

SA123 + Zn(II) LC-MS run 2: 123_Zn_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	54	374.09	b2°b2b3°b3b4°b4b5°b5b6°b6b7°b7b8°b8b9b12°b12b13b14°b14b15b17b18b21y1y2y3y4y5y6°y6y7°y7*y7y8y9y10y11°y11*y11y12*y12y13°y13y14*y14y15°y15y16°y16y17*y17y18y21	2216.11	96.198	496962	2	1108.56	6.28
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	2		YSYVDENGETK	96	11	12	113.03	b6y2y3y4y5y6y7y8y9y10°y10y11	1304.56	32.198	103748	2	652.79	-0.19
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	3	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	8	32.08	b2b7y1y5y8°y8y9y13	1624.76	92.297	44890	2	812.88	7.06
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	4		TPAVIKK	114	7	7	50.41	b1b3y1y3y5y6y7	756.49	19.192	38481	2	378.75	-12.26
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	5		EEESAAAAEVEER	41	13	5	41.11	y4y7y8y11y13	1419.63	34.046	12768	2	710.32	6.97
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	6		LEV VVNERR	32	9	3	38.08	y3y4y8	1113.62	54.270	6815	2	557.31	-14.91
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	7		YSYVDENGETKTWTGQGR	96	18	14	132.82	b3°b3y4y6y8°y8y11*y11y12y13y14y15y16y17	2090.93	46.463	169043	3	697.65	-6.31
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	8		TPAVIKK	114	7	4	53.42	y3y4y5y6	756.49	18.462	19595	2	378.75	-12.02
[P0A1S2]HNS_SALTY DNA-binding protein H-NS	9	Oxidation+M(7)	LQQYREMLIADGIDPNELLNSMAAAK	57	26	5	15.65	b3b6y7y10*y10	2920.43	136.252	1858	3	974.15	-7.19
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	1		YQINPQGMDTSSMDVFVQQYADTVK	176	25	20	113.37	b2°b2b3b4°b4b7b13b15b17b21y1y5y6y7°y7*y7y8y9y12y25	2865.30	85.725	110437	3	955.77	-2.30
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	2		AAADLQLQGV PAMFVNGK	158	18	29	262.9	b2b4b5b6b7°b7b8b9b10b13b14b15b17y1y2y3*y3y5y6y7y8°y8y9y10y11*y11y12y13y18	1829.96	79.970	108037	2	915.48	2.33
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	3		TQTVQSAADIR	116	11	8	41.26	b2b3°b8y2y7y8y9y11	1189.61	34.558	35764	2	595.31	-4.31
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	4		ELTQAWAVAMALGVEDK	88	17	4	16.18	b5b16°b16y4	1831.90	119.563	1644	3	611.31	-11.59
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	5		SLVAQQEK	150	8	4	32.9	b4°b4b5y7	902.48	39.862	8073	2	451.74	-17.18
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	6		VFVDAGVKGEDYDAAWSFVVK	128	22	5	25.36	b6b13b15y13y21	2416.16	80.719	5432	2	1208.58	-8.99
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	7		GEDYDAAWSFVVKSLVAQQEK	136	22	3	34.67	y3y4y5	2484.18	91.257	4799	3	828.73	-11.50
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	8	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	3	16.18	b4b10y5	1847.90	55.853	9412	4	462.73	-8.59
[P0A2H9]DSBA_SALTY Thiol:disulfide interchange protein dsbA	9	Oxidation+M()	YQINPQGMDTSSMDVFVQQYADTVK	176	25	6	39.08	b3b4b5y8y10°y10	2881.31	72.540	2038	2	1441.16	2.46

P0A1H5 EFTU_SALTY Elongation factor Tu	1		AIDKPFLLPIDVFSISGR	205	19	13	93.78	b7b8b12y2y3y4y5y6y7y9°y 9y11y19	2117.15	104.993	602343	3	706.39	-8.88
P0A1H5 EFTU_SALTY Elongation factor Tu	2		ELLSQYDFPGDDTPIVR	155	17	26	190.05	b2°b2b3°b3b5°b5b6b7b15y 1y3y4y5y6y8y9°y9y10y11y 12°y12y13°y13y14°y14y17	1964.97	76.075	358238	2	982.99	4.54
P0A1H5 EFTU_SALTY Elongation factor Tu	3		TTLTAAITTVLAK	25	13	11	74.4	b2°b2b13y2y3y6y7y8y9y10 y13	1303.78	84.098	314338	2	652.39	-3.37
P0A1H5 EFTU_SALTY Elongation factor Tu	4		AGENVGVLLR	270	10	16	112.61	b2b4b5°b5°b5b7°b7y1y2y3 y4y5y6y7y9y10	1027.58	55.898	302300	2	514.29	-11.88
P0A1H5 EFTU_SALTY Elongation factor Tu	5		IIELAGFLDSYIPEPER	188	17	29	245.36	b2b3b4b5b7b11°b11b12°b 12b14y2°y2y3°y3y4°y4y5y 6y7y8°y8y9y10y11y12y13y 14y15y17	1962.03	101.341	299390	2	981.52	3.67
P0A1H5 EFTU_SALTY Elongation factor Tu	6		GITINTSHVEYDTPTR	59	16	33	220.41	b2b3°b3b8°b8b9°b9b10b1 2b13b16y1y3y4°y4y5°y5y6 °y6y7°y7y8°y8y9y10°y10y 11y12°y12y13y14°y14y16	1803.87	49.114	282074	3	601.96	-11.30
P0A1H5 EFTU_SALTY Elongation factor Tu	7		TTDVTGTIELPEGVEMVMPGDNI K	334	24	47	315.81	b1b2°b2b3°b3b4b5°b5b7b8 °b8b10°b10b11b12b13b14 b17°b17b18y3y4y5°y5y6°y 6°y6y7°y7°y7y8y9°y9°y9y 10y12y13°y13y14°y14y15y 16°y16y17y20y24°y24	2546.24	85.926	250488	2	1273.63	2.97
P0A1H5 EFTU_SALTY Elongation factor Tu	8		QVGVPYIIVFLNK	124	13	10	76.09	b3b4°b4b13y4y5y6y9y11y 13	1489.87	98.552	243241	2	745.44	-1.97
P0A1H5 EFTU_SALTY Elongation factor Tu	9		ALEGDAEWEAK	177	11	3	31.12	y4y5y8	1218.56	45.827	166433	2	609.79	-0.30
P0A1H5 EFTU_SALTY Elongation factor Tu	10	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	10	67.8	b2°b2y2y3y4y6y7y8°y8y10	1187.52	52.401	115548	2	594.26	-1.03
P0A1H5 EFTU_SALTY Elongation factor Tu	11	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEV	137	18	15	96.66	b2b3b4y2y4y5°y5y6y7y8°y 8y9y14°y14y18	2224.00	105.481	87097	2	1112.50	7.36
P0A1H5 EFTU_SALTY Elongation factor Tu	12		VGEEVEIVGIK	238	11	5	31.12	b2y4y5y10y11	1171.66	59.650	60354	2	586.33	-0.52
P0A1H5 EFTU_SALTY Elongation factor Tu	13		MVVTLIHPIAMDDGLR	358	16	19	192.21	b3b4b5°b5y3y4y5°y5y6y7y 8y9°y9y10°y10y11y12y13y 15	1780.92	78.706	708245	3	594.31	-15.01
P0A1H5 EFTU_SALTY Elongation factor Tu	14		TVGAGVVAK	382	9	6	78.78	b4b7y3y5y7y8	801.47	27.718	211302	2	401.24	-15.38
P0A1H5 EFTU_SALTY Elongation factor Tu	15		LLDEGR	264	6	3	39.86	b4y4y5	702.38	25.917	20077	1	702.38	2.61
P0A1H5 EFTU_SALTY Elongation factor Tu	16		NMITGAAQMDGAILVVAATDGP MPQTR	90	27	4	35.2	b8b9b10y6	2729.31	105.003	17980	3	910.44	-13.06
P0A1H5 EFTU_SALTY Elongation factor Tu	17	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	3	17.99	b3y5y9	1768.81	81.294	7164	3	590.28	15.39
P0A1H5 EFTU_SALTY Elongation factor Tu	18		TKPHVNVGTIGHVDHGK	8	17	5	25.94	b3y3y7°y7y9	1795.92	39.397	1938	5	359.99	-19.64
P0A1H5 EFTU_SALTY Elongation factor Tu	19	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLE LVEMEV	124	31	7	62	b4°b4y3y4y5y6y7	3694.83	126.915	40603	3	1232.28	-4.29
P0A1H5 EFTU_SALTY Elongation factor Tu	20		GSALKALEGDAEWEAK	172	16	5	24.72	y6°y6y8y10°y10	1674.83	85.822	8944	2	837.92	0.66
P0A1H5 EFTU_SALTY Elongation factor Tu	21		TTLTAAITTVLAKTYGGAAR	25	20	3	14.26	b5y6y9	1980.13	103.432	1649	3	660.72	9.68
P0A1H5 EFTU_SALTY Elongation factor Tu	22	Oxidation+M(1)	MVVTLIHPIAMDDGLR	358	16	6	35.16	b4°b4b12y8y9y13	1796.92	73.274	44233	3	599.65	-9.65

P0A1H5 EFTU_SALTY Elongation factor Tu	23	Oxidation+M(16)	TTDVTGTIELPEGVEMVMPGDNI K	334	24	4	12.62	b3b12°b12y8	2562.24	78.619	4562	2	1281.62	2.38
P0A1H5 EFTU_SALTY Elongation factor Tu	24		TINTSHVEYDTPTR	61	14	3	14.28	b4*b4b10	1633.79	49.100	17189	2	817.40	6.87
P0A1H5 EFTU_SALTY Elongation factor Tu	25		TTDVTGTIELPEGVEM	334	16	3	12.26	y3°y3y13	1691.78	85.965	3095	3	564.60	-12.05
P0A1H5 EFTU_SALTY Elongation factor Tu	26		GITINTSHVEYDTPTR	59	16	0	4.52		1785.87	49.106	19525	3	595.96	-0.89
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	1		SGFAEDEVVAVSK	35	13	16	117	b2b3b4°b4b10y1y2°y2y3y4y7y8y9y10y12y13	1337.66	53.825	199892	2	669.33	-0.46
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	2		LGEIEYR	48	7	11	63.56	b2b3°b3y1y2y3y4y5y6°y6y7	879.45	41.653	187778	2	440.23	-10.13
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	3		MITGIQITK	0	9	11	64.38	b1b2b3y1y2y3y4°y4y6y7y9	1004.57	54.523	173150	2	502.79	-9.54
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	4		EIPMEVKPEVR	55	11	10	86.73	b4y1y2y3y4y5y6y8y9y11	1326.71	48.332	166178	2	663.86	-2.30
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	5		VEGGQHLNVNVLR	66	13	14	84.68	b2°b2b5b7°b7b11°b11y3y4°y4y6y7y8y13	1434.77	49.966	113441	3	478.93	-10.89
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	6		FNSLTPEQQR	106	10	21	112.61	b2°b2b3°b3b5b10y2y3°y3y4°y4y5°y5°y5y6y7y8°y8y9°y9y10	1219.60	37.402	103979	2	610.31	-3.20
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	7		FNSLTPEQQRDVIAR	106	15	10	52	b3°b3b11y1y4y6y10°y10y13y15	1773.91	47.028	48297	3	591.98	-7.71
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	8		AANDDLLNSFWLLDSEK	9	17	4	23.58	b8b10b13°b13	1950.94	98.288	3483	2	975.97	-4.07
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	9		TFTESL	121	6	5	39.86	b4°b4b5°b5y4	697.34	54.751	71604	1	697.34	-1.58
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	10		AANDDLLNSFWLLDSEKGEAR	9	21	28	255.75	b3b4b5°b5b6°b6b7°b7y3y4y5y7°y7y8°y8y9y10y11°y11y12y13y14°y14y15y16°y16y17y19	2364.14	92.119	426348	3	788.72	-3.61
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	11		HPEKYPQLTIR	88	11	4	50.29	b4b5b7b9	1381.76	72.434	9999	3	461.26	2.39
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	12		PMEVKPEVR	57	9	2	21.77	b3b4	1084.58	48.345	142483	2	542.79	-2.70
Q7CQ05 GRCA_SALTY Autonomous glycy radical cofactor	13		EIPMEVKPEVR	55	11	0	2.46		1308.68	48.364	49905	3	436.90	-9.33
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	1		IAAANVPAFVSGK	70	13	26	208.9	b2b3b4b5°b5b6°b6b8b10y1y2y3y4y5y6y7°y7y8y9y10°y10y11°y11°y11y12y13	1244.70	58.966	727916	2	622.85	0.39
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	2		AALESTLAAITESLKEGDAVQLVG FGTFK	22	29	13	56.85	b2b3b4b7°b7b23y3y6°y6y7y8y14y29	2966.56	115.501	351796	3	989.53	-3.46
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	3		NPQTGKEIK	61	9	15	93.69	b1b2°b2b3°b3b4°b4°b4b6y2y3°y3y5y6y8	1014.55	14.382	4799	2	507.78	-3.61
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	4		TQLIDVIADKAELSK	3	15	19	179.74	b3°b3b4b5°b5b6°b6y3y4°y4y5y6y7y8°y8y10y11y12y13	1643.90	71.486	642679	3	548.64	-14.70
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	5		AALESTLAAITESLKEGDAVQLVG FGTFK	22	29	4	11.47	b5°b5y3y5	2966.56	117.870	3106	2	1483.78	-3.87
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	6	Phosphoryl STY(6)	AALESTLAAITESLK	22	15	5	44.41	b5b10b12b14y10	1597.81	115.769	2903	2	799.41	6.57
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha	7		PQTGKEIK	62	8	2	8.77	b5°b5	900.53	14.285	8613	2	450.77	14.57
P64076 ENO_SALTY Enolase	1		FNQIGSLTETLAAIK	342	15	22	183.56	b2°b2b3°b3b4°b4b5b7°b7b14y2y3y4y6y7y8y9y10y11y12y13y15	1605.88	85.107	331598	2	803.45	-0.99

P64076 ENO_SALTY Enolase	2		SGETEDATIADLAVGTAAGQIK	371	22	32	251.46	b2b3b4b5b10b11b12°b12b13°b13b14°b14b18y2y3y4y5y6°y6y7°y7y8°y8°y8y9y10y12y13y14y16y17y22	2118.07	74.547	230748	2	1059.54	5.19
P64076 ENO_SALTY Enolase	3		GMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	200	31	30	209.9	b2b3b4b5°b5b6°b6°b6b13b16b17°b17b26b27b30y1y2y3y4y5y6y7y8y10y11y14y15y18y19y31	2989.46	94.298	176502	3	997.16	-0.25
P64076 ENO_SALTY Enolase	4		YSMPVPMMNIIINGGEHADNNVDIQEFMIQPVGAK	143	34	12	72.42	b2b4b5y3y5y9y11y12y13y29y31y34	3759.76	97.872	142533	3	1253.93	-0.13
P64076 ENO_SALTY Enolase	5		AVGAVNGPIAQAILGK	66	16	11	92.53	b2b3b4b5y3y4y10y11y12y14y16	1478.87	74.445	141302	2	739.94	-2.06
P64076 ENO_SALTY Enolase	6		DAGYTAVISHR	360	11	16	176.41	b2b3b4b5b7b8b9y3y4°y4y5y6y7y8y9y11	1189.59	40.971	114008	2	595.30	-2.46
P64076 ENO_SALTY Enolase	7		GIANSILIK	333	9	6	54.24	y2y3y5y6y7y9	928.58	60.470	109771	2	464.79	-7.43
P64076 ENO_SALTY Enolase	8		GMPLYEHIAELNGTPGK	126	17	4	16.18	b12y2y6y12	1826.90	66.915	78910	3	609.64	-8.09
P64076 ENO_SALTY Enolase	9		IQLVGDDLFVTNTK	311	14	15	99.79	b2°b2b3b13y1y2y4y5°y5y6y9y10y11y12y14	1562.84	76.895	73466	2	781.92	0.00
P64076 ENO_SALTY Enolase	10		AVGAVNGPIAQAILGKDAK	66	19	5	21.77	b1y3°y3y5y13	1793.01	68.220	65200	3	598.34	-10.21
P64076 ENO_SALTY Enolase	11		ILKEGIEK	325	8	5	40.68	y4y5°y5y6y8	929.56	29.534	33822	2	465.28	-7.75
P64076 ENO_SALTY Enolase	12		IEEALGEK	411	8	6	35.91	b2b5y1y3y7y8	888.46	30.490	31597	2	444.73	-7.21
P64076 ENO_SALTY Enolase	13		AVGAVNGPIAQAILGKDAKDQAGIDK	66	26	4	21.84	b3b4y7°y7	2520.34	86.998	11339	3	840.79	-13.37
P64076 ENO_SALTY Enolase	14		EALELRDGDK	46	10	4	33.72	b4b5b8y10	1145.57	53.887	7856	2	573.29	-10.34
P64076 ENO_SALTY Enolase	15		YVLAGEGNK	257	9	5	54.24	y3°y3y5y6y7	950.51	32.660	116811	2	475.76	19.59
P64076 ENO_SALTY Enolase	16		QYPIVSIEDGLDESDDWGFAYQTK	282	24	8	32.6	b8°b8b13y6°y6y8y10y11	2776.29	93.027	78056	3	926.10	9.50
P64076 ENO_SALTY Enolase	17		EALELR	46	6	1	13.56	b4	730.41	40.203	19750	1	730.41	-4.43
P64076 ENO_SALTY Enolase	18		IMIDLDGTENK	92	11	6	24.13	b6y3°y3°y3y5°y5	1248.61	109.937	9680	2	624.81	-4.01
P64076 ENO_SALTY Enolase	19		AAAAAKGMPLYEHIAELNGTPGK	120	23	4	12.95	b3y4y9°y9	2310.17	66.957	46918	4	578.30	-10.89
P64076 ENO_SALTY Enolase	20		GKGMNTAVGDEGGYAPNLGSNAEALAVIAEAVK	198	33	5	17.64	b7b15b17y4y18	3174.58	89.348	32434	3	1058.86	0.92
P64076 ENO_SALTY Enolase	21		IEEALGEKAPYNGR	411	14	3	27.7	y5y7y9	1546.77	39.193	15826	3	516.26	-9.08
P64076 ENO_SALTY Enolase	22	Phosphoryl STY(8)	FNQIGSLTETLAAIK	342	15	3	24.01	b6y9y10	1685.83	60.008	9225	3	562.61	-9.05
P64076 ENO_SALTY Enolase	23	Oxidation+M(2)	GMPLYEHIAELNGTPGK	126	17	7	43.27	b11°b11b12b13y6y8°y8	1842.89	127.119	3044	2	921.95	-10.40
P64076 ENO_SALTY Enolase	24		GYTAVISHR	362	9	1	7.83	b3	1003.53	40.998	43823	2	502.27	0.49
P64076 ENO_SALTY Enolase	25		ANSILIK	335	7	5	38.08	b3b4°b4°b4b5	758.48	60.472	20912	1	758.48	0.72
P64076 ENO_SALTY Enolase	26		AGYTAVISHR	361	10	0	2.46		1074.56	40.901	7615	2	537.79	-4.66
P64076 ENO_SALTY Enolase	27		TAVISHR	364	7	0	2.46		783.44	40.985	4903	2	392.22	-6.93
P64076 ENO_SALTY Enolase	28		YSMPVPMMNIIINGGEHA	143	17	4	36.38	y9y13y14y15	1860.85	97.895	3541	3	620.95	1.05
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	1		VINDNFGIIEGLMTTVHATTATQK	160	24	45	308.91	b2b3b4°b4b5°b5°b5b6°b6b7°b7°b7b8°b8°b8y1y3y5y6y7°y7°y7y8°y8y9y10°y10y11y13y14°y14y15°y15y16°y16y17y18°y18y19y20y21y22°y22y24°y24	2574.32	97.415	638106	3	858.78	-2.85
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	2		GASQNIIPSSTGAAK	198	15	22	155.8	b5°b5°b5b6°b6°b6b7°b7°b7b14b15y2y3y4y5y6y7y8y9y10y11y15	1401.73	40.219	288327	2	701.37	-1.57
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	3		AGIALNDNFVK	296	11	18	139.32	b3b4b5b10y1y2y3y4y5°y5°y5y6°y6y7°y7y8y9y11	1161.62	60.916	284328	2	581.31	-4.62

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	4		LVSWYDNETGYSNK	307	14	15	133.87	b2b9b12y1y3y4y5y6y8y9y10y11*y11y12y14	1675.77	57.769	236017	2	838.39	6.92
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	5		VLDLIAHISK	321	10	4	33.72	y5y6y8y10	1108.66	65.758	144446	2	554.84	-8.26
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	6		AATYEQIK	249	8	9	40.68	b1b8y2y4°y4y5*y5y6y8	923.47	30.324	135531	2	462.24	-11.90
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	7		VPTPNVSVVDLTVR	232	14	14	117.71	b2b3°b3b5y2y4y5y6y7y8y9y11y12y14	1495.85	70.316	110941	2	748.43	-0.08
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	8		SDIEIVAINDLLDAEYMAYMLK	24	22	12	63.85	b4b5b7°b7b13°b13y3y5y7y9y11°y11	2530.24	126.724	89777	3	844.09	-1.74
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	9		LTGMAFR	225	7	4	40.27	y4y5y6y7	795.41	48.821	85843	2	398.21	-9.90
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	10		VVLTGPSKDNTPMFVK	116	16	6	34.86	y5y7*y7y8y13y16	1732.91	57.228	61170	3	578.31	-9.93
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	11		VLPELNGK	217	8	9	66.98	y3*y3y4*y4y5y6*y6y7y8	869.50	44.195	54259	2	435.25	-9.41
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	12	Carbamidomethyl+C(12) ;Carbamidomethyl+C(16))	YEQDIVSNASCTTNCLAPLAK	138	22	3	13.33	b7y8y12	2412.09	106.358	9995	3	804.70	-11.94
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	13	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEGQDIVSNASCTTNCLAPLAK	132	28	43	357.15	b3b4b5*b5b6b7b8b10*b10b11°b11b12°b12b13°b13*b13b15b16b17b22b23b24*b24b26b27y3y4y5y8y9y10*y10y11y12°y12*y12y13°y13y14y15°y15*y15y16	3044.41	66.256	347363	3	1015.47	-0.08
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	14		GGRGASQNIIPSSTGAAK	195	18	7	32.48	b6°b6b8y8y9°y9y12	1671.87	36.205	5656	3	557.96	-7.16
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	15		RSDIEIVAINDLLDAEYMAYMLK	23	23	3	12.95	b3b16y20	2686.36	93.007	4623	3	896.13	5.63
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	16		YDSTHGRFDGTVEVK	46	15	4	26.07	y8y11°y11y12	1710.83	78.069	4111	3	570.95	10.77
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	17		DLIAHISK	323	8	0	2.05		896.51	65.715	48521	2	448.76	-12.87
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	18		LDLIAHISK	322	9	0	2.05		1009.59	65.714	45747	2	505.30	-9.98
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	19		AATYEQIK	249	8	0	1.23		905.46	30.325	52469	2	453.24	-5.53
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase	20		LTGMAFR	225	7	0	0.82		777.40	48.822	7784	2	389.20	-3.85
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	1		LADVLAANAR	57	11	14	113.82	b2b3b4y1y3*y3y4y5*y5y6y7y9y10y11	1084.60	52.822	175936	2	542.80	-11.70

Q8ZK80 RL9_SALTY 50S ribosomal protein L9	2		VANLGLGDQVNVK	8	14	24	217.09	b2b3b4b6b7*b7b9*b9b11b13*b13y3y4y6y7*y7y8y9*y9y10*y10y11y12y14	1413.77	56.054	147601	2	707.39	-0.17
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	3		DIADAVTAAGVDVAK	97	15	11	91.96	b2b5b6b8y4y6y7y8y9y10y15	1415.74	65.556	97084	2	708.37	0.43
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	4		NVEYFEAR	42	8	5	40.68	b1y2y4y5y6	1027.48	46.337	81388	2	514.25	-1.19
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	5		INALETVTIASK	71	12	6	49.38	b3y4y9y10y11y12	1259.72	60.641	57335	2	630.36	-0.68
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	6		TTGEHEVNFQVHSEVFAK	123	18	3	15.45	b5b7y13	2058.96	94.159	10193	3	686.99	-12.69
Q8ZK80 RL9_SALTY 50S ribosomal protein L9	7		AGDEGKLFGSIGTR	83	14	3	34.69	y6y7y8	1407.70	54.579	81798	3	469.91	-13.70
P65702 PGK_SALTY Phohoglycerate kinase	1		VLPAVAMLEER	373	11	15	113.03	b1b2b3y1y2*y2y3y4y5y6y7y8y9y10y11	1227.67	79.521	295882	2	614.34	-4.67
P65702 PGK_SALTY Phohoglycerate kinase	2	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	20	159.86	b2b6*b6b7*b7b9*b9b12b13y1y2y3y5y7y8y9y10y11y12y14	1599.84	67.997	207114	2	800.43	0.99
P65702 PGK_SALTY Phohoglycerate kinase	3	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	21	208.49	b2b3b4b5b6b7y1y2y3y4y5y6y7y8y9y10y13y14y15y16y20	2002.04	98.442	193645	2	1001.52	3.90
P65702 PGK_SALTY Phohoglycerate kinase	4		VATEFSETAPATLK	258	14	26	173.01	b1b2b3*b3b4*b4b6*b6b7b9y1y2y3y5*y5y6y7y9*y9y10y11*y11y12*y12y13y14	1464.76	51.995	138452	2	732.88	1.92
P65702 PGK_SALTY Phohoglycerate kinase	5		TILWNGPVGVFEFPNFR	302	17	19	115.77	b4b6b13*b13y4*y4y5y6*y6*y6y7*y7y8*y8y11y12*y12y13y17	1993.04	105.985	124121	2	997.03	5.51
P65702 PGK_SALTY Phohoglycerate kinase	6		SLYEADLVDEAKR	231	13	11	95.26	b4b5*b5y4y5*y5y6y9y10y11y13	1508.74	53.871	122841	3	503.59	-11.97
P65702 PGK_SALTY Phohoglycerate kinase	7		ADLNVPVKEGK	19	11	9	52.65	b3y2y4y6*y6y7y8*y8y11	1169.65	36.344	110429	2	585.33	0.63
P65702 PGK_SALTY Phohoglycerate kinase	8		MTDLDLAGKR	5	10	7	70.81	b2y3y4y5y7y9y10	1119.58	42.487	42316	2	560.29	-3.05
P65702 PGK_SALTY Phohoglycerate kinase	9		MTDLDLAGK	5	9	4	30.3	b6y5y8y9	963.48	47.843	27120	2	482.24	-6.27
P65702 PGK_SALTY Phohoglycerate kinase	10		AQASTHGIGK	146	10	15	120.4	b2*b2b3b4b6b7y1y2y3y4y5y7y8*y8y10	969.51	15.385	26881	2	485.26	-5.79
P65702 PGK_SALTY Phohoglycerate kinase	11		SVNDVKEDEQILDIGDASAQQLAEILK	272	27	3	11.84	b9b12y13	2941.48	100.533	11448	2	1471.24	-7.30
P65702 PGK_SALTY Phohoglycerate kinase	12		ASLPTIELALK	38	11	3	24.13	b7y6y8	1155.69	76.616	91360	2	578.35	-8.45
P65702 PGK_SALTY Phohoglycerate kinase	13		LTVLDSLK	197	9	3	38.08	y4y6y7	975.56	61.523	82757	2	488.29	-7.38
P65702 PGK_SALTY Phohoglycerate kinase	14		IADQLIVGGGIANTFVAAQGHSVGK	206	25	4	16.15	b3b5y4y10	2423.29	77.538	50968	3	808.44	-4.03
P65702 PGK_SALTY Phohoglycerate kinase	15		SVNDVK	272	6	1	13.56	b5	661.35	78.125	13959	1	661.35	-9.51
P65702 PGK_SALTY Phohoglycerate kinase	16		ISYISTGGGAFLEFVEGK	355	18	3	15.45	b3y3y14	1874.95	102.296	1713	2	937.98	-2.86
P65702 PGK_SALTY Phohoglycerate kinase	17		LVKDYLDGVDVAEGELVLENVR	90	23	3	12.95	b10y5y15	2544.35	97.403	39384	3	848.79	-1.06
P65702 PGK_SALTY Phohoglycerate kinase	18		SVIKMTDLDLAGK	1	13	3	20.48	b12y7y10	1390.78	79.132	3605	2	695.89	14.66
P65702 PGK_SALTY Phohoglycerate kinase	19	Carbamidomethyl+C(6)	KYAALCDVFVMDAFGTAHR	127	19	4	14.82	b11*b11b15y9	2172.03	80.369	3501	4	543.76	-4.27
P65702 PGK_SALTY Phohoglycerate kinase	20		ISYISTGGGAFLEFVEGKVLPAVAMLEER	355	29	8	35.46	b7b10b11y7*y7y8*y8y23	3083.62	136.303	2869	4	771.66	1.98

P65702 PGK_SALTY Phohoglycerate kinase	21		YEADLVDEAKR	233	11	1	7.4	b3	1308.64	53.865	32371	2	654.83	0.47
P65702 PGK_SALTY Phohoglycerate kinase	22		PAVAMLEER	375	9	2	18.76	b3b5	1015.52	79.559	28164	2	508.26	-3.67
P65702 PGK_SALTY Phohoglycerate kinase	23		DLNVPVKEGK	20	10	3	18.76	b3b6°b6	1098.61	36.315	21192	2	549.81	-7.78
P65702 PGK_SALTY Phohoglycerate kinase	24		LNVPVKEGK	21	9	0	2.46		983.59	36.320	15337	2	492.30	-1.80
P65702 PGK_SALTY Phohoglycerate kinase	25		TDLDLAGKR	6	9	1	8.21	b6	988.54	42.434	13628	2	494.78	0.74
P65702 PGK_SALTY Phohoglycerate kinase	26		ASTHGIGK	148	8	7	67.8	b3b4b5°b5b6b7°b7	770.41	15.389	4445	2	385.71	-12.12
P0A2A3 RL1_SALTY 50S ribosomal protein L1	1		VAVFTQGPNAEAAK	74	14	25	158.61	b5°b5b8b9b11°b11b13b14y1y2y3y4°y4y7y8y9°y9y10°y10y11°y11°y11y12°y12y14	1402.73	44.619	131860	2	701.87	1.04
P0A2A3 RL1_SALTY 50S ribosomal protein L1	2		VGTVTPNVAEAVK	141	13	17	139.48	b2b3°b3b4°b4b13y3y5y6y7y8°y8y9y10y11y12y13	1284.72	47.457	129204	2	642.86	-0.57
P0A2A3 RL1_SALTY 50S ribosomal protein L1	3		VVGQLGQVLGPR	122	12	9	68.55	b2b4y3y6y7y8y10°y10y12	1222.72	58.675	128556	2	611.86	-3.79
P0A2A3 RL1_SALTY 50S ribosomal protein L1	4		QYDINEAIALLK	19	12	5	26.09	b4b12y3y4y12	1390.76	84.732	50038	2	695.88	-0.44
P0A2A3 RL1_SALTY 50S ribosomal protein L1	5		AAGAELVGMEDLADQIK	88	17	9	54.84	b2b7b8y7y10°y10y11y12y17	1730.87	79.033	42216	2	865.94	4.87
P0A2A3 RL1_SALTY 50S ribosomal protein L1	6		GATVLPHGTR	60	11	5	50.29	y4y5y6y7y11	1065.58	29.416	24208	2	533.29	-1.72
P0A2A3 RL1_SALTY 50S ribosomal protein L1	7		VSISTTMGAGVAVDQAGLSASAN	211	23	3	12.95	b9y16y18	2107.01	102.421	1526	2	1054.01	-9.39
P0A2A3 RL1_SALTY 50S ribosomal protein L1	8		NGIIHTTIGKVDFDADK	167	17	3	24.83	y4y8y9	1843.98	78.314	9914	2	922.49	11.19
P0A2A3 RL1_SALTY 50S ribosomal protein L1	9	Oxidation+M(9)	AAGAELVGMEDLADQIK	88	17	4	16.18	b5b13y9°y9	1746.88	75.878	6507	2	873.94	13.84
P0A2A3 RL1_SALTY 50S ribosomal protein L1	10		TVLPHGTGR	62	9	0	2.46		937.51	29.416	17461	2	469.26	-11.78
P0A7W4 RS5_SALTY 30S ribosomal protein S5	1		VFMQPASEGTGIIAGGAMR	93	19	20	176.1	b2b3b4b10b12b13b14y4y5y6y7y11y12y13y14y15y16°y16°y16y19	1892.94	67.528	230752	2	946.97	1.93
P0A7W4 RS5_SALTY 30S ribosomal protein S5	2		AVLEVAGVHNVLAK	112	14	8	75.41	b4y3y6y9y10y11y12y14	1419.84	60.536	156256	2	710.42	2.41
P0A7W4 RS5_SALTY 30S ribosomal protein S5	3		AYGSTNPINVVR	126	12	14	109.46	b2b3b6y2y3y4°y4y6y7y8y9y10°y10y12	1290.68	50.683	134453	2	645.84	0.38
P0A7W4 RS5_SALTY 30S ribosomal protein S5	4		ATIDGLENMNSPEMVAAK	138	18	22	132.93	b2b4b8b15°b15b16y1y2y3y4y7y10y11y12°y12°y12y13y14°y14y15°y15y18	1890.90	62.733	117758	2	945.95	4.52
P0A7W4 RS5_SALTY 30S ribosomal protein S5	5		ATIDGLENMNSPEMVAAKR	138	19	14	135.48	b4b7b11y3y4y5y8y9y10y11y12°y12y16y17	2046.99	58.538	70651	3	683.00	-2.09
P0A7W4 RS5_SALTY 30S ribosomal protein S5	6		IFSFTALTVVGDGNGR	29	16	9	68.64	y6y7°y7y8y9y11°y11y12y16	1653.86	85.867	36454	2	827.43	-1.85
P0A7W4 RS5_SALTY 30S ribosomal protein S5	7		VGFGYGK	45	7	5	40.27	b1y3y4y6y7	727.37	39.320	21418	2	364.19	-7.13
P0A7W4 RS5_SALTY 30S ribosomal protein S5	8		MAHIEK	0	6	1	13.56	y3	728.38	65.668	6061	1	728.38	7.46
P0A7W4 RS5_SALTY 30S ribosomal protein S5	9		MAHIEKQAGELQEK	0	14	4	38.51	y5y6y8y10	1611.81	110.148	2285	2	806.41	-3.33

P0A7W4 RS5_SALTY 30S ribosomal protein S5	10		LEVAGVHNVLAK	114	12	1	7.3	b8	1249.71	60.609	3359	3	417.24	-11.92
P0A1D5 CH10_SALTY 10 kDa chaperonin	1		VGDIVIFNDGYGVK	60	14	26	219.45	b3b4°b4b5°b5b6b10°b10b11°b11°b11b13°b13y1y2y3y4y5y6y7y8y9y10y11y12y14	1495.78	72.863	345143	2	748.39	-0.90
P0A1D5 CH10_SALTY 10 kDa chaperonin	2		ILDNGTVQPLDVK	47	13	26	176.58	b2b4b7°b7b8°b8b10b11°b11b13y2y3y5°y5y6°y6°y6y7y8y9y10y11°y11°y11y12y13	1411.78	56.861	273659	2	706.39	-0.69
P0A1D5 CH10_SALTY 10 kDa chaperonin	3		SAGGIVLTGSAAGK	20	14	18	125.78	b2b3°b3b4b5°b5b10b14y1y2y3y4y6y7y8y9y12y14	1188.65	43.120	190137	2	594.83	-4.21
P0A1D5 CH10_SALTY 10 kDa chaperonin	4		GEIIVGK	37	8	7	53.83	b2y2y3y4y5y6y8	786.47	41.080	26086	2	393.74	-8.54
P0A1D5 CH10_SALTY 10 kDa chaperonin	5		IDNEEVLIMSESILAIVEA	77	20	11	54.67	b7°b7b8°b8°b8b9b10°b10°b10y3y9	2203.08	136.297	6116	2	1102.04	-10.64
P0A1D5 CH10_SALTY 10 kDa chaperonin	6		MSIRPLHDR	0	9	3	30.3	b5b8y4	1124.60	125.208	1546	2	562.80	-2.39
P0A1D5 CH10_SALTY 10 kDa chaperonin	7		SEKIDNEEVLIMSESILAIVEA	74	23	5	28.64	b4b5b9b21°b21	2547.28	136.264	8969	2	1274.14	2.01
P0A1D5 CH10_SALTY 10 kDa chaperonin	8		SAGGIVLTGSAAGK	20	14	0	3.7		1170.65	43.128	34802	2	585.83	3.02
P0A297 RL10_SALTY 50S ribosomal protein L10	1		LATLPTYEEAIAR	125	13	14	105.4	b2b3°b3b9y1y4y6y7y8y9°y9y10y11y13	1447.78	64.580	113196	2	724.39	-1.52
P0A297 RL10_SALTY 50S ribosomal protein L10	2		AAAFEGELIPASQIDR	109	16	22	138.96	b1b5b8b9y1y2y3°y3y5°y5y7°y7y8y9y10y11°y11y12y13°y13°y13y16	1687.87	68.106	79202	2	844.44	3.83
P0A297 RL10_SALTY 50S ribosomal protein L10	3		GALSAVVADSR	20	11	4	31.12	y2y4y5y8	1045.56	48.169	42232	2	523.29	-0.23
P0A297 RL10_SALTY 50S ribosomal protein L10	4		DTFVGPTLIAYSMHEPGAAAR	73	21	7	30.94	b3°b3b4°b4b6b11y8	2204.09	81.967	11473	3	735.37	4.32
P0A297 RL10_SALTY 50S ribosomal protein L10	5		LMATMK	138	6	2	26.71	y4y5	694.35	38.421	2984	1	694.35	-13.01
P0A297 RL10_SALTY 50S ribosomal protein L10	6	Carbamidomethyl+C(9)	VVEGTQFECLK	62	11	6	35.06	b7b10y5°y5y8°y8	1309.62	97.390	2212	1	1309.62	-18.18
P0A297 RL10_SALTY 50S ribosomal protein L10	7		LATLPTYEEAIARLMATMK	125	19	3	22.6	b11b12y6	2123.09	57.427	109244	3	708.37	-14.26
P0A297 RL10_SALTY 50S ribosomal protein L10	8	Carbamidomethyl+C(9)	VVEGTQFECLKDTFVGPTLIAYSM EHPGAAAR	62	32	3	11.11	b8y6y12	3494.68	91.730	61480	4	874.43	-7.06
P0A297 RL10_SALTY 50S ribosomal protein L10	9		AGREAGVYMR	43	10	4	39.88	b6y5y7y8	1109.54	87.129	2563	1	1109.54	-11.44
P0A297 RL10_SALTY 50S ribosomal protein L10	10	Phosphoryl STY(11)	DTFVGPTLIAYSMHEPGAAAR	73	21	3	13.77	b5b11y10_H3PO4 y10	2284.03	73.782	9786	4	571.76	-4.49
P67091 UF_SALTY Universal stress protein F	1		TILVPIDISDSELTQR	3	16	18	139.16	b1b2°b2b3b4y3y5y6°y6y7y8y9y10y12°y12°y12y14y16	1799.98	81.341	85116	2	900.49	1.29
P67091 UF_SALTY Universal stress protein F	2		VHFLTVPISLPYYASLGLAYSALP AMDDLK	34	31	4	22.71	y3°y3y4y9	3394.74	125.695	4092	3	1132.25	-6.69
P67091 UF_SALTY Universal stress protein F	3		VQAHVAEGSPK	85	11	7	47.42	b3b8°b8y6°y6y7y9	1122.57	17.473	11431	2	561.79	-19.46
P0A1E3 CYSK_SALTY Cysteine synthase A	1		IQGIGAGFIPGNLDLK	226	16	11	59.54	b2°b2b3b4b9y1y2y7y10y12y14	1612.90	82.855	166853	2	806.96	-0.83
P0A1E3 CYSK_SALTY Cysteine synthase A	2		LTLTMPETMSIER	87	13	12	102.09	b5°b5b6b8y6y7y8°y8y9y10y11y13	1521.77	73.270	127329	2	761.39	1.85
P0A1E3 CYSK_SALTY Cysteine synthase A	3		YLLQQFSNPANPEIHEK	137	18	12	62.58	b2b3b4y3°y3y7y8°y8y9y11°y11y18	2141.09	73.498	100378	3	714.37	-4.90

[P0A1E3 CYSK_SALTY Cysteine synthase A	4		YLSTALFADLFTEKELQQ	305	18	6	15.45	b2b16y2y7y10y18	2117.09	101.956	96039	2	1059.05	6.23
[P0A1E3 CYSK_SALTY Cysteine synthase A	5		ALGANLVLTGAK	105	13	7	27.96	b2y1y2y3y5y6y13	1256.72	60.762	50347	2	628.87	2.14
[P0A1E3 CYSK_SALTY Cysteine synthase A	6		NIVVILPSSGER	293	12	9	79.36	b2b3b4y5y6y8y9y10y12	1283.73	63.540	44823	2	642.37	0.67
[P0A1E3 CYSK_SALTY Cysteine synthase A	7		AEEIVASDPQK	126	11	11	70.57	b2b3y3y6y7*y7y8y9*y9y11*y11	1186.59	30.742	30829	2	593.80	-1.85
[P0A1E3 CYSK_SALTY Cysteine synthase A	8		VVGITNEEAISTAR	246	14	6	42.12	b3y4y9y10y12*y12	1459.78	48.873	29758	2	730.39	3.09
[P0A1E3 CYSK_SALTY Cysteine synthase A	9		IGANMIWDAEK	44	11	3	27.14	b3y7y8	1247.62	67.515	5033	2	624.32	12.13
[P0A1E3 CYSK_SALTY Cysteine synthase A	10		GVLKPGVELVEPTSGNTGIALAYVAAAR	56	28	4	22.19	b3y6y7y17	2753.52	81.273	3450	2	1377.27	1.42
[P0A1E3 CYSK_SALTY Cysteine synthase A	11		LQEDESFTNK	283	10	4	28.49	b3b10y5y6	1210.58	53.701	2847	3	404.20	13.51
[P0A1E3 CYSK_SALTY Cysteine synthase A	12		IGANMIWDAEKR	44	12	3	26.09	b5y7y8	1403.70	59.990	87970	3	468.57	-10.35
[P0A1E3 CYSK_SALTY Cysteine synthase A	13		LIDKVVGITNEEAISTAR	242	18	4	41.4	y4y5y12y13	1929.08	59.999	60225	2	965.04	8.73
[P0A1E3 CYSK_SALTY Cysteine synthase A	14		GAIQKAEEIVASDPQK	121	16	4	23.55	b14*b14y4y5	1683.90	90.200	56769	2	842.45	4.64
[P0A1E3 CYSK_SALTY Cysteine synthase A	15		LQEDESFTNKNIVVILPSSGER	283	22	5	24.05	b3b12*b12b13y6	2475.28	68.897	23832	3	825.76	2.66
[P0A1E3 CYSK_SALTY Cysteine synthase A	16		IYEDNSLTIGHTPLVRLNR	3	19	3	23.99	b10b11b13	2211.19	73.815	21711	3	737.73	0.22
[P0A1E3 CYSK_SALTY Cysteine synthase A	17		SKIYEDNSLTIGHTPLVR	1	18	3	24.37	b7b8b12	2043.11	117.484	11732	3	681.71	12.91
[P41031 CY_SALTY Thiosulfate-binding protein	1		AYLNWLYSPQAQTIIITHYYR	265	21	13	51.07	b1b2b8b10*b10b13y2y3y4y5y13*y13y21	2664.34	93.171	118834	3	888.78	5.59
[P41031 CY_SALTY Thiosulfate-binding protein	2		LPNNSSPFYSTMGFLVR	110	17	11	105.08	b7b8y3y5y6y9y11y13*y13y15y17	1929.96	91.435	77318	2	965.48	3.61
[P41031 CY_SALTY Thiosulfate-binding protein	3		QYEAQGFEVVIPK	226	13	8	33.84	b4b10*b10*b10b12y2y11y13	1507.78	69.304	74881	2	754.40	3.16
[P41031 CY_SALTY Thiosulfate-binding protein	4		ELFAALNPPEQQWAK	37	16	23	153.04	b3*b3b5*b5b6b7*b7b11b12*b12b15y1y2y4*y4y6y8y9*y9y11*y11y12y13	1888.97	89.299	70699	2	944.99	4.07
[P41031 CY_SALTY Thiosulfate-binding protein	5		VNNPEIMGK	286	9	9	74.52	b2b3y2y3y4y6y7y8y9	1001.50	35.508	70659	2	501.26	-4.33
[P41031 CY_SALTY Thiosulfate-binding protein	6		LIFPNPK	146	7	8	50.41	b2b5y2y4*y4y5y6y7	828.49	55.587	59734	2	414.75	-11.12
[P41031 CY_SALTY Thiosulfate-binding protein	7		NVEVFDTGGR	189	10	9	86.32	b3b8y4y5y6y7y8*y8y10	1093.53	46.686	56234	2	547.27	0.78
[P41031 CY_SALTY Thiosulfate-binding protein	8		GLGDVLISFESEVNNIR	208	17	4	16.18	b11b15y10y17	1861.96	106.844	13512	2	931.48	-4.00
[P41031 CY_SALTY Thiosulfate-binding protein	9		ADVVTYNQVTDVQILHDK	81	18	3	15.45	b3b10y10	2058.04	63.310	9225	3	686.68	-7.35
[P41031 CY_SALTY Thiosulfate-binding protein	10		FGSWPEVMK	311	9	3	30.3	b7y3y5	1080.52	68.348	80793	2	540.76	-0.34
[P41031 CY_SALTY Thiosulfate-binding protein	11		GATTTFAER	199	9	4	45.21	b3y4y5y6	953.46	30.256	24428	2	477.24	-4.80
[P41031 CY_SALTY Thiosulfate-binding protein	12		QSHAGSSK	63	8	4	35.91	b5y3*y3y6	801.38	80.091	13652	1	801.38	-9.82
[P41031 CY_SALTY Thiosulfate-binding protein	13		TNILAEFPVAWVDKNVQANGTEK	239	23	6	38.68	b3b4b7y7y19y20	2544.30	90.332	141585	3	848.77	-2.11
[P41031 CY_SALTY Thiosulfate-binding protein	14		NVEVFDTGGRGATTTFAER	189	19	3	14.82	b4b6y6	2027.97	56.190	15738	3	676.66	-4.76

[P41031 CY_SALTY Thiosulfate-binding protein	15		TSGNARYTYLAAWGAADNADGG DK	153	24	3	12.62	b11y4y15	2445.11	90.104	6239	2	1223.06	0.50
[P41031 CY_SALTY Thiosulfate-binding protein	16		YTYLAAWGAADNADGGDKAK	159	20	7	46.35	b12y7y11y12y15*y15y16	2057.99	117.893	4370	3	686.67	14.83
[P41031 CY_SALTY Thiosulfate-binding protein	17		VNNPEIMGKQADK	286	13	3	20.48	b4b10y11	1443.71	62.257	3114	2	722.36	-8.96
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	1		IAAGADISK	9	9	14	124.76	b2b4b6b8y1y2*y2y3y4y5y6y7y8y9	845.46	27.556	259301	2	423.23	-13.86
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	2		NPQTGKEITIAAAK	61	14	12	99.35	b1b7y1y2y3y4y5y6y8y11y13y14	1441.78	36.065	81977	3	481.26	-14.48
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	3		EITIAAAK	67	8	9	62.21	b2b3*b3y2y3y4y5y6y8	816.47	37.872	58725	2	408.74	-14.13
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	4		ALDAIIASVTESLKEGDDVALVGF GTFAVK	23	30	12	75.73	b2b3b4b5b24y1y6y7y8y9y15y30	3036.61	136.200	41680	3	1012.87	-2.09
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	5		ALKDAVN	83	7	8	56.43	b1b4b6y5*y5y6*y6y7	730.41	22.008	4368	2	365.71	6.10
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	6		SQLEK	3	6	1	13.56	b4	717.42	49.448	20740	2	359.21	6.55
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	7		ALDAIIASVTESLKEGDDVALVGF GTFAVK	23	30	9	66.56	b3b5y3y4y6y8y9y10y11	3036.60	137.425	13547	3	1012.87	-4.66
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	8		AGADISK	11	7	3	38.08	b3b4b5	661.35	27.566	40116	1	661.35	-1.38
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	9		AAGADISK	10	8	3	23.17	b3b5°b5	732.39	27.542	16962	1	732.39	0.33
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	10		GDDVALVGFGTFAVK	38	15	2	22.77	b9b10	1495.79	136.296	2901	2	748.40	4.00
[P0A1R8 DBHB_SALTY DNA-binding protein HU-beta	11		EITIAAAK	67	8	0	1.23		798.46	37.879	16505	2	399.73	-9.48
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	1		AEQQLDKDSAIVPVYYYVNAR	494	21	18	130.74	b4b6b10b11°b11b12°b12y1y3y4y5y6*y6y7y9y10y11y21	2442.23	72.493	99123	3	814.75	-1.50
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	2		NQGDLPAYSYTPPYTDGAK	333	19	6	34.85	b11y5y9y11y14y19	2057.96	58.451	64764	2	1029.49	9.13
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	3		SGEIDMTYNNMPIELFQK	263	18	13	51.41	b2b3b4b14y1y3y10y11*y11*y11y12*y14y18	2130.01	85.877	50230	2	1065.51	10.43
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	4		TVINQVTYLPISSEVTDVNR	241	20	12	99.66	b2b9y3y4y5y6y7y9y11y12y14y20	2248.19	76.398	44033	2	1124.60	3.04
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	5		NLGVNVNLENQEWK	410	14	11	78.42	b2b12y1y3y4y6y8y11y12*y12y14	1656.84	66.292	37499	2	828.92	1.25
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	6		WSDGTPVTAHDFVYSWQR	107	18	11	60.61	b7b14°b14y4*y4y5*y5y6y7*y7y12	2151.99	85.861	14320	2	1076.50	-0.68
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	7	Carbamidomethyl+C(4)	AGWCADYNEPTSLNTMLSDSSN NTAHYK	439	29	5	24.93	b4b6y3y4y10	3294.41	89.554	84743	3	1098.81	0.37
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	8		LVEPEWFK	352	8	3	40.68	y3y5y6	1047.54	70.654	71758	2	524.28	-6.99
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	9		LALDR	320	5	1	13.15	y4	587.35	57.054	18400	1	587.35	-8.11
[P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	10		ALDDHTFEVTLSEVPYFYK	163	20	3	14.26	b10y6y9	2371.13	58.539	7922	3	791.05	-8.34

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	11		IEGVPE\$NVSR	56	11	5	38.07	b8b9*b9y4y6	1186.63	63.273	6915	2	593.82	16.05
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	12		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	6	24.68	b3°b3b7°b7b9b13	3091.50	132.726	4577	3	1031.17	-12.08
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	13		WTQPANIVTNGAYK	204	14	4	26.91	b4*b4b5b11	1562.81	89.403	3101	3	521.61	11.33
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	14		SNITK	1	5	1	13.15	b4	562.32	26.261	2240	1	562.32	-6.40
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	15	Carbamidomethyl+C(6)	VDPYLCTYYYEINNQK	291	16	5	35.16	b3b5b6y4y12	2082.95	83.762	1685	4	521.49	-1.17
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	16		FGDKWTQPANIVTNGAYK	200	18	4	15.45	b8°b8b10y3	2009.99	78.668	55886	2	1005.50	-8.56
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	17		TVINQVTYLPISSEVTDVNRYR	241	22	5	20.69	b8°b8y13y16y19	2567.34	76.535	53030	3	856.45	-3.33
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	18	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYEINNQK	284	23	8	40.72	b4b6b9b12b21y7°y7*y7	2920.39	75.603	29107	3	974.13	2.01
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	19		KNLGVNVNLENQEWK	409	15	5	29.22	b10y3y9y10*y10	1784.92	54.851	15435	2	892.97	-2.80
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	20		VKNQGDLPAYSYTPPYTDGAK	331	21	3	13.77	b8y7y10	2285.13	54.515	14995	3	762.38	9.19
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	21		NNGSEVQSLDPHKIEGVPE\$NVSR	43	24	4	35.3	b13b14y6y7	2592.29	84.391	8682	3	864.77	11.11
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	22		SAVEKFGDK	195	9	3	30.3	b4b7y6	980.49	124.224	6798	1	980.49	-10.33
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	23		NPQYWDNAKTVINQVTYLPISSEV TDVNR	232	29	8	28.71	b5b13*b13y3y5y6°y6y11	3364.66	119.467	1944	4	841.92	-5.01
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein	24	Phosphoryl STY(13)	TVINQVTYLPISSEVTDVNR	241	20	4	25.07	b15y6y7y13	2328.13	82.021	3864	3	776.72	-3.15
Q7CR87 SURA_SALTY Chaperone surA	1		IQELPGIFAQALSTAK	235	16	10	30.58	b1b2*b2b3°b3b4*b4y1y12 y14	1686.94	89.365	40148	2	843.98	0.14
Q7CR87 SURA_SALTY Chaperone surA	2		LNAGQAGQQLPDDATLR	50	17	14	101.24	b7b9y4y7°y7y8y9y11°y11* y11y12y13y14y17	1767.91	50.249	34681	2	884.46	6.84
Q7CR87 SURA_SALTY Chaperone surA	3		LAYDGLNYSTYR	117	12	6	31.95	b4b9y2y8y10y12	1435.70	58.127	30231	2	718.35	8.50
Q7CR87 SURA_SALTY Chaperone surA	4		ITDEQLDQAIAIAK	90	15	5	25.58	b6b13y2y5y8	1642.87	79.649	30065	2	821.94	3.64
Q7CR87 SURA_SALTY Chaperone surA	5		ITVLPQEVDALAK	149	13	11	45.81	b2b3°b3b4y1y2y3y9°y9y10 y13	1396.81	70.087	28149	2	698.91	0.44
Q7CR87 SURA_SALTY Chaperone surA	6		QIGTQNDASTELNLSHILIALPENP TSEQVNDAQR	162	35	9	27.28	b3b4b6°b6y6y12°y12y14y3 5	3816.90	88.020	19866	3	1272.97	0.83
Q7CR87 SURA_SALTY Chaperone surA	7		GQSQSISVTEVHAR	274	14	6	58.28	b8y3y5y8y9y10	1498.75	36.432	14695	3	500.25	-7.33
Q7CR87 SURA_SALTY Chaperone surA	8		LIMDQIILQMGQK	73	13	3	27.96	y4y5y11	1530.82	87.528	2766	3	510.95	-9.65

Q7CR87 SURA_SALTY Chaperone surA	9		GQISAPVHSSFGWHLIELLDTR	362	22	5	28.71	b4b13b14y3y6	2463.26	99.819	2446	3	821.76	-6.54
Q7CR87 SURA_SALTY Chaperone surA	10		QAESIVEEAR	197	10	3	28.49	b6b7y6	1131.59	71.353	26543	2	566.30	19.85
Q7CR87 SURA_SALTY Chaperone surA	11		VAAVVNNGVVLESDVDGLMQSV K	27	23	4	12.95	b4y7*y7y9	2343.18	90.293	24414	3	781.73	-17.82
Q7CR87 SURA_SALTY Chaperone surA	12		LAITYSADQQALKGGQMGWGR	214	21	6	29.51	b8°b8b15y8y18y19	2251.12	64.774	23689	3	751.05	-2.82
Q7CR87 SURA_SALTY Chaperone surA	13		SRLAYDGLNYSTYR	115	14	3	19.13	b7y4y11	1678.81	66.313	9955	2	839.91	-6.98
Q7CR87 SURA_SALTY Chaperone surA	14		NGADFGKLAITYSADQQALK	207	20	5	14.26	b14y6°y6y9°y9	2111.06	84.649	9760	4	528.52	-9.37
Q7CR87 SURA_SALTY Chaperone surA	15		LNAGQAGQQLPDDATLRHQILER	50	23	4	28.64	b3b6b9b15	2544.34	102.617	2935	3	848.78	3.93
Q7CR87 SURA_SALTY Chaperone surA	16		EMIIEVRNNEVR	134	13	3	29.72	b4b9b12	1588.81	85.045	1855	3	530.27	-0.77
Q7CR87 SURA_SALTY Chaperone surA	17	Oxidation+M(19)	VAAVVNNGVVLESDVDGLMQSV K	27	23	3	12.95	b3y7y13	2359.19	114.768	4420	3	787.07	-10.45
Q7CR87 SURA_SALTY Chaperone surA	18		GQSQSISVTEVHAR	274	14	0	3.7		1481.73	36.335	1947	3	494.58	-1.48
P66313 RL6_SALTY 50S ribosomal protein L6	1		APVVVPAGVDVK	6	12	13	114.23	b2b3b4b5y1y2y3y5y7y8y9 y10y12	1150.68	52.815	124143	2	575.84	-4.99
P66313 RL6_SALTY 50S ribosomal protein L6	2		TLNDAVEVK	35	9	10	54.24	b2°b2y2y3°y3y6°y6y7y8y9	988.52	37.886	96533	2	494.77	-7.66
P66313 RL6_SALTY 50S ribosomal protein L6	3		INGQVITIK	18	9	10	64.38	b2°b2b3y2y3y4y7y8*y8y9	985.60	48.018	68178	2	493.30	-5.76
P66313 RL6_SALTY 50S ribosomal protein L6	4		DGYADGWAQAGTAR	55	14	10	58.28	b3y1y4°y4y6y7y9*y9y10y1 4	1438.64	49.083	65390	2	719.82	1.02
P66313 RL6_SALTY 50S ribosomal protein L6	5		HADNALTFGPR	44	11	8	64.55	b1b3°b3b5b7y4y5y9	1198.59	46.887	53542	2	599.80	-2.14
P66313 RL6_SALTY 50S ribosomal protein L6	6		ALLNSMVIGVTEGFTK	69	16	4	24.72	y3y6°y6y8	1679.90	94.088	56077	2	840.45	-0.94
P66313 RL6_SALTY 50S ribosomal protein L6	7		GADKQVIGQVAADLR	134	15	3	17.99	b5y5y7	1540.84	59.933	36747	2	770.93	0.40
P66313 RL6_SALTY 50S ribosomal protein L6	8		GKNGELTR	27	8	5	35.91	b7y3y6°y6*y6	874.47	54.652	9958	2	437.74	-0.28
P66313 RL6_SALTY 50S ribosomal protein L6	9		HADNALTFGPRDGYADGWAQAG TAR	44	25	5	22.51	b9b11b13y5y11	2618.24	89.199	2086	4	655.31	9.32
P67904 RS10_SALTY 30S ribosomal protein S10	1		LIDQSTAEIVETAKR	16	15	12	119.44	b2y1y4y5y6y7y8y9y10y11 y13y15	1673.89	51.800	137440	3	558.63	-12.11
P67904 RS10_SALTY 30S ribosomal protein S10	2		LIDQSTAEIVETAK	16	14	11	99.35	b2b10y3y5y7y8y9y10y12* y12y14	1517.81	54.913	102171	2	759.41	0.08
P67904 RS10_SALTY 30S ribosomal protein S10	3		LVDIVEPTEK	72	10	9	87.11	b2b3y3y4y5y6y8y9y10	1142.63	51.280	50052	2	571.82	-2.99
P67904 RS10_SALTY 30S ribosomal protein S10	4		LDLAAGVDVQISLG	89	14	7	30.52	b6b8°b8b9°b9y7*y7	1370.74	80.033	27971	2	685.87	-8.55
P67904 RS10_SALTY 30S ribosomal protein S10	5		FTVLISPHVNK	48	11	3	24.13	b7y5y7	1254.70	58.502	22100	3	418.91	-12.74
P67904 RS10_SALTY 30S ribosomal protein S10	6		RLVDIVEPTEK	71	11	4	36.49	b3b4b10y7	1298.73	51.483	47952	2	649.87	-0.09
P67904 RS10_SALTY 30S ribosomal protein S10	7		DARDQYEIR	59	9	9	61.37	b3°b3y4y5°y5y6y7°y7*y7	1165.55	136.277	1955	1	1165.55	-10.89
P67904 RS10_SALTY 30S ribosomal protein S10	8		LIDQSTAEIVE	16	11	0	3.7		1217.61	54.974	4438	2	609.31	-12.83
P0AA28 THIO_SALTY Thioredoxin-1	1		MIAPILDEIADEYQGK	37	16	18	142.77	b2b3b13y2y3*y3y5°y5y6y7 y8*y8y10y11y13y14y15y1 6	1805.91	92.999	214342	2	903.46	5.41

P0AA28 THIO_SALTY Thioredoxin-1	2		LNIDQNPGETAPK	58	12	28	178.59	b2*b2b3b4*b4*b4b6*b6*b6b7b10b11y2y3y6*y6y7*y7y8*y8*y8y9*y9*y9y10*y10y11y12	1267.66	37.879	161072	2	634.33	-4.62
P0AA28 THIO_SALTY Thioredoxin-1	3		GIPTLLLLFK	74	9	10	74.52	b2b3y1y2y3y4y5y6y7y9	1001.63	90.444	90148	2	501.32	-12.37
P0AA28 THIO_SALTY Thioredoxin-1	4		MIAPILDEIADEYQGKLTVAK	37	21	9	69.35	b3b4b11y7y11y12y15y18y19	2318.22	94.162	121983	3	773.41	-4.74
P02910 HISJ_SALTY Histidine-binding periplasmic protein	1		VGVLQGTQTETFGNEHWAPK	135	20	11	59.8	b2b3b4y2y3y9y10*y10y11y17y20	2199.07	63.203	150443	3	733.70	-3.77
P02910 HISJ_SALTY Histidine-binding periplasmic protein	2		IGTDPTYAPFESK	29	13	14	139.48	b4b5*b5y3y5y6y7y8y9*y9y10y11y12y13	1425.69	54.749	98703	2	713.35	-1.20
P02910 HISJ_SALTY Histidine-binding periplasmic protein	3		NSDIQPTVASLK	120	12	17	97.28	b1b2*b2*b2b3*b3*b3b4*b4y3y4y7y8*y8y9y10y12	1272.68	47.540	77769	2	636.84	-0.19
P02910 HISJ_SALTY Histidine-binding periplasmic protein	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	16	99.49	b2b3*b3b4*b4b9b10b12b13b16*b16y2y4y5y6y20	2273.20	103.227	63945	2	1137.10	6.23
P02910 HISJ_SALTY Histidine-binding periplasmic protein	5		FGGPAVKDEK	201	10	6	54.65	b2y1y3y5y6y9	1047.54	26.343	21332	2	524.27	-6.06
P02910 HISJ_SALTY Histidine-binding periplasmic protein	6		GIEIVSYQGQDNIYSDLTAGR	155	21	4	13.77	b11y3y8y21	2299.13	77.899	10674	2	1150.07	4.67
P02910 HISJ_SALTY Histidine-binding periplasmic protein	7		LFGVGTGMGLR	211	11	3	27.14	b3y7y8	1107.59	72.341	35591	2	554.30	-3.53
P02910 HISJ_SALTY Histidine-binding periplasmic protein	8		AFAEMR	234	6	1	13.56	b3	724.35	35.875	8672	1	724.35	5.06
P02910 HISJ_SALTY Histidine-binding periplasmic protein	9	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLKAK	62	22	6	13.33	b4*b4b14*b14y20*y20	2472.32	98.084	159894	3	824.78	1.68
P02910 HISJ_SALTY Histidine-binding periplasmic protein	10		IRIGTDPTYAPFESK	27	15	4	31.6	b12b13y4y6	1694.87	125.716	7848	2	847.94	0.00
P02910 HISJ_SALTY Histidine-binding periplasmic protein	11		QQEIAFTDKLYAADSR	99	16	7	44.19	b10*b10b11b12*b12y3y12	1855.91	112.684	1783	2	928.46	-6.31
P02910 HISJ_SALTY Histidine-binding periplasmic protein	12	Oxidation+M(8)	LFGVGTGMGLR	211	11	3	24.13	b5b7y7	1123.59	38.196	4910	3	375.20	-3.59
P0A283 PTGA_SALTY Glucose-ecific phohottransferase enzyme IIA component	1		STLTPVVISNMDEIKELIK	133	19	11	46.56	b2*b2b3*b3b4*b4y3y11y12y15y19	2130.15	92.493	360059	3	710.72	-9.40
P0A283 PTGA_SALTY Glucose-ecific phohottransferase enzyme IIA component	2		MVAPVDGTIGK	59	11	12	110.81	b2b3b8y2y3y5y6y7y8y9y10y11	1087.58	45.537	165088	2	544.29	-2.92
P0A283 PTGA_SALTY Glucose-ecific phohottransferase enzyme IIA component	3		VGDPIVIEFDLPLEEK	115	16	17	122.93	b1b2b3b4*b4b5b6b7y2y4y6y9y10*y10y11y13y16	1812.97	98.949	138114	2	906.99	3.91
P0A283 PTGA_SALTY Glucose-ecific phohottransferase enzyme IIA component	4		LSGSVTVGETPVIR	152	14	4	31.31	b4y4y7y9	1414.79	54.919	20520	2	707.90	-0.52
P0A283 PTGA_SALTY Glucose-ecific phohottransferase enzyme IIA component	5		DTGTIEIVAPLSGEIVNIEDVPDVVFAEK	16	29	4	14.39	b8b15y8y11	3069.60	110.791	5730	3	1023.87	2.70
P0A283 PTGA_SALTY Glucose-ecific phohottransferase enzyme IIA component	6		IVGDGIAIKPTGNK	45	14	13	142.32	b4b5y3y5*y5*y5y6y7y8y9y10y11y13	1382.78	43.114	262302	3	461.60	-17.66
P0A283 PTGA_SALTY Glucose-ecific phohottransferase enzyme IIA component	7		IFETNHAFSIESDSGIELFVHFGIDTVELK	70	30	3	22.67	b6b7b16	3394.68	78.153	6321	4	849.43	-0.58
P0A283 PTGA_SALTY Glucose-ecific phohottransferase enzyme IIA component	8		VKVGDPIVIEFDLPLEEK	113	18	9	52.16	b7b11*b11y3*y3y4y6y8y10	2040.11	95.441	152053	3	680.71	-8.56

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component	9		PVDGTIGK	62	8	4	35.89	b3b4b5°b5	786.43	45.543	2748	1	786.43	-11.33
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	1	Carbamidomethyl+C(10)	YVIDELDQICQR	77	12	8	59.22	b2b9b11y3y8y9y10y12	1551.76	67.633	27210	2	776.38	8.02
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	2		TVVADGIGQGYKEVQEISPNLR	55	22	11	32.72	b1b2b4b9b11y4*y4y7*y7y8°y9	2373.24	71.364	25265	3	791.75	-2.16
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	3	Carbamidomethyl+C(10)	YVIDELDQICQRDR	77	14	6	46.52	b5b10y9*y9y10y11	1822.85	54.772	9201	2	911.93	-11.72
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	4		ISEIEADLDK	114	10	4	41.5	y4y7y9y10	1132.56	50.723	7611	2	566.79	-8.51
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	5		TVVADGIGQGYK	55	12	7	43.85	b8b11y4y8°y8*y8y9	1207.62	31.138	78340	2	604.31	-7.78
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	6		MYDNLK	0	6	1	13.56	y5	783.37	32.760	6217	2	392.19	-7.09
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	7	Carbamidomethyl+C(10)	YVIDELDQICQRDR	77	14	3	19.13	b6b9y9	1822.87	53.491	6477	4	456.47	-3.55
Q7CR64 YAEH_SALTY UPF0325 protein yaeH	8	Carbamidomethyl+C(7)	DELDQICQRDR	80	11	1	7.3	b9	1447.68	54.737	7848	2	724.34	13.58
P25077 MDH_SALTY Malate dehydrogenase	1	Carbamidomethyl+C(2)	ACVGIITNPVNTTVAIAAEVLKK	111	23	14	93.11	b2b3b4b5b6b8*b8y3y4y15y16y18y20y23	2382.34	104.565	189607	3	794.78	-2.87
P25077 MDH_SALTY Malate dehydrogenase	2		NQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVK	21	33	26	94.42	b1*b1b2*b2b3*b3b7°b7b10*b10b12°b12b13*b13b15°b15b32y1y5y6y15y18y19y30y31y33	3388.80	93.180	180150	3	1130.27	0.65
P25077 MDH_SALTY Malate dehydrogenase	3		VAVLGAAGGIGQALALLK	2	19	17	153.41	b3b5b6b7b9b10y2y3y4y5y6y9y11y12y13y15y19	1735.09	119.607	153025	2	868.05	1.41
P25077 MDH_SALTY Malate dehydrogenase	4		FFSQPLLLGK	262	10	7	54.65	b2y2y3y4y6y8y10	1149.66	75.377	124112	2	575.33	-6.26
P25077 MDH_SALTY Malate dehydrogenase	5		IQNAGTEVVEAK	205	12	22	147.65	b2b3b10b11y1y3°y3y4°y4y5y6y7y8y9y10°y10*y10y11°y11*y11y12*y12	1258.66	33.908	121578	2	629.83	-3.10
P25077 MDH_SALTY Malate dehydrogenase	6		DIQLGEDFINK	301	11	8	41.08	b3b4y2y8°y8y9°y9y11	1291.65	67.231	76875	2	646.33	-3.12
P25077 MDH_SALTY Malate dehydrogenase	7		AGGGSATLSMGQAAAR	217	16	9	83.55	y5y7y8y9y10°y10y11y12y16	1405.69	39.343	68001	2	703.35	0.87
P25077 MDH_SALTY Malate dehydrogenase	8		FGLSLVR	233	7	6	53.42	b2y3y4y5y6y7	791.47	66.753	64049	2	396.24	-14.57
P25077 MDH_SALTY Malate dehydrogenase	9		SDLFNVNAGIVK	87	12	6	26.09	b1b2b3b4y8y12	1276.69	69.251	37146	2	638.85	-1.05
P25077 MDH_SALTY Malate dehydrogenase	10		SIGTLSAFEQHSLDAMLDTLKK	279	22	4	23.21	b11b12b14°b14	2405.25	85.134	35588	3	802.42	6.09
P25077 MDH_SALTY Malate dehydrogenase	11	Carbamidomethyl+C(5)	GVVECAYVEGDGQYAR	246	16	3	25.39	y3y5y6	1772.81	49.205	3568	2	886.91	8.33
P25077 MDH_SALTY Malate dehydrogenase	12		RIQNAGTEVVEAK	204	13	7	50	b7°b7b8b10*b10b11y8	1414.78	71.451	7188	2	707.90	13.46
P0A7K0 RL11_SALTY 50S ribosomal protein L11	1		AQLQEIAQTK	103	10	16	120.4	b2*b2b3*b3b6b8y2y3°y3*y3y4y5y6y8y9y10	1129.62	38.362	174997	2	565.31	-5.51
P0A7K0 RL11_SALTY 50S ribosomal protein L11	2		AADMTGADIEAMTR	113	14	12	93.84	b3b4°b4y2y3y4°y4y6y7y9y10y14	1452.65	56.898	91803	2	726.83	4.71
P0A7K0 RL11_SALTY 50S ribosomal protein L11	3		TPPAAVLLK	72	9	6	30.3	b2b3y2y5y7y9	909.57	53.965	84215	2	455.29	-9.13
P0A7K0 RL11_SALTY 50S ribosomal protein L11	4	Carbamidomethyl+C(29)	LQVAAGMANPSPVGPALGQQGVNIMEFCK	10	30	8	29.73	b3b8b11*b11y8*y8y9°y9	3081.56	95.365	3913	4	771.15	9.35

P0A7K0 RL11_SALTY 50S ribosomal protein L11	5	Carbamidomethyl+C(29) ;Oxidation+M(7)	LQVAAGMANPSPVGPALGQQG VNIMEFCK	10	30	7	29.64	b7*b7b8b16y8y13y25	3097.52	132.678	2872	3	1033.18	-2.92
P66593 RS6_SALTY 30S ribosomal protein S6	1		YSAAITGAEGK	24	11	16	100.67	b3b4b11*b11y1y2y3*y3y5y 6y7y9*y9y10*y10y11	1067.53	32.730	136573	2	534.27	-6.75
P66593 RS6_SALTY 30S ribosomal protein S6	2		AHYVLMNVEAPQEVIDELETFR	56	23	10	93.88	b4b5b11y3y4y5y6y11y12y 13	2704.32	112.571	111632	3	902.11	-2.44
P66593 RS6_SALTY 30S ribosomal protein S6	3		FNDAVIR	79	7	4	40.27	y3y4y6y7	834.44	41.898	84977	2	417.72	-12.00
P66593 RS6_SALTY 30S ribosomal protein S6	4		HAVTEASPMVK	93	11	4	31.12	y6y8y9*y9	1169.60	30.842	58592	2	585.30	-1.15
P66593 RS6_SALTY 30S ribosomal protein S6	5		SMVMR	86	5	1	13.15	y3	623.30	26.157	5018	1	623.30	2.15
P66038 RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	11	42.53	b3b4*b4b11*b11b12b14y2 y9y15y29	3110.68	97.911	104393	3	1037.56	-0.39
P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	19	119.39	b2*b2b12b13*b13b14 *b14y2y4y5y6y8y9y10y13y 14*y14y19	2109.08	101.069	64950	2	1055.04	6.71
P66038 RISB_SALTY 6	3		GAEAALTALEMINVLK	136	16	5	28.13	b6*b6b7b12y4	1643.90	102.806	23135	2	822.45	-2.45
P66038 RISB_SALTY 6	4		VAITIR	14	7	4	40.27	y3y4y6y7	743.47	43.734	10619	2	372.24	-13.63
P66038 RISB_SALTY 6	5		ANVAAPDAR	5	9	3	30.3	b8y3y8	884.44	59.162	14570	2	442.73	-16.63
P66038 RISB_SALTY 6	6		DDNITVVWVPGAYELPLATEALA K	45	24	6	23.38	b4b6*b6b12y13y15	2585.33	104.030	1601	2	1293.17	-6.80
P0A1D3 CH60_SALTY 60 kDa chaperonin	1		GYLSPYFINKPETGAVELESPFILL ADKK	197	29	10	52.94	b2b3b4b10b13b14y2y5y6y 29	3239.71	95.871	257861	4	810.68	-4.60
P0A1D3 CH60_SALTY 60 kDa chaperonin	2		EMLPVLEAVAK	231	11	11	70.57	b2b3*b3y1y2y3y4y5y6y8y1 1	1199.66	79.530	196300	2	600.34	-5.39
P0A1D3 CH60_SALTY 60 kDa chaperonin	3		ANDAAGDGTTTATVLAQSIITEGL K	80	25	21	144.21	b2*b2b3*b3b4*b4b5b14b1 5*b15b25y1y3y4y5y6y7y8y 9y10y25	2418.22	91.354	159213	3	806.75	-6.26
P0A1D3 CH60_SALTY 60 kDa chaperonin	4		AVAAAVEELK	122	10	9	60.81	b2b3y1y3*y3y5y6y8y10	1000.56	46.933	101711	2	500.78	-5.49
P0A1D3 CH60_SALTY 60 kDa chaperonin	5		SFGAPTITK	42	9	6	30.3	b2b3*b3b6y2y7	921.50	44.475	97596	2	461.25	-7.42
P0A1D3 CH60_SALTY 60 kDa chaperonin	6		QQIEEATSDYDREK	350	14	12	90.97	y3y4y5*y5y6*y6y7y8*y8y9 y14*y14	1711.76	32.957	91635	3	571.26	-11.98
P0A1D3 CH60_SALTY 60 kDa chaperonin	7		LAGGVAVIK	371	9	8	59.61	b3b4b5y1y2y7y8y9	827.53	44.663	88701	2	414.27	-11.73
P0A1D3 CH60_SALTY 60 kDa chaperonin	8	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	19	96.08	b6b12*b12b18y3y5*y5y6*y 6y9y12*y12y13*y13y14*y 14y15*y15y18	1957.02	61.133	74084	2	979.01	6.92
P0A1D3 CH60_SALTY 60 kDa chaperonin	9		GVNVLADAVK	18	10	9	73.96	b2b9y1y3y4y5y6y8y10	985.56	55.806	63510	2	493.28	-7.68
P0A1D3 CH60_SALTY 60 kDa chaperonin	10	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	8	51.64	b2y2y3*y3y5y6y7y10	1063.50	34.541	59805	2	532.26	-4.02
P0A1D3 CH60_SALTY 60 kDa chaperonin	11		AIAQVGTISANSDETVGK	142	18	7	34.38	b13y1y8y10y13y14y18	1760.91	47.792	46546	2	880.96	6.10
P0A1D3 CH60_SALTY 60 kDa chaperonin	12		VEDALHATR	395	9	7	45.21	b2b7y1y3y4y6y9	1011.52	25.997	39782	2	506.26	-5.55
P0A1D3 CH60_SALTY 60 kDa chaperonin	13		LIAEAMDK	160	8	3	40.68	y3y6y7	890.46	38.782	37389	2	445.73	-8.29
P0A1D3 CH60_SALTY 60 kDa chaperonin	14		AVAAGMNPMDLK	105	12	8	49.38	b11y2y5y8*y8y9y10y12	1217.60	58.014	37074	2	609.31	1.80
P0A1D3 CH60_SALTY 60 kDa chaperonin	15		GGDGNYGYNAAATEEYGNMIDMG ILDPTK	470	28	10	59.23	b2y2y3y4y8y9y12y13*y13y 28	2966.30	87.602	36952	3	989.44	6.83
P0A1D3 CH60_SALTY 60 kDa chaperonin	16	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDL PK	501	25	10	31.68	b1b3*b3b6b7*b7b10y16y2 0y25	2670.31	85.938	34507	3	890.77	-3.93

[P0A1D3 CH60_SALTY 60 kDa chaperonin	17		AGKPLLIIAEDVEGEALATLVVNTMR	242	26	8	61.95	b6b7b8y1y4y5*y5y6	2723.50	136.250	33135	3	908.50	-0.63
[P0A1D3 CH60_SALTY 60 kDa chaperonin	18		AVAAGMNPMDLKR	105	13	12	112.6	b2b5y2y3y4y6y7y8y9y10y11y13	1373.71	50.704	22792	2	687.36	4.44
[P0A1D3 CH60_SALTY 60 kDa chaperonin	19		GQNEQNVGIK	430	11	9	65.2	b2y1y3y6y7y8y9*y9y11	1201.58	26.239	22305	2	601.29	1.22
[P0A1D3 CH60_SALTY 60 kDa chaperonin	20		ATLEDLGQAKR	311	11	3	31.12	y4y7y8	1201.65	38.864	20183	2	601.33	-1.93
[P0A1D3 CH60_SALTY 60 kDa chaperonin	21		VVINKDTTIIIDGVGEEAAIQGR	322	23	5	34.8	b2y3y4y5y23	2399.28	67.324	7947	2	1200.14	1.73
[P0A1D3 CH60_SALTY 60 kDa chaperonin	22		VTLGPK	28	6	2	29.72	y3y5	614.39	27.566	5215	1	614.39	-1.59
[P0A1D3 CH60_SALTY 60 kDa chaperonin	23		IADLKGQNEQNVGIK	425	16	11	115.22	b3b4y3y4y8y9y10*y10y11y13y14	1741.89	39.710	159657	3	581.30	-7.99
[P0A1D3 CH60_SALTY 60 kDa chaperonin	24		EIELEDKFENMGAMVK	58	17	4	38.95	y6y7y8y10	2010.94	73.019	147825	3	670.98	-6.50
[P0A1D3 CH60_SALTY 60 kDa chaperonin	25	Carbamidomethyl+C(16)	AVAAAVEELKALSVPSCDSK	122	20	8	46.65	b8*b8b9y4y6y8y10*y10	2045.05	71.508	41118	3	682.35	-5.97
[P0A1D3 CH60_SALTY 60 kDa chaperonin	26		AMLQDIATLTGGTVISEEIGMELEKATLEDLGQAK	286	35	11	51.21	b4b6b7*b7b8b9*b9b13*b13y3*y3	3675.85	122.644	38983	3	1225.96	-4.91
[P0A1D3 CH60_SALTY 60 kDa chaperonin	27		VGKEGVITVEDGTGLQDELDVVEGMQFDR	168	29	3	11.47	b15y4y12	3135.50	72.607	35575	4	784.63	-3.43
[P0A1D3 CH60_SALTY 60 kDa chaperonin	28	Carbamidomethyl+C(13)	AMEAPLRQIVLNCGEPSVVANTVK	445	25	8	54.61	b3b4b5y5*y5y11y13y14	2725.40	73.503	21937	3	909.14	-0.81
[P0A1D3 CH60_SALTY 60 kDa chaperonin	29		AIAQVGTISANSDETVGKLI AEAMDK	142	26	3	18.21	b3b14b17	2632.34	91.229	10864	3	878.12	-2.13
[P0A1D3 CH60_SALTY 60 kDa chaperonin	30		DGVSVAREIELEDK	51	14	4	27.35	b5b10y8y10	1559.77	37.382	2613	3	520.60	-12.29
[P0A1D3 CH60_SALTY 60 kDa chaperonin	31		DTTIIIDGVGEEAAIQGRVAQIR	327	23	4	12.95	b10*b10b12y5	2413.24	98.596	2236	2	1207.13	-10.42
[P0A1D3 CH60_SALTY 60 kDa chaperonin	32		AAAVEELK	124	8	0	2.05		830.46	46.932	12185	1	830.46	-7.20
[P0A1D3 CH60_SALTY 60 kDa chaperonin	33		GMNPMDLKR	109	9	2	21.13	b3b4	1061.53	50.732	11441	2	531.27	9.66
[P0A1D3 CH60_SALTY 60 kDa chaperonin	34		NVLADAVK	20	8	2	22.33	b6b7	829.48	55.744	8706	1	829.48	0.88
[P0A1D3 CH60_SALTY 60 kDa chaperonin	35		LEDLGQAKR	313	9	0	2.46		1029.56	38.821	5884	2	515.28	-13.04
[P0A1D3 CH60_SALTY 60 kDa chaperonin	36		EMLPVLEAVAK	231	11	0	2.46		1181.64	79.472	9362	2	591.32	-12.40
[P0A1D3 CH60_SALTY 60 kDa chaperonin	37		QQIEEATSDYDREK	350	14	0	3.7		1693.77	32.865	5619	3	565.26	5.41
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	1		YAMIGDPTGALTR	93	13	9	67.55	b2b4b5b6b8y7y10y11y13	1365.68	62.588	79552	2	683.35	1.16
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	2	Carbamidomethyl+C(13)	AAQYVAAHGPEVCPAK	153	16	10	84.08	b3b6b8y3y5y8y9y11y12y16	1668.79	34.736	71628	3	556.94	-13.53
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	3		ATFVVDPQGIQAEIVTAEGIGR	120	23	13	102.56	b3*b3b4b5y2y5*y5y6y7y8y9y10y23	2384.27	128.740	47325	3	795.43	-6.04
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	4		EGEATLAPSLDLVGK	171	15	3	17.99	b9y3y5	1499.78	52.723	25981	2	750.39	-9.03
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	5		NQAFK	12	5	1	13.15	b3	607.31	51.815	19318	1	607.31	-11.36
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	6	Carbamidomethyl+C(15)	WSVFFFYPADFTFVCPTELGDVA DHYEELQK	32	31	4	13.73	b3b9y9y11	3757.74	119.606	10854	3	1253.25	6.37
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	7	Carbamidomethyl+C(15)	IKAAQYVAAHGPEVCPAK	151	18	4	15.45	b17y6*y6y15	1910.02	83.406	5873	3	637.34	12.59
[P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	8		NGEFIEVTEKDTEGR	17	15	6	29.22	b12y3y7*y7y8*y8	1723.81	72.428	2453	2	862.41	-1.27

P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	9	Carbamidomethyl+C(10)	YVAAHPGEVCPAK	156	13	0	4.52		1398.69	34.749	2088	2	699.85	7.68
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C	10	Carbamidomethyl+C(11)	QYVAAHPGEVCPAK	155	14	0	4.52		1526.73	34.740	2086	3	509.58	-10.15
Q8ZP65 TPX_SALTY Probable thiol peroxidase	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	26	169.39	b2b3b5b9b10*b10b11b12°b12b16b17y2y4y5°y5*y5y6°y6y7y8y9y10y12*y12y17y23	2379.23	64.045	167446	3	793.75	-3.59
Q8ZP65 TPX_SALTY Probable thiol peroxidase	2		AQAFTLVAK	24	9	6	38.08	y1y2y3y6y7y9	948.54	52.842	94046	2	474.77	-11.26
Q8ZP65 TPX_SALTY Probable thiol peroxidase	3	Carbamidomethyl+C(13)	VLNIFPSIDTGVCAASVR	48	18	12	58.68	b1b2b3b5b11y1y2y9y10y13y14y18	1919.02	84.611	93889	2	960.01	5.09
Q8ZP65 TPX_SALTY Probable thiol peroxidase	4	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	7	39.47	b2b3b4y4y6y15y17	1837.96	85.526	92065	2	919.48	4.98
Q8ZP65 TPX_SALTY Probable thiol peroxidase	5		DLSDVSLSQYAGK	33	13	9	76.09	b4b5y5y6*y6y7y9y11y13	1382.69	58.601	69575	2	691.85	5.47
Q8ZP65 TPX_SALTY Probable thiol peroxidase	6		NYGVEIVDGPLK	116	12	7	49.38	b2b3y4y5y8y10y12	1303.69	64.396	32624	2	652.35	-1.87
Q8ZP65 TPX_SALTY Probable thiol peroxidase	7	Carbamidomethyl+C(15)	FNQLATEVENTVVLCSADLPFAQSR	67	26	4	12.06	b12°b12y13y19	2908.42	109.456	2994	4	727.86	-11.58
Q8ZP65 TPX_SALTY Probable thiol peroxidase	8		AVIVLDENDNVIFSQLVDEITHEPDYDAALNVLKA	133	35	21	156.1	b3b4b5b6b10b11y3y4y5y6y11*y11y12y13°y13*y13y20y22y24y30y31	3882.95	120.118	125401	3	1294.99	-2.77
Q8ZP65 TPX_SALTY Probable thiol peroxidase	9	Phosphoryl STY(13)	MSQTVHFQGNPVTVANVIPQAGSK	0	24	6	23.27	b11°b11y5*y5y6y12	2590.21	85.950	51913	3	864.08	-10.93
P0A1Z2 SKP_SALTY Chaperone protein skp	1		METDLQSK	59	8	6	40.68	b2y2y4y5y6y8	951.44	25.884	145803	2	476.22	-8.79
P0A1Z2 SKP_SALTY Chaperone protein skp	2		IAIVNMGNLFQQVAQK	23	16	15	88.55	b1b2b3b7y1y2y3y6y7y9*y9y10y11y12y16	1773.97	89.325	129204	2	887.49	1.72
P0A1Z2 SKP_SALTY Chaperone protein skp	3		TGVSNTLENEFK	39	12	11	75.38	b6°b6b10y2y5y6y7y10*y10y11y12	1338.65	57.539	108047	2	669.83	0.64
P0A1Z2 SKP_SALTY Chaperone protein skp	4		VANDQSIDLVDANTVAYNSSDV K DITADVLK	126	32	7	23.42	b1b5b7b9b11*b11y1	3392.70	89.273	64185	3	1131.57	-0.58
P0A1Z2 SKP_SALTY Chaperone protein skp	5		QTFAQK	91	6	2	13.56	y4*y4	722.37	42.152	8060	1	722.37	-11.91
P0A1Z2 SKP_SALTY Chaperone protein skp	6		VANDQSIDLVDANTVAYNSSDV K	126	24	3	18.93	b6b12b14	2537.21	98.750	2924	2	1269.11	-10.78
P0A1Z2 SKP_SALTY Chaperone protein skp	7		AYNSSDV K DITADVLK	142	16	3	16.92	b4b8b13	1738.87	89.214	5968	2	869.94	-8.78
P0A1Z2 SKP_SALTY Chaperone protein skp	8		ETDLQSK	60	7	0	1.23		820.40	25.958	2362	1	820.40	-9.23
P0A1Z2 SKP_SALTY Chaperone protein skp	9		IAIVNMGNLFQQVAQK	23	16	0	4.52		1756.91	89.378	1793	3	586.31	-12.71
P64052 EFTS_SALTY Elongation factor Ts	1		ITDVEVLK	104	8	12	90.27	b2°b2b3b4y1y2y3y4y5y6y7y8	916.52	48.198	150362	2	458.77	-11.12
P64052 EFTS_SALTY Elongation factor Ts	2		VASLEGDVLGSYQHGAR	134	17	13	111.83	b2b6y3y4y5*y5y7y8y10y11y12y13y17	1758.86	58.705	138656	3	586.96	-8.74
P64052 EFTS_SALTY Elongation factor Ts	3		AEITASLVK	1	9	6	30.3	b3°b3y1y5y6y9	931.54	48.299	122807	2	466.27	-8.06
P64052 EFTS_SALTY Elongation factor Ts	4		IGENINIR	125	8	5	40.68	y4y5y7*y7y8	928.51	44.078	97093	2	464.76	-8.55
P64052 EFTS_SALTY Elongation factor Ts	5		IGVLVAAK	151	8	7	56.84	b2b3y1y3y5y7y8	770.50	46.899	69565	2	385.76	-12.52
P64052 EFTS_SALTY Elongation factor Ts	6		VLDAAVAGK	95	9	7	64.38	b2b5y3y4y6y8y9	843.48	33.062	28209	2	422.25	-10.78
P64052 EFTS_SALTY Elongation factor Ts	7		AGNVAADGVIK	52	11	5	31.12	y2y4y6y7y11	1014.55	36.128	21333	2	507.78	-4.51

P64052 EFTS_SALTY Elongation factor Ts	8		FTGEVSLTGQPFVMEPSK	222	18	8	30.72	b6°b6b11b15°b15y6y9*y9	1953.95	81.021	7060	2	977.48	-5.31
P64052 EFTS_SALTY Elongation factor Ts	9		EYQVQLDIAMQSGKPK	193	16	3	34.42	b8b9b10	1834.95	70.215	4435	3	612.32	8.71
P64052 EFTS_SALTY Elongation factor Ts	10		DAGFQAFADK	85	10	3	28.49	b3y8y9	1069.51	27.699	10047	2	535.26	15.07
P64052 EFTS_SALTY Elongation factor Ts	11		QLAMHVAASKPEFVKPEDVSADV VEK	167	26	11	55.38	b3b7°b7b8b9°b9°b9b19y6 y10y11	2824.47	136.311	5789	3	942.16	5.10
P64052 EFTS_SALTY Elongation factor Ts	12		ALTEANGDIELAIENMR	25	17	4	16.18	b6y7°y7y12	1859.89	88.907	4964	3	620.63	-16.34
P64052 EFTS_SALTY Elongation factor Ts	13	Carbamidomethyl+C(13)	IDGNVAFILEVNCQTDFVAK	65	20	3	34.47	b4b5b6	2253.14	82.756	2038	2	1127.07	6.72
P64052 EFTS_SALTY Elongation factor Ts	14		FEVGEGIEK	258	9	4	45.21	b3b5b6y5	1007.49	75.587	1507	2	504.25	-15.51
P64052 EFTS_SALTY Elongation factor Ts	15		DAGFQAFADKVLDAAVAGK	85	19	5	14.82	b14°b14y3y7°y7	1893.98	98.774	25057	2	947.49	2.84
P64052 EFTS_SALTY Elongation factor Ts	16		KALTEANGDIELAIENMR	24	18	6	32.37	y9*y9y11y13*y13y14	1988.01	66.231	14452	2	994.51	1.23
P64052 EFTS_SALTY Elongation factor Ts	17	Carbamidomethyl+C(15)	TKIDGNVAFILEVNCQTDFVAK	63	22	4	36.98	y8y10y11y12	2482.24	68.951	2505	2	1241.62	-9.15
P64052 EFTS_SALTY Elongation factor Ts	18	Phosphoryl STY(12)	EYQVQLDIAMQSGKPKEIAEK	193	21	3	13.77	b7b11y11	2485.19	67.283	4972	3	829.07	-2.26
P64052 EFTS_SALTY Elongation factor Ts	19	Oxidation+M(14)	FTGEVSLTGQPFVMEPSK	222	18	3	15.45	b3b14y10	1969.94	73.014	7443	2	985.47	-7.81
P64052 EFTS_SALTY Elongation factor Ts	20	Oxidation+M(16)	ALTEANGDIELAIENMRK	25	18	4	15.45	b9°b9b14y4	2004.01	71.467	2495	2	1002.51	2.74
P64052 EFTS_SALTY Elongation factor Ts	21		ITASLVK	3	7	0	1.64		731.46	48.316	23755	1	731.46	-6.68
P64052 EFTS_SALTY Elongation factor Ts	22		SLEGDVLSYQHGAR	136	15	2	20.81	b8b9	1588.78	58.755	2894	2	794.90	7.22
P64052 EFTS_SALTY Elongation factor Ts	23		LDAAVAGK	96	8	0	1.64		744.43	33.042	2433	1	744.43	1.64
P67093 UG_SALTY Universal stress protein G	1		TIIMPVDVFEMELSDK	3	16	13	66.35	b1b2b3b4y1y6y9y12°y12y 13y14°y14y16	1866.93	104.062	90197	2	933.97	6.28
P67093 UG_SALTY Universal stress protein G	2		NPSITTHLLGSNASSVVR	114	18	6	26.38	b4°b4b6b7y8y18	1852.98	58.688	43951	3	618.33	-2.37
P67093 UG_SALTY Universal stress protein G	3		DVVNEMGEELDADVVVIGSR	94	20	6	27.75	b4°b4b6b8y12y14	2146.07	118.075	2741	2	1073.54	17.86
P67093 UG_SALTY Universal stress protein G	4		TIIMPVDVFEMELSDKAIR	3	19	3	21.77	y4y11y16	2207.13	100.305	29310	3	736.38	-8.74
P67093 UG_SALTY Universal stress protein G	5		MYKTIIMPVDVFEMELSDK	0	19	3	23.99	y8y12y13	2289.12	98.108	2377	3	763.71	-0.43
P67093 UG_SALTY Universal stress protein G	6	Oxidation+M(24)	HAEFLAQDQGVIIHLHLVLPGSAS MSLHR	22	28	5	26.7	y3y5y7°y7y8	3079.61	137.300	41093	3	1027.21	6.58
P67093 UG_SALTY Universal stress protein G	7	Oxidation+M(11)	TIIMPVDVFEMELSDK	3	16	6	45.6	b9b13b15y11y12y15	1882.91	76.862	3704	3	628.31	-3.70
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	1		TVVFHDTSANEYVK	10	14	12	105.23	b1b11°b11b12y3y4y8y9y1 0y11y12y14	1609.77	46.731	263303	3	537.26	-12.36
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	2		TFDSESSAAR	62	10	9	60.81	b3°b3y1y4y5y7y8°y8y10	1070.47	23.916	67943	2	535.74	-4.11
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	3		VGSTIKTER	24	9	4	57.25	y3y4y7y8	990.55	17.627	34736	2	495.78	-6.72
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	4		QKTFDSESSAAR	60	12	3	26.09	b3y3y4	1326.61	22.050	23129	3	442.87	-14.72
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	5		TVVFHDTSANEYVKVGSTIK	10	20	8	61.49	b6b7°b7b8b9b10°b10*b10	2195.12	136.227	1762	2	1098.06	-7.45
P66193 RL31B_SALTY 50S ribosomal protein L31 type B	6	Phosphoryl STY(11)	TEREIELDGVITYPYVTIDVSSK	30	22	3	13.33	b5b9y12	2594.21	82.176	3550	2	1297.61	-2.07

P66193 RL31B_SALTY 50S ribosomal protein L31 type B	7		VFHDTSANEYVK	12	12	5	54.67	b3b5b9b10b11	1409.66	46.692	21723	2	705.34	-4.42
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	1		TQFMGPEGVANVSLNIAGESAE GLLVTKPK	240	31	12	56.05	b2b3b4b11y1y3y13y14y22 y27y28y31	3144.63	87.803	119986	3	1048.88	2.64
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	2		NYDQVPANKPIVDAIK	271	16	9	35.16	b2*b2b4b9b10y3y11*y11y 16	1784.94	53.495	118789	3	595.65	-9.44
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	3		TTGLDSDQGPTAAK	137	14	16	111.17	b2°b2b3°b3b4b12y5y7*y7y 8y9y10°y10y11y12y14	1361.65	28.632	79571	2	681.33	-0.63
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	4	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILM ITPAATAPELTAR	92	38	12	55.45	b2b12b25b27y6y8y10y11° y11y12y13y38	4077.98	88.875	64487	3	1360.00	-0.24
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	5		VAVVGAMSGPVAQYGDQEFTGA EQAIADINAK	25	32	16	60.52	b1b2b4b15y2y3y4y5*y5y6° y6y8y10*y10y25y32	3207.57	89.191	59134	3	1069.86	2.21
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	6		ENIDFVYYGGYHPMGQILR	212	20	3	22.39	b9y9y10	2401.16	79.874	8558	2	1201.08	11.39
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	7		GATVDTVMGPLSWDEK	326	16	3	14.28	b5°b5b13	1705.83	59.023	6866	3	569.28	13.17
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	8		GGVNVVFFDGITAGEK	185	16	3	34.42	y10y11y12	1609.81	70.179	3943	2	805.41	-9.10
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	9	Carbamidomethyl+C(6)	TLLAGCIALSLSHMAFADDIK	4	21	6	30.94	b8y5°y5y10y11y14	2247.13	78.159	5353	3	749.71	-10.65
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	10		GFEFGVFDWHANGTATDAK	346	19	6	41.78	b6°b6b7b8y4y10	2069.98	58.518	5110	3	690.66	21.11
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	11		KQDPSGAFVWTTYAALQSLQAGL NHSDDPAEIAK	289	34	9	39.26	b3b7b14b15y8y10y11y14* y14	3629.77	102.836	116319	4	908.20	-5.99
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	12		GDLKGFEFGVFDWHANGTATDA K	342	23	3	12.95	b15y5y8	2483.19	90.156	28604	3	828.40	9.73
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein	13		SGPVAQYGDQEFTGAEQAIADINA K	32	25	0	11.09		2580.24	89.197	5271	3	860.75	5.68
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	1		AGLGMMEGVLENVPSAR	78	17	9	49.4	b13b14*b14y4y6°y6y7y12 y17	1730.86	81.269	54318	2	865.93	3.53
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	2		VLVLVAAPEGIAALEK	155	16	7	77.99	b3b4b5b6y9y10y11	1592.96	85.383	36954	2	796.99	1.38
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	3		ITVVPILR	70	8	5	53.83	y2y4y5y6y7	910.60	69.590	14387	2	455.80	-6.90
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	4		ELASEVGSLLTYEATADLETEK	29	22	6	20.69	b3b7b15y2°y2y6	2369.17	108.399	3160	2	1185.09	4.12
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	5		LVSNI DER	116	8	3	40.68	y3y6y7	945.49	32.138	21999	2	473.25	-7.62
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	6		NEETLEPVVPYFQK	103	13	5	34.21	b10b11°b11y5y7	1593.78	64.911	17243	2	797.39	0.69
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	7		ISVVGMYRNEETLEPVVPYFQK	95	21	3	13.77	b11b13y6	2499.30	102.412	28232	3	833.77	14.65
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	8		NEETLEPVVPYFQKLVSNI DER	103	21	3	22.22	b12y3y4	2520.28	116.949	7229	3	840.77	8.72
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase	9	Phosphoryl.STY(3)	LVSNI DER	116	8	4	32.9	b5y4°y4y5	1025.47	94.319	1532	1	1025.47	14.05
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	1		TMNTPHGDAITVFDLR	23	16	6	39.63	y2y6y10°y10y11y12	1787.86	71.033	40692	3	596.62	-9.35
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	2	Carbamidomethyl+C(2)	FCIPNKEVMPEK	39	12	5	29.31	b2y1y4y9y10	1491.72	52.147	32454	3	497.91	-10.64
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	3	Carbamidomethyl+C(15)	VQDQNQIPELNVYQCGTYQMHS LSEAQDIAR	113	31	12	65.59	b6°b6b7b9y1y7y8y9y10y1 2y24y31	3635.69	74.319	26066	3	1212.57	1.54
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	4	Carbamidomethyl+C(18)	DHLNGNGVEIIDSPMGCR	65	19	7	34.85	b2b12y4y8y11y14y19	2096.97	66.064	7000	3	699.66	-5.94
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	5		TGFYMSLIGTPDEQR	84	15	6	29.22	b3°b3b12b14*b14y10	1714.85	81.990	8577	3	572.29	20.29

Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	6		GIHTLEHLFAGFMR	51	14	4	19.13	b9°b9b11y11	1628.84	75.572	4513	2	814.92	3.67
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	7		PLLDSDFAVDHTR	1	12	4	44.68	y3y5y7y8	1370.70	57.354	3571	3	457.57	-6.68
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	8	Carbamidomethyl+C(18)	TMNTPHGDAITVFDLRFCIPNK	23	22	4	13.33	b3b11y7*y7	2547.28	71.374	2678	2	1274.15	14.28
Q9L4T0 LUXS_SALTY S-ribosylhomocysteine lyase	9		TGFYMSLIGTPDEQRVADAWK	84	21	3	23.42	y6y11y12	2385.16	108.361	2409	3	795.73	3.48
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	1		VALTGLTMAEK	219	11	10	100.67	b2b3b5y3y4y5y7°y7y8y9	1133.62	58.772	52382	2	567.31	-1.72
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	2		YTLAGTEVSALLGR	247	14	7	27.7	b2°b2y1y4y6y11y14	1450.79	79.573	49123	2	725.90	-1.09
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	3		TVNMMELIR	156	9	6	30.3	b3b9y3y7y9*y9	1106.56	75.679	48163	2	553.79	-4.74
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	4		QLDPLVVQGEHYDTAR	343	16	13	115.08	b2y3y4y5y6y9°y9y10y11°y11*y11y13y14	1840.91	57.557	43335	3	614.31	-7.16
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	5	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	8	70.16	b3b9y5y6y7y8°y8y10	1193.59	80.270	40925	2	597.30	-12.58
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	6		FLSQPFFVAEVFTGSPGK	399	18	6	22.61	y7°y7y10°y10y14y18	1958.02	99.347	35184	2	979.51	7.04
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	7		MPSAVGYQPTLAEEMGVLQER	261	21	6	23.42	b21y4y6y7°y7y21	2306.13	80.831	31551	2	1153.57	4.66
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	8		VGLFGGAGVGK	145	11	3	31.12	y4y7y8	961.54	58.655	28249	2	481.27	-5.90
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	9		QIASLGIYPAVDPLDSTSR	324	19	7	38.78	b5b9y4y11y12y14y19	2003.06	79.708	27635	2	1002.03	5.42
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	10		AAPSYEELSNSQELLETK	112	20	9	41.18	b1b13b14°b14b15y1y12y18y20	2179.09	72.923	23111	2	1090.05	7.62
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	11		TIAMGSSDGLRR	53	12	4	29.31	b4b5b9y12	1263.64	32.792	16361	2	632.32	-5.22
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	12		NIAIEHSGYSVFAGVGER	165	18	7	30.72	b8b15°b15b17y5°y5y11	1905.93	83.412	7098	2	953.47	-8.58
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	13		TIAMGSSDGLR	53	11	3	35.89	y3y5y10	1107.55	46.003	3425	2	554.28	5.40
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	14		GIMEGEYDHLPEQAFYMVGSIDE AVEK	429	27	5	27	y5y6°y6y11y13	3057.43	91.948	33903	3	1019.82	16.13
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	15		YQELK	367	5	2	26.3	b3b4	680.36	30.286	5445	1	680.36	-3.41
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	16		DEGRDVLLFVDNIYR	232	15	3	17.99	b6b12y7	1823.95	99.005	303151	2	912.48	12.92
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	17	Carbamidomethyl+C(6)	VIDLMCPFAKGGK	132	13	3	20.48	b3b7y3	1435.74	65.396	2971	3	479.25	-0.51
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	18	Oxidation+M(11)	IMNVLGEPVDMK	87	12	3	26.09	b6b7y9	1361.69	33.122	17571	3	454.57	3.77
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	19	Oxidation+M(13)	YQELKDIIAILGMDELSEEDK	367	21	4	13.77	b4b14y14°y14	2468.20	97.852	2583	3	823.40	-6.03
Q7CPE2 ATPB_SALTY ATP synthase subunit beta	20		QLDPLVVQGEHYDTAR	343	16	0	4.52		1823.88	57.472	1908	3	608.63	-6.22
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	1		VVGYSQDYSNAIVEAVKK	61	18	10	50.08	b1b2y1y2y4y6y12y14y16y18	1970.01	62.863	134380	3	657.34	-7.31
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	2		ESSVPFSYYDNQK	47	14	12	102.8	b4°b4b11y4y5y6y7y8y9y10°y10y14	1691.76	54.791	118734	2	846.38	3.54
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	3		AVAFMMDDALLAGER	198	15	9	62.81	b1b3b5y4y10y11y13y14y15	1609.78	83.863	110284	2	805.39	4.32

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	4		VVGYSQDYSNAIVEAVK	61	17	16	103	b2b3b6b7b12y2y3y4y5y10y11°y11y13°y13y15y17	1841.93	67.230	98609	2	921.47	0.93
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	5	Carbamidomethyl+C(13)	IPLLQNGTFDFECGSTTNNLER	98	22	7	30.04	b11y5y7y9*y9y10y22	2526.19	80.985	30165	3	842.73	-1.74
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	6		GGDIKDFPDLK	141	11	4	27.14	b8y9y10y11	1204.63	69.283	29932	2	602.82	5.78
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	7	Carbamidomethyl+C(19)	KPDNWEIVGKPSQEAYGCMLR	217	22	11	45.42	b4°b4*b4b5b8°b8*b8b20y5y6y9	2606.26	136.259	21101	3	869.43	5.06
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	8		LMDDTIAQAQTSGEAEK	247	17	4	24.83	y3y10y11°y11	1807.85	45.411	6445	2	904.43	7.90
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	9		NDPEFK	240	6	1	13.56	y5	749.35	79.067	5823	1	749.35	8.39
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	10		WFDK	264	4	1	12.74	y3	595.29	32.437	2181	1	595.29	10.77
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	11	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTFDFECGSTTNNLER	89	31	9	50.59	b3b13y4y6y9y10y12y21y27	3548.79	86.255	269134	3	1183.60	1.65
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	12		AVVVTSGTTSEILLHLNREEQK	154	22	10	68.56	b3b13y3y5y8y9y10y18°y18y19	2396.29	63.261	50787	3	799.43	-6.83
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	13		LMDDTIAQAQTSGEAEKWFDK	247	21	6	29.83	y3°y3y4y9y13*y13	2384.10	88.412	16726	4	596.78	-2.97
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	14		KLMDDTIAQAQTSGEAEK	246	18	6	21.55	b12b14y9°y9y11°y11	1935.94	83.433	7582	2	968.48	6.31
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	15	Carbamidomethyl+C(19)	KPDNWEIVGKPSQEAYGCMLRK	217	23	5	28.64	y6y7y10y12°y12	2734.36	89.295	5644	3	912.12	5.80
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	16	Oxidation+M(8)	LTTAMLVMGLSAGLAHAEDGAP AAGSTLDDK	5	30	4	11.33	b5b9°b9y6	2885.40	109.463	8797	3	962.47	-11.68
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein	17		DIKDFPDLK	143	9	0	2.46		1090.58	69.363	9614	2	545.79	-0.67
P00924 ENO1_YEAST Enolase 1	1		NVNDVIAPAFVK	67	12	13	102.64	b2b4b5°b5b6°b6b9y5y6y7y8y10y12	1286.71	65.643	104876	2	643.86	-3.79
P00924 ENO1_YEAST Enolase 1	2		VNQIGTLESSEIK	346	12	12	75.38	b2*b2b3b9y1y2y5y6y8y9y10y12	1288.71	53.904	65475	2	644.86	-0.28
P00924 ENO1_YEAST Enolase 1	3		SIVPSGASTGVHEALEMR	32	18	7	43.41	b8b14b15y2y10y14y15	1840.91	61.812	62661	3	614.31	-8.49
P00924 ENO1_YEAST Enolase 1	4		AADALLLK	338	8	4	40.68	y4y5y6y8	814.49	53.480	62535	2	407.75	-11.76
P00924 ENO1_YEAST Enolase 1	5		TFAEALR	178	7	6	69.58	b3b6y4y5y6y7	807.43	45.205	50340	2	404.22	-7.71
P00924 ENO1_YEAST Enolase 1	6		IGSEVYHNLK	185	10	4	28.49	b2b3y5y6	1159.60	38.946	39533	3	387.20	-9.05
P00924 ENO1_YEAST Enolase 1	7		GNPTVEVELTTEK	15	13	5	20.48	b2b8b12y6y13	1416.72	62.386	33062	2	708.86	-4.05
P00924 ENO1_YEAST Enolase 1	8		IATAIEK	330	7	7	37.26	b2b4°b4y1y5y6y7	745.44	27.623	25465	2	373.22	-12.77
P00924 ENO1_YEAST Enolase 1	9		AVDDFLISLDGTANK	88	15	5	37.67	b7y1y6y7y8	1578.80	81.569	13562	2	789.90	-1.70
P00924 ENO1_YEAST Enolase 1	10		YDLDFK	258	6	2	26.71	y4y5	800.37	54.570	65765	2	400.69	-10.90
P00924 ENO1_YEAST Enolase 1	11		IEEELGDNAVFAGENFHHGDK	415	21	5	27.2	b9b14y12y13*y13	2328.09	80.806	39407	3	776.70	14.58
P00924 ENO1_YEAST Enolase 1	12		WLTGPQLADLYHSLMK	272	16	4	39.63	y6y7y8y10	1872.98	101.120	27978	2	936.99	7.76
P00924 ENO1_YEAST Enolase 1	13		NVPLYK	126	6	1	13.56	y4	733.42	36.551	8971	1	733.42	-9.15
P00924 ENO1_YEAST Enolase 1	14		AAQDSFAAGWGVMVSHR	358	17	4	16.18	b14*b14y9y15	1789.86	103.562	6214	2	895.43	10.09

[P00924]ENO1_YEAST Enolase 1	15		SGETEDTFIADLVVGLR	375	17	3	23.58	b10b12b16	1821.96	72.565	4943	3	607.99	18.49
[P00924]ENO1_YEAST Enolase 1	16		NPNSDK	264	6	2	26.71	y4y5	674.31	111.837	1676	1	674.31	-6.88
[P00924]ENO1_YEAST Enolase 1	17	Carbamidomethyl+C(7)	VKIGLDCASSEFFK	241	14	4	32.79	b10b12y5y6	1600.78	41.076	9178	2	800.89	-13.88
[P00924]ENO1_YEAST Enolase 1	18		GVFRSIVPSGASTGVHEALEMR	28	22	3	13.33	b10y3y10	2300.18	48.488	7388	3	767.40	0.21
[P00924]ENO1_YEAST Enolase 1	19	Phosphoryl STY(8)	VNQIGTLSESIK	346	12	6	34.01	b6b8°b8b9y10°y10	1368.65	57.225	118022	2	684.83	-14.63
[P00924]ENO1_YEAST Enolase 1	20	Phosphoryl STY(8)	AVDDFLISLDGTANK	88	15	5	44.41	b3b6b9b12y6	1658.74	69.217	9516	3	553.58	-10.74
[P00924]ENO1_YEAST Enolase 1	21	Oxidation+M(15)	WLTGSQLADLYHSLMKR	272	17	4	16.18	b9b11°b11y6	2045.05	116.563	19220	2	1023.03	-6.57
[P00924]ENO1_YEAST Enolase 1	22	Oxidation+M(17)	SIVPSGASTGVHEALEMR	32	18	7	39.88	b10°b10b11y3y4°y4y6	1856.91	136.159	2804	2	928.96	-5.85
[P00924]ENO1_YEAST Enolase 1	23		GSEVYHNLK	186	9	0	2.05		1046.52	38.947	24664	2	523.76	-9.68
[P00924]ENO1_YEAST Enolase 1	24		IATAIEK	330	7	0	0.82		727.42	27.604	2661	2	364.21	-12.33
[P66541]RS2_SALTY 30S ribosomal protein S2	1		WLGGMLTNWK	95	10	10	52.24	b3b7°b7b10y1y3°y3y4y8y10	1205.61	85.854	93549	2	603.31	-5.27
[P66541]RS2_SALTY 30S ribosomal protein S2	2		MATVSMRMDLK	0	11	5	27.14	b4b5y1y6y11	1282.63	58.962	44309	3	428.21	-2.09
[P66541]RS2_SALTY 30S ribosomal protein S2	3	Carbamidomethyl+C(6)	EAANSCDQFFVNHR	81	14	5	44.53	y1y3y4y7y8	1694.72	46.955	40760	3	565.58	-8.72
[P66541]RS2_SALTY 30S ribosomal protein S2	4		EANNLGIPVFAIVDTNSDPDGVDF VIPGNDDAIR	174	34	15	67.23	b5°b5b6°b6b7°b7°b7b17y3y4y7y8y13y16y34	3569.75	103.782	28842	3	1190.59	3.35
[P66541]RS2_SALTY 30S ribosomal protein S2	5		TVPMFNEALAE LNK	45	14	8	54.67	b3°b3b4b5b7b10°b10y14	1576.83	67.930	16558	2	788.92	13.55
[P66541]RS2_SALTY 30S ribosomal protein S2	6		ILFVGTK	66	7	5	40.27	b2y2y3y4y6	777.48	56.828	15971	2	389.24	-8.95
[P66541]RS2_SALTY 30S ribosomal protein S2	7		DLETQSQDGTFEK	115	13	7	34.95	b1b2y9y10°y10y11°y11	1497.69	39.745	11156	2	749.35	13.77
[P66541]RS2_SALTY 30S ribosomal protein S2	8		YWNPK	21	5	1	13.15	b4	707.36	21.569	12562	1	707.36	8.46
[P66541]RS2_SALTY 30S ribosomal protein S2	9		EGRSQDLASQAEE SFVEAE	222	19	3	14.82	b7y6y13	2081.96	73.917	8909	2	1041.48	14.07
[P66541]RS2_SALTY 30S ribosomal protein S2	10	Oxidation+M(5)	WLGGMLTNWK	95	10	4	33.72	y4°y4y6y7	1221.60	136.335	2794	1	1221.60	-8.99
[P66541]RS2_SALTY 30S ribosomal protein S2	11	Oxidation+M(2)	DMGGLPDALFVIDADHEHIAIK	152	22	3	22.08	b13b14y7	2393.19	77.887	2500	4	599.05	2.35
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	1		DQIIEAVSAMSVM DVVELISAMEE K	5	25	23	161.02	b2°b2°b2b3b4b5b6b7b8b9°b9b10b20y2°y2y4y5y6y7y9°y9y10y25	2737.33	137.082	59058	3	913.11	-2.50
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	2		DLVESAPAALK	85	11	6	35.06	b4b8°b8y4y9y11	1113.60	52.978	35307	2	557.31	-9.76
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	3		EGVSKDDAEALK	96	12	6	22.11	b2°b2b3y7y9y12	1261.64	34.672	9362	2	631.32	11.61
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	4		SLEEAGAEVEVK	109	12	3	22.11	b9b11y11	1260.63	48.481	4290	2	630.82	1.55
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	5		SITKDQIIEAVSAMSVM DVVELISAMEEK	1	29	4	21.89	b4b5°b5y21	3166.58	136.285	4048	3	1056.20	-5.63
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	6		EAKDLVESAPAALK	82	14	4	15.52	b5°b5b12y2	1441.79	60.591	3444	2	721.40	1.19
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	7		VAVIK	66	5	1	13.15	y4	529.37	25.604	2926	1	529.37	-6.00
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	8		AAGANK	60	6	1	13.56	b3	531.29	29.827	2444	1	531.29	9.42
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	9		SITKDQIIEAVSAMSVM DVVELISAMEEK	1	29	3	11.47	b16y8y13	3166.62	114.125	8234	3	1056.21	9.17
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	10		EGVSKDDAEALK	96	12	3	22.11	b3b11y11	1261.63	111.315	1679	2	631.32	2.81
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12	11	Phosphoryl STY(5)	DLVESAPAA LKEGVSK	85	16	4	17.02	b3°b3b11y11	1693.84	68.015	11040	3	565.29	7.28
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	1		SMQDPIADMLTR	1	12	12	65.54	b2b4y1y2y4y5°y5y6°y6y8y9y12	1377.65	77.716	150120	2	689.33	1.95

[P0A7X0]RS8_SALTY 30S ribosomal protein S8	2		AAVTMPSSK	22	9	10	67.39	b2y2y3y4°y4y5y6y7°y7y9	891.46	30.658	84900	2	446.23	-4.11
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	3		AVVESIQR	69	8	10	62.21	b2b3y2*y2y3y4y5°y5y6y8	901.50	32.155	77587	2	451.25	-9.14
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	4		NGQAANKAAVTMPSSK	15	16	4	27.46	b12y3y5y7	1574.82	112.004	3128	2	787.91	12.87
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	5		VTMPSSK	24	7	0	1.64		749.39	30.610	14341	1	749.39	0.08
[P0A7X0]RS8_SALTY 30S ribosomal protein S8	6		AVTMPSSK	23	8	0	1.64		820.43	30.664	4733	2	410.72	6.99
[O54297]RS4_SALTY 30S ribosomal protein S4	1		VVNIASYQVSPNDVVSIR	128	18	17	100.53	b3b7*b7b9°b9*b9b17y3y5y7y8y9*y9y11*y13y14y18	1960.06	71.475	64488	2	980.53	5.98
[O54297]RS4_SALTY 30S ribosomal protein S4	2		LSDYGVQLR	47	9	7	44.7	b2b3°b3b7y1y7y8	1050.56	50.635	47807	2	525.78	-1.05
[O54297]RS4_SALTY 30S ribosomal protein S4	3		KPER	184	4	1	12.74	y3	529.31	44.621	19867	1	529.31	-3.00
[O54297]RS4_SALTY 30S ribosomal protein S4	4		MGFGATR	104	7	3	40.27	b6y3y5	739.35	35.594	7290	2	370.18	-9.49
[O54297]RS4_SALTY 30S ribosomal protein S4	5		AALELAEQR	156	9	6	61.37	b3y4y6°y6y7y8	1000.54	42.784	5826	1	1000.54	-1.28
[O54297]RS4_SALTY 30S ribosomal protein S4	6		IEQAPGQHGAR	33	11	5	65.2	y4y5y6y7y8	1163.57	15.293	3909	3	388.53	-17.73
[O54297]RS4_SALTY 30S ribosomal protein S4	7		KPERSDLSADINEHLIVELYSK	184	22	4	13.33	b11b14*b14y6	2556.30	96.837	2701	3	852.77	-10.89
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	1		ISQHPGWEIVTTQFGYNDATK	177	22	6	26.75	b10b11b22y4°y4y9	2521.21	72.377	49060	3	841.07	2.42
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	2		AYPDLDAIIPDANALPAAQAEE NLKR	209	28	8	51.42	b2b8b9b10y6y10y12y19	2863.50	86.911	48004	3	955.17	0.85
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	3		VAFFYSSPTVTDQNQWVK	154	18	7	46.5	b10b12y3y11y12y13y18	2117.05	77.044	26982	2	1059.03	5.42
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	4		NMPMNVGDSLDIPGIGK	284	17	7	29.71	b12°b12b13y5y15*y15y17	1757.87	78.923	26705	2	879.44	6.67
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	5		VTVSPNSEQGYHYEAK	301	16	12	55.74	b6°b6b8b9°b9*b9y2y4y7y8y10y16	1808.83	35.926	24156	3	603.61	-8.30
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	6		EFGLWDVVQQ GK	261	12	9	34.01	b11*b11y2y3*y3y4*y4y8°y8	1405.71	82.051	16159	2	703.36	-2.00
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	7		LVGVGFFTSGGNGAQEAGK	35	19	8	51.4	b10b11b14y3y10y13y18°y18	1795.87	93.132	3550	2	898.44	-14.21
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	8	Carbamidomethyl+C(12)	ILTWSDTKPECR	111	13	3	27.96	b6b11b12	1620.80	69.218	74524	2	810.90	19.81
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	9		MIALLTAFLASAAAMTVQAAER	7	22	5	30.42	b3y3y5y10y16	2236.15	72.419	13525	2	1118.58	-14.41
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	10		NGGIVLLPER	317	10	3	36.73	y3y4y5	1067.61	61.002	11199	2	534.31	-8.00
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	11		NNLAIVGFSTPNVMRPYVQR	237	20	3	14.26	b4b13y5	2276.21	112.792	10108	3	759.41	4.18
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	12		SYIINQGTPK	124	10	7	57.8	b4b7b8b9y5°y5*y5	1170.59	39.887	2281	2	585.80	8.34
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	13		AKVAFFYSSPTVTDQNQWVK	152	20	3	14.26	b8b14y7	2316.16	82.134	9230	2	1158.58	-1.48
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	14	Oxidation+M()	QLGSMLEVMAAHQVDK	134	16	5	37.16	b11y4y5°y5y6	1772.86	45.581	2712	3	591.63	-1.51
[Q8ZKQ1]LSRB_SALTY Autoinducer 2-binding protein lsrB	15		ISQHPGWEIVTTQFGYNDATK	177	22	0	6.98		2503.19	72.373	8342	3	835.07	1.76
[P66643]RS9_SALTY 30S ribosomal protein S9	1		SLEQYFGR	33	8	6	49.06	b4y3y4y6°y6y8	999.49	60.212	72233	2	500.25	-2.63
[P66643]RS9_SALTY 30S ribosomal protein S9	2		AENQYYGTGR	1	10	7	51.64	b1y4y5y6y8*y8y10	1158.52	26.273	54759	2	579.76	-0.32

P66643 RS9_SALTY 30S ribosomal protein S9	3		GGGISGQAGAIR	68	12	9	43.85	b2b3b11y2y5y7y8°y8y12	1043.55	32.826	50568	2	522.28	-5.50
P66643 RS9_SALTY 30S ribosomal protein S9	4		SLEQYFGRETAR	33	12	3	26.09	b3y4y5	1456.73	55.779	5027	3	486.25	11.06
P66643 RS9_SALTY 30S ribosomal protein S9	5		AGFVTRDAR	100	9	3	30.3	b4y7y8	992.52	84.839	21175	2	496.76	-6.09
P66643 RS9_SALTY 30S ribosomal protein S9	6		AENQYYGTGRR	1	11	3	27.14	b7y9y10	1314.61	50.439	8292	2	657.81	-5.57
P66643 RS9_SALTY 30S ribosomal protein S9	7		ALMEYDESLRGELR	85	14	3	26.91	b9b10b13	1681.80	79.690	5372	3	561.27	-14.37
P66643 RS9_SALTY 30S ribosomal protein S9	8		SLEQYFG	33	7	0	1.23		843.40	60.289	9102	1	843.40	8.68
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	1		SSIPVFGVDALPEALALVK	250	19	7	42.25	y2y3y4y8y13y16y19	1926.10	107.255	36163	2	963.55	3.80
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	2		ALAINLVDPAAGTVIEK	84	18	5	24.62	b3y2y7y11y14	1766.01	79.741	27583	2	883.51	4.84
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	3		SGAMAGTVLNDANNQAK	269	17	11	96.17	b3b9b10b13y7°y7y8y9y10y12y13	1661.80	45.596	26302	2	831.40	5.80
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	4		HWQANQGWDLNK	148	12	6	22.11	b7b11y2y6°y6y12	1496.71	75.772	8556	3	499.58	5.38
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	5		SAPDVQLLMNDSQNDQSK	52	18	6	41.65	b6b7b10y8y10y13	1989.96	75.845	46203	2	995.48	20.80
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	6		ALDSYDK	120	7	5	50.41	b3b4°b4b6y3	811.40	71.433	3383	1	811.40	19.18
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	7		TTYVVKELNDK	181	11	4	27.14	b3b4y5°y5	1309.69	75.801	87620	2	655.35	-11.09
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	8		ELNDKGIQTEQLALDTAMWDTAQAK	187	25	3	12.32	b6b10y5	2790.38	124.286	9532	3	930.80	5.34
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	9		ESGVIQGDLIAKHWQANQGWDLNK	136	24	3	22.91	b3b4b13	2707.35	104.970	7967	2	1354.18	-4.42
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	10		DGKSAPDVQLLMNDSQNDQSK	49	21	3	13.77	b6b11y3	2290.06	58.685	7563	3	764.02	-0.64
P23905 DGAL_SALTY D-galactose-binding periplasmic protein	11		NLAEGKGAADGTSWK	293	15	3	26.07	b5b10b11	1504.72	101.706	5531	3	502.24	-12.82
Q8ZQT5 TOLB_SALTY Protein tolB	1		VSDYDGYNQFVVHR	183	14	6	38.51	b1y3y10*y10y11y13	1698.77	53.636	96312	3	566.93	-12.07
Q8ZQT5 TOLB_SALTY Protein tolB	2		SNNTEPTWFPDSQTLAFTSDQAGRPQVYK	287	29	11	24.03	b2b5°b5y1y2y12y14y22y24°y24y29	3285.54	76.919	70386	3	1095.85	-2.15
Q8ZQT5 TOLB_SALTY Protein tolB	3		IEITQGVSARPIGVVPPFK	24	19	7	14.82	b2b9y1y2y3y16y19	2026.12	70.022	48348	3	676.05	-6.09
Q8ZQT5 TOLB_SALTY Protein tolB	4		WAGPGAAPEDIGGIVAADLR	43	20	10	72.37	b5b6b7b8y2y5y6y9y13y20	1936.00	84.856	43435	2	968.50	2.96
Q8ZQT5 TOLB_SALTY Protein tolB	5		LPATDGQVK	413	9	6	54.24	y2y4y6y7y8y9	928.51	27.109	38054	2	464.76	-1.84
Q8ZQT5 TOLB_SALTY Protein tolB	6		MNINGGAAQR	316	10	9	42.89	b2*b2b3y1y6y7*y7y8y10	1031.51	27.233	29341	2	516.26	2.84
Q8ZQT5 TOLB_SALTY Protein tolB	7		LAYVTFESGR	213	10	4	26.73	b9y4y9y10	1142.58	57.287	28948	2	571.79	-7.05

Q8ZQT5 TOLB_SALTY Protein tolB	8		SALVIQTLANGAVR	223	14	5	38.3	b3y2y9y10y11	1412.82	70.338	25404	2	706.91	-0.26
Q8ZQT5 TOLB_SALTY Protein tolB	9		SPQPLMSPAWSPDGSK	197	16	4	17.02	b2b14y3y10	1684.82	46.983	9605	3	562.28	12.61
Q8ZQT5 TOLB_SALTY Protein tolB	10		YAGHTASDEVFEK	142	13	3	20.48	b3b5y9	1453.66	37.905	32059	3	485.22	-2.94
Q8ZQT5 TOLB_SALTY Protein tolB	11		TGSLNLYVMDLASGQIR	264	17	3	23.58	b3b6b8	1837.94	63.473	3334	3	613.32	-4.91
Q8ZQT5 TOLB_SALTY Protein tolB	12		LPATDGQVKSPAWSPYL	413	17	3	16.18	b8y4y12	1829.97	88.346	110539	3	610.66	13.54
Q8ZQT5 TOLB_SALTY Protein tolB	13		TRIAYVVQTNGGQFPYELR	164	19	6	36.09	b4y10y11*y11y12°y12	2212.15	90.162	44847	3	738.06	0.99
Q8ZQT5 TOLB_SALTY Protein tolB	14		ITWEGSQNQDADVSSDGKFMVM VSSNNGQQHIAK	326	34	3	10.96	b5b16y10	3708.70	96.053	20112	3	1236.91	0.33
Q8ZQT5 TOLB_SALTY Protein tolB	15		SNNTPTWFPDSQTLAFTSDQAG RPQVYKMNINGGAAQR	287	39	4	21.58	y6y8y11y15	4298.05	105.634	3860	3	1433.36	5.34
Q8ZQT5 TOLB_SALTY Protein tolB	16		TGSLNLYVMDLASGQIRQITDGR	264	23	3	12.95	b6b13y11	2508.30	73.365	3363	2	1254.65	4.77
Q8ZQT5 TOLB_SALTY Protein tolB	17	Phosphoryl STY(7)	IAYVVQTNGGQFPYELR	166	17	3	24.83	y5y9y10	2034.98	106.416	1736	2	1018.00	12.30
Q8ZQT5 TOLB_SALTY Protein tolB	18		VIQTLANGAVR	226	11	0	3.7		1141.65	70.430	34282	2	571.33	-13.58
Q56073 DNAK_SALTY Chaperone protein dnaK	1		IINEPTAAALAYGLDKEVGNR	167	21	12	68.72	b1b2b3y1y5y6y7y10y12y1 7y19y21	2215.16	74.294	66322	3	739.06	-5.73
Q56073 DNAK_SALTY Chaperone protein dnaK	2		SLGQFNLDGINPAPR	452	15	18	137.29	b2°b2b4°b4b8b14y1y4y5y7 y8°y8y10*y10y11y13y14y1 5	1598.84	71.368	38241	2	799.92	5.57
Q56073 DNAK_SALTY Chaperone protein dnaK	3		ASSGLNEEEIQK	502	12	9	81.77	b1y3y5y7°y7y8y9y10y12	1304.63	33.956	26479	2	652.82	-0.37
Q56073 DNAK_SALTY Chaperone protein dnaK	4		MQELAQVSQK	587	10	6	47.66	b2b3y3y6y8y10	1161.59	36.546	24056	2	581.30	-0.84
Q56073 DNAK_SALTY Chaperone protein dnaK	5		TAEDYLGPVTEAVITVPAYFNDA QR	125	26	9	54.56	b6b7y1y5y6y8y9y16y26	2869.39	92.879	20357	3	957.14	0.68
Q56073 DNAK_SALTY Chaperone protein dnaK	6		FQDEEVQR	76	8	4	40.68	y4y6y7*y7	1050.48	27.687	14312	2	525.74	-8.02
Q56073 DNAK_SALTY Chaperone protein dnaK	7		NDPLAMQR	253	8	5	49.06	b5y4y6y7y8	944.46	38.843	10009	2	472.73	-4.07
Q56073 DNAK_SALTY Chaperone protein dnaK	8		QAVTNPQNTLFAIK	56	14	3	19.13	b3b7y11	1544.84	66.843	9686	2	772.93	0.63
Q56073 DNAK_SALTY Chaperone protein dnaK	9		DDDVVDAEFEEVKDK	622	15	3	26.07	y5y7y12	1752.81	71.213	8537	2	876.91	14.35
Q56073 DNAK_SALTY Chaperone protein dnaK	10		TIAYVDLGGGTFDISIIEIDEVDGE K	188	26	6	36.02	b7b8y4y5°y5y8	2769.32	119.099	43554	3	923.78	-19.75
Q56073 DNAK_SALTY Chaperone protein dnaK	11		SIEPLK	315	6	1	13.56	b3	686.42	51.697	17301	1	686.42	12.09
Q56073 DNAK_SALTY Chaperone protein dnaK	12		LMEIAQQQHAQQAGSADASAN NAK	597	25	4	12.32	b13*b13y4y6	2610.21	84.729	4403	3	870.74	-7.01
Q56073 DNAK_SALTY Chaperone protein dnaK	13		VLENAEGDR	25	9	3	38.08	y3y4y5	1002.49	22.080	3492	2	501.75	7.91
Q56073 DNAK_SALTY Chaperone protein dnaK	14		AAIEAK	581	6	1	13.56	y5	602.35	30.701	2478	1	602.35	-4.36
Q56073 DNAK_SALTY Chaperone protein dnaK	15		SIEPLKVALQDAGLSVSDINDVILV GGQTR	315	30	4	21.93	b15y5°y5y6	3107.69	104.215	33761	3	1036.57	-2.44
Q56073 DNAK_SALTY Chaperone protein dnaK	16		DQGIDLRNDPLAMQR	246	15	3	26.07	b8b9b14	1741.89	71.750	10597	2	871.45	14.23
Q56073 DNAK_SALTY Chaperone protein dnaK	17		VLENAEGDRTPPSIIAYTDGETL VGQPAK	25	30	5	29.73	b6b13b26y11y12	3173.62	69.941	5278	3	1058.54	6.15
Q56073 DNAK_SALTY Chaperone protein dnaK	18		MQELAQVSQKLMEIAQQQHAQQ QAGSADASANNAK	587	35	4	14.99	b14y5y8y13	3752.80	114.734	3623	4	938.96	-1.43

Q56073 DNAK_SALTY Chaperone protein dnaK	19	Carbamidomethyl+C(14)	GKIIGIDLGTNSCVAIMDGTQAR	1	24	5	35.31	b22y7y8°y8y9	2491.29	128.088	1850	3	831.10	11.07
Q56073 DNAK_SALTY Chaperone protein dnaK	20	Phosphoryl STY(9)	TTPSIIAYTQDGETLVGQPAK	34	21	3	13.77	b3b8y11	2270.07	82.875	27394	3	757.36	-8.60
P0A1P8 GLRX1_SALTY Glutaredoxin-1	1	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14)	MFTVIFGRPGCPYCVR	0	16	3	25.39	b3b4b8	1959.92	76.998	44880	3	653.98	-10.03
P0A1P8 GLRX1_SALTY Glutaredoxin-1	2		TVGKPVETVPQIFVDQK	50	17	9	45.42	b3b9y2*y2y3y6y8y13y17	1885.02	64.582	39712	3	629.01	-11.53
P0A1P8 GLRX1_SALTY Glutaredoxin-1	3	Carbamidomethyl+C(5)	HIGGCTDFEAWAKENLNLFA	67	20	3	22.39	b3b4y11	2293.08	83.033	1963	2	1147.04	3.94
P0A1P8 GLRX1_SALTY Glutaredoxin-1	4	Carbamidomethyl+C(11) ;Carbamidomethyl+C(14) ;Oxidation+M(1)	MFTVIFGRPGCPYCVR	0	16	4	38.66	y5y9y11y13	1975.93	73.973	31644	3	659.31	-3.46
P0A1P8 GLRX1_SALTY Glutaredoxin-1	5	Carbamidomethyl+C(4)	IGGCTDFEAWAKENLNLFA	68	19	0	6.16		2155.99	83.027	22239	3	719.34	-9.06
P0A1P8 GLRX1_SALTY Glutaredoxin-1	6		PQIFVDQK	59	8	0	4.93		974.53	64.471	5153	1	974.53	3.13
P22107 TRAT_SALTY TraT complement resistance protein	1		ATVTTDNVAALR	177	12	9	75.38	b9b11y3y4y8y9y10y12*y12	1231.66	44.852	31831	2	616.34	-0.59
P22107 TRAT_SALTY TraT complement resistance protein	2		IQTSTETGNQHK	196	12	13	83.46	b2b3y2y5*y5y6y7°y7*y7y8°y8y9y10	1343.64	14.097	14385	3	448.55	-12.90
P22107 TRAT_SALTY TraT complement resistance protein	3		GYTVVTSPDK	79	10	4	36.73	y2y5y6y7	1066.54	35.586	2378	1	1066.54	-4.58
P22107 TRAT_SALTY TraT complement resistance protein	4		ESQGWLNR	107	8	4	35.91	b4b6°b6y7	989.47	107.486	1630	1	989.47	-10.55
P22107 TRAT_SALTY TraT complement resistance protein	5		DIQAKGYTVVTSPDK	74	15	5	31.6	b3b13*b13y4y5	1621.82	67.988	26239	2	811.42	-11.89
P22107 TRAT_SALTY TraT complement resistance protein	6		IQTSTETGNQHKYQTR	196	16	5	23.55	b5°b5*b5b6y12	1891.94	58.936	4964	2	946.47	7.03
P22107 TRAT_SALTY TraT complement resistance protein	7	Carbamidomethyl+C(16) ;Phosphoryl STY(5)	LMMVTLVSSTLALSGCGAMSTAI KK	5	25	4	21.86	b3b4y11°y11	2650.27	136.229	5593	3	884.10	-10.87
P22107 TRAT_SALTY TraT complement resistance protein	8	Carbamidomethyl+C(16) ;Oxidation+M()	LMMVTLVSSTLALSGCGAMSTAI KK	5	25	5	18.68	b3b8b16y10°y10	2586.33	102.497	2088	3	862.78	-3.87
P22107 TRAT_SALTY TraT complement resistance protein	9		TSTETGNQHK	198	10	0	2.88		1102.51	14.097	1607	2	551.76	-1.99
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	1		DIGAQYIIHGSERR	84	15	9	52	b3b12°b12y4y6y8y10°y10y15	1727.91	58.677	79794	3	576.64	-4.52
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	2		SATPAQAQAVHK	176	12	18	124.37	b2b3b5°b5b11y12y4y5*y5y6*y6y7*y7y8y9y10y12	1208.64	17.590	75906	2	604.82	-2.53
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	3	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	7	42.56	b17y4y10y11y12y19y24	2589.30	82.176	67634	3	863.77	-3.39
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	4		TQGAAAFEGAVIAYEPVWAIGTG K	152	24	15	51.28	b1b2*b2b3b5°b5b11b12b14y1y2y7y11y12y24	2407.24	93.098	21004	2	1204.12	4.97
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	5	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	4	23.04	y3y10y11y23	2433.21	87.535	13642	2	1217.11	3.81
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	6	Carbamidomethyl+C(14)	FAVLKEQGLTPVLCIGETEAENEA GK	112	26	5	18.21	y1y7°y7y9y14	2803.38	114.876	10768	3	935.13	-12.80
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	7		AAAGSHIMLGAQNVDLNLGSAFT GETSAEMLK	52	32	3	11.11	b3y11y15	3204.54	87.757	2578	5	641.71	-9.52
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	8		DIGAQYIIHGSER	84	14	6	48.14	b3b4b6b7y6°y6	1571.79	39.942	4202	3	524.60	-20.66

Q8ZKP7 TPIS_SALTY Triosephohate isomerase	9	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAENEAGKTEE VCAR	117	28	26	232.59	b5°b5b6b7°b7b11b12b25y3y4y5y7y10y12y13*y13y14y15y16y18y20y21y23°y23y24y26	3090.44	71.525	187126	3	1030.82	1.58
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	10		DIGAQYIIIGHSERR	84	15	5	42.83	b4b5b7y5y6	1727.92	112.856	10660	2	864.46	0.78
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	11	Oxidation+M(5)	HPLVMGNWK	2	9	4	44.7	b5b6y4y6	1097.55	67.113	2530	2	549.28	-4.78
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	12	Carbamidomethyl+C(8); Oxidation+M(17)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	4	19.29	b7b14b18y10	2605.27	89.224	1595	3	869.10	-9.75
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	13		TPAQQAQAVHK	178	10	7	44.68	b3°b3b4°b4°b4b7b9	1050.56	17.596	30268	2	525.78	-8.02
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	14		PAQAQAVHK	179	9	9	78.76	b3b4°b4b5b6°b6b7°b7b8	949.51	17.597	29074	2	475.26	-8.93
Q8ZKP7 TPIS_SALTY Triosephohate isomerase	15		SATPAQAQAVHK	176	12	0	2.88		1190.61	17.608	24336	3	397.54	-13.23
P06179 FLIC_SALTY Flagellin	1		AQILQQAGTSVLAQANQVPQNVLSLLR	468	27	11	43.97	b2°b2b3b4b6b7b18y1y4y9y27	2860.61	104.739	92342	3	954.21	2.65
P06179 FLIC_SALTY Flagellin	2		SQSALGTAIER	20	11	8	65.2	b2y3y6y7y8y9°y9y11	1132.59	41.443	45123	2	566.80	-4.31
P06179 FLIC_SALTY Flagellin	3		VSGQTQFNGVK	125	11	6	27.14	b9y9*y9y10*y10y11	1164.60	32.535	40923	2	582.80	-3.88
P06179 FLIC_SALTY Flagellin	4		INSAKDDAAGQAIANR	37	16	11	88.85	b3°b3b6b11y3y4y5y6y10*y10y11	1614.80	29.782	36400	3	538.94	-9.00
P06179 FLIC_SALTY Flagellin	5		AQVINTNSLSLLTQNNLNK	1	19	7	21.77	b2°b2y2y7y12y15y19	2085.14	73.959	35242	2	1043.07	3.86
P06179 FLIC_SALTY Flagellin	6		FNSAITNLGNTVNNLTSAR	432	19	6	23.46	b2b3b7b14y11y19	2007.03	77.850	30678	2	1004.02	3.41
P06179 FLIC_SALTY Flagellin	7		IDAALAQVDTLR	411	12	6	34.01	b2b4y4y6y7y12	1285.71	60.671	24450	2	643.36	-0.47
P06179 FLIC_SALTY Flagellin	8		AQPDLAEEAAATTENPLQK	392	19	5	20.51	b9b11y7°y7y15	1968.98	94.040	101007	2	984.99	-2.42
P06179 FLIC_SALTY Flagellin	9		QINSQTLGLDTLNVQQK	161	17	4	23.58	y8y12y14°y14	1899.99	64.713	26488	2	950.50	-10.60
P06179 FLIC_SALTY Flagellin	10		VSDTAATVTGYADTTIALDNSTFK	180	24	4	12.62	b7°b7b12y13	2462.18	91.331	26106	3	821.40	-5.35
P06179 FLIC_SALTY Flagellin	11		DGSISINTTK	339	10	4	39.88	b3b4b9y6	1035.53	114.705	8984	2	518.27	-5.78
P06179 FLIC_SALTY Flagellin	12		FTANIK	53	6	1	13.56	y5	693.39	33.600	6670	2	347.20	-10.83
P06179 FLIC_SALTY Flagellin	13		LGGADGKTEVVSIGGK	363	16	3	17.02	b12y5y8	1487.79	42.344	29361	3	496.60	-11.73
P06179 FLIC_SALTY Flagellin	14		IDGDLKFDDTTGK	216	13	5	29.44	b5b8y10°y10y12	1424.71	64.494	13807	2	712.86	14.14
P06179 FLIC_SALTY Flagellin	15		DGSISINTTKYTADDGTSK	339	19	4	14.82	b6°b6b11y5	1973.93	84.858	8336	3	658.65	0.12
P06179 FLIC_SALTY Flagellin	16		YKVSDTAATVTGYADTTIALDNS TFK	178	26	3	12.06	b5y6y14	2753.34	110.195	7004	3	918.45	-5.94
P06179 FLIC_SALTY Flagellin	17		TYAASKAEGHNFK	379	13	3	20.48	b4b7y9	1423.70	58.421	3714	3	475.24	3.09
P06179 FLIC_SALTY Flagellin	18	Phosphoryl STY(11)	FNSAITNLGNTVNNLTSAR	432	19	5	23.46	b8y7y9°y9y13_H3PO4 y13	2087.01	122.828	3860	2	1044.01	11.35
P52616 FLJB_SALTY Phase 2 flagellin	1		AQILQQAGTSVLAQANQVPQNVLSLLR	479	27	11	43.97	b2°b2b3b4b6b7b18y1y4y9y27	2860.61	104.739	92342	3	954.21	2.65
P52616 FLJB_SALTY Phase 2 flagellin	2		SQSALGTAIER	20	11	8	65.2	b2y3y6y7y8y9°y9y11	1132.59	41.443	45123	2	566.80	-4.31
P52616 FLJB_SALTY Phase 2 flagellin	3		TAANQLGGVDGK	369	12	8	63.99	b8b9b10°b10b11y4y7y12	1130.58	35.938	41217	2	565.79	-1.51
P52616 FLJB_SALTY Phase 2 flagellin	4		VSGQTQFNGVK	125	11	6	27.14	b9y9*y9y10*y10y11	1164.60	32.535	40923	2	582.80	-3.88
P52616 FLJB_SALTY Phase 2 flagellin	5		INSAKDDAAGQAIANR	37	16	11	88.85	b3°b3b6b11y3y4y5y6y10*y10y11	1614.80	29.782	36400	3	538.94	-9.00
P52616 FLJB_SALTY Phase 2 flagellin	6		AQVINTNSLSLLTQNNLNK	1	19	7	21.77	b2°b2y2y7y12y15y19	2085.14	73.959	35242	2	1043.07	3.86
P52616 FLJB_SALTY Phase 2 flagellin	7		YFVTIGGFTGADAAK	234	15	3	17.99	b12b14y14	1517.76	72.855	70474	2	759.39	0.64
P52616 FLJB_SALTY Phase 2 flagellin	8		AYANNGTTLDVSGLDAAIK	189	20	4	21.05	y3y8°y8y19	2008.94	73.193	24683	3	670.32	-19.14
P52616 FLJB_SALTY Phase 2 flagellin	9		DDAAGQAIANR	42	11	3	27.14	b3y8y9	1101.52	27.110	11844	2	551.27	-3.55

P52616 FLJB_SALTY Phase 2 flagellin	10		AQPELAEEAAK	403	11	4	31.12	b3b5°b5b6	1098.56	59.009	6962	2	549.78	-20.78
P52616 FLJB_SALTY Phase 2 flagellin	11		ELAVQSANSTNSQSDLDSIQAEIT QR	93	26	6	26.24	b9b12b13y3*y3y6	2805.36	69.631	2264	2	1403.18	2.61
P52616 FLJB_SALTY Phase 2 flagellin	12		VLAQDNTLTIQVGANDGETIDIDL K	136	25	4	12.32	b14y9y11°y11	2656.41	114.711	2135	2	1328.71	15.07
P52616 FLJB_SALTY Phase 2 flagellin	13		QINSQTLGLDSLNVQK	161	16	4	17.02	b4°b4b11y4	1757.93	45.921	1627	3	586.65	-7.15
P52616 FLJB_SALTY Phase 2 flagellin	14		NALIAGGVDATDANGAELVKMSY TDK	299	26	4	12.06	b10b16y4°y4	2624.28	75.621	82525	4	656.83	-3.07
P52616 FLJB_SALTY Phase 2 flagellin	15		FDADNNKYFVTIGGFTGADAAK	227	22	4	24.05	b12y6y7y12	2322.10	78.278	10905	4	581.28	-2.52
P52616 FLJB_SALTY Phase 2 flagellin	16		TEVVITIDGKTYNASK	381	15	7	52	b3b5b10b12y6y11*y11	1625.83	69.966	9444	2	813.42	-3.98
P52616 FLJB_SALTY Phase 2 flagellin	17		QINSQTLGLDSLNVQKAYDVK	161	21	5	23.42	b3*b3b4*b4b10	2334.22	89.228	8067	3	778.74	-5.75
P52616 FLJB_SALTY Phase 2 flagellin	18		LNEIDRVSGQTQFNGVK	119	17	4	23.17	b12y7*y7y8	1905.01	50.396	3876	2	953.01	13.33
P52616 FLJB_SALTY Phase 2 flagellin	19		AATGGTNGTASVTGGAVKFDAD NNK	209	25	5	22.94	b4b16b17°b17y24	2324.13	136.397	2812	2	1162.57	7.88
P52616 FLJB_SALTY Phase 2 flagellin	20		AKTTSYTAADGTTK	355	14	4	19.13	b4°b4y5y11	1415.72	38.035	1860	3	472.58	11.12
P52616 FLJB_SALTY Phase 2 flagellin	21	Phosphoryl STY(6)	QINSQTLGLDSLNVQK	161	16	4	17.02	b4b13°b13y12	1837.91	78.673	4620	2	919.46	7.11
P52616 FLJB_SALTY Phase 2 flagellin	22	Phosphoryl STY()	VRELAVQSANSTNSQSDLSIQAE ITQR	91	28	4	17.19	b3b12b14y26	3140.49	82.250	3281	3	1047.50	3.42
P61179 RL22_SALTY 50S ribosomal protein L22	1		IFVDEGPSMK	73	10	7	60.81	b2b4y5y6y8y9y10	1122.55	50.612	62762	2	561.78	-2.17
P61179 RL22_SALTY 50S ribosomal protein L22	2		IFVDEGPSMKR	73	11	4	36.49	b6y5y8y9	1278.64	45.034	40265	3	426.89	-7.83
P61179 RL22_SALTY 50S ribosomal protein L22	3		LVADLIR	18	7	5	53.42	y3y4y5y6y7	799.49	57.058	37917	2	400.25	-13.51
P61179 RL22_SALTY 50S ribosomal protein L22	4		AAVLVK	42	6	1	13.56	b3	600.41	41.063	14816	1	600.41	3.96
P61179 RL22_SALTY 50S ribosomal protein L22	5		VLESAIANAEHNDGADIDDLK	49	21	5	22.22	b5°b5y5°y5y6	2210.05	60.839	3974	3	737.35	-4.97
P61179 RL22_SALTY 50S ribosomal protein L22	6		VLESAIANAEHNDGADIDDLKVT K	49	24	3	21.91	b10y11y12	2538.24	61.042	41857	4	635.31	-12.41
P61179 RL22_SALTY 50S ribosomal protein L22	7		KVLESAIANAEHNDGADIDDLK	48	22	7	20.69	b13*b13y4°y4y7°y7y9	2338.18	112.814	9992	2	1169.59	10.86
P0A1H3 EFG_SALTY Elongation factor G	1		VYSGVVNSGDTVLSNVK	337	17	13	90.3	b2b4b5°b5y4y5y8y10y11* y11y12y15y17	1737.91	61.682	75131	2	869.46	3.79
P0A1H3 EFG_SALTY Elongation factor G	2		IATDPFVGNLTFFR	323	14	11	78.42	b2b4y1y3y4y7*y7y8y10y1 2y14	1597.84	92.759	65438	2	799.42	3.06
P0A1H3 EFG_SALTY Elongation factor G	3		SGPLAGYPVVDLGVR	562	15	10	47.23	b5°b5b7°b7y2y4y8y10y11y 15	1499.82	75.935	59696	2	750.41	-0.33
P0A1H3 EFG_SALTY Elongation factor G	4		IGEVHDGAATMDWMEQEQR	39	20	4	14.26	b7b12y6y20	2331.99	62.039	49280	3	778.00	-2.62
P0A1H3 EFG_SALTY Elongation factor G	5		GQYGHVVIDMYPLEPGSNPK	512	20	7	27.75	b2b4b7b11y6*y6y9	2201.07	70.032	33274	3	734.36	-1.44
P0A1H3 EFG_SALTY Elongation factor G	6		LGANPVPLQLAIGAEEGFTGVVDL VK	161	26	5	15.65	b4b6y1y3y5	2607.42	119.525	21685	3	869.81	-7.58
P0A1H3 EFG_SALTY Elongation factor G	7		AINWNADQGVTFEYEDIPADMQ DLANEWHQNLIESAAEASEELME K	189	47	12	42.41	b5b7b11b14y2°y2y3y8y9°y 9y10y29	5380.36	125.750	8412	4	1345.85	-4.36
P0A1H3 EFG_SALTY Elongation factor G	8		VEVETPEENTGDVIGDLSR	618	19	4	21.77	b1y5y9y14	2058.97	79.527	6116	4	515.50	-8.30
P0A1H3 EFG_SALTY Elongation factor G	9		YLGGEELTEEEIK	236	13	3	20.48	b10b12y11	1509.75	57.441	3075	2	755.38	12.13

P0A1H3 EFG_SALTY Elongation factor G	10		YDDAPNNVAQAVIEAR	686	16	4	27.46	b3y4y8y12	1745.85	64.517	20136	2	873.43	4.20
P0A1H3 EFG_SALTY Elongation factor G	11		ILFYTGVNHK	29	10	3	36.73	y7y8y9	1191.63	55.075	19174	3	397.88	-21.61
P0A1H3 EFG_SALTY Elongation factor G	12		VVGQIK	153	6	1	13.56	b4	643.41	44.662	14638	1	643.41	0.38
P0A1H3 EFG_SALTY Elongation factor G	13		QYEPHR	77	6	1	13.56	y4	829.38	100.935	9362	1	829.38	-14.50
P0A1H3 EFG_SALTY Elongation factor G	14		HASDDEPFSALAFK	309	14	3	19.13	b11b13y9	1534.75	62.982	6570	2	767.88	20.84
P0A1H3 EFG_SALTY Elongation factor G	15		GYEFINDIK	532	9	3	30.3	b6b7y4	1098.55	102.811	3106	1	1098.55	-1.44
P0A1H3 EFG_SALTY Elongation factor G	16		IHAEVPLSEMFGYATQLR	653	18	5	36.38	b11°b11b12b13y13	2062.00	75.775	1710	2	1031.50	-22.38
P0A1H3 EFG_SALTY Elongation factor G	17		INIIDTPGHVDFTIEVERSMR	83	21	4	20.41	y5y10y12°y12	2442.27	81.027	29540	3	814.76	11.50
P0A1H3 EFG_SALTY Elongation factor G	18		VWTDEESNQTIAGMGELHLDIIV DRMK	446	28	3	11.64	b13y11y13	3213.61	136.638	11051	2	1607.31	5.70
P0A1H3 EFG_SALTY Elongation factor G	19		GQESEVTGVKIHAEVPLSEMFGY ATQLR	643	28	3	17.66	b4b9b13	3076.53	123.793	7649	3	1026.18	-3.25
P0A1H3 EFG_SALTY Elongation factor G	20		GYEFINDIKGGVIPGEYIPAVDK	532	23	5	29.24	b5b10b11b13y9	2494.25	82.962	7507	3	832.09	-13.90
P0A1H3 EFG_SALTY Elongation factor G	21		SGPLAGYPVVDLGVRLHFGSYHD VDSSELAFK	562	32	6	24.69	b6b7b9b11°b11y15	3432.68	104.123	5115	3	1144.90	-11.95
P0A1H3 EFG_SALTY Elongation factor G	22	Carbamidomethyl+C(10)	VLDGAVMVVYCAVGGVQPQSETV WRQANK	104	28	6	40.09	b5b6b7b10b14y10	3062.54	132.711	3326	3	1021.52	6.94
P0A1H3 EFG_SALTY Elongation factor G	23	Oxidation+M(10)	GQYGHVVIDMYPLEPGSNPK	512	20	4	22.43	b8y10y13y18	2217.04	72.888	5786	3	739.68	-11.12
P0A1H3 EFG_SALTY Elongation factor G	24	Carbamidomethyl+C(10) ;Oxidation+M(7)	VLDGAVMVVYCAVGGVQPQSETV WR	104	24	4	23.27	b5y6y7y11	2637.27	94.236	1802	2	1319.14	-2.50
P63411 ACKA_SALTY Acetate kinase	1	Carbamidomethyl+C(19)	FAIDAVNGDEYLSGLAECFHLPE AR	17	26	9	29.88	b2b3b11y2y4y7y9y19y26	2907.40	104.193	40024	3	969.80	0.34
P63411 ACKA_SALTY Acetate kinase	2		EGTRPAVVIPTNEELVIAQDASR	374	23	8	69.15	b8b9b14b15y4y6y7y8	2465.29	68.454	37695	3	822.44	-3.27
P63411 ACKA_SALTY Acetate kinase	3	Carbamidomethyl+C(14)	ESGLLGLTEVTSDCR	272	15	7	29.22	b12y2y8y9°y9y11y15	1636.79	71.276	23365	2	818.90	5.52
P63411 ACKA_SALTY Acetate kinase	4		LDAVVFTGGIGENAAMVR	324	18	15	85.04	b3b4b8b15°b15*b15y4y6* y6y7y10°y10y11y13y18	1819.92	93.087	20726	2	910.46	-12.01
P63411 ACKA_SALTY Acetate kinase	5	Carbamidomethyl+C(1)	CVDTSMGLTPLEGLVMGTR	224	19	7	33.09	b2b13y1y4y7y8y10	2036.99	94.172	18592	2	1019.00	6.59
P63411 ACKA_SALTY Acetate kinase	6		YIGSYTALMDGR	312	12	4	32.32	b1y3y8y10	1346.64	64.310	7902	2	673.83	2.81
P63411 ACKA_SALTY Acetate kinase	7		NVAVFDATAFHQTMPEESYLYALP YSLYK	144	28	4	11.64	b6b10*b10y5	3297.57	109.395	2945	3	1099.86	-4.89
P63411 ACKA_SALTY Acetate kinase	8		SGDIDPAIIFHLHDTLGMSVDQINK	243	25	3	18.55	b6b8b12	2736.38	89.357	2398	4	684.85	6.07
P63411 ACKA_SALTY Acetate kinase	9		SGFINKEGTRPAVVIPTNEELVIAQ DASR	368	29	6	14.39	b3°b3b10*b10y5y12	3111.64	102.227	5551	3	1037.89	-0.16
P63411 ACKA_SALTY Acetate kinase	10		RYGAHGTSHFYVTQEAAK	177	18	3	15.45	b11y10y16	2022.99	103.569	2969	2	1012.00	6.40
P63411 ACKA_SALTY Acetate kinase	11	Carbamidomethyl+C(18) ;Phosphoryl.STY(6)	MLTKESGLLGLTEVTSDCR	268	19	3	14.82	b5b8y13	2190.00	120.761	4637	3	730.67	-3.01
P63411 ACKA_SALTY Acetate kinase	12	Carbamidomethyl+C(1)	CVDTSMLTPLEGLVMGT	224	18	0	5.75		1880.91	94.174	3155	3	627.64	14.73

P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	1		ILLINPTDSDAVGNAVK	84	17	14	82.01	b2b3b4b5b12y2y11y12°y12*y12y13*y13y14y17	1739.96	70.178	58845	2	870.48	3.93
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	2		LAATIAQLPDQIGAK	253	15	9	62.81	b3b8y3y4y7y9*y9y11y15	1509.86	65.669	55714	2	755.43	-5.58
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	3		VIELQGIAGTSAAR	150	14	5	27.7	b1b2y7y10y12	1385.77	58.472	31125	2	693.39	-1.67
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	4		ADVMVVGFDGTPDGEK	231	16	4	24.05	b8b12y5y11	1636.77	63.168	12221	2	818.89	11.04
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	5		DGAQK	45	5	1	13.15	y4	518.26	34.934	22961	1	518.26	6.60
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	6		LVIK	291	4	1	12.74	y3	472.35	56.490	21281	1	472.35	-6.01
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	7		GDVVSHIASDNVLGGK	119	16	4	17.02	b15y9y14°y14	1567.84	68.101	6046	2	784.42	18.22
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	8		FNVLASQPADFDRTK	178	15	3	34.52	y5y6y7	1708.88	89.325	12048	2	854.94	5.86
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein	9		EADKLGYNLVVLDSQNNPAK	50	20	7	38.94	b5°b5b6b7°b7b9y11	2188.10	76.611	3044	2	1094.55	-13.17
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	1		MYAVFQSGGK	0	10	7	60.81	b3y1y4y5y7y8y10	1087.52	52.023	67343	2	544.27	-1.12
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	2		IGVPFVDGGVIK	48	12	4	22.11	b3y2y6y9	1200.69	76.311	36661	2	600.85	-8.03
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	3		ITGISA	97	6	1	13.56	b5	561.33	27.644	8435	1	561.33	4.35
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	4		VSEGQTVR	13	8	3	40.68	y5y6y7	875.45	15.825	3006	2	438.23	-8.58
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	5		LDIATGETIEFAEVLMIANGEEVK	24	24	11	41.05	b3b11°b11y6°y6y7°y7y8°y8*y8y12	2592.26	136.284	2397	3	864.76	-21.57
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	6		QQGHRQWFTDVK	85	12	3	26.09	b6y6y7	1529.75	70.115	20674	2	765.38	-8.62
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	7		YAVFQSGGKQHR	1	12	3	22.11	b6y3y9	1377.70	45.770	12307	3	459.90	-2.84
Q7CPP7 RL21_SALTY 50S ribosomal protein L21	8	Oxidation+M(16)	LDIATGETIEFAEVLMIANGEEVK	24	24	4	19.29	b8y4y6y12	2608.33	75.603	66203	3	870.12	10.95
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1		AVLPGMVER	115	9	4	54.24	y4y5y6y7	971.53	52.655	28752	2	486.27	-5.59
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	2		VTDIEPLVGGETFSSVR	171	18	9	49.65	b2b5b13b15y9y13y14y17y18	1862.96	68.574	23009	2	931.98	5.90
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	3		AAIEEMMASLPAQWR	58	15	7	36.49	y4y5y8°y8y11*y11y15	1703.83	90.248	13279	2	852.42	5.37
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	4	Carbamidomethyl+C(14)	IVLVTGATAGFGECIAR	1	17	3	23.58	y4y7y14	1734.88	81.020	13942	2	867.94	-22.16
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	5	Carbamidomethyl+C(15)	MIVLVTGATAGFGECIAR	0	18	3	24.37	y7y11y12	1865.98	72.464	8602	2	933.49	8.11
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	6		GHIINIGSTAGSWPYAGGNVYGATK	126	25	10	41.64	b6b10b12°b12b14*b14y6y8y9*y9	2491.28	122.908	1952	3	831.10	18.03
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	7		TYENTTALTPEdITEAVWWVATLPAHVNINTVEMMPVTQSFAGLSVHRS	199	49	3	11.53	b8b11y33	5427.61	136.409	12821	4	1357.66	-9.72
P69936 YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	8		VTDIEPLVGGETFSSVRFK	171	20	4	14.26	b7°b7b16y9	2138.09	71.107	4841	2	1069.55	-10.05

[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	9	Carbamidomethyl+C(14) ;Phosphoryl STY(5)	IVLVTGATAGFGECIAR	1	17	6	50.78	b6y4y5y6y8y11	1814.90	63.294	4849	3	605.64	12.85
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	10	Carbamidomethyl+C(15) ;Phosphoryl STY(9)	MIVLVTGATAGFGECIARR	0	19	9	56.17	b9b11_H3PO4 b11°b11b12y6y7y8y10°y10	2102.04	136.294	2048	2	1051.52	9.52
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	11	Carbamidomethyl+C(15) ;Oxidation+M(1)	MIVLVTGATAGFGECIAR	0	18	3	24.37	y8y9y16	1881.96	119.645	14898	2	941.48	2.46
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	12	Oxidation+M()	AAIEEMMASLPAQWR	58	15	4	25.58	b5b12y8y13	1719.84	93.147	12368	2	860.42	12.63
[P60446]RL3_SALTY 50S ribosomal protein L3	1		VTVQSLDVVR	169	10	7	67.8	y2y3y5y6y7y8y10	1115.64	56.025	142372	2	558.32	-3.72
[P60446]RL3_SALTY 50S ribosomal protein L3	2		IFTEDGVSIPTVIEVEANR	13	20	8	51.49	b2y4°y4y5y6y7y13y20	2188.16	87.614	88404	2	1094.59	6.47
[P60446]RL3_SALTY 50S ribosomal protein L3	3		MAGQMGNER	160	9	6	57.25	b2y4*y4y5y7y8	993.42	19.550	25593	2	497.21	-2.40
[P60446]RL3_SALTY 50S ribosomal protein L3	4		AVQVTTGAK	46	9	7	61.37	b8y3y4y5y7*y7y9	874.49	21.000	11636	2	437.75	-14.59
[P60446]RL3_SALTY 50S ribosomal protein L3	5	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	4	32.37	y4y5y11y15	1738.92	53.660	40389	3	580.31	-15.79
[P60446]RL3_SALTY 50S ribosomal protein L3	6		NLLLVK	184	6	3	39.86	y3y4y5	699.48	56.473	35427	1	699.48	1.13
[P60446]RL3_SALTY 50S ribosomal protein L3	7		VTKPEAGHFAK	59	11	3	31.12	y3y7y8	1184.63	25.717	21750	3	395.55	-14.32
[P60446]RL3_SALTY 50S ribosomal protein L3	8		GLWEFR	77	6	2	26.71	b4y4	807.40	70.069	14295	2	404.21	-13.98
[P60446]RL3_SALTY 50S ribosomal protein L3	9		LAEGEETVQGSISEVELFADV K	83	22	4	13.33	b11y4°y4y11	2384.18	136.402	4903	2	1192.60	-1.02
[P60446]RL3_SALTY 50S ribosomal protein L3	10	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	10	108.25	b3b4b5b6y5y6y7y8y9y13	1809.97	55.842	102389	3	604.00	-8.84
[P60446]RL3_SALTY 50S ribosomal protein L3	11		IFTEDGVSIPTVIEVEANRVTVK	13	25	4	12.32	b7°b7y16y18	2743.49	94.528	68051	3	915.17	-0.62
[P60446]RL3_SALTY 50S ribosomal protein L3	12		TQDATHGNSLSHRVPGSIGQNQT PGK	128	26	4	27.33	y4y10y11y13	2687.32	54.202	29888	4	672.59	-1.91
[P60446]RL3_SALTY 50S ribosomal protein L3	13		WNFRTQDATHGNSLSHR	124	17	5	27.19	b10°b10b12b13y14	2026.93	72.618	8175	2	1013.97	-12.65
[P60446]RL3_SALTY 50S ribosomal protein L3	14	Phosphoryl STY(6)	AVQVTTGAKK	46	10	3	28.49	b3b4y5	1082.56	71.535	15774	2	541.78	5.30
[P60446]RL3_SALTY 50S ribosomal protein L3	15		QVTTGAK	48	7	0	1.64		704.39	21.031	3858	1	704.39	-7.71
[P26982]DEGP_SALTY Protease do	1		AGDVITSLNGKPISSFAALR	332	20	8	33.2	b3°b3y1y3y7y9y15y20	2017.09	74.354	45713	3	673.03	-10.47
[P26982]DEGP_SALTY Protease do	2		NLT SQMVEYGQVK	275	13	9	45.23	b1b12y5y8y9°y9y11*y11y1 3	1496.75	57.497	38222	2	748.88	5.30
[P26982]DEGP_SALTY Protease do	3		VGDYTV AIGNPFLGETVTSGIVS ALGR	186	28	15	85.57	b2b3b4b6°b6b8b9y2y3y4y 5y6y9y14y28	2750.43	116.054	34314	3	917.48	-2.31
[P26982]DEGP_SALTY Protease do	4		GAFVSQVMPNSSAAK	313	15	9	43.62	b3y1y2y7y8y9y11°y11y15	1493.74	52.817	29525	2	747.38	1.23
[P26982]DEGP_SALTY Protease do	5		SDIALIQINPK	160	12	6	40.03	b3b4b5°b5y6y12	1339.76	63.572	28223	2	670.38	-1.28
[P26982]DEGP_SALTY Protease do	6		FMALGSGVIIDAAK	110	14	8	60.04	b3b5b7b8°b8b10y1y4	1392.75	75.738	21713	2	696.88	-2.28
[P26982]DEGP_SALTY Protease do	7		SGLNVENYENFIQTDAAINR	214	20	7	14.26	b2°b2b6y3y7*y7y20	2268.10	76.852	11994	2	1134.56	6.14
[P26982]DEGP_SALTY Protease do	8		AQVGTMPVGSK	352	11	8	68.21	y3°y3y5y8°y8y9y10*y10	1074.56	34.050	25655	2	537.78	0.45
[P26982]DEGP_SALTY Protease do	9		AITVNLELQQSSQSQVDSSTIFSGI EGAEMSNK	373	33	6	23.66	b6b7b12°b12y4y7	3498.64	106.398	6152	3	1166.88	-15.42

P26982 DEGP_SALTY Protease do	10	Carbamidomethyl+C(13) ;Carbamidomethyl+C(25)	NFQQFFGGDDSPFCQDGSPFQNSPF CQGGGNGGNGGQQK	71	39	6	21.28	b6*b6b7*b7b12y8	4240.74	90.129	3606	3	1414.25	-3.22
P26982 DEGP_SALTY Protease do	11		GELGIMGTELNSELAK	289	16	6	17.02	b6y6°y6*y6y10*y10	1661.83	72.573	1792	2	831.42	-6.32
P26982 DEGP_SALTY Protease do	12		VDAQRGAFVSQVMPNSSAAK	308	20	3	23.68	b6b7b10	2063.03	48.219	3449	4	516.51	-3.08
P26982 DEGP_SALTY Protease do	13	Oxidation+M(6)	NLTSQMVEYGQVK	275	13	5	20.48	b3°b3b8y6°y6	1512.74	38.423	27629	3	504.92	1.37
P26982 DEGP_SALTY Protease do	14	Oxidation+M(6)	GELGIMGTELNSELAK	289	16	3	17.02	b6b15y10	1677.82	87.069	1555	3	559.95	-7.93
P26982 DEGP_SALTY Protease do	15		GAFVSQVMPNSSAAK	313	15	0	4.11		1476.73	52.759	3738	2	738.87	12.56
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	1		TGEDIPITAR	66	10	9	54	b1b3°b3b4°b4y5y7y8y10	1072.56	42.334	52949	2	536.78	-1.37
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	2		ELVELFFEEIRR	24	12	4	29.31	b3b4°b4b6	1579.83	93.164	3602	3	527.28	-10.59
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	3		VENASPK	90	7	5	37.26	b6y4y5°y5*y5	744.38	52.043	6752	1	744.38	-15.66
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	4		LSGFGNFDLR	45	10	4	26.73	b3°b3b5y6	1125.55	73.740	2566	2	563.28	-19.41
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	5		MALTKAEMSEYLFDK	0	15	3	26.07	y8y9y11	1776.88	74.292	4089	2	888.94	12.98
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	6		ALTKAEMSEYLFDK	1	14	4	19.13	b8°b8y6y8	1645.80	58.180	3737	2	823.41	-6.30
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	7		ALENGEQVKLSGFGNFDLR	36	19	3	22.6	b8y7y8	2094.08	68.155	2179	3	698.70	10.38
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	8		FFEEIRR	29	7	0	2.88		996.52	93.143	2045	2	498.76	-6.25
P0A1S0 IHFA_SALTY Integration host factor subunit alpha	9		ELVELFFEEIRR	24	12	0	2.88		1561.81	93.176	2084	3	521.28	-11.41
O33921 AGP_SALTY Glucose-1- phohatase	1		TPIGGQLVFQR	335	11	4	31.12	y3y8y9y11	1215.67	61.109	65716	2	608.34	-8.13
O33921 AGP_SALTY Glucose-1- phohatase	2		MGTMDFTFNPVITDDSAAFR	141	20	13	58.22	b3b12b13°b13°b13y1y2y3 y6y11y12y15y20	2186.01	77.731	42239	2	1093.51	7.37
O33921 AGP_SALTY Glucose-1- phohatase	3	Carbamidomethyl+C(14)	EWLVAQGLIPSGECPADPTVYAY ANSLQR	87	29	12	57.85	b4b14°b14y5y6°y6y7*y7y 10y13y15y20	3205.58	93.232	26756	3	1069.20	5.48
O33921 AGP_SALTY Glucose-1- phohatase	4		DTFSANYQQEPGVQGPLK	208	18	6	21.55	b10b13°b13y8y12y18	1978.97	55.954	17133	2	989.99	9.50
O33921 AGP_SALTY Glucose-1- phohatase	5		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDR	226	31	6	39.78	y3y4y6°y6y13y14	3486.66	104.154	15092	3	1162.89	3.92
O33921 AGP_SALTY Glucose-1- phohatase	6	Carbamidomethyl+C(14)	LLEQITHYQDSPSCK	182	15	3	17.99	b5b7y11	1818.89	51.386	5061	2	909.95	14.03
O33921 AGP_SALTY Glucose-1- phohatase	7	Carbamidomethyl+C(14)	LLEQITHYQDSPSCKEK	182	17	3	16.18	b8b10y10	2076.02	48.015	3380	3	692.68	4.35
O33921 AGP_SALTY Glucose-1- phohatase	8		APLANNGSVLAQSTPNAWPAWD VPGGQLTTK	43	31	9	27.55	b10b11b14°b14b18y8°y8y 13*y13	3161.61	82.764	16802	3	1054.54	1.39
O33921 AGP_SALTY Glucose-1- phohatase	9		SQLHLDESYK	172	10	5	28.49	b3°b3b4°b4y3	1219.58	20.552	7933	3	407.20	-11.21
O33921 AGP_SALTY Glucose-1- phohatase	10	Carbamidomethyl+C(16)	TVATAQFFFITGAFPGCDIPVHHQE K	116	25	3	12.32	b7b13y8	2771.37	84.753	5045	4	693.60	3.52
O33921 AGP_SALTY Glucose-1- phohatase	11		GGVLEVYMGHYTR	74	13	3	20.48	b5b10y8	1481.73	48.930	2918	2	741.37	9.31
O33921 AGP_SALTY Glucose-1- phohatase	12		NGYQDSLFTSPTVAR	266	15	3	17.99	b13y6y10	1655.77	68.033	2066	3	552.60	-18.73
O33921 AGP_SALTY Glucose-1- phohatase	13		IEYVYQSARQLR	358	12	6	47.69	b5b6°b6b8°b8b9	1525.79	44.603	27447	3	509.27	-12.08
O33921 AGP_SALTY Glucose-1- phohatase	14		ARSQLHLDESYK	170	12	5	22.11	b11°b11°b11y4y7	1446.71	75.619	24706	2	723.86	-13.16
O33921 AGP_SALTY Glucose-1- phohatase	15		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDRQWK	226	34	5	10.96	b7b10°b10y7*y7	3928.84	83.509	23253	3	1310.28	-9.69
O33921 AGP_SALTY Glucose-1- phohatase	16	Carbamidomethyl+C(16)	TVATAQFFFITGAFPGCDIPVHHQE KMGTMDFTFNPVITDDSAAFR	116	45	4	21.53	b15y5y6y11	4938.40	121.321	6307	4	1235.35	13.15

O33921 AGP_SALTY Glucose-1-phohatase	17		NYQQEPGVQGPLK	213	13	0	5.34		1457.75	55.964	1981	2	729.38	10.97
P02936 OMPA_SALTY Outer membrane protein A	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	14	85.47	b2b3b4y1y2y5y6y10y11°y1ly13y15y17y19	2032.90	37.209	62019	3	678.31	-7.75
P02936 OMPA_SALTY Outer membrane protein A	2		GVKDVVTQPQA	339	11	6	24.13	b8y1y3*y3y9y11	1141.62	36.982	35368	2	571.31	-3.31
P02936 OMPA_SALTY Outer membrane protein A	3		IGSDAYNQGLSEKR	267	14	5	32.79	b2b3b4y3y11	1537.75	33.965	23373	3	513.25	-9.92
P02936 OMPA_SALTY Outer membrane protein A	4		IGSDAYNQGLSEK	267	13	6	32.08	b2b4°b4b5b9y8	1381.65	37.351	8963	2	691.33	-9.01
P02936 OMPA_SALTY Outer membrane protein A	5		LGYPITDDLDVYTR	103	14	5	39.53	b11b13y4y9y11	1640.82	75.429	8445	2	820.91	1.19
P02936 OMPA_SALTY Outer membrane protein A	6		FGQQEAAPVVAPAPAPAEVQTK	194	23	10	58.91	b3b13y5y8y9°y9*y9y10y12y13	2303.20	53.247	6840	3	768.41	-0.32
P02936 OMPA_SALTY Outer membrane protein A	7		DGSVVVLGFTDR	255	12	4	29.31	b5°b5b6b11	1264.65	97.370	25213	2	632.83	1.06
P02936 OMPA_SALTY Outer membrane protein A	8		STLKPEGQQALDQLYSQLSNLDPK	231	24	4	12.62	b6b8y9*y9	2673.32	74.384	8502	3	891.78	-19.09
P02936 OMPA_SALTY Outer membrane protein A	9		DVVTQPQA	342	8	4	35.91	b7y3y7°y7	857.44	84.752	2184	1	857.44	3.35
P02936 OMPA_SALTY Outer membrane protein A	10		SDVLFNFNK	222	9	13	93.69	b3b5°b5b6°b6*b6b8°b8y3*y3y4*y4y5	1083.52	136.298	2047	1	1083.52	-20.50
P02936 OMPA_SALTY Outer membrane protein A	11		HFTLKSDVLFNFNK	217	14	3	19.13	b4b7y8	1709.91	58.421	11009	3	570.64	5.43
P02936 OMPA_SALTY Outer membrane protein A	12		GDNINGAYKAQGVQLTAK	85	18	3	22.86	b12b13y14	1847.96	77.591	4253	3	616.66	-1.06
P02936 OMPA_SALTY Outer membrane protein A	13	Carbamidomethyl+C(6)	AALIDCLAPDRR	321	12	5	43.85	b3b10y4y5y7	1370.71	56.094	3345	3	457.58	-6.77
P02936 OMPA_SALTY Outer membrane protein A	14		LGYPITDDLVDYTRLGGMVWR	103	21	3	13.77	b12y5y7	2440.26	134.290	2099	2	1220.63	11.31
P02936 OMPA_SALTY Outer membrane protein A	15	Phosphoryl STY(7)	GVKDVVTQPQA	339	11	3	35.89	b4b6b8	1221.59	45.613	7055	2	611.30	6.30
P02936 OMPA_SALTY Outer membrane protein A	16		DAYNQGLSEKR	270	11	0	3.7		1280.64	33.871	10235	2	640.82	14.39
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	1	Carbamidomethyl+C(6)	LLVDACYSPVER	170	12	9	75.38	b5b7y5y6°y6y8y9y10y12	1421.71	58.851	62488	2	711.36	3.09
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	2		LVDIEQVSSTHAK	12	13	4	32.08	b7y3y4y7	1426.74	45.039	62144	3	476.25	-11.46
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	3		VTLEPLER	25	8	8	66.98	y1y3y4°y4y5y6y7y8	956.53	51.723	50718	2	478.77	-10.08
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	4		IAYNVEAAR	182	9	6	67.39	y1y3y4y6y7y8	1006.53	38.428	27764	2	503.77	-3.52
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	5	Carbamidomethyl+C(9)	ILLSSMPGCAVTEVEIDGVLHEYS TK	45	26	7	27.79	b9°b9b13b15y6y10y13	2848.47	109.453	23295	3	950.16	22.03
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	6		TDLDK	195	5	1	13.15	b3	591.30	38.035	4976	1	591.30	-3.61
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	7		LVIEMETNGTIDPEEAIR	200	18	9	51.65	b9*b9b12*b12b15*b15y9y10y11	2030.02	104.139	4729	3	677.34	4.51
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	8		GLSLGMR	310	7	4	50.41	b6y3y4y5	733.39	49.971	2878	1	733.39	-18.06

P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	9		GYVPASTRIHSEEDERPIGR	150	20	3	14.26	b11b13y3	2269.13	68.663	29368	3	757.05	0.43
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	10		TDLDKLVIEMETNGTIDPEEAIR	195	23	4	12.95	b10y7y13*y13	2602.28	102.285	2020	3	868.10	-4.60
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	11	Phosphoryl STY(10)	LVIEMETNGTIDPEEAIRR	200	19	4	20.51	b8b13y8y12	2266.04	98.077	3660	4	567.27	-13.04
P0A7Z7 RPOA_SALTY DNA-directed RNA polymerase subunit alpha	12		DIEQVSSTHAK	14	11	2	7.4	b10°b10	1214.61	45.094	12402	2	607.81	8.64
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	1		DATGNTPFMLIAR	103	13	4	20.48	b3b9y3y13	1406.72	51.757	35867	2	703.86	6.86
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	2		TLWFYNPFEQATATWLK	85	18	13	66.1	b2b5°b5b6b9y1y2y4y10y12y13y14y18	2215.12	115.741	22893	2	1108.06	-2.54
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	3		FTFTPPQGVTTIDDQR	187	15	7	51.21	b1b4b6b7b8y5y9	1721.87	61.878	16859	3	574.63	11.63
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	4		DGTIHQFSAVEQDDQR	154	16	4	17.02	b3°b3b12y13	1845.86	83.549	4393	3	615.96	12.50
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	5		VTDGSGAAVQEGQGDLWVK	44	19	5	31.37	b7b11y9y13y14	1916.97	83.569	2545	2	958.99	17.89
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	6		RPNLFNWHMTQPDESILVSDGK	63	22	4	20.69	b3b7b18y14	2584.24	104.967	1909	3	862.08	-9.83
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	7	Carbamidomethyl+C(6)	KMAIACALLSSVVASSVWADAAS SLK	2	26	4	12.06	b7b16y12°y12	2636.40	86.234	15092	4	659.85	6.39
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	8		SQQNGAVDP SKFTFTPPQGVTTIDD QR	176	26	4	21.84	b12b13y3°y3	2833.38	101.127	1746	3	945.13	1.12
Q8ZQD4 LOLA_SALTY Outer-membrane lipoprotein carrier protein	9		SAYQLKSQQNGAVDPSK	170	17	3	23.58	y7y10y13	1820.92	87.876	1528	2	910.97	5.36
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	1		LNSAVFPSAQGGPLMHVIAGK	251	21	9	43.32	b4°b4*b4b16y3y4y5y15y21	2094.10	77.881	65974	3	698.71	-6.18
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	2		SPFVTSGIR	354	9	5	61.37	b8y4y5y6y7	963.53	48.820	54404	2	482.27	-0.76
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	3	Carbamidomethyl+C(5)	VLDICAR	405	7	5	40.27	b2y4y5y6y7	846.44	44.235	46217	2	423.72	-9.66
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	4		VMQAQGSQTLNK	42	12	13	115.99	b2b3b5b10y2y3y4y6y7y9y10*y10y12	1304.66	29.057	44742	2	652.83	-1.59
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	5		EMNIADYDAELWQAMEQEK	4	19	9	97.72	y4y5y6y7y10y11y12y13y19	2314.01	92.005	30013	2	1157.51	5.59
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	6	Carbamidomethyl+C(7)	ELAGWMCDVLDNINDEATIER	380	21	10	38.35	b2°b2b11y2°y2y5y11y12y13y21	2464.13	101.337	17658	2	1232.57	7.93
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	7		MIIGFSAYSGVVDWAK	168	17	9	48.56	b15y8°y8y11y13°y13y14°y14y16	1800.89	102.659	7601	3	600.97	-4.95
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	8		LYNIVPYGIDESGK	138	14	5	32.79	b12b13y2y3y13	1567.81	69.827	4362	2	784.41	3.74
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	9	Carbamidomethyl+C(5)	YYGGCEYVDVVEQLAIDR	63	18	4	15.45	b4y4y12°y12	2149.02	109.434	1841	3	717.01	11.47
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	10		EMNIADYDAELWQAMEQEKVR	4	21	3	13.77	b5b19y19	2569.14	73.843	46428	3	857.05	-11.97

P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	11		NSVPNDPKSPFVTSGIR	346	17	3	24.83	y8y9y14	1814.92	51.907	32631	3	605.65	-8.81
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	12		QEEHIELIASENYTSPRVMAQGS QLTK	25	29	3	11.47	b9b12y15	3301.61	83.512	25541	4	826.16	-1.85
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	13		VMQAQGSQLTNKYAEGYPGK	42	20	8	49.35	b11*b11b15b19y5y6y7*y7	2170.06	67.102	11365	4	543.27	1.24
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	14		EHKPKMIIGGFSAYSGVVDWAK	163	22	5	24.05	b18y9y10*y10y12	2420.26	104.590	9677	4	605.82	5.55
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	15		LYNIVPYGIDESGKIDYDEMAK	138	22	8	47.54	b10*b10b12b14y9y10*y10y11	2533.21	87.245	5379	3	845.08	-1.45
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	16		MIIGGFSAYSGVVDWAKMR	168	19	3	14.82	b4b15y8	2088.05	103.847	4592	3	696.69	4.09
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	17	Oxidation+M(15)	LNSAVFPSAQGGPLMHVIAGK	251	21	3	23.42	y3y4y18	2110.09	84.635	42792	3	704.03	-11.34
P0A2E1 GLYA_SALTY Serine hydroxymethyltransferase	18		IGGFSAYSGVVDWAK	170	15	1	7.29	b10	1556.79	102.698	7107	2	778.90	6.98
P66932 TIG_SALTY Trigger factor	1		NVALEEQAWEAVLAK	399	15	7	31.6	b2b3b11y1y2y11y12	1583.86	79.557	109314	2	792.44	-0.39
P66932 TIG_SALTY Trigger factor	2		SQAIEGLVK	287	9	7	30.3	b2b3*b3y1y3y4y9	944.54	46.959	35003	2	472.77	-4.26
P66932 TIG_SALTY Trigger factor	3		GLIEEMASAYEDPKVIEFYK	368	22	7	25.36	b2b8b18y4y8y12y22	2548.18	80.975	26426	3	850.07	-13.51
P66932 TIG_SALTY Trigger factor	4		VEERELPELTEEFIK	239	15	3	17.99	b10y6y9	1860.95	76.866	17219	2	930.98	-4.00
P66932 TIG_SALTY Trigger factor	5		INPAGAPNYVPGEYK	83	15	10	69.99	y3y5*y5y7y8*y8y9*y9y13y15	1589.81	50.355	16783	2	795.41	7.76
P66932 TIG_SALTY Trigger factor	6		ANDIDVPSALIDSEIDVLR	296	19	9	38.78	b3b6b7*b7b10y1y3y13y19	2055.07	94.061	16639	2	1028.04	2.97
P66932 TIG_SALTY Trigger factor	7		QALELPRELFEEQAK	327	15	3	17.99	b9y3y10	1800.92	56.453	9766	3	600.98	-14.17
P66932 TIG_SALTY Trigger factor	8		AGEEFTIDVTFPEEYHAENLK	206	21	5	37.96	b7b11b12y12y13	2439.10	101.248	2526	3	813.71	-13.31
P66932 TIG_SALTY Trigger factor	9		YGASVR	57	6	1	13.56	b4	652.34	26.510	20668	1	652.34	3.93
P66932 TIG_SALTY Trigger factor	10		FGVEDGSVAGLR	255	12	5	43.85	b5b10y7y9y10	1206.62	40.223	16314	3	402.88	7.79
P66932 TIG_SALTY Trigger factor	11		VTIDFTGSVDGEEFEGGK	163	18	4	21.55	b5b14y4y8	1886.83	120.459	14636	3	629.62	-17.27
P66932 TIG_SALTY Trigger factor	12		ATDFVLAMGQGR	181	12	5	31.95	b3*b3b7y3y10	1265.60	79.560	11351	3	422.54	-21.51
P66932 TIG_SALTY Trigger factor	13		ELFEEQAK	334	8	8	66.98	b3*b3b6y3*y3y6*y6y7	993.49	136.308	2549	1	993.49	1.23
P66932 TIG_SALTY Trigger factor	14		QDVLGDLMSR	63	10	3	41.5	y3y5y8	1133.54	76.662	2493	2	567.27	-19.71
P66932 TIG_SALTY Trigger factor	15	Oxidation+M(1)	MQVSVETQQLGRR	0	14	3	19.13	b7y9y11	1577.81	97.889	2027	2	789.41	-0.85
P58661 AAT_SALTY Aartate aminotransferase	1		MFENITAAPADPILGLADLFR	0	21	11	73.03	b2b3b5b8b10b11y1y3y4y13y14	2275.19	120.229	12921	2	1138.10	4.51
P58661 AAT_SALTY Aartate aminotransferase	2		TAQTPGGTGALR	96	12	5	26.09	b5*b5y8y9y12	1129.60	28.824	11598	2	565.30	1.84
P58661 AAT_SALTY Aartate aminotransferase	3		NYLGIDGIPEFAR	63	13	4	20.48	b2b3y5y10	1464.74	80.396	9310	2	732.88	-2.33
P58661 AAT_SALTY Aartate aminotransferase	4		VWVSNPSPWPNHK	122	12	3	22.11	b4y3y8	1450.71	53.673	6024	3	484.24	-11.86
P58661 AAT_SALTY Aartate aminotransferase	5		ANYSNPAPHGASIVATILSNDALR	280	24	3	21.91	b13y4y5	2452.21	58.956	4783	3	818.07	-21.40
P58661 AAT_SALTY Aartate aminotransferase	6		AIWEQELTDMR	304	11	5	36.49	b10*b10y3y9y10	1391.66	136.555	4625	1	1391.66	0.00

P58661 AAT_SALTY Aartate aminotransferase	7		DQVLR	355	5	1	13.15	b3	630.35	40.809	3486	1	630.35	-13.85
P58661 AAT_SALTY Aartate aminotransferase	8		QLFVNTLQEK	322	10	4	26.73	b6y5*y5y7	1219.68	58.843	3139	2	610.34	7.51
P58661 AAT_SALTY Aartate aminotransferase	9		AFSQMKSAIR	270	10	3	26.73	b4b6y8	1138.60	79.344	10118	2	569.80	-5.57
P58661 AAT_SALTY Aartate aminotransferase	10		GWLPLFD FayQG FARGLEEDAEG LR	204	25	4	22.94	b13y13y14y22	2857.40	136.578	7621	2	1429.20	1.62
P0A9Y9 CC_SALTY Cold shock-like protein cC	1		GFGFITPADGSK	15	12	20	154.64	b2b3b4b5b6b12y2°y2y3°y3y4y5y6°y6y7°y7y8y9y10y12	1196.59	63.890	494959	2	598.80	-4.90
P0A9Y9 CC_SALTY Cold shock-like protein cC	2		DVVFHFSAIQNGNGFK	27	15	6	44.41	b3°b3b5b8b12y11	1665.85	85.929	18082	2	833.43	4.32
P0A9Y9 CC_SALTY Cold shock-like protein cC	3		TLAEGQNVEFEIQDGQKGPAAVN VTAI	42	27	7	25.47	b3b11b22°b22b24y3°y3	2799.42	75.281	80888	3	933.81	2.35
P0A9Y9 CC_SALTY Cold shock-like protein cC	4		DVVFHFSAIQNGNGFKTLAEGQNV EFEIQDGQK	27	32	3	11.11	b8y6y9	3552.79	98.315	5759	3	1184.93	13.54
P0A9Y9 CC_SALTY Cold shock-like protein cC	5		TPADGSK	20	7	3	21.39	b4b5°b5	675.33	63.996	4949	1	675.33	1.72
P0A9Y9 CC_SALTY Cold shock-like protein cC	6		GFITPADGSK	17	10	2	17.41	b3b8	992.50	63.850	1874	1	992.50	-3.01
Q8ZRP4 DAPD_SALTY 2	1		EAVNQVISLLDSGALR	28	16	4	42.64	y5y6y9y10	1684.92	91.757	41463	2	842.97	1.09
Q8ZRP4 DAPD_SALTY 2	2		INDNQVIDGAESR	68	13	6	63.01	y5y6y7y8y9y13	1430.69	40.589	28590	2	715.85	4.01
Q8ZRP4 DAPD_SALTY 2	3		VPAGSVVVSGNLP SKDGK	226	18	5	15.45	b4b6y2y3y18	1710.92	42.996	26814	3	570.98	-10.56
Q8ZRP4 DAPD_SALTY 2	4		FADYDEAR	89	8	4	32.9	b2b3y5y6	986.43	33.974	25540	2	493.72	7.12
Q8ZRP4 DAPD_SALTY 2	5		IDGQWVTHQWLK	48	12	7	44.68	b2b3b4b7b10°b10y12	1510.76	90.165	22323	2	755.88	-14.46
Q8ZRP4 DAPD_SALTY 2	6		MQQLQNVIAFERR	0	15	3	26.07	b3b9b12	1862.96	62.763	12818	3	621.66	2.10
Q8ZRP4 DAPD_SALTY 2	7		ETGEVHYGRVPAGSVVVSGNLP S K	217	24	3	22.91	b9b10b12	2439.25	110.156	4861	3	813.75	-5.50
Q8ZRP4 DAPD_SALTY 2	8	Phosphoryl STY(7)	IDGQWVTHQWLKK	48	13	5	34.95	b4b5b6°b6*b6	1718.83	101.020	2059	3	573.62	-0.14
Q8ZRP4 DAPD_SALTY 2	9		IDGQWVTHQ	48	9	0	2.88		1083.51	90.202	1946	1	1083.51	-6.87
P0A1V4 KAD_SALTY Adenylate kinase	1		LVEYHQMTAPLIGYYQK	167	17	4	24.83	y5y6y11y17	2054.02	68.964	71561	3	685.35	-9.75
P0A1V4 KAD_SALTY Adenylate kinase	2		YGIPQISTGDMLR	23	13	7	33.84	b5°b5y7y10*y10y12y13	1450.74	72.187	44395	2	725.87	1.60
P0A1V4 KAD_SALTY Adenylate kinase	3		NGFLLDGFPR	78	10	6	42.89	b3y4y5y6°y6y10	1135.58	80.440	32025	2	568.30	-5.80
P0A1V4 KAD_SALTY Adenylate kinase	4		IILLGAPGAGK	2	11	5	36.49	b2b3y4y5y9	1009.63	60.678	27546	2	505.32	-8.16
P0A1V4 KAD_SALTY Adenylate kinase	5		IILLGAPGAGKGTQAQFIMEK	2	21	4	21.52	b3y7y17y19	2143.18	72.296	35720	3	715.07	-5.58
P0A1V4 KAD_SALTY Adenylate kinase	6		GTQAQFIMEKYGIPQISTGDMLR	13	23	4	12.95	b3°b3b8y7	2584.28	90.381	5393	3	862.10	-2.55
P0A1V4 KAD_SALTY Adenylate kinase	7		QAKDIMDAGK	47	10	3	26.73	b3b7y5	1076.55	25.807	4046	3	359.52	9.30
P0A1V4 KAD_SALTY Adenylate kinase	8		RLVEYHQMTAPLIGYYQK	166	18	3	22.61	y4y6y11	2210.11	84.677	2383	2	1105.56	-13.48
P0A1V4 KAD_SALTY Adenylate kinase	9		NGFLLDGFPR TIPQADAMK	78	19	4	14.82	b3°b3y3y9	2091.09	87.980	2150	2	1046.05	7.71
P0A1V4 KAD_SALTY Adenylate kinase	10	Oxidation+M(7)	LVEYHQMTAPLIGYYQK	167	17	5	16.18	b6°b6b13y11*y11	2070.04	94.992	2764	2	1035.52	2.83
P0A1V4 KAD_SALTY Adenylate kinase	11		LVEYHQMTAPLIGY	167	14	2	7.29	y9°y9	1634.81	68.960	2574	2	817.91	-8.51
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	1		LAEAGIPTQMER	60	12	9	83.46	b4y3y5y6y8y9y10*y10y12	1315.67	49.364	42246	2	658.34	1.11
P65889 PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase	2	Carbamidomethyl+C(7)	LLSDTECLVK	72	10	5	33.72	b2y1y5y7y8	1177.61	52.909	37899	2	589.31	-0.83

P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	3		TVYSTENPDLLVLEFR	13	16	4	17.02	b3y4°y4y10	1895.98	88.014	32249	2	948.50	4.57
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	4		QSLGGLIEAYEAVHR	215	16	5	27.46	b13y6°y6y10y14	1713.86	84.906	29179	3	571.96	-16.60
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	5		GMVNNK	46	6	1	13.56	b5	662.33	41.432	12909	1	662.33	5.53
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	6		FNHFIMTK	52	8	9	96.29	b5b6b7y3y4y6°y6y7°y7	1037.52	136.265	2342	1	1037.52	-8.24
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	7		LGVEEGMELNPPIFDLFLK	104	19	3	14.82	b4b14y12	2161.12	76.859	2121	2	1081.07	-0.34
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	8		FRQSLGGLIEAYEAVHR	213	18	5	36.38	b14y8y9y10°y10	2017.06	69.936	54797	4	505.02	-1.94
P65889 PUR7_SALTY Phohoribosylaminoimidazole- succinocarboxamide synthase	9		ETLDKMDK	203	8	4	35.91	b4b6°b6y5	979.46	120.033	1670	1	979.46	-13.46
P0A2A7 RL30_SALTY 50S ribosomal protein L30	1		GMVNAVSMVK	45	11	8	47.42	b2b4b5b10y1y2y5y8	1182.60	72.809	103403	2	591.80	-1.86
P0A2A7 RL30_SALTY 50S ribosomal protein L30	2		ATLLGLGLR	21	9	3	38.08	y5y6y7	913.57	73.550	44847	2	457.29	-12.29
P0A2A7 RL30_SALTY 50S ribosomal protein L30	3		EDTPAVRGMVNAVSMVK	38	18	4	21.55	b9b11y4y8	1950.97	100.432	6989	2	975.99	-2.63
P0A2A7 RL30_SALTY 50S ribosomal protein L30	4		ATLLGLGLR	21	9	0	1.64		895.56	73.545	1592	2	448.29	-4.63
P0A1P6 GLNA_SALTY Glutamine synthetase	1		LVPGYEAPVMLAYSAR	322	16	11	73.64	b2b5b15y4y5°y5y9y11y13° y13y14	1736.91	76.881	37328	2	868.96	2.46
P0A1P6 GLNA_SALTY Glutamine synthetase	2		AINALANPTTNSYKR	307	15	7	52.07	b2y4y8y9y10y13y15	1633.87	42.381	28744	3	545.29	1.64
P0A1P6 GLNA_SALTY Glutamine synthetase	3		GGYFPVPPVDSAQDIR	177	16	9	48.43	b2b3b12y2y5y7y10y12y16	1717.87	69.523	28027	2	859.44	6.68
P0A1P6 GLNA_SALTY Glutamine synthetase	4		AINALANPTTNSYK	307	14	5	27.7	y2y5y9y12°y12	1477.77	47.334	15882	2	739.39	1.65
P0A1P6 GLNA_SALTY Glutamine synthetase	5		ATGIADTVLFGPEPEFFLFDDIR	117	23	11	58.91	b2b4b6y2y3y5y6y9y10y11 y23	2570.26	116.898	11626	3	857.43	-7.03
P0A1P6 GLNA_SALTY Glutamine synthetase	6		EIPQVAGSLEEALNALDLDR	406	20	6	31.95	b16y6y7y10y13y20	2153.10	80.911	3233	2	1077.05	-5.10
P0A1P6 GLNA_SALTY Glutamine synthetase	7		GINESDMVLPDASTAVIDPFFAD STLIIR	59	30	9	58.7	b3b5b8b9b10b17y3y4y13	3238.58	113.078	16395	3	1080.20	-5.65
P0A1P6 GLNA_SALTY Glutamine synthetase	8		SAEHVLTMLNEHEVK	1	15	6	36.81	b5°b5b6b8y6y12	1736.83	50.245	2002	3	579.62	-19.12
P0A1P6 GLNA_SALTY Glutamine synthetase	9		NLYDLPPEEAK	395	11	3	24.13	b8b10y8	1288.65	58.975	1657	3	430.22	5.49
P0A1P6 GLNA_SALTY Glutamine synthetase	10		GKEQHVTIPAHQVNAEFFEFGK	26	22	4	24.05	b6b7b14y14	2495.23	96.988	4231	3	832.42	-0.29
P0A1P6 GLNA_SALTY Glutamine synthetase	11		IHPGEAMDKNLYDLPPPEEAK	386	20	3	14.26	b12y10y13	2267.12	79.415	1831	2	1134.06	6.35
P0A1P6 GLNA_SALTY Glutamine synthetase	12	Oxidation+M(9)	MSAEHVLTMLNEHEVK	0	16	6	24.05	b8b11y10°y10*y10y14	1883.90	75.616	21267	2	942.45	0.52
P0A1P6 GLNA_SALTY Glutamine synthetase	13	Oxidation+M(8)	SAEHVLTMLNEHEVK	1	15	3	17.99	b12y7y12	1752.87	94.975	1608	2	876.94	6.69
P0A1P6 GLNA_SALTY Glutamine synthetase	14		NALANPTTNSYKR	309	13	0	4.11		1449.74	42.418	2092	2	725.37	-4.72
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	1		LFNELGPR	78	8	10	66.98	b7*y3y4y5°y5y6*y6y7*y7y 8	945.51	54.930	103038	2	473.26	-7.55

Q7CPL7 RL17_SALTY 50S ribosomal protein L17	2		AGDNAPMAYIELVDR	103	15	4	17.99	b4y5y10y15	1634.79	78.542	52429	2	817.90	3.88
Q7CPL7 RL17_SALTY 50S ribosomal protein L17	3		LAFAR	64	5	1	13.15	y3	577.35	142.599	3403	1	577.35	13.64
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	1		YISMNVTQKPFDNPK	269	15	4	17.99	b11b14y11y15	1781.88	75.782	115614	2	891.44	-5.89
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	2		DIGFHPVGTGPYQLETWNQTD FV K	176	24	3	12.62	b9b15y10	2749.33	82.629	16862	3	917.11	0.18
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	3		NLTGFWIMPDTGFSFDDADLK	491	21	11	50.21	b2b3b11y1y2y6y7y8y13y15y21	2390.13	106.351	15788	2	1195.57	10.11
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	4		FQDGADFNAAAVK	97	13	4	11.52	b5y9*y11y13	1353.65	49.115	15626	2	677.33	1.98
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	5		TEVVDPATVK	134	10	9	67.8	b1b2y2y5y6y7y8y9y10	1058.57	38.374	15016	2	529.79	-1.04
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	6		VLQFTQQQLAIGVK	362	15	3	14.84	b4*b4b10	1700.98	71.476	10985	2	850.99	5.17
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	7		ITAMDAGQR	379	9	6	54.24	b2y5°y5y6y7y8	962.47	28.443	10558	2	481.74	-3.23
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	8		SFYQGLFGLDKDMK	56	14	4	31.31	b7b9b11y13	1648.80	80.979	2577	2	824.90	-2.07
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	9		NLELVASPSIMQR	256	13	4	20.48	b4*b4y8y11	1457.77	68.068	10326	2	729.39	-4.19
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	10		YGKDIGFHPVGTGPYQLETWNQ TDFVK	173	27	12	75.28	b6°b6b7b8°b8y4y5°y5y6*y6y7°y7	3097.55	136.173	4071	3	1033.19	14.19
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	11		QGVKFQDGADFNAAAVK	93	17	3	16.18	b4b11y9	1765.88	59.029	4065	2	883.44	-4.36
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	12		VKNVLAEGYTVSDDGLTYTITLR	70	23	3	23.04	y3y4y11	2528.33	54.706	3330	3	843.45	0.48
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	13		ARITAMDAGQR	377	11	3	31.12	y5y8y9	1189.62	106.478	2990	2	595.32	10.16
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	14		DIGFHPVGTGPYQLETWNQTD FV KVK	176	26	3	18.21	b5b14b23	2976.48	101.624	2694	4	744.87	-4.18
Q8ZQM3 GSIB_SALTY Glutathione-binding protein gsiB	15		TGFSFDDADLK	501	11	1	7.68	b4	1215.57	106.249	1550	2	608.29	12.95
P02906 SUBI_SALTY Sulfate-binding protein	1		YLYSPEGQEIAAK	263	13	13	82.92	b2b3b4°b4b11y1y2y6y7y9y10y11y13	1468.74	50.109	68479	2	734.87	2.16
P02906 SUBI_SALTY Sulfate-binding protein	2		LFTIDEVFGGWAK	298	13	5	33.84	b2b7y5y10y12	1482.77	101.753	46386	2	741.89	2.31
P02906 SUBI_SALTY Sulfate-binding protein	3		NVEVLDSGAR	183	10	4	33.72	b2y4y5y8	1059.54	39.539	41018	2	530.27	-2.19
P02906 SUBI_SALTY Sulfate-binding protein	4		QATSVINGIEADVVTALAYDVD AIAER	66	28	9	25.32	b7b13°b13°b13y2y5y8°y8y9	2917.51	128.457	14932	3	973.17	-3.35
P02906 SUBI_SALTY Sulfate-binding protein	5		WNYLAAWGYALHHNNNDQAK	153	20	5	22.43	b8°b8b11b13y3	2386.12	92.112	65498	3	796.05	5.73
P02906 SUBI_SALTY Sulfate-binding protein	6		FEIVTPSESILAEPTVSVDK	226	21	5	21.52	b10°b10y5y7y10	2260.22	76.766	61118	3	754.08	10.05
P02906 SUBI_SALTY Sulfate-binding protein	7		DIQLLNVSYPTR	20	13	3	20.48	b3y5y9	1533.77	82.173	10810	2	767.39	-13.85
P02906 SUBI_SALTY Sulfate-binding protein	8		NVEVLDSGARGSTNTFVER	183	19	20	97.13	b4b5b8°b8b10°b10b12°b12y3y7°y7*y7y8*y8y9°y9*y9y10*y10y13	2051.04	136.273	2954	2	1026.03	14.28
P02906 SUBI_SALTY Sulfate-binding protein	9		LFTIDEVFGGWAKAQK	298	16	4	17.02	b6b9°b9y13	1809.98	101.128	2421	2	905.49	13.15
P02906 SUBI_SALTY Sulfate-binding protein	10	Phosphoryl STY(1)	YLYSPEGQEIAAK	263	13	4	41.11	y7y9y11y12	1548.71	79.693	27442	2	774.86	13.79
Q8ZP20 TREA_SALTY Periplasmic trehalase	1		VAAAAQAHLLQPGGLATTSVK	428	21	3	22.22	b4b5y19	2004.11	57.392	19969	3	668.71	-8.41

Q8ZP20 TREA_SALTY Periplasmic trehalase	2		TFADAIPNSDPLMILADYR	68	19	11	49.64	b6b7°b7b9*b13y2y4y5°y5y11y13	2123.06	101.017	12815	2	1062.03	4.71
Q8ZP20 TREA_SALTY Periplasmic trehalase	3		SNPNRPATEIYR	296	12	4	26.09	b7b8y10y12	1417.71	32.759	3892	2	709.36	-4.22
Q8ZP20 TREA_SALTY Periplasmic trehalase	4		TTTIAPVDLNALLYQLEK	335	18	6	28.95	b3°b3b8°b8y13y14	2003.10	103.215	18254	2	1002.05	-5.00
Q8ZP20 TREA_SALTY Periplasmic trehalase	5		DQLTAAALFPLYVNAAAK	405	18	3	22.61	b4b7b14	1877.00	96.526	8364	2	939.00	-10.99
Q8ZP20 TREA_SALTY Periplasmic trehalase	6	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPTK	534	29	3	21.89	b5b6y7	3199.58	63.520	2814	3	1067.20	-1.22
Q8ZP20 TREA_SALTY Periplasmic trehalase	7		FLTNVQHTYDR	486	11	4	24.13	b7b9y5°y5	1393.72	80.040	1879	2	697.36	21.37
Q8ZP20 TREA_SALTY Periplasmic trehalase	8		SAAASGWDFSSR	311	12	4	34.01	b3y6y7y10	1241.54	35.939	1782	3	414.52	-7.77
Q8ZP20 TREA_SALTY Periplasmic trehalase	9	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPTKTPSAATQ	534	36	4	10.88	b4°b4y8y21	3855.88	63.391	16244	4	964.73	-2.41
Q8ZP20 TREA_SALTY Periplasmic trehalase	10		YWDDRDTPRPESWVEDIATAK	275	21	3	22.22	b10y14y15	2550.18	87.221	10420	3	850.73	-3.06
Q8ZP20 TREA_SALTY Periplasmic trehalase	11		FLTNVQHTYDREK	486	13	4	29.72	b8°b8b10b12	1650.81	84.389	6688	3	550.94	-10.65
Q8ZP20 TREA_SALTY Periplasmic trehalase	12		ASAAAGDRAK	357	10	6	39.88	b3°b3b4°b4b6y8	917.49	21.960	4858	2	459.25	9.25
Q8ZP20 TREA_SALTY Periplasmic trehalase	13		MQRNQSGFDLR	87	11	4	41.26	b4b6b10y7	1351.67	93.023	3982	2	676.34	11.20
Q8ZP20 TREA_SALTY Periplasmic trehalase	14	Oxidation+M(4)	VADMVANFGYEIDAWGHIPNGNR	183	23	4	12.95	b3b6°b6y11	2562.18	56.934	39105	3	854.73	-2.10
Q8ZP20 TREA_SALTY Periplasmic trehalase	15		LATTSVK	442	7	0	6.57		719.43	57.471	1902	2	360.22	-0.85
Q8ZP20 TREA_SALTY Periplasmic trehalase	16		TFADAIPNSDPLMILADYR	68	19	1	7.44	b8	2105.03	100.918	2706	3	702.35	-3.36
P67179 YEB_C_SALTY UPF0082 protein yebC	1		LGGGDPDANPR	37	11	10	70.57	b2b6y2y4y5°y5y6y9y10y11	1068.50	22.011	16914	2	534.75	-5.26
P67179 YEB_C_SALTY UPF0082 protein yebC	2	Carbamidomethyl+C(1)	CGGNLGTDGSAYLFSK	119	17	4	24.83	y6y11y12y17	1745.82	72.572	11960	2	873.41	3.01
P67179 YEB_C_SALTY UPF0082 protein yebC	3		DALEAAGLKADSAEVSMIPSTK	183	22	5	13.33	b3°b3b12°b12y4	2204.10	67.194	19538	3	735.37	-5.43
P60726 RL4_SALTY 50S ribosomal protein L4	1		FSVEAPK	123	7	5	40.27	y1y2y3y5y6	777.41	40.862	44754	2	389.21	-9.26
P60726 RL4_SALTY 50S ribosomal protein L4	2		DATGIDPVSLIAFDK	170	15	6	17.99	b4y2y4°y4y10y15	1561.81	87.464	39117	2	781.41	2.34
P60726 RL4_SALTY 50S ribosomal protein L4	3		DFNEALVHQVVVAYAAGAR	21	19	6	41.78	b2b10b15y6y7y8	2030.05	83.231	23629	3	677.36	2.59
P60726 RL4_SALTY 50S ribosomal protein L4	4		QVEEMLA	194	7	4	40.27	b3b6y6y7	819.39	50.868	20283	1	819.39	3.43
P60726 RL4_SALTY 50S ribosomal protein L4	5		DAQSALTVSETTFGRDFNEALVH QVVVAYAAGAR	6	34	3	10.96	b7b12y16	3593.75	104.933	5934	4	899.19	-13.45
P60726 RL4_SALTY 50S ribosomal protein L4	6		VVMTADAVK	185	9	3	30.3	b3y5y8	933.52	44.538	11670	2	467.26	14.25
P60726 RL4_SALTY 50S ribosomal protein L4	7		SGGVTF AARPQDHSQK	79	16	11	60.51	b5b6b7b10y5°y5*y5y7°y7y8*y8	1685.81	93.014	3729	2	843.41	-17.31
P60726 RL4_SALTY 50S ribosomal protein L4	8		DATGIDPVSLIAFDKVVMTADAV K	170	24	7	44.06	b3b9y7°y7y8y18y19	2476.30	101.460	46218	3	826.11	0.99
P60726 RL4_SALTY 50S ribosomal protein L4	9		LKDMALEDVLIITGELDENLFLAA R	137	25	6	39.08	b5°b5b6b7y3y5	2802.50	136.340	11147	3	934.84	1.05
P60726 RL4_SALTY 50S ribosomal protein L4	10		SPIWRSGGVTF AARPQDHSQK	74	21	4	22.22	b11b12°b12y8	2325.21	98.211	9203	3	775.74	10.92

[P60726]RL4_SALTY 50S ribosomal protein L4	11		DFNEALVHQVVVAYAAGARQGT R	21	23	3	21.98	b8b9y10	2472.28	63.156	6486	3	824.76	0.59
[P60726]RL4_SALTY 50S ribosomal protein L4	12		ELVLKDAQSALTVSETTFGR	1	20	3	23.68	y7y9y10	2165.17	108.200	4219	3	722.40	12.74
[P60726]RL4_SALTY 50S ribosomal protein L4	13		VVMTADAVKQVEMLA	185	16	8	59.84	b4b5b6*b6b10y4y9y14	1733.86	87.778	3304	2	867.43	-14.29
[P60726]RL4_SALTY 50S ribosomal protein L4	14	Phosphoryl STY(7)	VDVRDATGIDPVSLIAFDK	166	19	4	14.82	b5*b5y4y13	2111.02	71.485	8941	3	704.34	-7.52
[P60726]RL4_SALTY 50S ribosomal protein L4	15	Phosphoryl STY(4)	A EVTGSGKKPWR	49	12	5	34.01	b3b10b11*b11y9	1395.68	68.093	8354	3	465.90	5.16
[P60726]RL4_SALTY 50S ribosomal protein L4	16	Oxidation+M(4)	LKDMALEDVLIITGELDENLFLAA R	137	25	4	35.25	b6b7b8y12	2818.51	88.640	24466	3	940.17	6.15
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	1	Carbamidomethyl+C(3)	FICIADASK	112	9	7	52.99	b1b2b5y3y5y7y9	1024.51	50.588	30881	2	512.76	-0.71
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	2		GADVALIGTPDGVK	201	14	6	31.31	b6y2y3y5y7y14	1312.71	56.854	27126	2	656.86	2.05
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	3		GQIEGAVSSSDASTEK	43	16	4	17.02	b2b3b9y9	1565.74	30.995	8174	2	783.37	4.83
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	4		AVGWAALQYVQPGTIVGVGTGST AAHFIDALGTMK	8	35	5	16.83	b4b9b11y9y19	3487.80	107.195	67255	3	1163.27	-1.19
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	5		GLGIHVFDLNEVDSLGIYVDGADE INGHMQMIK	61	33	6	51.31	b11b12b15b16y9y10	3599.73	103.674	5788	3	1200.58	-7.12
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A	6		GQIEGAVSSSDASTEKLK	43	18	7	34.38	b3*b3b4*b4b7b11y11	1806.90	38.518	4355	2	903.95	-4.05
[P66170]RL29_SALTY 50S ribosomal protein L29	1		MQAASGQLQQSHLLK	29	15	17	110.69	b1b2*b2b3y1y2y3y5y7*y7 *y7y8y9y11y12y13y15	1639.84	44.603	258083	3	547.28	-12.21
[P66170]RL29_SALTY 50S ribosomal protein L29	2		SVEELNTELLNLLR	9	14	9	56.36	b1b3b4b9*b9b10y4y9y14	1642.90	101.028	134914	2	821.96	1.49
[P66170]RL29_SALTY 50S ribosomal protein L29	3		EQFNLR	23	6	4	26.71	y3*y3y4*y4	806.41	41.694	72324	2	403.71	-6.96
[P66170]RL29_SALTY 50S ribosomal protein L29	4		AASGQLQQSHLLK	31	13	5	26.07	b5*b5*b5b10b12	1380.75	44.588	4500	2	690.88	-3.80
[O54296]RS11_SALTY 30S ribosomal protein S11	1		ALNAAGFR	98	8	5	40.68	y4y5y6*y6y8	819.45	41.593	30825	2	410.23	-1.04
[O54296]RS11_SALTY 30S ribosomal protein S11	2		QGNALGWATAGGSGFR	37	16	7	42.37	b5y2y6y10y11y12y16	1549.76	65.556	21754	2	775.38	3.70
[O54296]RS11_SALTY 30S ribosomal protein S11	3		QVSDGVAHIHASFNNTIVTTDR	14	23	10	44.74	b3*b3*b3b4*b4b14b15*b15 y3y5	2495.23	101.180	5166	2	1248.12	-11.94
[O54296]RS11_SALTY 30S ribosomal protein S11	4	Carbamidomethyl+C(13)	STPFAAQVAAERCADAVK	57	18	3	15.45	b4b7y6	1891.92	135.609	2527	2	946.46	-7.87
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	1		FGSELLAK	17	8	6	40.68	b2y2y3y4y7y8	864.47	51.212	96912	2	432.74	-9.32
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	2		WIVEAAR	102	7	7	50.41	b1b4y4*y4y5y6y7	844.46	50.043	52636	2	422.73	-8.17
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	3		FVNILMVDGKK	25	11	4	47.28	y3y5y6y7	1263.70	66.820	52107	3	421.90	-12.56
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	4		VGGSTYQVPVEVRPVR	79	17	3	24.83	b3b6b7	1899.04	49.992	19636	4	475.51	-10.93
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	5		STAESIVYSALETLAQR	36	17	3	23.17	b11y4y5	1838.92	106.648	29896	3	613.65	-15.60
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	6		LANELSDAADNK	119	12	3	35.33	y7y8y9	1260.62	36.980	8345	2	630.81	6.68
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	7		NALAMR	96	6	2	26.71	y4y5	675.36	35.491	6075	1	675.36	0.36
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	8		ILPDPK	11	6	1	13.56	y4	682.41	31.885	3413	1	682.41	-1.88
[P0A2B3]RS7_SALTY 30S ribosomal protein S7	9		LANELSDAADNKGTA VK	119	17	13	112.25	b3*b3b4*b4b14y5y8y9y10 y12y13y15y16	1716.86	38.622	146558	3	572.96	-11.09

P0A2B3 RS7_SALTY 30S ribosomal protein S7	10		RNALAMR	95	7	3	40.27	y3y5y6	831.46	30.544	6705	2	416.23	-3.01
P0A2B3 RS7_SALTY 30S ribosomal protein S7	11		AFAHYRW	149	7	3	37.26	b6y5y6	950.46	114.660	1596	1	950.46	-6.36
P0A2B3 RS7_SALTY 30S ribosomal protein S7	12	Oxidation+M(6)	FVNILMVDGK	25	10	3	28.49	b3b4y7	1151.61	36.283	2880	3	384.54	-0.32
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	1		IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	7	14.79	b2b13y2y3y7°y7y14	3950.88	95.720	55147	4	988.48	-1.11
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	2		DSVGAVVMGPYADLAEGMK	68	19	9	49.64	b5b6b8b12y1y2y10y11y13	1909.91	82.965	39781	2	955.46	4.41
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	3		AVDSMIPIGR	151	10	4	33.72	y4y5y8y10	1058.56	59.523	36720	2	529.79	-2.77
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	4		ILEVPVGR	93	8	4	40.68	y4y5y6y8	882.53	52.088	31001	2	441.77	-9.20
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	5		QSVDQPQVTGYK	139	12	6	44.68	b12y7y8y9y11y12	1349.67	33.353	21286	2	675.34	0.09
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	6		ELAAFSQFASDLDDATRK	401	18	5	24.62	b12*b14y6y8y10	1984.98	72.461	3969	2	992.99	7.99
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	7		MQLNSTEISELIK	0	13	6	45.81	b10b11°b11y3y10y11	1505.79	76.238	38757	2	753.40	-1.86
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	8		ELAAFSQFASDLDDATR	401	17	3	16.18	b12y6y9	1856.88	88.089	22186	2	928.94	7.49
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	9		GYLADVELAK	453	10	4	39.09	b6b8y6y8	1078.57	68.052	19766	2	539.79	-9.51
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	10		DHAPLMQEINQSGGYNDEIEGK	477	22	6	45.5	b3b8y8y9y13y14	2445.13	93.134	7906	4	612.04	12.88
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	11		IAQFNVVSEAHNEGATIVSVSDGVI R	15	25	5	12.32	b16°b16y4y13°y13	2641.40	136.697	6325	2	1321.21	17.75
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	12	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	3	14.82	b3b7y4	2098.99	47.003	2634	3	700.33	3.02
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	13		VVNTLGAPIDGKGPVDNDGFSAV EAIAPGVIDR	106	33	11	37.03	b4°b4b5°b5b27y3°y3y6°y6 y7y10	3263.70	83.535	54472	3	1088.57	1.35
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	14		VNADYVEAFTKGEVK	303	15	3	17.99	b6y7y9	1669.83	63.145	39845	3	557.28	-10.60
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	15		AARVNADYVEAFTK	300	14	4	24.57	b13°b13y9y10	1554.77	77.744	5666	2	777.89	-12.80
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	16	Carbamidomethyl+C(33)	KLEEHGALANTIVVVATASESAAL QYLAPYAGCAMGEYFR	210	40	7	34.72	b4°b4y3y4°y4y5y7	4272.12	136.248	5559	4	1068.78	1.14
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	17	Oxidation+M(8)	DSVGAVVMGPYADLAEGMK	68	19	7	38.78	b3b8°b8y4y6y7y13	1925.93	57.479	4885	3	642.65	14.45
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	18	Carbamidomethyl+C(32) ;Oxidation+M(34)	LEEHGALANTIVVVATASESAALQ YLAPYAGCAMGEYFRDR	211	41	8	15.02	b4b8°b8b10°b10y5°y5y7	4431.11	136.216	4524	5	887.03	-6.28
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha	19	Oxidation+M(17)	YAIALNLERDSVGAVVMGPYADL AEGMK	59	28	3	22.66	y5y12y13	2969.50	122.750	1818	4	743.13	6.91
P77983 KPYK1_SALTY Pyruvate kinase I	1		GDLGVEIPVEEVIFAQK	244	17	9	54.28	b2°b2b6b7b8y1y3y4y12	1842.99	94.198	31672	2	922.00	3.31
P77983 KPYK1_SALTY Pyruvate kinase I	2		IENQEGLNNFDEILEASDGIMVAR	220	24	5	35.3	b9b10y1y3y4	2677.28	95.773	10976	3	893.10	2.37
P77983 KPYK1_SALTY Pyruvate kinase I	3	Carbamidomethyl+C(3)	IVCTIGPK	5	8	5	49.06	b5y3y6y7y8	887.49	35.467	9899	2	444.25	-9.49
P77983 KPYK1_SALTY Pyruvate kinase I	4		AEAGDVANAILDGTDAVMLSGES AK	292	25	3	18.55	y6y11y16	2405.16	91.623	5375	2	1203.08	3.76
P77983 KPYK1_SALTY Pyruvate kinase I	5		YFPDATILALTNEVTAR	389	18	4	22.86	b7b8y10°y10	1996.03	51.556	14970	3	666.01	-4.40
P77983 KPYK1_SALTY Pyruvate kinase I	6		KYFPDATILALTNEVTAR	388	19	4	23.46	b4b6b8y7	2124.12	83.430	5773	3	708.71	-6.67
P77983 KPYK1_SALTY Pyruvate kinase I	7	Carbamidomethyl+C(3)	VICKVLNNGDLGENK	141	15	5	26.07	y3y4*y4y10°y10	1672.88	125.743	5347	2	836.95	9.19

[P77983]KPYK1_SALTY Pyruvate kinase I	8		NPRPTRAEAGDVANAILDGTDAV MLSGESAK	286	31	4	11.21	b8b10*b10y23	3126.50	75.495	3753	3	1042.84	-14.68
[P77983]KPYK1_SALTY Pyruvate kinase I	9	Oxidation+M(18)	AEAGDVANAILDGTDAVMLSGES AK	292	25	6	22.94	b18y7y8°y8y12°y12	2421.14	81.921	8715	3	807.72	-3.73
[P77983]KPYK1_SALTY Pyruvate kinase I	10	Carbamidomethyl+C(13) ;Oxidation+M(9)	YPLEAVSIMATICER	319	15	4	17.99	b6°b6b11y4	1768.88	100.103	1879	3	590.30	13.46
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	1	Carbamidomethyl+C(20)	GMPVDIHPEEGVPAVELILCR	72	21	8	71.14	b6b7b8b9b13b14y13y15	2331.19	97.247	21007	3	777.74	4.29
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	2		TELFLVEGDSAGGSAK	411	16	5	17.02	b2b15y6y9y16	1580.77	81.113	15348	2	790.89	-8.26
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	3	Carbamidomethyl+C(11)	QGLLDAMREFCEYR	284	14	3	19.13	b3y11y13	1787.82	78.496	4356	3	596.61	-0.34
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	4	Carbamidomethyl+C(2)	QCAAFVSGVVKDAFSLWLNQNV QAAEQLAEMAIAAQR	340	38	6	15.82	b4b12b15y8*y8y10	4122.02	115.930	3261	4	1031.26	-9.24
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	5		LSAEDIWDR	306	9	6	30.3	b4b9y2y4y6y9	1104.54	81.941	3187	1	1104.54	9.28
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	6		LVQLTISDEDDQR	585	13	4	25.25	b11y11°y11y12	1531.79	98.759	20725	2	766.40	19.21
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	7		EYQAIMPLK	432	9	3	38.08	b3b4b8	1092.58	53.678	5194	2	546.79	-0.34
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	8		GDLADLDV	622	8	5	49.06	b3y4y5°y5y6	817.40	128.712	1511	1	817.40	7.24
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	9	Carbamidomethyl+C(14)	LTSGPALPGKLADCTAQDLNR	390	21	4	23.42	y5y6°y6y17	2198.10	115.143	29087	3	733.37	-10.11
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	10		NWLQEKGDLADLDV	616	14	3	19.13	b9b11y5	1615.78	78.706	3548	3	539.27	-7.63
[P0A2I5]PARE_SALTY DNA topoisomerase 4 subunit B	11	Phosphoryl STY(10)	VDVILHADQSLEVIDDGR	54	18	6	39.88	b12*b12b13y7y9_H3PO4 y9y10_H3PO4 y10_HPO3 y10	2073.97	117.913	5920	3	691.99	-3.77
[P65882]PURA_SALTY Adenylosuccinate synthetase	1	Carbamidomethyl+C(19)	VGAGPFPTELFDETGEFLCK	273	20	7	33.2	b11y2y3y6y8y14y20	2214.05	99.535	18103	2	1107.53	5.51
[P65882]PURA_SALTY Adenylosuccinate synthetase	2		VLDDTMAVADILTSMVVDVSDLL DQAR	186	27	7	49.65	b7y4y5y6y7y10°y10	2905.45	138.696	11473	3	969.15	-1.26
[P65882]PURA_SALTY Adenylosuccinate synthetase	3	Carbamidomethyl+C(7)	LLLSEACPLILDYHVALDNAR	97	21	7	41.36	b7y5°y5y6y8y9°y9	2396.26	91.223	9315	3	799.43	-1.53
[P65882]PURA_SALTY Adenylosuccinate synthetase	4		EVTTTPLAADDWK	354	13	3	25.25	b10b11y11	1446.71	80.298	7072	3	482.91	-0.34
[P65882]PURA_SALTY Adenylosuccinate synthetase	5		MGNNVVVLGTQWGDEGK	0	17	11	72.51	b8b15y3y4°y4y5y6°y6y8y1 5°y15	1803.84	75.779	38385	3	601.95	-17.46
[P65882]PURA_SALTY Adenylosuccinate synthetase	6		EVMEYHNFQLVNYK	163	15	3	24.01	b10b11y9	1976.91	83.530	4495	3	659.64	-5.62
[P65882]PURA_SALTY Adenylosuccinate synthetase	7		GLRVGDLFDK	145	10	3	26.73	b9y5y7	1119.63	64.557	10379	2	560.32	13.63
[P65882]PURA_SALTY Adenylosuccinate synthetase	8		GNNVVVLGTQWGDEGKGK	1	18	5	26.38	b6y11y13*y13y14	1857.93	58.355	9455	3	619.98	-8.80
[P65882]PURA_SALTY Adenylosuccinate synthetase	9		EVMEYHNFQLVNYKAEAVDYQ K	163	23	6	37.11	y4y6y7y11y14°y14	2881.36	93.079	5125	3	961.12	1.95
[P65882]PURA_SALTY Adenylosuccinate synthetase	10	Carbamidomethyl+C(19)	VGAGPFPTELFDETGEFLCKQGNE YGATTGR	273	31	4	11.21	b8b16°b16y12	3348.59	94.979	3116	3	1116.87	11.23
[P65882]PURA_SALTY Adenylosuccinate synthetase	11		EMKELEDR	82	8	4	32.9	b3b4y3°y3	1049.49	84.652	2157	2	525.25	-2.09
[P65882]PURA_SALTY Adenylosuccinate synthetase	12	Carbamidomethyl+C(2)	LCVAYRMPDGR	343	11	6	55.2	b7b8y3y7y9°y9	1337.65	119.496	1529	1	1337.65	-0.09
[P65882]PURA_SALTY Adenylosuccinate synthetase	13	Carbamidomethyl+C(11) ;Phosphoryl STY(6)	AVQLNSLSGFCLTK	318	14	3	19.13	b3y7y10	1617.77	39.735	325248	3	539.93	4.83
[P65882]PURA_SALTY Adenylosuccinate synthetase	14	Phosphoryl STY(4)	YVDYVLGILK	258	10	3	26.73	b3y3y8	1262.63	80.296	5448	2	631.82	-5.80

P65882 PURA_SALTY Adenylosuccinate synthetase	15	Oxidation+M(1)	MGNNVVVLGTQWGDEGK	0	17	3	24.83	y4y10y11	1819.87	59.457	5158	3	607.29	1.68
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	1	Carbamidomethyl+C(2); Carbamidomethyl+C(24)	SCPVIELTQQLIRRPSPDDAGCQALMIER	1	31	3	17.07	b5b8b10	3553.78	92.386	11179	3	1185.27	-2.75
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	2		FSTELTDEMIK	257	11	9	64.55	b2b3b6b10y3y5°y5y6y11	1313.62	67.198	7359	2	657.32	-3.72
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	3	Carbamidomethyl+C(4)	LDYCLVGEPSSTEIVGDVVK	154	20	5	40.56	b7b8b11b12b20	2180.05	85.712	5096	2	1090.53	-12.21
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	4		YTVDWWLSGQPFLTAR	281	16	3	25.39	b4b6b7	1939.94	137.285	2001	2	970.48	-13.78
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	5		GETLAFAGHTDVVPAGDVDR	57	20	5	27.75	b7b9b13y11y17	2027.00	104.342	12434	3	676.34	9.88
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	6		GNDFFPATSMQVANIQAGTGSNNVIPGELFVQFNFR	221	36	5	22.22	y3*y3y6y9y18	3887.84	106.003	3108	3	1296.62	-9.36
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	7	Carbamidomethyl+C(5)	GS LTCNLTIHG VQGHVAYPHLADNPVHR	178	28	3	21.85	b9b10y13	3063.48	132.705	2497	4	766.63	-17.93
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	8		LAF LITSDEEASAKNGTVK	124	19	3	22.6	b14b15y11	1994.03	89.391	9186	3	665.35	-6.00
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	9		GRGETLAFAGHTDVVPAGDVDR	55	22	13	74.64	b3b5b7°b7b9b11°b11y3y4y10°y10y11°y11	2240.09	136.245	2681	2	1120.55	-5.23
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	10	Carbamidomethyl+C(2); Carbamidomethyl+C(24)	SCPVIELTQQLIRRPSPDDAGCQALMIER	1	31	3	11.21	b9y11y13	3553.75	116.035	2636	4	889.19	-10.99
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	11	Carbamidomethyl+C(4)	LDYCLVGEPSSTEIVGDVVKNGR	154	23	3	19.36	b3b6b13	2507.22	84.915	1615	2	1254.11	-10.71
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	12	Carbamidomethyl+C(11);Oxidation+M(15)	RPSLSPDDAGCQALMIER	14	18	4	28.95	b14b15y10y13	2031.95	78.672	26389	3	677.99	-2.64
Q8ZN75 DAPE_SALTY Succinyl-diaminopimelate desuccinylase	13	Oxidation+M(8)	IGFTIEHMDFGDTQNFVAWR	35	20	4	19.58	b6b8y5y8	2487.08	101.374	12959	3	829.70	-14.43
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	1	Carbamidomethyl+C(3)	FACGVIEK	169	8	9	66.98	y1y2°y2y3y4y5y6y7y8	923.46	40.759	98462	2	462.23	-7.20
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	2		GGDNYSDKPAPLGGGGAR	151	18	10	40.48	b2b5*b5b10y7y8y10y13°y13y18	1688.78	32.694	71735	3	563.60	-10.70
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	3		EV PALMAGGHLDPEK	84	15	5	25.58	b6b13y10°y10y13	1563.80	57.038	9498	2	782.40	11.94
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	4	Carbamidomethyl+C(21)	GGDNYSDKPAPLGGGGARFACGVIEK	151	26	3	12.06	b17y7y14	2593.24	75.760	4255	4	649.07	-1.13
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	5		GHSLMIHKGGDNYSDKPAPLGGGAR	143	26	4	15.65	b11b13y4y15	2592.25	81.006	2988	3	864.76	-8.29
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	6	Oxidation+M(9)	DGKEVPALMAGGHLDPEK	81	18	3	15.45	b11y7y9	1879.94	72.612	55540	3	627.32	7.99
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1	7	Oxidation+M(6)	EV PALMAGGHLDPEK	84	15	5	36.81	b6b12y4y8y13	1579.78	110.006	1810	2	790.40	2.78
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltri glutamate--homocysteine methyltransferase	1	Carbamidomethyl+C(7)	LWVNPDCLK	719	10	5	41.5	y4y6°y6y8y10	1201.61	60.335	51152	2	601.31	4.47
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltri glutamate--homocysteine methyltransferase	2		QAGIDLLPVGDFAWYDHVLT TSL LLGNV PAR	52	31	11	44.08	b5*b5b6*b6y3y6*y6y7y13y24y31	3351.78	119.216	34842	3	1117.93	2.77
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltri glutamate--homocysteine methyltransferase	3		LA AITAQDSQRENPYEVR	395	18	8	49.88	b2b3b4y1y2y13y14y15	2061.03	46.993	31038	3	687.68	-4.86
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltri glutamate--homocysteine methyltransferase	4		LPVDWLLSAGLINGR	279	15	5	24.01	b4b5°b5y12y15	1623.92	101.237	12930	2	812.46	-3.91

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	5		LAAITAQDSQR	395	11	7	36.49	b2b3y2*y2y3y4y7	1173.62	33.342	11663	2	587.32	2.29
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	6		SDWDAYLEWGVEAFR	611	15	5	17.99	b1b12y6y8°y8	1843.82	113.945	4960	3	615.28	-2.12
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	7		DALNSGETAALEEWSAPIQAR	360	21	5	13.77	b14y3*y3y12°y12	2229.05	88.204	3810	2	1115.03	-13.36
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	3	23.55	b5b6y12	1834.94	98.963	38501	2	917.97	4.46
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	9		WFNTNYHYIVPEFSK	117	15	4	17.99	b9y4°y4y6	1944.90	51.687	21282	2	972.95	-15.00
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	10		LPAPWPTTTIGSFQTTEIR	422	19	3	23.99	y10y11y13	2116.08	77.882	6193	3	706.03	-13.15
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	11		GEPFDR	174	6	2	26.71	y4y5	720.34	54.827	3377	1	720.34	7.71
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	12		NDMVEYFGEHLDDGFVFTQNGWV QSYGSR	487	28	7	34.54	y3y5°y5y10y12*y12y14	3282.52	94.256	2611	3	1094.85	19.26
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	13		RSDWDAYLEWGVEAFR	610	16	3	17.02	b3y6y11	1999.96	101.322	81249	3	667.32	13.12
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	14		FKLPAPWPTTTIGSFQTTEIR	420	21	4	13.77	b14y7*y7y9	2391.26	88.445	40006	3	797.76	-4.29
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	15		LPAPWPTTTIGSFQTTEIRGLR	422	22	6	48.96	b3b4b5b6°b6y21	2442.29	136.263	8959	3	814.77	-8.20
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	16		TRGWPETR	729	8	3	32.9	b4b5y6	1002.50	110.688	2877	1	1002.50	-11.20
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	17		LAAITAQDSQRENPYEVR	395	18	4	22.86	b13°b13y9y10	2061.01	62.926	2180	2	1031.01	-10.66
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	18	Oxidation+M(12)	APTGEPA AAAEMTK	103	14	3	24.57	b9y3y4	1360.65	57.508	13739	2	680.83	7.00
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	19		SQRENPYEVR	403	10	1	7.35	b9	1277.62	47.075	2275	2	639.31	-6.40
P66955 TALB_SALTY Transaldolase B	1		LSYDTEASIAK	100	11	4	35.89	y8y9y10y11	1197.60	43.827	17034	2	599.30	-0.10
P66955 TALB_SALTY Transaldolase B	2		ELAESEGAIER	250	11	5	35.89	y7y8y9°y9y11	1203.59	35.906	15858	2	602.30	7.00
P66955 TALB_SALTY Transaldolase B	3	Carbamidomethyl+C(11)	NVGEILELAGCDR	228	13	3	20.48	b12y4y8	1445.71	73.616	13059	2	723.36	3.88
P66955 TALB_SALTY Transaldolase B	4		LYNDAGISNDR	117	11	3	24.13	b7y4y7	1237.59	35.415	17312	2	619.30	6.12
P66955 TALB_SALTY Transaldolase B	5		MIGDLL	311	6	1	13.56	b4	661.36	17.539	1778	2	331.18	2.03
P66955 TALB_SALTY Transaldolase B	6		LIDDAVAWAKQSSDR	50	16	4	28.13	b4y3y4y9	1802.91	53.862	2078	3	601.64	1.83
P05989 ILVC_SALTY Ketol-acid reductoisomerase	1		GFGVPTLIAPHENDPQGEGMAIA K	167	25	10	52.15	b2b3b4b13y3y8y12y14y21 y25	2548.28	76.738	51403	3	850.10	-0.67

P05989 ILVC_SALTY Ketol-acid reductoisomerase	2		LIQFGWETITEALK	252	14	4	19.13	b2b6y3y11	1648.88	101.237	22286	2	824.95	-5.92
P05989 ILVC_SALTY Ketol-acid reductoisomerase	3		TAFETAPQYEGK	336	12	4	22.11	b3y5y7y12	1341.64	41.123	19307	2	671.32	3.73
P05989 ILVC_SALTY Ketol-acid reductoisomerase	4	Carbamidomethyl+C(6)	VVIVGCGAQGLNQLNMR	39	18	5	24.62	b12y3*y3y5y12	1885.98	63.864	5299	2	943.49	1.42
P05989 ILVC_SALTY Ketol-acid reductoisomerase	5		LVAEGTDPAYAEK	239	13	3	20.48	b11y5y11	1363.67	37.206	5169	2	682.34	-1.61
P05989 ILVC_SALTY Ketol-acid reductoisomerase	6		ANYFNTLNLR	1	10	3	28.49	b5y6y7	1225.63	67.640	23724	2	613.32	-4.58
P05989 ILVC_SALTY Ketol-acid reductoisomerase	7		DITVVMVAPK	145	10	3	26.73	b3b8y6	1072.63	60.393	8361	2	536.82	21.28
P05989 ILVC_SALTY Ketol-acid reductoisomerase	8		LLTWR	326	5	1	13.15	y4	688.42	54.311	3383	2	344.71	9.66
P05989 ILVC_SALTY Ketol-acid reductoisomerase	9		DEFADGASYLQGK	25	13	3	20.48	b3y7y10	1400.66	44.743	2072	2	700.83	19.87
P05989 ILVC_SALTY Ketol-acid reductoisomerase	10		AWAAATGGHR	192	10	3	26.73	b6y3y5	997.48	111.178	1994	1	997.48	-17.44
P05989 ILVC_SALTY Ketol-acid reductoisomerase	11		DGAALGYSHGFNIVEVGEQIR	123	21	10	44.37	b5b8b9b12°b12y7°y7*y7y8°y8	2232.14	136.276	1786	3	744.72	16.95
P05989 ILVC_SALTY Ketol-acid reductoisomerase	12		VGTYEELIPQADLVVNLTDPDKQHS DVVR	88	28	4	17.19	b8y6y14y20	3135.61	81.254	32389	4	784.66	-7.01
P05989 ILVC_SALTY Ketol-acid reductoisomerase	13	Carbamidomethyl+C(11)	DITVVMVAPKCPGTEVR	145	17	9	57.32	b12b14y3y6°y6y7y8°y8y11	1871.97	57.392	18667	2	936.49	-0.91
P05989 ILVC_SALTY Ketol-acid reductoisomerase	14	Carbamidomethyl+C(11) ;Carbamidomethyl+C(21))	SDLMGEQTILCGMLQAGSLLCFD KLVAEGTDPAYAEK	215	37	6	37.44	b3b12y6°y6y7y8	4031.91	117.634	16330	3	1344.64	-0.97
P05989 ILVC_SALTY Ketol-acid reductoisomerase	15		TAFETAPQYEGKIGEYFDK	336	21	6	29.51	b5b6b9y3y10°y10	2451.11	80.087	3147	3	817.71	-11.55
P05989 ILVC_SALTY Ketol-acid reductoisomerase	16		EETGKTAFETAPQYEGK	331	17	5	25.94	b5°b5b8b14y11	1885.86	72.636	2427	3	629.29	-13.27
P05989 ILVC_SALTY Ketol-acid reductoisomerase	17	Oxidation+M(6)	SVQPLMKDGAALGYSHGFNIVEV GEQIR	116	28	12	65.61	b3°b3b5b8°b8*b8b9b11°b11b14b18b24	3031.53	136.250	6432	3	1011.18	0.64
P05989 ILVC_SALTY Ketol-acid reductoisomerase	18	Oxidation+M(21)	GFGVPTLIAVHPENDPQGEGMAIA K	167	25	4	12.32	b6y10°y10y15	2564.28	99.415	2322	3	855.43	-0.19