

MA6926 + Zn(II) LC-MS run 3: 6926_Zn_220709_1a2_03

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)
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	1		AAADLQLQGVPAMFVNGK	158	18	28	247.05	b2b4b5b6b7b8b9b10b12b14b18y2y3*y3y4y5y6y7y8*y8y9y10y11*y11y12*y12y14y18	1829.97	80.521	219558	2	915.49	4.54
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	2		YQINPQGMDTSSMDVVFVQQYADTVK	176	25	21	125.73	b2*b2b3b4b6b7b9y1y3y4y5y6y7*y7y8*y8y9*y9y12*y12y25	2865.31	86.186	113273	3	955.78	1.62
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	3		TQTVQSAADIR	116	11	14	55.96	b2°b2*b2b3°b8b11y2y6y7°y7*y7y8y9y11	1189.61	35.194	57732	2	595.31	-4.82
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	4		YHVEFLGPLGK	77	11	8	52.95	b2b3b4b5b10y1y2y3	1259.67	70.518	36297	2	630.34	-6.88
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	5		ELTQAWAVAMALGVEDK	88	17	4	16.31	b5°b5b10y10	1831.90	45.372	1869	3	611.31	-13.39
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	6		SLVAQQEKAAADLQLQGVPAMFVNGK	150	26	5	18.28	b14°b14y6y10y13	2713.42	81.337	11995	3	905.14	-6.12
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	7		VFVDAGVKGEDYDAAWSFVVVK	128	22	4	13.43	b6b13°b13y11	2416.20	71.370	9131	3	806.07	6.06
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	8	Phosphoryl STY(3)	ELTQAWAVAMALGVEDK	88	17	4	23.3	b14y13y14°y14	1911.91	101.287	1643	3	637.97	13.86
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	9	Oxidation+M(10)	ELTQAWAVAMALGVEDK	88	17	8	40.98	b7°b7b8°b8b11°b11y8y9	1847.90	136.258	2777	2	924.45	-11.43
P0A2H9 DSBA_SALTY Thiol:disulfide interchange protein dsbA;	10		PAMFVNGK	168	8	2	20.9	b3b4	863.44	80.515	7059	1	863.44	-8.77
P0A1D5 CH10_SALTY 10 kDa chaperonin;	1		VGDIVIFNDGYGVK	60	14	19	202.1	b3b4b5°b5b6b13°b13y3y4y5y6y7y8y9y10y11y12y13y14	1495.77	73.295	202249	2	748.39	-4.49
P0A1D5 CH10_SALTY 10 kDa chaperonin;	2		ILDNGTVQPLDVK	47	13	26	195.47	b2b7°b7b8°b8b9b10b11°b11y2y3y4y5y6*y6y7y8y9y10y11°y11*y11y12*y12y13*y13	1411.78	57.325	189411	2	706.39	-2.51
P0A1D5 CH10_SALTY 10 kDa chaperonin;	3		SAGGIVLTGSAAGK	20	14	20	141.45	b2b3°b3b4b5°b5b6°b6b11b14y2y3y4y6y7y8°y8y9y12y14	1188.65	43.672	116246	2	594.83	-6.88
P0A1D5 CH10_SALTY 10 kDa chaperonin;	4		GEIIAVGK	37	8	6	54.08	y2y3y4y5y6y8	786.46	41.597	23811	2	393.74	-10.79
P0A1D5 CH10_SALTY 10 kDa chaperonin;	5		SIRPLHDR	1	8	6	36.09	b1b3°b3b7y5y8	993.55	26.969	4087	2	497.28	-9.21
P0A1D5 CH10_SALTY 10 kDa chaperonin;	6		STRGEIIAVGK	34	11	5	55.5	b3b5b8y3y4	1130.65	37.928	50233	2	565.83	-6.80
P0A1D5 CH10_SALTY 10 kDa chaperonin;	7		SEKIDNEEVLIMSESILAIVEA	74	23	5	19.45	b5°b5b10°b10b18	2547.29	136.252	2032	3	849.77	4.41
P0A1D5 CH10_SALTY 10 kDa chaperonin;	8	Phosphoryl STY(10)	IDNEEVLIMSESILAIVEA	77	20	3	14.37	b3b8y10	2283.04	98.400	9111	4	571.52	-7.91
P0A1D5 CH10_SALTY 10 kDa chaperonin;	9		SAGGIVLTGSAAGK	20	14	0	3.64		1170.64	43.617	18736	2	585.82	-2.29

[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	1		EMLIADGIDPNELLNSMAAAK	62	21	47	342.54	b2°b2b3°b3b4°b4b5°b5b6° b6b7°b7b8°b8b9b10b12°b1 2b13b14°b14b18b21y1y2y 3y4y5y6y7°y7*y7y8y9y10y 12*y12y13°y13y14°y14y15 y16y17°y17y18y21	2216.11	96.512	436549	2	1108.56	9.36
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	2		YSYVDENGETK	96	11	9	84.74	b2y2y3y5y7y8y9y10y11	1304.56	32.779	64190	2	652.79	-0.19
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	3		REEESAAAAEVEER	40	14	7	38.52	b6b7°b7b8y2y3y14	1575.73	31.873	41221	2	788.37	4.88
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	4		TPAVIKK	114	7	10	50.67	b1°b1b2°b2b3y2y3y4y5y7	756.49	19.422	22788	2	378.75	-14.12
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	5	Carbamidomethyl+C(6)	AQARECTLETLEEMLEK	15	17	7	27.39	b1b5°b5°b5b6b11y10	2050.99	56.626	4481	3	684.33	4.64
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	6	Carbamidomethyl+C(2)	ECTLETLEEMLEK	19	13	4	20.63	b7°b7y7y9	1624.77	88.106	1582	3	542.26	16.98
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	7		YSYVDENGETKTWTGQGR	96	18	17	108.51	b3°b3y4°y4y5y6y7y8*y8y1 1°y11y12*y12y14*y14y17° y17	2090.93	46.733	147245	3	697.65	-7.24
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	8	Carbamidomethyl+C(2)	ECTLETLEEMLEKLEV VNER	19	21	3	22.32	b14y3y4	2563.24	71.954	12713	3	855.09	-8.29
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	9		EMLIADGIDPNELLNSMAAAKSGT K	62	25	3	35.19	b7b8b9	2589.28	90.400	10016	3	863.77	-2.45
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	10	Carbamidomethyl+C(6)	AQARECTLETLEEMLEK	15	17	4	26.14	b8b10b12y4	2050.95	63.158	2132	2	1025.98	-12.97
[P0A1S2]HNS_SALTY DNA-binding protein H-NS;	11	Oxidation+M(17)	EMLIADGIDPNELLNSMAAAK	62	21	9	44.84	b3b5b8°b8b10°b10y5y10y1 2	2232.06	104.270	1868	3	744.69	-13.89
[P0A1H5]EFTU_SALTY Elongation factor Tu;	1		AIDKPFLPIEDVFSISGR	205	19	21	153.38	b2b3b4°b4b7b8b9y1y2y3y 4y5y6°y6y7y8y9°y9y11y15 y19	2117.14	104.358	364011	3	706.39	-9.57
[P0A1H5]EFTU_SALTY Elongation factor Tu;	2		TTLTAAITVLAK	25	13	16	140.17	b2°b2b4°b4b5°b5y2y3y4y5 y6y7y8y9y10y11	1303.77	84.312	284800	2	652.39	-6.83
[P0A1H5]EFTU_SALTY Elongation factor Tu;	3		ELLSQYDFPGDDTPIVR	155	17	26	188.84	b2°b2b6°b6°b6b7b9b13b1 6y1y2y3y4y5y6y8y9°y9y10 °y10y11y12°y12y13y14y17	1964.97	76.619	229683	2	982.99	6.15
[P0A1H5]EFTU_SALTY Elongation factor Tu;	4		IIELAGFLDSYIPEPER	188	17	31	251.41	b2b3b4b5b6b7b12°b12b14 y1y2y3°y3y4°y4y5°y5y6y7 y8°y8y9°y9y10°y10y11y12 y13y14y15y17	1962.03	101.590	209617	2	981.52	3.61
[P0A1H5]EFTU_SALTY Elongation factor Tu;	5		AGENVGVLLR	270	10	7	68.11	y2y3y4y5y6y7y10	1027.58	56.240	191403	2	514.29	-11.29
[P0A1H5]EFTU_SALTY Elongation factor Tu;	6		GITINTSHVEYDTPTR	59	16	20	180.45	b2b3°b3b9b10b12y3y4y5y 6y7°y7y8y9y10y12*y12y13 y14y16	1803.86	49.410	185236	3	601.96	-13.40
[P0A1H5]EFTU_SALTY Elongation factor Tu;	7		QVGVPYIIVFLNK	124	13	8	47.86	b3b4°b4b13y4y9y11y13	1489.87	98.706	183214	2	745.44	-4.59
[P0A1H5]EFTU_SALTY Elongation factor Tu;	8		TTDVTGTIELPEGVEMVMPGDNI K	334	24	32	190.07	b1b2b3°b3b4b5°b5b8°b8b1 0°b10b16b17°b17b18°b18y 3y5y6°y6°y6y7y8y9y10*y1 0y12y14°y14y15y20y24	2546.26	86.406	180617	2	1273.63	8.73
[P0A1H5]EFTU_SALTY Elongation factor Tu;	9		ALEGDAEWEAK	177	11	11	81.94	b2b6b9y1y2y4y6y7y8y9y1 1	1218.56	46.108	118469	2	609.78	-3.51
[P0A1H5]EFTU_SALTY Elongation factor Tu;	10	Carbamidomethyl+C(3)	STCTGVEMFR	253	10	6	51.88	y4y6y7°y7y8y10	1187.51	52.686	99774	2	594.26	-3.19

P0A1H5 EFTU_SALTY Elongation factor Tu;	11	Carbamidomethyl+C(1)	CDMVDDEELLELVEMEV	137	18	10	54.85	b2b3y2y3y5°y5y6y7y8y18	2224.00	105.670	34829	2	1112.51	9.99
P0A1H5 EFTU_SALTY Elongation factor Tu;	12		VGEEVEIVGIK	238	11	9	50.52	b2b4b7°b7b8b10b11y2y11	1171.67	44.920	19547	2	586.34	9.38
P0A1H5 EFTU_SALTY Elongation factor Tu;	13		GQVLAKPGTIKPHTK	289	15	5	18.13	b5°b5y2y3y9	1574.92	29.474	3663	3	525.64	-11.24
P0A1H5 EFTU_SALTY Elongation factor Tu;	14		MVVTLIHPIAMDDGLR	358	16	20	193.16	b3b4°b4b5°b5y3y4y5y6°y6y7y8°y8y9y10°y10y11y12y13y15	1780.91	78.779	502983	3	594.31	-17.62
P0A1H5 EFTU_SALTY Elongation factor Tu;	15		TVGAGVVAK	382	9	3	38.26	y3y7y8	801.47	28.367	118292	2	401.24	-17.59
P0A1H5 EFTU_SALTY Elongation factor Tu;	16		EHILLGR	117	7	3	37.45	b3y4y5	837.48	40.751	35597	2	419.24	-16.62
P0A1H5 EFTU_SALTY Elongation factor Tu;	17		LLDEGR	264	6	2	26.84	b4y5	702.37	28.183	7085	1	702.37	-12.34
P0A1H5 EFTU_SALTY Elongation factor Tu;	18	Carbamidomethyl+C(7)	HYAHVDCPGHADYVK	75	15	3	18.13	b9y4y6	1768.76	35.823	6310	4	442.95	-12.15
P0A1H5 EFTU_SALTY Elongation factor Tu;	19		NMITGAAQMDGAILVVAATDGP MPQTR	90	27	3	11.9	b10y7y13	2729.36	92.435	6302	3	910.46	5.28
P0A1H5 EFTU_SALTY Elongation factor Tu;	20		TKPHVNVGTIGHVDHGK	8	17	4	16.31	b7y4y10°y10	1795.92	39.323	2603	4	449.74	-19.78
P0A1H5 EFTU_SALTY Elongation factor Tu;	21		GTVVTGRVER	224	10	3	26.9	b9y3y8	1073.60	25.814	60094	2	537.30	-8.53
P0A1H5 EFTU_SALTY Elongation factor Tu;	22	Carbamidomethyl+C(14)	QVGVPYIIVFLNKCDMVDDEELLE LVEMEV	124	31	6	62.25	b7y4y5y6y7y8	3694.87	127.074	23825	3	1232.29	7.07
P0A1H5 EFTU_SALTY Elongation factor Tu;	23		ALEGDAEWEAKIILAGFLDSYIPE PER	177	28	8	53.76	b11b12y4y5y6y9y12°y12	3161.55	124.236	5438	3	1054.52	-4.40
P0A1H5 EFTU_SALTY Elongation factor Tu;	24		AFDQIDNAPEEKAR	45	14	4	27.57	b3b5y11y13	1603.78	83.356	4876	2	802.39	3.58
P0A1H5 EFTU_SALTY Elongation factor Tu;	25		ARGITINTSHVEYDTPTR	57	18	5	26.57	b4y6y10°y10y11	2031.03	40.022	2095	3	677.68	3.91
P0A1H5 EFTU_SALTY Elongation factor Tu;	26	Oxidation+M(1)	MVVTLIHPIAMDDGLR	358	16	3	25.53	y5y8y9	1796.91	73.480	19930	3	599.64	-14.61
P0A1H5 EFTU_SALTY Elongation factor Tu;	27	Oxidation+M(2)	NMITGAAQMDGAILVVAATDGP MPQTR	90	27	7	21.9	b8y5°y5°y5y6°y6°y6	2745.31	71.193	2525	4	687.08	-10.58
P0A1H5 EFTU_SALTY Elongation factor Tu;	28	Oxidation+M(18)	TTDVTGTIELPEGVEMVMPGDNI K	334	24	4	35.46	b13y7y8y9	2562.25	79.167	1981	2	1281.63	5.81
P0A1H5 EFTU_SALTY Elongation factor Tu;	29		ENVGVLLR	272	8	0	2.02		899.52	56.315	3846	2	450.26	-13.77
P0A1H5 EFTU_SALTY Elongation factor Tu;	30		PIEDVFSISGR	213	11	2	13.18	b5b7	1219.62	104.354	1874	2	610.31	-12.71
P0A1H5 EFTU_SALTY Elongation factor Tu;	31		GITINTSHVEYDTPTR	59	16	0	4.45		1785.86	49.406	11101	3	595.96	-7.04
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha;	1		IAAANVPAFVSGK	70	13	27	190.7	b2b3b4b5°b5b6°b6b10y1y2y3°y3y4°y4y5y6y7°y7y8y9y10°y10y11°y11°y11y12y13	1244.69	59.409	830104	2	622.85	-4.41
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha;	2		AALESTLAAITESLKEGDAVQLVG FGTFK	22	29	33	262.01	b2b3b4b6°b6b7b8b9b12b13b16b23b26y1y2y3y4y6°y6y7y8y10y11°y11y13y14y17y19y21y22y24y25y29	2966.57	114.615	525740	3	989.53	0.74
P0A1R6 DBHA_SALTY DNA-binding protein HU-alpha;	3		AALESTLAAITESLK	22	15	6	48.38	b3b6b7y5y12y14	1517.81	96.656	14720	2	759.41	-20.83

[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	1		LADPNTASPYASYLQYGHIANIDD IIAGKKPATDLGVK	125	38	36	232.74	b2b3b4°b4b5°b5b6°b6°b6b7°b7°b7b8°b8°b8b10b11b13y2y3y4y6y8y9y11y12y16y19y22y23y27y30y31y35y36y38	4001.01	82.901	371412	5	801.01	-13.30
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	2		AEQQLDKDSAIVPVYYYVNAR	494	21	27	212.59	b2b4b5°b5b6b7°b7b8b9°b9b10°b10b11°b11b12y1y3°y3y4y5y6y7y8y9°y9y10y21	2442.22	72.882	178788	3	814.75	-3.60
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	3		LVEPEWFK	352	8	9	67.3	y2y3y4°y4y5y6°y6y7y8	1047.54	70.879	155000	2	524.27	-9.21
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	4		WSDGTPVTAHDFVYSWQR	107	18	15	162.93	b12y3y4y5y6y7y8y9y10y11y12y13y15°y15y18	2151.98	72.201	108938	3	718.00	-5.33
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	5		SGEIDMTYNNMPIELFQK	263	18	12	77.57	b2b3b11b15y2y3y4y5y9y11y14y18	2130.00	86.336	89886	2	1065.51	7.22
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	6	Carbamidomethyl+C(4)	AGWCADYNEPTSFLNTMLSDSSN NTAHYK	439	29	15	99.15	b4y2y3y4y6°y6y7y8y9y10°y10y11y13y20y29	3294.43	89.809	86702	3	1098.81	4.89
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	7		ALDDHTFEVTLSEPVYFYK	163	20	10	49.71	b6b9b10°b10y5y7y9°y9y11y20	2371.14	85.833	86535	3	791.05	-4.12
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	8		TVINQVTYLPISSEVTDVNR	241	20	29	166.13	b2°b2b3b4b5°b5b8°b8°b8b9°b9y2°y2y3y4°y4y5°y5y6°y6y7y8°y8y11y12°y12y14y15y20	2248.20	76.972	77903	2	1124.60	8.04
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	9		NLGVNVNLENQEWK	410	14	13	80.13	b1°b1b2b3b10b11y1y7y8y10y11y12y14	1656.84	66.611	76650	2	828.92	3.17
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	10		NQGDLPAYSYTPPYTDGAK	333	19	13	98.7	b5b11°b11y3y5y6y8°y8y11y13y14y16y19	2057.96	58.990	71961	2	1029.49	9.49
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	11		HQGTFDVAR	430	9	6	61.68	b5y3y4y5y6°y6	1030.50	32.501	61395	2	515.75	-9.24
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	12		LADPNTASPYASYLQYGHIANIDD IIAGK	125	29	7	25.98	b3b12b13b15y1y3y29	3091.55	88.031	27832	3	1031.19	4.26
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	13		NPQYWDNAK	232	9	4	30.48	b8y3y6°y6	1135.51	39.388	44318	2	568.26	-3.23
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	14		NWVVNER	220	7	3	37.45	b4b5y3	916.46	43.536	42021	2	458.73	-5.53
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	15		TFLDTR	424	6	1	13.62	b4	752.39	43.704	18746	1	752.39	-3.41
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	16		NNGSEVQSLDPHK	43	13	5	41.33	b4b6y4y7y8	1424.68	92.360	3666	2	712.84	2.48
[P06202]OPPA_SALTY Periplasmic oligopeptide-binding protein;	17		DLFEGLLISDVEGHPSPGVAEK	67	22	3	13.43	b7y6y11	2309.12	69.832	3225	3	770.38	-21.25

P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	18	Carbamidomethyl+C(6)	VDPYLCTYYYEINNQK	291	16	8	35.43	b3b6°b6y6*y6y9*y9y10	2082.98	116.916	2902	3	695.00	15.59
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	19		TVINQVTYLPISSEVTDVNRYS	241	22	12	116.79	y5*y5y9y13*y13y14y15y16y17y18y19y20	2567.34	76.857	110357	3	856.45	-2.47
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	20		FGDKWTQPANIVTNGAYK	200	18	3	15.58	b16y3y7	2009.99	63.133	45172	3	670.67	-7.41
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	21		VADDTQRSELYAK	481	13	3	20.63	b10y3y11	1495.72	30.574	38305	3	499.24	-14.12
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	22	Carbamidomethyl+C(13)	EIPNEVRVDPYLCTYYYEINNQK	284	23	4	13.04	b13°b13y12y21	2920.39	75.979	31037	3	974.14	3.43
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	23	Carbamidomethyl+C(6)	VDPYLCTYYYEINNQKAPFNDVR	291	23	4	35.56	b9y3y4y5	2882.36	76.163	21449	3	961.46	4.49
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	24		VKNQGDLPAYSYPPTYDGAK	331	21	6	61.77	y7y8°y8y9y10y11	2285.10	54.942	19313	3	762.37	-2.56
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	25		NLGVNVNLENQEWKTFDTR	410	20	5	22.61	b4b11b13°b13y9	2390.20	84.768	18151	3	797.41	-2.86
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	26		NPQYWDNAKTVINQVTYLPISSEVTDVNR	232	29	8	39.87	b3y4y7*y7y10y11y12°y12	3364.70	101.587	15676	3	1122.24	6.53
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	27		IVLERNPQYWDNAK	227	14	3	27.85	y3y5y9	1745.92	87.818	9665	2	873.46	11.40
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	28		DLFEGLLISDVEGHSPGVAEKWENK	67	26	3	12.14	b4y7y14	2866.45	99.303	4643	3	956.15	8.26
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	29		NNGSEVQSLDPHKIEGVPESNVSR	43	24	3	12.7	b4b14y8	2592.27	116.992	3917	3	864.76	0.09
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	30		ASYLQYGHIANIDDIAGKKPATDLGVK	135	28	4	36.82	b3b6b7b8	2971.63	82.897	3395	4	743.66	14.71
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	31		LADPNTASPYASYLQYGHIANIDDIAG	125	28	0	13.35		2963.44	82.916	1952	2	1482.22	-0.82
P06202 OPPA_SALTY Periplasmic oligopeptide-binding protein;	32		HQGTFDVAR	430	9	0	1.62		1013.47	32.535	6982	2	507.24	-9.46
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	1		VINDNFGIIEGLMTTVHATTATQK	160	24	44	296.9	b2b3*b3b4°b4*b4b5*b5b6°b6*b6b7°b7*b7y1y3y4y5y6y7°y7*y7y8y9y10y11*y11y14*y14y15°y15*y15y16°y16*y16y17y18y19y20y22°y22y23y24*y24	2574.32	97.615	502605	3	858.78	-0.57
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	2		AGIALNDNFVK	296	11	17	115.36	b3b4b5y1y2y3y4*y4y5°y5*y5y6*y6y7*y7y8y11	1161.62	61.253	218910	2	581.31	-7.15
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	3		LVSWYDNETGYSNK	307	14	13	123.46	b3b6b7b11y3y5y6y9y10y11y12*y12y14	1675.76	58.134	164628	2	838.39	2.33

[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	4		GASQNIIPSSTGAAK	198	15	23	168.29	b3b6°b6*b6b7°b7*b7b8b1 1b15y2y3y4y5y6y7°y7y8y9 y10y11*y11y15	1401.72	40.849	157800	2	701.37	-7.58
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	5		AATYEQIK	249	8	7	49.31	b5b8y4°y4y5y6y8	923.47	30.833	107351	2	462.24	-11.43
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	6		VLDLIAHISK	321	10	8	88.52	b3b4y2y3y4y5y6y8	1108.66	65.065	106007	2	554.83	-9.25
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	7		SDIEIVAINDLLDAEYMAYMLK	24	22	15	133.93	b3°b3b4b5b6b7y4y5y7y8y 9y10y11°y11y22	2530.24	125.851	76228	3	844.08	-2.22
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	8		VPTPNVSVVDLTVR	232	14	5	38.73	y5y8y11y12y14	1495.85	70.778	52516	2	748.43	0.16
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	9		VLPELNGK	217	8	8	54.08	b2y3y4y5°y5y6°y6y8	869.50	44.749	41714	2	435.25	-13.83
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	10		TVDGPSHKDWR	184	11	8	41.32	b8b9°b9y2y7°y7y8y11	1297.62	28.070	18460	2	649.32	-3.29
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	11		VGINGFGR	4	8	7	51.07	b2b5b7y6*y6y7y8	819.45	41.961	14137	2	410.23	2.76
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	12		WDEVGVDVVAEATGIFLTDETAR	84	23	6	17.48	b8b13°b13y10y13°y13	2493.19	69.043	3397	4	624.05	-9.01
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	13		DNTPMFVK	124	8	3	33.08	b6y4y5	951.47	48.327	3002	1	951.47	10.46
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	14		GANFDK	132	6	1	13.62	y4	651.31	52.260	2985	1	651.31	7.50
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	15		AAAEGEMK	261	8	3	36.09	b4y4y6	806.38	112.198	1759	1	806.38	6.81
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	16	Carbamidomethyl+C(18) ;Carbamidomethyl+C(22))	GANFDKYEGQDIVSNASCTTNCL APLAK	132	28	32	246.11	b4b5b7b8b10*b10b11*b11 b12°b12*b12b13b16b22b2 4*b24b27y3y4y5y6y8y10y 11y12°y12*y12y13y14y15 *y15y16	3044.41	66.489	234802	3	1015.47	0.24
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	17		TVDGPSHKDWR	184	11	3	27.31	b3y7y8	1297.63	27.055	8921	2	649.32	-2.54
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	18		KHITAGAK	107	8	5	57.09	b3y3y5°y5y7	825.49	12.583	7512	2	413.25	-10.13
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	19		DNTPMFVKGANFDK	124	14	4	19.28	b10b13y12*y12	1583.75	136.800	7108	1	1583.75	1.62
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	20		SDIEIVAINDLLDAEYMAYMLKYD STHGR	24	29	5	16.9	b4b6b15y11°y11	3346.60	81.973	4682	3	1116.20	-0.07
[P0A1P0]G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	21		VINDNFGIIEGLMTTVHATTATQK TVDGPSHK	160	32	3	11.14	b5y5y8	3395.74	119.139	2907	3	1132.59	4.96

P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	22		AAVKAAAE GEMK	257	12	3	22.27	b4y7y9	1175.60	82.947	2568	2	588.30	-6.33
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	23	Oxidation+M()	SDIEIVAINDLLAEY MAYMLK	24	22	3	13.43	b5y8y13	2546.23	121.116	2651	3	849.42	-2.49
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	24		DLIAHISK	323	8	1	8.25	b6	896.51	65.062	32519	2	448.76	-14.09
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	25		LDLIAHISK	322	9	1	8.25	b6	1009.59	65.070	32054	2	505.30	-11.43
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	26		LNDNFVK	300	7	2	21.87	b3b4	849.44	61.208	7203	1	849.44	-9.99
P0A1P0 G3P1_SALTY Glyceraldehyde-3-phohate dehydrogenase;	27		AATYEQIK	249	8	0	1.21		905.46	30.813	37803	2	453.23	-6.74
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	1		SSIPVFGVDALPEALALVK	250	19	20	172.71	b4°b4b6°b6b9y1y2y3y4y6y8y9y10y11y12y13y14y15y16y19	1926.10	107.465	91307	2	963.55	3.04
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	2		ALAINLVDPAAGTVIEK	84	18	15	87.19	b2b3b4b5°b5b6y2°y2y3y6y10y11°y11y14y18	1766.01	80.255	73088	2	883.51	3.87
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	3		SGAMAGTVLNDANNQAK	269	17	21	117.69	b2°b2b3b4b9b17y1y2y4*y4y5y6y8y9*y9y10y11y12°y12*y12y17	1661.80	46.111	68069	2	831.40	3.67
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	4		VPYVGVDKDNLSFTQK	315	17	7	43.82	b3b12b13y4y6y13y17	1938.96	61.485	33214	3	646.99	-8.37
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	5		MDAWLSGPNANK	214	12	5	44.91	y3y9y10*y10y11	1303.60	49.332	19094	2	652.31	-5.43
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	6		GIQTEQLALDTAMWDTAQAKDK	192	22	6	29.74	b3b8b11°b11°b11b13	2434.22	63.239	18712	4	609.31	10.43
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	7		ESGVIQGDLIAK	136	12	5	34.24	b7°b7y3y6y7	1229.66	53.666	8507	2	615.34	-7.94
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	8		HWQANQGWDLNK	148	12	4	37.25	b4y7y9y11	1496.72	62.486	2267	3	499.58	8.97
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	9		GIQTEQLALDTAMWDTAQAK	192	20	6	25.24	b7°b7b11b12°b12y4	2191.12	84.712	5997	3	731.04	20.95
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	10		NLAEGK	293	6	2	26.84	b5y3	631.33	46.713	5529	1	631.33	-10.05
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	11		GEPGHPDAEAR	170	11	6	38.31	b3b5y6°y6y7°y7	1135.50	98.406	2614	1	1135.50	-9.03
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	12		SAPDVQLLMNDSQNDQSKQNDQIDVLLAK	52	29	3	21.94	b9b10y15	3227.57	93.588	60456	3	1076.53	-3.40
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	13		ATFDLAKNLAEGK	286	13	4	39.2	b5b6y4y5	1377.74	72.772	18848	2	689.37	-1.59

P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	14		IGVTIYKYDDNFMSVVR	27	17	3	16.31	b12y8y12	2020.00	77.796	16835	3	674.01	-9.13
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	15		GAADGTSWKIENK	299	13	5	49.11	b3b5b8b12*b12	1376.66	54.100	12061	3	459.56	-12.50
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	16		ESGVIQGDLIAKHWQANQGWDL NK	136	24	3	19.01	b3b5b11	2707.38	72.746	7337	5	542.28	9.56
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	17		SGAMAGTVLNDANNQAKATFDL AK	269	24	4	19.01	b3°b3b6b10	2408.17	57.714	5415	2	1204.59	-5.47
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	18		SSIPVFGVDALPEALALVKSGAMA GTVLNDANNQAK	250	36	5	10.89	b10b13°b13y3*y3	3568.82	73.731	5345	4	892.96	-13.34
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	19		DGKSAPDVQLLMNDSQNDQSK	49	21	3	22.32	b6y3y4	2290.04	58.923	4154	3	764.02	-11.30
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	20		GEPGHPDAEARTTYVVK	170	17	4	16.31	b3°b3b6y11	1826.91	80.298	2462	3	609.64	3.01
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	21		NLAEGKGAADGTSWK	293	15	5	37.88	b9y4y5°y5y6	1504.73	63.310	2321	2	752.87	-2.84
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	22		ELNDKGIQTEQLALDTAMWDTAQ AK	187	25	3	18.62	y6y8y13	2790.39	79.803	1675	2	1395.70	8.84
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	23	Oxidation+M(4)	SGAMAGTVLNDANNQAK	269	17	4	16.31	b3°b3b9y3	1677.80	44.892	13802	3	559.94	10.11
P23905 DGAL_SALTY D-galactose-binding periplasmic protein;	24	Oxidation+M(8)	VLTL SAVMASLLFGAHAHAADTR	4	23	3	23.13	y6y7y11	2368.23	78.306	11487	3	790.08	-7.22
P64076 ENO_SALTY Enolase;	1		FNQIGSLTETLAAIK	342	15	27	217.94	b2*b2b3*b3b4*b4b5b6b9b 12*b12b13b14*b14b15y1y 2y3y4y5y6y7y8y9y11y12y 15	1605.88	85.415	246537	2	803.44	-3.50
P64076 ENO_SALTY Enolase;	2		SGETEDATIADLAVGTAAGQIK	371	22	32	247.62	b2b3b4b7b9°b9b10b11b12 °b12b13b14°b14b16b22y1 y2y3y4y5*y5y6y7y8*y8y9y 12y13y14y16y17y22	2118.07	75.168	222048	2	1059.54	6.34
P64076 ENO_SALTY Enolase;	3		GMNTAVGDEGGYAPNLGSNAEA LAVIAEAVK	200	31	22	149.87	b2b3b4b5°b5b6°b6°b6b8b 13y2y3y4y5y6y7y8y14y15 y16y18y31	2989.47	94.703	125308	3	997.16	2.94
P64076 ENO_SALTY Enolase;	4		DAGYTAVISHR	360	11	15	111.38	b2b3b10y1y2y3°y3y4y5y6y 7y8y9°y9y11	1189.59	41.322	88605	2	595.30	-4.52
P64076 ENO_SALTY Enolase;	5		GIANSILIK	333	9	7	45.46	b2b5y1y3y6y7y9	928.57	60.464	81566	2	464.79	-12.16
P64076 ENO_SALTY Enolase;	6		YSMPVPMMNIIINGGEHADNNVDI QEFMIQPVGAK	143	34	9	23.51	b2°b2b5b23y5y7y29y31y3 4	3759.79	98.064	77432	3	1253.94	8.12
P64076 ENO_SALTY Enolase;	7	Carbamidomethyl+C(16)	AAGYELGKDITLAMDCAASEFYK DGK	231	26	10	69.66	b3b4b5b7°b7b9b10b11y7° y7	2824.29	98.418	58038	4	706.83	-10.03
P64076 ENO_SALTY Enolase;	8		GMPLYEHIAELNGTPGK	126	17	5	16.31	b2b10y2y3y5	1826.89	66.959	51916	3	609.64	-8.82
P64076 ENO_SALTY Enolase;	9		IQLVGDDLFTVNTNK	311	14	9	42.4	b2*b2b4y2y4y9y11y12y14	1562.85	77.402	35786	2	781.93	3.75
P64076 ENO_SALTY Enolase;	10		IEEALGEK	411	8	6	33.08	b1b5y6°y6y7y8	888.46	31.077	22193	2	444.73	-6.32
P64076 ENO_SALTY Enolase;	11		AVGAVNGPIAQAILGK	66	16	5	37.87	b5y5y10y11y14	1478.87	74.944	74627	2	739.94	0.33
P64076 ENO_SALTY Enolase;	12		QYPIVSIEDGLDESDWDGFAYQTK	282	24	4	12.7	b9y6*y6y14	2776.30	93.397	21581	2	1388.65	11.87

P64076 ENO_SALTY Enolase;	13		EALELR	46	6	1	13.62	y4	730.41	30.561	18402	1	730.41	-3.76
P64076 ENO_SALTY Enolase;	14		GNPTVEAEVHLEGGFVGVMAAAPS GASTGSR	16	30	4	22.72	y7y8y14°y14	2856.36	61.541	9390	4	714.85	1.97
P64076 ENO_SALTY Enolase;	15		SNFGANAILAVSLANAK	103	17	4	33.71	b3b4b11b16	1660.88	77.116	7805	2	830.95	-11.25
P64076 ENO_SALTY Enolase;	16		GMPLYEHIAELNGTPGKYSMPP MMNIINGGEHADNNVDIQEFMIQP VGAK	126	51	6	17.15	b4b14°b14b22b26y3	5567.62	97.800	106281	5	1114.33	-6.49
P64076 ENO_SALTY Enolase;	17		VLGDKIQLVGDDLFVNTNK	306	19	9	52.21	y4y5y6°y6*y6y10*y10y11° y11	2075.12	79.474	102249	3	692.38	-7.18
P64076 ENO_SALTY Enolase;	18		DGKYVLAGEGK	254	12	5	32.18	b5b11y3y9°y9	1250.63	43.537	81640	2	625.82	-8.78
P64076 ENO_SALTY Enolase;	19		GKGMNTAVGDEGGYAPNLGSNA EALAVIAEAVK	198	33	4	13.29	b9b16y3y5	3174.58	89.596	37623	3	1058.87	3.46
P64076 ENO_SALTY Enolase;	20		AAAAAKGMPLYEHIAELNGTPGK	120	23	3	13.04	b11b13y13	2310.22	75.232	15427	3	770.74	12.26
P64076 ENO_SALTY Enolase;	21		IEEALGEKAPYNGR	411	14	3	27.06	y5y6y9	1546.77	39.575	8095	3	516.26	-10.65
P64076 ENO_SALTY Enolase;	22		DQAGIDKIMIDLDTENK	85	18	3	24.5	y6y7y9	1975.99	70.531	1806	2	988.50	11.18
P64076 ENO_SALTY Enolase;	23	Oxidation+M(2)	GMPLYEHIAELNGTPGK	126	17	3	34.51	y6y7y8	1842.91	36.329	2945	3	614.97	0.13
P64076 ENO_SALTY Enolase;	24		GYTAVISHR	362	9	2	7.86	b3°b3	1003.53	41.354	36920	2	502.27	-2.86
P64076 ENO_SALTY Enolase;	25		ANSILK	335	7	2	8.81	b4°b4	758.47	60.463	15127	1	758.47	-5.23
P64076 ENO_SALTY Enolase;	26		AGYTAVISHR	361	10	0	2.43		1074.57	41.291	13716	2	537.79	5.00
P64076 ENO_SALTY Enolase;	27		YSMPVPMMNINGGEHA	143	17	0	11.73		1860.84	98.010	6423	3	620.95	-1.31
P64076 ENO_SALTY Enolase;	28		DAGYTAVISHR	360	11	1	7.86	b4	1171.58	41.293	1579	3	391.20	-1.35
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	1		VGVLQGTQTETFGNEHWAPK	135	20	22	133.4	b1b2b3b4b14y1y2y3y7°y7 *y7y8y9y10y11°y11y15y16 *y16y17y19y20	2199.08	63.240	237580	3	733.70	-3.00
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	2		IGTDPTYAPFESK	29	13	20	153.39	b2b3b4°b4y1y2y3°y3y4y5° y5y6°y6y7y8y9y10y11y12y 13	1425.69	55.320	126593	2	713.35	-2.65
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	3		NSDIQPTVASLK	120	12	17	111.78	b2°b2b3°b3°b3b4°b4b5y3 y4y8°y8*y8y9y10y11y12	1272.67	48.101	102352	2	636.84	-6.43
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	4	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLK	62	20	21	122.21	b3°b3b9b10°b10b14b16°b1 6°b16y1y2y4°y4y5y6y7y8y 10y12y15y20	2273.20	103.498	94941	2	1137.10	7.84
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	5		FGGPAVKDEK	201	10	6	36.9	y3°y3y4y5°y5y10	1047.54	26.721	32230	2	524.27	-5.36
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	6		QQEIAFTDK	99	9	5	45.46	b5b6b8y1y4	1079.54	42.778	13129	2	540.27	-0.90
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	7		GIEIVSYQGQDNIYSDLTAGR	155	21	4	23.52	y2y7y8y12	2299.13	77.078	2004	4	575.54	2.12
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	8		EDNELR	223	6	1	13.62	y4	775.36	58.553	2717	1	775.36	7.01
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	9	Carbamidomethyl+C(5)	INTQCTFVENPLDALIPSLKAK	62	22	4	13.43	b4b9°b9y20	2472.32	98.313	109610	3	824.78	0.20
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	10		IGTDPTYAPFESKNAQGLVGFDI DLAK	29	28	4	35.32	b13b14y3y4	2996.52	95.550	70741	3	999.51	9.94
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	11	Carbamidomethyl+C(6)	RINTQCTFVENPLDALIPSLK	61	21	3	13.87	b11y4y6	2429.26	97.434	59998	3	810.43	-8.94
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	12		IRIGTDPTYAPFESK	27	15	3	26.21	y5y7y11	1694.87	125.807	4541	2	847.94	-2.23
P02910 HISJ_SALTY Histidine-binding periplasmic protein;	13		GGPAVKDEK	202	9	0	2.02		900.47	26.641	6277	2	450.74	-12.00
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor;	1		MITGIQITK	0	9	5	38.26	y2y3y6y7y9	1004.57	54.831	86304	2	502.79	-11.12
Q7CQ05 GRCA_SALTY Autonomous glycyl radical cofactor;	2		SGFAEDEVVAVSK	35	13	12	83.41	b3b4°b4b9y1y2y4y6y8y9y1 0y13	1337.65	54.188	84903	2	669.33	-2.83

Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	3		FNSLTPEQQRDVIAR	106	15	8	39.92	b2*b2b3y3y4y6y13y15	1773.90	47.386	68984	3	591.97	-11.84
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	4		LGEIEYR	48	7	8	40.46	b2b3y1y2y4°y4y6y7	879.45	42.043	52949	2	440.23	-8.81
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	5		VEGGQHNLNVNVLr	66	13	8	78.94	b10y3y4*y4y6y7y8y11	1434.76	50.048	50261	3	478.93	-13.10
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	6		FNSLTPEQQR	106	10	14	86.76	b2*b2b3°b3b9°b9y3y5*y5y6y7y8°y8y10	1219.60	37.919	46813	2	610.31	-3.10
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	7		EIPMEVKPEVR	55	11	6	50.52	y2y4y6y8y9y11	1326.71	48.514	30408	2	663.86	-2.39
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	8		VSGYAVR	99	7	5	37.45	b3y2y5y6y7	751.40	26.972	10978	1	751.40	-7.07
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	9		AANDDLLNSFWLLDSEK	9	17	4	39.15	b7b12b13b14	1950.93	98.757	5602	2	975.97	-6.95
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	10		AANDDLLNSFWLLDSEKGEAR	9	21	23	192.68	b5°b5b6*b6b7°b7*b7y4y5y7y8y9y10°y10y11y12y13y14*y14y15y16y19*y19	2364.13	92.328	209821	3	788.72	-5.47
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	11	Carbamidomethyl+C(1)	CIVAKSGFAEDVVAVSK	30	18	6	29.14	b11°b11b12y11y13°y13	1908.97	120.420	21597	2	954.99	-4.54
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	12		MITGIQITKAANDDLLNSFWLLDSEK	0	26	3	22.81	y5y12y13	2936.47	105.029	7658	3	979.50	-11.47
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	13		SGFAEDVVAVSKLGEIEYR	35	20	4	36.01	b4b5y3y4	2198.10	97.619	5813	3	733.37	1.11
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	14		ETLEDAVKHPEK	80	12	4	37.25	b4b8b10y4	1395.70	76.215	3365	2	698.35	-7.61
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	15		VSGYAVRFNSLTPEQQR	99	17	3	16.31	b14y5y9	1951.98	102.383	2549	3	651.33	-8.69
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	16		PMEVKPEVR	57	9	2	21.87	b3b4	1084.58	48.522	35038	2	542.79	-6.42
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	17		TGIQITK	2	7	3	8.81	b4°b4*b4	760.46	54.803	3939	1	760.46	-1.44
Q7CQ05 GRCA_SALTY Autonomous glycyI radical cofactor;	18		EIPMEVKPEVR	55	11	0	2.43		1308.68	48.524	10059	3	436.90	-10.17
P0AA28 THIO_SALTY Thioredoxin-1;	1		LNIDQNPGTAPK	58	12	30	198.08	b2*b2b4*b4b5b6*b6b7*b7b9°b9b10y1y2y3y4y5y6°y6y7*y7y8°y8*y8y9°y9*y9y10y11y12	1267.65	38.475	114170	2	634.33	-8.47
P0AA28 THIO_SALTY Thioredoxin-1;	2		MIAPILDEIADEYQGK	37	16	10	62.96	b2y2y3*y3y4y6y12y13y14y16	1805.91	93.323	105256	2	903.46	8.11
P0AA28 THIO_SALTY Thioredoxin-1;	3		GIPTLLLFK	74	9	10	74.9	b2b3y1y2y3y4y5y6y7y9	1001.63	90.429	68183	2	501.32	-11.39
P0AA28 THIO_SALTY Thioredoxin-1;	4		VGALSK	91	6	2	13.62	b5°b5	574.35	38.378	14593	1	574.35	-12.75
P0AA28 THIO_SALTY Thioredoxin-1;	5		MIAPILDEIADEYQGKLTVAK	37	21	9	71.2	b3b14y4y11y12y15y16y18y20	2318.22	94.434	164562	3	773.41	-3.58
P0AA28 THIO_SALTY Thioredoxin-1;	6	Oxidation+M(1)	MIAPILDEIADEYQGK	37	16	3	17.15	b4y10y14	1821.90	120.977	1857	2	911.46	5.23
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	1		VVGYSQDYSNAIVEAVKK	61	18	13	113.28	b2b11y2y4y5y6y7y9y12y14y16y17y18	1970.00	63.090	164916	3	657.34	-9.17
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	2		AVAFMMDDALLAGER	198	15	13	124.17	b3b5b6y3°y3y4y5y8y10y11y12y13y15	1609.77	84.267	135549	2	805.39	0.91
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	3		ESSVPFSYYDNQKK	47	14	17	115.6	b2°b2b4°b4b7b11y1y4y5y6y7y8y9y10°y10*y10y14	1691.76	55.360	135103	2	846.38	2.67

Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	4		VVGYSQDYSNAIVEAVK	61	17	24	182.98	b3b6b7b11*b11b13*b13b14b15b17y2y3y4y5y6y10*y10y11*y11y12*y12y13y15y17	1841.93	67.672	116841	2	921.47	2.12
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	5		LNKPDLQVK	80	9	5	30.48	b3*b3y4y6y9	1054.61	37.746	36398	2	527.81	-10.65
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	6	Carbamidomethyl+C(13)	IPLLQNGTDFECGSTNNLER	98	22	10	28.95	b3b13y1y2*y2y5y6y8*y8y22	2526.20	81.503	33111	3	842.74	1.45
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	7		LIPITSQNR	89	9	6	54.49	b2y5y6y7y8y9	1041.59	42.880	30143	2	521.30	-13.59
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	8		IISAKDHGDSFR	180	12	4	32.18	b9b11y3y10	1345.67	31.626	23480	3	449.23	-13.88
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	9		GGDIKDFPDLK	141	11	5	24.3	b2b7b9y10y11	1204.63	69.863	21084	2	602.82	6.38
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	10		LMDDTIAQAQTSGEAEK	247	17	3	16.31	b7b9y11	1807.85	46.034	5383	2	904.43	7.83
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	11		NGVIVVGHR	38	9	4	54.49	y4y5y6y7	950.54	32.820	117989	2	475.77	-14.96
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	12	Carbamidomethyl+C(19)	KPDNWEIVGKPKSQEAYGCMLR	217	22	7	35.38	b3b9*b9y4y6y10y13	2606.27	136.215	17273	3	869.43	8.06
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	13	Carbamidomethyl+C(22)	LIPITSQNRIPLLQNGTDFECGSTNNLER	89	31	18	153.09	b3b9b10b11b14y6y7y8y9*y9y10y11y12y13y14*y14y16y21	3548.79	86.588	294061	3	1183.60	3.58
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	14		NLNMNFELSDMKALFK	277	17	3	23.3	b5b6y9	2043.98	91.198	6013	3	682.00	-4.72
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	15		TLESGRAVAFMMDDALLAGER	192	21	8	54.33	b6b9b11b13y4y10y13y14	2253.08	106.064	1769	3	751.70	-11.05
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	16	Oxidation+M(5)	LTTAMLVMGLSAGLAHAEDGAP AAGSTLDK	5	30	3	11.38	b5b8y6	2885.47	87.343	18892	3	962.50	12.61
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	17		NKPDQLQVK	81	8	0	1.62		941.54	37.748	25192	2	471.27	-1.75
Q9ZF60 GLTI_SALTY Glutamate/aartate periplasmic-binding protein;	18		SAKDHGDSFR	182	10	0	2.83		1119.53	31.580	6698	2	560.27	10.14
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	1		NNLAIVGFSTPNVMRPYVQR	237	20	15	100.07	b2*b2b3b4*b4b5y5y10y12y14*y14y15y16y17y20	2276.17	77.944	113048	3	759.39	-12.98
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	2		AYPDLDAIIPDANALPAAQAEE NLKR	209	28	19	124.74	b1b2b8b9b10b13y3y4y5*y5y6y9y10*y10y12y18y19y20y28	2863.50	87.340	101507	3	955.17	1.62
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	3		ISQEHPGWEIVTTQFGYNDATK	177	22	14	99.39	b5b9b10b11b12b19y1y6*y6*y6y7y8y9y22	2521.19	72.715	73575	3	841.07	-1.84
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	4		LVGVGFFTSGGNGAQEAGK	35	19	15	86.93	b2b3b15b17y2y3y4y8*y8y12y14y15*y15y17y19	1795.90	71.494	68554	2	898.45	1.29
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	5		SYIINQGTTPK	124	10	11	74.33	b2b3y3y4*y4y5y7*y7y8*y8y10	1170.58	38.309	67063	2	585.79	-1.67

Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	6	Carbamidomethyl+C(12)	ILTWSDTKPECR	111	13	9	77.77	b1b2y2y4y6y8y9y10y11	1620.75	50.188	62182	3	540.92	-9.34
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	7		VAFFYSSPTVTDQNQWVK	154	18	12	92.03	b5b7b12y5y6y8y11y12y13°y13y14y18	2117.05	77.484	56164	2	1059.03	6.46
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	8		ISVYVANALLK	273	11	5	36.06	y2y6y7y8y11	1190.71	73.596	52429	2	595.86	-5.23
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	9		VTVSPNSEQGYHYEAK	301	16	14	115.62	y2y4y5y6y7°y7y8°y8*y8y10y11y12y14y16	1808.82	36.407	48472	3	603.61	-12.89
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	10		NMPMNVGDSLDPGIGK	284	17	12	48.89	b1b2b6b17y1y5y7y11y14y15*y15y17	1757.87	79.387	43643	2	879.44	5.90
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	11		SLQTAEGIIK	199	10	8	58.11	b1b2b9y4y5y6y7y10	1059.60	51.005	42725	2	530.30	-8.06
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	12		EFLWDVVQQGK	261	12	8	47.92	y2y3*y3y4*y4y7y8y12	1405.71	82.385	33490	2	703.36	0.00
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	13		GNGIVLLPER	317	10	7	51.88	b2*b2y3y4y5y6y10	1067.61	61.384	25577	2	534.31	-7.55
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	14		QLGSMLEVMAAHQVDK	134	16	3	25.53	y3y6y7	1756.88	56.519	5927	2	878.95	6.32
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	15		IAFIPK	29	6	2	26.84	y4y5	688.43	54.181	14644	2	344.72	-13.65
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	16		MIALLTAFLASAAMTVQAAER	7	22	5	19.95	y3y5°y5*y5y11	2236.17	72.900	6560	2	1118.59	-4.04
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	17		AYPDLDAIIAPDANALPAAQAAE NLK	209	27	6	26.93	b4b9b10*b10b16y12	2707.38	94.543	2729	4	677.60	-3.70
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	18		AKISQEHPGWEIVTTQFGYNDAT K	175	24	13	66.27	b9*b9b10*b10b13y5y6°y6y7y12°y12y20y22	2720.33	69.048	7882	3	907.45	-1.35
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	19		AKVAFFYSSPTVTDQNQWVK	152	20	6	45.71	b10b11y7y8y11y13	2316.15	81.166	1560	2	1158.58	-4.85
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	20	Phosphoryl STY(17)	NNLAIVGFSTPNVMRPYVQR	237	20	3	21.16	y3y5y12_H3PO4 y12	2356.14	94.431	14330	4	589.79	-7.67
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	21	Oxidation+M(4)	NMPMNVGDSLDPGIGK	284	17	4	29.9	b12b13y4y14	1773.84	71.367	1848	2	887.43	-4.68
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	22		NNLAIVGFSTPNVM	237	14	4	21.04	y6°y6y7*y7	1476.76	77.958	17109	2	738.88	6.70
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	23		PDANALPAAQAENLKR	219	18	5	17.72	b4b6°b6*b6b9	1820.94	87.295	1983	3	607.65	-10.79
Q8ZKQ1 LSRB_SALTY Autoinducer 2-binding protein lsrB;	24		VSPNSEQGYHYEAK	303	14	0	4.45		1608.72	36.411	1677	2	804.87	-2.73
P67093 UG_SALTY Universal stress protein G;	1		HATLPVLVVR	132	10	7	51.88	b2y2y4y6y7y8y10	1104.68	60.853	72056	2	552.84	-10.50
P67093 UG_SALTY Universal stress protein G;	2		TIIMPVDVFEMELSDK	3	16	18	144.48	b2°b2b3b4°b4b13y1y3y5°y5y6y7y8y9y10y12y14y16	1866.93	104.252	65278	2	933.97	5.69
P67093 UG_SALTY Universal stress protein G;	3		NPSITTHLLGSNASSVVR	114	18	6	34.64	b5°b5y4y5y10y14	1852.97	58.698	37539	3	618.33	-9.88
P67093 UG_SALTY Universal stress protein G;	4		HAEFLAQDGVIIHLHLVPGSAS MSLHR	22	28	4	11.7	b10*b10y6y13	3063.53	83.287	19819	4	766.64	-22.31
P67093 UG_SALTY Universal stress protein G;	5		LQTMVGHFSDPSR	69	14	3	27.06	b6b7b11	1587.78	89.618	1901	2	794.39	-9.00
P67093 UG_SALTY Universal stress protein G;	6		TIIMPVDVFEMELSDKAIR	3	19	8	90.91	b3y4y6y9y11y13y15y17	2207.13	100.310	51249	3	736.38	-6.75
P67093 UG_SALTY Universal stress protein G;	7		RFEHLQHEAETR	56	13	4	20.63	b4°b4y3y5	1681.79	40.858	3953	4	421.20	-10.31
P67093 UG_SALTY Universal stress protein G;	8	Oxidation+M(4)	LQTMVGHFSDPSR	69	14	4	19.28	b6y6°y6y9	1603.80	49.663	9082	3	535.27	3.73

P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	1		STLTPVVISNMDEIKELIK	133	19	23	138.36	b2°b2b3°b3b4°b4b19y1y2y3y4°y4y5y6y11°y11*y11y12y13y15y16y17y19	2130.15	92.426	242018	3	710.72	-9.86
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	2		MVAPVDGTIGK	59	11	14	111.38	b2b3b8y1y2y3y5°y5y6y7y8y9y10y11	1087.57	46.140	107960	2	544.29	-7.18
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	3		VGDPVIEFDLPLLEEK	115	16	14	109.81	b1b4b5b6b7y2°y2y4y6y9y10y11y13y16	1812.97	99.289	107787	2	906.99	4.11
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	4		STLTPVVISNMDEIK	133	15	5	26.21	y2y3y5°y5y11	1646.88	72.947	7711	2	823.94	8.52
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	5		DTGTIEIVAPLSGEIVNIEDVPDVVFAEK	16	29	8	28.97	b6b9b10b14y1y2y3y8	3069.59	110.989	3570	3	1023.87	1.27
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	6		MGLFDK	0	6	1	13.62	b5	710.35	96.742	2333	1	710.35	-8.68
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	7		VKVGDPVIEFDLPLLEEK	113	18	5	21.74	b7b11y3°y3y6	2040.11	95.037	126283	3	680.71	-9.33
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	8		VGDPVIEFDLPLLEEKAK	115	18	3	15.58	b4y5y13	2012.07	91.268	15615	3	671.36	-14.44
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	9		APVDGTIGK	61	9	5	47.51	b4b5b6°b6b8	857.47	46.165	3713	1	857.47	-7.83
P0A283 PTGA_SALTY Glucose-ecific phohotransferase enzyme IIA component;	10		PVDGTIGK	62	8	5	47.51	b3b4b5°b5b7	786.43	46.141	2826	1	786.43	-7.14
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	1		TQFMGPEGVANVSLNIAGESAEGLLVTKPK	240	31	23	199.01	b2°b2b3b4b5b11b12y3y4y5y6y8y13y14y17y19y22y24y26y27y28y29y31	3144.63	88.165	316718	3	1048.88	2.10
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	2		TTGLDSDQGPTAAK	137	14	30	194.11	b2°b2b3°b3b4b5°b5b7b8°b8°b8b11°b11b12°b12y1y2y3y5y6°y6y8y9*y9y10°y10y11*y11y12y14	1361.65	29.407	147345	2	681.33	-4.21
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	3	Carbamidomethyl+C(7)	YVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTAR	92	38	16	94.39	b2b12°b12b24b25b26b27°b27y6y8y10y11y12y13y15y38	4078.01	89.141	144313	3	1360.01	7.60
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	4		VAVVGAMSGPVAQYGDQEFTGAEQAIADINAK	25	32	24	111.45	b1b2b3b4b6b9°b9b14y1y2y3y4*y4y5°y5*y5y6°y6y7y12y13°y13y14y32	3207.58	89.639	109540	3	1069.86	4.11
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	5		GGVNVVFFDGITAGEKDFSTLVAR	185	24	11	48.92	b3b4b6°b6b12y2y10y13y18y19y24	2499.28	101.852	90343	3	833.77	-1.47
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	6		ENIDFVYYGGYHPMGQILR	212	20	5	21.16	b2y9y12y14y20	2401.13	79.843	72180	3	801.05	1.42
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	7		QQYGEGLAR	168	9	5	38.26	y1y4y6y7y9	1021.50	32.930	67933	2	511.25	-5.92
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	8		QDPSGAFVWTTYAALQSLQAGLNHSDDPAEIAK	290	33	7	21.59	b2b8y2y8y10y11y33	3501.73	108.942	9905	3	1167.91	9.97
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	9		NYDQVPANKPIVDAIK	271	16	8	51.5	b3°b3b4y5y7y11°y11y12	1784.92	53.666	307791	3	595.65	-17.51
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	10	Carbamidomethyl+C(6)	TLLAGCIALSLSHMAFADDIK	4	21	4	35.82	b7b8y4y5	2247.14	67.455	15450	3	749.72	-5.65

P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	11		GATVDTVMGPLSWDEK	326	16	5	27.66	b5°b5b8b14y14	1705.83	81.452	1571	3	569.28	12.88
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	12		KQDPSGAFVWTTYAALQSLQAGL NHSDDPAEIAK	289	34	30	218.5	b3*b3b6b7°b7b8*b8b9°b9 b10b13°b13b15y3y6y10y1 1y12y14y15y17°y17y18*y1 8y19y20y21y22y23y24	3629.76	102.376	335923	4	908.20	-6.86
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	13		GDLKGFEGVFDWHANGTATDA K	342	23	3	19.45	y9y11y15	2483.19	90.177	27712	3	828.40	12.29
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	14	Carbamidomethyl+C(10)	LVAVKYDDACDPK	64	13	5	25.41	b10b11°b11y3°y3	1493.73	50.693	1700	3	498.58	-0.41
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	15	Oxidation+M(8)	GATVDTVMGPLSWDEK	326	16	3	17.15	b5y6y11	1721.83	90.570	8346	3	574.61	11.56
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	16	Carbamidomethyl+C(6); Oxidation+M(14)	TLLAGCIALSLSHMAFADDIK	4	21	3	22.32	b14y4y5	2263.15	63.058	4967	3	755.06	2.16
P17215 LIVJ_SALTY Leu/Ile/Val/Thr-binding protein;	17		SGPVAQYGDQEFTHAEQAIADINA K	32	25	1	9.83	b7	2580.26	89.663	2250	2	1290.63	14.48
P0A1S0 IHFA_SALTY Integration host factor subunit alpha;	1		TGEDIPITAR	66	10	11	101.74	b2b3b4°b4y3y5y6y7y8y9y1 0	1072.56	42.949	52058	2	536.78	-7.40
P0A1S0 IHFA_SALTY Integration host factor subunit alpha;	2		LSGFGNFDLR	45	10	8	47.9	b5b10y3y6°y6y8°y8y10	1125.58	58.522	14794	2	563.30	12.47
P0A1S0 IHFA_SALTY Integration host factor subunit alpha;	3		AEMSEYLFDK	5	10	3	26.9	b7b9y9	1232.57	31.738	1990	3	411.53	14.56
P0A1S0 IHFA_SALTY Integration host factor subunit alpha;	4		DAKELVELFFEEIR	21	14	8	68.17	b3°b3b5b7b9y4y5y8	1737.92	33.071	16320	4	435.24	9.62
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	1		VVGQLGQVLGPR	122	12	12	97.78	b2b4b5y2y3y6y7y8y10*y1 0y11y12	1222.72	59.069	99102	2	611.86	-8.89
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	2		VAVFTQGPNAEAAK	74	14	16	126.47	b3b11b12b13b14y4y5y7y8 y9*y9y10*y10y11°y11y14	1402.73	45.175	77659	2	701.87	0.00
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	3		VGTVPNVAEAVK	141	13	12	116.17	b3°b3y1y3y5y6y7y8y9y10y 12y13	1284.71	48.031	68215	2	642.86	-1.62
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	4		GATVLPHTGR	60	11	6	50.52	y2y3y4°y4y5y6	1065.57	29.640	20625	2	533.29	-5.61
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	5		AAGAELVGMEDLADQIK	88	17	7	53.82	b3b4b6y7y10y11y15	1730.87	79.494	14484	2	865.94	5.22
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	6		GEMNFDVVIASPDAMR	106	16	3	17.15	b8b13y3	1751.84	62.284	4361	3	584.62	17.28
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	7		FNESVDVAVNLGIDAR	37	16	3	17.15	b4b13y5	1718.85	76.799	1574	4	430.47	-12.14
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	8		KGEMNFDVVIASPDAMR	105	17	3	16.31	b8y5y9	1879.88	40.222	58107	3	627.30	-14.22
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	9		AAGAELVGMEDLADQIKK	88	18	5	26.57	b3b4b13y11°y11	1858.94	72.933	4641	3	620.32	-8.60
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	10		SVRVAVFTQGPNAEAAK	71	17	6	26.14	b13y12y14°y14*y14y16	1744.93	136.791	1891	1	1744.93	-3.29
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	11	Oxidation+M(9)	AAGAELVGMEDLADQIKK	88	18	3	22.74	b3b5b15	1874.97	94.988	5147	3	625.66	10.48
P0A2A3 RL1_SALTY 50S ribosomal protein L1;	12		TVLPHGTGR	62	9	0	2.43		937.51	29.641	15722	2	469.26	-11.78
P25077 MDH_SALTY Malate dehydrogenase;	1		NQLPSGSELSLYDIAPVTPGVAVD LSHIPTAVK	21	33	32	135.42	b1b2*b2b3*b3b5°b5b6b10 °b10b12*b12b13*b13b15* b15b16*b16b27y1y2y3y4y 5°y5y6y12y15y18y19y30y3 3	3388.82	93.558	181176	3	1130.28	5.55
P25077 MDH_SALTY Malate dehydrogenase;	2	Carbamidomethyl+C(2)	ACVGITNPVNTTVAIAAEVLKK	111	23	16	90.46	b2b3b4b5b13*b13y1y2y3y 4y13y15y18y20y21y23	2382.33	104.383	157236	3	794.78	-3.69

P25077 MDH_SALTY Malate dehydrogenase;	3		FFSQPLLLGK	262	10	9	61.12	b2b3°b3y2y3y4y6y8y10	1149.66	75.679	156696	2	575.33	-6.16
P25077 MDH_SALTY Malate dehydrogenase;	4		VAVLGAAGGIGQALALLK	2	19	20	180.78	b2b3b6b7b8b9b10y1y2y3y4y5y6y7y9y11y12y13y15y19	1735.08	119.517	131770	2	868.04	-1.48
P25077 MDH_SALTY Malate dehydrogenase;	5		IQNAGTEVVEAK	205	12	28	163.86	b2°b2b3b4°b4b9b11°b11y1y2y3°y3y4y5y6y7°y7y8°y8y9y10°y10*y10y11°y11*y11y12*y12	1258.66	34.582	110361	2	629.83	-4.56
P25077 MDH_SALTY Malate dehydrogenase;	6		AGGGSATLSMGQAAAR	217	16	15	93.86	b4b6b16°b16y5y7y8y9°y9*y9y10*y10y11*y11y12	1405.68	39.970	71198	2	703.35	-1.56
P25077 MDH_SALTY Malate dehydrogenase;	7		DIQLGEDFINK	301	11	6	36.72	b3b4b8°b8y8*y8	1291.64	67.651	62835	2	646.33	-6.33
P25077 MDH_SALTY Malate dehydrogenase;	8		SDLFNVNAGIVK	87	12	6	34.24	b2b3y6y8y9y12	1276.68	69.508	36128	2	638.85	-5.35
P25077 MDH_SALTY Malate dehydrogenase;	9		LFGVTTLDIIR	142	11	5	24.3	b2b3y1y3y9	1247.73	88.812	26320	2	624.37	-7.53
P25077 MDH_SALTY Malate dehydrogenase;	10		GFSGEDATPALEGADVVLISAGVAR	56	25	3	21.94	b3b4y4	2402.23	90.609	9184	2	1201.62	5.39
P25077 MDH_SALTY Malate dehydrogenase;	11		SIGTLSAFEQHSLDAMLDTLK	279	21	3	13.87	b9y8y13	2277.13	101.069	1651	3	759.72	-5.04
P25077 MDH_SALTY Malate dehydrogenase;	12		FGLSLVR	233	7	4	53.68	y3y4y5y6	791.46	66.619	75236	2	396.24	-17.20
P25077 MDH_SALTY Malate dehydrogenase;	13	Carbamidomethyl+C(5)	GVVECAYVEGDGQYAR	246	16	4	17.15	b10y4*y4y7	1772.82	49.875	5413	2	886.91	15.08
P25077 MDH_SALTY Malate dehydrogenase;	14	Carbamidomethyl+C(11)	ALQGEKGVVECAYVEGDGQYAR	240	22	3	13.43	b13y7y9	2399.12	51.857	19870	3	800.38	-3.46
P25077 MDH_SALTY Malate dehydrogenase;	15		GKLPTEVEVPVIGGHSGVTILPLLSQIPGVSFTEQEAAELTK	162	42	4	21.4	b17b20b21y4	4341.35	112.734	13722	4	1086.09	-2.59
P25077 MDH_SALTY Malate dehydrogenase;	16		IQNAGTEVVEAKAGGGSATLSMGQAAAR	205	28	4	22.32	b7b8b16y16	2645.34	90.631	3422	4	662.09	3.23
P25077 MDH_SALTY Malate dehydrogenase;	17		SIGTLSAFEQHSLDAMLDTLKK	279	22	5	25.59	b11b16y10y15y19	2405.23	136.833	2550	2	1203.12	-2.94
P25077 MDH_SALTY Malate dehydrogenase;	18		AGGGSATLSMGQAAARFGLSLVR	217	23	4	28.8	b6b8b10b13	2178.12	105.205	1966	2	1089.56	-13.11
P25077 MDH_SALTY Malate dehydrogenase;	19		NQLPSGSEL	21	9	1	10.07	y5	944.47	93.511	1753	1	944.47	-1.94
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	1		AVLEVAGVHNVLAK	112	14	12	95.06	b2b6y1y2y3y6y8y9y10y11y12y14	1419.83	60.415	107369	2	710.42	0.17
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	2		VFMQPASEGTHIAGGAMR	93	19	19	188.1	b2b3b4b7b12b13b14b16y4y5y6y7y11y12y13y14y15y16y19	1892.95	67.926	104616	2	946.98	5.09
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	3		AYGSTNPINVVR	126	12	13	93.8	b2b3b5y2y3y4*y4y6y7y8y10y12*y12	1290.68	51.007	93117	2	645.84	-2.46
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	4		ATIDGLENMNSPEMVAAGR	138	19	12	92.68	b2°b2b5b11y4y8y9y11y12y13y15y17	2046.99	58.931	70468	3	683.00	-4.59
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	5		SVEEILGK	159	8	4	40.86	y3y4y6y8	874.48	50.225	59544	2	437.74	-8.03
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	6		ATIDGLENMNSPEMVAAG	138	18	16	114.67	b2°b2b11b15y2y3y4y7y10y11y12*y12y14y15y16y18	1890.90	63.114	56574	2	945.96	5.36
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	7		AREVPAAIQK	52	10	5	28.66	b6b7y2y3*y3	1082.63	28.684	10933	2	541.82	-1.69
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	8		IFSFTALTVVGDGNR	29	16	3	23.69	b7y6y7	1653.84	70.308	11445	2	827.42	-11.88
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	9		LIAVNR	14	6	1	13.62	y4	685.43	32.803	6448	1	685.43	-1.42

P0A7W4 RS5_SALTY 30S ribosomal protein S5;	10		AVLEVAGVHNVLAKAYGSTNPIN VVR	112	26	3	21.91	b3b4y12	2691.49	96.717	192339	3	897.84	0.00
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	11		MAHIEKQAGELQEK	0	14	5	27.06	b5b6°b6b9°b9	1611.79	54.875	16455	2	806.40	-13.71
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	12	Oxidation+M()	ATIDGLENMNSPEMVA AK	138	18	6	30.97	b6°b6b9b15y7y13	1906.91	82.484	3780	2	953.96	12.55
P0A7W4 RS5_SALTY 30S ribosomal protein S5;	13	Oxidation+M(3)	VFMQPASEGTGIIAGGAMR	93	19	3	14.93	b5y5y15	1908.94	60.031	2689	2	954.97	4.60
Q8ZP20 TREA_SALTY Periplasmic trehalase;	1		VAAAAQAHL LQPGGLATT SVK	428	21	16	108.72	b1b2b3b4b5b9b10b11b12b14y9y10y12°y12y19y21	2004.11	57.736	59094	3	668.71	-8.34
Q8ZP20 TREA_SALTY Periplasmic trehalase;	2		TTTIAPVDL NALLYQLEK	335	18	14	67.54	b1b3°b3b5°b5y1y3y4y5*y5y11y13y14y18	2003.12	103.493	55755	2	1002.06	5.97
Q8ZP20 TREA_SALTY Periplasmic trehalase;	3		WMDNPQQLSTIR	323	12	9	65.9	b2b11y2y4y8y9y10y11y12	1488.73	62.381	45833	2	744.87	3.20
Q8ZP20 TREA_SALTY Periplasmic trehalase;	4		TFADAIPNSDPLMILADYR	68	19	22	143.68	b3°b3b5°b5b6°b6b11b14y2y3y4°y4y5°y5y6y7y9y10y13°y13y14y19	2123.07	101.225	42806	2	1062.04	9.54
Q8ZP20 TREA_SALTY Periplasmic trehalase;	5	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPTK	534	29	5	16.9	b4°b4b6b10y14	3199.57	63.812	13562	4	800.65	-3.43
Q8ZP20 TREA_SALTY Periplasmic trehalase;	6		SNPNRPATEIYR	296	12	5	29.47	b2y6y7y10y12	1417.72	32.786	10395	2	709.36	1.12
Q8ZP20 TREA_SALTY Periplasmic trehalase;	7		WDSLLPLPESYVVP GGR	142	17	4	16.31	b4b11°b11y12	1885.00	91.261	6581	2	943.00	6.48
Q8ZP20 TREA_SALTY Periplasmic trehalase;	8		TYYLSR	206	6	2	26.84	y3y4	802.40	37.762	19262	2	401.71	-5.78
Q8ZP20 TREA_SALTY Periplasmic trehalase;	9		DQLTAAALFLYVNAAAK	405	18	7	26.57	b7°b7b10°b10°b10b11y5	1877.01	96.806	12192	2	939.01	-3.64
Q8ZP20 TREA_SALTY Periplasmic trehalase;	10		DTPRPESWVEDIATAK	280	16	11	70.74	b4°b4b5°b5b7°b7b8°b8b12b13°b13	1814.89	111.790	3255	2	907.95	-0.67
Q8ZP20 TREA_SALTY Periplasmic trehalase;	11		VADMVANFGYEIDA WGHIPNGNR	183	23	5	42.98	b3b5b6b8b9	2546.23	123.178	1786	3	849.41	15.53
Q8ZP20 TREA_SALTY Periplasmic trehalase;	12	Carbamidomethyl+C(6); Carbamidomethyl+C(12)	MLDLICPQEKPCDSVPSTRPASLS ATPTKTPSAATQ	534	36	6	25.53	b3b5y8y10y11y21	3855.88	63.732	60495	4	964.72	-4.18
Q8ZP20 TREA_SALTY Periplasmic trehalase;	13		NVEKWDSLLPLPESYVVP GGR	138	21	5	31.18	b9y4y7y9y10	2355.24	87.961	55053	3	785.75	3.42
Q8ZP20 TREA_SALTY Periplasmic trehalase;	14		ASAAAGDRAK	357	10	3	33.89	b4b7b8	917.47	54.078	50544	2	459.24	-9.85
Q8ZP20 TREA_SALTY Periplasmic trehalase;	15		DTPRPESWVEDIATAKSNPNRPAT EIYR	280	28	3	22.72	b4b8b9	3213.59	120.929	18927	3	1071.87	0.46
Q8ZP20 TREA_SALTY Periplasmic trehalase;	16		LFPDQKTFADAIPNSDPLMILADY R	62	25	5	16.3	b4b9y7°y7y13	2851.44	101.847	12266	3	951.15	2.40
Q8ZP20 TREA_SALTY Periplasmic trehalase;	17		LEDGSVLNRYWDDR	266	14	3	19.28	b7y5y12	1737.82	71.346	6878	2	869.41	-0.91
Q8ZP20 TREA_SALTY Periplasmic trehalase;	18		SNPNRPATEIYRDLR	296	15	6	29.43	b8b9b13°b13y14*y14	1801.92	88.224	3839	2	901.46	-4.34
Q8ZP20 TREA_SALTY Periplasmic trehalase;	19		TFADAIPNSDPLMILADYRMQR	68	22	6	23.31	b12°b12b17°b17b18°b18	2538.22	136.825	2281	2	1269.61	-11.45
Q8ZP20 TREA_SALTY Periplasmic trehalase;	20	Oxidation+M(4)	VADMVANFGYEIDA WGHIPNGNR	183	23	6	24.55	b5b8y4°y4y8y10	2562.18	72.851	13800	3	854.73	-0.29
Q8ZP20 TREA_SALTY Periplasmic trehalase;	21	Oxidation+M(9)	SQPPFFAFMVELLAQHEGDDALK	212	23	4	13.04	b4b7y6°y6	2606.29	74.557	1876	3	869.43	10.12
Q8ZP20 TREA_SALTY Periplasmic trehalase;	22		PNRPATEIYR	298	10	0	2.83		1216.64	32.712	14227	2	608.83	-0.30
Q8ZP20 TREA_SALTY Periplasmic trehalase;	23		TFADAIPNSDPLMILADYR	68	19	0	5.66		2106.02	101.197	1877	3	702.68	2.55

Q8ZP20 TREA_SALTY Periplasmic trehalase;	24		SNPNRPATEIYR	296	12	0	2.83		1400.67	32.798	1531	3	467.56	-12.46
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	1		VANLGLSGDQVNVK	8	14	23	125.23	b1b2b3b6°b6b9*b9b10°b10°b10b13b14y1y3y7*y7y8*y8y9y10*y10y12y14	1413.77	56.576	68876	2	707.39	1.47
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	2		NVEYFEAR	42	8	8	67.3	y2y3y4y5°y5y6y7y8	1027.48	46.616	65831	2	514.24	-5.82
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	3		DIADAVTAAGVDVAK	97	15	10	63.64	b2b4b7b9y4°y4y7y9y13y15	1415.74	66.013	59415	2	708.37	0.17
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	4		LADVLAANAR	57	11	8	24.3	b2b5y1y2y5*y5y10*y10	1084.62	38.311	29725	2	542.81	5.51
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	5		VIINVVAE	141	8	3	33.08	b5b6y5	856.51	63.390	69436	1	856.51	-6.27
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	6		NFLVPK	27	6	2	26.84	b3y4	717.42	51.089	21397	1	717.42	-11.23
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	7		TTGEHEVNFQVHSEVFAK	123	18	4	15.58	b12*b12y9y14	2058.99	94.502	6805	3	687.00	-1.42
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	8		DIADAVTAAGVDVAKSEVR	97	19	4	34.52	b12b13b14°b14	1886.95	75.306	54796	3	629.66	-14.62
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	9		VANLGLSGDQVNVKAGYAR	8	19	4	34.52	b9°b9b10b11	1932.05	67.357	7803	2	966.53	12.00
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	10		LPNGVLRTTGEHEVNFQVHSEVFAK	116	25	11	53.27	b12b13*b13y11°y11*y11y12*y12y15y16°y16	2808.44	136.814	3218	2	1404.72	-0.96
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	11		KNVEYFEAR	41	9	3	30.48	b6y4y8	1155.59	70.418	2072	2	578.30	8.24
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	12	Phosphoryl STY(5)	AVPATKK	35	7	4	40.46	b3b6y6°y6	794.41	45.090	4262	1	794.41	2.84
Q8ZK80 RL9_SALTY 50S ribosomal protein L9;	13		ADVLAANAR	58	10	1	7.86	b9	971.52	38.299	46234	2	486.27	-2.01
P0A297 RL10_SALTY 50S ribosomal protein L10;	1		LATLPTYEEAIAR	125	13	11	96.93	b2b4y4y6y7y8y9y10°y10y11y13	1447.77	64.950	75090	2	724.39	-4.05
P0A297 RL10_SALTY 50S ribosomal protein L10;	2	Carbamidomethyl+C(9)	VVEGTQFECLKDTFVGPTLIAYSM EHPGAAAR	62	32	10	49.47	b2b3y6y12y13y15y16°y16y17y32	3494.70	91.986	70853	4	874.43	-3.07
P0A297 RL10_SALTY 50S ribosomal protein L10;	3		AAAFEGELIPASQIDR	109	16	10	70.74	b1b4b5y2y7y8y9y11y12y16	1687.87	68.552	52019	2	844.44	4.85
P0A297 RL10_SALTY 50S ribosomal protein L10;	4		GALSAVVADSR	20	11	9	52.49	b3b5°b5y2y5y6°y6y7y11	1045.57	48.259	37079	2	523.29	5.84
P0A297 RL10_SALTY 50S ribosomal protein L10;	5		AGREAGVYMR	43	10	5	61.12	b6y3y4y6y8	1109.55	46.156	9628	2	555.28	2.53
P0A297 RL10_SALTY 50S ribosomal protein L10;	6	Carbamidomethyl+C(9)	VVEGTQFECLK	62	11	5	31.29	b3b9b10b11y11	1309.66	86.052	3289	2	655.33	12.68
P0A297 RL10_SALTY 50S ribosomal protein L10;	7		LMATMK	138	6	1	13.62	b4	694.37	40.905	12415	1	694.37	6.86
P0A297 RL10_SALTY 50S ribosomal protein L10;	8		DTFVGPTLIAYSM EHPGAAAR	73	21	3	13.87	b5y3y13	2204.10	115.252	7826	3	735.37	9.19
P0A297 RL10_SALTY 50S ribosomal protein L10;	9		EASAGK	144	6	3	29.85	b3b5°b5	562.29	43.602	2615	1	562.29	13.79
P0A297 RL10_SALTY 50S ribosomal protein L10;	10		LATLPTYEEAIARLMATMK	125	19	3	14.93	b12y6y18	2123.09	57.772	234798	3	708.37	-14.72
P0A297 RL10_SALTY 50S ribosomal protein L10;	11		AAAFEGELIPASQIDRLATLPTYEEAIAR	109	29	8	33.3	b9b11b13°b13*b13b18b25y9	3116.59	99.848	5800	3	1039.53	-12.06
P0A297 RL10_SALTY 50S ribosomal protein L10;	12	Phosphoryl STY(4)	GALSAVVADSR	20	11	3	24.3	b3y6y10	1125.51	40.209	11617	2	563.26	-11.93
P0A297 RL10_SALTY 50S ribosomal protein L10;	13	Oxidation+M(2)	LMATMKEASAGK	138	12	3	26.25	b6b7y8	1253.61	61.352	15212	3	418.54	-9.15

Q8ZQT5 TOLB_SALTY Protein tolB;	1		SNNTEPTWFPDSQTLAFTSDQAG RPQVYK	287	29	15	77.34	b2b4b5°b5y2y1y14y16y2 0y21y22y24°y24y25y29	3285.56	77.421	98276	3	1095.86	4.46
Q8ZQT5 TOLB_SALTY Protein tolB;	2		WAGPGAAPEDIGGIVAADLR	43	20	12	66.83	b1b7b15b17°b17y2y4y5y6 y13y14y20	1936.00	85.314	66345	2	968.50	4.16
Q8ZQT5 TOLB_SALTY Protein tolB;	3		IEITQGVSARPIGVVPFK	24	19	14	92.73	b2b9b11b12°b12b15b16y3 y14°y14y15y16y17y19	2026.11	70.368	63384	3	676.04	-11.63
Q8ZQT5 TOLB_SALTY Protein tolB;	4		LAYVTFESGR	213	10	6	51.88	b1y4y5y6y8y10	1142.58	57.526	46940	2	571.79	-3.10
Q8ZQT5 TOLB_SALTY Protein tolB;	5		SPQPLMSPAWSPDGSK	197	16	12	85	b2°b2b9y3y4y5y9°y9y10y1 3y14y16	1684.81	62.580	41529	2	842.91	8.62
Q8ZQT5 TOLB_SALTY Protein tolB;	6		IAYVVQTNGGQFPYELR	166	17	8	52.74	b3b4y2y5y8y11y13°y13	1955.01	73.143	35772	2	978.01	5.93
Q8ZQT5 TOLB_SALTY Protein tolB;	7		SALVIQTLANGAVR	223	14	9	89.55	b3b4y4y5y8y9y10y11y14	1412.82	70.689	34021	2	706.91	-2.42
Q8ZQT5 TOLB_SALTY Protein tolB;	8		MNINGGAAQR	316	10	11	87.55	b2°b2b3y2y3y5y6y7°y7y8 y9	1031.50	27.876	30874	2	516.25	-8.76
Q8ZQT5 TOLB_SALTY Protein tolB;	9		LPATDGQVK	413	9	7	45.46	b5b9y4y5y8°y8y9	928.51	27.975	1915	1	928.51	3.62
Q8ZQT5 TOLB_SALTY Protein tolB;	10		YAGHTASDEVFEK	142	13	4	20.63	b5°b5b10y9	1453.64	37.606	24339	3	485.22	-13.35
Q8ZQT5 TOLB_SALTY Protein tolB;	11		QVASFPR	237	7	3	40.46	y3y4y5	804.43	38.354	22141	2	402.72	-9.94
Q8ZQT5 TOLB_SALTY Protein tolB;	12		LAFALSK	257	7	3	37.45	b4y5y6	749.45	56.362	10014	2	375.23	-12.46
Q8ZQT5 TOLB_SALTY Protein tolB;	13		HNGAPAFSPDGTK	244	13	8	74.96	b5b6b7°b7y4y5y6y9	1298.62	67.191	4627	2	649.81	3.10
Q8ZQT5 TOLB_SALTY Protein tolB;	14		FNPLDR	67	6	1	13.62	b4	761.38	37.365	3078	2	381.20	-14.51
Q8ZQT5 TOLB_SALTY Protein tolB;	15		ITWEGSQNQDADVSSDGK	326	18	3	15.58	b11y5y11	1936.89	65.519	1657	2	968.95	19.66
Q8ZQT5 TOLB_SALTY Protein tolB;	16		SPQPLMSPAWSPDGSKLAYVTFES GR	197	26	6	49.93	b8b9y4y5y6y13	2808.37	80.926	39400	3	936.80	1.56
Q8ZQT5 TOLB_SALTY Protein tolB;	17		NSGKFNPLDR	63	10	3	33.89	y5y6y8	1147.57	41.952	18936	2	574.29	-12.98
Q8ZQT5 TOLB_SALTY Protein tolB;	18		LPATDGQVKSPAWSPYL	413	17	3	16.31	b3b6y6	1829.92	119.570	8950	2	915.46	-12.34
Q8ZQT5 TOLB_SALTY Protein tolB;	19		HNGAPAFSPDGTKLAFALSK	244	20	3	23.79	b5b8b9	2029.05	61.718	6488	3	677.02	-0.42
Q8ZQT5 TOLB_SALTY Protein tolB;	20		QALRVAFGFLMLWAAVLHAEVR	2	22	6	51.2	b12b14b15y16y17y18	2498.39	136.839	3334	2	1249.70	2.05
Q8ZQT5 TOLB_SALTY Protein tolB;	21		VIQTLANGAVR	226	11	0	3.64		1141.65	70.725	18705	2	571.33	-12.94
O33921 AGP_SALTY Glucose-1- phohatase;	1		TPIGGQLVFQR	335	11	7	65.5	b2y3y4y7y8y9y11	1215.68	61.356	161176	2	608.34	-6.83
O33921 AGP_SALTY Glucose-1- phohatase;	2		MGTMDPTEFNPVITDDSAAFR	141	20	21	137.51	b2b3°b3b5°b5y2y3y5°y5y6 y7y8y9°y9y11y12y14°y14y 15y16y20	2186.01	78.235	94338	2	1093.51	7.37
O33921 AGP_SALTY Glucose-1- phohatase;	3		IEYVYQSAR	358	9	9	89.37	b2b3b6y3y5y6y7y8y9	1128.56	42.584	82251	2	564.79	-3.89
O33921 AGP_SALTY Glucose-1- phohatase;	4		NVAAPLVK	281	8	5	49.31	b5y4y5y6y8	811.49	40.155	80453	2	406.25	-12.41
O33921 AGP_SALTY Glucose-1- phohatase;	5		QQAQAMEK	161	9	12	74.9	b3°b3b9y3y4°y4y5°y5°y5y 6y7y9	1032.50	26.249	70025	2	516.76	-9.46
O33921 AGP_SALTY Glucose-1- phohatase;	6	Carbamidomethyl-C(14)	EWLVQAQLIPSGECPAPDVTYAY ANSLQR	87	29	26	152.26	b3°b3b4b6b7°b7b9°b9b12 b16y2y3y4y5°y5y6y7y9y1 0y11y13°y13°y13y15y20y2 9	3205.58	93.585	47906	3	1069.20	5.79

O33921 AGP_SALTY Glucose-1-phohatase;	7		APLANNGSVLAQSTPNAWPAWD VPGGQLTTK	43	31	18	92.81	b4b6b8b9°b9b14*b14b18y 2y8y10y11y12*y12y13y14 *y14y31	3161.61	83.345	39926	3	1054.54	3.63
O33921 AGP_SALTY Glucose-1-phohatase;	8		DTFSANYQQEPGVQGPLK	208	18	7	22.74	b2°b2y1y8y10y12y18	1978.97	56.473	33532	2	989.99	7.90
O33921 AGP_SALTY Glucose-1-phohatase;	9		NGYQDSLFTSPTVAR	266	15	4	26.21	b2y3y5y11	1655.80	62.918	27539	2	828.40	-1.62
O33921 AGP_SALTY Glucose-1-phohatase;	10		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDR	226	31	6	26.13	b3b6b7b15°b15*b15	3486.66	104.156	25620	3	1162.89	5.46
O33921 AGP_SALTY Glucose-1-phohatase;	11		VTVLVGHDNSNIASLLTALDFKPYQ LHDQYER	304	31	5	25.2	b9y4y5y10y15	3542.77	96.058	171470	5	709.36	-15.30
O33921 AGP_SALTY Glucose-1-phohatase;	12		NAEALTLK	370	8	5	51.07	b3*b3b5y6y7	859.48	41.138	85461	2	430.24	-15.20
O33921 AGP_SALTY Glucose-1-phohatase;	13		SQLHLDSEYK	172	10	5	28.66	b4°b4b5y4°y4	1219.58	40.916	20789	3	407.20	-14.71
O33921 AGP_SALTY Glucose-1-phohatase;	14	Carbamidomethyl+C(2); Carbamidomethyl+C(10)	GCPVDANGFCPLDKFDNMNTA AK	389	24	9	56.8	b4b22y3y10y12*y12y14y1 8y22	2641.18	78.262	71975	3	881.07	-0.74
O33921 AGP_SALTY Glucose-1-phohatase;	15		LKNGYQDSLFTSPTVAR	264	17	10	84.05	b7b9b10°b10y3y4y5y6y8y 15	1896.96	58.786	70510	3	632.99	-8.88
O33921 AGP_SALTY Glucose-1-phohatase;	16		MGTMDPTFNPVITDDSAFRQQA VQAMEK	141	29	6	25.98	b3y3y4°y4y7y24	3199.50	81.574	32009	3	1067.17	4.88
O33921 AGP_SALTY Glucose-1-phohatase;	17		VGNSLVDAFTLQYYEGFPMQVA WGGIHTDRQWK	226	34	6	21.51	b13*b13y7y8y12*y12	3928.87	84.054	26913	3	1310.29	-2.49
O33921 AGP_SALTY Glucose-1-phohatase;	18		QQAVQAMEKAR	161	11	4	41.49	b4y4y8y10	1259.66	63.718	16963	2	630.33	4.55
O33921 AGP_SALTY Glucose-1-phohatase;	19	Carbamidomethyl+C(27) ;Oxidation+M(8)	GGVLEVYMGHYTREWLVAQGLIP SGECPAPDTVYAYANSLQR	74	42	3	10.94	b8b11y4	4684.29	57.644	5434	4	1171.83	6.36
P41031 CY_SALTY Thiosulfate-binding protein;	1		AYLNWLYSPQAQTIIHHYYR	265	21	18	137.91	b2b3b4b5*b5b6*b6y1y3y4 y5y7y9y11y13y15y16y21	2664.33	92.929	181927	3	888.78	0.64
P41031 CY_SALTY Thiosulfate-binding protein;	2		GLGDVLISFESEVNNIRK	208	18	12	62.21	b2b5°b5b10b12b14°b14y6 y11y12y16y18	1990.04	101.166	160070	3	664.02	-10.49
P41031 CY_SALTY Thiosulfate-binding protein;	3		FGSWPEVMK	311	9	7	45.46	b2b3°b3y2y3y5y6	1080.51	68.505	150774	2	540.76	-4.41
P41031 CY_SALTY Thiosulfate-binding protein;	4		ELFAALNPPEQQWAK	37	16	19	94.82	b5b7°b7b14°b14*b14b15° b15y1y2y4*y4y6°y6y7y9y1 0y12y16	1888.97	89.613	98826	2	944.99	6.53
P41031 CY_SALTY Thiosulfate-binding protein;	5		QYEAQGFEEVIPK	226	13	19	102.65	b2*b2b3*b3b4°b4*b4b11° b11b13y1y2y3y5y8y9y10y 11y13	1507.78	69.700	95063	2	754.39	-0.57
P41031 CY_SALTY Thiosulfate-binding protein;	6		VNNPEIMGK	286	9	10	61.68	b1b2°b2b3y2y4y6y7y8y9	1001.50	36.114	94183	2	501.25	-9.81
P41031 CY_SALTY Thiosulfate-binding protein;	7		LPNNSPFYSTMGFLVR	110	17	16	122.46	b6°b6b7b8°b8y1y2y3y5y8 y9y11y12y13y14y17	1929.97	91.691	91611	2	965.49	7.46
P41031 CY_SALTY Thiosulfate-binding protein;	8		NVEFDTGGR	189	10	8	58.11	b2b8y4y6y7y8°y8y10	1093.52	47.125	63117	2	547.26	-4.35
P41031 CY_SALTY Thiosulfate-binding protein;	9		NIHDWSDLVR	132	10	7	26.9	b2b8y1y3y6°y6y10	1254.62	63.090	60328	2	627.81	-0.78
P41031 CY_SALTY Thiosulfate-binding protein;	10		LIFPNPK	146	7	9	63.88	b5y2y3*y3y4*y4y5y6y7	828.49	55.872	60096	2	414.75	-14.37
P41031 CY_SALTY Thiosulfate-binding protein;	11		QALAILQLK	71	10	8	74.33	b3°b3b10y3y5y6y7y8	1054.65	74.840	46161	2	527.83	-9.95
P41031 CY_SALTY Thiosulfate-binding protein;	12		GATTTFAER	199	9	5	54.49	y4y5y6y7y9	953.46	30.737	31056	2	477.23	-11.20
P41031 CY_SALTY Thiosulfate-binding protein;	13		GLGDVLISFESEVNNIR	208	17	5	23.3	b5y1y10*y10y11	1861.97	106.998	29419	2	931.49	2.16

[P41031 CY_SALTY Thiosulfate-binding protein;	14		ADVVTYNQVTDVQILHDK	81	18	6	22.74	b2°b2b3°b3b10b12	2058.04	63.600	8958	3	686.68	-5.81
[P41031 CY_SALTY Thiosulfate-binding protein;	15		ELFAALNPPFEQQWAKDNGGDK	37	22	6	24.22	b15y2y7y13°y13y14	2475.18	97.084	2693	3	825.73	-6.41
[P41031 CY_SALTY Thiosulfate-binding protein;	16		TNLAIEFPVAWVDK	239	14	5	44.75	y5y7y9y11°y11	1602.84	97.042	7221	2	801.93	-5.18
[P41031 CY_SALTY Thiosulfate-binding protein;	17		RPLTLAAMLLLAGQAQATELLNS SYDVSR	8	29	16	76.67	b11b18°b18b19y12*y12y13y14°y14*y14y15*y15y16y18°y18*y18	3102.61	136.800	5936	2	1551.81	-15.50
[P41031 CY_SALTY Thiosulfate-binding protein;	18		TEQFMTQFLK	179	10	7	73.54	b3b9y3y5y7y8°y8	1272.63	75.258	4203	1	1272.63	-1.82
[P41031 CY_SALTY Thiosulfate-binding protein;	19		VEEK	307	4	1	12.81	b3	504.27	46.446	3781	1	504.27	1.15
[P41031 CY_SALTY Thiosulfate-binding protein;	20		TNLAIEFPVAWVDKNVQANGTEK	239	23	17	132.25	b3b4b5°b5y5y6°y6y7*y7y9y10*y10y13y17y18y19y20	2544.30	90.353	194803	3	848.77	-4.13
[P41031 CY_SALTY Thiosulfate-binding protein;	21		NVEVFDTGGRGATTTFATER	189	19	14	100.01	b3°b3b5b8b12°b12b14y5y8y13°y13y14y15y17	2027.96	56.513	62103	3	676.66	-7.76
[P41031 CY_SALTY Thiosulfate-binding protein;	22		YTYLAAWGAADNADGGDKAK	159	20	3	21.16	y3y6y13	2057.95	61.984	61848	3	686.65	-5.10
[P41031 CY_SALTY Thiosulfate-binding protein;	23		TSGNARYTYLAAWGAADNADGGDK	153	24	4	19.44	b8b10b13y15	2445.13	90.423	6637	2	1223.07	10.18
[P41031 CY_SALTY Thiosulfate-binding protein;	24		GNPKNIHDWSDLVR	128	14	3	27.85	y7y9y13	1650.81	84.784	5487	3	550.94	-14.12
[P41031 CY_SALTY Thiosulfate-binding protein;	25		LIPADWQSRLPNNSSPFYSTMGFLVR	101	26	4	12.14	b21y10°y10y13	2996.51	84.731	4873	3	999.51	0.73
[P41031 CY_SALTY Thiosulfate-binding protein;	26		QADKFPQTELFRR	295	12	4	35.49	y4y5y6°y6	1479.75	58.955	4248	2	740.38	-5.53
[P41031 CY_SALTY Thiosulfate-binding protein;	27		VEEKFGSWPEVMK	307	13	4	34.43	b4b5y4y8	1565.75	46.658	2285	2	783.38	-11.46
[P41031 CY_SALTY Thiosulfate-binding protein;	28		VNNPEIMGKQADK	286	13	3	20.63	b3b11y9	1443.74	76.664	1756	2	722.37	6.43
[P41031 CY_SALTY Thiosulfate-binding protein;	29	Phosphoryl STY(6)	ADVVTYNQVTDVQILHDK	81	18	5	29.14	b4b5°b5y13_H3PO4y13y16	2138.04	69.025	13547	3	713.35	13.93
[P41031 CY_SALTY Thiosulfate-binding protein;	30		EVFDTGGR	191	8	0	2.02		880.41	47.099	1676	1	880.41	-3.40
[P41031 CY_SALTY Thiosulfate-binding protein;	31		GATTTFAER	199	9	0	1.62		935.45	30.742	11884	2	468.23	-3.78
[P41031 CY_SALTY Thiosulfate-binding protein;	32		FGSWPEVMK	311	9	0	1.62		1062.51	68.562	3819	1	1062.51	10.23
[P41031 CY_SALTY Thiosulfate-binding protein;	33		NIHDWSDLVR	132	10	1	8.25	y4	1237.59	63.097	3496	3	413.20	1.18
[P67091 UF_SALTY Universal stress protein F;	1		TILVPIDISDSELTQR	3	16	21	135.07	b1b2b3°b3b4°b4y2*y2y3y5°y5*y5y7y8y9y10y12y13°y13y14y16	1799.98	81.861	133178	2	900.49	2.71
[P67091 UF_SALTY Universal stress protein F;	2		VISHVEAEAK	19	10	3	36.9	y5y6y7	1082.58	25.079	24740	2	541.79	-4.51
[P67091 UF_SALTY Universal stress protein F;	3		VHFLTVPISLPYYASLGLAYSALPAMDDLK	34	31	6	39.96	y1y4y7y9y10y11	3394.77	125.702	3511	3	1132.26	0.65
[P67091 UF_SALTY Universal stress protein F;	4		ILEMAK	98	6	1	13.62	y4	704.40	38.381	6797	2	352.70	-8.66
[P67091 UF_SALTY Universal stress protein F;	5		VQAHVAEGSPK	85	11	3	24.3	b6b10y5	1122.58	69.549	2127	2	561.80	-5.76
[P67091 UF_SALTY Universal stress protein F;	6		MNRTILVPIDISDSELTQR	0	19	3	34.52	y8y9y10	2201.16	68.895	2812	2	1101.08	-0.22

P65702 PGK_SALTY Phohoglycerate kinase;	1		SVNDVKEDEQILDIGDASAQQLAELK	272	27	23	152.37	b1b4°b4b5°b5b11b13b14°b14b17b25b26y2y3y4°y4y5y6y7y13y14y15y27	2941.52	99.963	162667	3	981.18	5.81
P65702 PGK_SALTY Phohoglycerate kinase;	2		VLPVAMLEER	373	11	12	87.16	b1b3y2y3°y3y4y6y7y8°y8y9y11	1227.67	79.922	161940	2	614.34	-5.67
P65702 PGK_SALTY Phohoglycerate kinase;	3	Carbamidomethyl+C(6)	FADVACAGPLLAELDALGK	156	20	19	168.75	b2b3b5b7b8b12b13y2y3y4y5y6y8y9y13y14y15y16y20	2002.04	98.698	161686	2	1001.52	4.94
P65702 PGK_SALTY Phohoglycerate kinase;	4	Carbamidomethyl+C(5)	LLTTCDIPVPTDVR	244	14	15	95.57	b2b6°b6b7°b7b9y2y5°y5y7y9y10y11y12y14	1599.85	68.493	118680	2	800.43	2.75
P65702 PGK_SALTY Phohoglycerate kinase;	5		VATEFSETAPATLK	258	14	18	152.24	b2b3°b3b4°b4b5b9y1y3y5y7y9y10y11°y11y12y13y14	1464.76	52.477	98684	2	732.88	-1.75
P65702 PGK_SALTY Phohoglycerate kinase;	6		TILWNGPVGVFEPNFR	302	17	17	112.92	b2b5b6°b6b12y1y4y5y6y7y11°y11y12y13°y13y15y17	1993.05	106.027	83609	2	997.03	8.15
P65702 PGK_SALTY Phohoglycerate kinase;	7		ADLNVPVKEGK	19	11	12	66.96	b2°b2b3b9y2y3y4°y4y6y8*y8y11	1169.65	36.834	73826	2	585.33	-3.24
P65702 PGK_SALTY Phohoglycerate kinase;	8		ASLPTIELALK	38	11	5	31.29	y1y3y4y8y11	1155.69	77.090	65205	2	578.35	-6.13
P65702 PGK_SALTY Phohoglycerate kinase;	9		LVKDYLDGVDVAEGELVLENVR	90	23	3	23.13	y3y4y12	2544.36	96.950	42488	3	848.79	0.10
P65702 PGK_SALTY Phohoglycerate kinase;	10		IADQLIVGGGIANTFVAAQGHSVGK	206	25	11	54.29	b2b3b4b5y2y5°y5y9y11y14*y14	2423.28	77.950	41713	3	808.43	-9.77
P65702 PGK_SALTY Phohoglycerate kinase;	11		MTDLDLAGKR	5	10	8	81.32	b2y3y4y5y6y7y9y10	1119.58	42.686	34482	2	560.29	-5.89
P65702 PGK_SALTY Phohoglycerate kinase;	12		TILWNGPVGVFEPNFRK	302	18	8	26.57	b2b13y1y10y13y14°y14y18	2121.12	96.495	24833	3	707.71	-5.87
P65702 PGK_SALTY Phohoglycerate kinase;	13		MTDLDLAGK	5	9	5	38.26	y2y3y4y8y9	963.47	48.320	21214	2	482.24	-8.17
P65702 PGK_SALTY Phohoglycerate kinase;	14		AQASTHGIGK	146	10	8	40.12	b2°b2b6y2y4y7y8y10	969.50	15.982	7711	2	485.26	-6.86
P65702 PGK_SALTY Phohoglycerate kinase;	15		VMVTSHLGRPTEGEYNEEFSLLPV VNYLK	53	29	5	16.9	b4b6°b6b13y15	3321.69	136.288	2766	4	831.18	3.68
P65702 PGK_SALTY Phohoglycerate kinase;	16	Carbamidomethyl+C(5)	YAALCDVFMDFAGTAHR	128	18	3	24.5	b6b11b12	2043.96	62.989	12123	2	1022.48	9.26
P65702 PGK_SALTY Phohoglycerate kinase;	17		LSNPVR	84	6	2	29.85	y3y5	685.39	27.742	5031	2	343.20	-11.04
P65702 PGK_SALTY Phohoglycerate kinase;	18		SVNDVK	272	6	1	13.62	b4	661.35	106.657	2507	1	661.35	3.97
P65702 PGK_SALTY Phohoglycerate kinase;	19		ISYISTGGGAFLEFVEGK	355	18	3	24.5	b3b5b6	1874.99	61.904	2453	2	938.00	20.83
P65702 PGK_SALTY Phohoglycerate kinase;	20		DYLDGVDVAEGELVLENVR	93	20	4	22.5	b13b14y16°y16	2204.09	95.413	1777	3	735.37	-7.64
P65702 PGK_SALTY Phohoglycerate kinase;	21		SLYEADLVDEAK	231	12	5	54.15	b7b8y9y10y11	1352.65	136.272	1742	1	1352.65	-5.87
P65702 PGK_SALTY Phohoglycerate kinase;	22		VATEFSETAPATLKSVNDVK	258	20	3	22.5	b13b14y15	2107.09	74.564	28543	3	703.04	1.04
P65702 PGK_SALTY Phohoglycerate kinase;	23		ISYISTGGGAFLEFVEGKVLPVAMLEER	355	29	9	37.81	b4b8b10°b10b14y4y7°y7y8	3083.61	136.319	3979	4	771.66	0.48
P65702 PGK_SALTY Phohoglycerate kinase;	24	Carbamidomethyl+C(5); Oxidation+M(10)	YAALCDVFMDFAGTAHR	128	18	4	24.81	b5b7b14y11	2059.95	78.116	2057	3	687.32	7.59
P65702 PGK_SALTY Phohoglycerate kinase;	25		DLDLAGKR	7	8	2	20.68	b3b7	887.50	42.653	16435	2	444.25	6.74
P65702 PGK_SALTY Phohoglycerate kinase;	26		TDLDLAGKR	6	9	0	2.02		988.54	42.707	14491	2	494.77	-5.12

P65702 PGK_SALTY Phohoglycerate kinase;	27		DLNVPVKEGK	20	10	2	7.86	b3°b3	1098.61	36.834	10931	2	549.81	-8.22
P65702 PGK_SALTY Phohoglycerate kinase;	28		PAVAMLEER	375	9	2	18.86	b3b5	1015.51	79.922	7786	2	508.26	-10.34
P06179 FLIC_SALTY Flagellin;	1		AQILQQAGTSVLAQANQVPQNVLSLLR	468	27	20	106.92	b2*b2b3b4b5*b5b7b8b17b18y1y2y4y6y9y10y12*y12y13y27	2860.60	104.953	132071	3	954.21	0.51
P06179 FLIC_SALTY Flagellin;	2		SQSALGTAIER	20	11	9	41.49	b2*b2b3y1y5y7y9°y9y11	1132.59	41.984	45416	2	566.80	-6.25
P06179 FLIC_SALTY Flagellin;	3		FNSAITNLGNTVNNLTSAR	432	19	12	50.03	b3b4°b4b8°b8y3y7*y7y13y14°y14y19	2007.04	78.164	32657	2	1004.02	5.78
P06179 FLIC_SALTY Flagellin;	4		INSAKDDAAGQAIANR	37	16	11	65.76	b2b9°b9y3y4y5y7*y7y10y11y16	1614.80	30.181	30742	3	538.94	-12.78
P06179 FLIC_SALTY Flagellin;	5		VSGQTQFNGVK	125	11	8	36.72	b10y3y9°y9y10°y10*y10y11	1164.60	33.207	21905	2	582.80	-3.04
P06179 FLIC_SALTY Flagellin;	6		VRELAVQSANSTNSQSDLSIQAEITQR	91	28	3	11.7	b3y3y9	3060.54	66.837	16127	3	1020.85	7.98
P06179 FLIC_SALTY Flagellin;	7		VSDTAATVTGYADTTIALDNSTFK	180	24	7	19.44	b6°b6b10b15°b15y8y24	2462.17	71.311	14507	3	821.39	-10.01
P06179 FLIC_SALTY Flagellin;	8		QINSQTLGLDTLNVQQK	161	17	7	39.73	b6b11b13*b13y3y4y17	1899.99	66.700	4738	2	950.50	-12.14
P06179 FLIC_SALTY Flagellin;	9		AQPDLAEEAAATTENPLQK	392	19	5	21.89	b3b5*b5b10*b10	1968.99	94.362	82775	2	985.00	0.25
P06179 FLIC_SALTY Flagellin;	10		TEVVSIGGK	370	9	3	30.48	b3b6y7	889.50	33.838	15448	2	445.25	1.24
P06179 FLIC_SALTY Flagellin;	11		DGSISINTTK	339	10	4	26.9	b4b7°b7y4	1035.55	64.927	7095	2	518.28	14.62
P06179 FLIC_SALTY Flagellin;	12		ASATGLGGTDQK	204	12	5	48.12	b4b10b11y4y5	1105.54	48.340	3127	2	553.27	-8.39
P06179 FLIC_SALTY Flagellin;	13		IDAALAQVDTLRSDLGAVQNR	411	21	3	13.87	b10y9y18	2226.19	63.267	22995	3	742.73	1.54
P06179 FLIC_SALTY Flagellin;	14		FNSAITNLGNTVNNLTSARSR	432	21	8	36.23	b4b6b7b9°b9°b9y11y13	2250.17	111.860	5999	2	1125.59	4.88
P06179 FLIC_SALTY Flagellin;	15		SDLGAVQNRFNNSAITNLGNTVNNLTSAR	423	28	9	44.79	b13b15°b15b16b17y11y14y18°y18	2947.53	136.823	4745	2	1474.27	9.69
P06179 FLIC_SALTY Flagellin;	16		YKVSDTAATVTGYADTTIALDNSTFK	178	26	3	22.81	b7b12b13	2753.34	90.936	3172	3	918.45	-3.64
P06179 FLIC_SALTY Flagellin;	17		DGSISINTTKYTADDGTSK	339	19	3	14.93	b3y6y15	1973.91	91.671	1557	3	658.64	-9.15
P06179 FLIC_SALTY Flagellin;	18	Phosphoryl STY(13)	TNGEVTLAGGATSPLTGGLPATATEDVK	252	28	6	28.12	b4b7b12b16y13y16	2708.28	86.388	2693	2	1354.64	-4.06
P0A1D3 CH60_SALTY 60 kDa chaperonin;	1		GYLSPYFINKPETGAVELESPFILLADKK	197	29	17	68.56	b2b3b4°b4b6b7b9°b9b14y1y2y5y9y13y25y26y29	3239.71	95.455	135869	4	810.68	-3.62
P0A1D3 CH60_SALTY 60 kDa chaperonin;	2		ANDAAGDGTTTATVLAQSIITEGLK	80	25	20	148.12	b1b2b3b4*b4b5b14b15y1y3y4y5°y5y6y7y8y9y10y14y25	2418.23	91.817	110229	3	806.75	-4.34
P0A1D3 CH60_SALTY 60 kDa chaperonin;	3		EMLPVLEAVAK	231	11	10	73.95	b2b3°b3y2y3y5y6y8y9y11	1199.67	79.894	105476	2	600.34	-3.36
P0A1D3 CH60_SALTY 60 kDa chaperonin;	4		QQIEEATSDYDREK	350	14	9	42.4	b7y2y5y7y8°y8y10y14*y14	1711.76	33.470	71660	3	571.26	-11.48
P0A1D3 CH60_SALTY 60 kDa chaperonin;	5		VVINKDTTTHIDGVGEEAAIQGR	322	23	10	38.01	b1b3y2y3y5y6y8*y8y13y23	2399.27	67.411	65685	3	800.43	-4.68
P0A1D3 CH60_SALTY 60 kDa chaperonin;	6		LAGGVAVIK	371	9	5	44.94	b5b6y7y8y9	827.52	45.086	62970	2	414.27	-14.01
P0A1D3 CH60_SALTY 60 kDa chaperonin;	7		AVAAAVEELK	122	10	7	40.12	b2b3y2y5y7y8y10	1000.56	47.337	58126	2	500.78	-7.20
P0A1D3 CH60_SALTY 60 kDa chaperonin;	8		VEDALHATR	395	9	11	104.34	b2b3b4b5°b5y3y4y5y6y7y9	1011.51	26.260	41360	2	506.26	-9.90
P0A1D3 CH60_SALTY 60 kDa chaperonin;	9	Carbamidomethyl+C(6)	QIVLNCGEEPSVVANTVK	452	18	7	32.73	b7b13°b13y5y14y15y18	1957.02	61.663	40141	2	979.01	5.55
P0A1D3 CH60_SALTY 60 kDa chaperonin;	10	Carbamidomethyl+C(18)	SALQYAASVAGLMITTECMVTDLPK	501	25	5	18.83	b6b8b10y20y25	2670.34	86.369	38825	2	1335.67	7.22

[P0A1D3]CH60_SALTY 60 kDa chaperonin;	11	Carbamidomethyl+C(6)	ALSVPCSDSK	132	10	11	74.33	b2b3°b3y2y3°y3y5y6y7y8y10	1063.51	35.249	37860	2	532.26	-3.21
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	12		GVNVLADAVK	18	10	9	52.54	b2b4b8°b8y1y3y5y6y10	985.56	56.095	35109	2	493.28	-10.34
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	13		AVAAGMNPMDLK	105	12	10	93.8	b3b8y2y3y5y6y8y9y10y12	1217.60	58.395	34625	2	609.30	-1.90
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	14		SFGAPTITK	42	9	12	79.16	b1b2b3°b3b8y1y2y3y5y7y8y9	921.50	44.926	33409	2	461.25	-8.61
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	15		AIAQVGTISANSDETVGK	142	18	10	63.88	b2b7y10y11y12y13°y13*y13y14y18	1760.91	48.408	28810	2	880.96	4.99
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	16		GGDGNYGYNAAATEEYGNMIDMG ILDPTK	470	28	6	26.83	y1y3y5y10y11y28	2966.32	88.094	25672	3	989.44	12.43
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	17		ATLEDLGQAKR	311	11	6	41.49	b2b5y3y5y9y11	1201.65	39.142	15396	2	601.33	-6.50
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	18		GQNEQNVGIK	430	11	10	47.72	b2°b2b4b10°b10y3y4y9*y9y11	1201.58	26.999	10140	2	601.30	2.34
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	19		DGVSVAREIELEDK	51	14	4	19.28	b6b10b14y3	1559.77	78.006	5289	2	780.39	-11.11
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	20		VGAATEVEMK	380	10	5	40.12	b1b3b4b8y7	1034.51	56.077	3581	2	517.76	-4.37
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	21		LIAEAMDK	160	8	6	62.53	b7°b7y3y5y6y7	890.45	39.237	20262	2	445.73	-18.23
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	22		NVVLDK	36	6	2	26.84	b5y4	687.40	44.057	19494	1	687.40	-6.93
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	23		ATLEDLGQAK	311	10	4	26.9	b7°b7b9y9	1045.53	43.563	8840	2	523.27	-22.30
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	24		DTTIIIDGVGEEAAIQGR	327	18	6	30.97	b3b5b7y7*y7y11	1845.96	63.251	8494	3	615.99	20.57
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	25		AGKPLIIAEDVEGEALATLVVNT MR	242	26	7	26.5	b6y3°y3y7y9°y9y23	2723.48	136.253	3675	3	908.50	-6.90
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	26		EGVITVEDGTGLQDELVDVEGMQ FDR	171	26	7	31.71	b9b11b13y11*y11y12°y12	2851.37	83.362	1816	3	951.13	14.73
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	27		EIELEDK	58	7	5	40.46	b3°b3b5°b5y3	875.43	68.985	1505	1	875.43	-11.16
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	28		EIELEDKFENMGAMVK	58	17	6	36.13	b9y6y7y10*y10y14	2010.94	73.234	114556	3	670.99	-5.04
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	29		IADLKGQNEQNVGIK	425	16	12	78.88	b3b9y3y4y8y9*y9y10°y10*y10y11°y11	1741.89	40.018	98093	3	581.30	-11.98
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	30	Carbamidomethyl+C(16)	AVAAAVEELKALSVPCSDSK	122	20	6	37.58	b4b14y6y10y11y18	2045.04	71.889	49552	3	682.35	-10.74
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	31		AMLQDIATLTGGTVISEEIGMELE KATLEDLGQAK	286	35	10	46.97	b3b5b6°b6b7°b7y5y21y25y29	3675.89	122.058	36505	3	1225.97	5.25
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	32	Carbamidomethyl+C(13)	AMEAPLRQIVLNCGEPSVVANT VK	445	25	6	23.09	b4b5°b5b7y13°y13	2725.40	73.906	22675	3	909.14	0.18
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	33		AVAAGMNPMDLKR	105	13	9	96.93	b3y3y4y5y6y7y8*y8y11	1373.70	50.810	17782	2	687.35	-2.13
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	34	Carbamidomethyl+C(6)	ALSVPCSDSKAIAQVGTISANSDE TVGK	132	28	6	25.11	b10b11°b11y12y14°y14	2805.36	70.261	12166	3	935.79	-13.49
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	35		LIAEAMDKVGK	160	11	4	24.3	b6b8y9°y9	1174.64	46.146	11117	2	587.82	-9.98
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	36		EVASKANDAAGDGTTTATVLAQS IITEGLK	75	30	3	17.28	b3b8b10	2932.50	87.268	9651	3	978.17	-2.58
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	37		ANDAAGDGTTTATVLAQSIITEGL KAVAAGMNPMDLK	80	37	5	20.22	b11y3y5y8y12	3616.81	131.511	4883	4	904.96	-2.90
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	38	Carbamidomethyl+C(6)	QIVLNCGEPSVVANTVKGGDGN YGYNAATEEYGNMIDMGILDPTK	452	46	3	24.53	y3y9y10	4904.29	89.214	3379	4	1226.83	3.39
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	39		VGKEGVITVEDGTGLQDELVDVVE GMQFDR	168	29	7	24.93	b14b15y4*y4y12°y12*y12	3135.52	72.859	3308	4	784.64	2.57

[P0A1D3]CH60_SALTY 60 kDa chaperonin;	40		DTTIIIDGVGEEAAIQGRVAQIR	327	23	6	19.45	b12°b12b16°b16b18°b18	2413.26	136.823	2991	2	1207.13	-5.06
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	41		DGVSVAREIELEDK	51	14	3	19.28	b13y3y9	1559.81	97.823	2878	2	780.41	14.63
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	42	Phosphoryl.STY(4)	DGVSVAREIELEDK	51	14	6	45.41	b3y7y8°y8y9y12	1639.75	40.141	23527	3	547.25	-0.89
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	43	Oxidation+M(22)	EGVITVEDGTGLQDELDVVEGMQ FDR	171	26	4	18.28	b4b7b10y14	2867.33	113.253	38029	3	956.45	2.21
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	44	Oxidation+M()	AMLQDIATLTGGTVISEEIGMELE K	286	25	4	23.09	b11y9y10y14	2665.32	92.186	10884	2	1333.16	-5.86
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	45	Oxidation+M(9)	VGAATEVEMK	380	10	3	33.89	b5b6b8	1050.51	109.973	1882	1	1050.51	-3.72
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	46		EDALHATR	396	8	0	1.62		912.45	26.279	28618	2	456.73	-6.09
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	47		AAAVEELK	124	8	0	2.02		830.45	47.341	8428	1	830.45	-13.74
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	48		EMLPVLEAVAK	231	11	1	7.86	y4	1181.64	79.878	7383	2	591.32	-12.71
[P0A1D3]CH60_SALTY 60 kDa chaperonin;	49		QQIEEATSDYDREK	350	14	2	15.6	y4y6	1694.75	33.447	3253	3	565.59	0.50
[Q7CR46]IRAP_SALTY Anti-adaptor protein iraP;	1		QVEGALEGVKPDASVPDHDTELL R	50	24	13	91.78	b7°b7b9°b9b14y3y5y7y8y9y10y11y19	2575.26	59.642	31051	4	644.57	-13.65
[Q7CR46]IRAP_SALTY Anti-adaptor protein iraP;	2		NMAQNEQEMLIR	38	12	6	35.49	b2y8y9°y9y10y12	1476.70	55.947	27737	2	738.85	1.49
[Q7CR46]IRAP_SALTY Anti-adaptor protein iraP;	3	Oxidation+M(9)	NMAQNEQEMLIR	38	12	3	22.27	b4y5y7	1492.68	60.397	3269	2	746.84	-3.93
[Q7CR46]IRAP_SALTY Anti-adaptor protein iraP;	4		EGVKPDASVPDHDTELLR	56	18	0	7.69		1977.98	59.597	16334	3	660.00	-2.84
[P66313]RL6_SALTY 50S ribosomal protein L6;	1		APVVVPAGVDVK	6	12	14	141.23	b2b3b4b5y2y3y4y5y6y7y8y9y10y12	1150.67	53.272	65842	2	575.84	-8.38
[P66313]RL6_SALTY 50S ribosomal protein L6;	2		TLNDAVEVK	35	9	12	57.5	b1°b1b2°b2y1y3°y3y4y7°y7y8y9	988.52	38.412	50791	2	494.76	-9.94
[P66313]RL6_SALTY 50S ribosomal protein L6;	3		INGQVITIK	18	9	5	45.46	b3y3y4y8y9	985.60	48.446	42597	2	493.30	-7.56
[P66313]RL6_SALTY 50S ribosomal protein L6;	4		HADNALTFGPR	44	11	4	27.31	b5b6y9°y9	1198.59	46.450	22276	2	599.80	-7.23
[P66313]RL6_SALTY 50S ribosomal protein L6;	5		ALLNSMVIGVTEGFTK	69	16	3	24.86	y4y6y9	1679.90	94.147	50583	2	840.45	-0.73
[P66313]RL6_SALTY 50S ribosomal protein L6;	6		NGELTRTLNDAVEVK	29	15	4	29.43	b5b10b12y8	1658.85	81.941	10022	2	829.93	-9.57
[P0A1E3]CYSK_SALTY Cysteine synthase A;	1		YLSTALFADLFTEKELQQ	305	18	8	32.73	b2b5b16y2y7y8y11y18	2117.09	102.087	110055	2	1059.05	4.04
[P0A1E3]CYSK_SALTY Cysteine synthase A;	2		IQIGAGFIPGNLDLK	226	16	9	24.25	b2°b2b3b8y2y7°y7y10y16	1612.91	83.223	79541	2	806.96	2.19
[P0A1E3]CYSK_SALTY Cysteine synthase A;	3		LTLTMPETMSIER	87	13	13	101.4	b5°b5b10b12y6y8°y8y9°y9y10y11y12y13	1521.77	73.793	73443	2	761.39	1.93
[P0A1E3]CYSK_SALTY Cysteine synthase A;	4		YLLLQQFSNPANPEIHEK	137	18	12	62.17	b2b3y3°y3y6y7°y7y9°y9y11y15y18	2141.09	73.877	62348	3	714.37	-5.36
[P0A1E3]CYSK_SALTY Cysteine synthase A;	5		GVLKPGVELVEPTSGNTGIALAYV AAAR	56	28	5	25.32	y4y6y14y17y28	2753.52	81.346	60649	3	918.51	-0.27
[P0A1E3]CYSK_SALTY Cysteine synthase A;	6		ALGANLVLTEGAK	105	13	4	29.88	b2y3y5y7	1256.72	61.134	23507	2	628.86	-0.29
[P0A1E3]CYSK_SALTY Cysteine synthase A;	7		NIVVILPSSGER	293	12	10	82.8	b2b3b4y6°y6y7y8y9y10y12	1283.73	63.934	21894	2	642.37	-4.09
[P0A1E3]CYSK_SALTY Cysteine synthase A;	8		IGANMIWDAEK	44	11	5	35.3	b3b9°b9y6y9	1247.62	65.269	18480	2	624.31	4.89
[P0A1E3]CYSK_SALTY Cysteine synthase A;	9		VVGITNEEAISTAR	246	14	4	30.73	b3y9y10y12	1459.77	49.381	17860	2	730.39	-6.27

[P0A1E3]CYSK_SALTY Cysteine synthase A;	10		AEEIVASDPQK	126	11	6	52.49	b3b5y3y5y7y11	1186.59	31.501	16020	2	593.80	-3.39
[P0A1E3]CYSK_SALTY Cysteine synthase A;	11		LTLTMPETMSIERR	87	14	5	33.01	b9°b9b10y9y11	1677.87	67.795	3888	3	559.96	2.62
[P0A1E3]CYSK_SALTY Cysteine synthase A;	12		IYEDNSLTIGHTPLVR	3	16	4	24.25	b8b11y4y7	1827.94	61.563	26844	3	609.99	-8.81
[P0A1E3]CYSK_SALTY Cysteine synthase A;	13		GKTDLTITVAVEPTDSPVIAQALAG EEIKPGPHK	193	33	3	16.83	y5y10y22	3381.79	79.396	39337	4	846.20	-11.55
[P0A1E3]CYSK_SALTY Cysteine synthase A;	14		AEEIVASDPQKYLLQQFSNPANP EIHEK	126	29	9	38.75	b3b4°b4b5°b5b13y6y9*y9	3308.67	76.821	20199	4	827.92	-1.48
[P0A1E3]CYSK_SALTY Cysteine synthase A;	15		GAIQKAAEEIVASDPQK	121	16	5	17.15	b14y7°y7*y7y10	1683.91	67.427	6385	2	842.46	9.93
[P0A1E3]CYSK_SALTY Cysteine synthase A;	16		GYKLTLTMPETMSIER	84	16	3	17.15	b11y3y10	1869.95	75.238	5799	3	623.99	3.72
[P0A1E3]CYSK_SALTY Cysteine synthase A;	17		LMEEEGILAGISSGAAVAAALKLQ EDESFTNK	261	32	3	11.14	b8y11y23	3292.62	126.360	2463	3	1098.21	-11.79
[P0A1E3]CYSK_SALTY Cysteine synthase A;	18		SKIYEDNSLTIGHTPLVR	1	18	3	22.74	b6b10b12	2043.07	51.429	2386	3	681.70	-8.07
[P0A1E3]CYSK_SALTY Cysteine synthase A;	19	Phosphoryl STY(8)	IYEDNSLTIGHTPLVR	3	16	3	17.15	b4b7y9	1907.91	38.433	3637	3	636.64	-2.56
[P0A1E3]CYSK_SALTY Cysteine synthase A;	20	Oxidation+M(5)	LTLTMPETMSIERR	87	14	5	30.73	b7b8°b8b12y8	1693.84	67.847	11058	3	565.29	-12.18
[P0A1E3]CYSK_SALTY Cysteine synthase A;	21		LTMPETMSIER	89	11	1	7.42	b7	1307.64	73.787	10187	3	436.55	1.77
[P52616]FLJB_SALTY Phase 2 flagellin;	1		AQILQQAGTSVLAQANQVPQNVLSLLR	479	27	20	106.92	b2*b2b3b4b5°b5b7b8b17b18y1y2y4y6y9y10y12*y12y13y27	2860.60	104.953	132071	3	954.21	0.51
[P52616]FLJB_SALTY Phase 2 flagellin;	2		SQSALGTAIER	20	11	9	41.49	b2*b2b3y1y5y7y9°y9y11	1132.59	41.984	45416	2	566.80	-6.25
[P52616]FLJB_SALTY Phase 2 flagellin;	3		INSAKDDAAGQAIANR	37	16	11	65.76	b2b9°b9y3y4y5y7*y7y10y11y16	1614.80	30.181	30742	3	538.94	-12.78
[P52616]FLJB_SALTY Phase 2 flagellin;	4		VSGQTQFNGVK	125	11	8	36.72	b10y3y9°y9y10°y10*y10y11	1164.60	33.207	21905	2	582.80	-3.04
[P52616]FLJB_SALTY Phase 2 flagellin;	5		TAANQLGGVDGK	369	12	6	22.27	b4°b4*b4y5y8y12	1130.58	35.365	20326	2	565.79	-2.70
[P52616]FLJB_SALTY Phase 2 flagellin;	6		VRELAVQSANSTNSQSDLDISIAEITQR	91	28	3	11.7	b3y3y9	3060.54	66.837	16127	3	1020.85	7.98
[P52616]FLJB_SALTY Phase 2 flagellin;	7		FNSAITNLGNTVNNLSEAR	443	19	3	14.93	b5b10y6	2035.01	57.300	4280	4	509.51	-6.06
[P52616]FLJB_SALTY Phase 2 flagellin;	8		DTPAVVSADAK	288	11	3	24.3	b7b9y4	1073.56	27.012	1518	2	537.28	11.48
[P52616]FLJB_SALTY Phase 2 flagellin;	9		AQVINTNSLSLLTQNNLNK	1	19	4	14.93	b7*b7y10y15	2085.15	74.555	37560	2	1043.08	7.38
[P52616]FLJB_SALTY Phase 2 flagellin;	10		AYANNGTTLDSVGLDDAAIK	189	20	6	19.76	b3b11°b11y6°y6y14	2008.99	78.259	16029	3	670.34	4.19
[P52616]FLJB_SALTY Phase 2 flagellin;	11		SDLGAVQNR	434	9	3	38.26	y4y6y7	959.48	27.649	14798	2	480.24	-10.94
[P52616]FLJB_SALTY Phase 2 flagellin;	12		ELAVQSANSTNSQSDLDISIAEITQR	93	26	5	12.14	b13°b13y3y11*y11	2805.36	99.748	6427	3	935.79	2.00
[P52616]FLJB_SALTY Phase 2 flagellin;	13		TTSYTAADGTTK	357	12	4	26.25	b6°b6b7y6	1216.58	59.639	6299	3	406.20	7.63
[P52616]FLJB_SALTY Phase 2 flagellin;	14		AATGGTNGTASVTGGAVK	209	18	7	36.54	b4°b4b5°b5y13y14°y14	1519.74	57.730	3592	2	760.38	-17.99
[P52616]FLJB_SALTY Phase 2 flagellin;	15		MAQVINTNSLSLLTQNNLNK	0	20	7	39.19	b4b5b6°b6b8y7*y7	2216.14	98.387	3382	2	1108.57	-15.53
[P52616]FLJB_SALTY Phase 2 flagellin;	16		NANDGISIAQTTEGALNEINNNLQ R	66	25	3	12.4	b8b11y6	2670.34	61.959	3313	3	890.78	10.24
[P52616]FLJB_SALTY Phase 2 flagellin;	17		SRIEDSDYATEVSNMSR	462	17	7	51.19	b4b5b7b8y6*y6y9	1959.89	50.812	34241	2	980.45	10.40

P52616 FLJB_SALTY Phase 2 flagellin;	18		SDLGAVQNRFSAITNLGNTVNN LSEAR	434	28	4	21.91	b9y10*y10y11	2975.48	93.434	9897	3	992.50	-5.83
P52616 FLJB_SALTY Phase 2 flagellin;	19		AATGGTNGTASVTGGAVKFDAD NNK	209	25	7	42.66	b11b12b20y8y9y12y17	2324.14	96.908	9601	2	1162.57	11.98
P52616 FLJB_SALTY Phase 2 flagellin;	20		TEVVTDIDGKTYNASK	381	15	3	18.13	b3b10y8	1625.83	70.337	9489	2	813.42	-2.25
P52616 FLJB_SALTY Phase 2 flagellin;	21		TAANQLGGVDGKTEVVTDIDGK	369	21	7	31.18	b5°b5b10b13b14*b14y18	2073.10	89.768	6071	3	691.70	6.36
P52616 FLJB_SALTY Phase 2 flagellin;	22		AAGHDFKAQPELAEEAAK	396	18	5	15.58	b10*b10b12°b12y3	1824.95	72.103	5324	3	608.99	12.58
P52616 FLJB_SALTY Phase 2 flagellin;	23		TIEGGYALKAGDK	328	13	4	28.12	b3°b3b6b7	1322.68	89.724	3151	2	661.84	-12.46
P52616 FLJB_SALTY Phase 2 flagellin;	24		AKTTSYTAADGTTK	355	14	5	42.4	b6b9b10b12y10	1415.72	75.995	2628	2	708.36	12.24
P52616 FLJB_SALTY Phase 2 flagellin;	25		TTSYTAADGTTKTAANQLGGVD GK	357	24	4	12.7	b3b6y12°y12	2328.11	69.946	2502	3	776.71	-10.17
P52616 FLJB_SALTY Phase 2 flagellin;	26		AQVINTNSLSLLTQNNLNKSQSAL GTAIER	1	30	6	24.34	b3b5*b5b8*b8b10	3198.66	136.228	1965	3	1066.89	-14.27
P00924 ENO1_YEAST Enolase 1;	1		NVNDVIAPAFVK	67	12	16	111.78	b2b4*b4b5°b5b6y2y3y5y6 y7y9y10°y10*y10y12	1286.71	65.979	96092	2	643.86	-3.98
P00924 ENO1_YEAST Enolase 1;	2		VNQIGTLSSEIK	346	12	13	105.76	b2b3b4b6y1y3y5y6y8y9°y9 y10y12	1288.71	54.224	73954	2	644.86	-2.75
P00924 ENO1_YEAST Enolase 1;	3		TFAEALR	178	7	8	63.88	b3y1y3y4y5°y5y6y7	807.43	45.505	65152	2	404.22	-13.30
P00924 ENO1_YEAST Enolase 1;	4		SIVPSGASTGVHEALEMR	32	18	12	108.51	b13y2y3y4y5y6°y6y9y10y1 ly14y15	1840.91	61.423	65045	3	614.31	-9.15
P00924 ENO1_YEAST Enolase 1;	5		TAGIQIVADDLTVTNPK	312	17	8	63.36	b14y3y7y8y10y11y13y17	1755.95	72.304	50827	2	878.48	2.29
P00924 ENO1_YEAST Enolase 1;	6		AAQDSFAAGWGMVSHR	358	17	6	24.96	y3y6°y6y7°y7y17	1789.86	50.740	30539	3	597.29	9.55
P00924 ENO1_YEAST Enolase 1;	7		AVDDFLISLDGTANK	88	15	8	58.36	b3b5b7b10y5y6°y6y15	1578.80	82.005	26117	2	789.91	1.78
P00924 ENO1_YEAST Enolase 1;	8		IEEELGDNAVFAGENFHHGDK	415	21	8	54.46	b1b3b4b12y4y5y6y13	2328.02	57.653	24429	4	582.76	-12.58
P00924 ENO1_YEAST Enolase 1;	9		AADALLK	338	8	5	67.3	y3y4y5y6y7	814.49	53.706	74562	2	407.75	-20.16
P00924 ENO1_YEAST Enolase 1;	10		IATAIEK	330	7	7	63.88	b4°b4y3y4y5y6°y6	745.43	28.295	33399	2	373.22	-16.70
P00924 ENO1_YEAST Enolase 1;	11		LNQLLR	409	6	5	40.06	y3y4*y4y5*y5	756.46	42.680	30286	2	378.73	-14.60
P00924 ENO1_YEAST Enolase 1;	12		NVPLYK	126	6	1	13.62	y4	733.42	36.966	19824	1	733.42	-7.49
P00924 ENO1_YEAST Enolase 1;	13		YGASAGNVGDEGGVAPNIQTAE ALDLIVDAIK	201	33	4	11.05	b3b5y13°y13	3257.65	62.425	11819	6	543.78	11.39
P00924 ENO1_YEAST Enolase 1;	14		YPIVSIEDPFAEDDWEAWSHFFK	289	23	5	28.23	b4b9y3y4y6	2828.33	124.266	2041	4	707.84	15.19
P00924 ENO1_YEAST Enolase 1;	15		SVYDSRGNPTVEVELTTEK	9	19	4	28.47	b8b9y8y10	2124.03	48.305	3468	3	708.68	-5.40
P00924 ENO1_YEAST Enolase 1;	16		VNQIGTLSSEIKAAQDSFAAGWG VMVSHR	346	29	3	22.71	y3y13y14	3059.51	97.830	2290	3	1020.51	-8.54
P00924 ENO1_YEAST Enolase 1;	17	Oxidation+M(15)	WLTGPQLADLYHSLMK	272	16	6	30.79	b4°b4b13°b13y8y9	1888.98	85.390	23121	2	944.99	9.37
P00924 ENO1_YEAST Enolase 1;	18	Oxidation+M(17)	SIVPSGASTGVHEALEMRDGD K	32	22	5	20.86	b7b10b13°b13y9	2272.09	109.063	5745	3	758.03	-0.75
P00924 ENO1_YEAST Enolase 1;	19	Oxidation+M(15)	WLTGPQLADLYHSLMKR	272	17	3	16.31	b9b12y8	2045.05	73.948	2781	2	1023.03	-5.49
P00924 ENO1_YEAST Enolase 1;	20	Oxidation+M(13)	AAQDSFAAGWGMVSHR	358	17	5	26.14	b5y6y10°y10y12	1805.85	50.722	1502	2	903.43	8.04
P00924 ENO1_YEAST Enolase 1;	21		FAAGWGMVSHR	363	12	0	4.85		1317.67	50.727	5768	2	659.34	13.62
P00924 ENO1_YEAST Enolase 1;	22		AVDDFLISLDGTAN	88	14	0	4.05		1450.71	81.966	4419	2	725.86	0.67
P00924 ENO1_YEAST Enolase 1;	23		PSGASTGVHEALEMR	35	15	1	7.34	b11	1541.75	61.406	2674	2	771.38	6.10
P0A299 RL7_SALTY 50S ribosomal protein L7/L12;	1		DQIIEAVSAMSVMDEVVELISAMEE K	5	25	22	159.07	b2°b2*b2b3b4b5b6b7b8b1 0°b10y2°y2y3y4y5y6y7y8y 9°y9y25	2737.34	137.042	22668	3	913.12	1.16
P0A299 RL7_SALTY 50S ribosomal protein L7/L12;	2		EAKDLVESAPAALK	82	14	3	27.06	b3b4b13	1441.80	60.422	4886	2	721.41	9.40
P0A299 RL7_SALTY 50S ribosomal protein L7/L12;	3		DLVESAPAALKEGVSK	85	16	5	17.15	b2°b2b5b9y5	1613.86	56.618	3911	3	538.63	-8.17

[P0A299]RL7_SALTY 50S ribosomal protein L7/L12;	4		SITKDKIIEAVSAMSVM DVVELISA MEEK	1	29	4	22.71	b1y9y11y12	3166.63	114.401	3836	3	1056.22	12.49
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12;	5		DLVESAPAALK	85	11	3	31.29	y4y5y9	1113.59	53.385	19128	2	557.30	-21.59
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12;	6		SLEEAGAEVEVK	109	12	4	32.18	b3b10y3y7	1260.63	64.225	8578	2	630.82	0.68
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12;	7		AAGANK	60	6	1	13.62	b4	531.29	30.342	6390	1	531.29	-2.30
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12;	8		AAGANK VAVIK	60	11	9	97.37	b3b6*b6b7b9b10y4y5y7	1041.63	29.327	39411	2	521.32	-6.91
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12;	9		FGVSAAA AVAVAAGPAEAAEEKT EFDVILK	30	30	4	22.72	b6b7*b7b10	2932.53	136.302	7920	3	978.18	1.08
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12;	10	Oxidation+M(1)	MSITKDKIIEAVSAMSVM DVVELI SAMEEK	0	30	4	24.77	b3b10y6y7	3313.65	123.480	2079	3	1105.22	7.29
[P0A299]RL7_SALTY 50S ribosomal protein L7/L12;	11		DLVESAPAALK	85	11	1	7.32	b4	1113.60	60.367	4269	2	557.30	-14.36
[P0A1Z2]SKP_SALTY Chaperone protein skp;	1		IAIVNMG NLFQQVAQK	23	16	17	117.58	b2b3b4b5b15y1y2*y2y3y5y6y7*y7y11y12y13y16	1773.97	89.613	164578	2	887.49	1.03
[P0A1Z2]SKP_SALTY Chaperone protein skp;	2		VANDQSIDL VVDANTVAYNSSDV K DITADVLK	126	32	16	72.69	b1b2b4b5b6b7*b7b8*b8b10*b10b18b31*b31y1y3	3392.72	89.604	122369	3	1131.58	3.09
[P0A1Z2]SKP_SALTY Chaperone protein skp;	3		TGVSNTLENEFK	39	12	6	47.92	y2y4y5y7y8y12	1338.65	57.687	107252	2	669.83	-1.00
[P0A1Z2]SKP_SALTY Chaperone protein skp;	4		AQAFEKDR	97	8	4	36.09	b3y4y6y8	964.48	17.621	41314	2	482.74	-7.66
[P0A1Z2]SKP_SALTY Chaperone protein skp;	5		VANDQSIDL VVDANTVAYNSSDV K	126	24	4	12.7	b5b15*b15y9	2537.24	84.277	30374	3	846.42	2.69
[P0A1Z2]SKP_SALTY Chaperone protein skp;	6		AAELQKMETDLQSK	53	14	4	27.57	b9b12y9y12	1591.78	51.252	129455	3	531.27	-10.51
[P0A1Z2]SKP_SALTY Chaperone protein skp;	7		KVANDQSIDL VVDANTVAYNSSD VK	125	25	3	12.4	b4b8y5	2665.33	87.388	5593	4	667.09	-1.47
[P0A1Z2]SKP_SALTY Chaperone protein skp;	8		LQSMKAGSDR	70	10	3	33.89	y4y6y7	1092.54	87.738	1612	1	1092.54	-6.26
[P0A1Z2]SKP_SALTY Chaperone protein skp;	9		QAFEKDR	98	7	0	1.21		893.45	17.682	3911	2	447.23	-2.87
[P66593]RS6_SALTY 30S ribosomal protein S6;	1		YSAAITGAEGK	24	11	12	84.95	b2*b2b3*b3b4y2y5y6y7y9y10y11	1067.53	33.378	88414	2	534.27	-6.40
[P66593]RS6_SALTY 30S ribosomal protein S6;	2		FNDAVIR	79	7	6	50.67	b3y4y5y6y7*y7	834.44	42.105	72246	2	417.72	-13.46
[P66593]RS6_SALTY 30S ribosomal protein S6;	3		HAVTEASPMVK	93	11	7	47.72	b2b3b8y4y9y10y11	1169.59	30.829	40317	2	585.30	-4.07
[P66593]RS6_SALTY 30S ribosomal protein S6;	4		LEDWGR	38	6	2	26.84	y3y4	775.37	38.406	11906	2	388.19	-7.56
[P66593]RS6_SALTY 30S ribosomal protein S6;	5		SMVMR	86	5	1	13.22	b3	623.29	30.911	5636	1	623.29	-13.22
[P66593]RS6_SALTY 30S ribosomal protein S6;	6		MRHYEIVFMVHPDQSEQVPGMIE R	0	24	3	19.01	b3b7b10	2928.36	66.833	10675	3	976.79	-11.67
[P66593]RS6_SALTY 30S ribosomal protein S6;	7		YSAAITGAEGKIHR	24	14	4	27.06	b3b4*b4b9	1473.80	136.386	1778	2	737.40	14.00
[P66593]RS6_SALTY 30S ribosomal protein S6;	8		AVTEASPMVK	94	10	0	2.43		1032.55	30.754	2172	2	516.78	6.38
[P26982]DEGP_SALTY Protease do;	1		AGDVITSLNGKPISSF AALR	332	20	11	63.65	b3b4b5*b5b10y1y2y4y7y9y15	2017.08	74.718	98619	3	673.03	-11.86
[P26982]DEGP_SALTY Protease do;	2		GYVVTTNNH VVDNASVIK	124	17	7	36.13	b2b3y7y10y14y15y17	1828.93	50.077	43782	3	610.32	-11.41
[P26982]DEGP_SALTY Protease do;	3		SDIALIQINPK	160	12	10	96.81	b3b4b5y3y4*y4y5y6y7y12	1339.76	63.961	43135	2	670.38	-2.00

P26982 DEGP_SALTY Protease do;	4		GAFVSQVMPNSSAAK	313	15	11	77.53	b3b4b5b7b8y2y8y10y11*y11y15	1493.74	53.237	40645	2	747.37	-1.96
P26982 DEGP_SALTY Protease do;	5		AQVGTMPVGSK	352	11	11	73.95	b2*b2b5y3y5*y5y6y8*y8y9y11	1074.56	34.802	40012	2	537.78	-5.34
P26982 DEGP_SALTY Protease do;	6		NLTSQMVEYGQVK	275	13	13	71.74	b2b6b8b13y5y6*y6y8y9*y9y11*y11y13	1496.75	57.686	38970	2	748.88	4.00
P26982 DEGP_SALTY Protease do;	7		VGDYTVAIGNPFLGETVTSGIVS ALGR	186	28	19	102.78	b2b3b5*b5b6*b6b7*b7b8y1y2y3y4y5y6y8y10y14y28	2750.43	116.233	32979	3	917.48	-2.22
P26982 DEGP_SALTY Protease do;	8		GELGIMGTELNSELAk	289	16	5	35.43	b4b5b10y11y13	1661.85	74.920	8118	2	831.43	2.35
P26982 DEGP_SALTY Protease do;	9		AITVNLELQQSSQSQVDSSTIFSGI EGAEMSNK	373	33	3	22.19	b6y6y7	3498.65	106.632	3703	3	1166.89	-10.89
P26982 DEGP_SALTY Protease do;	10		SGLNVENYENFIQTDAAINR	214	20	5	14.37	b3*b3b6y12*y12	2268.10	66.743	3667	3	756.71	6.57
P26982 DEGP_SALTY Protease do;	11		VMPSVVSINVEGSTTVNTPR	48	20	4	22.61	b4b7b16y5	2087.09	87.495	2657	3	696.37	6.32
P26982 DEGP_SALTY Protease do;	12		ILDSKPSVLALNIQR	450	15	5	29.43	b3*b3y3y4y10	1666.96	65.148	39813	3	556.32	-17.65
P26982 DEGP_SALTY Protease do;	13	Carbamidomethyl+C(13) ;Carbamidomethyl+C(25))	NFQQFFGDDSPFCQDGSFPQNSPF CQGGGNGGNGGQQQK	71	39	5	15.66	b5b8y4y8y14	4240.78	90.591	5761	3	1414.27	7.37
P26982 DEGP_SALTY Protease do;	14		NIAELR	443	6	3	40.06	b4y3y4	715.41	33.833	4461	2	358.21	-5.37
P26982 DEGP_SALTY Protease do;	15		VDAQRGAfVSQVMPNSSAAK	308	20	8	38.76	b6*b6*b6b7*b7b11y5y6	2063.03	48.289	10973	4	516.51	-3.79
P26982 DEGP_SALTY Protease do;	16		RGELGIMGTELNSELAk	288	17	4	27.39	b15y6y9y10	1817.93	77.199	7616	2	909.47	-5.77
P26982 DEGP_SALTY Protease do;	17		GAFVSQVMPNSSAAKAGIK	313	19	4	24.11	b7*b7b8b10	1862.98	100.338	4504	2	931.99	1.25
P26982 DEGP_SALTY Protease do;	18		ILDSKPSVLALNIQRGDSSIYLLMQ	450	25	4	18.62	b11b14*b14b16	2774.53	136.857	3654	2	1387.77	7.30
P26982 DEGP_SALTY Protease do;	19		NLTSQMVEYGQVKR	275	14	3	19.28	b7b11y10	1652.83	83.258	3120	2	826.92	-4.58
P26982 DEGP_SALTY Protease do;	20		GELGIMGTELNSELAkAMK	289	19	6	49.49	b3b5b9b13b17y14	1992.03	93.543	2005	3	664.68	8.33
P26982 DEGP_SALTY Protease do;	21	Phosphoryl.STY(8)	GELGIMGTELNSELAk	289	16	3	24.86	y8y10_HPO3 y10y13_HPO3_y13	1741.81	90.734	2832	2	871.41	5.47
P26982 DEGP_SALTY Protease do;	22	Oxidation+M(8)	GAFVSQVMPNSSAAK	313	15	3	18.13	b6b8y8	1509.75	39.117	15723	2	755.38	9.62
P26982 DEGP_SALTY Protease do;	23	Oxidation+M(6)	GELGIMGTELNSELAk	289	16	5	17.15	b7y3y10*y10*y10	1677.82	62.917	9091	2	839.41	-8.88
P26982 DEGP_SALTY Protease do;	24		NLTSQMVEYGQV	275	12	0	3.24		1368.65	57.634	224310	2	684.83	2.05
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein;	1		ILLINPTDSDAVGNAVK	84	17	19	127.23	b2b3b4b5y2y5y9y10y11*y11y12*y12y13*y13y14*y14*y14y15y17	1739.96	70.662	105741	2	870.48	0.84
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein;	2		IPVITLDR	107	8	10	75.74	b2b3y1y3*y3y4y5y6y7y8	926.56	61.810	76603	2	463.78	-12.05
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein;	3		LAATIAQLPDQIGAK	253	15	14	118.89	b1b3b4*b4y3y4y7y8y9*y9y10y11y13y15	1509.86	66.212	52682	2	755.43	-2.75
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein;	4		VIELQGIAGTSAAR	150	14	11	75.83	b1b2b3y6y7y9y10y11*y11y12y14	1385.77	58.970	30687	2	693.39	0.18
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein;	5		GLNVMQNLTLAHPDVQAVFAQN DEMALGALR	193	31	14	55.57	b2b3b4*b4b5b11b22y2y4y9y11*y11y12y31	3336.69	102.478	22688	3	1112.90	1.02
P0A2C5 RBSB_SALTY D-ribose-binding periplasmic protein;	6		IAGDYIAK	135	8	5	40.86	y1y3y6y7y8	850.46	35.747	18422	2	425.73	-11.20

[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	7		ELANVQDLTVR	70	11	6	52.49	b4b7b10y3y6y11	1257.67	57.645	15753	2	629.34	-9.32
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	8		DTIALVISTLNNPFFVSLKDGAQK EADK	26	28	5	24.92	b14y3y8y12y25	3034.57	114.300	9706	4	759.40	-13.03
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	9		FNVLASQPADFDR	178	13	3	25.41	b7y10y11	1479.73	105.070	1619	2	740.37	5.03
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	10		QATKGDVVSHIASDNVLGGK	115	20	4	14.37	b6*b6b12y10	1996.03	51.413	50377	3	666.01	-8.87
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	11		FNVLASQPADFDRTK	178	15	3	24.15	b3y11y12	1708.84	54.845	4154	3	570.29	-13.72
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	12		ADVMVVGFDGTPDGEKAVK	231	19	5	36.28	b3b4b5°b5y9	1934.97	60.171	1793	2	967.99	7.32
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	13	Phosphoryl STY(11)	LATLVSAVALSATVSANAMAK	5	21	4	13.87	b15y9y12°y12	2069.08	73.886	7597	3	690.37	11.09
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	14	Phosphoryl STY(9)	ELANVQDLTVR	70	11	11	99.13	b7b8b9y3_H3PO4 y3°y3y4y7°y7y8°y8y9	1337.63	136.297	1591	1	1337.63	-8.03
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	15	Oxidation+M(4)	ADVMVVGFDGTPDGEK	231	16	5	37.87	b6y4y6y11y12	1652.77	66.193	2548	3	551.59	11.74
[P0A2C5]RBSB_SALTY D-ribose-binding periplasmic protein;	16		AGDYIAK	136	7	0	1.21		737.38	35.729	3191	1	737.38	-4.47
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	1		QQYGEGLAR	170	9	5	38.26	y1y4y6y7y9	1021.50	32.930	67933	2	511.25	-5.92
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	2		TAGLDSSQGPTAAK	139	14	16	84.11	b5°b5b10b14y6°y6y8y9°y9*y9y10°y10y11y12°y12y14	1303.65	28.784	49094	2	652.33	-2.43
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	3		LQKENIDFVYYGGYYPEMGMLR	211	23	7	28.23	b10b14y6*y6y8*y8y9	2814.33	84.857	45208	3	938.78	2.60
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	4		TQFMGPEGVGNASLSNIAGGAAE GMLVTMPK	242	31	13	52.19	b2b3b4b9y1y3y4y8y9°y9y13°y13y31	3035.48	92.364	38115	3	1012.50	6.76
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	5		GYQYIMR	132	7	9	37.45	b2b5*b5b7y1y2y4y5y7	930.46	47.570	30620	2	465.73	9.71
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	6		TQFMGPEGVGNASLSNIAGGAAE GMLVTMPKR	242	32	6	15.86	b2b3°b3b6b16y14	3191.61	120.942	19373	3	1064.54	14.61
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	7	Carbamidomethyl+C(10)	LVGVEYDDACDPK	66	13	3	20.63	b10y9y11	1480.66	46.945	11283	2	740.83	-0.08
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	8		QGNANIVFFDGITAGEK	186	17	3	23.3	b6b7y3	1780.88	64.534	8921	3	594.30	-4.52
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	9		KDPSGPYVWITYAAVQSLATAMT R	292	24	4	16.86	b6b17y5y12	2626.35	81.248	5997	3	876.12	6.23
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	10		YILETVKPQR	153	10	6	73.54	b4b8b9y4y6y9	1246.69	45.561	56285	3	416.24	-16.45
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	11		VAIVGAMSGPVAQWGDMEFNGA R	27	23	3	22.08	b11y5y6	2363.10	57.843	4210	3	788.37	-11.67
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	12		ENIDFVYYGGYYPEMGMLR	214	20	5	25.24	b5b6°b6b8y7	2445.13	99.925	3033	3	815.71	15.68
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	13		DPSGPYVWITYAAVQSLATAMTR	293	23	3	13.04	b10y9y13	2498.26	133.921	2741	3	833.43	10.36
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	14		VAIVGAMSGPVAQWGDMEFNGA RQAIK	27	27	4	21.9	b14b15*b15y13	2803.40	115.073	10996	3	935.14	-2.18
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	15		GDLKGFEFGVFQWHADGSSTVA K	346	23	3	13.04	b9b11y12	2483.21	99.075	10771	3	828.41	4.03
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	16		TQFMGPEGVGNASLSNIAGGAAE GMLVTMPKR	242	32	3	11.14	b12b22y14	3191.59	106.029	8259	4	798.65	9.18
[P0A1W6]LIVK_SALTY Leucine-ecific-binding protein;	17		LQKENIDFVYYGGYYPEMGMLR	211	23	4	13.04	b10y6*y6y18	2814.37	89.788	4414	3	938.79	13.88
[Q8ZRP4]DAPD_SALTY 2	1		MQQLQNVIETAFER	0	14	9	56.71	b3b12y1y3y7y9y12*y12y14	1706.86	85.769	53792	2	853.93	2.43
[Q8ZRP4]DAPD_SALTY 2	2		EAVNQVISLLDSGALR	28	16	6	50.32	y4y5y6y9y13y16	1684.93	91.893	42502	2	842.97	1.45

Q8ZRP4 DAPD_SALTY 2	3		INDNQVIDGAESR	68	13	13	102.65	b3b4b7°b7y5y6y7y8y9°y9*y9y10y13	1430.69	41.154	29037	2	715.85	1.79
Q8ZRP4 DAPD_SALTY 2	4		FADYDEAR	89	8	4	51.07	b3b4y4y6	986.42	34.487	13615	2	493.71	-1.73
Q8ZRP4 DAPD_SALTY 2	5	Carbamidomethyl+C(30)	NTVLMPSYVNIGAYYDEGTMVD TWATVGSQAQIGK	119	35	4	10.93	b12°b12b19y13	3747.81	98.747	3601	4	937.71	11.66
Q8ZRP4 DAPD_SALTY 2	6		VPMKFADYDEAR	85	12	4	22.27	b5b11y9°y9	1441.67	47.678	19103	2	721.34	-4.83
Q8ZRP4 DAPD_SALTY 2	7		IYDRETGEVHYGR	213	13	5	41.33	b3b12y6y7y9	1594.77	57.509	19002	3	532.26	6.58
Q8ZRP4 DAPD_SALTY 2	8		MQQLQNVIAFAFERR	0	15	3	24.15	b5y10y11	1862.93	137.695	4734	2	931.97	-11.93
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	1		TMNTPHGDAITVFDLR	23	16	5	24.86	b2y2y4y6y10	1787.85	71.107	47357	3	596.62	-11.61
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	2	Carbamidomethyl+C(15)	VQDQNQIPELNVYQCGTYQMHS LSEAQDIAR	113	31	11	61.98	b7b12b14y3y4y8y9y10y19 y24y31	3635.71	74.909	20754	3	1212.58	7.72
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	3	Carbamidomethyl+C(18)	DHLNGNGVEIIDISPMGCR	65	19	5	28.47	b2b3b6y10y11	2096.96	66.640	5096	3	699.66	-11.41
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	4		PLLDsFAVDHTR	1	12	6	61.13	y4y5y9y10°y10y11	1370.68	62.172	60711	3	457.57	-17.81
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	5		TGFYMSLIGTPDEQR	84	15	4	24.15	b13y3*y3y4	1714.84	76.371	8576	2	857.92	15.16
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	6		VADAWK	99	6	2	26.84	b3b4	689.37	36.678	6385	1	689.37	14.08
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	7		MPLLDsFAVDHTR	0	13	4	20.63	b3b6°b6y6	1501.76	46.166	4696	3	501.26	7.56
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	8		EVMPEK	45	6	1	13.62	b3	732.35	71.982	1641	1	732.35	-8.75
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	9		EVMPEKGIHTLEHLFAGFMR	45	20	3	21.16	y3y5y11	2342.19	86.265	3373	3	781.40	5.00
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	10	Oxidation+M(2)	TMNTPHGDAITVFDLR	23	16	3	23.69	b14y13y14	1803.88	81.323	4844	2	902.45	8.05
Q9L4T0 LUXS_SALTY S- ribosylhomocysteine lyase;	11	Carbamidomethyl+C(18) ;Oxidation+M(16)	DHLNGNGVEIIDISPMGCR	65	19	3	24.11	b3b10b11	2112.98	63.601	2503	3	705.00	2.08
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C;	1	Carbamidomethyl+C(13)	AAQYVAAHPEVCPAK	153	16	7	55.3	b3b4y3y5y8y11y16	1668.79	35.305	42622	3	556.94	-13.02
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C;	2		YAMIGDPTGALTR	93	13	8	62.72	b2b4y5y7y8y10y11y13	1365.68	62.920	35770	2	683.34	-3.22
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C;	3		ATFVVDPPQGIHIAIEVTAEIGR	120	23	13	94.56	b3°b3b4°b4b9b10y2y5y6y7 y8y9y23	2384.27	128.461	28509	3	795.43	-4.40
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C;	4		NGEFIEVTEKDTEGR	17	15	4	26.21	y4y6°y6y8	1723.82	49.815	5221	2	862.42	6.51
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C;	5		AWHSSSETIAK	80	11	4	27.31	b4y7°y7y8	1216.60	60.417	2004	2	608.81	7.53
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C;	6		EGEATLAPSLDLVGKI	171	16	6	45.65	b6b7b11°b11b12y3	1612.87	84.747	39035	2	806.94	-7.95
P0A251 AHPC_SALTY Alkyl hydroperoxide reductase subunit C;	7	Carbamidomethyl+C(13)	AAQYVAAHPEVCPAKWK	153	18	3	15.58	b8b10y10	1982.99	46.831	2406	3	661.67	-1.60
Q7CQJ0 SRA_SALTY Stationary-phase- induced ribosome-associated protein;	1		VVTEGDTSSVVNNPTGR	22	17	8	66.37	b13y3y4y5y6y8y13y17	1731.86	39.321	11679	2	866.43	3.88
Q7CQJ0 SRA_SALTY Stationary-phase- induced ribosome-associated protein;	2		VVTEGDTSSVVNNPTGRK	22	18	6	22.98	b1b2b5y6y7*y7	1859.92	35.478	2619	3	620.65	-12.60
Q7CQJ0 SRA_SALTY Stationary-phase- induced ribosome-associated protein;	3		ISNQR	16	5	1	13.22	y3	617.34	103.525	4032	1	617.34	1.88
Q7CQJ0 SRA_SALTY Stationary-phase- induced ribosome-associated protein;	4		KVVTEGDTSSVVNNPTGR	21	18	12	108.86	b10°b10b11°b11y4y5y6y7y 8y9y13y15	1859.92	36.337	112403	3	620.64	-14.11
P66692 RPIA_SALTY Ribose-5-phohate isomerase A;	1		AVGWAALQYVQPGTIVGVGTGST AAHFIDALGTMK	8	35	14	77.84	b3b5b6b7b9b11y3y4y6y11 y17y19y24y35	3487.82	107.309	58356	3	1163.28	3.36

[P66692]RPIA_SALTY Ribose-5-phohate isomerase A;	2		GADVALIGTPDGVK	201	14	6	31.53	b6y2y3y5y7y14	1312.70	57.346	22404	2	656.86	-5.67
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A;	3	Carbamidomethyl+C(3)	FICIADASK	112	9	8	61.68	b2b5y2y3y5y6y7y9	1024.51	51.028	20578	2	512.76	-3.46
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A;	4		GLGIHVFDLNEVDSLGIYVDGADE INGHMQMIK	61	33	5	13.29	b11b16y6y10°y10	3599.78	95.956	8923	3	1200.60	9.29
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A;	5		GGGAALTR	94	8	3	36.09	b3y5y7	702.38	34.994	2302	1	702.38	-9.04
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A;	6		QVDILGKFPLPVEVIPMAR	121	19	4	23.65	b3y4y7y9	2122.19	99.855	39817	3	708.07	-6.79
[P66692]RPIA_SALTY Ribose-5-phohate isomerase A;	7		GADVALIGTPDG	201	12	0	3.64		1085.55	57.359	3017	2	543.28	-0.79
[P0A1H3]EFG_SALTY Elongation factor G;	1		VYSGVVNSGDTVLSNVK	337	17	14	111.84	b2b4b5°b5y4y5*y5y9y10y 11y12y14y15y17	1737.91	62.073	59148	2	869.46	2.67
[P0A1H3]EFG_SALTY Elongation factor G;	2	Carbamidomethyl+C(11)	VLNNEILVTCGSAFK	255	16	6	35.43	b2b12b14y5y8y9	1777.97	106.036	46765	3	593.33	10.64
[P0A1H3]EFG_SALTY Elongation factor G;	3		SGPLAGYPVVDLGVR	562	15	11	74.52	b3°b3b5°b5b7y3y4y8y10y1 1y15	1499.83	76.407	39107	2	750.42	2.28
[P0A1H3]EFG_SALTY Elongation factor G;	4		IGEVHDGAATMDWMEQEQR	39	20	8	36.24	b3b10b12y3*y3y5y9y20	2331.99	62.112	23534	3	778.00	-1.88
[P0A1H3]EFG_SALTY Elongation factor G;	5		IHAEVPLSEMFGYATQLR	653	18	4	15.58	b1b5b11y8	2062.02	90.025	23363	3	688.01	-11.37
[P0A1H3]EFG_SALTY Elongation factor G;	6		EFNVEANVGKPVAYR	475	16	6	17.15	b2b3°b3b11y8y16	1820.91	53.293	21488	3	607.64	-12.20
[P0A1H3]EFG_SALTY Elongation factor G;	7		GQYGHVVIDMYPLEPGSNPK	512	20	7	60.18	b4b5b7b10b11y9y10	2201.06	70.136	21015	3	734.36	-5.88
[P0A1H3]EFG_SALTY Elongation factor G;	8		LGANPVPLQLAIGAEEGFTGVVDL VK	161	26	5	15.79	b4b6y3y12y26	2607.41	119.681	19982	3	869.81	-10.58
[P0A1H3]EFG_SALTY Elongation factor G;	9		YLGGEELTEEEIK	236	13	7	53.09	b5b6b7y8°y8y9y13	1509.73	89.082	11680	2	755.37	-1.37
[P0A1H3]EFG_SALTY Elongation factor G;	10		REFNVEANVGKPVAYREAIR	474	21	5	26.73	b6b11b15y7y9	2446.29	64.484	9032	5	490.06	-3.49
[P0A1H3]EFG_SALTY Elongation factor G;	11		AINWNDADQGVTFEYEDIPADMQ DLANEWHQNLIESAAEASEELME K	189	47	16	59.5	b2b3b5b6b11*b11y1y2°y2 y3y4y5y7y8y10y29	5380.40	125.675	7250	4	1345.86	3.63
[P0A1H3]EFG_SALTY Elongation factor G;	12		VEVETPEENTGDVIGDLR	618	19	3	14.93	b7y5y10	2058.97	79.992	5151	4	515.50	-4.98
[P0A1H3]EFG_SALTY Elongation factor G;	13	Carbamidomethyl+C(20)	AGDIAAAIGLKDVTTGDTLCDPEN PIILER	378	30	6	21.98	b6b7°b7y2°y2y11	3138.56	121.118	2741	3	1046.86	-12.52
[P0A1H3]EFG_SALTY Elongation factor G;	14		VVGQIK	153	6	1	13.62	b4	643.41	45.085	12139	1	643.41	-3.23
[P0A1H3]EFG_SALTY Elongation factor G;	15		GIQEQLK	555	7	3	37.45	b5y3y4	815.46	51.998	9662	1	815.46	-4.87
[P0A1H3]EFG_SALTY Elongation factor G;	16	Carbamidomethyl+C(10)	VLDGAVMVYCAVGGVQPQSETV WR	104	24	3	12.7	b5b16y3	2621.29	85.766	6897	3	874.43	1.68
[P0A1H3]EFG_SALTY Elongation factor G;	17		LHFGSYHDVDSSELAFK	577	17	3	23.71	b5b10b12	1951.95	84.089	5234	3	651.32	17.39
[P0A1H3]EFG_SALTY Elongation factor G;	18		MEFPEPVISIAVEPK	408	15	7	44.69	b4b9b12°b12b14°b14y4	1685.86	93.539	3295	2	843.43	-14.70
[P0A1H3]EFG_SALTY Elongation factor G;	19		AGDIAAAIGLK	378	11	3	27.31	b3y6y7	999.58	65.308	1821	2	500.29	-7.33
[P0A1H3]EFG_SALTY Elongation factor G;	20		TTTTTERILFYTGVNHK	23	16	4	17.15	b12y3y8*y8	1880.98	48.304	50449	3	627.67	-1.23
[P0A1H3]EFG_SALTY Elongation factor G;	21		GYEFINDIKGGVIPGEYIPAVDK	532	23	4	23.13	b10b11*b11b14	2494.29	98.321	11788	3	832.10	3.23
[P0A1H3]EFG_SALTY Elongation factor G;	22		HASDDEPFSALAFKIATDPFVGNL TFFR	309	28	5	22.72	y4y5y12°y12*y12	3113.54	88.037	7076	3	1038.52	-0.16

P0A1H3 EFG_SALTY Elongation factor G;	23		GQSEVTGVKIHAEVPLSEMFY ATQLR	643	28	3	17.72	b8b12b14	3076.56	119.950	2918	3	1026.19	7.30
P0A1H3 EFG_SALTY Elongation factor G;	24	Carbamidomethyl+C(13)	SMRVLDGAVMVVYCAVGGVQPQS ETVWR	101	27	6	21.19	b8b12°b12y6y12y16	2995.50	97.172	2057	3	999.17	13.86
P0A1H3 EFG_SALTY Elongation factor G;	25	Phosphoryl.STY(4)	LAASIAFKEGFK	594	12	5	22.27	b4_HPO3 b4°b4b8°b8y8	1361.69	37.487	2942	3	454.57	12.46
P0A1H3 EFG_SALTY Elongation factor G;	26	Phosphoryl STY(15)	EFNVEANVGKQPQVAYREAIR	475	20	4	25.24	b10y5y6y11	2370.17	115.037	2248	3	790.73	7.31
P0A1H3 EFG_SALTY Elongation factor G;	27	Oxidation+M(5)	GVQAMLDIVIDYLPSPVDVPAIN GILDDGK	273	30	4	16.52	b4b6b9y3	3111.58	94.424	7465	3	1037.86	-5.10
P0A1H3 EFG_SALTY Elongation factor G;	28	Oxidation+M(10)	IHAEVPLSEMFYATQLR	653	18	8	32.73	b10b12y8y9°y9*y9y16*y16	2078.03	111.821	3157	2	1039.52	-3.29
P0A1H3 EFG_SALTY Elongation factor G;	29		SGPLAGYP	562	8	0	4.05		761.38	76.425	1942	1	761.38	0.08
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	1		IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	9	54.19	b5b6b7b8b22y2y5y7y11	3950.89	95.202	68560	4	988.48	1.67
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	2		MQLNSTEISELIK	0	13	8	45.52	b2b3b13y3y8y10y11y13	1505.79	76.699	43695	2	753.40	0.65
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	3		ILEVPVGR	93	8	4	40.86	y4y5y6y8	882.53	52.408	37350	2	441.77	-12.03
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	4		GYLADVELAK	453	10	9	40.12	b2b8°b8y1y2y6y7y9y10	1078.57	60.401	36021	2	539.79	-6.34
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	5		QYAPMSVAQQLVLFAAER	434	19	8	31.62	b3°b3b6y2y5y6y16y19	2109.10	92.963	31804	2	1055.05	8.91
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	6	Carbamidomethyl+C(7)	IHGLADCMQGEMISLPGNR	40	19	13	40.86	b2b3b13°b13y4y6°y6*y6y10°y10*y10y13y19	2098.98	69.070	31541	3	700.33	-0.35
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	7		DSVGAVVMGPYADLAEGMK	68	19	7	53.96	b5y7y11y12y13y14y19	1909.92	83.368	29745	2	955.46	7.54
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	8	Carbamidomethyl+C(1)	CIYVAIGQK	192	9	4	38.26	b3b4b6y9	1051.55	57.365	18373	2	526.28	-5.57
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	9		ELAAFSQFASDLDDATR	401	17	7	42.57	b5b10b14y5y11y13y17	1856.89	88.324	17709	2	928.95	10.91
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	10		QSVDQPVTGYK	139	12	15	93.8	b4°b4°b4b8b12y4°y4y5*y5y6y7°y7y8y10y12	1349.67	34.062	16008	2	675.34	-2.80
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	11		ELAAFSQFASDLDDATRK	401	18	5	36.98	b6y6y9y11y13	1984.93	83.179	13226	3	662.32	-13.71
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	12		GEDALIIYDDLK	252	13	4	20.63	b12°b12y4y10	1451.72	68.259	42532	2	726.36	-7.23
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	13		AVDSMIPIGR	151	10	3	26.9	b7y5y8	1058.56	59.863	33031	2	529.78	-6.34
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	14		TALAIIDAINQR	175	12	4	29.47	y3*y3y4y9	1298.74	73.958	20444	2	649.87	-3.29
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	15		DHAPLMQEINQSGGYNDEIEGK	477	22	3	22.18	b3b4y3	2445.14	93.424	5871	4	612.04	17.87
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	16		VELLK	426	6	1	13.62	y5	702.43	39.922	4838	2	351.72	-13.12
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	17		IGSFEAALLAYVDRDHAPLMQEIN QSGGYNDEIEGK	463	36	5	21.4	b6y7°y7y8y11	3950.84	84.053	45693	3	1317.62	-10.81
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	18		VVNTLGAPIDGKGPVDNDGFSAV EAIAPGVIDR	106	33	11	51.35	b16°b16b27y5y6°y6y7y15y16y28°y28	3263.71	83.998	33480	3	1088.57	4.41
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	19		AARVNADYVEAFTK	300	14	3	24.72	b13y9y10	1554.77	89.738	5097	2	777.89	-12.80
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	20		GILDSFKATQSW	501	12	3	22.27	b6y8y11	1352.70	87.826	3429	2	676.85	12.45
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	21	Carbamidomethyl+C(6)	DSGIKCIYVAIGQK	187	14	4	27.85	b7b9b13°b13	1551.83	84.062	2171	2	776.42	6.53

Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	22		DSVGAVVMGPYADLAEGMKVK	68	21	3	13.87	b5b9y14	2137.09	78.367	2076	2	1069.05	9.60
Q7CPE1 ATPA_SALTY ATP synthase subunit alpha;	23	Oxidation+M(18)	DSVGAVVMGPYADLAEGMK	68	19	4	23.65	b8y3y9y11	1925.91	66.296	2949	2	963.46	6.40
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	1		AGLGMMEGVLENVPSAR	78	17	7	43.82	b11b13b14y4y7y12y17	1730.87	81.616	34906	2	865.94	5.78
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	2		VLVLVAAPEGIAALEK	155	16	8	58.19	b1b2b3b4b5b6y9y11	1592.96	85.812	27151	2	796.98	-0.54
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	3		ITVVPILR	70	8	5	40.86	b2*b2y4y5y6	910.60	69.752	10687	2	455.80	-7.37
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	4		NEETLEPVYPYFQK	103	13	7	25.41	b1b2*b2b9b10y6y13	1593.77	52.156	7578	2	797.39	-7.66
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	5		VTIEGWNGPVEIDQIK	51	16	4	17.15	b1b8b12y11	1797.96	75.294	3902	2	899.48	10.18
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	6		ELASEVGSLTYEATADLETEK	29	22	5	26.91	b13*b13b14y7y15	2369.15	91.470	2064	2	1185.08	-3.09
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	7		ISVVGMYRNEETLEPVYPYFQK	95	21	4	13.87	b8b11*b11y17	2499.23	72.809	11426	3	833.75	-10.94
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	8		ELASEVGSLTYEATADLETEKVT IEGWNGPVEIDQIK	29	38	5	19.87	b6b12b15b20y4	4148.04	111.906	3958	3	1383.35	-10.83
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	9	Oxidation+M(6)	AGLGMMEGVLENVPSAR	78	17	5	39.14	b5b10b14b16y13	1746.84	63.203	13602	3	582.95	-6.15
P0A2M5 UPP_SALTY Uracil phohoribosyltransferase;	10		MEGVLENVPSAR	83	12	0	4.85		1301.64	81.598	2770	2	651.33	-6.66
P02906 SUBI_SALTY Sulfate-binding protein;	1		YLYSPEGQEIAAK	263	13	13	90.4	b2b3b4b7*b7b10*b10b11y 9y10*y10y11y13	1468.73	50.579	70556	2	734.87	0.58
P02906 SUBI_SALTY Sulfate-binding protein;	2		LFTIDEVFGGWAK	298	13	8	45.52	b2b3*b3y5y6y8y11y13	1482.76	101.754	57142	2	741.88	-0.49
P02906 SUBI_SALTY Sulfate-binding protein;	3		NVEVLDSGAR	183	10	9	39.33	b2*b2b3*b3b9b10y5y8y10	1059.53	40.029	53449	2	530.27	-7.60
P02906 SUBI_SALTY Sulfate-binding protein;	4		AVAEAYLK	255	8	7	40.86	b1b2y1y4y5y6y8	864.47	40.916	32309	2	432.74	-10.38
P02906 SUBI_SALTY Sulfate-binding protein;	5		GSTNTFVER	193	9	9	67.7	b2y3y4*y4y5y6*y6y7y9	1010.48	32.269	30701	2	505.75	-7.13
P02906 SUBI_SALTY Sulfate-binding protein;	6		QATSVINGIEADVTLALAYDVD AIAER	66	28	8	49.65	b2b11y2y3y4y9y10y11	2917.52	128.001	25028	3	973.18	0.42
P02906 SUBI_SALTY Sulfate-binding protein;	7		WNYLAAWGYALHHNNNDQAK	153	20	9	30.63	b2b3b4*b4b8y8y12*y12y2 0	2386.14	79.123	5883	2	1193.57	10.95
P02906 SUBI_SALTY Sulfate-binding protein;	8		FEIVTPSESILAEPVSVVDK	226	21	4	24.7	b8y5y10y11	2260.24	77.096	85781	3	754.08	18.15
P02906 SUBI_SALTY Sulfate-binding protein;	9		QIHDWNDLIKPGSVITPNPK	126	21	10	57.47	b3*b3b4*b4b9b10y4y5*y5 y17	2371.23	72.907	74954	4	593.56	-20.39
P02906 SUBI_SALTY Sulfate-binding protein;	10		DIQLLNVSYPTR	20	13	4	29.88	y4y6y10*y10	1533.77	82.458	10612	2	767.39	-12.02
P02906 SUBI_SALTY Sulfate-binding protein;	11		VVEK	247	4	2	26.03	b3y3	474.29	66.621	7032	1	474.29	4.95
P02906 SUBI_SALTY Sulfate-binding protein;	12		LPDNSAPYTSTIVFLVR	104	17	6	24.96	b4b6*b6*b6b7*b7	1893.00	86.052	2448	2	947.00	-5.42
P02906 SUBI_SALTY Sulfate-binding protein;	13		RLPDNSAPYTSTIVFLVR	103	18	3	22.98	b9b10y5	2049.09	82.723	23505	3	683.70	-9.41
P02906 SUBI_SALTY Sulfate-binding protein;	14		DIQLLNVSYPDPTRELYEQYNK	20	21	6	18.92	b10b16y9*y9y15*y15	2601.30	136.840	3019	2	1301.15	7.23
P02906 SUBI_SALTY Sulfate-binding protein;	15		AVAEAYLKLYLSPEGQEIAAK	255	21	5	37.41	y7y9*y9y10y11	2314.17	114.333	2156	3	772.06	-9.81
Q7CR87 SURA_SALTY Chaperone surA;	1		LAYDGLNYSTYR	117	12	5	37.25	b8y4y8y10y12	1435.69	58.450	58752	2	718.35	3.32
Q7CR87 SURA_SALTY Chaperone surA;	2		IQELPGIFAQALSTAK	235	16	14	41.29	b2*b2b3*b3*b3b4*b4*b4y 1y2y3y12y14y16	1686.94	89.691	58289	2	843.97	-1.16

Q7CR87 SURA_SALTY Chaperone surA;	3		ITDEQLDQAIANIAK	90	15	11	63.64	b2°b2b3b5b12b14y1y4y5y13y15	1642.87	80.088	47369	2	821.94	2.23
Q7CR87 SURA_SALTY Chaperone surA;	4		ITVLPQEVDALAK	149	13	13	62.72	b2°b2b3°b3y1y2y4y5y9°y9y10y11y13	1396.80	70.492	45067	2	698.90	-1.84
Q7CR87 SURA_SALTY Chaperone surA;	5		LNAGQAGQQLPDDATLR	50	17	11	57.72	b2b3b7°b7y4y5y7°y7y11y12y17	1767.91	50.768	44785	2	884.46	4.49
Q7CR87 SURA_SALTY Chaperone surA;	6		QIGTQNDASTELNLSHILALPENP TSEQVNDAQR	162	35	6	15.08	b6y3y6y12*y12y35	3816.93	88.449	22707	3	1272.98	8.57
Q7CR87 SURA_SALTY Chaperone surA;	7		GQSQSISVTEVHAR	274	14	5	45.41	b8y6y8y9y10	1498.74	36.922	13455	3	500.25	-14.66
Q7CR87 SURA_SALTY Chaperone surA;	8		VAAVVNNGVVLESDDGLMQSV K	27	23	7	28.23	b3b4b14°b14y8y11*y11	2343.24	90.737	11851	2	1172.12	7.40
Q7CR87 SURA_SALTY Chaperone surA;	9		TTFAAAAKEYSQDPGSANQGDDL GWATPDIFDPAFRDALTK	318	41	5	21.31	b2b4b9b11b13	4301.02	91.394	9817	4	1076.01	-3.97
Q7CR87 SURA_SALTY Chaperone surA;	10		QAESIVEEAR	197	10	4	26.9	b4b6y5°y5	1131.58	71.534	14458	2	566.29	12.62
Q7CR87 SURA_SALTY Chaperone surA;	11		EYSQDPGSANQGDDLGWATPDIF DPAFR	326	28	6	28.12	b3b11y4y7y11y13	3011.39	93.432	3669	2	1506.20	16.62
Q7CR87 SURA_SALTY Chaperone surA;	12		DALTK	354	5	1	13.22	b4	547.30	43.538	3560	1	547.30	-11.71
Q7CR87 SURA_SALTY Chaperone surA;	13		LIMDQIILQMGGK	73	13	7	74.76	y4y5y6y7y11°y11y12	1530.81	87.831	3180	3	510.94	-20.81
Q7CR87 SURA_SALTY Chaperone surA;	14		GQISAPVHSSFGWHLIELLDTR	362	22	12	66.11	b6°b6b8°b8b9b10°b10b12y3y6y12y13	2463.28	94.437	1993	3	821.76	-0.59
Q7CR87 SURA_SALTY Chaperone surA;	15		LAITYSADQQALKGGQMGWGR	214	21	10	112.41	y4y5y7y8y9y10y11y12y16y18	2251.12	65.034	30042	3	751.05	-2.71
Q7CR87 SURA_SALTY Chaperone surA;	16		KFSEEAATWMQEQR	404	14	6	39.02	b6b7b10y5°y5y9	1740.81	56.566	9490	2	870.91	7.92
Q7CR87 SURA_SALTY Chaperone surA;	17		SRLAYDGLNYSTYR	115	14	4	19.28	b6°b6b8y8	1678.80	66.678	6835	3	560.27	-13.52
Q7CR87 SURA_SALTY Chaperone surA;	18		GQSQSISVTEVHARHILLKPSIMN DQQR	274	30	3	11.38	b3y8y14	3340.70	97.197	6391	4	835.93	-14.76
Q7CR87 SURA_SALTY Chaperone surA;	19	Oxidation+M(19)	VAAVVNNGVVLESDDGLMQSV K	27	23	4	35.54	b3b4y7y8	2359.22	114.747	15259	3	787.08	0.62
Q7CR87 SURA_SALTY Chaperone surA;	20		GQSQSISVTEVHAR	274	14	0	3.64		1481.73	36.914	1636	3	494.58	-2.80
P66038 RISB_SALTY 6	1		IGQVKDDNITVVWVPGAYELPLA TEALAK	40	29	18	114.31	b3b8b9b10°b10b11°b11°b11b12b13b14°b14y4y9y12y15y16y29	3110.69	98.082	93377	3	1037.57	4.32
P66038 RISB_SALTY 6	2		FNQFINDSLLDGAVDALTR	21	19	12	98.7	b4b10b13°y4y5y6y8y9y10y14y15y19	2109.08	101.076	68524	2	1055.05	10.65
P66038 RISB_SALTY 6	3		GAEAALTALEMINVLK	136	16	4	17.15	b6b13y1y4	1643.90	102.746	26226	2	822.46	-0.37
P66038 RISB_SALTY 6	4		VAITIAR	14	7	3	40.46	y4y5y6	743.46	44.224	12653	2	372.24	-18.06
P66038 RISB_SALTY 6	5		ANVAAPDAR	5	9	3	30.48	b3y6y7	884.45	22.673	11370	2	442.73	-7.52
P65882 PURA_SALTY Adenylosuccinate synthetase;	1	Carbamidomethyl+C(7)	LLLSEACPLILDYHVALDNAR	97	21	6	30.01	b2y3y5°y5y8y9	2396.25	91.455	28086	3	799.42	-7.64
P65882 PURA_SALTY Adenylosuccinate synthetase;	2		EVTTTPLAADDWK	354	13	5	29.66	b3b9y8y11y13	1446.72	76.070	15355	2	723.86	3.04
P65882 PURA_SALTY Adenylosuccinate synthetase;	3		GVEPIYETMPGWSESTFGVK	367	20	4	22.61	b8b11b13y13	2214.08	99.765	15303	2	1107.54	14.89
P65882 PURA_SALTY Adenylosuccinate synthetase;	4		VLDDTMAVADILTSMVVDVSDLL DQAR	186	27	17	124.12	b2b3b4b5b6b7b9y3*y3y4y5*y5y7y8y10y11*y11	2905.45	138.295	10714	3	969.16	0.50
P65882 PURA_SALTY Adenylosuccinate synthetase;	5		MGNNVVVLGTQWGDEGK	0	17	4	23.3	b14°b14y4y5	1803.89	87.621	2164	2	902.45	10.90
P65882 PURA_SALTY Adenylosuccinate synthetase;	6		IEELTGVPIDIISTGPDR	402	18	3	15.58	b7y5y13	1924.99	87.552	34351	3	642.33	-18.01

P65882 PURA_SALTY Adenylosuccinate synthetase;	7	Carbamidomethyl+C(2)	LCVAYR	343	6	1	13.62	b5	781.40	30.816	19666	1	781.40	1.48
P65882 PURA_SALTY Adenylosuccinate synthetase;	8		GNNVVVLGTQWGDEGK	1	16	3	17.15	b15y5y14	1672.83	81.872	18552	3	558.28	-1.31
P65882 PURA_SALTY Adenylosuccinate synthetase;	9		TGWLDTVAVR	307	10	4	28.66	b3°b3y5y6	1117.59	68.919	4986	2	559.30	-5.02
P65882 PURA_SALTY Adenylosuccinate synthetase;	10		AYSTR	268	5	1	13.22	b4	597.29	49.346	2866	1	597.29	-12.47
P65882 PURA_SALTY Adenylosuccinate synthetase;	11		YVDYVLGILK	258	10	3	33.89	b3b6b7	1182.67	44.956	2193	2	591.84	-5.26
P65882 PURA_SALTY Adenylosuccinate synthetase;	12		VGDLFDK	148	7	4	40.46	b4°b4y3y6	793.39	70.551	1913	1	793.39	-20.00
P65882 PURA_SALTY Adenylosuccinate synthetase;	13		AEAVDYQK	178	8	4	36.09	b4°b4b7y3	923.44	88.680	1583	1	923.44	-2.71
P65882 PURA_SALTY Adenylosuccinate synthetase;	14		GIGPAYEDK	132	9	3	30.48	b5b6y8	949.46	83.143	1538	1	949.46	-0.64
P65882 PURA_SALTY Adenylosuccinate synthetase;	15		GNNVVVLGTQWGDEGKGK	1	18	4	15.58	b13y5y7°y7	1857.92	40.213	78305	2	929.47	-11.37
P65882 PURA_SALTY Adenylosuccinate synthetase;	16		AIGTTGRGIGPAYEDK	125	16	3	17.15	b5y5y7	1605.81	82.240	17604	2	803.41	-7.45
P65882 PURA_SALTY Adenylosuccinate synthetase;	17		VLDDTMAVADILTSMVVDVSDLLDQARQR	186	29	3	22.71	b8b9b11	3189.62	109.058	6288	3	1063.88	0.69
P65882 PURA_SALTY Adenylosuccinate synthetase;	18		EVMHEYHNFQLVNYKAEAVDYQK	163	23	7	29.46	b20y4°y4*y4y7y10y19	2881.39	93.547	3644	3	961.13	12.12
P65882 PURA_SALTY Adenylosuccinate synthetase;	19		LKEVMEYHNFQLVNYK	161	17	4	16.31	b9y5y10*y10	2218.09	112.832	3398	2	1109.55	-3.19
P65882 PURA_SALTY Adenylosuccinate synthetase;	20	Oxidation+M()	ENVTSIIGNGVVLSPSALMKEMKELEDRL	62	28	7	25.52	b4°b4b8*b8y6y7y9	3075.54	132.607	4998	3	1025.85	-8.34
P65882 PURA_SALTY Adenylosuccinate synthetase;	21	Oxidation+M(15)	VLDDTMAVADILTSMVVDVSDLLDQAR	186	27	4	11.9	b11°b11y10y12	2921.45	122.318	3086	3	974.49	1.75
Q7CPZ4 GRPE_SALTY Protein grpE;	1		FVNELLPVIDSLDR	90	14	7	60.39	b4y4y5°y5y6y8y9	1629.89	96.676	28510	2	815.45	2.02
Q7CPZ4 GRPE_SALTY Protein grpE;	2		IANLEVQLAEAQTR	43	14	4	44.75	y5y7y10y13	1555.85	63.262	6153	2	778.43	5.18
Q7CPZ4 GRPE_SALTY Protein grpE;	3		FGVEVIAETNPVLDPNVHQAIAI VESEVPAGNVLGIMQKGYTLNG R	136	47	7	22.77	b7b8b10°b10b15y15y24	5006.47	69.015	4215	4	1252.37	-13.26
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	1	Carbamidomethyl+C(10)	YVIDELDQICQRDR	77	14	6	27.57	b1b5b9y3y11y14	1822.89	53.657	50965	3	608.30	5.56
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	2	Carbamidomethyl+C(10)	YVIDELDQICQR	77	12	8	49.67	b2b8y1y3y8y9y10y12	1551.75	68.054	38427	2	776.38	4.48
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	3		TVVADGIGQGYKEVQEISPNLR	55	22	6	18.16	b2b5b13y4y8y22	2373.23	71.699	34127	3	791.75	-4.84
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	4		TVVADGIGQGYK	55	12	4	22.27	b8b11y4y12	1207.62	48.233	1803	2	604.31	-9.10
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	5		SLGITNPPEIDR	6	12	4	44.91	y6y7y9y11	1343.70	81.528	14408	2	672.36	17.99
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	6		ILDDLRL	99	6	1	13.62	b5	744.42	51.776	12394	1	744.42	-10.41
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	7		IYFQK	31	5	1	13.22	y3	698.38	38.383	4053	2	349.69	-10.49
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	8		HLESVVANK	105	9	3	30.48	b4y3y5	996.53	37.545	2627	2	498.77	-17.27
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	9		TVVADGIGQGYKEVQEISPNLR	55	22	3	13.43	b11y3y5	2373.25	91.487	71401	3	791.75	2.47
Q7CR64 YAEH_SALTY UPF0325 protein yaeH;	10		SLGITNPPEIDRYSRLR	6	16	3	17.15	b11y9y12	1862.98	79.042	6706	3	621.67	10.81
Q7CPH8 SECB_SALTY Protein-export protein secB;	1		GTFPQLNLAPVNFDAFMNYLQQ QAGEGTTEHQDA	120	35	7	51.04	b6b7b8b9y4y26y35	3893.84	115.911	16186	3	1298.62	8.78

Q7CPH8 SECB_SALTY Protein-export protein secB;	2		LDLDTASSQLADDVYEVVLR	41	20	15	55.41	b2b4°b4b6°b6b8°b8b9y3y6y9y10°y10y20*y20	2222.14	109.125	12574	2	1111.57	10.44
Q7CPH8 SECB_SALTY Protein-export protein secB;	3		DVSFEAPNAPHVFQK	19	15	5	29.43	b4b5b13y2y13	1685.82	73.820	2286	2	843.41	-5.21
Q7CPH8 SECB_SALTY Protein-export protein secB;	4		SEQNNTMAFQIQR	1	14	3	19.28	b9b13y9	1695.81	83.967	3543	2	848.41	21.52
Q7CPH8 SECB_SALTY Protein-export protein secB;	5		IYTKDVSFEAPNAPHVFQK	15	19	6	46.19	b8b10b11b13b14*b14	2191.11	69.010	9332	3	731.04	-5.68
P64052 EFTS_SALTY Elongation factor Ts;	1		VASLEGDVLGSYQHGAR	134	17	16	131.67	b1b3y3y4y5y6y7y8°y8y10y11°y11y12*y12y13y17	1758.85	58.924	167126	3	586.96	-13.46
P64052 EFTS_SALTY Elongation factor Ts;	2		ITDVEVLK	104	8	6	40.86	b2y2y3y6y7y8	916.53	48.616	86659	2	458.77	-10.12
P64052 EFTS_SALTY Elongation factor Ts;	3		AEITASLVK	1	9	5	54.49	y4y5y6y7y9	931.54	48.688	81602	2	466.27	-7.27
P64052 EFTS_SALTY Elongation factor Ts;	4		FTGEVSLTGQPFVMEPSK	222	18	6	24.81	b11y1y3y5y13y18	1953.98	74.548	69258	2	977.49	8.37
P64052 EFTS_SALTY Elongation factor Ts;	5		IGENINIR	125	8	6	40.86	b2y2y5y6y7y8	928.51	44.512	68981	2	464.76	-12.75
P64052 EFTS_SALTY Elongation factor Ts;	6		ALTEANGDIELAIENMRK	25	18	8	50.04	b7b9b12y4*y4y5y14y16	1988.00	74.110	47604	3	663.34	-6.63
P64052 EFTS_SALTY Elongation factor Ts;	7	Carbamidomethyl+C(8)	TGAGMMDCKK	15	10	3	36.9	y4y5y6	1098.47	20.977	23221	2	549.74	-1.89
P64052 EFTS_SALTY Elongation factor Ts;	8		SVGQLLK	240	7	6	40.46	b1b6y2y3y5y7	744.45	44.959	10330	2	372.73	-14.92
P64052 EFTS_SALTY Elongation factor Ts;	9		EYQVQLDIAMQSGKPK	193	16	7	46.6	b4b5b7y4y9y10*y10	1834.94	70.416	7440	3	612.32	2.20
P64052 EFTS_SALTY Elongation factor Ts;	10		ALTEANGDIELAIENMR	25	17	4	16.31	b11y3y6y17	1859.92	81.853	5580	2	930.46	2.30
P64052 EFTS_SALTY Elongation factor Ts;	11		FEVGEGIEK	258	9	3	46.04	b3b5b7	1007.48	34.972	75254	2	504.25	-20.96
P64052 EFTS_SALTY Elongation factor Ts;	12		IGVLVAAK	151	8	6	77.5	b3b4y3y5y6y7	770.50	47.173	48521	2	385.75	-16.00
P64052 EFTS_SALTY Elongation factor Ts;	13		AGNVAADGVIK	52	11	5	36.72	b8y4y6y7°y7	1014.54	36.787	25258	2	507.77	-15.04
P64052 EFTS_SALTY Elongation factor Ts;	14		MVEGR	214	5	1	13.22	y4	591.29	38.372	5894	1	591.29	2.27
P64052 EFTS_SALTY Elongation factor Ts;	15		DAGFQAFADK	85	10	4	28.66	b7°b7b8y5	1069.47	27.975	5583	2	535.24	-19.29
P64052 EFTS_SALTY Elongation factor Ts;	16	Carbamidomethyl+C(13)	IDGNVAFILEVNCQTDFVAK	65	20	5	19.76	b3°b3b8y6y10	2253.08	74.808	3467	4	564.02	-19.94
P64052 EFTS_SALTY Elongation factor Ts;	17		DAGFQAFADKVLDAAVAGK	85	19	4	31.59	y3y6y7y17	1893.95	97.732	113928	3	631.99	-9.22
P64052 EFTS_SALTY Elongation factor Ts;	18		KAGNVAADGVIK	51	12	7	48.12	b10b11y8y10y11°y11*y11	1142.65	32.000	55814	2	571.83	-6.30
P64052 EFTS_SALTY Elongation factor Ts;	19		GADEELVKQLAMHVAASKPEFVK PEDVSADVVEK	159	34	4	10.98	b7°b7b13y12	3665.88	78.308	4358	4	917.22	1.00
P64052 EFTS_SALTY Elongation factor Ts;	20		KFTGEVSLTGQPFVMEPSK	221	19	4	22.71	b13°b13y13y14	2082.07	78.321	3428	2	1041.54	4.57
P64052 EFTS_SALTY Elongation factor Ts;	21		FEVGEGIEKVETDFAAEVAAMSK	258	23	6	33.9	b3b10y3y5y12y13	2457.16	59.483	2053	3	819.72	-12.32
P64052 EFTS_SALTY Elongation factor Ts;	22	Oxidation+M(4)	QLAMHVAASKPEFVKPEDVSADV VEK	167	26	7	21.93	b7b10b12°b12y11°y11y20	2840.43	61.526	11720	3	947.48	-5.93
P64052 EFTS_SALTY Elongation factor Ts;	23	Oxidation+M(14)	FTGEVSLTGQPFVMEPSK	222	18	3	15.58	b12b15y10	1969.96	79.416	9525	2	985.48	0.00
P64052 EFTS_SALTY Elongation factor Ts;	24	Oxidation+M(16)	ALTEANGDIELAIENMRK	25	18	8	24.81	b8b10°b10°b10b14°b14y11*y11	2003.99	69.032	4942	2	1002.50	-8.71

[P64052]EFTS_SALTY Elongation factor Ts;	25		ITASLVK	3	7	0	1.62		731.46	48.695	11323	1	731.46	-12.43
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase;	1		LAEAGIPTQMER	60	12	12	71.55	b2b3°b3b4b6y1y6y8y9y10*y10y12	1315.67	49.862	39148	2	658.34	-1.11
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase;	2		QSLGGLIEAYEAVHR	215	16	4	17.15	b5b11°b11y7	1713.87	84.811	38020	3	571.96	-12.61
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase;	3		TVYSTENPDLLVLEFR	13	16	6	23.69	b2°b2b4b5y3y16	1895.97	88.283	18473	2	948.49	-0.39
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase;	4	Carbamidomethyl+C(8)	LEMVPVECVVR	83	11	3	36.06	b3b5b9	1330.67	94.941	3441	2	665.84	-13.03
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase;	5	Carbamidomethyl+C(9)	KLEMVPVECVVR	82	12	6	63.56	b5b6y4y5y7y11	1458.79	62.520	27255	2	729.90	3.35
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase;	6		TVYSTENPDLLVLEFRNDTSAGD GAR	13	26	3	22.81	y3y4y8	2840.38	80.412	12726	3	947.47	3.78
[P65889]PUR7_SALTY Phohoribosylaminoimidazole-succinocarboxamide synthase;	7		GEVVLGDEFSPDGSRLWDK	184	19	5	25.86	b3b4°b4b6y10	2106.00	104.349	3104	2	1053.51	-4.64
[P0A7V6]RS3_SALTY 30S ribosomal protein S3;	1		LVADSITSQLER	114	12	12	87.78	b2b3b4b10y2y5°y5y6y8y9y10y12	1331.71	60.443	27472	2	666.36	-2.93
[P0A7V6]RS3_SALTY 30S ribosomal protein S3;	2		ADIDYNTSEAHTTYGVIGVK	179	20	3	22.5	b13y17y18	2154.03	56.289	23121	3	718.68	-4.19
[P0A7V6]RS3_SALTY 30S ribosomal protein S3;	3	Phosphoryl STY(7)	LVADSITSQLERR	114	13	4	25.41	b4°b4b5y8	1567.76	59.490	14868	2	784.39	-6.62
[P0A7V6]RS3_SALTY 30S ribosomal protein S3;	4	Phosphoryl STY(10)	LGIVKPWNSTWFANTK	11	16	3	23.69	b14y5y6	1941.93	35.641	2075	3	647.98	-9.99
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	1		SQTVHFQGNPVTVANVIPQAGSK	1	23	24	98.65	b2°b2*b2b4°b4b5b7°b7b9°b9b10°b10*b10b11b12°b12y4y6°y6y7y9y12*y12y23	2379.23	64.386	108136	3	793.75	-3.90
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	2	Carbamidomethyl+C(13)	VLNIFPSIDTGVCASVR	48	18	6	50.14	b3b4b5y13y14y18	1919.01	85.014	50355	2	960.01	4.26
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	3		DLSDVSLSQYAGK	33	13	5	20.63	b2b10y6y11y13	1382.68	59.171	35054	2	691.85	2.21
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	4	Carbamidomethyl+C(2)	FCGAEGLSNVITLSTLR	93	17	8	54.61	b2b3b4b7y4y5y6y17	1837.96	85.877	34158	2	919.48	4.65
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	5		DLSDVSLSQYAGKR	33	14	6	19.28	b2°b2b7b12y10y14	1538.78	54.773	4285	2	769.89	-0.95
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	6		AQAFTLVAK	24	9	5	57.5	y3y4y6°y6y7	948.54	53.204	63728	2	474.77	-17.18
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	7		GLAAR	128	5	1	13.22	b3	487.29	54.229	17951	1	487.29	-13.97
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	8		NYGVEIVDGPLK	116	12	3	22.27	b3y4y10	1303.68	64.652	16063	2	652.35	-4.87
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	9		MSQTVHFQGNPVTVANVIPQAGS K	0	24	3	19.01	b9b12b17	2510.23	68.278	5531	3	837.41	-21.10
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	10		AVIVLDENDNVIFSQLVDEITHEPD YDAALNVLKA	133	35	21	162.1	b3b4b5b8b11°b11b15b16b32y3y5y6y7y8y12y18y24y28y29y30y31	3882.98	119.952	80826	3	1295.00	4.97
[Q8ZP65]TPX_SALTY Probable thiol peroxidase;	11	Carbamidomethyl+C(13) ;Phosphoryl STY(7)	VLNIFPSIDTGVCASVRK	48	19	3	14.93	b6b10y14	2127.04	96.742	10955	2	1064.02	-7.23

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	1		TGYLPITTAAYELTR	343	15	12	99.2	b3b4b5°b5y4y5y6y7y9°y9y11y15	1669.88	84.722	98863	2	835.45	2.85
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	2		TIVDEELESVWTGKK	397	15	5	25.79	b4b6y8y13y15	1733.88	75.479	39388	3	578.63	-11.19
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	3		TGNAPAILQVYEVGTATMMASK	77	22	4	26.91	b3b4y6y15	2253.16	93.817	24752	2	1127.08	14.41
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	4		FNYGVGMMPYDADIK	282	15	7	36.7	b2y2y3y7y8y10y15	1720.79	74.431	15469	2	860.90	10.78
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	5		TIVDEELESVWTGK	397	14	5	31.53	b6y7y11y13°y13	1605.81	94.495	4817	2	803.41	6.46
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	6		TGYLPITTAAYELTREQGYDDK	343	22	6	20.86	b14y2y5y8°y8y10	2553.24	78.228	3671	3	851.75	-4.59
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	7		FLDFLAKPENAAEWHQK	326	17	4	22.92	b3b8y4y7	2043.99	74.067	73732	4	511.75	-21.02
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	8		QMLNKPPLPFTK	374	12	4	26.25	b7y3y4°y4	1413.77	61.554	63073	3	471.93	-13.30
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	9		LGNMPQIR	389	8	3	33.08	b5y6y7	928.51	27.829	45046	2	464.76	3.22
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	10		NNGFDGTDAVLEFNKPEQVK	212	20	5	33.45	b11y6y8y11y18	2222.08	65.225	23415	3	741.37	4.18
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	11		GNYEQNLASAGIAAFR	62	15	3	18.13	b13y4y8	1610.79	72.949	18540	2	805.90	0.53
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	12		TWQELADYTAK	167	11	4	24.3	b5°b5y4y9	1325.63	28.785	8916	2	663.32	-7.83
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	13		EVDSLAQR	39	8	5	36.09	b5°b5b7y7°y7	917.47	41.655	7336	2	459.24	4.12
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	14		SGHLLSQPFNSSTPVLYYNK	132	20	6	21.16	b3b8°b8*b8b11°b11	2252.16	68.317	3868	2	1126.58	9.97
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	15		GAPQNAIIGGASLWVMQGK	297	19	3	14.93	b3b11y9	1897.97	114.295	2110	2	949.49	-13.51
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	16		DAGINFDESQFVPTVAGYYTDAK	109	23	7	24.55	b8b13*b13y8°y8y10y14	2508.15	124.320	1531	3	836.72	-3.02
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	17		AGLDPEQPPKTWQELADYTAK	157	21	6	37.02	b4b15y3y6y14y17	2358.15	72.555	92214	3	786.72	-4.04
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	18		NPGADIATRQMLNKPPLPFTK	365	21	4	20.51	b4*b4b8b10	2309.22	67.355	3571	3	770.41	-8.99
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	19		ETYTGVAKFLDFLAKPENAAEWHQK	318	25	5	18.83	b6y3y8y10°y10	2893.45	115.998	2341	3	965.15	-1.94

Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	20	Phosphoryl STY(12)	GAPQNAIIGGASLWVMQ GKDK	297	21	3	13.87	b3b13y8	2221.09	115.178	2857	3	741.04	8.68
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	21	Oxidation+M(19)	TGNAPAILQVYEVGTATMMASK	77	22	7	18.16	b11*b11b18y4°y4y13°y13	2269.14	69.037	69074	3	757.05	7.96
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	22	Oxidation+M(8)	HIALLEEMNK	232	10	3	26.9	b7y4y6	1213.63	28.211	4805	3	405.21	2.11
Q7CPK0 UGPB_SALTY sn-glycerol-3-phohate-binding periplasmic protein ugpB;	23	Oxidation+M()	FNYGVGMMPYDADIK	282	15	5	31.81	b5*b5b6y3y13	1736.77	71.486	4259	3	579.60	2.74
O54297 RS4_SALTY 30S ribosomal protein S4;	1		VVNIASYQVSPNDVVSIR	128	18	14	88.94	b4b8b10b14y1y2y3y4y9y10y11*y11y13y18	1960.06	72.026	28405	2	980.53	4.61
O54297 RS4_SALTY 30S ribosomal protein S4;	2		IEQAPGQHGAR	33	11	5	24.3	b2b9y2y8y10	1163.59	27.041	2011	2	582.30	-4.51
O54297 RS4_SALTY 30S ribosomal protein S4;	3		GNTGENLLALLEGR	83	14	5	30.73	b4b5b9y4°y4	1456.80	94.487	4613	2	728.90	16.42
O54297 RS4_SALTY 30S ribosomal protein S4;	4		SDLSADINEHLIVELYSK	188	18	7	40.21	b5b8*b8b13y6y10y13	2046.06	79.237	2922	3	682.69	9.90
O54297 RS4_SALTY 30S ribosomal protein S4;	5		AALELAEQR	156	9	5	45.46	b3y3y4y7*y7	1000.53	43.331	2524	1	1000.53	-10.19
O54297 RS4_SALTY 30S ribosomal protein S4;	6		IEQAPGQH GARKPR	33	14	4	27.85	b4b6*b6b11	1544.85	54.059	11270	3	515.62	8.22
O54297 RS4_SALTY 30S ribosomal protein S4;	7	Carbamidomethyl+C(1)	CKIEQAPGQHGAR	31	13	4	20.63	b12y5y11*y11	1451.70	56.581	9146	3	484.57	-12.28
O54297 RS4_SALTY 30S ribosomal protein S4;	8		KPERSDLSADINEHLIVELYSK	184	22	3	13.43	b8b12y3	2556.32	111.273	8899	3	852.78	-2.58
O54297 RS4_SALTY 30S ribosomal protein S4;	9		KPRLSDYGVQLR	44	12	3	22.27	b9y5y7	1431.79	77.070	8780	2	716.40	-11.25
O54297 RS4_SALTY 30S ribosomal protein S4;	10		LSDYGVQLREK	47	11	6	73.28	b3b4b6b8*b8b10	1307.70	88.079	3458	2	654.35	1.31
Q8ZLD7 UA_SALTY Universal stress protein A;	1		AVSMARPYNAK	22	11	11	90.17	b2b5b6b9y2y3y5°y5y7y9y11	1207.62	31.397	83867	2	604.31	-6.47
Q8ZLD7 UA_SALTY Universal stress protein A;	2		QLINTVHVDMLIVPLRDEEE	124	20	9	39.19	b12y1y7y8y9°y9y11°y11y20	2363.22	86.355	74730	3	788.41	-5.27
Q8ZLD7 UA_SALTY Universal stress protein A;	3		VLVEK	17	5	1	13.22	y3	587.38	41.146	6151	1	587.38	11.43
Q8ZLD7 UA_SALTY Universal stress protein A;	4		ISEETHHALTELSTNAGYPITETLSGSGDLGQVLVDAIK	61	39	3	10.86	b4b6y13	4067.08	88.756	1717	3	1356.36	7.62
Q8ZLD7 UA_SALTY Universal stress protein A;	5		AYKHILIAVDLSPESK	1	16	3	17.15	b12b14y15	1783.98	136.757	1665	1	1783.98	-7.46
Q8ZLD7 UA_SALTY Universal stress protein A;	6		SMARPYNAK	24	9	2	18.86	b4b6	1037.51	31.326	81736	2	519.26	-7.65
Q8ZLD7 UA_SALTY Universal stress protein A;	7		VSMARPYNAK	23	10	0	2.43		1136.58	31.317	8654	2	568.79	-4.94
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	1		LGSVFSSTGTGGGQEQTITSTWTT LAHHGMVIVPIGYAAQELFDVSQVR	106	49	18	52.38	b2b7b8°b8b9b12°b12b16b35y1y2y3y4*y4y7y9y13*y13	5134.58	116.094	28928	4	1284.40	3.33
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	2		FGNMSGQMR	79	9	5	38.26	y2y4y5y6y9	1027.45	38.317	16831	2	514.23	1.07
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	3		TQNAPVATPQELADYDAIIFGTPT R	54	25	19	78.9	b2°b2*b2b4b5*b5b6b7°b7°b7b14°b14*b14y6y13°y13y14y15y25	2689.35	89.682	12270	3	897.12	-0.54
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	4		ILVLYYSMYGHITMAHAVAEGA K	3	24	4	19.44	b9y5y11y17	2667.36	66.576	6717	4	667.60	10.34
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	5		QPSQEELSIAR	172	11	3	31.29	b6b9b10	1257.62	49.681	4662	2	629.31	-19.02

Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	6		VPETMPPEIFAK	38	12	3	22.27	b5b11y10	1358.73	57.738	3294	3	453.58	20.93
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	7		TFLDQTGGLWASGSLYGK	88	18	5	15.58	b11y8°y8y14*y14	1900.91	97.039	1719	2	950.96	-18.11
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	8		GGTPYGATTIAGDGSRQPSQEEL SIAR	155	28	7	40.35	b9y10*y10y18y23y24y25	2776.35	54.951	17117	3	926.12	0.79
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	9		TQNAPVATPQELADYDAIIFGTPT RFGNMSGQMR	54	34	4	22.92	b6b9b10°b10	3697.82	122.059	17020	4	925.21	13.80
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	10		MAKILVLYYSMYGHETMAHAVA EGAK	0	27	3	17.98	y5y8y15	2997.53	88.836	4547	3	999.85	10.18
Q8ZQ40 WRBA_SALTY Flavoprotein wrbA;	11		LGSVFSSTGTGGGQEQTITSTWTT LA	106	26	0	17.8		2587.26	116.086	1872	3	863.09	1.32
Q56073 DNAK_SALTY Chaperone protein dnaK;	1		IINEPTAAALAYGLDKEVGNR	167	21	18	114.17	b2b3b7y1y3y5°y5y7*y7y10°y10y11y12*y12y14y17y19y21	2215.16	74.814	42791	3	739.06	-5.84
Q56073 DNAK_SALTY Chaperone protein dnaK;	2		QAVTNPQNTLFAIKR	56	15	4	34.67	b15y4y5y6	1700.92	58.746	25800	3	567.65	-11.91
Q56073 DNAK_SALTY Chaperone protein dnaK;	3		TAEDYLGEVPVTEAVITVPAYFNDA QR	125	26	7	34.79	y3y9y11y12*y12y23y26	2869.40	93.291	21497	3	957.14	5.11
Q56073 DNAK_SALTY Chaperone protein dnaK;	4		ASSGLNEEEIQK	502	12	11	68.92	b2°b2y1y3y5y7°y7y9°y9y10y12	1304.63	34.672	15968	2	652.82	-2.06
Q56073 DNAK_SALTY Chaperone protein dnaK;	5		MQELAQVSQK	587	10	6	28.66	b1b2b7b8y3y10	1161.59	37.193	15089	2	581.30	-6.31
Q56073 DNAK_SALTY Chaperone protein dnaK;	6		NDPLAMQR	253	8	6	33.08	b3°b3y3y4*y4y8	944.46	39.255	13947	2	472.73	-3.94
Q56073 DNAK_SALTY Chaperone protein dnaK;	7		QAVTNPQNTLFAIK	56	14	6	30.73	b4°b4b11°b11b12y3	1544.84	67.255	5457	2	772.92	-2.92
Q56073 DNAK_SALTY Chaperone protein dnaK;	8		TFEVLATNGDTHLGGEDFDTR	214	21	4	21.69	b6b8b11y10	2295.07	65.257	4938	4	574.52	7.45
Q56073 DNAK_SALTY Chaperone protein dnaK;	9		TTPSIIAYTQDGETLVGQPAK	34	21	5	23.52	b3b4b12b21°b21	2190.10	92.404	2998	3	730.70	-14.94
Q56073 DNAK_SALTY Chaperone protein dnaK;	10		GMPQIEVTFDIDADGILHVSADKDK	467	24	3	12.7	b12b14y13	2599.32	102.723	1767	3	867.11	4.60
Q56073 DNAK_SALTY Chaperone protein dnaK;	11		TIAYVDLGGGTFDISIIEIDEVDGE K	188	26	10	49.1	b6°b6b12b13y3y5y10°y10y11y13	2769.38	123.879	29098	3	923.80	3.00
Q56073 DNAK_SALTY Chaperone protein dnaK;	12		SIEPLK	315	6	2	13.62	b3°b3	686.41	49.233	7431	1	686.41	6.67
Q56073 DNAK_SALTY Chaperone protein dnaK;	13		AAIEAK	581	6	1	13.62	b4	602.35	31.904	7229	1	602.35	-8.21
Q56073 DNAK_SALTY Chaperone protein dnaK;	14		FEELVQTR	528	8	4	33.08	b6y6y7°y7	1021.54	64.457	6034	2	511.27	4.48
Q56073 DNAK_SALTY Chaperone protein dnaK;	15		MPMVQK	345	6	1	13.62	y4	733.37	31.608	5392	1	733.37	-5.24
Q56073 DNAK_SALTY Chaperone protein dnaK;	16		MAPPQISAEVLK	109	12	3	32.48	b4b6b10	1283.70	82.346	4123	2	642.35	-5.90
Q56073 DNAK_SALTY Chaperone protein dnaK;	17		NQGDHLLHSTR	536	11	5	38.31	b4b6y4°y4y5	1277.63	43.590	4119	2	639.32	-0.38
Q56073 DNAK_SALTY Chaperone protein dnaK;	18		VLENAEGDR	25	9	3	30.48	b3b4y5	1002.50	110.877	2584	1	1002.50	17.72
Q56073 DNAK_SALTY Chaperone protein dnaK;	19		MQELAQVSQKLMEIAQQQHAQQ QAGSADASANNAK	587	35	4	15.08	b9y4y9y16	3752.86	66.858	35512	5	751.38	13.73
Q56073 DNAK_SALTY Chaperone protein dnaK;	20		KTAEDYLGEVPVTEAVITVPAYFND AQR	124	27	3	11.9	b9y10y12	2997.50	85.453	17624	3	999.84	4.56
Q56073 DNAK_SALTY Chaperone protein dnaK;	21		DVSIMPYKIIGADNGDAWLVDK	84	22	3	13.43	b3b9y13	2420.25	104.386	13450	4	605.82	12.21
Q56073 DNAK_SALTY Chaperone protein dnaK;	22		KQVEEAGDK	547	9	5	30.48	b8°b8°b8y4y7	1003.49	37.756	9546	2	502.25	-12.16

Q56073 DNAK_SALTY Chaperone protein dnaK;	23	Carbamidomethyl+C(12)	IIGIDLGTNSCVAIMDGTQARVLE NAEGDR	3	31	14	44.17	b12°b12*b12b14*b14b16* b16b18*b18b19y13y14°y14y16	3289.65	136.792	6186	2	1645.33	9.35
Q56073 DNAK_SALTY Chaperone protein dnaK;	24		VLENAEGDRTPPSIIAYTQDGETL VGQPAK	25	30	5	14.16	b11*b11b13y11y14	3173.61	70.411	3228	3	1058.54	3.23
Q56073 DNAK_SALTY Chaperone protein dnaK;	25	Phosphoryl STY(9)	QAVTNPQNTLFAIKR	56	15	8	39.92	b4*b4b7*b7b8*b8b10y12	1780.91	81.293	7212	2	890.96	6.31
Q56073 DNAK_SALTY Chaperone protein dnaK;	26	Phosphoryl STY(9)	TTPSIIAYTQDGETLVGQPAK	34	21	6	35.19	b3b5b10_H3PO4 b10y11y12*y12	2270.12	136.258	3336	2	1135.56	14.20
Q56073 DNAK_SALTY Chaperone protein dnaK;	27	Oxidation+M(2)	GMPQIEVTFDIDADGILHVS AK	467	22	5	13.43	b6°b6b13°b13y13	2372.19	93.460	3611	2	1186.60	2.88
Q56073 DNAK_SALTY Chaperone protein dnaK;	28		QAVTNPQNTLFAIK	56	14	0	3.64		1526.83	67.272	3923	3	509.62	2.00
P0A1P6 GLNA_SALTY Glutamine synthetase;	1		LVPGYEAPVMLAYSAR	322	16	6	37.87	b15y4y5y9y14y16	1736.91	77.431	27446	2	868.96	3.51
P0A1P6 GLNA_SALTY Glutamine synthetase;	2		AINALANPTTNSYKR	307	15	9	57.57	b2b3*b3b4y5y7y8y9y15	1633.86	42.804	25281	3	545.29	-5.23
P0A1P6 GLNA_SALTY Glutamine synthetase;	3	Carbamidomethyl+C(1)	CDILEPGTLQGYDRDPR	89	17	7	22.92	b2b3b10y1y2y7y11	2004.94	59.923	21814	3	668.98	-2.13
P0A1P6 GLNA_SALTY Glutamine synthetase;	4		GGYFPVPPVDSAQDIR	177	16	5	17.15	b14b16y1y5y8	1717.88	57.259	17315	3	573.30	12.51
P0A1P6 GLNA_SALTY Glutamine synthetase;	5		AGGVFTDEAIDAYIALR	430	17	3	23.71	b4b10b16	1781.93	76.064	12578	3	594.65	10.89
P0A1P6 GLNA_SALTY Glutamine synthetase;	6		FGASISGSHVAIDIEGAWNSSTK	140	24	7	32.89	b6b15°b15y4y8y9y15	2449.18	82.295	9969	3	817.06	5.68
P0A1P6 GLNA_SALTY Glutamine synthetase;	7		ATGIADTVLFGPEPEFFLFDDIR	117	23	10	43.65	b13°b13y1y2y4°y4y5y8y12y13	2570.27	116.971	9393	3	857.43	-5.98
P0A1P6 GLNA_SALTY Glutamine synthetase;	8		GINESDMVLPDASTAVIDPFFAD STLIIR	59	30	3	21.98	b10y11y12	3238.61	113.240	9516	3	1080.21	1.58
P0A1P6 GLNA_SALTY Glutamine synthetase;	9		AINALANPTTNSYK	307	14	3	19.28	b11y7y9	1477.76	47.867	8329	2	739.38	-2.89
P0A1P6 GLNA_SALTY Glutamine synthetase;	10		NGTNLFSGDK	277	10	4	41.67	y3y6y8°y8	1052.51	59.865	7857	2	526.76	4.87
P0A1P6 GLNA_SALTY Glutamine synthetase;	11		MSAEHVLTMLNEHEVK	0	16	3	17.15	b8y7y14	1867.89	99.295	5827	3	623.30	-5.10
P0A1P6 GLNA_SALTY Glutamine synthetase;	12	Carbamidomethyl+C(1)	CDILEPGTLQGYDR	89	14	5	19.28	b7y3°y3y6°y6	1636.77	30.170	4554	3	546.26	3.73
P0A1P6 GLNA_SALTY Glutamine synthetase;	13		SAEHVLTMLNEHEVK	1	15	6	31.81	b12b14°b14y12°y12y13	1736.84	136.782	4066	1	1736.84	-13.56
P0A1P6 GLNA_SALTY Glutamine synthetase;	14		AEDYLR	111	6	2	26.84	y4y5	766.37	41.986	3845	1	766.37	-1.43
P0A1P6 GLNA_SALTY Glutamine synthetase;	15		EIPQVAGSLEEALNALDLDR	406	20	11	36.24	b4°b4*b4b8b10°b10y3y7°y7y9°y9	2153.10	93.490	3716	3	718.37	-3.86
P0A1P6 GLNA_SALTY Glutamine synthetase;	16		IHPGEAMDKNLYDLPEEAK	386	20	5	36.13	b9b10y6y8y14	2267.12	98.420	56241	3	756.38	6.46
P0A1P6 GLNA_SALTY Glutamine synthetase;	17		LVPGYEAPVMLAYSARNR	322	18	3	22.98	b7b8y4	2007.07	100.906	18089	2	1004.04	11.98
P0A1P6 GLNA_SALTY Glutamine synthetase;	18	Carbamidomethyl+C(11)	FPDPAANPYLCFAALLMAGLDGIK NK	360	26	9	34.79	b3b5b10°b10*b10b11°b11b13y18	2807.41	128.570	10972	3	936.48	-4.70
P0A1P6 GLNA_SALTY Glutamine synthetase;	19	Carbamidomethyl+C(4); Oxidation+M()	SEMCLVMEQMGLVVEAHHHEVA TAGQNEVATR	193	32	4	22.79	y11y13y14*y14	3579.66	84.874	4764	3	1193.89	3.89
P0A1P6 GLNA_SALTY Glutamine synthetase;	20		FTDEAIDAYIALR	434	13	2	13.88	b6b10	1497.76	76.089	9821	2	749.38	1.55
P0A1P6 GLNA_SALTY Glutamine synthetase;	21		NALANPTTNSYKR	309	13	0	4.05		1449.73	42.803	2421	2	725.37	-7.83
P0A1P6 GLNA_SALTY Glutamine synthetase;	22		LVPGYEAPVMLAY	322	13	1	7.25	y12	1422.75	77.426	2193	2	711.88	12.10
P26976 PHON_SALTY Non-ecific acid phohatase;	1		IFSPVVGAK	85	9	5	38.26	y1y3y6y7y9	917.54	51.173	55085	2	459.27	-10.24

[P26976]PHON_SALTY Non-ecific acid phohatase;	2		LQTIPAFQK	215	9	9	54.49	b2*b2y2y3y4y5*y5y7y9	1045.59	55.037	51256	2	523.30	-12.38
[P26976]PHON_SALTY Non-ecific acid phohatase;	3		NGSYPSGHTAYGTLLALVLSEARPER	150	26	8	12.14	b2b3°b3*b3y2y16y22y26	2759.37	96.158	39597	4	690.60	-13.54
[P26976]PHON_SALTY Non-ecific acid phohatase;	4		NLLTMGGYYATASAK	108	15	5	29.43	b11y1y9y11y12	1560.77	69.694	35262	2	780.89	0.31
[P26976]PHON_SALTY Non-ecific acid phohatase;	5		YVGAVEFAR	206	9	5	59.92	b3b4y4y7y8	1011.52	51.287	27169	2	506.26	-9.90
[P26976]PHON_SALTY Non-ecific acid phohatase;	6		DTPETWNMLK	98	10	4	41.67	y4y6y8*y8	1234.58	65.048	10246	2	617.80	5.34
[P26976]PHON_SALTY Non-ecific acid phohatase;	7		QAAEDADVSVENIAR	70	15	4	37.88	b4y3y4y5	1587.78	40.134	9353	2	794.40	14.84
[P26976]PHON_SALTY Non-ecific acid phohatase;	8		VREELNDK	228	8	5	33.08	b4°b4y3y4y8	1002.54	25.386	7550	2	501.77	14.12
[P26976]PHON_SALTY Non-ecific acid phohatase;	9	Carbamidomethyl+C(3)	VICGAHWQSDVDAGR	191	15	6	47.57	b6b7b11b13y6y9	1670.81	59.734	34177	2	835.91	21.41
[P26976]PHON_SALTY Non-ecific acid phohatase;	10		YTSAETVQPFHSPPEESVNSQFYLP PPPGNDDPAYR	16	35	3	10.93	b7b12y7	3936.84	122.075	1694	3	1312.95	10.98
[P26976]PHON_SALTY Non-ecific acid phohatase;	11		WKQAAEDADVSVENIAR	68	17	6	36.13	b4b6b7b10°b10y12	1901.96	72.868	4069	3	634.66	11.17
[P26976]PHON_SALTY Non-ecific acid phohatase;	12		YVGAVEFARLQTIPAFQK	206	18	4	15.58	b6°b6b8y5	2038.11	82.592	3182	3	680.04	0.24
[P26976]PHON_SALTY Non-ecific acid phohatase;	13	Oxidation+M(12)	INPKDTPETWNMLK	94	14	4	24.72	b10°b10y8y9	1702.85	79.383	4349	2	851.93	3.66
[P26976]PHON_SALTY Non-ecific acid phohatase;	14	Oxidation+M(5)	NLLTMGGYYATASAK	108	15	7	58.87	b9b11b12y4y10y11y13	1576.77	81.642	1855	3	526.26	1.32
[P26976]PHON_SALTY Non-ecific acid phohatase;	15		GAVEFAR	208	7	0	1.62		749.39	51.299	4534	1	749.39	-7.90
[P26976]PHON_SALTY Non-ecific acid phohatase;	16		IFSPVVGAK	85	9	0	1.62		899.53	51.168	5403	2	450.27	-2.37
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	1		IGTDTTYAPFSSK	29	13	4	29.88	y3y5y12y13	1387.67	53.084	41232	2	694.34	-2.29
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	2	Carbamidomethyl+C(1)	CTWVASDFDALIPSLK	66	16	7	44.97	b3b12y3y4y11y13y16	1822.92	97.991	38844	2	911.96	6.03
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	3		LDAALQDEVAASEGFLK	176	17	5	16.31	b9°b9y2y5y14	1776.88	123.834	2387	2	888.94	-13.12
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	4		HVGVLQGSTQEAYANDNWR	134	19	5	31.62	b4b12y6y7y9	2145.00	54.128	37849	3	715.67	-6.15
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	5		YFGDGTGVGLR	211	11	3	27.31	b10y9y10	1141.57	55.798	13956	2	571.29	1.92
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	6		AAFDK	229	5	1	13.22	y4	551.29	35.788	7006	1	551.29	11.74
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	7		QPAGK	193	5	1	13.22	b3	500.28	45.487	6866	1	500.28	1.77
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	8		GVDVVAYANQDLIYSDLTAGR	155	21	3	13.87	b8y7y9	2240.12	91.081	4518	3	747.38	1.74
[P02911]ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	9		DDTELK	223	6	1	13.62	y5	720.35	84.816	1734	1	720.35	14.74

[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	10		GVDVVAYANQDLIYSDLTAGRLD AALQDEVAASEGFLK	155	38	4	14.51	b11y5y11y14	3997.98	102.585	38241	4	1000.25	-4.52
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	11		QQEIAFSDKLYAADSR	99	16	7	56.14	b4b7b8b10y5y6y9	1841.89	93.450	8259	2	921.45	-5.63
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	12		RQQEIAFSDK	98	10	3	33.89	b3b4b9	1221.63	79.858	6365	2	611.32	8.89
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	13		IGTDTTYAPFSSKDAK	29	16	5	41.67	b4b7b11b14y7	1701.83	112.604	2198	2	851.42	-2.22
[P02911 ARGT_SALTY Lysine-arginine-ornithine-binding periplasmic protein;	14	Carbamidomethyl+C(15) ;Oxidation+M(14)	GEFIGFDIDLGNECK	45	16	3	17.15	b11y3y7	1860.81	26.904	5373	3	620.94	-0.52
[P0A1V4 KAD_SALTY Adenylate kinase;	1		VDGTQAVADVR	195	11	8	41.49	b4°b4y2y4°y4y8°y8y10	1130.58	36.632	48804	2	565.79	-0.22
[P0A1V4 KAD_SALTY Adenylate kinase;	2		LVEYHQMTAPLIGYYQK	167	17	9	33.99	b7°b7b11b17y1y5y6y10y17	2054.03	69.088	39210	3	685.35	-6.06
[P0A1V4 KAD_SALTY Adenylate kinase;	3		YGIPQISTGDMLR	23	13	6	34.06	b2b5y4y7y10y13	1450.73	72.603	35911	2	725.87	-1.09
[P0A1V4 KAD_SALTY Adenylate kinase;	4		NGFLLDGFPR	78	10	7	55.55	b2b6b9y4y5y6y10	1135.59	80.525	33400	2	568.30	-3.98
[P0A1V4 KAD_SALTY Adenylate kinase;	5		IILLGAPGAGK	2	11	7	52.95	b2b3y2y5y6y7y9	1009.63	61.069	16093	2	505.32	-10.94
[P0A1V4 KAD_SALTY Adenylate kinase;	6		LVEYHQMTAPLIGYYQKEAEGN TK	167	25	3	21.94	b7b8y6	2854.37	96.980	6702	3	952.13	-14.80
[P0A1V4 KAD_SALTY Adenylate kinase;	7		DDVTGEDLTTR	145	11	3	31.29	y6y8y9	1221.54	69.033	5026	1	1221.54	-15.69
[P0A1V4 KAD_SALTY Adenylate kinase;	8		IILLGAPGAGKGTQAQFIMEK	2	21	6	44.75	b3y9y12y15y17y19	2143.18	72.619	26847	3	715.06	-8.09
[P0A1V4 KAD_SALTY Adenylate kinase;	9		GTQAQFIMEKYGIPQISTGDMLR	13	23	3	13.04	b12y6y9	2584.27	75.371	3881	3	862.10	-7.27
[P0A1V4 KAD_SALTY Adenylate kinase;	10		VEGKDDVTGEDLTTR	141	15	3	18.13	b3b9y9	1634.81	84.669	2553	3	545.61	12.84
[P0A1V4 KAD_SALTY Adenylate kinase;	11	Phosphoryl STY(8)	LVEYHQMTAPLIGYYQK	167	17	5	46.47	b3b5b6b8b10_HPO3 b10	2134.01	42.698	1758	4	534.26	5.61
[P0A1V4 KAD_SALTY Adenylate kinase;	12	Oxidation+M(8)	GTQAQFIMEK	13	10	9	65.76	b3°b3b5°b5b6y3y4°y4y8	1168.57	60.414	4618	2	584.79	6.27
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	1		VIGAGQVYGLSAR	158	13	7	41.33	b2y6y7y9*y9y11*y11	1290.71	55.612	31749	2	645.86	-2.93
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	2		FVIIPGRDVTVDVQSK	219	16	4	25.53	b2y4y12y13	1772.97	64.755	26436	3	591.66	-11.70
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	3		GLAIDTALPSGEEFPR	171	16	8	52.75	b2b6b11y2y8y9y12y13	1672.85	72.894	12772	2	836.93	-4.09
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	4		YADYQQIQFNSDK	55	13	4	20.63	b8b10y9*y9	1619.74	52.174	7535	2	810.37	4.07
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	5		YSPDYFNFGNVQHDK	107	15	7	46.91	b12y6*y6y7y9*y9y10	1830.81	36.407	4971	3	610.94	0.93
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	6		QPDGTIAFVVDFVGADMK	419	18	4	21.74	b6b8y4y10	1909.93	117.124	4745	2	955.47	-1.92
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	7		VELVEIPTNDETNDNIWAYWTPDQ LPEPGK	347	30	6	35.35	b11b12y1y6y11y12	3396.62	120.431	3754	3	1132.88	-8.91
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	8		SNLPSVFRDMK	44	11	4	38.31	b6b8y8y9	1293.66	56.041	2665	2	647.33	-1.60
[P67557 OPGG_SALTY Glucans biosynthesis protein G;	9		LGVAPLTSMFLEGPNQPSPTTNYR PELHDSNGLSIHAGNGEWIWRPLN NPK	244	51	6	13.52	b14b16y11*y11y19y29	5640.71	136.743	4862	5	1128.95	-20.43

[P67557]OPGG_SALTY Glucans biosynthesis protein G;	10		WLGAAIMLTLYASSSWAFSIDDV AK	5	25	4	18.62	y6y8y10°y10	2716.42	81.374	3277	2	1358.72	19.77
[P67557]OPGG_SALTY Glucans biosynthesis protein G;	11		YDLRPSAWITPKGDWGK	328	17	4	26.14	b3b5b14y4	1989.99	79.112	6265	2	995.50	-12.02
[P67557]OPGG_SALTY Glucans biosynthesis protein G;	12		IKYSPDYFNFNGVQHDK	105	17	4	16.31	b9°b9y11y13	2071.99	110.348	4577	2	1036.50	2.47
[P67557]OPGG_SALTY Glucans biosynthesis protein G;	13		TPFKLEFYHQGMFYDTPVK	75	19	4	20.69	b3b6y4y9	2348.14	42.661	2947	3	783.38	-3.02
[P67557]OPGG_SALTY Glucans biosynthesis protein G;	14		FREFWIERPKPTDK	187	14	4	27.57	b7b11y6y12	1848.97	106.739	2128	3	616.99	-4.82
[P67557]OPGG_SALTY Glucans biosynthesis protein G;	15	Phosphoryl STY(6)	YDLRPSAWITPK	328	12	4	22.27	b4y8y11°y11	1526.71	80.048	296162	2	763.86	-12.07
[P67557]OPGG_SALTY Glucans biosynthesis protein G;	16	Oxidation+M(7)	NDEIVSMLGASYFR	144	14	7	46.8	b4b5b6°b6y5°y5y8	1617.75	55.625	10625	2	809.38	-3.47
[P67557]OPGG_SALTY Glucans biosynthesis protein G;	17	Oxidation+M(10)	SNLPVSFRDMK	44	11	3	24.3	b7y4y7	1309.65	37.697	10354	3	437.22	-4.38
[P67557]OPGG_SALTY Glucans biosynthesis protein G;	18		YFNFGNVQHDK	111	11	0	4.05		1368.65	36.364	2678	2	684.83	10.26
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	1		SATPAQAQAVHK	176	12	22	138.22	b2b3b5°b5b7°b7y1y2y3y4y5°y5y6°y6y7°y7y8°y8y9y10°y10y12	1208.63	18.734	44726	2	604.82	-3.03
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	2		TQGAAAFEGAVIAYEPVWAIGTG K	152	24	16	58.18	b1°b1b2°b2b3°b3b4b7°b7b8b9b12b15°y7y12y24	2407.26	93.455	43844	2	1204.14	13.89
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	3	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAKR	28	24	8	23.42	b2°b2b7y9y11°y11y12y24	2589.31	82.588	40895	3	863.77	1.79
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	4	Carbamidomethyl+C(8)	ELTGVAGCDVAIAPPEMYIDLAK	28	23	8	37.26	b5b6y1y8y10°y10y11y23	2433.22	88.017	17764	2	1217.11	5.42
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	5		QIDAVLK	145	7	3	37.45	b6y3y4	786.46	42.741	30032	2	393.73	-12.18
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	6	Carbamidomethyl+C(9)	EQGLTPVLCIGETEAENEAGK	117	21	6	43.63	b6b7b8b10y10y12	2245.03	100.333	3645	4	562.01	-15.99
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	7		HMVNELVANLR	16	11	4	31.29	b3b4°b4b6	1295.67	40.894	2402	2	648.34	-10.74
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	8	Carbamidomethyl+C(9); Carbamidomethyl+C(26)	EQGLTPVLCIGETEAENEAGKTEE VCAR	117	28	21	163.97	b3°b3b5°b5b7°b7y3y4y5°y5y6y7y10y12y14y18y20y21y23y24y26	3090.45	72.112	102844	3	1030.82	3.32
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	9		MRHPLVMGNWK	0	11	3	31.29	b3b4b9	1368.69	54.851	15879	3	456.90	-7.31
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	10		TYHKESDELIAK	99	12	5	32.18	b9b11°b11y3y8	1433.75	72.783	5268	3	478.59	12.94
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	11		QIDAVLKTQGAAAFEGAVIAYEPV WAIGTGK	145	31	4	11.25	b3°b3b16y18	3174.66	108.035	2324	3	1058.89	-8.61
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	12	Carbamidomethyl+C(9)	KELTGVAGCDVAIAPPEMYIDLAK	27	24	4	28.3	y3y4y9y12	2561.27	69.046	1715	2	1281.14	-12.01
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	13		TPAQQAQAVHK	178	10	12	79.12	b3°b3b4°b4b6°b6b7°b7b8°b8°b8b9	1050.56	18.751	16373	2	525.79	-5.93
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	14		PAQAQAVHK	179	9	11	79.12	b3°b3b4b5°b5b6°b6b7°b7b8°b8	949.52	18.756	13745	2	475.26	-4.50
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	15	Carbamidomethyl+C(8)	ELTGVAGC	28	8	0	7.28		806.38	88.076	1934	1	806.38	13.62
[Q8ZKP7]TPIS_SALTY Triosephohate isomerase;	16		SATPAQAQAVHK	176	12	0	2.83		1190.61	18.753	12910	3	397.54	-14.46
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	1		VTDIEPGLVGGTEFSSVR	171	18	18	119.64	b2°b2b5b6°b6b14b15b17°b17y5y6°y6y7y9°y9y11y13y17	1862.96	69.059	25938	2	931.98	4.72

[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	2	Carbamidomethyl+C(15)	MIVLVTGATAGFGECIARR	0	19	4	14.93	b2b3y7y14	2022.06	80.004	21066	2	1011.54	0.97
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	3		AVLPGMVER	115	9	3	38.26	y5y6y7	971.52	52.962	17180	2	486.27	-9.74
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	4		AAIEEMMASLPAQWR	58	15	4	25.79	b4b14y5y12	1703.85	90.318	9191	2	852.43	12.61
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	5		GHIINIGSTAGSWPYAGGNVYGAT K	126	25	3	12.4	b9y5y19	2491.26	64.844	37617	4	623.57	8.62
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	6		DELGENVLTAQLDVR	41	15	8	54.56	b3b4b7*b7b8y5*y5y7	1671.83	33.083	17963	3	557.95	-13.58
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	7		TDLHGTAVR	162	9	6	79.16	b4b5y3y5y6y8	969.49	23.060	5457	2	485.25	-18.57
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	8		ASVEDWETMIDTNNKGLIYMTR	93	22	4	22.18	b3b4*b4y4	2587.25	123.983	5677	3	863.09	12.27
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	9	Phosphoryl STY(21)	GHIINIGSTAGSWPYAGGNVYGAT K	126	25	9	50.58	b12b14_H3PO4 b13b14b19*b19b20*b20y18*y18	2571.17	136.844	4573	2	1286.09	-9.31
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	10	Carbamidomethyl+C(14) ;Phosphoryl STY(5)	IVLVTGATAGFGECIARR	1	18	5	21.74	b6*b6b9y11y13	1971.01	93.538	2413	3	657.67	14.49
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	11	Oxidation+M(6)	AAIEEMMASLPAQWR	58	15	5	18.13	b14y9°y9y14*y14	1719.84	93.421	31755	2	860.43	13.63
[P69936]YDFG_SALTY NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	12	Carbamidomethyl+C(15) ;Oxidation+M(1)	MIVLVTGATAGFGECIAR	0	18	3	22.98	b14b15y7	1881.97	106.431	5896	2	941.49	5.51
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	1		QLDPLVVGQEHYDTAR	343	16	8	68.98	b2*b2y3y4y5y6y9y10	1840.90	57.814	52076	3	614.30	-12.27
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	2		VALTGLTMAEK	219	11	7	65.5	y5y7y8y9y10°y10y11	1133.62	59.212	46480	2	567.31	-5.60
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	3		TVNMMELIR	156	9	8	45.46	b2b3y1y4y7°y7y8y9	1106.57	75.852	35477	2	553.79	-3.86
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	4		VGLFGGAGVGK	145	11	5	27.31	b1b3y7y8y11	961.54	58.978	34304	2	481.27	-8.70
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	5		FLSQPFFVAEVFTGSPGK	399	18	5	24.5	y3y6°y6y7y18	1958.02	99.461	33455	2	979.51	8.10
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	6		QIASLGIYPAVDPLDSTSR	324	19	7	46.19	y4y6y11°y11y12y13y19	2003.06	80.248	33030	2	1002.03	7.50
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	7		MPSAVGYQPTLAEEMGVLQER	261	21	13	86.63	b5b7b21y3*y3y4y6y7y8y10y11y13y21	2306.13	81.361	32319	2	1153.57	6.56
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	8	Carbamidomethyl+C(6)	VIDLMCPFAK	132	10	5	47.9	b7y4y6y8y10	1193.60	80.513	30091	2	597.30	-2.97
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	9		TIAMGSSDGLRR	53	12	8	34.24	b2b6y1y2y4y9y10y12	1263.65	37.367	23677	2	632.33	-1.74
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	10		VSLVYQMNPEPPGNR	202	15	6	29.43	b11y5*y5y7y11y15	1660.80	54.139	23161	2	830.90	-8.38
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	11		AAPSYEELSNSQELLETKIK	112	20	5	14.37	b8y1y12y15y20	2179.09	73.506	19525	2	1090.05	5.04
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	12		YQELKDIIAILGMDDELSEEDK	367	21	4	22.32	b5b6y1y13	2452.25	86.069	11012	3	818.09	13.94
[Q7CPE2]ATPB_SALTY ATP synthase subunit beta;	13		TREGNDFYHEMTDSNVIDK	183	19	3	14.93	b4y7y12	2271.02	66.545	6434	3	757.68	11.18

Q7CPE2 ATPB_SALTY ATP synthase subunit beta;	14		VYDALEVQNGNEK	25	13	3	20.63	b3b11y3	1478.74	70.377	1988	3	493.58	18.66
Q7CPE2 ATPB_SALTY ATP synthase subunit beta;	15	Carbamidomethyl+C(26)	AAPSYEELSNSQELLETGKVIDLM C PFAK	112	30	13	86.42	b5b7°b7b8b15y4y5y6y7y9y10y22y28	3353.67	120.430	42726	3	1118.56	1.02
Q7CPE2 ATPB_SALTY ATP synthase subunit beta;	16		FLSQPFFVAEVFTGSPGKYVSLK	399	23	4	19.45	b6*b6b9b14	2548.31	87.257	2802	4	637.83	-13.51
Q7CPE2 ATPB_SALTY ATP synthase subunit beta;	17		TIAMGSSDGLRR	53	12	4	22.27	b4°b4b6y8	1263.65	42.724	1930	2	632.33	3.09
Q7CPE2 ATPB_SALTY ATP synthase subunit beta;	18		IMNVLGEPVDMKGEIGEEER	87	20	3	14.37	b11y7y11	2245.06	84.856	1560	2	1123.03	-12.07
Q7CPE2 ATPB_SALTY ATP synthase subunit beta;	19	Oxidation+M(1)	MPSAVGYQPTLAEEMGVLQER	261	21	5	22.32	b11°b11b12y10°y10	2322.13	74.194	2758	3	774.72	8.73
Q7CPE2 ATPB_SALTY ATP synthase subunit beta;	20		AMGSSDGLRR	55	10	0	2.83		1049.51	37.374	11683	2	525.26	-4.77
Q7CPE2 ATPB_SALTY ATP synthase subunit beta;	21		QLDPLVVQGEHYDTAR	343	16	0	4.45		1822.89	57.831	2261	3	608.30	-8.30
P66932 TIG_SALTY Trigger factor;	1		NVALEEQAWEAVLAK	399	15	8	39.92	b2b3y2y3y4y11y13y15	1583.86	79.882	54833	2	792.43	-1.00
P66932 TIG_SALTY Trigger factor;	2		ANDIDVPSALIDSEIDVLRR	296	20	6	25.24	b2b3b4b8y1y4	2211.15	90.304	31411	3	737.72	-5.63
P66932 TIG_SALTY Trigger factor;	3		GLIEEMASAYEDPKEVIEFYSK	368	22	5	49.16	b6b7y4y5y6	2548.18	81.503	26779	3	850.07	-13.70
P66932 TIG_SALTY Trigger factor;	4		ANDIDVPSALIDSEIDVLR	296	19	9	47.81	b2b3b4b10b15y1y3y8y13	2055.06	94.394	14558	2	1028.04	1.90
P66932 TIG_SALTY Trigger factor;	5		INPAGAPNYVPGEYK	83	15	9	79.24	b2b10b11y3y5y7y9y13y15	1589.80	50.802	11889	2	795.40	-0.08
P66932 TIG_SALTY Trigger factor;	6		FGVEDGSVAGLR	255	12	4	29.47	y5y9°y9y10	1206.60	46.374	24229	2	603.80	-8.60
P66932 TIG_SALTY Trigger factor;	7		SQAIEGLVK	287	9	7	45.46	b4*b4b7°b7°b7b8y5	944.55	68.954	5383	2	472.78	10.47
P66932 TIG_SALTY Trigger factor;	8		VTIDFTGSVDGEEFEGGK	163	18	3	15.58	b5y5y8	1886.83	120.842	4487	3	629.61	-20.12
P66932 TIG_SALTY Trigger factor;	9		MIPGFEDGVK	193	10	4	51.88	b4b5b6b9	1092.53	115.133	2907	1	1092.53	-9.50
P66932 TIG_SALTY Trigger factor;	10		ATDFVLAMGQGR	181	12	4	36.16	b7b8y6y11	1265.63	69.063	2273	1	1265.63	-2.70
P66932 TIG_SALTY Trigger factor;	11		ELPELTEEFIK	243	11	4	24.3	b3b7y8°y8	1347.71	44.896	2210	2	674.36	1.99
P66932 TIG_SALTY Trigger factor;	12		GLIEEMASAYEDPKEVIEFYSK	368	22	4	18.16	b6b13y5y12	2548.22	98.265	14521	3	850.08	0.38
P66932 TIG_SALTY Trigger factor;	13		EKINPAGAPNYVPGEYK	81	17	4	39.15	y6y11y12y13	1846.93	75.991	8448	3	616.31	-3.57
P66932 TIG_SALTY Trigger factor;	14		RFGVEDGSVAGLR	254	13	4	20.63	b9°b9b11y7	1362.71	49.208	5307	3	454.91	-3.67
P66932 TIG_SALTY Trigger factor;	15		QALELPRELFEEQAK	327	15	4	18.13	b3y5°y5y12	1800.97	119.478	1779	3	601.00	13.96
P66932 TIG_SALTY Trigger factor;	16		VSEKATSFNELMNQQA	416	16	3	23.69	b3b4y6	1796.82	82.270	1586	3	599.61	-13.25
P66932 TIG_SALTY Trigger factor;	17	Oxidation+M(6)	GLIEEMASAYEDPKEVIEFYSK	368	22	3	13.43	b6b10y8	2564.25	81.812	4360	2	1282.63	14.47
P0A9Y9 CC_SALTY Cold shock-like protein cC;	1		GFGFITPADGSK	15	12	21	155.41	b2b3b4b5b6°b6y2°y2y3°y3y4°y4y5y6°y6y7°y7y8y9y10y12	1196.59	64.256	259247	2	598.80	-6.32
P0A9Y9 CC_SALTY Cold shock-like protein cC;	2		GFGFITPADGSKDVFVHFSAIQGN GFK	15	27	9	34.97	b6b17b22y2y4y11y13y22y27	2843.38	87.435	58363	4	711.60	-12.11
P0A9Y9 CC_SALTY Cold shock-like protein cC;	3		DVFVHFSAIQGN GFK	27	15	4	29.43	b4b11b12y10	1665.82	73.481	40830	3	555.95	-9.53
P0A9Y9 CC_SALTY Cold shock-like protein cC;	4		GPAAVNVTAI	59	10	3	41.67	b3b6b9	912.51	59.693	11274	1	912.51	-6.02

[P0A9Y9]CC_SALTY Cold shock-like protein cC;	5		TLAEGQNVEFEIQDGQK	42	17	4	16.31	b6y4°y4y6	1905.92	57.643	9815	3	635.98	-0.64
[P0A9Y9]CC_SALTY Cold shock-like protein cC;	6		WFNESKGFGFITPADGSK	9	18	5	24.81	b7b10°b10b13y5	1987.95	75.836	13517	3	663.32	-4.05
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	1	Carbamidomethyl+C(7)	LWVNPDCGLK	719	10	10	58.11	b2b9°b9y4y67°y7y8y10*y10	1201.60	60.538	36315	2	601.30	-2.03
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	2		LAAITAQDSQRENPYEVR	395	18	8	36.54	b2b3b4y2y14*y14y15y18	2061.02	47.409	35576	3	687.68	-5.33
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	3		QAGIDLLPVGDFAWYDHVLTTSLLGNVPAR	52	31	9	35.2	b6°b6°*b6b7°b7y6y7y24y31	3351.79	119.136	27939	3	1117.93	3.79
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	4		WFNTNYHYIVPEFSK	117	15	5	29.43	b9y9y11y12°y12	1944.91	78.180	15996	3	648.98	-8.85
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	5		AQESYWAGNTTR	21	12	7	64.15	y6y7y8y9y10*y10y12	1383.63	40.819	11709	2	692.32	2.29
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	6		APTGEPA AAAEMTK	103	14	9	39.81	b1b2b7b9°b9b12y9y12°y12	1344.65	39.199	10319	2	672.83	0.00
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	7		LPVDWLLSAGLINGR	279	15	6	24.15	b2b4b5°b5y3*y3	1623.93	101.280	9146	2	812.47	2.26
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	8		LAAITAQDSQR	395	11	6	36.06	b2y5y6y7°y7y11	1173.62	34.085	7911	2	587.31	-1.66
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	9	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPREDVTR	549	21	4	21.69	b5b12b14y10	2435.23	92.501	2675	3	812.41	2.01
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	10	Carbamidomethyl+C(11)	GMLTGPVTILCWSFPR	549	16	3	17.15	b5y5y13	1834.94	99.308	24986	2	917.97	3.06
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	11		LTWTQLLEEVDEALALGHK	137	19	5	20.69	b4b11*b11y11y13	2166.12	118.952	17709	3	722.71	-10.37
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	12		AALANMVK	737	8	3	40.86	y4y5y6	817.44	43.628	15686	2	409.23	-20.23
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	13		DALNSGETAALEEWSAPIQAR	360	21	5	30.8	b3b5b11*b11b18	2229.03	96.111	5074	3	743.68	-20.70
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	14		GWPETR	731	6	1	13.62	b5	745.37	41.731	3146	1	745.37	13.18
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	15	Carbamidomethyl+C(8)	ALWVASSCSLLHSPIDLSVETR	315	22	4	18.16	b7b12y5y7	2441.23	97.587	2894	3	814.41	-9.30
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	16		GQQFR	132	5	1	13.22	b3	635.32	41.912	2856	1	635.32	-4.03
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	17		GEPFDR	174	6	2	26.84	y3y4	720.33	55.984	1644	1	720.33	0.85
[Q9L6N1]METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	18		RSDWDAYLEWGVAEFR	610	16	4	17.15	b3b12y4°y4	1999.95	101.599	59688	3	667.32	12.33

Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	19		FKLPAWPTTTIGSFQTTTEIR	420	21	4	30.01	y6y7y10y12	2391.28	87.944	41622	3	797.76	1.94
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	20		KAQESYWAGNTTR	20	13	3	20.63	b8b12y5	1511.70	76.144	6363	3	504.57	-14.62
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	21		WFNTNYHYIVPEFSKGQQFR	117	20	4	23.79	b3b4b11°b11	2561.22	79.156	2475	3	854.41	-6.01
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	22		LAAITAQDSQRENPYEV	395	18	5	15.58	b5b13°b13y5°y5	2061.01	63.302	2474	2	1031.01	-12.32
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	23		AAQRIPAQR	710	9	3	30.48	b3b5y4	1010.57	18.652	2117	2	505.79	-12.38
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	24	Carbamidomethyl+C(11) ;Oxidation+M(2)	GMLTGPVTILCWSFPR	549	16	6	34.76	b3b6b11y7°y7y10	1850.93	90.686	2756	2	925.97	2.97
Q9L6N1 METE_SALTY 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	25	Carbamidomethyl+C(11) ;Oxidation+M(2)	GMLTGPVTILCWSFPREDVTR	549	21	4	21.69	b5y6y13y20	2451.25	97.431	2387	3	817.76	14.14
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	1		AAPNTIPTAAK	149	11	7	81.73	y3y4y5y6y7y8y11	1054.58	32.162	21580	2	527.79	-6.60
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	2		SVDGIQVGEGR	266	11	5	36.06	b1y4y6y9y11	1116.56	41.315	15855	2	558.79	0.00
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	3		AGGNYLSLLVGSEARR	160	17	7	26.14	b5b7*b7b14y1y15y17	1749.90	72.896	15733	3	583.97	-12.42
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	4		ESLYLADEVFMSGTAAEITPVR	244	22	6	25.59	b3b15y13°y13y15y21	2399.16	117.945	3770	4	600.54	-9.87
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	5		WGWLDPVNS	300	9	5	30.48	b3b8y6°y6y9	1073.52	89.625	3399	1	1073.52	13.76
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	6		AGGNYLSLLVGSEAR	160	16	5	24.86	y3y5°y5y15*y15	1593.80	69.059	3336	3	531.94	-14.02
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	7	Carbamidomethyl+C(14)	FPVSQSIDELMEACRDVIR	69	19	5	22.71	b9y8y9°y9y19	2265.11	70.518	1978	2	1133.06	4.74
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	8		ELGIEVR	231	7	3	40.46	b3b5y4	815.45	35.420	2310	2	408.23	-17.89
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	9	Carbamidomethyl+C(12)	SVDGIQVGEGRGCPVTK	266	17	5	22.92	b4b8*b8y12y16	1758.88	103.055	3017	2	879.94	-1.32
P0A1A5 ILVE_SALTY Branched-chain-amino-acid aminotransferase;	10		ADYIWFNGEMVRWEDAK	5	17	3	16.31	b12y8y12	2129.96	101.071	2799	4	533.25	-7.45
P0A7K0 RL11_SALTY 50S ribosomal protein L11;	1		AQLQEIAQTK	103	10	10	58.11	b2*b2b3y2y5y6°y6y7y8y10	1129.61	38.957	76340	2	565.31	-8.21
P0A7K0 RL11_SALTY 50S ribosomal protein L11;	2		AADMTGADIEAMTR	113	14	8	48.42	b3y1y4y5y7y8°y8y14	1452.65	57.337	57897	2	726.83	1.68
P0A7K0 RL11_SALTY 50S ribosomal protein L11;	3		TPPAAVLLK	72	9	3	30.48	b5y5y7	909.57	54.299	40804	2	455.29	-12.62
P0A7K0 RL11_SALTY 50S ribosomal protein L11;	4		SGSGKPNKDK	87	10	3	26.9	b6b9y3	1017.53	33.131	5836	2	509.27	-1.92
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain;	1	Carbamidomethyl+C(12)	FLETDIPLFGICLGHQLLALASGAK	257	25	16	72.85	b2b3°b3b5b6°b6y2y3y5°y5y8y14y19y20y23y25	2684.45	127.591	44934	3	895.49	-0.36
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain;	2		LTVVPAQTSAEVVK	215	15	6	18.13	b12b14*b14y1y11°y11	1584.89	63.291	11291	2	792.95	3.47
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain;	3	Carbamidomethyl+C(6)	GAQNGCIIAGDSPDAK	125	16	3	24.86	y3y5y12	1573.75	62.156	3011	2	787.38	11.32
P14845 CARA_SALTY Carbamoyl-phosphate synthase small chain;	4	Carbamidomethyl+C(18)	MNPDGIFLSNGPGDPAPCDYAITA IQK	230	27	5	22.75	b2y9y11y12*y12	2862.36	121.341	2231	3	954.79	6.14

P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	5		QIVTLTYPHIGNVGTNK	50	17	3	23.3	b3y8y9	1854.97	53.108	38904	3	618.99	-20.99
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	6		SALLVLEDGTQFHGR	3	15	3	26.21	y5y7y12	1642.86	124.884	3668	2	821.93	1.41
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	7		AIGATGSAVGEVVFNTSMTGYQEILTDPSYSR	18	32	4	24.52	b12b16y6y7	3321.61	102.603	3478	5	665.13	5.59
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	8		SEDDLPHFHVYAYDFGAK	185	17	3	23.3	b8b9y3	1909.90	29.823	2185	3	637.31	2.49
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	9		AFPGLNGMDLAK	148	12	3	22.27	b4y7y10	1233.64	37.335	2163	2	617.32	4.95
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	10		NTEDLSSYLK	93	10	3	28.66	b3y4y5	1169.55	28.855	1614	3	390.52	-19.83
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	11		EVTTAETRYRWTQGSWTLK	160	18	6	41.97	b3b6b8y10y11y13	2157.08	82.364	25232	2	1079.04	9.39
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	12	Carbamidomethyl+C(7)	MLVDRGCR	207	8	3	36.09	b5b7y3	1006.48	27.047	8394	2	503.75	-8.19
P14845 CARA_SALTY Carbamoyl-phohate synthase small chain;	13	Phosphoryl.STY(2)	LTVVPAQTSAAEVLK	215	15	3	18.13	b3b14y12	1664.84	124.858	3035	2	832.92	0.15
P66491 RS19_SALTY 30S ribosomal protein S19;	1		QHVPVFVSDEMVGHK	55	15	5	36.7	b5b9b11b12y15	1708.86	62.235	42121	2	854.93	4.43
P66491 RS19_SALTY 30S ribosomal protein S19;	2		LGEFAPTR	70	8	7	54.08	b2y1y3y4y5y7y8	890.46	41.984	37474	2	445.74	-9.12
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	1		TFDTPPTYNSLALSADGK	308	18	8	41.97	b3b4b7y2y5y11y14y18	1897.93	65.513	28962	2	949.47	5.40
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	2		EQEATQPDDVIR	338	12	8	64.15	b1y2y3y6y8y9y10y12	1400.67	39.421	20838	2	700.84	-0.09
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	3		QAGQVSVIDAK	291	11	6	31.29	y1y2y3y4y9y11	1115.60	37.605	18700	2	558.30	-4.49
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	4		EHFFINLSLDTAGHR	229	15	5	29.43	b11*b11y5y6y13	1756.91	95.556	8417	2	878.96	17.72
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	5		TGDVK	119	5	1	13.22	b3	519.27	64.980	3978	1	519.27	-12.46
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	6		LYTTNADGEFTIDTASNK	198	19	3	14.93	b10y9y14	2074.02	103.706	2782	3	692.01	12.83
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	7		ELVADAATNTIYISGVGK	144	18	9	75.53	b9b10*b10b11b12b13*b13b14*b14	1821.93	124.205	1995	2	911.47	-18.16
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	8		GSLLLGSLLVASSFSTLAAEDMLR	12	24	5	36.4	y7y9y11y13y14	2451.34	84.598	1670	3	817.79	11.35
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	9		NEAYVTHRQAGQVSVIDAK	283	19	4	23.65	b5b11b14y12	2086.07	64.350	8731	3	696.03	-0.35
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	10		STREQEATQPDDVIR	335	15	4	29.43	b6b10b13y10	1744.84	94.685	3399	2	872.93	-1.33
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	11		TTIENTGKMSTGLALDSK	177	18	3	15.58	b6b10y13	1866.95	61.549	3145	2	933.98	-0.59
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	12		AQRLYTTNADGEFITIDTASNK	195	22	8	51.94	b10y3*y3y4y5y8y9*y9	2429.18	136.275	1821	2	1215.09	-5.23
Q8ZPD6 YNCE_SALTY Uncharacterized protein yncE;	13		LLDDGKEHFFINLSLDTAGHR	223	21	3	13.87	b3b6y6	2398.23	75.188	1524	2	1199.62	6.92
P58661 AAT_SALTY Aartate aminotransferase;	1		VWVSNPSWPNHK	122	12	4	26.25	b7*b7b8y4	1450.70	53.651	12578	3	484.24	-13.04
P58661 AAT_SALTY Aartate aminotransferase;	2		FENITAAPADPILGLADLFR	1	20	8	40.95	b6b8*b8b11*b11b15*b15b16	2144.16	99.872	7821	3	715.39	11.39
P58661 AAT_SALTY Aartate aminotransferase;	3		MFENITAAPADPILGLADLFR	0	21	11	44.05	b8*b8b11b14*b14y1y3y4y7y13y21	2275.15	120.336	7447	3	759.05	-14.59
P58661 AAT_SALTY Aartate aminotransferase;	4	Carbamidomethyl+C(4)	VGACTLVAADAETVDR	254	16	6	34.76	b11b14y7y10y12y16	1647.79	70.304	4767	3	549.94	-6.07
P58661 AAT_SALTY Aartate aminotransferase;	5		TAQTPGGTGALR	96	12	4	26.25	b4*b4y7y8	1129.59	29.546	7259	2	565.30	-2.70

P58661 AAT_SALTY Aartate aminotransferase;	6		NYLGIDGIPEFAR	63	13	7	45.52	b3*b3b4b9*b9b12y8	1464.78	89.656	4217	2	732.89	22.08
P58661 AAT_SALTY Aartate aminotransferase;	7		AFSQMK	270	6	2	13.62	y5°y5	711.35	108.418	3047	1	711.35	0.77
P58661 AAT_SALTY Aartate aminotransferase;	8		GWLPLFD FayQG FAR	204	15	5	37.09	b11b12b14y11y13	1787.87	136.745	2980	1	1787.87	-9.08
P58661 AAT_SALTY Aartate aminotransferase;	9		EEFGVYAVASGR	362	12	3	26.25	b3b4y11	1284.62	75.936	2945	2	642.81	-1.71
P58661 AAT_SALTY Aartate aminotransferase;	10		NFGLYNER	246	8	7	54.08	b4*b4b7°b7y5*y5y7	1012.48	101.711	1996	1	1012.48	-1.45
P58661 AAT_SALTY Aartate aminotransferase;	11		FENTAAPADPILGLADLFRADDRP GK	1	27	4	11.9	b4°b4y6y8	2883.46	63.197	10544	5	577.50	-13.63
P58661 AAT_SALTY Aartate aminotransferase;	12	Carbamidomethyl+C(12)	NFGLYNERVGACTLVAADAETVD R	246	24	4	12.7	b9°b9b13y11	2641.29	75.885	4156	3	881.10	6.75
P58661 AAT_SALTY Aartate aminotransferase;	13		DFSFIKQNGMFSFSGLTK	336	19	3	14.93	b6b12y12	2167.07	66.126	3212	3	723.03	-8.00
P58661 AAT_SALTY Aartate aminotransferase;	14	Carbamidomethyl+C(4)	VGACTLVAADAETVDRAFSQMK	254	22	4	24.22	b3b4b19y4	2340.10	67.944	3030	3	780.71	-13.04
P58661 AAT_SALTY Aartate aminotransferase;	15		ELIVASSYSKNFGLYNER	236	18	4	22.98	b13*b13y8y9	2090.03	110.354	1538	3	697.35	-13.43
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1;	1	Carbamidomethyl+C(3)	FACGVIEK	169	8	8	67.3	y2°y2y3y4y5y6y7y8	923.46	41.061	160980	2	462.23	-10.18
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1;	2		GGDNYSDKPAPLGGGGAR	151	18	13	101.31	b2b10*b10y5y6y7y8y10y11y12y13°y13y18	1688.78	33.269	81334	3	563.60	-13.52
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1;	3		EVPALMAGGHLDPEK	84	15	4	18.13	b2b3b10y14	1563.78	57.311	18873	3	521.93	-2.73
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1;	4		GHSLMIHK	143	8	4	40.86	b3°b3b4b6	922.49	12.592	1808	2	461.75	-4.37
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1;	5		HLGPYNDKGHLGDLPLGVVNAD GTATYPLLAPR	102	33	3	11.05	b11y3y20	3441.76	82.534	12703	4	861.20	-7.66
P53636 SODC1_SALTY Superoxide dismutase [Cu-Zn] 1;	6		DGKEVPALMAGGHLDPEK	81	18	5	30.97	b6b11b16y7y14	1863.92	83.354	3591	2	932.47	-2.16
P67904 RS10_SALTY 30S ribosomal protein S10;	1		LIDQSTAEIVETAK	16	14	13	80.93	b2b3b7b9b14y2y3y4y5y9°y9y10y14	1517.81	55.436	64198	2	759.41	0.64
P67904 RS10_SALTY 30S ribosomal protein S10;	2		LVDIVEPTEK	72	10	8	47.9	b2b3y2y4y6°y6y8y10	1142.63	51.744	41730	2	571.82	-4.59
P67904 RS10_SALTY 30S ribosomal protein S10;	3		FTVLISPHVNKDAR	48	14	3	27.85	y5y7y9	1596.88	54.636	4450	2	798.94	-6.04
P67904 RS10_SALTY 30S ribosomal protein S10;	4		DQYEIR	62	6	1	13.62	y4	823.39	32.229	20433	2	412.20	-1.33
P67904 RS10_SALTY 30S ribosomal protein S10;	5		AFDHRLIDQSTAEIVETAK	11	19	4	14.93	b5b9y12*y12	2144.08	111.056	1505	3	715.37	-7.29
P67904 RS10_SALTY 30S ribosomal protein S10;	6		SPHVNKDAR	53	9	0	3.64		1023.52	54.577	3035	2	512.26	-14.49
P60446 RL3_SALTY 50S ribosomal protein L3;	1		VTVQSLDVVR	169	10	8	68.11	b2°b2y3y5y6y7y8y10	1115.64	56.481	69377	2	558.32	-5.91
P60446 RL3_SALTY 50S ribosomal protein L3;	2		IFTEDGVSPVTVIEVEANR	13	20	8	51.74	y2y4°y4y5y6y7y15y20	2188.17	87.974	38699	2	1094.59	8.59
P60446 RL3_SALTY 50S ribosomal protein L3;	3		MAGQMGNER	160	9	10	59.92	b2b3b4y1y2°y2y4y5°y5y8	993.44	20.449	10666	2	497.22	14.50
P60446 RL3_SALTY 50S ribosomal protein L3;	4		LAEGEETYVGQISVELFADVK	83	22	5	20.86	b3y1y4y9y12	2384.18	136.301	3299	2	1192.59	-4.61
P60446 RL3_SALTY 50S ribosomal protein L3;	5		VDVTGTSK	106	8	4	36.09	b3b7y6°y6	806.44	38.417	73161	2	403.72	13.25
P60446 RL3_SALTY 50S ribosomal protein L3;	6		TQDATHGNSLSHR	128	13	5	25.41	b8y7°y7*y7y8	1423.69	40.843	29676	3	475.23	13.20
P60446 RL3_SALTY 50S ribosomal protein L3;	7		NLLLVK	184	6	1	13.62	y4	699.47	56.454	17679	1	699.47	-7.07

[P60446]RL3_SALTY 50S ribosomal protein L3;	8		VGMTR	8	5	2	26.43	b3y4	563.30	50.265	16096	1	563.30	-2.28
[P60446]RL3_SALTY 50S ribosomal protein L3;	9		GLWEFR	77	6	2	26.84	y3y4	807.41	69.873	12457	2	404.21	-9.68
[P60446]RL3_SALTY 50S ribosomal protein L3;	10	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVK	190	18	4	24.81	b12y4y6y15	1738.92	53.937	11284	3	580.31	-17.34
[P60446]RL3_SALTY 50S ribosomal protein L3;	11	Carbamidomethyl+C(9)	GGVPGATGCDLIVKPAVKA	190	19	5	33.34	b7y5y6y12y16	1809.97	56.166	61075	3	603.99	-11.80
[P60446]RL3_SALTY 50S ribosomal protein L3;	12		WNFRTQDATHGNSLSHR	124	17	3	16.31	b3b9y7	2026.98	74.238	6770	3	676.33	10.36
[P60446]RL3_SALTY 50S ribosomal protein L3;	13		LAEGEETYVGQSIGVELFADVKK	83	23	4	28.8	b4b5b11b15	2512.25	98.344	2726	3	838.09	-12.63
[P60446]RL3_SALTY 50S ribosomal protein L3;	14		VTQVKDLANDGYR	33	13	3	20.63	b3b6y7	1478.75	71.623	2627	2	739.88	-5.12
[P60446]RL3_SALTY 50S ribosomal protein L3;	15		DLANDGYRAVQVTTGAK	38	17	3	23.71	b4b8b14	1778.89	76.263	1544	3	593.64	-6.24
[P60446]RL3_SALTY 50S ribosomal protein L3;	16		IFTEDGVSIPTVIEVEANR	13	20	0	6.07		2170.12	87.967	5177	3	724.05	-4.50
[P60726]RL4_SALTY 50S ribosomal protein L4;	1		DAQSALTVSETTFGR	6	15	4	18.13	b4b6y5°y5	1582.77	46.124	17334	3	528.26	1.00
[P60726]RL4_SALTY 50S ribosomal protein L4;	2		VVMTADAVK	185	9	4	30.48	b6°b6y3y7	933.52	45.048	13965	2	467.26	11.70
[P60726]RL4_SALTY 50S ribosomal protein L4;	3		DAQSALTVSETTFGRDFNEALVH QVVVAYAAGAR	6	34	3	10.98	b9b15y7	3593.79	99.515	11405	4	899.20	-2.24
[P60726]RL4_SALTY 50S ribosomal protein L4;	4		MELVLKDAQSALTVSETTFGR	0	21	5	23.52	y1y4y6y7°y7	2296.16	120.392	3002	2	1148.58	-12.33
[P60726]RL4_SALTY 50S ribosomal protein L4;	5		DATGIDPVSLIAFDK	170	15	4	18.13	b5y5y10°y10	1561.81	87.907	12781	2	781.41	-0.31
[P60726]RL4_SALTY 50S ribosomal protein L4;	6		SGGVTFARPQDHSQK	79	16	8	49.74	b3°b3b6b7b8y6°y6y8	1685.82	60.415	9156	3	562.61	-9.49
[P60726]RL4_SALTY 50S ribosomal protein L4;	7		DATGIDPVSLIAFDKVVMTADAV K	170	24	7	39.63	b3b5b8b9y3y7y19	2476.30	101.731	21521	3	826.10	-1.18
[P60726]RL4_SALTY 50S ribosomal protein L4;	8		DAQSALTVSETTFGRDFNEALVH QVVVAYAAGAR	6	34	3	10.98	b8b12y10	3593.81	85.266	3303	3	1198.61	3.46
[P60726]RL4_SALTY 50S ribosomal protein L4;	9	Phosphoryl STY(9)	ELVLKDAQSALTVSETTFGR	1	20	5	37.73	y8y9°y9y10y13_H3PO4 y13	2245.11	80.384	1537	2	1123.06	3.59
[P60726]RL4_SALTY 50S ribosomal protein L4;	10	Oxidation+M(4)	LKDMALEDVLIITGELDENLFLAA R	137	25	3	12.4	b4b6y13	2818.50	89.053	12144	3	940.17	3.12
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	1		LFAGNATPELAQR	5	13	6	28.12	y6*y6y10°y10y11y13	1387.74	53.817	17230	2	694.37	1.85
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	2		ITAVIPYFGYAR	84	12	4	37.25	b4y5y7y9	1370.75	80.397	15468	2	685.88	1.34
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	3	Carbamidomethyl+C(10)	NSVIDEVVVCDTIPTLDEIK	262	20	6	30.63	b2b12b14b15y5y7	2259.15	88.094	6544	2	1130.08	2.16
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	4		VVADFLSSVGVDNR	111	13	3	25.41	b5b6y6	1363.71	74.854	10200	2	682.36	-10.29
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	5		ANVSQVMHIIGDVAGR	198	16	5	27.66	b4b6b9*b9y11	1666.85	75.275	3273	2	833.93	-13.18
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	6		VFAYATHPIFSGNAANNLR	243	19	5	25.86	b7y8y13*y13y14	2063.02	103.541	2889	3	688.35	-11.12
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	7	Carbamidomethyl+C(11)	GGDIFIQSTCAPTNDNLMELVVM VDALR	49	29	3	22.71	b4b5b9	3192.62	105.148	2791	3	1064.88	14.45
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	8		FSDGEVSVQINENVR	34	15	4	29.43	b5b8b13y7	1692.80	59.725	2095	2	846.90	-11.18
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	9		RISNEESISAMFEH	301	14	4	27.06	b7°b7b9b10	1649.76	47.706	10424	2	825.39	3.40
[P0A1V6]KPRS_SALTY Ribose-phohate pyrophohokinase;	10		AIAKLLNDTDMAIIDK	178	16	3	17.15	b11y7y11	1744.94	66.499	4228	2	872.98	-4.27

P66541 RS2_SALTY 30S ribosomal protein S2;	1		TVPMFNEALAE LNK	45	14	9	39.02	b2b3°b3b7b8°b8y9*y9y12	1576.81	84.269	67772	2	788.91	2.63
P66541 RS2_SALTY 30S ribosomal protein S2;	2		DMGGLPDALFVIDADHEHIAIK	152	22	3	19.95	b5b11b14	2377.18	83.388	9922	2	1189.10	-0.82
P66541 RS2_SALTY 30S ribosomal protein S2;	3		SQDLASQAEE SFVEAE	225	16	5	17.15	b6b9y1y5y16	1739.78	72.985	9686	2	870.39	9.12
P66541 RS2_SALTY 30S ribosomal protein S2;	4		EANNLGIPVFAIVD TNSDPDGVDF VIPGNDDAIR	174	34	16	65.17	b6°b6*b6b7°b7°b7b14y5°y 5y7y8y12y13y14*y14y16	3569.76	104.121	13824	3	1190.59	6.02
P66541 RS2_SALTY 30S ribosomal protein S2;	5		YWNPK	21	5	1	13.22	b3	707.35	34.055	11716	2	354.18	-5.26
P66541 RS2_SALTY 30S ribosomal protein S2;	6		WLGGMLTNWK	95	10	3	26.9	b3b8y7	1205.64	82.735	4603	2	603.32	18.53
P66541 RS2_SALTY 30S ribosomal protein S2;	7		AGVHFHGQTR	11	10	5	40.12	b7y5y8y9°y9	1109.54	87.615	2469	1	1109.54	-17.16
P66541 RS2_SALTY 30S ribosomal protein S2;	8		TVPMFNEALAE LNKISAR	45	18	5	24.81	b4°b4b6b10y4	2004.04	95.501	18583	3	668.69	-7.67
P66541 RS2_SALTY 30S ribosomal protein S2;	9	Phosphoryl STY(4)	LENSLGGIK	143	9	3	30.48	b3y7y8	1010.48	21.428	9900	2	505.75	2.30
P66541 RS2_SALTY 30S ribosomal protein S2;	10	Oxidation+M(2)	DMGGLPDALFVIDADHEHIAIK	152	22	4	13.43	b9b14y11°y11	2393.17	71.339	170164	4	599.05	-5.71
P0A7X0 RS8_SALTY 30S ribosomal protein S8;	1		SMQDPIADMLTR	1	12	15	100.12	b1b2b4b12y1y2y3y4y5y6y 8y9y10°y10y12	1377.65	78.069	139210	2	689.33	-2.48
P0A7X0 RS8_SALTY 30S ribosomal protein S8;	2		AVVESIQR	69	8	6	40.86	b2y4y5y6°y6y8	901.50	32.735	58448	2	451.25	-11.71
P0A7X0 RS8_SALTY 30S ribosomal protein S8;	3		AAVTMPSSK	22	9	10	67.7	b2y2y3y4°y4y6y7°y7y8y9	891.46	31.372	54212	2	446.23	0.14
P55900 SERC_SALTY Phohoserine aminotransferase;	1	Carbamidomethyl+C(7)	LAQQELCDWHGLGTSVMEISHR	20	22	9	57.25	b5b6b7y1y3y6°y6y10y11	2567.19	73.903	25660	4	642.55	-10.65
P55900 SERC_SALTY Phohoserine aminotransferase;	2		AQVFNFSSGPAMLPAEVLK	1	19	8	20.69	b2°b2b6°b8b14y6y13y19	2006.06	91.189	20843	2	1003.53	7.18
P55900 SERC_SALTY Phohoserine aminotransferase;	3		MNVPFQLADNTLDK	297	14	3	19.28	b5y7y12	1605.78	57.790	49657	3	535.93	-6.23
P55900 SERC_SALTY Phohoserine aminotransferase;	4		ASIYNAMPIEGVK	335	13	4	32.3	b11y6y9y10	1392.72	64.707	20997	2	696.86	0.18
P55900 SERC_SALTY Phohoserine aminotransferase;	5		YGVIIYAGA QK	188	10	3	41.67	y5y7y9	1069.55	43.299	15174	2	535.28	-14.04
P55900 SERC_SALTY Phohoserine aminotransferase;	6		ITVDGK	122	6	1	13.62	b5	632.36	28.295	10532	1	632.36	-5.50
P55900 SERC_SALTY Phohoserine aminotransferase;	7		EFIQVAEEAEQDFR	44	14	4	19.28	b6°b6y9y12	1710.80	72.879	3540	3	570.94	-0.14
P55900 SERC_SALTY Phohoserine aminotransferase;	8	Carbamidomethyl+C(3)	KYCAPQIIDAK	111	11	5	36.72	b4b7b8°b8y9	1306.67	66.846	95868	2	653.84	-9.81
P55900 SERC_SALTY Phohoserine aminotransferase;	9		GKEFIQVAEEAEQDFR	42	16	3	17.15	b8b13y3	1895.93	52.401	11451	3	632.65	7.28
P55900 SERC_SALTY Phohoserine aminotransferase;	10		ASIYNAMPIEGVKAL TDFMIDFER	335	24	4	22.99	b3°b3b12b13	2731.35	98.466	4488	4	683.59	0.27
P55900 SERC_SALTY Phohoserine aminotransferase;	11		AQGGVAAMHKINQ QK	257	15	4	43.69	y9y10y12y13	1580.81	136.792	2628	1	1580.81	-14.90
P55900 SERC_SALTY Phohoserine aminotransferase;	12	Phosphoryl STY(8)	MAQVFNFSSGPAMLPAEVLK	0	20	4	14.37	b4b6°b6y13	2217.01	82.556	9738	3	739.67	-13.77
P55900 SERC_SALTY Phohoserine aminotransferase;	13	Carbamidomethyl+C(7); Oxidation+M(17)	LAQQELCDWHGLGTSVMEISHR	20	22	8	25.59	b3°b3b8y7y9°y9y13°y13	2583.21	69.018	2504	3	861.74	1.98
P55900 SERC_SALTY Phohoserine aminotransferase;	14	Oxidation+M(13)	MAQVFNFSSGPAMLPAEVLK	0	20	3	21.16	b3b7b14	2153.05	102.131	1770	3	718.36	-10.77
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	1		IVELEAPQLPR	178	11	8	55.96	b2b3°b3y5y6y7y8y11	1264.72	66.108	67288	2	632.86	-4.63

Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	2		DGIFVEDKDSPYVNLIVTREDNKD AENVK	215	29	5	22.13	b4y8y9y12y29	3322.63	70.314	30130	4	831.41	-3.89
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	3		LKDGVGLLPTSLDIVENPK	156	19	6	24.11	y1y2y4y5y7y19	2008.12	79.270	19916	3	670.04	-6.32
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	4		DGSQVAVPNDPTNLGR	128	16	5	17.15	b3°b3b10y9y16	1639.81	34.441	12917	3	547.27	3.35
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	5		FVQAYQSDEVYEAANK	245	16	7	65.97	y3y6y10y11y12y13y16	1861.88	50.856	11601	2	931.45	12.52
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	6	Carbamidomethyl+C(17)	TFAAVGALIGSLALAGCGQDEK	6	22	4	24.22	b4b7b8y3	2149.07	101.064	6769	2	1075.04	-10.00
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	7		DSPYVNLIVTREDNKDAENVK	223	21	7	23.52	b7b11°b11°b11b12°b12y2 1	2419.19	62.525	3925	3	807.07	-7.97
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	8		DGIFVEDK	215	8	5	48.06	b3b4y3y4°y4	922.45	93.450	8749	1	922.45	-2.78
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	9		GDIDANAFQHKKPYLDQQIK	78	19	5	38.12	b3b10b11°b11b12	2201.09	89.585	8679	3	734.37	-3.22
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	10		SLDDAQIALAVINTTYASQIGLTPA K	189	26	3	12.14	b3b9y13	2674.37	100.847	3279	3	892.13	-20.54
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	11		VFNGGAVKGW	261	10	4	41.09	b4b6y7y8	1034.56	30.181	215861	2	517.78	13.10
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	12		SLDELKDGSQVAVPNDPTNLGR	122	22	6	28.95	b10b12°b12b13y3y19	2325.18	57.822	3608	2	1163.09	5.88
Q8ZRN1 METQ_SALTY D-methionine-binding lipoprotein metQ;	13	Phosphoryl STY(13)	YGLDVELVTFNDYVLPNEALSK	56	22	5	18.16	b5°b5b11y11y13	2579.22	80.090	3705	3	860.41	-1.14
P02936 OMPA_SALTY Outer membrane protein A;	1	Carbamidomethyl+C(13)	GMGESNPVTGNTCDNVKPR	302	19	18	158.7	b3b4b12y2y5y7y8y9y10y1 1°y11y12y13°y13y14y15y1 7y19	2032.90	37.624	74537	3	678.30	-9.85
P02936 OMPA_SALTY Outer membrane protein A;	2		IGSDAYNQGLSEKR	267	14	5	27.85	y4y8*y8y13y14	1537.74	34.435	21816	3	513.25	-14.45
P02936 OMPA_SALTY Outer membrane protein A;	3		LGYPITDDLVDYTR	103	14	4	41.74	y4y9y10y11	1640.83	75.920	11887	2	820.92	5.13
P02936 OMPA_SALTY Outer membrane protein A;	4		FGQQEAAPVVAPAPAPEVQTK	194	23	6	20.11	b2b3y6y10y12y23	2303.18	53.847	8803	3	768.40	-8.69
P02936 OMPA_SALTY Outer membrane protein A;	5		GDNINGAYK	85	9	4	38.26	b4b5b7b9	951.44	26.878	7250	1	951.44	-14.05
P02936 OMPA_SALTY Outer membrane protein A;	6		IGSDAYNQGLSEK	267	13	6	29.66	b7b9y7*y7y12y13	1381.67	31.605	4934	2	691.34	4.06
P02936 OMPA_SALTY Outer membrane protein A;	7		DGSVVVLGFTDR	255	12	3	32.48	b4b8b11	1264.67	49.877	4180	3	422.23	11.10
P02936 OMPA_SALTY Outer membrane protein A;	8		SDVLFNFNK	222	9	3	30.48	b3y5y6	1083.53	68.580	27702	2	542.27	-15.55
P02936 OMPA_SALTY Outer membrane protein A;	9		DHDTGVSPVFAGGIEYAITPEIATR	138	25	6	25.84	b14b15°b15y10y13°y13	2616.25	136.825	4662	2	1308.63	-16.61
P02936 OMPA_SALTY Outer membrane protein A;	10		GIPSDKISAR	292	10	5	54.89	y3y5y7°y7y8	1043.57	32.061	20748	2	522.29	-13.33
P02936 OMPA_SALTY Outer membrane protein A;	11		MPYKGDNINGAYK	81	13	3	20.63	b9y4y7	1470.72	60.435	15931	2	735.86	12.20

[P02936]OMPA_SALTY Outer membrane protein A;	12		DGSVVVLGFTDRIGSDAYNQGLS EK	255	25	3	18.62	b3b9b13	2627.27	66.191	5687	4	657.57	-9.20
[P02936]OMPA_SALTY Outer membrane protein A;	13		AQGVQLTAKLGYPITDDLDVYTR	94	23	4	22.08	b3b4y5°y5	2537.30	124.932	4986	3	846.44	-10.10
[P02936]OMPA_SALTY Outer membrane protein A;	14		LGYPITDDLDVYTRLGGMVWR	103	21	4	21.69	b12y4y10y12	2440.20	71.243	3974	3	814.07	-11.61
[Q8ZR01]RLPA_SALTY Rare lipoprotein A;	1		LSQQFSVPGR	329	10	10	99.98	b3*b3b7y2y3y5y6y7y8y9	1118.59	47.635	19353	2	559.80	-3.27
[Q8ZR01]RLPA_SALTY Rare lipoprotein A;	2		FSQAGLAAIYDAEPGSNLTASGEM FDPMQLTAAHPTLPIPSYAR	78	44	10	34.39	b3b5b7b8b10*b10b13y5y7 y14	4607.21	99.756	14277	4	1152.56	-2.76
[Q8ZR01]RLPA_SALTY Rare lipoprotein A;	3		FVVQVGAVSDQTR	309	13	3	20.63	b6b9y7	1405.73	64.721	2940	3	469.25	-9.12
[Q8ZR01]RLPA_SALTY Rare lipoprotein A;	4		QTYALPPRPDLSGMGSSASSAPA QPQGDVLPVSNSTLK	191	38	3	22.76	b13b14y11	3794.98	112.966	6720	4	949.50	20.39
[Q8ZR01]RLPA_SALTY Rare lipoprotein A;	5		AAADRLNTSNNTK	152	13	4	20.63	b4°b4b7y7	1375.70	42.657	6385	3	459.24	7.63
[Q8ZR01]RLPA_SALTY Rare lipoprotein A;	6		AQQYQQRLSQQFSVPGR	322	17	3	23.3	b10y5y6	2021.03	86.991	2239	2	1011.02	-1.57
[Q8ZR01]RLPA_SALTY Rare lipoprotein A;	7		AVSDQTR	315	7	0	3.24		776.38	64.791	1910	1	776.38	-14.07
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	1		MASVSSGMQLPPGFK	91	15	6	25.79	b4b10y11y13°y13y15	1536.75	66.583	32804	2	768.88	-2.30
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	2	Carbamidomethyl+C(9)	VTINGAHNCR	43	10	3	33.89	y4y6y7	1141.55	20.434	4764	2	571.28	-4.49
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	3		VEIDPSLLEDDK	54	12	5	51.13	b3b7b9y8y9	1372.67	34.108	4095	3	458.23	-12.09
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	4		MQEEIAQLEVTGESGAGLVK	23	20	5	27.88	b9b15*b15y10y11	2089.05	118.030	2043	3	697.02	0.93
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	5		GGLGNLMKQAQQMQEK	4	16	7	60.22	b3b5b13b14b15y4y13	1760.90	72.988	11612	2	880.96	14.70
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	6		EKMASVSSGMQLPPGFK	89	17	9	52.57	b5b6b11b15°b15y5y11*y1 y13	1793.90	111.799	2849	2	897.45	2.99
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	7		MASVSSGMQLPPGFKMPF	91	18	3	15.58	b12y12y16	1911.91	67.598	2318	2	956.46	-1.79
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	8	Carbamidomethyl+C(8)	TINGAHNCR	44	9	2	8.25	b7*b7	1042.47	20.414	3831	2	521.74	-11.94
[P0A8B8]YBAB_SALTY UPF0133 protein ybaB;	9	Carbamidomethyl+C(7)	INGAHNCR	45	8	0	2.02		941.43	20.485	3732	2	471.22	-5.83
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	1		GFGVPTLIAVHPENDPQGEGMAIA K	167	25	10	40.84	b2b3b4y1y2y8y10y14y21y 25	2548.29	77.134	57241	3	850.10	1.53
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	2		LIQFGWETITEALK	252	14	5	27.06	b3b12b13y1y14	1648.88	101.284	14629	2	824.94	-7.85
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	3	Carbamidomethyl+C(6)	VVIVGCGAQQGLNQLNMR	39	18	4	15.58	b1b3b13y5	1885.97	71.921	8737	3	629.33	-3.43
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	4		FMGRDEFADGASYLQGK	21	17	3	23.3	b3b4y9	1891.88	50.877	5610	3	631.30	7.29
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	5		ANYFNTLNL	1	10	3	26.9	b3y4y6	1225.63	67.827	19387	2	613.32	-3.98
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	6		TAFETAPQYEGK	336	12	3	26.25	b3b4y5	1341.66	27.925	3274	2	671.33	20.74
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	7		VGTYEELIPQADLVVNLTDPKQHS DVVR	88	28	4	22.72	b3°b3b4b7	3135.61	81.524	25141	4	784.66	-6.62
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	8	Carbamidomethyl+C(11)	DITVVMVAPKCPGTEVR	145	17	6	32.74	b3b14y6y9°y9y11	1871.97	57.834	23425	2	936.49	0.65
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	9		ANYFNTLNLRQQLAQLGK	1	18	4	24.81	b3b7b10y3	2092.13	89.591	12125	2	1046.57	-0.35
[P05989]ILVC_SALTY Ketol-acid reductoisomerase;	10		QGGITLMMDRLSNPAK	266	16	4	25.53	b4b5b12*b12	1731.87	110.962	3206	2	866.44	-12.33

P05989 ILVC_SALTY Ketol-acid reductoisomerase;	11	Phosphoryl STY(6)	LVAEGTDPAYAEK	239	13	4	32.3	b5y4y6y7	1443.65	82.416	3316	3	481.89	9.98
P05989 ILVC_SALTY Ketol-acid reductoisomerase;	12	Oxidation+M(21)	GFGVPTLIAPHENDPQGEGMAIAK	167	25	3	12.4	b5y3y11	2564.27	108.037	2652	3	855.43	-4.67
P67286 YBJQ_SALTY UPF0145 protein ybjQ;	1		AREIAFQELGEQAK	56	14	6	19.28	b11*b11y2y7°y7y9	1589.82	60.396	12640	2	795.41	-4.22
P67286 YBJQ_SALTY UPF0145 protein ybjQ;	2		EIAFQELGEQAK	58	12	11	79.12	b2b3°b3b5b6b9b10b11*b11b12y2	1362.69	60.398	12613	2	681.85	0.00
P63411 ACKA_SALTY Acetate kinase;	1		DSASFAPLHNPAHLIGIAEALK	114	22	5	13.43	b10°b10b13*b13y8	2272.22	86.252	28603	3	758.08	6.98
P63411 ACKA_SALTY Acetate kinase;	2		EGTRPAVV IPTNEEL VIAQDASR	374	23	9	42.03	b6b8°b8y5y6y7°y7y14y23	2465.30	68.887	19475	3	822.44	-0.20
P63411 ACKA_SALTY Acetate kinase;	3		LGVLGFEVDHER	348	12	5	37.25	b3y3y6y8y12	1370.69	67.605	18524	3	457.57	-13.71
P63411 ACKA_SALTY Acetate kinase;	4		QEALGAGAAHSEALNFIVNTILAKPELSAQLTAIGHR	52	39	9	36.15	b14b17°b17b18b19y14*y14y17*y17	4011.11	136.838	8767	3	1337.71	-8.95
P63411 ACKA_SALTY Acetate kinase;	5		NVAVFDTAFHQTMPEESYLYALPYSLYK	144	28	3	17.72	b3b7b10	3297.61	94.305	2111	4	825.16	8.14
P63411 ACKA_SALTY Acetate kinase;	6		LDVVFTGGIGENAA MVR	324	18	6	38.58	y9*y9y10*y10y11y16	1819.92	93.446	54331	2	910.46	-8.59
P63411 ACKA_SALTY Acetate kinase;	7	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPEAR	17	26	5	18.28	b3y4°y4y12y23	2907.40	104.240	26594	3	969.81	1.93
P63411 ACKA_SALTY Acetate kinase;	8	Carbamidomethyl+C(1)	CVDTSMGLTPLEGLVMGTR	224	19	8	57.94	b3y4y5y7y10y11y13°y13	2037.03	94.524	21835	2	1019.02	21.45
P63411 ACKA_SALTY Acetate kinase;	9		SGDIDPAIIFHLHDTLGMSVDQINKMLTK	243	29	7	25.98	b8b12°b12b13°b13b15y15	3209.64	94.507	27166	3	1070.55	1.83
P63411 ACKA_SALTY Acetate kinase;	10		YTSSVVIDESVIQGIKDSASFAPLHNPAHLIGIAEALK	98	38	7	27.69	b12y12°y12y15y16y22y32	3991.11	136.830	5532	3	1331.04	-1.10
P63411 ACKA_SALTY Acetate kinase;	11	Carbamidomethyl+C(19)	FAIIDAVNGDEYLSGLAECFHLPEARIK	17	28	4	17.32	b12b14b17y10	3148.56	96.971	3369	2	1574.78	-4.96
P63411 ACKA_SALTY Acetate kinase;	12	Phosphoryl STY(15)	SGDIDPAIIFHLHDTLGMSVDQINK	243	25	3	22.88	b11b14b15	2816.36	84.148	41223	3	939.46	14.13
P63411 ACKA_SALTY Acetate kinase;	13	Carbamidomethyl+C(18);Phosphoryl STY(3)	MLTKESGLLGLTEVTSDCR	268	19	9	50.02	b4b12y5y9y12y14°y14y15°y15	2190.01	86.305	36333	2	1095.51	-1.23
P63411 ACKA_SALTY Acetate kinase;	14	Carbamidomethyl+C(18);Oxidation+M(1)	MLTKESGLLGLTEVTSDCR	268	19	4	20.69	b4b6y9y13	2126.07	126.623	1988	2	1063.54	9.42
P63411 ACKA_SALTY Acetate kinase;	15		QEALGAGAAHSEALNFI	52	18	2	11.66	y15°y15	1769.88	136.786	2952	1	1769.88	-0.21
P63411 ACKA_SALTY Acetate kinase;	16		DSASFAPLHNPAHLIGIAE	114	19	1	7.79	y3	1960.00	86.216	2365	3	654.00	2.43
P22107 TRAT_SALTY TraT complement resistance protein;	1		ATVTTDNVAALR	177	12	8	35.49	y2y8y9*y9y10*y10y12*y12	1231.66	45.436	58063	2	616.33	-2.28
P22107 TRAT_SALTY TraT complement resistance protein;	2		FEEAKPVLEEQLAK	223	14	10	66.92	b2b3b4b6b9b10y2y6y9y14	1630.85	53.330	33509	3	544.29	-13.92
P22107 TRAT_SALTY TraT complement resistance protein;	3	Carbamidomethyl+C(16)	LMMVTLVSSTLALSGCGAMSTAIK	5	24	4	22	b8y2y12y13	2442.28	136.135	8349	3	814.76	11.90
P22107 TRAT_SALTY TraT complement resistance protein;	4		AYYWIQANVLK	89	11	3	36.06	b6b8b10	1368.74	90.696	4395	2	684.88	9.72
P22107 TRAT_SALTY TraT complement resistance protein;	5		IQTSTETGNQHK	196	12	5	44.91	y5y6y8°y8y10	1343.63	14.598	9809	3	448.55	-16.90
P22107 TRAT_SALTY TraT complement resistance protein;	6		TKATVTTDNVAALR	175	14	5	42.4	b8y3y8y9y11	1460.79	41.187	13655	3	487.60	-14.79
P22107 TRAT_SALTY TraT complement resistance protein;	7		IQTSTETGNQHKYQTR	196	16	4	23.69	b5b6°b6y12	1891.95	59.444	6439	2	946.48	13.10
P22107 TRAT_SALTY TraT complement resistance protein;	8		NTSDKDMSDLQSLIAK	58	16	4	17.15	b3b5y11*y11	1765.89	116.175	2260	2	883.45	14.10

P22107 TRAT_SALTY TraT complement resistance protein;	9	Carbamidomethyl+C(16) ;Phosphoryl STY(5)	LMMVTLVSSTLALSGCGAMSTAI KK	5	25	4	27.86	b3b4b12b14	2650.26	87.940	1781	2	1325.64	-12.99
P22107 TRAT_SALTY TraT complement resistance protein;	10	Carbamidomethyl+C(16) ;Oxidation+M()	LMMVTLVSSTLALSGCGAMSTAI KK	5	25	4	23.09	b3b4b9y12	2586.32	104.274	1703	3	862.78	-6.89
P22107 TRAT_SALTY TraT complement resistance protein;	11	Oxidation+M(2)	DMSDLQSLIAKDIAK	63	16	3	23.69	b10b11y12	1791.93	136.750	1523	1	1791.93	6.68
P22107 TRAT_SALTY TraT complement resistance protein;	12		TDNVAALR	181	8	0	2.83		859.47	45.435	2515	2	430.24	6.75
Q7CQV9 DPS_SALTY DNA protection during starvation protein;	1		AVQLGGVALGTTQVINSK	83	18	8	24.81	b1b2b4y3y11y14°y14y18	1756.00	67.311	20694	2	878.50	0.42
Q7CQV9 DPS_SALTY DNA protection during starvation protein;	2		ASNLLYTR	10	8	5	40.86	y1y3y4y5y8	937.50	44.185	16776	2	469.25	-9.31
Q7CQV9 DPS_SALTY DNA protection during starvation protein;	3		TALTDHLDTMAER	70	13	6	56.31	b5b10y3y7y8y9	1473.68	52.316	40172	3	491.90	-16.65
Q7CQV9 DPS_SALTY DNA protection during starvation protein;	4		FLWFIESNIE	157	10	4	47.9	b4b7b9y9	1297.62	71.328	27436	2	649.32	-16.84
Q7CQV9 DPS_SALTY DNA protection during starvation protein;	5		SYPLDIHNVQDHLK	105	14	3	24.72	b3y7y8	1678.87	70.049	11510	2	839.94	11.12
Q7CQV9 DPS_SALTY DNA protection during starvation protein;	6		ASNLLYTRNDVSESDK	10	16	4	24.86	b3b10*b10b14	1811.90	89.611	22272	3	604.64	10.98
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	1		MQAAGAQAAYLVNTGWNGTGK	426	20	8	33.45	b2b5y8y10y14*y14y16y20	2037.99	78.165	30204	3	680.00	4.01
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	2		LTANQTQYHFLSGFTAK	371	17	6	26.14	b11y1y6y10y15y17	1926.95	67.787	26230	3	642.99	-11.40
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	3		NTYASPEQWQEK	495	12	5	48.12	b3b4y7y8y10	1480.69	44.499	21073	2	740.85	11.46
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	4	Carbamidomethyl+C(21)	LIGDDEHGWDDDGVFNFEGGCY AK	263	24	3	12.7	b6b14y9	2716.13	79.079	11711	3	906.05	2.34
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	5		AYGINDVQDIVYNPSYDTLYQEEL NPGLEGYER	12	33	14	102.63	b4b5b10b11b12°b12b13y2 y3y4y6y8y9y10	3837.80	90.670	8763	3	1279.94	6.74
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	6		MQAAGAQAAYLVNTGWNGTGKR	426	21	5	22.32	b8*b8y2y10y11	2194.09	59.753	1965	2	1097.55	5.12
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	7		GVLTNLGAVAVDTGIFTGR	45	19	3	21.89	y4y8y10	1861.01	93.800	8688	2	931.01	-3.21
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	8		TTLSTDPK	253	8	5	67.3	b4b5b6y5y7	862.47	28.107	6308	2	431.74	17.20
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	9		NMFIRPTDEELVGFKPDFIVMNGA K	148	25	3	12.4	b5y3y13	2868.44	57.383	4468	3	956.82	-0.51
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	10		NDNKPLSQETWQHLLK	90	15	3	26.21	y7y9y10	1837.91	77.865	4169	3	613.31	-6.11

P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	11		LPLFDLAIPTELPGVDTHILDPR	472	23	3	34.89	y8y9y10	2542.34	107.005	3993	3	848.12	-19.21
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	12		DALLENVTVR	305	10	3	28.66	b5b6y3	1129.61	25.791	1994	2	565.31	-14.37
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	13		NTYASPEQWQEKATALAK	495	18	3	15.58	b10b13y12	2036.02	73.288	15306	3	679.34	3.84
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	14		GDVAVFFGLSGTGKTTLSTDPK	239	22	3	19.95	b4b15b19	2198.11	115.256	12474	3	733.37	-11.44
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	15		LFIEFEEKYTDTPAGEALVSAGPK	513	24	7	40.19	b5*b5b6*b6b8b9y12	2597.29	69.032	6015	3	866.44	-8.18
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	16		YIVRDDTTR	69	9	3	30.48	b7y6y7	1138.58	120.347	5481	1	1138.58	-7.29
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	17		DTRAIIDAILNGSLDNAETFR	451	21	3	23.52	y8y9y12	2305.18	78.366	5282	2	1153.09	-0.85
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	18		MQAAGAQAAYLVNTGWNGTGKR	426	21	4	13.87	b10b14°b14y7	2194.09	106.985	2118	3	732.03	1.67
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	19		RMQAAGAQAAYLVNTGWNGTGK	425	21	10	47.06	b9b11b12y5°y5y6*y6y10*y10y17	2194.11	136.266	1944	2	1097.56	14.58
P41033 PCKA_SALTY Phohoenolpyruvate carboxykinase [ATP];	20	Phosphoryl STY(12)	LTANQTQYHFLSGFTAK	371	17	7	48.69	b4°b4b7b9b10°b10b11	2006.91	94.360	8259	3	669.64	-10.16