.66	76.044	43672	2	575.33	-8.49
P25077 MDH_SALTY Malate dehydrogenase	4		IQNAGTEVV EAK	205	12	25	128.05	b2b3*b3b6°b6°b6b8*b8b10°b10y1y2y3°y3y4°y4y8°y8y9°y9y10*y10y11°y11y12	1258.66	35.184	35556	2	629.83	-2.42
P25077 MDH_SALTY Malate dehydrogenase	5		AGGGSATLSMGQAAAR	217	16	6	41.6	b1y7y8y10y11y16	1405.68	40.620	33996	2	703.35	-1.39
P25077 MDH_SALTY Malate dehydrogenase	6		SIGTSAFEQHS LDAMLDTLKK	279	22	4	17.16	b11b13y12y14	2405.22	85.711	17853	3	802.41	-5.48
P25077 MDH_SALTY Malate dehydrogenase	7		DIQLGEDFINK	301	11	3	26.28	b3y8y9	1291.64	68.048	2976	1	1291.64	-9.55
P25077 MDH_SALTY Malate dehydrogenase	8		IQNAGTEVV EAKAGGGSATLSMGQAAAR	205	28	7	38.23	b4b9*b9b10b17y7y8	2645.35	96.882	2230	4	662.09	8.68
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	1		TFDTP TYPNSLALSADGK	308	18	9	51.71	b3b4b12y2y5y8y11y14y18	1897.93	65.752	29742	2	949.47	3.86
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	2		LYT TNADGEFITIDTASNK	198	19	6	38.32	b1b5b6b7b10y7	2073.98	118.688	4587	3	692.00	-7.65
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	3		AFITDSK	244	7	8	39.27	b1b2b3b7y3y6°y6y7	781.40	35.149	3928	2	391.20	-14.53
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	4		ESAIWVVDGETIK	162	13	5	27.17	b2b4°b4b5b12	1446.74	81.682	2505	3	482.92	-4.39
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	5		ELVADAATNTIYISGVGK	144	18	4	23.75	b11b13*b13b14	1821.94	73.066	33326	3	607.98	-11.32
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	6		IAAPASLAVLFNPTR	268	15	5	23.29	b6y4*y4y5°y5	1540.86	90.048	12001	2	770.93	-16.87
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	7		IAAPASLAVLFNPTRNEAYVTHR	268	23	4	22.83	b4y11y12y20	2511.31	82.706	48446	4	628.58	-13.90
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	8		NEAYVTHRQAGQVSVIDAK	283	19	3	14.23	b8y3y12	2086.09	64.786	18653	3	696.03	9.13
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	9		AQRLYTTNADGEFITIDTASNK	195	22	6	12.85	b7°b7b15°b15y4°y4	2429.21	89.156	6347	3	810.41	7.24
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	10		EQEATQPPDDVIRIAL	338	15	3	25.35	b4b11b12	1697.86	78.781	2935	2	849.43	-5.68
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE	11	Phosphoryl STY(14)	ELVADAATNTIYISGVGK	144	18	5	29.38	b5b7y3y6y10	1901.92	56.936	15277	3	634.65	2.44
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		AGLGMMEGVLENVPSAR	78	17	6	34.5	b13y4y6y7y12y17	1730.86	81.954	73229	2	865.94	4.23
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		VLVLVAAPEGIAALEK	155	16	7	56.1	b2b3b4b5b6y9y11	1592.96	85.959	39411	2	796.99	1.00
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		NEETLEPVVPYFQK	103	13	5	27.17	b2y5y7y8y13	1593.78	65.691	16659	2	797.40	2.68
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		ITVVPILR	70	8	4	39.72	y2y4y5y6	910.60	70.191	15589	2	455.80	-7.57
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		LVS NIDER	116	8	3	39.72	y3y6y7	945.49	33.467	34576	2	473.25	-8.13
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	6		ELASEVGSLLTYEATADLETEK	29	22	7	47	b3b8b9b10b13y5y12	2369.14	136.372	1886	2	1185.07	-9.17
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	7		AHPDVELY TASIDQGLNEHGYIIPGLGDAGDKIFGTK	171	37	3	10.89	b5b10y15	3911.92	89.778	25183	4	978.73	-6.99
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	8		LGLMRENDISTK	14	12	4	32.83	b6b8b9y7	1376.73	33.607	2049	3	459.58	9.40
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	9	Oxidation+M()	AGLGMMEGVLENVPSAR	78	17	4	15.53	b12*b12b16y6	1746.86	94.981	18058	2	873.93	2.59
P26976 PHON_SALTY Non-ecific acid phohatase	1		LQTIPAFQK	215	9	7	55.97	y3y5*y5y7y8*y8y9	1045.60	55.603	99009	2	523.30	-6.65
P26976 PHON_SALTY Non-ecific acid phohatase	2		YVGAVEFAR	206	9	5	51.71	b5y3y5y7y9	1011.52	52.074	74122	2	506.26	-8.63

P26976 PHON_SALTY Non-ecific acid phohatase	3		NLLTMGGYYATASAKK	108	16	3	16.33	b12y8y12	1688.85	64.847	22378	3	563.62	-11.93
P26976 PHON_SALTY Non-ecific acid phohatase	4		NLLTMGGYYATASAK	108	15	8	36.54	b1b10b11°b11*b11y12y13°y13	1560.77	90.289	19154	2	780.89	-3.99
P26976 PHON_SALTY Non-ecific acid phohatase	5		NGSYPSGHTAYGTLLALVLSEARPER	150	26	5	11.72	b1b2b5b22y6	2759.37	96.771	18172	4	690.60	-13.18
P26976 PHON_SALTY Non-ecific acid phohatase	6	Carbamidomethyl+C(3)	VICGAHWQSDVDAGR	191	15	8	53.43	b3y2y3y5y8°y8y9y13	1670.79	47.009	7189	2	835.90	12.93
P26976 PHON_SALTY Non-ecific acid phohatase	7		IFSPVVGAK	85	9	7	78.55	y3y4y5y6y7y8°y8	917.53	51.735	110140	2	459.27	-15.96
P26976 PHON_SALTY Non-ecific acid phohatase	8		QAAEDADVSVENIAR	70	15	4	39.39	y8y11y12y13	1587.77	51.067	18204	2	794.39	3.08
P26976 PHON_SALTY Non-ecific acid phohatase	9	Carbamidomethyl+C(12)	TRPFVLFNHSTCRPEDENTLR	128	21	7	34.77	b12*b12b13y7°y7*y7y8	2589.26	92.688	14116	3	863.76	-1.51
P26976 PHON_SALTY Non-ecific acid phohatase	10		DTPETWNMLKNLLTMGGYYATASAK	98	25	4	22.42	b11b12°b12b14	2776.31	136.641	10523	2	1388.66	-8.88
P26976 PHON_SALTY Non-ecific acid phohatase	11		EDHPKLNy	242	8	3	31.94	b5b6y5	1015.50	61.774	2602	1	1015.50	11.48
P26976 PHON_SALTY Non-ecific acid phohatase	12		EAYFKGYAIK	54	10	5	27.6	b4°b4b5°b5y9	1189.61	32.343	1917	3	397.21	-9.85
P26976 PHON_SALTY Non-ecific acid phohatase	13	Oxidation+M(5)	NLLTMGGYYATASAK	108	15	5	42.98	b5b10b12b14y9	1576.78	81.666	4520	3	526.26	7.35
P26976 PHON_SALTY Non-ecific acid phohatase	14		GAVEFAR	208	7	0	1.78		749.39	52.112	4691	1	749.39	-0.57
P26976 PHON_SALTY Non-ecific acid phohatase	15		TIPAFQK	217	7	2	8.55	b6°b6	804.45	55.611	2437	1	804.45	-11.61
O54296 RS11_SALTY 30S ribosomal protein S11	1		STPFAAQVAAER	57	12	9	61.31	b1b2b3°b3b4y6y7y8y10	1247.65	50.284	110575	2	624.33	9.78
O54296 RS11_SALTY 30S ribosomal protein S11	2		QGNALGWATAGGSGFR	37	16	9	63.25	b5b16y6y7y8y11y12y14y16	1549.75	66.356	63425	2	775.38	2.28
O54296 RS11_SALTY 30S ribosomal protein S11	3		ALNAAGFR	98	8	6	47.74	b5y4y5y6°*y6y8	819.44	42.834	46883	2	410.22	-9.24
O54296 RS11_SALTY 30S ribosomal protein S11	4		ESTIR	93	5	2	25.59	b3b4	605.33	35.163	9056	1	605.33	8.77
O54296 RS11_SALTY 30S ribosomal protein S11	5	Carbamidomethyl+C(15)	ITNITDVTPIPHNGCRPPK	106	19	5	30.07	b3b8y6y7y13	2130.09	117.393	4056	2	1065.55	-11.23
O54296 RS11_SALTY 30S ribosomal protein S11	6		QGNALGWATAGGSGFRGSR	37	19	8	51.99	b6b9b10b11°b11b12°*b12y8	1849.92	61.914	17501	3	617.31	7.59
O54296 RS11_SALTY 30S ribosomal protein S11	7	Phosphoryl STY(12)	QVSDGVAHIHASFNNTIVTITDR	14	23	6	28.08	b3b8b9b11°b11y12	2575.23	111.666	5682	3	859.08	3.51
P0A1Z2 SKP_SALTY Chaperone protein skp	1		TGVSNTLENEFK	39	12	8	43.5	y2y5°y5y7y9y10°y10y12	1338.66	58.458	89155	2	669.83	1.55
P0A1Z2 SKP_SALTY Chaperone protein skp	2		IAIVNMGNLFFQVQAQK	23	16	13	62.74	b2b3b4b11b15y1y2y3y6°y6y7y12y16	1773.97	89.994	74442	2	887.49	1.58
P0A1Z2 SKP_SALTY Chaperone protein skp	3		VANDQSIDLVVDANTVAYNSSDV K DITADVLK	126	32	5	15.26	b7b9°b9b18y3	3392.70	89.912	47863	3	1131.57	-0.79
P0A1Z2 SKP_SALTY Chaperone protein skp	4		DVMSQR	85	6	1	13.24	b3	735.35	25.320	2497	1	735.35	10.38
P0A1Z2 SKP_SALTY Chaperone protein skp	5		AQAFEK	97	6	1	13.24	y5	693.35	28.282	2181	2	347.18	-11.88
P0A1Z2 SKP_SALTY Chaperone protein skp	6		TGVSNTLENEFKGR	39	14	4	23.81	b13y10°y10y11	1551.76	68.431	16119	2	776.39	-8.42
P0A1Z2 SKP_SALTY Chaperone protein skp	7		KVANDQSIDLVVDANTVAYNSSDVK	125	25	4	24.96	b7b8y8y13	2665.32	108.799	5245	3	889.11	-4.03
P0A1Z2 SKP_SALTY Chaperone protein skp	8	Oxidation+M(11)	WLLAAGLGLAMVTSAQAADK	3	20	5	24.16	b14y3y6°y6y7	2003.07	81.592	5358	2	1002.04	3.05
P0A1Z2 SKP_SALTY Chaperone protein skp	9	Oxidation+M(6)	LEKDVMSQR	82	9	5	43.93	b4b5b8°b8y8	1121.57	115.783	1616	2	561.29	6.64

P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	1		LAEVAGEYLR	63	10	6	35.84	b2b10y6y7y8y10	1120.59	55.040	48303	2	560.80	-7.73
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	2		VILVGNLGQDPEVR	8	14	6	37.4	y2y4y8y11y12y14	1508.85	66.079	35956	2	754.93	2.02
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	3		YTTEINVPIGGVMQMLGGR	97	20	14	86.96	b2b3b4b5b7*b7b10b12y4y5y7y10y14y20	2164.11	96.724	33930	2	1082.56	7.56
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	4		YMPSGGAVANLTLATSESWR	22	20	3	12.67	b16*y6y17	2111.01	72.142	8237	3	704.34	-6.71
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	5		VVMFGK	57	6	3	38.83	y3y4y5	680.38	46.127	8433	1	680.38	-4.58
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	6		GSQVYIEGQLR	74	11	4	23.27	b8b10y8*y8	1249.64	56.067	4887	2	625.32	-13.87
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	7		YMPSGGAVANLTLATSESWRDK	22	22	3	12.85	b13b15y6	2354.15	113.651	6735	3	785.39	3.73
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	8		KWTDQSGQER	87	10	5	25.84	b8y3*y3y5*y5	1234.58	118.552	2273	1	1234.58	-0.59
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	9	Oxidation+M(16)	YTTEINVPIGGVMQMLGGR	97	20	7	36.94	b5b6b14y5y12*y12y16	2180.07	86.283	4603	2	1090.54	-7.06
P0A2F6 SSB_SALTY Single-stranded DNA-binding protein	10		SGGAVANLTLATSESWR	25	17	1	7.71	b10	1719.89	72.213	14176	2	860.45	13.70
P55900 SERC_SALTY Phohoserine aminotransferase	1		AQVFNFSSGPAMLP AEVLK	1	19	11	47.64	b2*b2b6b12*b12b13y3y6y13y14y19	2006.05	91.506	60254	2	1003.53	4.99
P55900 SERC_SALTY Phohoserine aminotransferase	2		MNVPFQLADNTLDK	297	14	4	15.12	y4y11*y11y14	1605.81	55.725	12767	3	535.94	10.26
P55900 SERC_SALTY Phohoserine aminotransferase	3	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	4	19.86	b7b10b13y5	2567.19	119.339	7930	3	856.40	-8.84
P55900 SERC_SALTY Phohoserine aminotransferase	4		ALTDFMIDFERR	348	12	5	25.26	b1b8b9y10y12	1513.76	73.048	6165	2	757.39	11.05
P55900 SERC_SALTY Phohoserine aminotransferase	5		AQGGVAAMHK	257	10	3	25.84	b3b5y8	969.49	19.365	5878	2	485.25	-4.72
P55900 SERC_SALTY Phohoserine aminotransferase	6		ITVDGK	122	6	2	13.24	b5*b5	632.36	29.005	11221	1	632.36	-5.50
P55900 SERC_SALTY Phohoserine aminotransferase	7		MAQVFNFSSGPAMLP AEVLK	0	20	6	21.53	b3b8*b8b10y13*y13	2137.10	90.203	9000	2	1069.05	9.37
P55900 SERC_SALTY Phohoserine aminotransferase	8		ASIYNAMPIEGVK	335	13	4	34.16	b3*b3b4b5	1392.75	76.338	6035	2	696.88	21.21
P55900 SERC_SALTY Phohoserine aminotransferase	9		YGVIIYAGAQK	188	10	6	50.63	b3b9*b9y6y8y9	1069.56	44.026	4053	1	1069.56	-5.48
P55900 SERC_SALTY Phohoserine aminotransferase	10		TTADYVDAGYWAASAIK	91	17	3	22.52	b11y10y11	1802.84	40.852	2841	3	601.62	-9.07
P55900 SERC_SALTY Phohoserine aminotransferase	11		EFIQVAEEAEQDFR	44	14	6	38.06	b8b13*b13y3y7y13	1710.83	87.853	2169	2	855.92	21.55
P55900 SERC_SALTY Phohoserine aminotransferase	12		GQFAGVPLNLLGDKTTADYVDA GYWAASAIK	77	31	4	13.2	b5b25y10y25	3212.64	97.751	38934	3	1071.55	5.09
P55900 SERC_SALTY Phohoserine aminotransferase	13		GKEFIQVAEEAEQDFR	42	16	4	29.54	b10b13y6y7	1895.93	53.026	3290	3	632.65	8.89
P55900 SERC_SALTY Phohoserine aminotransferase	14		INQQKAELLYGVINDSDFYR	267	20	5	39.91	b4b19y3y4y5	2386.21	86.663	2584	2	1193.61	1.33
P55900 SERC_SALTY Phohoserine aminotransferase	15		MNVPFQLADNTLDK	297	14	0	4		1588.76	55.820	6332	2	794.88	-4.99
P0A1V4 KAD_SALTY Adenylate kinase	1		LVEYHQMTAPLIGYYQK	167	17	9	50.09	b6b7b9b11y4y8y12*y12y17	2054.03	69.626	53132	3	685.35	-5.35
P0A1V4 KAD_SALTY Adenylate kinase	2		YGIPQISTGDMLR	23	13	6	41.3	b3b12y3y8y10y13	1450.73	72.889	50121	2	725.87	-0.93
P0A1V4 KAD_SALTY Adenylate kinase	3		VDGTQAVADVRR	195	11	6	35.27	b4y2y4y9y10y11	1130.57	37.215	48056	2	565.79	-5.07
P0A1V4 KAD_SALTY Adenylate kinase	4		NGFLLDGFPR	78	10	5	27.6	b2b3y4y5y10	1135.58	81.085	38357	2	568.29	-6.45

P0A1V4 KAD_SALTY Adenylate kinase	5		IILLGAPGAGK	2	11	5	40.04	b2b3y3y5y7	1009.63	61.448	27667	2	505.32	-10.04
P0A1V4 KAD_SALTY Adenylate kinase	6		VEGKDDVTGEDLTTR	141	15	4	33.8	b1y9y10y11	1634.79	50.181	3278	3	545.60	1.79
P0A1V4 KAD_SALTY Adenylate kinase	7		GTQAQFIMEK	13	10	3	40.61	y3y5y7	1152.58	49.307	2101	1	1152.58	8.90
P0A1V4 KAD_SALTY Adenylate kinase	8		TIPQADAMK	88	9	4	43.93	b4b6b7y3	974.48	87.915	1734	1	974.48	-18.41
P0A1V4 KAD_SALTY Adenylate kinase	9	Carbamidomethyl+C(6)	IAQEDCRNGFLLDGFPR	71	17	3	15.53	b12y5y14	2007.97	88.779	38724	2	1004.49	2.01
P0A1V4 KAD_SALTY Adenylate kinase	10		IILLGAPGAGKGTQAQFIMEK	2	21	3	13.25	b3y17y19	2143.18	72.908	36193	3	715.06	-7.29
P0A1V4 KAD_SALTY Adenylate kinase	11		VDGTQAVADVRAALEK	195	16	3	16.33	b4b11y13	1642.87	80.461	20098	2	821.94	-6.24
P0A1V4 KAD_SALTY Adenylate kinase	12		NGFLLDGFPR TIPQADAMK	78	19	3	14.23	b11y6y9	2091.05	91.623	5443	3	697.69	-10.74
P0A1V4 KAD_SALTY Adenylate kinase	13		GTQAQFIMEKYGIPQISTGDMLR	13	23	3	12.5	b8b11y10	2584.32	109.357	2388	3	862.11	11.81
P0A1V4 KAD_SALTY Adenylate kinase	14		KDDQEETVR	156	9	4	37.15	y3y6*y6y7	1119.54	136.357	2160	1	1119.54	13.74
P0A1V4 KAD_SALTY Adenylate kinase	15		RLVEYHQMTAPLIGYYQK	166	18	5	33.75	y3*y3y4y5*y5	2210.13	72.035	1646	2	1105.57	-7.18
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	1	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLALASGAK	257	25	13	55.8	b2b3b6*b6b12y2y6y7y16y19y22y23y25	2684.45	128.579	104580	3	895.49	-1.09
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	2		LTVVPAQTSAEVLK	215	15	6	25.35	y1y2y4y8y11y15	1584.89	63.636	42334	2	792.95	0.62
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	3		AFPGLNGMDLAK	148	12	9	48.27	b1y7*y7y8y9y10*y10y12*y12	1233.63	72.095	25196	2	617.32	-2.87
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	4		SALLVLEDGTQFHGR	3	15	6	28.14	b7y5y7y8*y8y15	1642.87	125.431	22564	2	821.94	6.54
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	5		DLPLIASNFR	83	10	4	35.84	b2y4y5y6	1145.62	76.072	21684	2	573.31	-10.34
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	6		EVTTAETYR	160	9	8	55.97	y2y4*y4y5*y5y7y8y9	1069.51	29.128	11312	2	535.26	-5.25
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	7	Carbamidomethyl+C(6)	GAQNGCIIAGDSPDAK	125	16	7	33.09	b5b10b13*b13y11y13y16	1573.73	38.714	9707	2	787.37	4.03
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	8	Carbamidomethyl+C(18)	MNPDGIFLSNGPGDPAPCDYAITA IQK	230	27	5	11.52	b9*b9b14y13*y13	2862.38	77.272	8232	3	954.80	11.17
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	9		NVVMITAQNHGFAVDEDSL PANL R	302	24	5	22.5	b1b10y10y12y13	2611.28	82.776	7689	3	871.10	-4.21
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	10		SEDDLPHFVVAYDFGAK	185	17	5	32.36	b3b9b10y3y10	1909.87	47.185	3712	3	637.29	-14.70
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	11		MLVDR	207	5	1	12.79	b3	633.33	118.660	2390	1	633.33	-13.97
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	12		AIGATGSAGVEVVNTSMTGYQEI LTDPSSYSR	18	32	8	27.38	b10*b10b11b14y4y7*y7y14	3321.56	110.114	1696	3	1107.86	-9.63
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	13		MKFGHHGGNHPVK	285	13	4	37.92	b12y10y11y12	1445.72	59.023	1192810	3	482.58	0.51
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	14	Carbamidomethyl+C(8)	EKGAQNGCIIAGDSPDAK	123	18	4	40.43	b5b6b16b17	1830.89	93.710	11824	2	915.95	12.53
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	15		DGLPEAKSEDDLPHFVVAYDFGA K	178	24	6	26.23	b12b16b17*b17y14y16	2620.29	136.759	7109	2	1310.65	13.88
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	16		NVVMITAQNHGFAVDEDSL PANL RVTHK	302	28	3	22.38	b4b8b9	3076.61	82.529	3099	6	513.61	14.13
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	17	Oxidation+M(8)	AFPGLNGMDLAK	148	12	4	30.77	b6b10y5y7	1249.63	36.065	23361	3	417.22	8.01
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain	18		NVVMITAQNHGFAVDEDSL PANL R	302	24	0	8.45		2594.23	82.865	8677	2	1297.62	-13.08

P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	1		SSDVSLPVLVLTAR	68	14	7	54.97	y1y3y4y8y9y10y14	1456.84	86.729	84992	2	728.92	0.34
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	2		IQAQYPHDVITTVR	201	14	6	40.65	b2b10y7y9y10y12	1640.85	52.176	69714	3	547.62	-14.51
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	3		VLVVEDNALLR	3	11	8	54.09	b2b3y6y7*y7y8*y8y9	1240.71	67.772	52303	2	620.86	-9.64
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	4		VQLQDSGHQVDAEDAR	18	17	8	32.36	b1b8b9b15y2y3y15°y15	1838.84	36.892	19150	3	613.62	-12.55
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	5		ELSVNEEVIK	140	10	6	46.41	b3°b3b5b7y6°y6	1159.60	42.941	18854	2	580.30	-20.63
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	6		ESHTIDVLMGR	186	11	3	23.27	b4y3y10	1257.65	58.270	2730	2	629.33	20.58
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	7		MQALMR	112	6	1	13.24	b3	749.37	25.917	2488	2	375.19	-9.77
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	8		EGWQDKVEVLSSGADDYVTKPF HIEEVMAR	82	30	6	23.64	b7°b7b14y6y9y10	3435.64	126.189	3825	3	1145.88	-4.48
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	9	Phosphoryl STY(12)	VVSKDSLMLQLYPDAELR	168	18	4	20.57	b6b13y5y12	2157.07	82.570	21597	2	1079.04	6.11
P14146 PHOP_SALTY Virulence transcriptional regulatory protein phoP	10	Oxidation+M(8)	VVSKDSLMLQLYPDAELRESHTID VLMGR	168	29	3	17.18	y4y6y14	3331.67	77.199	6394	4	833.67	-10.48
P41031 CY_SALTY Thiosulfate-binding protein	1		VNNPEIMGK	286	9	5	44.93	b1y4y6y8y9	1001.50	36.808	71762	2	501.26	-5.73
P41031 CY_SALTY Thiosulfate-binding protein	2		AYLNWLYSPPAQTIITHYYR	265	21	8	30.51	b2b14°b14y4y8y15y19y21	2664.32	93.807	71252	3	888.78	-0.92
P41031 CY_SALTY Thiosulfate-binding protein	3		QYEAQGFEVVIK	226	13	12	48.5	b3°b3b4°b4b11°b11b12°b12b13y2y3y13	1507.78	70.050	48675	2	754.40	3.16
P41031 CY_SALTY Thiosulfate-binding protein	4		NVEVFDTGGR	189	10	4	35.84	y6y7y8y10	1093.53	47.903	47146	2	547.27	3.80
P41031 CY_SALTY Thiosulfate-binding protein	5		LPNNSSPFYSTMGFLVR	110	17	9	67	b7b8°b8y3y5y9y11y13y17	1929.96	92.131	44724	2	965.48	3.54
P41031 CY_SALTY Thiosulfate-binding protein	6		ELFAALNPPFEQQWAK	37	16	8	42.87	b3b15y1y6y7y9y12y16	1888.97	89.991	41864	2	944.99	5.17
P41031 CY_SALTY Thiosulfate-binding protein	7		GATTTFAER	199	9	4	37.15	y3y4y6y9	953.46	31.608	20281	2	477.24	-4.16
P41031 CY_SALTY Thiosulfate-binding protein	8		ELFAALNPPFEQQWAKDNGGDK	37	22	3	12.85	b12y4y11	2475.23	83.464	1789	2	1238.12	14.99
P41031 CY_SALTY Thiosulfate-binding protein	9		ADVVTYNQVTDVQILHDK	81	18	5	40.43	b4b5°b5b9b10	2058.03	64.054	4166	3	686.68	-7.59
P41031 CY_SALTY Thiosulfate-binding protein	10		TNILAEFPVAVWDKNVQANGTEK	239	23	8	42.41	b3°b3b4b12y5y6y10y19	2544.30	90.949	80259	3	848.77	-1.73
P41031 CY_SALTY Thiosulfate-binding protein	11		YTYLAAWGAADNADGGDKAK	159	20	3	23.12	y6y7y15	2057.94	62.609	28024	3	686.65	-7.36
P41031 CY_SALTY Thiosulfate-binding protein	12		LIPADWQSRLPNNSSPFYSTMGFL VR	101	26	3	11.72	b3y13y24	2996.50	96.167	27057	3	999.51	-1.47
P41031 CY_SALTY Thiosulfate-binding protein	13		NVEVFDTGGRGATTTFAER	189	19	3	14.23	b7b10y3	2028.00	73.096	8891	3	676.67	10.41
P41031 CY_SALTY Thiosulfate-binding protein	14		LPNNSSPFYSTMGFLVRK	110	18	5	33.75	b4b5°b5b6°b6	2058.06	83.418	6887	3	686.69	6.05

P41031 CY_SALTY Thiosulfate-binding protein	15		ADVVTYNQVTDVQILHDKGK	81	20	3	20.49	b4b6b9	2243.14	104.634	2193	3	748.38	-13.17
P41031 CY_SALTY Thiosulfate-binding protein	16	Oxidation+M(5)	TEQFMTQFLK	179	10	3	25.84	b3b7y7	1288.61	23.520	8412	2	644.81	-11.37
P41031 CY_SALTY Thiosulfate-binding protein	17		ELFAALNPPFEQQWAKDNGG	37	20	0	7.56		2232.10	83.436	3484	2	1116.55	13.67
P0A7V6 RS3_SALTY 30S ribosomal protein S3	1		LVADSITSQLER	114	12	14	97.02	b2b5y1y2y4y5y6*y6y8y9y10y11y12*y12	1331.71	60.897	48330	2	666.36	-3.94
P0A7V6 RS3_SALTY 30S ribosomal protein S3	2		VVADIAGVPAQINIAEVRKPELDAK	89	25	5	17.95	b3y4y11y17y25	2616.45	70.890	43862	4	654.87	-10.17
P0A7V6 RS3_SALTY 30S ribosomal protein S3	3		LGIVKPWNSTWFANTK	11	16	5	24.03	y6y10°y10y12°y12	1862.01	113.461	3227	3	621.34	8.46
P0A7V6 RS3_SALTY 30S ribosomal protein S3	4		ADIDYNTSEAHTTYGVIGVK	179	20	3	13.7	b9b18y4	2154.00	58.463	20938	3	718.67	-16.32
P0A7V6 RS3_SALTY 30S ribosomal protein S3	5		EFADNLDSDFK	27	11	4	26.28	b3b4y10*y10	1300.59	71.939	1618	3	434.20	15.02
P0A7V6 RS3_SALTY 30S ribosomal protein S3	6		RAVQNAMR	135	8	5	52.51	b3b7y4*y4y6	945.50	35.148	3222	2	473.25	-6.26
P0A7V6 RS3_SALTY 30S ribosomal protein S3	7		LVADSITSQLER	114	12	0	3.11		1314.68	60.883	25563	2	657.84	-4.46
P63411 ACKA_SALTY Acetate kinase	1	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPEAR	17	26	13	48.53	b2b3b10y1y2y4°y4y5y9y10y19y22y26	2907.40	105.023	49131	3	969.81	1.76
P63411 ACKA_SALTY Acetate kinase	2		EGTRPAVVIPTNEELVIAQDASR	374	23	10	61.42	b3b8b9b14y5y6y7y12y14y23	2465.29	69.172	42497	3	822.44	-3.47
P63411 ACKA_SALTY Acetate kinase	3	Carbamidomethyl+C(1)	CVDTSMGLTPLEGLVMGTR	224	19	8	45.42	b2b3b12b14y4y7y8y10	2037.00	94.924	32103	2	1019.00	6.77
P63411 ACKA_SALTY Acetate kinase	4	Carbamidomethyl+C(14)	ESGLLGLTEVTSDCR	272	15	7	30.52	b11b14y2y10y11°y11y15	1636.80	71.974	25117	2	818.90	6.86
P63411 ACKA_SALTY Acetate kinase	5		NVAVFDATFHQTMPEESYLALPYSLYK	144	28	4	35.61	y5y6y7y9	3297.61	99.347	10979	3	1099.88	9.77
P63411 ACKA_SALTY Acetate kinase	6	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPEARIK	17	28	3	17.38	b6b8b15	3148.60	98.698	63460	4	787.91	8.14
P63411 ACKA_SALTY Acetate kinase	7		ELSLGKLGVLGFVDHER	342	18	3	22.24	b3y3y4	1998.05	68.559	2353	3	666.69	-8.25
P63411 ACKA_SALTY Acetate kinase	8	Carbamidomethyl+C(18) ;Oxidation+M(1)	MLTKESGLLGLTEVTSDCR	268	19	4	14.23	b6y9°y9y15	2126.03	103.414	1601	3	709.35	-8.27
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	1		AGGNYLSLLVGSEARR	160	17	3	24.18	b5b6b8	1749.90	73.301	30360	3	583.97	-15.00
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	2		AAPNTIPTAAK	149	11	8	71.65	b5y3y5y7y8y9*y9y11	1054.58	32.674	28682	2	527.80	-4.86
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	3		SVDGIQVGEGR	266	11	12	76.67	b1b3°b3b4°b4b10y4°y4y6y8y9y11	1116.57	41.979	25296	2	558.79	2.08
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	4		AGGNYLSLLVGSEAR	160	16	8	23.01	b1b9b14°b14y2y3y5y16	1593.82	79.392	18113	2	797.41	-4.90
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	5		IQQAFFGFLTGETEDK	284	16	4	26.41	b6y5y9y13	1830.89	78.688	7489	2	915.95	0.60
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	6	Carbamidomethyl+C(14)	FPVSQSIDELMEACR	69	15	3	17.27	b3y3y11	1781.86	82.491	5707	2	891.43	20.14
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	7		AGGNYLSLLVGSEARR	160	17	3	22.52	b15b16y3	1749.91	113.719	17035	2	875.46	-6.84
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	8	Carbamidomethyl+C(12)	SVDGIQVGEGRCGPVTK	266	17	3	15.53	b11b13y10	1758.89	76.653	4803	2	879.95	6.39
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	9	Phosphoryl STY(11)	DGVLFTPPFTSSALPGITRDAIK	204	24	5	18.52	b9b15b17y14°y14	2596.30	103.338	2455	3	866.11	-12.13
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase	10	Phosphoryl STY(10)	VHVMShALHYGTSVFEGIR	22	19	3	23.41	b7b9b10	2220.06	46.077	2140	3	740.69	10.23
P67551 YAE_P_SALTY UPF0253 protein yaeP	1	Carbamidomethyl+C(18)	YAEIASGDLGYVPDALGCVLK	11	21	8	34.34	b3b11y1y9°y9y12y14y15	2211.11	103.659	14187	3	737.71	4.42

[P67551 YAEP_SALTY UPF0253 protein yaeP	2		AAAYAAANLLVSDYVNE	50	16	4	16.33	b2b7y4y11	1683.82	86.454	2917	2	842.41	-1.01
[P67551 YAEP_SALTY UPF0253 protein yaeP	3	Carbamidomethyl+C(19)	RYAEIASGDLGYVPDALGCVLK	10	22	3	12.85	b6b8y9	2367.19	88.887	15096	3	789.73	-4.85
[P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	23	161.66	b2b3b4b5b7b8y1y2°y2y3°y3y4°y4y5°y5y6°y6y7°y7y8y9y10y12	1196.59	64.696	593464	2	598.80	-3.26
[P0A9Y9 CC_SALTY Cold shock-like protein cC	2		GPAAVNVTAI	59	10	6	40.61	b3b6*b6b9*b9y10	912.51	60.012	32173	1	912.51	-7.69
[P0A9Y9 CC_SALTY Cold shock-like protein cC	3		TLAEGQNVEFEIQDGQK	42	17	6	39.95	b11y5y9y10y11°y11	1905.93	57.800	14626	2	953.47	6.47
[P0A9Y9 CC_SALTY Cold shock-like protein cC	4		GFGFITPADGSKDVFVHFSAIQGN GFK	15	27	7	50.54	b8b15y8*y8y9y10y11	2843.38	65.607	7507	3	948.46	-14.00
[P0A9Y9 CC_SALTY Cold shock-like protein cC	5		DVVFVHFSAIQNGGFK	27	15	3	25.35	y6y9y11	1665.85	73.948	34714	2	833.43	4.32
[P0A9Y9 CC_SALTY Cold shock-like protein cC	6		TLAEGQNVEFEIQDGQKGPAAVN VTAI	42	27	4	17.6	b3°b3b5b14	2799.42	75.967	133441	3	933.81	-0.35
[P0A9Y9 CC_SALTY Cold shock-like protein cC	7		GFITPADGSK	17	10	0	3.11		992.51	64.631	4231	1	992.51	2.89
[P0A9Y9 CC_SALTY Cold shock-like protein cC	8		TLAEGQNVEFEIQ	42	13	1	7.34	y11	1477.71	57.807	2692	2	739.36	-3.06
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		AVLPGMVER	115	9	6	37.15	y2y4°y4y6y7y9	971.52	53.643	34386	2	486.27	-9.80
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		VTDIEPGLVGGTEFSSVR	171	18	10	50.12	b2b5b14y1y5y7y9y13y14y18	1862.96	69.351	29598	2	931.99	7.54
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		AAIEEMMASLPAQWR	58	15	4	25.35	y5y9y13y15	1703.83	90.933	28908	2	852.42	5.52
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4		TDLHGTAVR	162	9	3	29.37	b3b6y5	969.50	24.111	9284	2	485.26	-8.56
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5	Carbamidomethyl+C(15)	MIVLVTGATAGFGECIARR	0	19	5	22.01	b2b3y2y13y14	2022.07	80.252	4489	3	674.69	2.72
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		GHIINIGSTAGSWPYAGGNVYGAT K	126	25	5	17.95	b3b5*b5b9y5	2491.28	36.118	2122	3	831.10	16.66
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		DELGENVLTAQLDVR	41	15	3	23.29	b11b12y12	1671.86	52.920	1762	2	836.43	4.31
[P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	8	Oxidation+M(9)	ASVEDWETMIDTNNK	93	15	3	17.27	b3y4y6	1768.76	42.957	22884	4	442.95	-6.14
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	1		VITDVHEASQAQPVADVVDVIQL PAFLAR	91	29	12	61.09	b2b8b9b10°b10b11b12*b12b23y1y2y6	3101.67	104.962	38331	3	1034.56	2.68
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	2		AGMAVGLAGLFLSHPDPANAK	226	22	3	21.6	b5b6y3	2166.12	120.390	9017	3	722.71	9.24
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	3		GANFGYDNLVVDMLGFSVMK	168	20	4	13.7	b10y2y9y14	2177.02	102.743	3408	3	726.34	-9.76
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	4		ASFDK	55	5	2	12.79	b3°b3	567.27	49.704	12989	1	567.27	-11.73
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	5		LGIPYVFK	47	8	4	47.74	b3y3y4y5	936.54	76.772	12933	2	468.77	-15.51
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	6	Carbamidomethyl+C(17)	VSGNSPVIFDVTHALQCR	189	18	5	23.65	b7°b7b10b12y3	2000.04	69.705	10303	2	1000.52	16.66
[P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphooctonate aldolase	7		QTDLVEAMAK	120	10	5	27.6	b8°b8b9y8°y8	1105.55	103.545	5859	1	1105.55	-3.75

P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	8	Carbamidomethyl+C(2)	ICEHYVTVTQK	36	11	3	26.28	b7b8y7	1377.70	81.534	3620	2	689.36	14.18
P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	9		DPFGAASGGR	207	10	3	25.84	b7y7y9	934.44	107.251	1567	1	934.44	6.66
P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	10		TGAVINVKKPQFVSPGQMGNIVDK	130	24	5	18.52	b3y8°y8y10y12	2527.33	109.356	3423	3	843.12	-14.30
P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	11		AIDDLVKSFDELDTEN	268	16	3	16.33	b3y4y13	1823.86	88.575	2405	2	912.44	4.95
P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	12	Oxidation+M(8)	GPGLGEGMK	70	9	5	57.97	b3b5y4y5y6	933.45	68.502	4498	1	933.45	13.73
P65215 KDSA_SALTY 2-dehydro-3-deoxyphosphoactonate aldolase	13	Oxidation+M(8)	QTDLVEAMAK	120	10	4	25.84	b4b6°b6y5	1121.54	46.061	2555	2	561.28	-5.99
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	1		VQALADAAR	102	9	9	59.73	b2*b2b3*b3y3y5y6y7y9	914.49	32.173	167211	2	457.75	-13.95
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	2		AIAEQLK	56	7	7	39.27	y2y3*y3y4*y4y5y7	772.45	32.853	44526	2	386.73	-12.41
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	3		GKDVSVFDR	85	9	5	43.93	b8y3y4y6y9	1036.53	43.214	35528	2	518.77	-7.18
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	4		SGFYQHGR	94	8	3	31.94	b4b5y4	951.43	27.281	93347	2	476.22	-8.85
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	5		HIYAQVIAPNGSEVLVAASTVEK	33	23	4	25.55	b3b11y6y7	2396.25	85.270	4165	3	799.42	-14.26
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	6		DAAAAVGK	68	8	4	31.94	b7°b7y5y6	702.37	35.135	2397	1	702.37	-9.21
Q7CPL6 RL18_SALTY 50S ribosomal protein L18	7	Phosphoryl STY()	HIYAQVIAPNGSEVLVAASTVEK	33	23	3	12.5	b4y3y5	2476.24	134.773	1767	3	826.09	1.97
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	1		LNSAVFPSAQGGPLMHVIAGK	251	21	12	36.73	b2b3°b3b4°b4°b4b10°b10b21y3y4y21	2094.10	78.527	68550	3	698.71	-7.23
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	2		VMQAQGSQLTNK	42	12	17	133.85	b2b3b5b9y1y2y3y4y5y6y7y8°y8y9y10°y10y12	1304.66	30.365	49236	2	652.83	-0.09
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	3		MIIGFSAYSQGVVDWAK	168	17	10	68.83	b8b12y4y6°y6y12y13°y13y14y16	1800.88	103.445	29617	3	600.97	-10.24
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	4	Carbamidomethyl+C(7)	ELAGWMCDVLDNINDEATIER	380	21	6	13.25	b2b4y2y8y11y21	2464.13	102.241	19733	2	1232.57	7.53
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	5		YAEGYPGKR	54	9	7	57.97	b4b8y4y6y7°y7y9	1040.51	25.293	7579	2	520.76	-7.39
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	6		QEEHIELIASENYTSR	25	17	3	22.52	b9y7y8	2015.97	118.453	1974	2	1008.49	1.94
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	7		NSVPNDPKSPFVTSGIR	346	17	7	51.34	b8b9b11y8y9y11y14	1814.91	52.895	37887	3	605.64	-14.19
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	8		QEEHIELIASENYTSRVMQAQGSQLTNK	25	29	3	21.64	b9y14y15	3301.62	84.139	22392	4	826.16	1.26
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	9		MIIGFSAYSQGVVDWAKMR	168	19	5	22.52	b9°b9b12b16y11	2088.03	101.713	10323	3	696.68	-7.25
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	10		LYNIVPYGIDESGKIDYDEMAK	138	22	5	34.67	b13°b13y8y9y10	2533.22	87.865	4327	3	845.08	-0.39
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	11		VRQEEHIELIASENYTSR	23	19	6	19.56	b5°b5b13°b13y8y11	2271.11	112.452	4074	3	757.71	-9.78
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	12		EHPKPMIIGFSAYSQGVVDWAK	163	22	8	55.75	b13b14y10y12y13y14y16°y16	2420.22	105.164	1704	4	605.81	-8.07
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	13	Oxidation+M(15)	LNSAVFPSAQGGPLMHVIAGK	251	21	5	13.25	b4°b4b7°b7y3	2110.09	85.122	33923	3	704.04	-8.91
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	14	Oxidation+M(1)	MIIGFSAYSQGVVDWAK	168	17	7	24.93	b7°b7b9b12°b12y5°y5	1816.90	66.888	11303	3	606.30	2.15
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	15	Carbamidomethyl+C(12);Oxidation+M(11)	EAEVKELAGWMCDVLDNINDEATIER	375	26	3	17.86	y3y8y13	3036.36	79.742	5723	4	759.85	-10.94

[P67605 YEEX_SALTY UPF0265 protein yeeX	1		METTKPSFQDVLEFVR	0	16	7	40.29	b10b11y4°y4y10y11y16	1926.95	85.477	59009	3	642.99	-8.49
[P67605 YEEX_SALTY UPF0265 protein yeeX	2		ETTKPSFQDVLEFVR	1	15	6	25.35	b4b6b10°b10b12°y15	1795.90	71.840	18218	2	898.45	-11.42
[P67605 YEEX_SALTY UPF0265 protein yeeX	3		EIQDIEK	26	7	12	49.06	b1b2b5°b5°b5y2°y2y3°y3y4y5y7	874.45	35.207	7888	2	437.73	-4.05
[P67605 YEEX_SALTY UPF0265 protein yeeX	4		NAEISK	82	6	3	26.03	b3b4*b4	661.35	28.933	39780	1	661.35	-5.91
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	1	Carbamidomethyl+C(1)	CTWVASDFDALIPSLK	66	16	5	27.08	b11b12b14y2y4	1822.92	98.654	18392	2	911.96	6.83
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	2		GVDVVAYANQDLIYSDLTAGR	155	21	5	17.87	b6b11y7y14*y14	2240.11	113.458	2442	2	1120.56	-5.89
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	3		IGTDTTYAPFSSK	29	13	7	43.73	b4b6b8b9°b9y4°y4	1387.66	47.132	2163	2	694.34	-7.57
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	4		RQQEIAFSDK	98	10	4	25.84	b3b5y4°y4	1221.64	80.155	17943	2	611.32	12.49
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	5		QQEIAFSDKLYAADSR	99	16	3	24.7	y5y14y15	1841.89	93.804	7429	2	921.45	-9.08
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein	6		QPAGKEYAFAGPSVK	193	15	4	28.14	b10b11b13y9	1549.81	80.972	5865	2	775.41	6.62
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1	Carbamidomethyl+C(6)	LLVDACYSPVER	170	12	9	92.68	b2y4y5y6y7y8y9y10y12	1421.71	59.681	60932	2	711.36	-1.72
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2		LVDIEQVSSTHAK	12	13	4	19.69	b2b10y3y6	1426.73	46.199	52511	3	476.25	-13.18
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3		VTLEPLER	25	8	7	52.51	y1y4°y4y5y6y7y8	956.53	52.730	48152	2	478.77	-13.21
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4		IAYNVEAAR	182	9	6	52.96	b2y3y6y7y8y9	1006.53	39.684	47164	2	503.77	-6.06
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5	Carbamidomethyl+C(9)	ILLSSMPGCAVTEVEIDGVLHEYS TK	45	26	4	21.49	b3y6°y6y7	2848.42	91.093	23097	3	950.14	2.31
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		LENWPPASIADE	317	12	4	21.29	b5b11y11y12	1341.63	57.569	12093	2	671.32	-4.64
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		LVIEMETNGTIDPEEAIRR	200	19	5	24.74	b7b8b12y12°y12	2186.08	115.602	6719	2	1093.54	-14.52
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8		AEAIHYIGDLVQR	271	13	4	19.69	b6b12*b12y9	1484.79	77.665	16087	2	742.90	1.64
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9		TPNLGK	291	6	2	13.24	b5*b5	629.37	29.160	8043	1	629.37	13.19
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	10		TEVELLK	284	7	4	39.27	b3b5°b5y6	831.49	36.071	4985	2	416.25	5.51
[P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	11		DVRQPEVK	235	8	3	34.95	b4b6y4	970.52	42.020	11379	2	485.76	-14.65

P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	12	Carbamidomethyl+C(18)	IHSEEDERPIGRLLVDACYSPPER	158	24	8	30.77	b3b9°b9y3°y3y6y8y10	2840.44	136.339	5623	3	947.49	14.70
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	13		DIEQVSSTHAK	14	11	1	7.32	b10	1214.61	46.182	10546	2	607.81	5.13
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	14		LVDIEQVSST	12	10	0	3.56		1090.58	46.242	2897	3	364.20	13.88
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	1		LLEQEMVSFLFEGK	64	14	10	38.06	b1b5°b5b9b12°b12y3°y3y9y14	1669.87	101.766	30289	2	835.44	10.67
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	2		QTMLINEK	45	8	8	34.95	b3b8y2°y2y3°y3y5y8	976.51	41.951	26329	2	488.76	-0.50
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	3		DAEQQDFQLYPGELGK	12	16	3	13.95	y4°y4y8	1766.80	69.890	15710	2	883.90	-13.40
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	4		IYNEISK	29	7	3	36.26	b4y5y6	866.47	41.957	7434	2	433.74	9.16
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	5	Carbamidomethyl+C(4)	TIFCTYLQR	3	9	3	29.37	b5b7y3	1201.62	55.759	7823	2	601.31	13.61
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	6		DAWAQWQHKTMLINEK	36	17	3	15.53	b10b16y3	2127.06	100.178	8954	3	709.69	7.12
P67617 FETP_SALTY Probable Fe(2+)-trafficking protein	7		KLNMMAEHR	53	10	6	56.2	b5b6b7b8y4°y4	1243.59	35.142	3102	3	415.20	-8.93
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	1		LAEAGIPTQMER	60	12	8	66.66	b2b4y3y6y8y9y10y12	1315.67	50.476	51169	2	658.34	-0.46
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	2		QSLGGLIEAYEAVHR	215	16	5	26.41	b15y8°y8y10y13	1713.87	85.454	44152	3	571.96	-13.60
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	3		FNHFIMTK	52	8	7	31.94	b7y2°y2y6y7°y7y8	1037.53	28.362	8737	2	519.27	10.47
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	4		LGVEEGMELNPPIFDLFLK	104	19	6	44.64	b4b7b12b13b14*b14	2161.10	100.690	3725	3	721.04	-10.39
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	5		TVYSTENPDLLVLEFR	13	16	5	33.09	b3b6b13y10y13	1895.98	88.663	57373	2	948.49	0.39
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	6		GMVNNK	46	6	1	13.24	y4	662.33	42.904	14220	1	662.33	-1.75
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	7	Carbamidomethyl+C(7)	LLSDTECLVK	72	10	3	35.84	y6y7y8	1177.61	87.783	5421	1	1177.61	0.93
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	8		TVYSTENPDLLVLEFRNDTSAGD GAR	13	26	3	11.72	b10b13y13	2840.35	109.839	18729	3	947.46	-6.79
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	1	Carbamidomethyl+C(14)	ILNTASVIPVDGLCVR	252	16	5	43.98	b15y5y6y8y9	1726.94	77.789	30649	2	863.98	-5.30
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	2		ELTPAAVTGTLTTPVGR	315	17	5	21.71	b3b6y4y14y17	1683.94	68.789	23658	2	842.47	5.07
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	3		NVGFIGWR	2	8	5	31.94	b5°b5b6y6y8	948.50	70.847	16676	2	474.75	-7.59
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	4	Carbamidomethyl+C(8)	ALDIIVTCQGGDYTNEIYPK	65	20	6	26.8	b11°b11b14°b14y7y8	2270.13	112.411	7073	2	1135.57	14.30
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	5		ELLTQMGQLYGHVADELATPSSAILEDIER	174	29	4	17.18	b5b14°b14b21	3170.60	98.699	6638	3	1057.54	-1.77
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	6		GMVGSVLMQR	10	10	7	38.63	b4b8°b8b9°b9*b9y5	1077.56	47.110	6597	2	539.29	8.84

P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	7		DFDAIRPVFFSTSQFGQAAPTFGD TSTGTLQDAFDLDALK	25	40	5	13.94	b14y7y9y13*y13	4298.03	106.474	3627	3	1433.35	-6.02
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	8		SGELPVDNFGVPLAGSLIPWIDK	210	23	6	12.5	b2b3b15°b15y5y23	2424.28	111.901	2195	2	1212.65	1.31
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	9		LNMGPEFLSAFTVGDQLLWGAAE PLRR	335	27	5	22.37	b8°b8b9°b9b15	2988.53	115.960	208957	4	747.89	-3.76
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	10		MVEERDFDAIRPVFFSTSQFGQAA PTFGDTSTGTLQDAFDLDALK	20	45	3	24.25	b5y9y10	4942.34	101.719	10082	4	1236.34	-3.16
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	11		SGELPVDNFGVPLAGSLIPWIDKQ LDNGQSR	210	31	5	15.53	b6b13b16y8*y8	3322.70	111.351	7956	3	1108.24	-2.87
P0A1F8 DHAS_SALTY Aartate-semialdehyde dehydrogenase	12	Oxidation+M(1)	MKDDAIIILDVPVNDVITDGLNNG VK	103	26	4	17.43	b7y9y11y14	2826.45	115.570	15129	3	942.82	-1.81
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	11	55.54	b2b3y2y5y6y10y11°y11y13 y17y19	2032.90	38.374	50216	3	678.30	-8.95
P02936 OMPA_SALTY Outer membrane protein A	2	Carbamidomethyl+C(6)	AALIDCLAPDR	321	11	7	50.62	b3b8y1y3y6y8y11	1214.62	62.233	49781	2	607.81	2.21
P02936 OMPA_SALTY Outer membrane protein A	3		GVKDVVTQPQA	339	11	6	23.27	b6b8y1y3*y3y11	1141.61	38.137	24857	2	571.31	-5.77
P02936 OMPA_SALTY Outer membrane protein A	4		GDNINGAYK	85	9	4	37.15	y4y5y7y9	951.44	29.156	9964	2	476.23	-10.14
P02936 OMPA_SALTY Outer membrane protein A	5		IGSDAYNQGLSEKR	267	14	10	43.66	b2b3°b3b4°b4b5b9°b9y3y1 4	1537.74	35.188	7490	3	513.25	-10.72
P02936 OMPA_SALTY Outer membrane protein A	6		HFTLK	217	5	1	12.79	b3	645.36	47.043	4762	1	645.36	-12.86
P02936 OMPA_SALTY Outer membrane protein A	7		LGGMVWR	117	7	3	39.27	b5y3y5	818.43	39.310	4263	1	818.43	-6.79
P02936 OMPA_SALTY Outer membrane protein A	8		DNTWYAGAK	24	9	6	65.75	y3y5y6y7°y7y8	1025.48	76.325	3120	1	1025.48	14.52
P02936 OMPA_SALTY Outer membrane protein A	9		IGSDAYNQGLSEK	267	13	6	19.69	b10°b10°b10y6*y6y9	1381.68	32.552	1623	2	691.34	14.49
P02936 OMPA_SALTY Outer membrane protein A	10		HFTLKSDVLFNFK	217	14	6	53.2	b3b4b6°b6b10b11	1709.89	86.795	14414	2	855.45	-8.14
P02936 OMPA_SALTY Outer membrane protein A	11		DGSVVVLGFTDRIGSDAYNQGLS EK	255	25	5	21.42	b10b13y3y11y17	2627.29	66.716	8158	4	657.58	-1.21
P02936 OMPA_SALTY Outer membrane protein A	12	Carbamidomethyl+C(6)	AALIDCLAPDRR	321	12	3	28.49	y4y5y8	1370.73	42.018	5599	3	457.58	4.81
P02936 OMPA_SALTY Outer membrane protein A	13		ADTKSNVPGGPSTK	124	14	4	30.2	b5y7y9y13	1358.67	67.575	1981	2	679.84	-12.94
P02936 OMPA_SALTY Outer membrane protein A	14		IGSDAYNQGLSEKR	267	14	8	42.71	b8b9y10°y10y12y13°y13*y 13	1537.76	118.521	1606	2	769.38	-3.25
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	1		LFNELGPR	78	8	5	55.52	y3y4y6y7y8	945.50	55.854	161914	2	473.26	-11.49
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	2		AGDNAPMAYIELVDR	103	15	8	41.4	b4b5°b5y1y5y10y11y15	1634.79	79.277	58428	2	817.90	3.06
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	3		TRDNEIVAK	69	9	6	43.93	b3b7b8y7°y7y9	1045.55	42.117	14334	2	523.28	-12.14
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	4		QAMFR	17	5	2	25.59	b3y4	652.32	32.136	4784	1	652.32	-5.61
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	5		RVVEPLITLAK	45	11	5	54.09	b3b4b6b8y5	1238.78	63.151	161394	2	619.89	-3.25
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	1		MYAVFQSGGK	0	10	6	50.63	b2b3b5y4y5y8	1087.52	53.167	91998	2	544.26	-4.49
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	2		VSEGQTVR	13	8	4	47.5	y3y5y7y8	875.45	16.822	4432	2	438.23	-7.25
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	3		YAVFQSGGK	1	9	3	29.37	b5y3y8	956.48	86.624	17637	1	956.48	-9.00
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	4	Oxidation+M(16)	LDIATGETIEFAEVLMIANGEEVK	24	24	5	22.25	b8b10y6y12y14	2608.27	76.290	10481	4	652.82	-14.79

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	7	33.09	b3b7b14y1y6y9y16	1834.94	99.784	41802	2	917.97	4.32
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2		QAGIDLLPVGDFAWYDHVLTTSLLGNVPAR	52	31	13	50.07	b4b5°b5*b5b6°b6*b6y1y3y6y7y24y31	3351.78	119.824	35976	3	1117.93	2.77
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	3	Carbamidomethyl+C(7)	LWVNPDCLK	719	10	6	50.39	y2y4y6y7y8y10	1201.61	61.068	35259	2	601.31	1.42
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	4		SDWDAYLEWGVEAFR	611	15	3	17.27	b13y4y11	1843.83	93.705	25296	3	615.28	-0.53
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	5		LAAITAQDSQRENPYEV	395	18	5	36.79	b3b5b8y13y14	2061.02	48.088	15951	3	687.68	-6.16
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	6		LAAITAQDSQR	395	11	5	23.27	b10y6y9°y9y11	1173.61	49.311	11895	2	587.31	-8.63
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	7		WENTNYHYIVPEFSK	117	15	3	17.27	b10y5y12	1944.90	83.384	2435	3	648.97	-14.31
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8	Carbamidomethyl+C(1)	CGELALLRDALNSGETAALEEWSAPIQAR	352	29	4	17.18	b6b10b18y2	3141.55	104.938	2216	5	629.12	-4.51
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	9	Carbamidomethyl+C(1)	CVKPPVIGDISRPAPITVEWAK	515	23	6	35.87	b6b7b10y3y4°y4	2532.36	76.327	34880	4	633.84	-16.87
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	10		GQQFR	132	5	1	12.79	b3	635.32	42.825	14054	1	635.32	-5.38
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	11		DALNSGETAALEEWSAPIQAR	360	21	3	13.25	b3b12y19	2229.11	80.235	5473	3	743.71	12.81
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	12	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETR	315	22	4	12.85	b7y7y10°y10	2441.25	98.219	2263	3	814.42	1.10
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	13		RSDWDAYLEWGVEAFR	610	16	3	24.7	y9y11y12	1999.96	102.148	79052	3	667.32	12.94
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	14	Carbamidomethyl+C(11) ;Oxidation+M(2)	GMLTGPVTILCWSFPR	549	16	4	23.01	b5b11y3y9	1850.92	115.083	4554	2	925.96	-6.79
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	11	38.79	b1b2b6*b6b17y1y4y12y16y17y18	1970.00	63.641	85458	3	657.34	-9.48
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		VVGYSQDYSNAIVEAVK	61	17	9	46.13	b4b12y2y3y11y12*y12y13y17	1841.94	68.030	58186	2	921.47	4.04
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		AVAFMMDDALLAGER	198	15	9	66.69	b5b6y3y4y8y10°y10y13y15	1609.78	84.475	53836	2	805.39	4.09
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		ESSVPFSYYDNQK	47	14	3	18.37	b11y6y10	1691.76	55.863	50220	2	846.38	3.68
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5	Carbamidomethyl+C(13)	IPLLQNGTDFECGSTTNNLER	98	22	5	21.6	b10y2y9y10y22	2526.20	81.682	10767	3	842.74	1.26

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6	Carbamidomethyl+C(19)	KPDNWEIVGK PQSQEAYGCMLR	217	22	5	25.91	b4b12°b12y4y5	2606.26	136.376	26261	3	869.43	5.25
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7		LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	3	21.72	b9y11y12	2869.50	137.196	2176	3	957.17	19.31
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTT NNLER	89	31	6	29.52	b3y9y10y14y21y27	3548.79	86.883	111803	3	1183.60	3.65
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9		AVVVTSGTTSEILLHKLNEEQK	154	22	5	36.63	b3y8y17y18y19	2396.29	63.910	25268	3	799.43	-6.93
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		LMDDTIAQAQTSGEAEKWFDK	247	21	3	13.25	b10b13y4	2384.11	88.969	7697	4	596.78	-0.72
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11		KLMDDTIAQAQTSGEAEK	246	18	5	23.65	b7b10b12y13*y13	1935.92	108.850	2455	2	968.46	-7.63
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12	Oxidation+M(6)	AVAFMMDDALLAGER	198	15	4	28.14	b3y3y7y10	1625.76	42.942	6929	3	542.59	-3.38
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	1		AYASLATSADK	594	11	14	110.04	b1b2b3b5b6b7b8y2y3°y3y5y9y10y11	1097.56	35.161	18956	2	549.28	9.57
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	2		LNPIVFVSGGPMMEAGK	135	17	7	21.71	b2b3*b3b16y6y14°y14	1728.94	89.626	12869	2	864.97	0.07
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	3		VYESQDDAVEAILGGK	453	16	3	16.33	b12b15y11	1693.83	74.901	8146	2	847.42	1.73
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	4		EFNTIAVDDGIAMGHGGMLYSLP SR	72	25	5	34.25	b4b5b9b11b13	2651.24	128.929	2759	3	884.42	-7.46
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	5	Carbamidomethyl+C(16)	DGGLAVLYGNFAENGCIK	418	19	3	14.23	b5b11y6	1996.98	92.712	2470	3	666.33	1.96
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	6		VVEGDVVVIR	469	10	3	25.84	b4b6y6	1084.62	39.357	38480	2	542.81	-16.09
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	7		LDLVDAMIQGADPK	161	14	4	23.81	b13*b13y6y7	1485.76	71.795	9993	3	495.93	1.31
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	8		YEGPK	479	5	1	12.79	y3	593.29	90.146	6409	1	593.29	-8.85
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	9		SLEYAYSK	410	8	3	34.95	b4b6y4	960.45	44.005	4855	2	480.73	-18.81
P40810 ILVD_SALTY Dihydroxy-acid dehydratase	10		GGPGMQEMLYPTSFLKSMGLGK	484	22	3	22.72	b12b14b15	2329.15	118.524	1615	2	1165.08	3.25
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	1		SFELPALPYAKDALAPHISAETLEY HYGK	1	29	8	48.79	b4°b4y5y9y10y11y13y14	3231.64	81.491	33392	4	808.67	2.42
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	2		SFELPALPYAK	1	11	7	50.62	b2b3b6b9y4y7y11	1235.66	79.254	22106	2	618.33	-5.33
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	3	Carbamidomethyl+C(22)	TSEGGIFNNAQVWNHTFYWNCL APNAGGEPTGK	58	34	10	40.95	b1b13°b13b14*b14y5y7y9y10y13	3708.72	96.822	18498	3	1236.91	7.64
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	4		GTAPEGK	44	7	4	52.07	b4b5y3y4	709.35	42.923	5313	1	709.35	1.12
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	5		DALAPHISAETLEYHYGK	12	18	5	31.15	b6b7b10y6y10	2014.95	104.885	1508	2	1007.98	-20.48
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	6		SFELPALPYAKDALAPHISAETLEY HYGK	1	29	5	13.79	b6b10°b10y3y10	3231.68	94.796	3353	3	1077.90	14.13
P0A2F4 SODF_SALTY Superoxide dismutase [Fe]	7	Phosphoryl STY(7)	HHQTYVTNLNNLIK	30	14	3	23.81	b5_H3PO4 b5b6y10	1774.84	77.635	4723	3	592.29	-6.47
P0A6B1 ACP_SALTY Acyl carrier protein	1		IIGQLGVK	10	9	5	37.15	b2y4y7y8y9	956.57	49.756	119061	2	478.79	-10.78
P0A6B1 ACP_SALTY Acyl carrier protein	2		MSTIEER	0	7	7	55.08	b2b3b4y2y3y6y7	865.41	27.289	12050	2	433.21	5.92

[P0A6B1 ACP_SALTY Acyl carrier protein	3		ITTVQAIDYINGHQA	62	16	5	40	b5y3y8y11y14	1714.88	82.670	20902	2	857.94	-0.21
[Q7CPL4 RL16_SALTY 50S ribosomal protein L16	1		VLYEMDGVPEELAR	100	14	19	170.12	b2b4b5b8b10b13y2y4°y4y6y7y8y9y10y11°y11y12y13y14	1620.80	69.986	168772	2	810.91	5.57
[Q7CPL4 RL16_SALTY 50S ribosomal protein L16	2		VLYEMDGVPEELAREAFK	100	18	5	23.75	b1b2b10b12b13	2096.06	110.212	2615	3	699.36	8.97
[Q7CPL4 RL16_SALTY 50S ribosomal protein L16	3		GLAAGADVSGFSGLK	18	16	7	36.2	b5b8°b8b14b15°b15y11	1496.74	58.377	23142	2	748.88	-20.55
[Q7CPL4 RL16_SALTY 50S ribosomal protein L16	4		AMTR	51	4	1	12.35	b3	478.24	42.026	8159	1	478.24	-13.02
[P58661 AAT_SALTY Aartate aminotransferase	1		TAQTPGGTGALR	96	12	4	25.26	b3y7y8y12	1129.60	30.153	13812	2	565.30	-0.76
[P58661 AAT_SALTY Aartate aminotransferase	2		MFENITAAPADPILGLADLFR	0	21	11	34.34	b2b5b8b9°b9b13°b13°b13y1y3y13	2275.15	120.891	6148	3	759.06	-12.34
[P58661 AAT_SALTY Aartate aminotransferase	3		ELIVASSYSK	236	10	3	27.6	b8b9y7	1096.60	69.847	34877	2	548.80	10.58
[P58661 AAT_SALTY Aartate aminotransferase	4		EEFGVYAVASGR	362	12	6	35.84	b8y5°y5y7°y7y11	1284.60	127.273	1965	1	1284.60	-15.96
[P58661 AAT_SALTY Aartate aminotransferase	5		ANYSNPPAHGASIVATILSNDALR	280	24	4	15.94	b14b16y5y16	2452.23	103.536	1575	2	1226.62	-11.25
[P58661 AAT_SALTY Aartate aminotransferase	6		RVWVSNPSPWPNHK	121	13	6	32.7	b4b7°b7°b7b10y3	1606.84	63.796	25163	3	536.29	11.09
[P58661 AAT_SALTY Aartate aminotransferase	7		ELIVASSYSKNFGLYNER	236	18	5	25.41	b7y3y4y7°y7	2090.08	88.672	5302	2	1045.54	11.91
[P58661 AAT_SALTY Aartate aminotransferase	8	Carbamidomethyl+C(4)	VGACTLVAADAETVDRAFSQMK	254	22	4	12.85	b18y8y10*y10	2340.13	68.397	2279	3	780.71	-2.92
[P58661 AAT_SALTY Aartate aminotransferase	9	Carbamidomethyl+C(14)	NYLGIDGIPEFARCTQELLFGK	63	22	3	19.37	b3b6b11	2541.27	74.280	2023	2	1271.14	-2.79
[P58661 AAT_SALTY Aartate aminotransferase	10	Phosphoryl STY(6)	QLFVNTLQEK	322	10	3	27.6	b9y3y4	1299.61	73.065	6597	3	433.87	-12.12
[P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	1		NIANPIAQILSLALLR	293	17	13	70.67	b1b2b3b4°b4b5b6b8y1y2y4y7y8	1833.15	137.352	7990	2	917.08	7.19
[P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	2		ELTGGIYFGQPK	138	12	7	32.83	b3°b3b4°b4b7°b7y11	1309.67	67.639	6328	2	655.34	-4.10
[P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	3		TGDLAR	335	6	1	13.24	y5	632.33	33.472	16120	1	632.33	-9.36
[P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	4		ALEEGVR	328	7	4	49.06	b4y4y5y6	773.41	27.306	5317	2	387.21	-7.26
[P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	5	Carbamidomethyl+C(12)	ADIAANGFDILCVR	124	14	3	18.37	b4y3y10	1534.77	76.653	4139	2	767.89	0.16
[P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	6	Carbamidomethyl+C(6)	ATVEGCEQADAILFGSVGGPK	59	21	4	20.64	b3y4y13y16	2106.05	101.760	2914	3	702.69	13.91
[P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	7		TYPDVELAHMYIDNATMQLIK	214	21	3	13.25	b5b12y13	2466.16	100.403	2741	2	1233.59	-16.43
[P37412 LEU3_SALTY 3-isopropylmalate dehydrogenase	8	Carbamidomethyl+C(6)	ATVEGCEQADAILFGSVGGPKWE NLPPEQPER	59	33	8	22.85	b4°b4b29y3°y3y11°y11y12	3568.74	115.619	5626	3	1190.25	10.54
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	1		AVGWAALQYVQPGTIVGVGTGST AAHFIDALGTMK	8	35	8	25.31	b5b7b11y4y17y25y28y35	3487.81	107.991	58581	3	1163.27	0.84
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	2	Carbamidomethyl+C(3)	FICIADASK	112	9	5	29.37	b2b7y5y7y9	1024.51	51.649	28278	2	512.76	-4.89
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	3		GADVALIGTPDGVK	201	14	9	45.05	b4b5°b5b6y1y2y3y7y14	1312.71	57.730	25119	2	656.86	-3.16
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	4		FPLPVEVIPMAR	128	12	3	21.29	b6y4y7	1368.74	91.053	6765	2	684.87	-22.21
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	5		GQIEGAVSSSDASTEK	43	16	6	42.87	b4b6b7b9y4y9	1565.74	32.283	4720	2	783.37	5.22
[P66692 RPIA_SALTY Ribose-5-phohate isomerase A	6		QVDILGKFLPVEVIPMAR	121	19	3	21.19	y4y7y9	2122.19	100.646	53705	3	708.07	-7.13

P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	1	Carbamidomethyl+C(10)	VAEVIDIPFCVAGGIR	68	16	4	16.33	b5y1y9y11	1715.92	90.856	48001	2	858.46	0.57
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	2		VTQWETLDWVQEVQQR	153	16	9	49.78	b9y1y2y3y5y6y9y11y16	2045.02	84.447	42837	2	1023.02	7.70
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	3		AYLAGQGVEIR	245	11	7	51.08	b2b3y5y7y8y9y11	1176.63	51.801	42668	2	588.82	-6.85
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	4	Carbamidomethyl+C(5)	FGVQCIVVGIDTWFDATGK	119	20	4	24.16	b6b12b13y14	2228.11	91.494	12365	3	743.38	19.61
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	5		SWVAR	63	5	1	12.79	y4	618.33	31.627	3300	1	618.33	-9.28
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	6		VPLIASGGAGTMEHFLEAFR	201	20	5	26.49	b3b12y4y8y10	2103.05	61.763	2752	4	526.52	-10.68
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	7		ILSFGADKISINSPALADPTLITR	91	24	4	22.5	b13y6y7y11	2513.39	84.634	63108	3	838.47	-2.43
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	8		GAGEIVLNMNMNQDGVNRNGYDLT QLK	169	25	4	22.42	b7b10b11°b11	2736.37	84.342	4751	3	912.80	9.55
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	9	Carbamidomethyl+C(3)	DVCRVPLIASGGAGTMEHFLEAFR	197	24	5	12.2	b3y9°y9y13°y13	2633.30	112.633	3587	2	1317.15	1.67
P0A1R2 HIS6_SALTY Imidazole glycerol phohate synthase subunit hisF	10	Oxidation+M(9)	GAGEIVLNMNMNQDGVR	169	16	6	27.08	b3y6°y6y7°y7y10	1719.80	72.013	6168	3	573.94	-7.03
P16326 FLGL_SALTY Flagellar hook- associated protein 3	1		LQMSNLVDVDWNSVISSYVMQQ AALQASYK	272	30	16	63.19	b4b6°b6b7°b7b8°b8y1y3y4 °y4y8°y8y9°y9°y9	3388.67	136.340	12825	3	1130.23	5.26
P16326 FLGL_SALTY Flagellar hook- associated protein 3	2		YIFAGYK	133	7	4	39.27	b2b5y3y6	861.44	28.281	2274	2	431.22	-11.62
P16326 FLGL_SALTY Flagellar hook- associated protein 3	3		VTNPSDDPIAASQAVVLSQAQAQ NSQYALAR	35	31	5	13.2	b11°b11b16y7y10	3213.61	125.123	14468	3	1071.88	-0.38
P16326 FLGL_SALTY Flagellar hook- associated protein 3	4		AELGTQLSELSTLDSLGS DR	247	20	4	13.7	b11°b11b14y3	2092.06	88.392	2897	3	698.03	11.09
P16326 FLGL_SALTY Flagellar hook- associated protein 3	5		TFATQK	66	6	3	13.24	y5°y5°y5	695.36	36.088	2459	1	695.36	-14.92
P16326 FLGL_SALTY Flagellar hook- associated protein 3	6		TEAAPFDQATGGYHGGEK	140	18	4	23.65	b12y4y9y12	1835.86	50.057	2055	3	612.62	21.94
P16326 FLGL_SALTY Flagellar hook- associated protein 3	7		TEAAPFDQATGGYHGGEKSVTQQ VDSAR	140	28	3	21.57	b4b5y15	2907.37	112.615	10440	3	969.80	7.98
P16326 FLGL_SALTY Flagellar hook- associated protein 3	8		LGEQMSTGKR	25	10	4	25.84	b3°b3b9y6	1106.57	35.256	7003	2	553.79	8.16
P16326 FLGL_SALTY Flagellar hook- associated protein 3	9	Phosphoryl.STY(9)	VSLEESVLSQVTTAIQTAEK	72	21	5	28.28	b6b7b10y3y6	2341.15	73.147	7563	3	781.05	1.04
P16326 FLGL_SALTY Flagellar hook- associated protein 3	10	Phosphoryl.STY(8)	NSLNNVLTVR	237	10	5	37.84	b3°b3b7y4y9	1209.61	66.320	4015	2	605.31	13.42
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	1		HPVDIATDLNAPVLGLYGQDTSI PQESVETMR	183	33	3	16.69	y6y10y16	3523.70	90.274	38703	4	881.68	-10.88
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	2		VPDSQVLADLDHVASWASR	114	19	5	27.85	b3b6b10y5y8	2066.02	84.441	23340	3	689.34	-6.74
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	3		AAVAWYGK	164	8	5	34.95	b1b3b8y4y7	865.45	36.073	8375	2	433.23	-12.69
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	4		MLEWFAQYGGK	257	11	6	49.08	y3y6y8y9°y9y11	1329.64	79.645	5656	2	665.32	7.53

Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	5		ITWLYAAHNPQLK	151	13	5	34.16	b8°b8b9°b9b10	1554.86	110.817	35170	2	777.93	12.40
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	6		LALEGYLAIAPELYFR	78	16	4	16.33	b5b8°b8y13	1838.96	109.525	12353	2	919.99	-22.10
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	7		TTTHPSGFAPAASPLAPTMHTPD GAISAGITSIPSGDDMPAYYARP K	1	49	9	27.24	b7b16y6y8y10y12°y12y15y 19	4965.37	78.634	9745	5	993.88	-10.62
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	8		VPDSQVLADLDHVASWASRNGG DAHR	114	26	4	11.72	b9°b9b14y13	2773.38	129.541	3135	3	925.13	12.59
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	9		MLEWFAQYGGKK	257	12	4	30.77	b3b5y7y9	1457.71	75.075	2895	2	729.36	-8.46
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	10	Phosphoryl STY(21)	AEIVVYPDAGHAFNADYRPGYHE ASAKDGWQR	225	32	8	27.38	b3b12b14y4°y4y10y11°y1 1	3670.69	104.648	2169	3	1224.23	12.44
Q9L6M9 DLHH_SALTY Putative carboxymethylenebutenolidase	11		HPVDIATDLNAPVLGLYGGQDTSI PQES	183	28	6	38.59	y4y7y13y14y15°y15	2907.44	90.240	15950	3	969.82	0.92
P61179 RL22_SALTY 50S ribosomal protein L22	1		IFVDEGPSMK	73	10	7	66.2	b2y4y5y6y8y9y10	1122.54	51.667	93799	2	561.78	-4.78
P61179 RL22_SALTY 50S ribosomal protein L22	2		IFVDEGPSMKR	73	11	4	30.26	y1y5y7y8	1278.64	46.149	83852	3	426.88	-12.60
P61179 RL22_SALTY 50S ribosomal protein L22	3		LVADLIR	18	7	5	61.85	b4y3y4y5y6	799.49	57.886	110717	2	400.25	-19.77
P61179 RL22_SALTY 50S ribosomal protein L22	4		VLESAIANAEHNDGADIDDLK	49	21	7	25.27	b8b11b15°b15y6°y6y15	2210.05	103.700	2960	4	553.27	-4.86
P61179 RL22_SALTY 50S ribosomal protein L22	5		ETIAK	1	5	1	12.79	y3	561.32	25.370	2674	1	561.32	-4.57
P61179 RL22_SALTY 50S ribosomal protein L22	6		METIAK	0	6	2	26.03	b3y3	692.36	25.374	1972	1	692.36	-7.41
P61179 RL22_SALTY 50S ribosomal protein L22	7	Phosphoryl STY(9)	VSQALDILTYTNK	28	13	7	39.54	b3°b3b5°b5y3y4_H3PO4 y4y12	1545.75	70.843	3094	2	773.38	0.87
P61179 RL22_SALTY 50S ribosomal protein L22	8	Oxidation+M(9)	IFVDEGPSMK	73	10	6	25.84	b4°b4b6°b6y5°y5	1138.54	136.332	1976	1	1138.54	-4.93
P61179 RL22_SALTY 50S ribosomal protein L22	9		FVDEGPSMKR	74	10	0	2.67		1165.56	46.111	11439	2	583.29	-3.04
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	1		LNDEVLSWR	22	9	10	59.73	b1b2b5°b5b6b7b8y8y9°y9	1131.59	72.067	20447	2	566.30	7.98
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	2		LIPLVNDEGWFATRDR	321	16	6	36.2	b12y6y11y12y14y16	1901.97	86.476	14292	2	951.49	-8.15
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	3	Carbamidomethyl+C(11)	TLLAWLALMQCGAR	64	14	7	42.71	b2°b2b12b13y3y4y10	1603.87	99.815	13231	2	802.44	13.93
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	4		AASMAEGYWR	308	10	3	25.84	b3b8y6	1141.53	27.338	13825	2	571.27	21.92
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	5		EFGHRPVAVVEYASQAGDVNLAE WVR	388	26	4	17.86	y5y7°y7y9	2899.50	122.896	6163	3	967.17	17.77
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	6		LVSMTLTSGSTGLPK	135	15	4	28.14	b11b13b14y14	1491.78	97.697	5040	3	497.93	-20.46
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	7		LDNLFFSGGEGIQPEEVER	350	19	5	19.56	b14b16y11°y11y13	2136.03	60.431	2574	3	712.68	4.91
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	8		AGNQPR	58	6	1	13.24	b5	642.33	20.874	2138	1	642.33	-7.13
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	9		STAAYAVAWQPQR	122	13	4	28.93	b4b7b10°b10	1448.75	122.749	2067	1	1448.75	18.54
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	10		WLTMPSELKNGGIK	425	14	3	18.37	b6b8y4	1573.83	52.849	3408	2	787.42	-6.67
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	11	Carbamidomethyl+C(10) ;Oxidation+M(6)	QPLEQMLAGCTHASLVPTQLWR	208	22	4	23.21	b4b14b15y18	2552.24	78.562	4696	3	851.42	-14.16
P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	12		PLVNDEGWFATRDR	323	14	2	13.95	b5b7	1675.81	86.555	11125	3	559.28	-2.77

P37418 MENE_SALTY 2-succinylbenzoate--CoA ligase	13	Carbamidomethyl+C(7)	WLALMQCGAR	68	10	0	4		1205.59	99.906	11040	1	1205.59	-4.15
P41782 HILD_SALTY Transcriptional regulator hiiD	1		IGNHNVNAVALK	267	12	7	32.83	b2b4b8b9y2y11y12	1249.71	61.030	62979	2	625.36	10.55
P41782 HILD_SALTY Transcriptional regulator hiiD	2	Carbamidomethyl+C(12)	LTISNNHDTIYCDEPGMLVLKK	59	22	4	22.72	y11y13y14y22	2561.25	136.709	6320	2	1281.13	-7.63
P41782 HILD_SALTY Transcriptional regulator hiiD	3	Carbamidomethyl+C(12)	LTISNNHDTIYCDEPGMLVLK	59	21	3	13.25	b9b11y3	2433.21	99.396	3937	3	811.74	11.44
P41782 HILD_SALTY Transcriptional regulator hiiD	4	Carbamidomethyl+C(1); Carbamidomethyl+C(12)	CGYDSTSFIQCFC	279	14	4	33.94	y6*y6y7y8	1775.76	70.465	2498	4	444.70	11.76
P41782 HILD_SALTY Transcriptional regulator hiiD	5		EVFEHLK	143	7	3	39.27	b4b6y4	901.48	28.240	1915	2	451.24	-2.30
P41782 HILD_SALTY Transcriptional regulator hiiD	6		MENVTFVSNShQRPAADNLQK	0	21	4	22.9	y4y11*y11y12	2386.13	92.760	79221	3	796.05	-12.89
P41782 HILD_SALTY Transcriptional regulator hiiD	7		LAEEGTSFSDIYLSAR	242	16	9	66.54	b3b4b8b10b13y3*y3y7y9	1758.89	82.534	26588	2	879.95	18.39
P41782 HILD_SALTY Transcriptional regulator hiiD	8	Carbamidomethyl+C(11)	NLYVSSFTLVCFR	43	13	4	33.06	b5b6y7y9	1605.81	122.822	2809	2	803.41	-1.06
P41782 HILD_SALTY Transcriptional regulator hiiD	9		VYNISSSPSRQWK	210	14	5	18.37	b8*b8y8*y8y10	1664.86	101.696	57874	3	555.62	-11.95
P41782 HILD_SALTY Transcriptional regulator hiiD	10	Carbamidomethyl+C(12)	EVFEHLKTAFSCTK	143	14	3	18.37	b3b5y5	1696.82	71.842	24247	2	848.91	-8.63
P41782 HILD_SALTY Transcriptional regulator hiiD	11		ENVTFVSNShQRPAADNLQKLK	1	22	6	42.2	b4b8*b8b9b10b13	2496.30	89.161	23831	3	832.77	0.98
P41782 HILD_SALTY Transcriptional regulator hiiD	12	Carbamidomethyl+C(11)	NLYVSSFTLVCFRSGK	43	16	3	16.33	b8y10y12	1877.94	110.471	5585	2	939.47	-9.56
P41782 HILD_SALTY Transcriptional regulator hiiD	13		QWKLTDVADHIFMSTSTLK	221	19	6	14.23	b6*b6*b6b9y7*y7	2221.11	136.326	5340	2	1111.06	-12.20
P41782 HILD_SALTY Transcriptional regulator hiiD	14		TTPSTFIKMANH	297	12	3	21.29	b4b7y8	1347.67	83.391	2003	2	674.34	-3.26
P41782 HILD_SALTY Transcriptional regulator hiiD	15	Carbamidomethyl+C(12)	LTISNNHDTIYCDEP	59	15	1	8.05	y11	1791.81	136.724	3063	1	1791.81	12.47
Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	7	22.86	b1b3*b3b4y1y2y12	1686.94	90.064	37265	2	843.97	-2.97
Q7CR87 SURA_SALTY Chaperone surA	2		LNAGQAGQQLPDDATLR	50	17	6	26.18	b9y4y10*y10y11y17	1767.90	51.345	12413	2	884.46	3.52
Q7CR87 SURA_SALTY Chaperone surA	3		QIGTQNDASTELNLSHILALPENP TSEQVNDAGR	162	35	7	29.55	y6y8y9*y9y12y14y35	3816.91	88.711	9812	3	1272.97	2.43
Q7CR87 SURA_SALTY Chaperone surA	4		LAYDGLNYSTYR	117	12	7	47.84	b1b6b7b9*b9b11y3	1435.69	82.404	3216	2	718.35	1.79
Q7CR87 SURA_SALTY Chaperone surA	5		VAAVVNNGVVLESVDGLMQSV K	27	23	3	12.5	b4b8y10	2343.22	91.062	6406	2	1172.11	-2.29
Q7CR87 SURA_SALTY Chaperone surA	6		GQSQSISVTEVHAR	274	14	4	18.37	b9b12*b12y5	1498.76	56.468	5558	2	749.88	-0.98
Q7CR87 SURA_SALTY Chaperone surA	7		QAESIVEEAR	197	10	3	25.84	b4b6y9	1131.54	119.790	1503	1	1131.54	-17.26
Q7CR87 SURA_SALTY Chaperone surA	8		LAITYSADQQALKGGQMGWGR	214	21	7	40.13	b11*b11y9y10*y10y12y13	2251.16	112.400	3918	2	1126.08	14.75
Q7CR87 SURA_SALTY Chaperone surA	9		NGADFGKLAITYSADQQALK	207	20	4	13.7	b9b13*b13y12	2111.07	104.752	2102	2	1056.04	-2.78
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		MQLNSTEISELIK	0	13	8	52.54	b2b3b9b12y3y10y11y13	1505.79	76.919	57800	2	753.40	-0.08
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2		AVDSMIPIGR	151	10	6	53.4	b1y4y5y7y8y10	1058.55	60.332	52852	2	529.78	-11.19
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	7	14.23	b2b7*b7y4*y4y6y19	2098.97	69.860	48346	3	700.33	-4.42
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4		GYLADVELAK	453	10	5	40.61	b2y2y3y6y9	1078.57	61.053	37726	2	539.79	-11.43

Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		ILEVPVGR	93	8	5	34.95	b3y2y4y6y8	882.53	53.056	35146	2	441.77	-13.07
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6		QYAPMSVAQQLVLFAAER	434	19	3	22.01	b3y5y6	2109.09	93.285	30954	2	1055.05	5.67
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		DSVGAVVMGPYADLAEGMK	68	19	4	14.23	b6b11y2y12	1909.92	83.597	29504	2	955.46	9.40
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		QSVDQPVTGYK	139	12	4	28.49	y7y9y10y12	1349.67	34.642	20963	2	675.34	-0.45
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9		ELAAFSQFASDLDDATR	401	17	6	21.71	b8b10°b10y4y13y17	1856.88	88.795	20933	2	928.94	5.65
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		RPPGREAFPGDVFYLHSR	278	18	3	23.75	y5y10y11	2101.09	79.574	1661	2	1051.05	8.71
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		TALAIDAIINQR	175	12	4	32.83	b7y4y7y8	1298.73	74.178	30139	2	649.87	-6.11
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12		VNADYVEAFTK	303	11	4	33.85	b3b8y4y6	1256.64	27.330	29511	3	419.55	21.66
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		GLLGR	101	5	2	25.59	b4y3	515.33	74.130	11210	1	515.33	-9.00
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		GEDALIYDDLK	252	13	3	19.69	b5b8y7	1451.69	68.581	3610	3	484.57	-21.95
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		VVNTLGAPIDGKGPVDNDGFSAV EAIAPGVIDR	106	33	14	61.08	b4°b4b5°b5°b5b27y5y6°y6 y7y10y13y17y28	3263.70	84.156	41191	3	1088.57	3.82
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16		EAFPGDVFYLHSRLLER	283	17	3	22.93	b4b9b11	2049.05	71.467	3425	3	683.69	-4.41
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17		VNADYVEAFTKGEVK	303	15	4	17.27	b3b13°b13y11	1669.84	78.670	3318	2	835.43	1.02
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18	Phosphoryl.STY(8)	QLNSTEISELIK	1	12	4	38.85	b7y5y6y7	1454.70	39.185	4732	2	727.85	-6.29
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	19	Carbamidomethyl+C(32) ;Oxidation+M(34)	LEEHGALANTIVVVATASESAALQ YLAPYAGCAMGEYFRDR	211	41	12	57.9	b4b8°b8b9b10°b10y4°y4y5 y6°y6y19	4431.20	136.249	6852	5	887.05	13.88
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	20	Oxidation+M(8)	DSVGAVVMGPYADLAEGMK	68	19	6	30.07	b5°b5b12y10y12y13	1925.90	66.689	3299	2	963.45	-0.51
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	21		DSMIPGR	153	8	0	2.22		888.47	60.347	10081	2	444.74	15.04
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		AEQQLDKDSAIVPVYYYVNAR	494	21	9	25.27	b4b11°b11y1y5y7°y7y9y2 1	2442.22	73.205	30072	3	814.75	-2.90
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		LADPNTASPYASYLQYGHIANIDD IAGKKPATDLGVK	125	38	5	16.54	b6b8b11°b11°b11	4001.04	83.371	22774	4	1001.02	-6.59
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3		TVINQVTYLPISSEVTDVNR	241	20	10	70.24	b4y3y5y6y10y11°y11y13y1 4y20	2248.18	77.116	19413	2	1124.59	-0.22
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4		NLGVNVNLENQEWK	410	14	5	29.41	b12y3°y3y4y6	1656.84	67.068	15322	2	828.92	2.36
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		LLAEAGFTADKPLTFDLLYNTSDL HK	372	26	7	26.38	b9b11b15y7°y7y9y12	2893.46	116.467	5284	3	965.16	-13.84
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		LVEPEWFK	352	8	3	39.72	y3y4y5	1047.54	71.423	29549	2	524.28	-7.81
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7		DSAIVPVYYYVNAR	501	14	4	30.2	b3b5b8y5	1629.83	93.910	22114	2	815.42	4.49
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8	Carbamidomethyl+C(4)	AGWCADYNEPTSLNTMLSDSSN NTAHYK	439	29	6	24.08	y6°y6°y6y8y10y13	3294.42	90.269	21991	3	1098.81	3.48

[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	9		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	4	11.23	b4b12y7°y7	3091.50	133.217	6199	3	1031.17	-12.24
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	10		DLFEGLLISDVEGHPSPGVAEK	67	22	3	12.85	b4y8y12	2309.16	64.782	5289	3	770.39	-1.59
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	11		NPQYWDNAKTVINQVTYLPISSEV TDVNR	232	29	4	13.79	b3b15y7y11	3364.68	102.306	26270	3	1122.23	-0.58
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	12		DPLDNIYVKNLYIIK	527	15	5	25.35	b7b8°b8b10°b10	1821.00	129.539	14335	2	911.01	-5.90
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	13		NNGSEVQSLDPHKIEGVPESNVSR	43	24	5	35.53	b4b5y5y6y11	2592.23	51.726	10362	4	648.81	-11.96
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	14	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYEINNQK	284	23	6	19.15	b4*b4b6b13y11°y11	2920.39	76.333	8342	3	974.13	2.09
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	15		DLFEGLLISDVEGHPSPGVAEKWE NK	67	26	5	11.72	b14y4*y4y13*y13	2866.46	95.055	6035	3	956.16	13.37
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein	16		FGDKWTQPANIVTNGAYK	200	18	4	21.99	b6b11*b11b15	2009.99	90.136	2241	4	503.25	-7.23
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTDSDAVGNAVK	84	17	10	75.36	b1b2b3b4b5y11y12y13y14 y17	1739.96	70.914	36017	2	870.48	2.95
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	2		DTIALVISTLNNPFFVSLKDGAQK EADK	26	28	4	24.56	y4y7y10y25	3034.57	114.816	15551	4	759.40	-14.56
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	3		ALQTAGK	224	7	6	39.27	b1b6y3y6*y6y7	688.40	35.190	3368	1	688.40	5.76
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	4		LVIK	291	4	1	12.35	y3	472.35	57.242	20024	1	472.35	-2.20
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	5		YPVDLK	285	6	3	38.83	b3b4b5	734.41	73.305	17684	1	734.41	1.16
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	6		GDVVSHIASDNVLGGK	119	16	10	57.73	b4b6b7b8°b8y3y7*y7y9°y9	1567.78	35.212	3911	3	523.27	-16.74
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	7		FNVLASQPADFDRTK	178	15	7	41.4	b7°b7b9°b9b13y8y9	1708.85	83.993	16638	2	854.93	-8.14
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	8		EADKLGYNLVVLDSQNNPAK	50	20	3	13.7	b9y8y11	2188.13	78.528	4656	3	730.05	3.79
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein	9	Oxidation+M(25)	GLNVMQNLLTAHPDVQAVFAQN DEMALGALR	193	31	3	11.03	b5b15y13	3352.69	84.002	1923	3	1118.24	5.02
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1		MIIPALDLIDGTVVR	0	15	8	53.43	b2b3y5y6y7y9y12y15	1625.93	103.121	82558	2	813.47	1.65
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	2		QVAVSGWQENSGVSLEQLVETYL PVGLK	138	28	5	11.36	b4y1y3y5y28	3030.61	118.445	13216	3	1010.87	10.55
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	3		GWFER	113	5	1	12.79	b3	694.33	51.625	15530	1	694.33	-7.56

[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	4		YPQIAFQSSGGIGDIDDIAALR	193	22	9	53.15	b3b6b7b11b14°b14b19y9y13	2307.12	118.573	6169	2	1154.07	-16.72
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	5		QIPLIK	60	6	1	13.24	y4	711.47	52.635	5149	2	356.24	-14.93
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	6		LQDYAAQGAGVLHLVDLTGAK	34	21	3	13.25	b8b14y3	2140.09	70.270	4785	2	1070.55	-20.99
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	7	Carbamidomethyl+C(4); Carbamidomethyl+C(25)	HVLCTDISRDGTLAGSNVSLYEEV CAR	166	27	5	14.52	b7b13°b13y3y10	3022.43	107.177	10017	4	756.36	-2.67
[P10372]HIS4_SALTY 1-(5-phohoribosyl)-5-[(5-phohoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	8		LHQGDYARQR	15	10	7	37.84	b3b8°b8*b8y6*y6y8	1243.61	36.052	4734	3	415.21	-14.63
[P66955]TALB_SALTY Transaldolase B	1		LSFSGEVK	262	8	4	34.95	b2b5b7y7	866.46	39.186	18671	2	433.73	-2.04
[P66955]TALB_SALTY Transaldolase B	2		LYQPQDATTNPSSLILNAAQIPEYR	25	24	6	22.49	b1y2y4y7y8y24	2716.39	81.479	15303	3	906.13	-2.97
[P66955]TALB_SALTY Transaldolase B	3		LSYDTEASIAK	100	11	4	23.27	b4b8y7y11	1197.60	45.058	15169	2	599.30	0.92
[P66955]TALB_SALTY Transaldolase B	4		ISTEVDAR	92	8	7	49.5	b6°b6b7b8y3y5y8	890.44	28.279	13532	2	445.73	-14.87
[P66955]TALB_SALTY Transaldolase B	5	Carbamidomethyl+C(11)	NVGEILELAGCDR	228	13	4	19.69	b4b12y8y13	1445.71	74.282	11932	2	723.36	1.44
[P66955]TALB_SALTY Transaldolase B	6		LIDDAVAWAK	50	10	4	25.84	b3b5y7y10	1101.60	47.189	9345	2	551.30	2.44
[P66955]TALB_SALTY Transaldolase B	7		DYAPAEDPGVVSVEIYEYYK	193	21	5	13.25	b2b5y4y6y21	2408.12	92.709	9325	3	803.38	0.61
[P66955]TALB_SALTY Transaldolase B	8		QFTTVVADTGDIAAMK	9	16	9	60.74	b3b8b14y10y11°y11y14y15y16	1667.84	96.916	4612	2	834.42	5.49
[P66955]TALB_SALTY Transaldolase B	9	Carbamidomethyl+C(2)	ACAEAGVYLISPFVGR	165	16	6	43.84	b9b12b15y3y4y6	1709.87	94.940	2773	2	855.44	-1.71
[P66955]TALB_SALTY Transaldolase B	10		FAVDQEK	301	7	8	49.06	b5y3°y3y5°y5y6°y6*y6	836.41	136.255	2122	1	836.41	-2.19
[P66955]TALB_SALTY Transaldolase B	11		ELAESEGAIER	250	11	6	35.27	b4b7°b7b8y7°y7	1203.58	118.536	2051	1	1203.58	-0.91
[P66955]TALB_SALTY Transaldolase B	12		QQSSDRAQQVVDATDK	60	16	5	40	b14y3y8y10y12	1775.88	75.011	9553	2	888.44	14.92
[P66955]TALB_SALTY Transaldolase B	13		LAVNIGLEILKLVPGR	76	16	4	27.08	b11b12b15y11	1705.09	136.737	3521	1	1705.09	12.24
[P66955]TALB_SALTY Transaldolase B	14		ILDWYKANTDK	181	11	4	49.08	y4y5y6y7	1366.68	72.020	2356	2	683.84	-14.74
[P66955]TALB_SALTY Transaldolase B	15		LYQPQDATTNPSSLILNA	25	17	0	8.45		1858.95	81.532	3603	3	620.32	-3.02
[P0A1S4]STPA_SALTY DNA-binding protein stpA	1		MNMLQNLNNIR	0	12	9	79.66	b2b3b4b11b12y4y7y9y11	1473.77	76.434	24839	2	737.39	0.25
[P0A1S4]STPA_SALTY DNA-binding protein stpA	2		INAFLELMK	57	9	3	29.37	b6b8y7	1078.59	84.878	22704	2	539.80	-9.62

P0A1S4 STPA_SALTY DNA-binding protein stpA	3		AMAREFSIDVLEEMLEK	15	17	4	26.18	b5b10b11y13	2010.99	91.375	2743	2	1006.00	0.12
P0A1S4 STPA_SALTY DNA-binding protein stpA	4		EFSIDVLEEMLEK	19	13	5	30.93	b7b10b11y10°y10	1581.78	104.622	23116	2	791.39	6.56
P0A1S4 STPA_SALTY DNA-binding protein stpA	5		ADGINPEELFAMDSAMPR	66	18	3	14.83	b7b16y11	1963.92	74.503	11289	3	655.31	15.85
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1	Carbamidomethyl+C(3)	FACGVIEK	169	8	9	52.51	y2°y2y4y5°y5y6°y6y7y8	923.46	41.892	120363	2	462.23	-9.32
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2		GGDNYSDKPAPLGGGGAR	151	18	7	60.3	y5y6y7y8y11y13y18	1688.78	34.008	89536	3	563.60	-11.06
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3		SLSELK	137	6	1	13.24	b5	676.39	37.265	2988	2	338.70	4.78
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	4		DGKEVPALMAGGHLDPK	81	18	5	29.38	b4b11y8y11y15	1863.92	83.836	1937	2	932.46	-3.67
P68684 RS21_SALTY 30S ribosomal protein S21	1		ENEPFDVALR	7	10	12	66.2	b2b10*b10y2y4y5y6y7°y7y9°y9y10	1189.58	63.824	83956	2	595.30	-0.92
P68684 RS21_SALTY 30S ribosomal protein S21	2		EFYEKPTTER	35	10	4	27.6	b7y4y5y10	1299.61	33.507	5689	3	433.87	-9.67
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	1	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	9	44.81	b6°b6b13y4y10y11y12y18y24	2589.30	82.787	70444	3	863.77	-3.11
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	2		SATPAQAQAVHK	176	12	21	121.06	b2b3°b3b5°b5b11y1y2y4y5*y5y6*y6y7*y7y8*y8y9*y9y10y12	1208.63	19.216	64809	2	604.82	-3.33
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	3		TQGAAAFEGAVIAYEPVWAIGTGK	152	24	16	37.43	b1°b1b2°b2°b2b5°b5b11b12b14y1y2y4y7y12y24	2407.24	93.767	47622	2	1204.12	4.16
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	4	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	5	25.55	b10b11y10y13y23	2433.22	88.163	40104	2	1217.11	5.02
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	5	Carbamidomethyl+C(14)	FAVLKEQGLTPVLCIGETEAEAEA GK	112	26	4	11.72	b23y1y5y9	2803.39	115.631	4219	3	935.14	-9.06
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	6		DIGAQYIIIGHSER	84	14	3	18.37	b6b10y7	1571.83	64.870	9687	2	786.42	8.39
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	7	Carbamidomethyl+C(9)	EQGLTPVLCIGETEAEAEAGK	117	21	3	19.89	y8y10y12	2245.09	109.888	5697	3	749.03	10.55
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	8	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAEAEAGKTEEVCAR	117	28	17	142.06	b4b5°b5b13y3y4y5y7y10y12y13y18y20y21y23y24y26	3090.44	72.312	277884	3	1030.82	-0.08
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	9	Oxidation+M(8)	AAAGSHIMLGAQNVLDNLSGAFTGETSAEMLK	52	32	8	25.83	b5b6b9b25°b25y5y8°y8	3220.58	136.390	3959	4	805.90	5.38
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	10		PAQAQAVHK	179	9	8	76.87	b3b4b5b6°b6b7b8°b8	949.51	19.209	27744	2	475.26	-11.89
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	11		TPAQAQAVHK	178	10	9	59.3	b3°b3b4b6°b6b7°b7b8°b8	1050.56	19.215	26416	2	525.79	-4.30
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	12		VAIAPPEMYIDLAK	37	14	0	8.01		1530.83	88.208	19339	2	765.92	6.22
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	13		TQGAAAFEGA	152	10	0	8.45		922.44	93.706	10263	1	922.44	13.30
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	1		MIQEQTMLNVADNSGAR	0	17	20	124.86	b2b3b8°b8b11b13°b13b17y3y5y6y7y8y9°y9y12°y12y14*y14y17	1877.89	59.434	106849	2	939.45	1.63
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	2		IISLAPEVL	114	9	6	29.37	b2b5y1y4y5y9	954.58	85.425	78408	1	954.58	-11.06
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	3	Carbamidomethyl+C(6)	FDGNACVILNNNSEQPIGTR	78	20	6	20.49	y3y9°y9°y9y11y20	2219.06	59.591	19158	2	1110.03	3.30
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	4	Carbamidomethyl+C(3)	VMCIK	18	5	1	12.79	y4	650.33	40.934	12476	1	650.33	-8.82
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	5		IQEQTMLNVADNSGAR	1	16	5	24.03	b3b9°b9b12°b12	1746.88	76.702	8450	2	873.94	19.43

Q7CPL5 RL14_SALTY 50S ribosomal protein L14	6		RPDGSVIR	70	8	3	34.95	b6y5y7	899.49	24.423	5190	2	450.25	-16.69
Q7CPL5 RL14_SALTY 50S ribosomal protein L14	7	Oxidation+M(7)	MIQEQTMLNVADNSGAR	0	17	3	22.93	y5y10y12	1893.89	96.006	7800	2	947.45	3.29
P65559 YFCD_SALTY Uncharacterized Nudix hydrolase yfcD	1		LASTEWVDIVNEDNEVIAQSSREQMR	6	26	6	20.66	b13b15y3*y3y13y17	3019.47	78.647	4364	3	1007.16	9.86
P65559 YFCD_SALTY Uncharacterized Nudix hydrolase yfcD	2		NEAALQEKPETE	171	13	5	24.46	b2*b2b8y9y10	1487.69	32.636	3400	2	744.35	5.09
P65559 YFCD_SALTY Uncharacterized Nudix hydrolase yfcD	3		DFLPGMLDATAGGVVQADEQLLESAR	61	26	5	11.72	b2b10*b10b12y4	2703.36	84.540	3109	3	901.79	11.56
P65559 YFCD_SALTY Uncharacterized Nudix hydrolase yfcD	4		TETKDFLPGMLDATAGGVVQADEQLLESAR	57	30	4	13.48	b8b11y4y16	3162.60	125.498	3036	3	1054.87	11.66
P65559 YFCD_SALTY Uncharacterized Nudix hydrolase yfcD	5		MVEQR	0	5	1	12.79	b3	662.33	42.012	9402	1	662.33	3.59
P65559 YFCD_SALTY Uncharacterized Nudix hydrolase yfcD	6		LASTEWVDIVNEDNEVIAQSSR	6	22	3	12.85	b8b13y11	2475.24	86.429	2542	3	825.75	15.88
P65559 YFCD_SALTY Uncharacterized Nudix hydrolase yfcD	7		HRATYIVVHDGMGK	37	14	5	37.4	y7y8*y8y10y12	1583.83	136.332	2108	2	792.42	11.33
P65559 YFCD_SALTY Uncharacterized Nudix hydrolase yfcD	8	Oxidation+M(10)	TETKDFLPGMLDATAGGVVQADEQLLESAR	57	30	5	15.84	b14y5y11*y11y13	3178.60	91.994	3952	3	1060.21	14.90
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	1		TQFMGPEGVGNASLSNIAGGAEEGMLVTMPK	242	31	6	21.17	b1b4b5b9y13y31	3035.47	92.602	6854	3	1012.49	1.69
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	2		TAGLDSSQGPTAAK	139	14	7	43.66	b1b12y6*y6y10y11y12	1303.65	29.265	6240	2	652.33	-0.28
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	3		GFEFGVFQWHADGSSTVAK	350	19	4	14.23	b3*b3b12y10	2070.01	122.746	2736	3	690.68	20.05
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	4		DINAKGGIK	54	9	3	29.37	b6y4y5	915.52	26.771	42118	2	458.27	-2.40
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	5		QQYGEGLARSVQDGLK	170	16	4	26.41	b3b10b14y8	1748.90	77.785	14968	2	874.96	6.00
P0A1W6 LIVK_SALTY Leucine-ecific-binding protein	6		SVQDGLKQGNANIVFFDGITAGEK	179	24	4	12.2	b3b11y3*y3	2508.31	74.082	4127	2	1254.66	12.85
P60726 RL4_SALTY 50S ribosomal protein L4	1		DFNEALVHQVVVAYAAGAR	21	19	6	48.27	b10b11y5y6y7y19	2030.05	83.820	48992	3	677.36	3.79
P60726 RL4_SALTY 50S ribosomal protein L4	2		VVMTADAVK	185	9	4	37.15	b2y5y6y8	933.50	37.311	44821	2	467.25	-9.74
P60726 RL4_SALTY 50S ribosomal protein L4	3		LKDMALEDVLIITGELDENLFLAAR	137	25	7	26.09	b5b7b10b20y2y9*y9	2802.50	136.363	18595	3	934.84	2.27
P60726 RL4_SALTY 50S ribosomal protein L4	4		FSVEAPK	123	7	3	39.27	b4y3y6	777.40	41.995	72990	2	389.20	-16.49
P60726 RL4_SALTY 50S ribosomal protein L4	5		DATGIDPVSLIAFDK	170	15	4	40.19	y4y7y10y13	1561.81	88.132	48739	2	781.41	-0.16
P60726 RL4_SALTY 50S ribosomal protein L4	6		DAQSALTVSETTFGR	6	15	10	45.44	b6*b6*b6b11*b11y5y8y9*y9y11	1582.78	47.152	22371	3	528.26	3.32
P60726 RL4_SALTY 50S ribosomal protein L4	7		KPWR	57	4	1	12.35	y3	586.35	35.137	14133	1	586.35	12.39
P60726 RL4_SALTY 50S ribosomal protein L4	8		DATGIDPVSLIAFDKVVMTADAVK	170	24	7	59.61	b3y3y4y7y8y12y13	2476.30	102.245	51901	3	826.10	-1.48
P60726 RL4_SALTY 50S ribosomal protein L4	9		VVMTADAVKQVEMLA	185	16	3	22.86	b5y4y5	1733.88	94.674	14416	2	867.45	0.92

P60726 RL4_SALTY 50S ribosomal protein L4	10		SGGVTFARPQDHSQKVNK	79	19	3	14.23	b7b10y10	2027.05	31.278	1611	2	1014.03	4.82
P60726 RL4_SALTY 50S ribosomal protein L4	11	Phosphoryl STY(13)	MELVLKDAQSALTVSETTFGR	0	21	3	13.25	b11b13y5	2376.17	73.394	2866	3	792.73	12.54
P60726 RL4_SALTY 50S ribosomal protein L4	12	Oxidation+M(1)	MELVLKDAQSALTVSETTFGR	0	21	4	22.9	y6°y6y7y9	2312.20	100.905	6860	3	771.41	10.14
P60726 RL4_SALTY 50S ribosomal protein L4	13	Oxidation+M(4)	LKDMALEDVLIITGELDENLFLAAR	137	25	9	47.05	b5b7°b7b10b11b15y10*y10y11	2818.47	103.427	6613	4	705.37	-6.32
Q8ZQT5 TOLB_SALTY Protein tolB	1		SNNTEPTWFPDSQTLAFTSDQAGRPQVYK	287	29	5	11.23	b4y14*y14y24y29	3285.55	77.683	43971	3	1095.85	1.11
Q8ZQT5 TOLB_SALTY Protein tolB	2		IEITQGVD SARPIGVVPFK	24	19	7	24.74	b2b9y1y3y15y16y19	2026.12	70.646	28289	3	676.05	-5.54
Q8ZQT5 TOLB_SALTY Protein tolB	3		WAGPGAAPEDIGGIVAADLR	43	20	5	13.7	b7y2y5y14y20	1936.00	85.508	24291	2	968.50	4.10
Q8ZQT5 TOLB_SALTY Protein tolB	4		LPATDGQVK	413	9	9	65.75	b9y4y5°y5y6y7y8*y8y9	928.51	28.360	23309	2	464.76	-0.33
Q8ZQT5 TOLB_SALTY Protein tolB	5		SALVIQTLANGAVR	223	14	5	31.68	b3b4y2y9y11	1412.82	71.040	18097	2	706.91	-2.59
Q8ZQT5 TOLB_SALTY Protein tolB	6		QVASFPR	237	7	3	39.27	y3y4y5	804.42	39.274	14428	2	402.71	-19.50
Q8ZQT5 TOLB_SALTY Protein tolB	7		TGSLNLYVMDLASGQIR	264	17	4	21.71	b7b11y6y16	1837.94	39.301	11656	3	613.32	-3.72
Q8ZQT5 TOLB_SALTY Protein tolB	8		HNGAPAFSPDGTK	244	13	4	30.93	b8b9b12y10	1298.61	57.836	9683	2	649.81	-3.29
Q8ZQT5 TOLB_SALTY Protein tolB	9		FNPLDR	67	6	3	26.03	y3°y3y4	761.39	36.050	6031	2	381.20	-3.37
Q8ZQT5 TOLB_SALTY Protein tolB	10		SPQPLMSPAWSPDGSK	197	16	6	23.01	b4*b4b10°b10y5y10	1684.83	36.061	3768	3	562.28	18.77
Q8ZQT5 TOLB_SALTY Protein tolB	11		MNINGGAAQR	316	10	3	25.84	b3b5y8	1031.49	94.919	1958	1	1031.49	-12.43
Q8ZQT5 TOLB_SALTY Protein tolB	12	Phosphoryl STY(7)	IAYVVQTNGGQFPYELR	166	17	6	44.84	b3b5b8°b8b9b12	2034.99	79.299	5906	3	679.00	13.26
P02906 SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQEIAAK	263	13	5	37.92	b4y9y10y11y13	1468.73	51.241	47288	2	734.87	-0.75
P02906 SUBI_SALTY Sulfate-binding protein	2		DIQLLNVSYPTR	20	13	5	19.69	b10y5y9*y9y13	1533.78	69.916	28982	2	767.40	-5.09
P02906 SUBI_SALTY Sulfate-binding protein	3		LFTIDEVFGGWAK	298	13	5	24.46	b10°b10b11y8y13	1482.76	102.556	27121	2	741.88	-2.80
P02906 SUBI_SALTY Sulfate-binding protein	4		QATSVINGIEADVVTALAYDVD AIAER	66	28	4	21.56	b16y12y13y15	2917.53	136.633	8213	2	1459.27	3.60
P02906 SUBI_SALTY Sulfate-binding protein	5		NVEVLDSGAR	183	10	4	25.84	b3°b3y5y8	1059.54	40.807	28764	2	530.27	-3.57
P02906 SUBI_SALTY Sulfate-binding protein	6		QSHGGSGKQATSVINGIEADVVTLALAYDVD AIAER	58	36	6	25.04	b11*b11b12b14b16°b16	3655.82	87.685	6810	5	731.97	-11.02
P02906 SUBI_SALTY Sulfate-binding protein	7		QETGDNV VIRQSHGGSGK	48	18	4	14.83	b9b16y4°y4	1868.92	99.803	4641	2	934.96	-0.13
P02906 SUBI_SALTY Sulfate-binding protein	8		AVAEAYLKLYSPEGQEIAAK	255	21	5	47.16	y9y10*y10y11y12	2314.20	115.045	2765	3	772.07	-0.21
P02906 SUBI_SALTY Sulfate-binding protein	9	Phosphoryl STY(15)	FEIVTPSESILAPTVSVVDK	226	21	4	19.89	y5y8°y8y10	2340.15	136.259	2090	2	1170.58	-2.71
Q9L9I8 THIE_SALTY Thiamine-phosphate pyrophosphorylase	1		LGLYPVDSVEWIER	12	15	5	38.21	b14y4y5y7y11	1774.94	95.348	30091	2	887.97	2.54
Q9L9I8 THIE_SALTY Thiamine-phosphate pyrophosphorylase	2		MYQPDFPTVPFR	0	12	3	21.29	b3y3y10	1497.73	78.076	27823	2	749.37	4.32
Q9L9I8 THIE_SALTY Thiamine-phosphate pyrophosphorylase	3		APAVLATGVGSI AVVSAITQAADWR	171	25	3	22.42	y4y5y8	2424.31	108.196	2286	3	808.78	-4.43
Q9L9I8 THIE_SALTY Thiamine-phosphate pyrophosphorylase	4		QMPSAPQGLAQLASHIER	137	18	6	23.65	b14°b14y6y9y16°y16	1933.97	75.394	31564	3	645.33	-10.23

Q9L9I8 THIE_SALTY Thiamine-phohate pyrophohorylase	5		LADYPTVAIGGISLER	155	16	3	16.33	b10y6y10	1674.90	36.079	17487	2	837.95	-6.05
Q9L9I8 THIE_SALTY Thiamine-phohate pyrophohorylase	6		LAIK	73	4	1	12.35	y3	444.31	46.025	10928	1	444.31	-10.03
Q9L9I8 THIE_SALTY Thiamine-phohate pyrophohorylase	7		AYGVHLGQEDLETTDLK	79	17	9	53.1	b4b6b10b14y8y10°y10y13°y13	1888.95	87.710	2829	3	630.32	13.76
P58580 GSHB_SALTY Glutathione synthetase	1		LYTAWFADLTPETLVTR	125	17	4	37.94	b6b7b8b10	1997.04	102.364	6598	2	999.03	3.55
P58580 GSHB_SALTY Glutathione synthetase	2		EGDPNIGVIAETLTELGNR	174	19	3	14.23	b9b15y6	1998.01	66.748	4663	4	500.26	-2.81
P58580 GSHB_SALTY Glutathione synthetase	3		EIEAEYPISITGMLMDAIEAR	291	21	8	49.14	b3b10b13°b13y5y6y7y10	2352.17	119.861	3778	2	1176.59	8.41
P58580 GSHB_SALTY Glutathione synthetase	4		KDPPFDTEFIYATYILER	86	18	7	23.65	b4b7b12°b12y2°y2y12	2218.10	126.545	3360	2	1109.55	-3.85
P58580 GSHB_SALTY Glutathione synthetase	5		WYEFGSEQEIK	65	11	3	23.27	b9y3y9	1415.67	47.090	6680	3	472.56	12.76
P58580 GSHB_SALTY Glutathione synthetase	6		GEPRPLSESDWEIARR	241	16	4	24.7	y3y9y10°y10	1897.95	71.784	2990	3	633.32	-2.83
P58580 GSHB_SALTY Glutathione synthetase	7		TLSVEQNYDKWYEFGSEQEIK	55	21	5	23.65	b7b9b10°b10y8	2593.19	126.985	2425	3	865.07	-9.32
P58580 GSHB_SALTY Glutathione synthetase	8	Phosphoryl STY(12)	DPPFDTEFIYATYILER	87	17	5	28.7	b9b10y7y10_H3PO4y10°y10	2169.98	86.520	2723	3	724.00	7.54
P58580 GSHB_SALTY Glutathione synthetase	9		LYTAWFADLT	125	10	0	5.34		1200.60	102.353	8699	2	600.80	2.24
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	1		AIAEHTDLQPILYNVPSR	120	18	13	41.72	b1b2b4°b4b5b7°b7y6y7*y7y12*y12y18	2037.05	72.065	36062	3	679.69	-13.24
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	2		LAAEGQFAEAR	219	11	4	35.03	y8y9y10y11	1162.59	41.763	15843	2	581.80	1.37
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	3		EATGNLTR	161	8	5	31.94	b1b3b4y7°y7	861.43	43.025	8488	2	431.22	-13.89
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	4	Carbamidomethyl+C(44)	ELVSDDFILLSGDDASALDFMQLG GHGVISVTANVAAREMADMCK	174	45	3	11.46	b5b11y3	4769.29	114.141	6025	4	1193.08	7.99
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	5		MFTGSIVALVTPMDEK	0	16	4	33.82	y3y5y7y8	1738.87	89.822	3763	2	869.94	-5.90
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	6		DIVK	279	4	1	12.35	y3	474.29	39.329	23716	1	474.29	-11.65
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	7	Carbamidomethyl+C(9)	FNDSGIVGCLTVPYYNRPTQEGL FQHFK	91	29	4	11.23	b11y9°y9y13	3388.71	95.925	22678	4	847.93	19.38
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	8		FTGSIVALVTPMDEK	1	15	4	17.27	b4°b4y7y10	1607.81	136.392	1657	2	804.41	-15.94
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	9		LPMTPTDHGRDIVK	268	15	3	17.27	b3b10y8	1692.90	137.364	2338	2	846.96	-3.32
Q8ZN71 DAPA_SALTY Dihydrodipicolinate synthase	10	Oxidation+M(3)	LPMTPTDHGR	268	11	5	45.85	b3b4b10y5y10	1253.63	46.054	2487	2	627.32	2.92