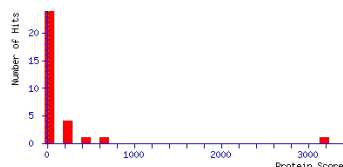


Cambridge Centre for Proteomics Mascot Search Results

User :
Email :
Search title : Himansha seq and Lactococcus 231115 Nov 2015 (\\prot-filesvrl\data\CORE\MASCOT\PARAMS\Julie\Himansha_plus_Lactococcus_Velos_Oct_2015.par), submitted from Daemon on CCP-PC152
MS data file : \\prot-filesvrl\data\CORE\RAW_DATA_2015_Velos\Himansha_November_2015\Himansha_MT_20_11_15.mgf
Database 1 : Himansha_Oct15_Oct_2015 (2 sequences; 928 residues)
Database 2 : Rik Nov 2015 proteome AUP000002195_AND_proteomecomponent_A_Chromosome (2225 sequences; 656950 residues)
Timestamp : 23 Nov 2015 at 10:13:30 GMT
Protein hits : 1:hs|HSFULL|HSFULL| full length MbaA
2:isp|Q9CR10|EFTU LACIA Elongation factor Tu OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=tuf PE=3 SV=1
2:itr|Q9CGH2|Q9CGH2 LACIA Fumarate reductase flavoprotein subunit OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=frdC PE=4 SV=1
2:isp|Q9CEK3|SYN LACIA Asparagine--tRNA ligase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=asnS PE=3 SV=1
2:itr|Q9CVD3|Q9CVD3 LACIA Dihydropolypyl dehydrogenase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=pdhD PE=4 SV=1
2:itr|Q9CHA0|Q9CHA0 LACIA 30S ribosomal protein S1 OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=rpsA PE=4 SV=1
2:itr|Q9CRM1|Q9CRM1 LACIA Transport protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ysaI PE=4 SV=1
2:itr|Q9CGJ6|Q9CGJ6 LACIA Nicotinate phosphoribosyltransferase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ylaF PE=3 SV=1
2:itr|Q9CF08|Q9CF08 LACIA l-deoxy-D-xylulose-5-phosphate synthase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=dxsB PE=4 SV=1
2:isp|Q9CD71|JSE LACIA Glutamate--tRNA ligase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=glx PE=3 SV=1
2:isp|Q9CD41|POTR LACIA Spermidine/putrescine import ATP-binding protein PotA OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=potA PE=3 SV=1
2:isp|Q9CDR6|EZR LACIA Septation ring formation regulator EzrA OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ezrA PE=3 SV=1
2:itr|Q9CRH2|Q9CRH2 LACIA Cell division protein FtsZ OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ftsZ PE=3 SV=1
2:itr|Q9CDR1|Q9CDR1 LACIA Aldehyde-alcohol dehydrogenase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=adhE PE=3 SV=1
2:itr|Q7DAV2|Q7DAV2 LACIA Alpha-acetolactate synthase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=als PE=3 SV=1
2:isp|Q9CF25|FTSK LACIA DNA translocase FtsK OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ftsK PE=3 SV=1
2:isp|Q9C175|PYRG LACIA CTP synthase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=pyrG PE=3 SV=1
2:isp|P0A493|RLJ6 LACIA 50S ribosomal protein L36 OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=rplJ PE=3 SV=1
2:itr|Q9CR09|Q9CR09 LACIA Uncharacterized protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=yvcA PE=4 SV=1
2:itr|Q9C176|Q9C176 LACIA Amino acids and amines aminotransferase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=yelG PE=3 SV=1
2:itr|Q9CGY3|Q9CGY3 LACIA Fructose-specific PTS system enzyme IIBC component OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=fraA PE=4 SV=1
2:isp|Q9C161|PNP LACIA Polynucleotide nucleotidyltransferase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=pnp PE=3 SV=1
2:itr|Q9CGA1|Q9CGA1 LACIA Citrate lyase alpha chain OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=citF PE=4 SV=1
2:isp|Q9CFV2|CARB LACIA Carbamoyl-phosphate synthase large chain OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=carB PE=3 SV=1
2:itr|Q9CHF3|Q9CHF3 LACIA Biotin carboxylase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=accC PE=4 SV=1
2:itr|Q9CFE6|Q9CFE6 LACIA ABC transporter ATP binding and permease protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ygpD PE=4 SV=1
2:itr|Q9CJAO|Q9CJAO LACIA ABC transporter ATP binding protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ybaB PE=3 SV=1
2:isp|P3514|DVAJ LACIA Chaperone protein DnaJ OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=dnaJ PE=3 SV=2
2:itr|Q9CH39|Q9CH39 LACIA NADH dehydrogenase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=noxH PE=4 SV=1
2:itr|Q9CDS2|Q9CDS2 LACIA Uncharacterized protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ywbA PE=4 SV=1
2:isp|Q9CJ85|SECA LACIA Protein translocase subunit SecA OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=secA PE=3 SV=1

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 16 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As	Peptide Summary	Help
Significance threshold p<	0.05	Max. number of hits
Standard scoring	MudPIT scoring	Ions score or expect cut-off
Show pop-ups	Suppress pop-ups	Sort unassigned
Select All	Select None	Search Selected
Error tolerant	Archive Report	

1. 1:hs|HSFULL|HSFULL| Mass: 64534 Score: 3180 Matches: 862 (862) Sequences: 48 (48) emPAI: 1347.72
full length MbaA
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
53	384.6910	767.3674	767.3670	0.54	0	(20)	0.0098	1	U	K.VVMTHR.R + 2 Oxidation (M)
54	384.6910	767.3674	767.3670	0.54	0	(20)	0.01	1	U	K.VVMTHR.R + 2 Oxidation (M)
55	384.6911	767.3677	767.3670	0.94	0	(23)	0.0058	1	U	K.VVMTHR.R + 2 Oxidation (M)
57	384.6913	767.3680	767.3670	1.26	0	23	0.0049	1	U	K.VVMTHR.R + 2 Oxidation (M)
248	432.2331	862.4517	862.4517	0.01	1	22	0.02	1	U	R.MRLQMK.M
284	447.7190	893.4234	893.4243	-1.04	0	51	1.9e-05	1	U	R.ATGDVEFR.N
285	447.7192	893.4239	893.4243	-0.49	0	(46)	5.2e-05	1	U	R.ATGDVEFR.N
286	447.7196	893.4246	893.4243	0.33	0	(24)	0.0098	1	U	R.ATGDVEFR.N
287	447.7196	893.4247	893.4243	0.40	0	(46)	6.1e-05	1	U	R.ATGDVEFR.N
288	447.7198	893.4251	893.4243	0.95	0	(46)	6.1e-05	1	U	R.ATGDVEFR.N
291	448.7687	895.5228	895.5239	-1.27	0	(25)	0.0028	1	U	R.TSLVIAHR.L
292	448.7690	895.5235	895.5239	-0.52	0	58	1.6e-06	1	U	R.TSLVIAHR.L
293	448.7694	895.5242	895.5239	0.30	0	(56)	2.5e-06	1	U	R.TSLVIAHR.L
342	458.2558	914.4970	914.4974	-0.38	0	(41)	0.00021	1	U	R.GVYALQK.M
343	458.2559	914.4973	914.4974	-0.11	0	46	7.1e-05	1	U	R.GVYALQK.M
400	473.2333	944.4521	944.4563	-4.41	0	(29)	0.0016	1	U	R.EQIEAAR.M
401	473.2344	944.4543	944.4563	-2.14	0	(25)	0.0036	1	U	R.EQIEAAR.M
402	473.2345	944.4544	944.4563	-2.01	0	(39)	0.00014	1	U	R.EQIEAAR.M
403	473.2349	944.4553	944.4563	-1.05	0	(23)	0.0064	1	U	R.EQIEAAR.M
404	473.2350	944.4554	944.4563	-0.92	0	(30)	0.0013	1	U	R.EQIEAAR.M
405	473.2351	944.4557	944.4563	-0.59	0	45	3.7e-05	1	U	R.EQIEAAR.M
406	473.2352	944.4558	944.4563	-0.46	0	(21)	0.0095	1	U	R.EQIEAAR.M
407	473.2353	944.4560	944.4563	-0.27	0	(38)	0.00018	1	U	R.EQIEAAR.M
408	473.2353	944.4560	944.4563	-0.27	0	(42)	8e-05	1	U	R.EQIEAAR.M
409	473.2354	944.4562	944.4563	-0.08	0	(41)	9.8e-05	1	U	R.EQIEAAR.M
410	473.2355	944.4565	944.4563	0.18	0	(39)	0.00015	1	U	R.EQIEAAR.M
411	473.2356	944.4566	944.4563	0.31	0	(45)	4e-05	1	U	R.EQIEAAR.M
412	473.2357	944.4568	944.4563	0.51	0	(21)	0.0097	1	U	R.EQIEAAR.M
413	473.2357	944.4569	944.4563	0.70	0	(40)	0.00011	1	U	R.EQIEAAR.M
414	473.2358	944.4570	944.4563	0.76	0	(27)	0.0025	1	U	R.EQIEAAR.M
415	473.2359	944.4572	944.4563	0.96	0	(24)	0.0044	1	U	R.EQIEAAR.M
416	473.2360	944.4574	944.4563	1.15	0	(41)	8.3e-05	1	U	R.EQIEAAR.M
417	473.2362	944.4579	944.4563	1.67	0	(28)	0.0021	1	U	R.EQIEAAR.M
418	473.2364	944.4583	944.4563	2.12	0	(24)	0.0065	1	U	R.EQIEAAR.M
419	473.2376	944.4607	944.4563	4.64	0	(27)	0.0029	1	U	R.EQIEAAR.M
420	473.2378	944.4610	944.4563	4.96	0	(21)	0.013	1	U	R.EQIEAAR.M
421	473.2422	944.4699	944.4563	14.4	0	(26)	0.0054	1	U	R.EQIEAAR.M
444	476.7577	951.5008	951.5025	-1.84	0	(32)	0.00099	1	U	R.EYTLASLR.N
445	476.7579	951.5013	951.5025	-1.33	0	(32)	0.00085	1	U	R.EYTLASLR.N

446	476.7580	951.5014	951.5025	-1.20	0	(43)	6.8e-05	1	U	R.EYTLASLR.N
447	476.7583	951.5021	951.5025	-0.49	0	(30)	0.0014	1	U	R.EYTLASLR.N
448	476.7583	951.5021	951.5025	-0.43	0	(44)	6.3e-05	1	U	R.EYTLASLR.N
449	476.7584	951.5023	951.5025	-0.24	0	(40)	0.00016	1	U	R.EYTLASLR.N
450	476.7585	951.5024	951.5025	-0.17	0	(30)	0.0014	1	U	R.EYTLASLR.N
451	476.7586	951.5026	951.5025	0.08	0	46	4.1e-05	1	U	R.EYTLASLR.N
452	476.7586	951.5027	951.5025	0.15	0	(32)	0.00097	1	U	R.EYTLASLR.N
455	476.7597	951.5049	951.5025	2.46	0	(27)	0.0026	1	U	R.EYTLASLR.N
484	481.2854	960.5562	960.5604	-4.36	0	(25)	0.0059	1	U	K.STIASLITR.F
485	481.2864	960.5582	960.5604	-2.27	0	(57)	3.5e-06	1	U	K.STIASLITR.F
486	481.2865	960.5584	960.5604	-2.07	0	(56)	5.1e-06	1	U	K.STIASLITR.F
487	481.2866	960.5587	960.5604	-1.76	0	(45)	5.4e-05	1	U	K.STIASLITR.F
488	481.2868	960.5591	960.5604	-1.38	0	(54)	7.7e-06	1	U	K.STIASLITR.F
489	481.2869	960.5593	960.5604	-1.12	0	82	9.7e-09	1	U	K.STIASLITR.F
490	481.2870	960.5594	960.5604	-1.00	0	(59)	2.1e-06	1	U	K.STIASLITR.F
491	481.2870	960.5595	960.5604	-0.87	0	(55)	5e-06	1	U	K.STIASLITR.F
492	481.2872	960.5598	960.5604	-0.55	0	(45)	6e-05	1	U	K.STIASLITR.F
493	481.2874	960.5603	960.5604	-0.04	0	(45)	4.8e-05	1	U	K.STIASLITR.F
494	481.2875	960.5605	960.5604	0.15	0	(62)	1.1e-06	1	U	K.STIASLITR.F
495	481.2876	960.5606	960.5604	0.28	0	(57)	3.2e-06	1	U	K.STIASLITR.F
496	481.2884	960.5622	960.5604	1.86	0	(31)	0.0013	1	U	K.STIASLITR.F
497	481.2887	960.5629	960.5604	2.63	0	(43)	8.3e-05	1	U	K.STIASLITR.F
500	481.7653	961.5160	961.5193	-3.36	0	(27)	0.0069	1	U	K.QSTOTLLSR.I
501	481.7664	961.5182	961.5193	-1.07	0	61	2.3e-06	1	U	K.QSTOTLLSR.I
502	481.7664	961.5183	961.5193	-0.95	0	(51)	2.5e-05	1	U	K.QSTOTLLSR.I
503	481.7668	961.5190	961.5193	-0.31	0	(46)	7.7e-05	1	U	K.QSTOTLLSR.I
504	481.7670	961.5195	961.5193	0.26	0	(51)	2.2e-05	1	U	K.QSTOTLLSR.I
505	481.7671	961.5197	961.5193	0.45	0	(57)	5.6e-06	1	U	K.QSTOTLLSR.I
506	481.7672	961.5198	961.5193	0.58	0	(31)	0.0026	1	U	K.QSTOTLLSR.I
507	481.7672	961.5198	961.5193	0.58	0	(55)	1.1e-05	1	U	K.QSTOTLLSR.I
776	527.7672	1053.5199	1053.5244	-4.25	0	(32)	0.0011	1	U	R.NVFTTTPGR.D
778	527.7676	1053.5207	1053.5244	-3.44	0	(22)	0.011	1	U	R.NVFTTTPGR.D
779	527.7684	1053.5223	1053.5244	-1.94	0	(22)	0.01	2	U	R.NVFTTTPGR.D
780	527.7687	1053.5228	1053.5244	-1.47	0	(22)	0.01	1	U	R.NVFTTTPGR.D
781	527.7688	1053.5230	1053.5244	-1.24	0	44	6e-05	1	U	R.NVFTTTPGR.D
782	527.7688	1053.5230	1053.5244	-1.24	0	(29)	0.0019	1	U	R.NVFTTTPGR.D
783	527.7689	1053.5232	1053.5244	-1.12	0	(34)	0.00074	1	U	R.NVFTTTPGR.D
784	527.7690	1053.5235	1053.5244	-0.78	0	(38)	0.00029	1	U	R.NVFTTTPGR.D
785	527.7690	1053.5235	1053.5244	-0.78	0	(26)	0.0042	1	U	R.NVFTTTPGR.D
786	527.7692	1053.5238	1053.5244	-0.55	0	(31)	0.0014	1	U	R.NVFTTTPGR.D
789	527.7697	1053.5248	1053.5244	0.38	0	(22)	0.01	1	U	R.NVFTTTPGR.D
790	527.7697	1053.5249	1053.5244	0.50	0	(26)	0.0043	1	U	R.NVFTTTPGR.D
791	527.7697	1053.5249	1053.5244	0.50	0	(23)	0.0079	1	U	R.NVFTTTPGR.D
792	527.7697	1053.5249	1053.5244	0.50	0	(39)	0.00018	1	U	R.NVFTTTPGR.D
793	527.7699	1053.5252	1053.5244	0.84	0	(39)	0.00018	1	U	R.NVFTTTPGR.D
795	527.7703	1053.5260	1053.5244	1.54	0	(21)	0.012	2	U	R.NVFTTTPGR.D
799	527.7714	1053.5282	1053.5244	3.62	0	(34)	0.00071	1	U	R.NVFTTTPGR.D
802	527.7726	1053.5306	1053.5244	5.94	0	(22)	0.011	1	U	R.NVFTTTPGR.D
803	527.7733	1053.5320	1053.5244	7.22	0	(21)	0.012	1	U	R.NVFTTTPGR.D
807	528.2621	1054.5096	1054.5084	1.19	0	(38)	0.00024	1	U	R.NVFTTTPGR.D + Deamidated (NQ)
808	528.2629	1054.5113	1054.5084	2.81	0	(34)	0.00064	1	U	R.NVFTTTPGR.D + Deamidated (NQ)
835	534.3329	1066.6513	1066.6498	1.41	1	(34)	0.00042	1	U	R.NINLKIPAGK.T
836	534.3331	1066.6516	1066.6498	1.64	1	41	8.8e-05	1	U	R.NINLKIPAGK.T
843	536.8127	1071.6109	1071.6117	-0.71	0	35	0.00075	1	U	R.LMPTIAPFK.A
844	536.8129	1071.6113	1071.6117	-0.37	0	(23)	0.012	1	U	R.LMPTIAPFK.A
1081	577.2845	1152.5545	1152.5564	-1.60	0	(37)	0.00057	1	U	K.DLSTWQTR.R
1083	577.2861	1152.5576	1152.5564	1.05	0	(28)	0.0043	1	U	K.DLSTWQTR.R
1084	577.2861	1152.5577	1152.5564	1.16	0	(49)	4e-05	1	U	K.DLSTWQTR.R
1085	577.2864	1152.5582	1152.5564	1.58	0	51	2.5e-05	1	U	K.DLSTWQTR.R
1135	389.5631	1165.6674	1165.6680	-0.48	1	41	8.1e-05	1	U	K.NRTSLVIAHR.L
1136	389.5632	1165.6679	1165.6680	-0.09	1	(39)	0.00012	1	U	K.NRTSLVIAHR.L
1200	397.8659	1190.5758	1190.5792	-2.88	0	(32)	0.0015	1	U	R.GTHNDLLEHR.G
1202	397.8669	1190.5787	1190.5792	-0.42	0	(32)	0.0013	1	U	R.GTHNDLLEHR.G
1203	397.8669	1190.5789	1190.5792	-0.26	0	(34)	0.001	1	U	R.GTHNDLLEHR.G
1205	397.8673	1190.5801	1190.5792	0.74	0	(25)	0.0071	1	U	R.GTHNDLLEHR.G
1206	397.8674	1190.5804	1190.5792	0.97	0	(25)	0.0068	1	U	R.GTHNDLLEHR.G
1207	397.8674	1190.5805	1190.5792	1.04	0	(26)	0.0054	1	U	R.GTHNDLLEHR.G
1208	596.2975	1190.5805	1190.5792	1.11	0	(45)	6.6e-05	1	U	R.GTHNDLLEHR.G
1209	596.2976	1190.5807	1190.5792	1.21	0	54	8.5e-06	1	U	R.GTHNDLLEHR.G
1211	596.7883	1191.5620	1191.5632	-1.05	0	(35)	0.00066	1	U	R.GTHNDLLEHR.G + Deamidated (NQ)
1212	598.1956	1191.5651	1191.5632	1.58	0	(38)	0.00038	1	U	R.GTHNDLLEHR.G + Deamidated (NQ)
1213	596.7902	1191.5658	1191.5632	2.13	0	(31)	0.0016	1	U	R.GTHNDLLEHR.G + Deamidated (NQ)
1214	598.1964	1191.5674	1191.5632	3.50	0	(35)	0.00077	1	U	R.GTHNDLLEHR.G + Deamidated (NQ)
1222	600.3315	1198.6485	1198.6557	-5.99	0	(43)	0.0001	1	U	R.AIQAALDELQK.N
1223	600.3341	1198.6537	1198.6557	-1.72	0	(61)	1.5e-06	1	U	R.AIQAALDELQK.N
1224	600.3345	1198.6545	1198.6557	-1.00	0	(24)	0.0079	1	U	R.AIQAALDELQK.N
1225	600.3345	1198.6545	1198.6557	-1.00	0	(46)	4.8e-05	1	U	R.AIQAALDELQK.N
1226	600.3346	1198.6546	1198.6557	-0.90	0	(34)	0.00082	1	U	R.AIQAALDELQK.N
1227	600.3346	1198.6546	1198.6557	-0.90	0	(59)	2.4e-06	1	U	R.AIQAALDELQK.N
1228	600.5589	1198.6549	1198.6557	-0.71	0	(39)	0.00024	1	U	R.AIQAALDELQK.N
1229	600.3349	1198.6552	1198.6557	-0.39	0	(70)	1.8e-07	1	U	R.AIQAALDELQK.N
1230	600.3350	1198.6554	1198.6557	-0.29	0	(71)	1.7e-07	1	U	R.AIQAALDELQK.N
1231	400.5591	1198.6556	1198.6557	-0.10	0	73	1e-07	1	U	R.AIQAALDELQK.N
1232	400.5591	1198.6556	1198.6557	-0.10	0	(38)	0.00032	1	U	R.AIQAALDELQK.N
1233	600.3351	1198.6556	1198.6557	-0.09	0	(40)	0.00021	1	U	R.AIQAALDELQK.N
1234	600.3354	1198.6562	1198.6557	0.42	0	(34)	0.00083	1	U	R.AIQAALDELQK.N
1235	400.5594	1198.6563	1198.6557	0.51	0	(58)	2.9e-06	1	U	R.AIQAALDELQK.N
1236	600.3354	1198.6563	1198.6557	0.53	0	(43)	9.8e-05	1	U	R.AIQAALDELQK.N
1237	600.3354	1198.6563	1198.6557	0.53	0	(49)	2.3e-05	1	U	R.AIQAALDELQK.N
1238	600.3355	1198.6565	1198.6557	0.63	0	(72)	1.4e-07	1	U	R.AIQAALDELQK.N
1239	600.3356	1198.6567	1198.6557	0.83	0	(51)	1.7e-05	1	U	R.AIQAALDELQK.N
1240	600.3358	1198.6570	1198.6557	1.03	0	(46)	5.1e-05	1	U	R.AIQAALDELQK.N
1241	600.3359	1198.6573	1198.6557	1.34	0	(72)	1.2e-07	1	U	R.AIQAALDELQK.N
1242	600.3362	1198.6579	1198.6557	1.85	0	(52)	1.2e-05	1	U	R.AIQAALDELQK.N
1243	600.3367	1198.6589	1198.6557	2.66	0	(48)	3.1e-05	1	U	R.AIQAALDELQK.N
1245	600.3369	1198.6593	1198.6557	2.97	0	(52)	1.2e-05	1	U	R.AIQAALDELQK.N
1246	600.3370	1198.6595	1198.6557	3.17	0	(46)	4.6e-05	1	U	R.AIQAALDELQK.N
1247	600.3370	1198.6595	1198.6557	3.17	0	(56)	4.2e-06	1	U	R.AIQAALDELQK.N
1248	600.3371	1198.6596	1198.6557	3.28	0	(46)	4.8e-05	1	U	R.AIQAALDELQK.N
1250	600.3376	1198.6607	1198.6557	4.19	0	(27)	0.0032	1	U	R.AIQAALDELQK.N
1251	600.3385	1198.6625	1198.6557	5.62	0	(27)	0.0038	1	U	R.AIQAALDELQK.N
1252	600.8311	1199.6476	1199.6397	6.53	0	(61)	2e-06	1	U	R.AIQAALDELQK.N + Deamidated (NQ)
1253	600.8311	1199.6477	1199.6397	6.63	0	(55)	7.3e-06	1	U	R.AIQAALDELQK.N + Deamidated (NQ)
1263	602.2745	1202.5345	1202.5464	-9.85	0	(29)	0.0013	1	U	R.MAYAMDFINK.M
1264	602.2771	1202.5396	1202.5464	-5.59	0	(43)	5.3e-05	1	U	R.MAYAMDFINK.M
1265	602.2773	1202.5401	1202.5464	-5.18	0	(46)	2.6e-05	1	U	R.MAYAMDFINK.M
1266	602.2777	1202.5409	1202.5464	-4.58	0	(42)	6.7e-05	1	U	R.MAYAMDFINK.M
1267	602.2784	1202.5422	1202.5464	-3.46	0	(25)	0.0032	1	U	R.MAYAMDFINK.M
1268	602.2784	1202.5422	1202.5464	-3.46	0	(31)	0.00098	1	U	R.MAYAMDFINK.M
1269	602.2789	1202.5432	1202.5464	-2.65	0	(31)	0.00081	1	U	R.MAYAMDFINK.M
1270	602.2789	1202.5432	1202.5464	-2.65						

1275	602.2808	1202.5470	1202.5464	0.50	0	(27)	0.0022	1	U	R.MAYAMDFINK.M
1276	602.2809	1202.5472	1202.5464	0.70	0	(39)	0.00013	1	U	R.MAYAMDFINK.M
1277	401.8565	1202.5477	1202.5464	1.10	0	(34)	0.00046	1	U	R.MAYAMDFINK.M
1278	602.2812	1202.5479	1202.5464	1.31	0	(51)	1e-05	1	U	R.MAYAMDFINK.M
1279	602.2814	1202.5482	1202.5464	1.51	0	(39)	0.00016	1	U	R.MAYAMDFINK.M
1280	602.2814	1202.5483	1202.5464	1.62	0	(26)	0.0028	1	U	R.MAYAMDFINK.M
1281	602.2815	1202.5484	1202.5464	1.72	0	(45)	4.2e-05	1	U	R.MAYAMDFINK.M
1282	602.2816	1202.5486	1202.5464	1.82	0	(48)	1.9e-05	1	U	R.MAYAMDFINK.M
1284	602.2817	1202.5488	1202.5464	2.02	0	(40)	0.00013	1	U	R.MAYAMDFINK.M
1285	602.2817	1202.5489	1202.5464	2.12	0	(42)	7.5e-05	1	U	R.MAYAMDFINK.M
1286	602.2819	1202.5492	1202.5464	2.33	0	(49)	1.7e-05	1	U	R.MAYAMDFINK.M
1287	602.2827	1202.5508	1202.5464	3.65	0	(29)	0.0017	1	U	R.MAYAMDFINK.M
1288	602.2827	1202.5509	1202.5464	3.75	0	(33)	0.00066	1	U	R.MAYAMDFINK.M
1289	602.2828	1202.5511	1202.5464	3.95	0	(27)	0.0025	1	U	R.MAYAMDFINK.M
1290	602.2831	1202.5517	1202.5464	4.46	0	(27)	0.0024	1	U	R.MAYAMDFINK.M
1297	602.7812	1203.5478	1203.5304	14.5	0	(30)	0.0017	1	U	R.MAYAMDFINK.M + Deamidated (NQ)
1298	602.7822	1203.5498	1203.5304	16.1	0	(22)	0.01	1	U	R.MAYAMDFINK.M + Deamidated (NQ)
1384	610.2716	1218.5287	1218.5413	-10.36	0	(27)	0.0019	1	U	R.MAYAMDFINK.M + Oxidation (M)
1385	610.2753	1218.5360	1218.5413	-4.35	0	(26)	0.0026	1	U	R.MAYAMDFINK.M + Oxidation (M)
1387	610.2763	1218.5381	1218.5413	-2.65	0	(60)	1.1e-06	1	U	R.MAYAMDFINK.M + Oxidation (M)
1388	610.2766	1218.5385	1218.5413	-2.25	0	(29)	0.0014	1	U	R.MAYAMDFINK.M + Oxidation (M)
1389	610.2769	1218.5393	1218.5413	-1.65	0	(62)	6.8e-07	1	U	R.MAYAMDFINK.M + Oxidation (M)
1390	407.1872	1218.5398	1218.5413	-1.18	0	(31)	0.00089	1	U	R.MAYAMDFINK.M + Oxidation (M)
1392	610.2773	1218.5401	1218.5413	-0.95	0	(46)	2.4e-05	1	U	R.MAYAMDFINK.M + Oxidation (M)
1393	610.2774	1218.5403	1218.5413	-0.85	0	(46)	2.4e-05	1	U	R.MAYAMDFINK.M + Oxidation (M)
1394	610.2774	1218.5403	1218.5413	-0.85	0	(57)	2.2e-06	1	U	R.MAYAMDFINK.M + Oxidation (M)
1397	610.2781	1218.5416	1218.5413	0.25	0	(57)	2.3e-06	1	U	R.MAYAMDFINK.M + Oxidation (M)
1398	610.2783	1218.5420	1218.5413	0.55	0	(51)	7.3e-06	1	U	R.MAYAMDFINK.M + Oxidation (M)
1399	610.2783	1218.5421	1218.5413	0.65	0	(51)	7.4e-06	1	U	R.MAYAMDFINK.M + Oxidation (M)
1400	610.2783	1218.5421	1218.5413	0.65	0	(56)	2.4e-06	1	U	R.MAYAMDFINK.M + Oxidation (M)
1401	610.2784	1218.5422	1218.5413	0.76	0	(23)	0.0047	1	U	R.MAYAMDFINK.M + Oxidation (M)
1402	610.2784	1218.5422	1218.5413	0.76	0	(56)	2.3e-06	1	U	R.MAYAMDFINK.M + Oxidation (M)
1403	610.2784	1218.5423	1218.5413	0.86	0	(63)	5.6e-07	1	U	R.MAYAMDFINK.M + Oxidation (M)
1404	610.2786	1218.5426	1218.5413	1.06	0	(68)	2.2e-07	1	U	R.MAYAMDFINK.M + Oxidation (M)
1409	407.1898	1218.5474	1218.5413	5.05	0	(26)	0.0031	1	U	R.MAYAMDFINK.M + Oxidation (M)
1478	410.2449	1227.7129	1227.7128	0.07	1	(26)	0.0062	1	U	R.RLNPTIAPFK.A
1481	614.8644	1227.7143	1227.7128	1.25	1	40	0.00019	1	U	R.RLNPTIAPFK.A
1482	614.8645	1227.7145	1227.7128	1.35	1	(34)	0.00072	1	U	R.RLNPTIAPFK.A
1500	618.2698	1234.5250	1234.5362	-9.08	0	(41)	8.6e-05	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1501	618.2711	1234.5276	1234.5362	-7.00	0	(25)	0.0029	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1503	618.2740	1234.5335	1234.5362	-2.16	0	(46)	2.8e-05	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1504	618.2749	1234.5353	1234.5362	-0.78	0	(46)	2.3e-05	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1505	618.2753	1234.5361	1234.5362	-0.08	0	(60)	1.1e-06	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1506	618.2754	1234.5362	1234.5362	0.02	0	(50)	1.1e-05	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1507	618.2755	1234.5365	1234.5362	0.21	0	(51)	8.1e-06	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1508	618.2756	1234.5367	1234.5362	0.41	0	(50)	1e-05	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1509	618.2757	1234.5368	1234.5362	0.51	0	(56)	2.2e-06	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1510	618.2758	1234.5371	1234.5362	0.71	0	(28)	0.0015	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1511	618.2759	1234.5372	1234.5362	0.81	0	(55)	3e-06	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1512	618.2759	1234.5373	1234.5362	0.91	0	(40)	0.00011	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1513	618.2759	1234.5373	1234.5362	0.91	0	(53)	5.5e-06	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1514	618.2760	1234.5375	1234.5362	1.01	0	(41)	7.7e-05	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1515	618.2761	1234.5376	1234.5362	1.10	0	(57)	2.1e-06	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1516	618.2764	1234.5382	1234.5362	1.60	0	(58)	1.5e-06	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1517	618.2783	1234.5420	1234.5362	4.66	0	(40)	0.00012	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1518	618.2792	1234.5439	1234.5362	6.25	0	(37)	0.00021	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1519	618.2834	1234.5522	1234.5362	13.0	0	(43)	7.1e-05	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1520	618.2842	1234.5539	1234.5362	14.4	0	(37)	0.00031	1	U	R.MAYAMDFINK.M + 2 Oxidation (M)
1745	639.3283	1276.6421	1276.6524	-8.09	0	(29)	0.0053	1	U	K.SLTWVNAQFOR.G
1746	639.3307	1276.6469	1276.6524	-4.26	0	(29)	0.0056	1	U	K.SLTWVNAQFOR.G
1747	639.3315	1276.6484	1276.6524	-3.12	0	(43)	0.00019	1	U	K.SLTWVNAQFOR.G
1748	639.3315	1276.6485	1276.6524	-3.02	0	(23)	0.022	1	U	K.SLTWVNAQFOR.G
1749	426.5573	1276.6501	1276.6524	-1.79	0	(61)	3.4e-06	1	U	K.SLTWVNAQFOR.G
1750	426.5573	1276.6502	1276.6524	-1.71	0	(59)	4.6e-06	1	U	K.SLTWVNAQFOR.G
1751	639.3325	1276.6505	1276.6524	-1.49	0	(34)	0.0016	1	U	K.SLTWVNAQFOR.G
1752	639.3330	1276.6515	1276.6524	-0.73	0	(31)	0.0034	1	U	K.SLTWVNAQFOR.G
1753	639.3333	1276.6521	1276.6524	-0.25	0	(57)	8.7e-06	1	U	K.SLTWVNAQFOR.G
1754	639.3336	1276.6527	1276.6524	0.23	0	65	1.3e-06	1	U	K.SLTWVNAQFOR.G
1755	639.3337	1276.6528	1276.6524	0.33	0	(46)	0.0001	1	U	K.SLTWVNAQFOR.G
1756	639.3340	1276.6535	1276.6524	0.90	0	(26)	0.011	1	U	K.SLTWVNAQFOR.G
1757	639.3341	1276.6537	1276.6524	0.99	0	(57)	8.4e-06	1	U	K.SLTWVNAQFOR.G
1758	639.3342	1276.6538	1276.6524	1.09	0	(52)	2.5e-05	1	U	K.SLTWVNAQFOR.G
1759	639.3342	1276.6539	1276.6524	1.19	0	(55)	1.3e-05	1	U	K.SLTWVNAQFOR.G
1760	639.3347	1276.6548	1276.6524	1.86	0	(52)	2.4e-05	1	U	K.SLTWVNAQFOR.G
1761	639.3347	1276.6549	1276.6524	1.95	0	(22)	0.022	1	U	K.SLTWVNAQFOR.G
1762	639.3362	1276.6578	1276.6524	4.25	0	(28)	0.007	1	U	K.SLTWVNAQFOR.G
1764	639.3393	1276.6640	1276.6524	9.12	0	(39)	0.00049	1	U	K.SLTWVNAQFOR.G
1766	639.8238	1277.6330	1277.6364	-2.63	0	(43)	0.00018	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1767	426.8855	1277.6347	1277.6364	-1.36	0	(40)	0.00032	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1768	426.8860	1277.6360	1277.6364	-0.28	0	(56)	9.1e-06	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1769	639.8255	1277.6364	1277.6364	0.04	0	(63)	1.7e-06	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1770	426.8861	1277.6366	1277.6364	0.15	0	(52)	2e-05	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1771	426.8865	1277.6376	1277.6364	0.94	0	(36)	0.00083	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1772	639.8261	1277.6377	1277.6364	1.00	0	(49)	4.8e-05	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1773	639.8262	1277.6378	1277.6364	1.09	0	(58)	5.3e-06	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1774	639.8284	1277.6422	1277.6364	4.53	0	(56)	9.1e-06	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1775	639.8290	1277.6434	1277.6364	5.49	0	(51)	2.6e-05	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1776	639.8305	1277.6465	1277.6364	7.87	0	(43)	0.00016	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
1777	639.8311	1277.6476	1277.6364	8.73	0	(45)	0.00011	1	U	K.SLTWVNAQFOR.G + Deamidated (NQ)
2065	459.9272	1376.7596	1376.7623	-1.96	1	41	0.00021	1	U	R.SGSGKSTIASLITR.F
2066	459.9282	1376.7627	1376.7623	0.30	1	(29)	0.0039	1	U	R.SGSGKSTIASLITR.F
2067	459.9283	1376.7630	1376.7623	0.50	1	(38)	0.00045	1	U	R.SGSGKSTIASLITR.F
2148	483.5920	1447.7543	1447.7559	-1.08	0	(70)	3.8e-07	1	U	K.EVLIFGGQEVETK.R
2150	724.8852	1447.7558	1447.7559	-0.02	0	(48)	5.7e-05	1	U	K.EVLIFGGQEVETK.R
2151	483.5926	1447.7559	1447.7559	-0.00	0	(53)	1.9e-05	1	U	K.EVLIFGGQEVETK.R
2152	724.8853	1447.7561	1447.7559	0.15	0	(71)	2.8e-07	1	U	K.EVLIFGGQEVETK.R
2153	724.8854	1447.7562	1447.7559	0.24	0	(52)	2.5e-05	1	U	K.EVLIFGGQEVETK.R
2154	724.8854	1447.7562	1447.7559	0.24	0	88	6.2e-09	1	U	K.EVLIFGGQEVETK.R
2155	724.8855	1447.7564	1447.7559	0.40	0	(85)	1.1e-08	1	U	K.EVLIFGGQEVETK.R
2156	724.8866	1447.7586	1447.7559	1.92	0	(69)	4.7e-07	1	U	K.EVLIFGGQEVETK.R
2157	724.8867	1447.7588	1447.7559	2.01	0	(84)	1.3e-08	1	U	K.EVLIFGGQEVETK.R
2158	724.8868	1447.7590	1447.7559	2.18	0	(62)	2.1e-06	1	U	K.EVLIFGGQEVETK.R
2159	724.8878	1447.7611	1447.7559	3.61	0	(63)	1.6e-06	1	U	K.EVLIFGGQEVETK.R
2161	724.8904	1447.7662	1447.7559	7.15	0	(68)	6.2e-07	1	U	K.EVLIFGGQEVETK.R
2202	735.4067	1468.7988	1468.7997	-0.64	1	(60)	1.6e-06	1	U	R.AIQALDELQKNR.T
2204	735.4070	1468.7995	1468.7997	-0.14	1	74	6.6e-08	1	U	R.AIQALDELQKNR.T
2205	490.6074	1468.8004	1468.7997							

2346	802.9355	1603.8564	1603.8570	-0.34	1	(71)	2.7e-07	1	U	K.EVLIFGGQEVETKR.F
2347	802.9359	1603.8573	1603.8570	0.19	1	77	7.3e-08	1	U	K.EVLIFGGQEVETKR.F
2349	401.9721	1603.8594	1603.8570	1.55	1	(27)	0.0063	1	U	K.EVLIFGGQEVETKR.F
2350	401.9724	1603.8603	1603.8570	2.08	1	(25)	0.01	1	U	K.EVLIFGGQEVETKR.F
2396	821.4340	1640.8535	1640.8621	-5.26	0	(55)	1e-05	1	U	K.ADEIVVVEDGVIVER.G
2397	821.4349	1640.8552	1640.8621	-4.22	0	(76)	8.4e-08	1	U	K.ADEIVVVEDGVIVER.G
2398	821.4352	1640.8559	1640.8621	-3.77	0	(68)	4.6e-07	1	U	K.ADEIVVVEDGVIVER.G
2399	821.4368	1640.8591	1640.8621	-1.84	0	(59)	4e-06	1	U	K.ADEIVVVEDGVIVER.G
2400	821.4374	1640.8602	1640.8621	-1.17	0	(80)	3.1e-08	1	U	K.ADEIVVVEDGVIVER.G
2401	821.4374	1640.8602	1640.8621	-1.17	0	(79)	4.4e-08	1	U	K.ADEIVVVEDGVIVER.G
2402	547.9608	1640.8606	1640.8621	-0.92	0	(83)	1.5e-08	1	U	K.ADEIVVVEDGVIVER.G
2403	547.9611	1640.8614	1640.8621	-0.47	0	(82)	1.9e-08	1	U	K.ADEIVVVEDGVIVER.G
2404	821.4381	1640.8617	1640.8621	-0.28	0	(85)	1e-08	1	U	K.ADEIVVVEDGVIVER.G
2405	547.9612	1640.8619	1640.8621	-0.13	0	(46)	8.2e-05	1	U	K.ADEIVVVEDGVIVER.G
2406	821.4383	1640.8620	1640.8621	-0.05	0	(91)	2.4e-09	1	U	K.ADEIVVVEDGVIVER.G
2407	547.9613	1640.8621	1640.8621	-0.02	0	(82)	1.8e-08	1	U	K.ADEIVVVEDGVIVER.G
2408	547.9613	1640.8621	1640.8621	-0.02	0	(78)	4.3e-08	1	U	K.ADEIVVVEDGVIVER.G
2409	821.4384	1640.8622	1640.8621	0.02	0	(69)	4.1e-07	1	U	K.ADEIVVVEDGVIVER.G
2410	821.4385	1640.8625	1640.8621	0.24	0	(78)	5.3e-08	1	U	K.ADEIVVVEDGVIVER.G
2411	821.4385	1640.8625	1640.8621	0.24	0	(76)	7e-08	1	U	K.ADEIVVVEDGVIVER.G
2412	821.4385	1640.8625	1640.8621	0.24	0	(91)	2.5e-09	1	U	K.ADEIVVVEDGVIVER.G
2413	547.9615	1640.8626	1640.8621	0.31	0	(46)	7.5e-05	1	U	K.ADEIVVVEDGVIVER.G
2414	547.9615	1640.8626	1640.8621	0.31	0	99	3.8e-10	1	U	K.ADEIVVVEDGVIVER.G
2415	547.9615	1640.8626	1640.8621	0.31	0	(71)	2.6e-07	1	U	K.ADEIVVVEDGVIVER.G
2416	547.9615	1640.8628	1640.8621	0.42	0	(40)	0.00032	1	U	K.ADEIVVVEDGVIVER.G
2417	547.9616	1640.8630	1640.8621	0.53	0	(25)	0.01	1	U	K.ADEIVVVEDGVIVER.G
2418	547.9616	1640.8630	1640.8621	0.53	0	(55)	1e-05	1	U	K.ADEIVVVEDGVIVER.G
2419	821.4388	1640.8630	1640.8621	0.54	0	(90)	3.1e-09	1	U	K.ADEIVVVEDGVIVER.G
2420	821.4388	1640.8630	1640.8621	0.54	0	(87)	5.5e-09	1	U	K.ADEIVVVEDGVIVER.G
2421	821.4388	1640.8631	1640.8621	0.62	0	(91)	2.7e-09	1	U	K.ADEIVVVEDGVIVER.G
2422	547.9617	1640.8634	1640.8621	0.76	0	(45)	9.1e-05	1	U	K.ADEIVVVEDGVIVER.G
2423	547.9617	1640.8634	1640.8621	0.76	0	(54)	1.2e-05	1	U	K.ADEIVVVEDGVIVER.G
2424	821.4390	1640.8634	1640.8621	0.77	0	(52)	2.2e-05	1	U	K.ADEIVVVEDGVIVER.G
2425	821.4390	1640.8635	1640.8621	0.84	0	(94)	1.3e-09	1	U	K.ADEIVVVEDGVIVER.G
2426	547.9618	1640.8635	1640.8621	0.87	0	(75)	1e-07	1	U	K.ADEIVVVEDGVIVER.G
2427	547.9622	1640.8646	1640.8621	1.54	0	(29)	0.0035	1	U	K.ADEIVVVEDGVIVER.G
2428	821.4400	1640.8655	1640.8621	2.03	0	(64)	1.3e-06	1	U	K.ADEIVVVEDGVIVER.G
2429	821.4405	1640.8664	1640.8621	2.63	0	(76)	6.6e-08	1	U	K.ADEIVVVEDGVIVER.G
2430	821.4407	1640.8668	1640.8621	2.85	0	(60)	2.8e-06	1	U	K.ADEIVVVEDGVIVER.G
2431	821.4412	1640.8678	1640.8621	3.44	0	(89)	3.6e-09	1	U	K.ADEIVVVEDGVIVER.G
2432	821.4413	1640.8681	1640.8621	3.67	0	(64)	1.3e-06	1	U	K.ADEIVVVEDGVIVER.G
2433	821.4416	1640.8687	1640.8621	4.04	0	(66)	7.5e-07	1	U	K.ADEIVVVEDGVIVER.G
2434	821.4416	1640.8687	1640.8621	4.04	0	(62)	1.8e-06	1	U	K.ADEIVVVEDGVIVER.G
2435	821.4435	1640.8724	1640.8621	6.27	0	(51)	2.4e-05	1	U	K.ADEIVVVEDGVIVER.G
2436	547.9657	1640.8753	1640.8621	8.01	0	(38)	0.00043	1	U	K.ADEIVVVEDGVIVER.G
2447	549.9341	1646.7806	1646.7801	0.29	1	(21)	0.017	1	U	M.HNKKDLSTWQTF.R
2448	549.9346	1646.7819	1646.7801	1.07	1	41	0.00018	1	U	M.HNKKDLSTWQTF.R
2507	853.4552	1704.8958	1704.8948	0.64	1	(21)	0.032	1	U	R.NVTFTYTPGRDVPALR.N
2508	569.3061	1704.8964	1704.8948	0.99	1	(20)	0.04	1	U	R.NVTFTYTPGRDVPALR.N
2509	569.3064	1704.8974	1704.8948	1.53	1	23	0.021	1	U	R.NVTFTYTPGRDVPALR.N
2510	570.6077	1708.8012	1708.8016	-0.25	1	(38)	0.0004	1	U	R.TEQYSRQIEEAAAR.M
2511	570.6084	1708.8034	1708.8016	1.04	1	42	0.00015	1	U	R.TEQYSRQIEEAAAR.M
2512	570.9356	1709.7850	1709.7856	-0.35	1	(36)	0.00058	1	U	R.TEQYSRQIEEAAAR.M + Deamidated (NQ)
2513	570.9361	1709.7865	1709.7856	0.50	1	(41)	0.00015	1	U	R.TEQYSRQIEEAAAR.M + Deamidated (NQ)
2520	872.4057	1742.7968	1742.7983	-0.83	0	(64)	5.9e-07	1	U	R.LFGHMGHMPVSFFDK.Q
2521	581.9398	1742.7974	1742.7983	-0.49	0	(30)	0.0016	1	U	R.LFGHMGHMPVSFFDK.Q
2522	581.9402	1742.7987	1742.7983	0.25	0	(33)	0.00084	1	U	R.LFGHMGHMPVSFFDK.Q
2525	872.4083	1742.8021	1742.7983	2.18	0	71	1.2e-07	1	U	R.LFGHMGHMPVSFFDK.Q
2534	587.2707	1758.7902	1758.7932	-1.69	0	(31)	0.0015	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2535	587.2710	1758.7912	1758.7932	-1.17	0	(31)	0.0014	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2536	587.2712	1758.7917	1758.7932	-0.86	0	(43)	9.7e-05	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2537	587.2714	1758.7923	1758.7932	-0.54	0	(30)	0.0018	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2538	587.2714	1758.7923	1758.7932	-0.54	0	(27)	0.0042	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2539	880.4039	1758.7932	1758.7932	-0.01	0	(54)	6.9e-06	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2540	587.2717	1758.7934	1758.7932	0.08	0	(22)	0.012	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2541	587.2718	1758.7935	1758.7932	0.19	0	(28)	0.0029	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2542	587.2719	1758.7939	1758.7932	0.40	0	(21)	0.014	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2543	587.2724	1758.7954	1758.7932	1.23	0	(37)	0.00039	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2544	587.2725	1758.7957	1758.7932	1.44	0	(21)	0.015	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2545	880.4061	1758.7976	1758.7932	2.48	0	(45)	5.7e-05	1	U	R.LFGHMGHMPVSFFDK.Q + Oxidation (M)
2612	590.9838	1769.9297	1769.9312	-0.87	1	(58)	4.8e-06	1	U	K.GHKEVLIFGGQEVETK.R
2613	590.9838	1769.9297	1769.9312	-0.87	1	(54)	1.3e-05	1	U	K.GHKEVLIFGGQEVETK.R
2614	885.9729	1769.9312	1769.9312	0.03	1	(81)	2.5e-08	1	U	K.GHKEVLIFGGQEVETK.R
2615	590.9844	1769.9313	1769.9312	0.06	1	(47)	5.5e-05	1	U	K.GHKEVLIFGGQEVETK.R
2616	443.4902	1769.9317	1769.9312	0.29	1	(32)	0.0018	1	U	K.GHKEVLIFGGQEVETK.R
2617	590.9847	1769.9322	1769.9312	0.57	1	(47)	5.8e-05	1	U	K.GHKEVLIFGGQEVETK.R
2618	443.4904	1769.9324	1769.9312	0.70	1	(49)	3.7e-05	1	U	K.GHKEVLIFGGQEVETK.R
2619	885.9735	1769.9325	1769.9312	0.72	1	93	1.5e-09	1	U	K.GHKEVLIFGGQEVETK.R
2620	592.6023	1774.7851	1774.7881	-1.73	0	(26)	0.0031	1	U	R.LFGHMGHMPVSFFDK.Q + 2 Oxidation (M)
2621	888.4005	1774.7864	1774.7881	-1.00	0	(58)	2.4e-06	1	U	R.LFGHMGHMPVSFFDK.Q + 2 Oxidation (M)
2622	592.6030	1774.7871	1774.7881	-0.60	0	(40)	0.00015	1	U	R.LFGHMGHMPVSFFDK.Q + 2 Oxidation (M)
2624	592.6040	1774.7902	1774.7881	1.16	0	(31)	0.0012	1	U	R.LFGHMGHMPVSFFDK.Q + 2 Oxidation (M)
2627	888.4044	1774.7943	1774.7881	3.47	0	(39)	0.00024	1	U	R.LFGHMGHMPVSFFDK.Q + 2 Oxidation (M)
2630	593.6138	1777.8197	1777.8206	-0.53	1	(23)	0.011	1	U	--HNKKDLSTWQTF.R
2631	593.6146	1777.8220	1777.8206	0.81	1	37	0.00049	1	U	--HNKKDLSTWQTF.R
2648	597.9344	1790.7815	1790.7831	-0.86	0	(25)	0.003	1	U	R.LFGHMGHMPVSFFDK.Q + 3 Oxidation (M)
2650	597.9352	1790.7837	1790.7831	0.37	0	(28)	0.0016	1	U	R.LFGHMGHMPVSFFDK.Q + 3 Oxidation (M)
2752	947.4555	1892.8965	1892.8979	-0.74	0	(80)	3.6e-08	1	U	R.GITSVSSYSCISMVSGK.V
2753	631.9736	1892.8989	1892.8979	0.54	0	(67)	7.9e-07	1	U	R.GITSVSSYSCISMVSGK.V
2754	631.9739	1892.9000	1892.8979	1.12	0	(62)	2.1e-06	1	U	R.GITSVSSYSCISMVSGK.V
2755	631.9745	1892.9018	1892.8979	2.09	0	(37)	0.00064	1	U	R.GITSVSSYSCISMVSGK.V
2756	947.4595	1892.9045	1892.8979	3.52	0	92	2.2e-09	1	U	R.GITSVSSYSCISMVSGK.V
2762	475.7322	1898.8996	1898.8994	0.11	1	(24)	0.012	1	U	R.RLFGHMGHMPVSFFDK.Q
2763	475.7327	1898.9018	1898.8994	1.27	1	29	0.0041	1	U	R.RLFGHMGHMPVSFFDK.Q
2786	482.5137	1926.0257	1926.0323	-3.43	2	(29)	0.003	1	U	K.GHKEVLIFGGQEVETKR.F
2787	482.5150	1926.0308	1926.0323	-0.76	2	(20)	0.024	1	U	K.GHKEVLIFGGQEVETKR.F
2788	482.5151	1926.0313	1926.0323	-0.51	2	(40)	0.00023	1	U	K.GHKEVLIFGGQEVETKR.F
2789	386.2136	1926.0314	1926.0323	-0.45	2	(28)	0.004	1	U	K.GHKEVLIFGGQEVETKR.F
2790	643.0178	1926.0315	1926.0323	-0.44	2	(60)	2.5e-06	1	U	K.GHKEVLIFGGQEVETKR.F
2791	482.5152	1926.0316	1926.0323	-0.38	2	(34)	0.00093	1	U	K.GHKEVLIFGGQEVETKR.F
2792	482.5154	1926.0323	1926.0323	-0.00	2	(40)	0.00024	1	U	K.GHKEVLIFGGQEVETKR.F
2793	482.5154	1926.0324	1926.0323	0.06	2	(45)	7.6e-05	1	U	K.GHKEVLIFGGQEVETKR.F
2794	386.2138	1926.0328	1926.0323	0.26	2	(29)	0.0033	1	U	K.GHKEVLIFGGQEVETKR.F
2795	482.5156	1926.0334	1926.0323	0.57	2	(35)	0.00074	1	U	K.GHKEVLIFGGQEVETKR.F
2796	643.0190	1926.0351	1926.0323	1.46	2	72	1.5e-07	1	U	K.GHKEVLIFGGQEVETKR.F
2797	482.5172	1926.0396	1926.0323	3.80	2	(28)	0.0034	1	U	K.GHKEVLIFGGQEVETKR.F
2800	644.3140	1929.9202	19							

2896	671.3094	2010.9063	2010.9173	-5.44	0	(43)	0.0001	1	U	K.NMQNTMGQVTTSAEQMLK.G
2897	671.3097	2010.9072	2010.9173	-4.98	0	(31)	0.0018	1	U	K.NMQNTMGQVTTSAEQMLK.G
2898	1006.4615	2010.9084	2010.9173	-4.40	0	(83)	1.1e-08	1	U	K.NMQNTMGQVTTSAEQMLK.G
2899	671.3102	2010.9087	2010.9173	-4.25	0	(25)	0.0082	1	U	K.NMQNTMGQVTTSAEQMLK.G
2900	671.3107	2010.9102	2010.9173	-3.52	0	(25)	0.0071	1	U	K.NMQNTMGQVTTSAEQMLK.G
2901	671.3111	2010.9115	2010.9173	-2.89	0	(31)	0.0019	1	U	K.NMQNTMGQVTTSAEQMLK.G
2902	671.3113	2010.9122	2010.9173	-2.52	0	(37)	0.00049	1	U	K.NMQNTMGQVTTSAEQMLK.G
2903	671.3113	2010.9122	2010.9173	-2.52	0	(32)	0.0017	1	U	K.NMQNTMGQVTTSAEQMLK.G
2904	671.3113	2010.9122	2010.9173	-2.52	0	(33)	0.0013	1	U	K.NMQNTMGQVTTSAEQMLK.G
2905	671.3120	2010.9140	2010.9173	-1.61	0	(38)	0.00042	1	U	K.NMQNTMGQVTTSAEQMLK.G
2906	671.3127	2010.9162	2010.9173	-0.52	0	(21)	0.018	1	U	K.NMQNTMGQVTTSAEQMLK.G
2907	671.3127	2010.9162	2010.9173	-0.52	0	(41)	0.00019	1	U	K.NMQNTMGQVTTSAEQMLK.G
2908	671.3130	2010.9173	2010.9173	0.03	0	(66)	5.9e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G
2909	671.3130	2010.9173	2010.9173	0.03	0	(37)	0.00054	1	U	K.NMQNTMGQVTTSAEQMLK.G
2910	671.3132	2010.9177	2010.9173	0.21	0	(27)	0.0005	1	U	K.NMQNTMGQVTTSAEQMLK.G
2911	1006.4663	2010.9181	2010.9173	0.40	0	(96)	6e-10	1	U	K.NMQNTMGQVTTSAEQMLK.G
2912	671.3134	2010.9182	2010.9173	0.48	0	(89)	3e-09	1	U	K.NMQNTMGQVTTSAEQMLK.G
2913	671.3137	2010.9192	2010.9173	0.94	0	(29)	0.003	1	U	K.NMQNTMGQVTTSAEQMLK.G
2914	671.3140	2010.9201	2010.9173	1.39	0	(28)	0.0041	1	U	K.NMQNTMGQVTTSAEQMLK.G
2916	671.3149	2010.9230	2010.9173	2.85	0	(45)	7.7e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G
2918	671.3160	2010.9261	2010.9173	4.40	0	(21)	0.022	1	U	K.NMQNTMGQVTTSAEQMLK.G
2926	671.6371	2011.8896	2011.9013	-5.80	0	(21)	0.013	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2927	1006.9546	2011.8946	2011.9013	-3.30	0	(90)	1.7e-09	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2928	1006.9573	2011.9001	2011.9013	-0.57	0	(73)	1e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2929	1006.9577	2011.9009	2011.9013	-0.21	0	(78)	2.9e-08	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2930	671.6411	2011.9013	2011.9013	0.03	0	(60)	2e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2931	671.6413	2011.9021	2011.9013	0.39	0	(76)	5e-08	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2932	1006.9590	2011.9035	2011.9013	1.12	0	(84)	9.3e-09	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2933	671.6422	2011.9046	2011.9013	1.66	0	(71)	1.5e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2934	671.6423	2011.9050	2011.9013	1.85	0	(57)	4.2e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2935	1006.9605	2011.9065	2011.9013	2.58	0	(76)	5.3e-08	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2936	671.6428	2011.9066	2011.9013	2.67	0	(61)	1.7e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2937	1006.9609	2011.9073	2011.9013	3.01	0	(94)	9e-10	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2938	671.6438	2011.9096	2011.9013	4.12	0	(46)	5.7e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2939	671.6443	2011.9112	2011.9013	4.94	0	(71)	1.7e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2940	671.6458	2011.9156	2011.9013	7.13	0	(36)	0.00054	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ)
2951	1014.4560	2026.8974	2026.9122	-7.28	0	(43)	7e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2952	1014.4601	2026.9056	2026.9122	-3.24	0	(92)	1.1e-09	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2953	676.6429	2026.9070	2026.9122	-2.56	0	(60)	1.6e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2954	1014.4612	2026.9079	2026.9122	-2.10	0	(70)	1.7e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2955	1014.4612	2026.9079	2026.9122	-2.10	0	(67)	3.7e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2956	1014.4615	2026.9084	2026.9122	-1.86	0	119	2e-12	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2957	676.6434	2026.9085	2026.9122	-1.83	0	(72)	1.1e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2958	1014.4617	2026.9089	2026.9122	-1.62	0	(42)	0.00011	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2959	1014.4618	2026.9090	2026.9122	-1.56	0	(109)	2.4e-11	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2960	1014.4620	2026.9095	2026.9122	-1.32	0	(94)	7.2e-10	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2961	1014.4623	2026.9101	2026.9122	-1.01	0	(54)	7e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2962	676.6440	2026.9103	2026.9122	-0.93	0	(56)	4.6e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2963	1014.4625	2026.9105	2026.9122	-0.83	0	(42)	0.00011	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2964	1014.4626	2026.9106	2026.9122	-0.77	0	(80)	1.6e-08	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2965	676.6442	2026.9107	2026.9122	-0.75	0	(60)	1.6e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2966	676.6442	2026.9108	2026.9122	-0.66	0	(57)	3.8e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2967	676.6442	2026.9108	2026.9122	-0.66	0	(65)	5.6e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2968	1014.4627	2026.9109	2026.9122	-0.65	0	(67)	3.8e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2969	676.6446	2026.9119	2026.9122	-0.12	0	(73)	9.1e-08	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2970	676.6446	2026.9119	2026.9122	-0.12	0	(59)	2.4e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2971	1014.4633	2026.9121	2026.9122	-0.05	0	(102)	1.1e-10	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2972	676.6447	2026.9121	2026.9122	-0.03	0	(49)	2.4e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2973	676.6448	2026.9127	2026.9122	0.24	0	(52)	1.2e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2974	676.6450	2026.9132	2026.9122	0.52	0	(43)	8.2e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2975	1014.4641	2026.9137	2026.9122	0.73	0	(89)	2.5e-09	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2976	1014.4643	2026.9140	2026.9122	0.91	0	(48)	2.8e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2977	676.6453	2026.9141	2026.9122	0.97	0	(49)	2.4e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2978	676.6454	2026.9143	2026.9122	1.06	0	(59)	2.5e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2979	676.6455	2026.9147	2026.9122	1.24	0	(44)	8e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2980	676.6456	2026.9151	2026.9122	1.42	0	(53)	9.1e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2981	676.6457	2026.9152	2026.9122	1.51	0	(88)	2.6e-09	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2982	1014.4664	2026.9182	2026.9122	2.96	0	(47)	3.3e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Oxidation (M)
2984	676.9716	2027.8928	2027.8962	-1.65	0	(46)	3.1e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ); Oxidation (M)
2985	676.9717	2027.8932	2027.8962	-1.47	0	(56)	3.1e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ); Oxidation (M)
2986	676.9721	2027.8945	2027.8962	-0.84	0	(56)	3.3e-06	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ); Oxidation (M)
2987	1014.9562	2027.8978	2027.8962	0.79	0	(73)	6.5e-08	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ); Oxidation (M)
2988	676.9744	2027.9014	2027.8962	2.59	0	(61)	9.4e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ); Oxidation (M)
2989	1014.9595	2027.9045	2027.8962	4.10	0	(63)	6.8e-07	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ); Oxidation (M)
2990	676.9756	2027.9051	2027.8962	4.40	0	(50)	1.2e-05	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ); Oxidation (M)
2991	1014.9621	2027.9096	2027.8962	6.63	0	(85)	4.4e-09	1	U	K.NMQNTMGQVTTSAEQMLK.G + Deamidated (NQ); Oxidation (M)
2996	1019.4601	2036.9057	2036.9149	-4.52	0	(89)	3.3e-09	1	U	R.FYDIDEGEILMDGHDRLR.E
2997	1019.4625	2036.9104	2036.9149	-2.25	0	(89)	3.3e-09	1	U	R.FYDIDEGEILMDGHDRLR.E
2998	679.9777	2036.9112	2036.9149	-1.86	0	(38)	0.00038	1	U	R.FYDIDEGEILMDGHDRLR.E
2999	679.9777	2036.9113	2036.9149	-1.77	0	(42)	0.00014	1	U	R.FYDIDEGEILMDGHDRLR.E
3000	679.9780	2036.9123	2036.9149	-1.32	0	(40)	0.00025	1	U	R.FYDIDEGEILMDGHDRLR.E
3001	679.9781	2036.9126	2036.9149	-1.14	0	(24)	0.0095	1	U	R.FYDIDEGEILMDGHDRLR.E
3004	679.9786	2036.9139	2036.9149	-0.51	0	(43)	0.00012	1	U	R.FYDIDEGEILMDGHDRLR.E
3005	679.9788	2036.9145	2036.9149	-0.24	0	(63)	1.2e-06	1	U	R.FYDIDEGEILMDGHDRLR.E
3006	679.9789	2036.9148	2036.9149	-0.06	0	(52)	1.6e-05	1	U	R.FYDIDEGEILMDGHDRLR.E
3007	679.9796	2036.9168	2036.9149	0.92	0	(42)	0.00016	1	U	R.FYDIDEGEILMDGHDRLR.E
3008	679.9796	2036.9170	2036.9149	1.01	0	(40)	0.00028	1	U	R.FYDIDEGEILMDGHDRLR.E
3009	679.9797	2036.9172	2036.9149	1.10	0	(31)	0.0018	1	U	R.FYDIDEGEILMDGHDRLR.E
3010	679.9797	2036.9172	2036.9149	1.10	0	(49)	3.1e-05	1	U	R.FYDIDEGEILMDGHDRLR.E
3011	679.9799	2036.9177	2036.9149	1.37	0	(47)	5.3e-05	1	U	R.FYDIDEGEILMDGHDRLR.E
3012	679.9799	2036.9179	2036.9149	1.46	0	(49)	3.7e-05	1	U	R.FYDIDEGEILMDGHDRLR.E
3013	679.9799	2036.9179	2036.9149	1.46	0	(48)	3.7e-05	1	U	R.FYDIDEGEILMDGHDRLR.E
3014	679.9800	2036.9181	2036.9149	1.55	0	(60)	2.8e-06	1	U	R.FYDIDEGEILMDGHDRLR.E
3015	679.9801	2036.9185	2036.9149	1.73	0	(39)	0.0003	1	U	R.FYDIDEGEILMDGHDRLR.E
3016	679.9802	2036.9187	2036.9149	1.82	0	(60)	2.7e-06	1	U	R.FYDIDEGEILMDGHDRLR.E
3017	679.9802	2036.9188	2036.9149	1.91	0	(52)	1.7e-05	1	U	R.FYDIDEGEILMDGHDRLR.E
3018	679.9803	2036.9190	2036.9149	2.00	0	(58)	4e-06	1	U	R.FYDIDEGEILMDGHDRLR.E
3019	679.9822	2036.9249	2036.9149	4.88	0	(30)	0.003	1	U	R.FYDIDEGEILMDGHDRLR.E
3036	1021.4792	2040.9438	2040.9496	-2.84	0	(75)	8.6e-08	1	U	R.GMAACQTLFTILDSRQEK.D
3037	1021.4825	2040.9504	2040.9496	0.39	0	77	5.5e-08	1	U	R.GMAACQTLFTILDSRQEK.D
3038	681.3246	2040.9519	2040.9496	1.13	0	(58)	5e-06	1		

3061	681.9764	2042.9075	2042.9071	0.19	0	(38)	0.00035	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3062	681.9766	2042.9079	2042.9071	0.37	0	(40)	0.0002	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3063	681.9766	2042.9080	2042.9071	0.46	0	(47)	4.1e-05	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3064	681.9767	2042.9084	2042.9071	0.64	0	(37)	0.00038	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3065	681.9767	2042.9084	2042.9071	0.64	0	(60)	2.2e-06	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3066	681.9767	2042.9084	2042.9071	0.64	0	(60)	2e-06	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3067	681.9768	2042.9086	2042.9071	0.73	0	(55)	6.6e-06	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3068	681.9770	2042.9091	2042.9071	1.00	0	(39)	0.00029	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3069	681.9771	2042.9093	2042.9071	1.09	0	(61)	1.6e-06	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3070	681.9772	2042.9099	2042.9071	1.36	0	(60)	2e-06	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3071	681.9772	2042.9099	2042.9071	1.36	0	(41)	0.00015	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3074	681.9775	2042.9108	2042.9071	1.80	0	(49)	2.4e-05	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3075	681.9776	2042.9110	2042.9071	1.89	0	(57)	4e-06	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3076	1022.4642	2042.9139	2042.9071	3.33	0	(71)	1.9e-07	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3077	681.9792	2042.9159	2042.9071	4.31	0	(68)	3.5e-07	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3078	1022.4670	2042.9194	2042.9071	6.02	0	(57)	4.8e-06	1	U	K.NMONTGQVTTSAEQMLK.G + 2 Oxidation (M)
3079	1022.9491	2043.8836	2043.8911	-3.66	0	(38)	0.00015	1	U	K.NMONTGQVTTSAEQMLK.G + Deamidated (NQ); 2 Oxidation (M)
3112	1027.4557	2052.8968	2052.9099	-6.35	0	95	6.2e-10	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3113	1027.4561	2052.8976	2052.9099	-6.00	0	(76)	4.4e-08	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3117	685.3099	2052.9080	2052.9099	-0.92	0	(57)	4.5e-06	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3118	685.3100	2052.9082	2052.9099	-0.83	0	(52)	1.7e-05	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3119	685.3107	2052.9104	2052.9099	0.24	0	(58)	4.3e-06	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3120	685.3109	2052.9107	2052.9099	0.42	0	(22)	0.014	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3121	685.3109	2052.9107	2052.9099	0.42	0	(49)	3.2e-05	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3122	685.3110	2052.9111	2052.9099	0.60	0	(39)	0.00032	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3123	685.3111	2052.9115	2052.9099	0.78	0	(42)	0.00016	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3124	685.3113	2052.9122	2052.9099	1.13	0	(46)	5.6e-05	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3125	685.3117	2052.9133	2052.9099	1.67	0	(48)	4e-05	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3127	685.3123	2052.9151	2052.9099	2.56	0	(28)	0.0037	1	U	R.FYDIDEGEILMDGHDLR.E + Oxidation (M)
3137	686.6572	2056.9497	2056.9445	2.50	0	(58)	4.9e-06	1	U	R.GMAACQTLFTILDSEQEK.D + Oxidation (M)
3138	686.6578	2056.9517	2056.9445	3.48	0	(63)	1.4e-06	1	U	R.GMAACQTLFTILDSEQEK.D + Oxidation (M)
3148	687.3077	2058.9012	2058.9020	-0.40	0	(24)	0.0059	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3149	687.3087	2058.9041	2058.9020	1.03	0	(39)	0.00018	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3150	687.3088	2058.9045	2058.9020	1.20	0	(51)	1.3e-05	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3151	1030.4596	2058.9046	2058.9020	1.27	0	(53)	8.2e-06	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3152	687.3088	2058.9047	2058.9020	1.29	0	(45)	5e-05	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3153	687.3088	2058.9047	2058.9020	1.29	0	(46)	3.6e-05	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3154	687.3088	2058.9047	2058.9020	1.29	0	(68)	2.5e-07	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3155	687.3092	2058.9058	2058.9020	1.83	0	(37)	0.00029	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3156	1030.4603	2058.9061	2058.9020	1.98	0	(48)	2.6e-05	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3158	687.3099	2058.9080	2058.9020	2.89	0	(50)	1.7e-05	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3164	687.3113	2058.9122	2058.9020	4.94	0	(25)	0.0057	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3165	687.3113	2058.9122	2058.9020	4.94	0	(26)	0.0039	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3167	687.3137	2058.9193	2058.9020	8.41	0	(26)	0.0046	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3170	687.3149	2058.9228	2058.9020	10.1	0	(23)	0.011	1	U	K.NMONTGQVTTSAEQMLK.G + 3 Oxidation (M)
3479	715.6741	2144.0004	2144.0532	-24.63	0	(41)	0.0003	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3480	1073.0153	2144.0160	2144.0532	-17.36	0	(24)	0.016	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3481	715.6806	2144.0200	2144.0532	-15.49	0	(47)	8.5e-05	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3482	715.6822	2144.0247	2144.0532	-13.27	0	(28)	0.0072	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3483	1073.0311	2144.0477	2144.0532	-2.56	0	(106)	1.2e-10	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3484	715.6901	2144.0484	2144.0532	-2.25	0	(58)	8.7e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3485	715.6913	2144.0520	2144.0532	-0.54	0	(72)	3.8e-07	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3486	715.6917	2144.0533	2144.0532	0.05	0	(46)	0.00014	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3487	1073.0339	2144.0533	2144.0532	0.06	0	(108)	8.8e-11	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3488	715.6922	2144.0548	2144.0532	0.74	0	(77)	1.1e-07	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q
3489	1073.5160	2145.0174	2145.0372	-9.22	0	(59)	6e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3490	1073.5250	2145.0355	2145.0372	-0.79	0	(84)	2.2e-08	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3491	1073.5250	2145.0355	2145.0372	-0.79	0	(121)	4.2e-12	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3492	1073.5262	2145.0379	2145.0372	0.34	0	(98)	9.1e-10	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3493	1073.5262	2145.0379	2145.0372	0.34	0	(110)	5.2e-11	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3494	1073.5262	2145.0379	2145.0372	0.34	0	(108)	8.5e-11	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3495	716.0200	2145.0382	2145.0372	0.48	0	(46)	0.00014	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3496	716.0201	2145.0384	2145.0372	0.57	0	(70)	5.3e-07	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3497	716.0201	2145.0386	2145.0372	0.65	0	(39)	0.00071	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3498	1073.5273	2145.0401	2145.0372	1.37	0	(119)	6.3e-12	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3499	716.0207	2145.0402	2145.0372	1.42	0	(61)	4.5e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3500	716.0207	2145.0402	2145.0372	1.42	0	(56)	1.3e-05	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3501	716.0208	2145.0404	2145.0372	1.50	0	(61)	4.1e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3502	716.0208	2145.0404	2145.0372	1.50	0	(57)	1.1e-05	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3503	716.0209	2145.0410	2145.0372	1.76	0	(53)	2.5e-05	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3504	716.0212	2145.0417	2145.0372	2.10	0	(74)	2.1e-07	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3505	716.0213	2145.0421	2145.0372	2.27	0	(63)	2.6e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3506	716.0214	2145.0424	2145.0372	2.44	0	(47)	0.00012	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3507	716.0221	2145.0445	2145.0372	3.38	0	(50)	5.1e-05	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3508	716.0221	2145.0445	2145.0372	3.38	0	(49)	5.9e-05	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3509	716.0224	2145.0454	2145.0372	3.81	0	(45)	0.00016	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3510	1073.5305	2145.0465	2145.0372	4.33	0	(64)	1.9e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3511	716.0236	2145.0489	2145.0372	5.43	0	(48)	7.7e-05	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3512	716.0242	2145.0509	2145.0372	6.37	0	(58)	9.7e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ)
3513	1074.0173	2146.0201	2146.0212	-0.51	0	(102)	3.1e-10	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3514	1074.0183	2146.0221	2146.0212	0.40	0	(106)	1.2e-10	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3515	1074.0183	2146.0221	2146.0212	0.40	0	(119)	6.4e-12	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3516	716.3485	2146.0237	2146.0212	1.16	0	(72)	2.8e-07	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3517	1074.0197	2146.0248	2146.0212	1.65	0	(108)	6.3e-11	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3518	716.3490	2146.0252	2146.0212	1.84	0	(78)	7.4e-08	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3519	716.3491	2146.0254	2146.0212	1.93	0	(83)	2.4e-08	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3520	716.3494	2146.0263	2146.0212	2.36	0	(64)	1.9e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3521	716.3497	2146.0274	2146.0212	2.87	0	(59)	5.5e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + 2 Deamidated (NQ)
3527	721.0231	2160.0474	2160.0481	-0.34	0	(64)	1.8e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Oxidation (M)
3528	721.0231	2160.0476	2160.0481	-0.25	0	(57)	8.4e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Oxidation (M)
3529	1081.5203	2161.0260	2161.0321	-2.84	0	124	1.4e-12	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ); Oxidation (M)
3530	1081.5206	2161.0267	2161.0321	-2.50	0	(87)	7e-09	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ); Oxidation (M)
3531	721.3502	2161.0286	2161.0321	-1.61	0	(45)	0.00011	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ); Oxidation (M)
3532	1081.5220	2161.0294	2161.0321	-1.26	0	(91)	3e-09	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ); Oxidation (M)
3533	1081.5229	2161.0313	2161.0321	-0.36	0	(107)	6.5e-11	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ); Oxidation (M)
3534	721.3513	2161.0319	2161.0321	-0.08	0	(53)	1.6e-05	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ); Oxidation (M)
3535	721.3513	2161.0321	2161.0321	0.00	0	(57)	7.3e-06	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ); Oxidation (M)
3536	1081.5234	2161.0323	2161.0321	0.09	0	(88)	5.4e-09	1	U	K.MDNGLDVTIGENGVLLSGGQR.Q + Deamidated (NQ); Oxidation (M)
3537	721.3516	2161.0329	2161.0321	0.34	0</					

3593	1088.0349	2174.0553	2174.0590	-1.72	0	(81)	2.9e-08	1	U	R.DSPILILDEATSALDTESER.A
3594	725.6926	2174.0559	2174.0590	-1.44	0	(34)	0.0014	1	U	R.DSPILILDEATSALDTESER.A
3595	725.6926	2174.0561	2174.0590	-1.36	0	(31)	0.003	1	U	R.DSPILILDEATSALDTESER.A
3596	1088.0354	2174.0562	2174.0590	-1.27	0	(76)	9.5e-08	1	U	R.DSPILILDEATSALDTESER.A
3597	1088.0356	2174.0567	2174.0590	-1.04	0	(80)	3.9e-08	1	U	R.DSPILILDEATSALDTESER.A
3598	1088.0358	2174.0570	2174.0590	-0.93	0	115	1.3e-11	1	U	R.DSPILILDEATSALDTESER.A
3599	1088.0363	2174.0580	2174.0590	-0.48	0	(103)	2.2e-10	1	U	R.DSPILILDEATSALDTESER.A
3600	725.6933	2174.0581	2174.0590	-0.43	0	(29)	0.0054	1	U	R.DSPILILDEATSALDTESER.A
3601	725.6933	2174.0581	2174.0590	-0.43	0	(68)	7.2e-07	1	U	R.DSPILILDEATSALDTESER.A
3602	725.6934	2174.0584	2174.0590	-0.26	0	(62)	2.3e-06	1	U	R.DSPILILDEATSALDTESER.A
3603	725.6934	2174.0584	2174.0590	-0.26	0	(73)	2e-07	1	U	R.DSPILILDEATSALDTESER.A
3604	1088.0365	2174.0584	2174.0590	-0.26	0	(98)	7.1e-10	1	U	R.DSPILILDEATSALDTESER.A
3605	725.6935	2174.0588	2174.0590	-0.10	0	(58)	6.9e-06	1	U	R.DSPILILDEATSALDTESER.A
3606	725.6936	2174.0590	2174.0590	-0.01	0	(65)	1.4e-06	1	U	R.DSPILILDEATSALDTESER.A
3607	725.6937	2174.0593	2174.0590	0.16	0	(76)	1e-07	1	U	R.DSPILILDEATSALDTESER.A
3608	725.6940	2174.0601	2174.0590	0.49	0	(72)	2.5e-07	1	U	R.DSPILILDEATSALDTESER.A
3609	1088.0375	2174.0604	2174.0590	0.64	0	(94)	1.5e-09	1	U	R.DSPILILDEATSALDTESER.A
3610	725.6941	2174.0604	2174.0590	0.66	0	(71)	3.6e-07	1	U	R.DSPILILDEATSALDTESER.A
3611	1088.0377	2174.0609	2174.0590	0.87	0	(106)	1.2e-10	1	U	R.DSPILILDEATSALDTESER.A
3612	1088.0387	2174.0628	2174.0590	1.76	0	(59)	5.1e-06	1	U	R.DSPILILDEATSALDTESER.A
3613	1088.0400	2174.0655	2174.0590	3.00	0	(77)	9.2e-08	1	U	R.DSPILILDEATSALDTESER.A
3619	1092.0607	2182.1068	2182.1117	-2.27	0	(88)	6.2e-09	1	U	R.ITYDSEQVASSSSGALITVVR.E
3620	728.3765	2182.1076	2182.1117	-1.91	0	(39)	0.00045	1	U	R.ITYDSEQVASSSSGALITVVR.E
3621	1092.0615	2182.1085	2182.1117	-1.49	0	(91)	3.4e-09	1	U	R.ITYDSEQVASSSSGALITVVR.E
3622	728.3769	2182.1088	2182.1117	-1.33	0	(77)	7.2e-08	1	U	R.ITYDSEQVASSSSGALITVVR.E
3623	728.3772	2182.1098	2182.1117	-0.91	0	(40)	0.00036	1	U	R.ITYDSEQVASSSSGALITVVR.E
3624	546.5347	2182.1098	2182.1117	-0.88	0	(54)	1.4e-05	1	U	R.ITYDSEQVASSSSGALITVVR.E
3625	728.3773	2182.1099	2182.1117	-0.82	0	(82)	2.5e-08	1	U	R.ITYDSEQVASSSSGALITVVR.E
3626	728.3775	2182.1107	2182.1117	-0.49	0	(58)	5.7e-06	1	U	R.ITYDSEQVASSSSGALITVVR.E
3627	728.3775	2182.1107	2182.1117	-0.49	0	(28)	0.0055	1	U	R.ITYDSEQVASSSSGALITVVR.E
3628	1092.0627	2182.1109	2182.1117	-0.37	0	(69)	5e-07	1	U	R.ITYDSEQVASSSSGALITVVR.E
3629	728.3777	2182.1114	2182.1117	-0.15	0	(64)	1.4e-06	1	U	R.ITYDSEQVASSSSGALITVVR.E
3631	728.3779	2182.1120	2182.1117	0.10	0	(62)	2.7e-06	1	U	R.ITYDSEQVASSSSGALITVVR.E
3632	728.3782	2182.1127	2182.1117	0.44	0	(38)	0.00057	1	U	R.ITYDSEQVASSSSGALITVVR.E
3633	728.3782	2182.1127	2182.1117	0.44	0	(62)	2.3e-06	1	U	R.ITYDSEQVASSSSGALITVVR.E
3634	728.3782	2182.1129	2182.1117	0.52	0	(23)	0.02	1	U	R.ITYDSEQVASSSSGALITVVR.E
3635	728.3782	2182.1129	2182.1117	0.52	0	(67)	6.9e-07	1	U	R.ITYDSEQVASSSSGALITVVR.E
3636	546.5355	2182.1130	2182.1117	0.57	0	(55)	1.2e-05	1	U	R.ITYDSEQVASSSSGALITVVR.E
3637	728.3783	2182.1131	2182.1117	0.60	0	(35)	0.0013	1	U	R.ITYDSEQVASSSSGALITVVR.E
3638	1092.0638	2182.1131	2182.1117	0.64	0	(74)	1.5e-07	1	U	R.ITYDSEQVASSSSGALITVVR.E
3639	728.3785	2182.1138	2182.1117	0.94	0	(36)	0.00087	1	U	R.ITYDSEQVASSSSGALITVVR.E
3640	728.3785	2182.1138	2182.1117	0.94	0	(46)	0.0001	1	U	R.ITYDSEQVASSSSGALITVVR.E
3641	728.3786	2182.1140	2182.1117	1.02	0	(36)	0.00085	1	U	R.ITYDSEQVASSSSGALITVVR.E
3642	728.3791	2182.1156	2182.1117	1.78	0	(21)	0.027	2	U	R.ITYDSEQVASSSSGALITVVR.E
3643	728.3791	2182.1156	2182.1117	1.78	0	(70)	3.8e-07	1	U	R.ITYDSEQVASSSSGALITVVR.E
3644	728.3792	2182.1158	2182.1117	1.86	0	(30)	0.0041	1	U	R.ITYDSEQVASSSSGALITVVR.E
3645	1092.0653	2182.1161	2182.1117	1.98	0	98	6.1e-10	1	U	R.ITYDSEQVASSSSGALITVVR.E
3646	1092.0654	2182.1163	2182.1117	2.09	0	(69)	4.6e-07	1	U	R.ITYDSEQVASSSSGALITVVR.E
3869	771.7527	2312.2362	2312.2475	-4.87	1	(42)	0.00015	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3870	771.7549	2312.2430	2312.2475	-1.94	1	(56)	6.7e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3871	771.7552	2312.2439	2312.2475	-1.55	1	(61)	2e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3872	771.7554	2312.2445	2312.2475	-1.31	1	(49)	2.9e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3873	579.0684	2312.2446	2312.2475	-1.26	1	(22)	0.014	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3874	771.7555	2312.2447	2312.2475	-1.23	1	(55)	7.1e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3875	771.7556	2312.2448	2312.2475	-1.15	1	(67)	5.2e-07	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3876	579.0686	2312.2453	2312.2475	-0.95	1	(26)	0.0065	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3877	771.7557	2312.2454	2312.2475	-0.91	1	(51)	1.9e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3878	771.7558	2312.2456	2312.2475	-0.84	1	(50)	2.1e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3879	771.7560	2312.2463	2312.2475	-0.52	1	(54)	8.3e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3880	1157.1305	2312.2464	2312.2475	-0.46	1	137	4.3e-14	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3881	771.7561	2312.2465	2312.2475	-0.44	1	(68)	3.3e-07	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3882	771.7562	2312.2467	2312.2475	-0.36	1	(60)	2.2e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3883	771.7562	2312.2467	2312.2475	-0.36	1	(58)	4.1e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3884	579.0690	2312.2468	2312.2475	-0.31	1	(42)	0.00014	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3885	771.7562	2312.2468	2312.2475	-0.28	1	(55)	7.9e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3886	771.7563	2312.2470	2312.2475	-0.20	1	(50)	2.3e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3887	771.7563	2312.2470	2312.2475	-0.20	1	(64)	9.3e-07	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3888	771.7563	2312.2472	2312.2475	-0.12	1	(45)	7e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3889	771.7566	2312.2479	2312.2475	0.19	1	(56)	5.4e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3890	771.7566	2312.2479	2312.2475	0.19	1	(53)	1e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3891	579.0693	2312.2480	2312.2475	0.22	1	(44)	9.3e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3892	1157.1313	2312.2481	2312.2475	0.28	1	(56)	6.3e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3893	771.7567	2312.2483	2312.2475	0.35	1	(47)	4.6e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3894	1157.1315	2312.2484	2312.2475	0.38	1	(124)	9.3e-13	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3895	771.7568	2312.2485	2312.2475	0.43	1	(61)	1.9e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3896	771.7568	2312.2485	2312.2475	0.43	1	(56)	6e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3897	579.0695	2312.2487	2312.2475	0.53	1	(25)	0.0075	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3898	771.7569	2312.2489	2312.2475	0.59	1	(57)	4.2e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3899	771.7570	2312.2490	2312.2475	0.67	1	(46)	5.7e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3900	771.7570	2312.2492	2312.2475	0.75	1	(63)	1e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3901	771.7571	2312.2494	2312.2475	0.83	1	(51)	1.6e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3902	771.7571	2312.2496	2312.2475	0.91	1	(45)	6.3e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3903	771.7571	2312.2496	2312.2475	0.91	1	(66)	5.2e-07	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3904	579.0698	2312.2502	2312.2475	1.17	1	(47)	4.4e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3905	771.7574	2312.2505	2312.2475	1.30	1	(56)	5e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3906	771.7574	2312.2505	2312.2475	1.30	1	(53)	1.1e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3907	579.0699	2312.2507	2312.2475	1.38	1	(45)	6.6e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3908	579.0700	2312.2509	2312.2475	1.48	1	(40)	0.00023	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3909	579.0700	2312.2509	2312.2475	1.48	1	(33)	0.001	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3910	579.0701	2312.2512	2312.2475	1.59	1	(32)	0.0015	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3911	771.7577	2312.2512	2312.2475	1.62	1	(53)	1e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3912	579.0701	2312.2514	2312.2475	1.69	1	(39)	0.00028	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3913	771.7578	2312.2514	2312.2475	1.70	1	(52)	1.4e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3914	579.0702	2312.2517	2312.2475	1.80	1	(35)	0.00067	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3915	579.0703	2312.2519	2312.2475	1.90	1	(54)	8.5e-06	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3916	579.0703	2312.2521	2312.2475	2.01	1	(41)	0.00017	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3917	579.0704	2312.2526	2312.2475	2.22	1	(34)	0.00093	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3918	579.0704	2312.2526	2312.2475	2.22	1	(28)	0.0033	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3919	579.0706	2312.2531	2312.2475	2.43	1	(29)	0.0027	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3920	771.7585	2312.2536	2312.2475	2.65	1	(66)	5.9e-07	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3921	771.7585	2312.2538	2312.2475	2.73	1	(44)	8.6e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3922	579.0711	2312.2553	2312.2475	3.38	1	(38)	0.00032	1	U	R.LSTIEKADEIVVVEDGVIVER.G
3923	771.7598	2312.2575	2312.2475	4.31	1	(45)	6.6e-05	1	U	R.LSTIEKADEIVVVEDGVIVER.G
4022	819.0599	2454.1578	2454.1552	1.04	1	(64)	1.4e-06	1	U	R.NISKQNTMGQVTTSAEQMLK.G + Deamidated (M0)
4023	819.0628	2454.1666	2454.1552	4.62	1	(60)	3.6e-06	1	U	R.NISKQNTMGQVTTSAEQMLK.G + Deamidated (M0)
4027	824									

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4447	1121.8589	3362.5548	3362.5469	2.37	1	(106)	6.8e-11	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4448	841.6461	3362.5551	3362.5469	2.46	1	(69)	3.5e-07	1	U	R.MAYAMDFINKQDGLDTVIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4449	1121.8590	3362.5552	3362.5469	2.48	1	(103)	1.6e-10	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4450	841.6461	3362.5554	3362.5469	2.53	1	(56)	7.2e-06	1	U	R.MAYAMDFINKQDGLDTVIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4451	841.6461	3362.5554	3362.5469	2.53	1	(53)	1.3e-05	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4452	841.6461	3362.5554	3362.5469	2.53	1	(60)	2.9e-06	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4453	841.6475	3362.5610	3362.5469	4.20	1	(69)	4.1e-07	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4454	1121.8612	3362.5618	3362.5469	4.44	1	(69)	3.8e-07	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4455	1121.8612	3362.5618	3362.5469	4.44	1	(90)	2.8e-09	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 2	Oxidation (M)
4462	1126.8538	3377.5395	3377.5578	-5.42	1	(75)	3.9e-08	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)
4463	845.3954	3377.5524	3377.5578	-1.58	1	(28)	0.0029	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)
4464	1126.8599	3377.5578	3377.5578	-0.00	1	(66)	4.7e-07	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)
4465	1126.8607	3377.5603	3377.5578	0.76	1	(82)	1.3e-08	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)
4466	845.3975	3377.5610	3377.5578	0.95	1	(63)	1.1e-06	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)
4467	1126.8627	3377.5662	3377.5578	2.49	1	(106)	4.8e-11	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)
4468	1127.1862	3378.5366	3378.5418	-1.52	1	(74)	9e-08	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)
4469	1127.1880	3378.5421	3378.5418	0.11	1	(67)	4.6e-07	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)
4470	845.6434	3378.5444	3378.5418	0.77	1	(81)	1.6e-08	1	U	R.MAYAMDFINKQDNGLDVTIGENGVLSSGGQR.Q + 2	Deamidated (NQ); 3	Oxidation (M)

2. 2::sp|Q9CR10|EFTU_LACLA Mass: 43185 Score: 562 Matches: 20(20) Sequences: 12(12) emPAI: 1.42

Elongation factor Tu OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=tuf PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
641	505.3075	1008.6005	1008.6008	-0.28	0	32	0.00059	1	U	K.LVLVFLNK.A
642	505.3084	1008.6022	1008.6008	1.41	0	(29)	0.0014	1	U	K.LVLVFLNK.A
962	561.8029	1121.5913	1121.5903	0.86	0	(59)	3.8e-06	1	U	K.AVVTGTEMFR.K
963	561.8031	1121.5916	1121.5903	1.19	0	59	3.3e-06	1	U	K.AVVTGTEMFR.K
1052	572.8315	1143.6484	1143.6499	-1.33	1	58	4.1e-06	1	U	R.TVGSQIVAEIKA.-
1053	572.8346	1143.6546	1143.6499	4.11	1	(48)	3.2e-05	1	U	R.TVGSQIVAEIKA.-
1784	642.3479	1282.6812	1282.6809	0.28	0	67	4.5e-07	1	U	K.LFEGEVTVLSK.E
1785	642.3485	1282.6825	1282.6809	1.23	0	(52)	1.3e-05	1	U	K.LFEGEVTVLSK.E
2240	746.8497	1491.6849	1491.6841	0.52	0	67	3.7e-07	1	U	K.ATDFASIDAAPER.E
2241	746.8498	1491.6850	1491.6841	0.61	0	(67)	4.1e-07	1	U	K.ATDFASIDAAPER.E
2342	800.4369	1598.8592	1598.8628	-2.22	0	77	6.8e-08	1	U	K.LTLEGAGNDVALLR.G
2441	548.9606	1643.8601	1643.8618	-1.04	1	35	0.0009	1	U	K.VGDEVEIVGIEETK.R
2490	424.2067	1692.7976	1692.8008	-1.94	0	(28)	0.0036	1	U	R.HYAHIDAPGHADTVK.N
2491	424.2082	1692.8038	1692.8008	1.74	0	30	0.0028	1	U	R.HYAHIDAPGHADTVK.N
2628	593.2834	1776.8283	1776.8278	0.29	1	43	0.00013	1	U	K.ATDFASIDAAPERER.G
2629	593.2842	1776.8309	1776.8278	1.73	1	(37)	0.00049	1	U	K.ATDFASIDAAPERER.G
2662	449.7440	1794.9470	1794.9489	-1.09	0	36	0.00096	1	U	R.SKPHVNIQTIQVHDGK.T
2686	604.6436	1810.9088	1810.9101	-0.70	1	35	0.0012	1	U	K.LFEGEVTVLSKEEGGR.H
2687	604.6451	1810.9134	1810.9101	1.83	1	(31)	0.0025	1	U	K.LFEGEVTVLSKEEGGR.H
2730	625.6580	1873.9520	1873.9534	-0.70	1	22	0.027	1	U	R.GTITNTAIEYETEK.R

3. 2::tr|Q9CGH2|Q9CGH2_LACLA Mass: 52877 Score: 530 Matches: 21(21) Sequences: 11(11) emPAI: 1.07

Fumarate reductase flavoprotein subunit OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=frdC PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
543	488.2505	974.4865	974.4855	1.07	0	(24)	0.013	1	U	K.MPIAGGNTSK.A
544	488.2515	974.4885	974.4855	3.07	0	25	0.012	1	U	K.MPIAGGNTSK.A
719	515.7988	1029.5830	1029.5818	1.10	0	51	2.1e-05	1	U	K.IINTNTQVLK.K
720	515.8002	1029.5859	1029.5818	3.95	0	(35)	0.00081	1	U	K.IINTNTQVLK.K
972	562.8009	1123.5873	1123.5873	-0.06	0	55	6.3e-06	1	U	K.TGYLVSESIR.G
973	562.8012	1123.5879	1123.5873	0.48	0	(49)	2.4e-05	1	U	K.TGYLVSESIR.G
1190	593.8107	1185.6068	1185.6063	0.38	0	47	4e-05	1	U	K.DAGMNPVILEK.M
1257	601.8085	1201.6024	1201.6013	0.94	0	(25)	0.0096	1	U	K.DAGMNPVILEK.M + Oxidation (M)
1346	404.2361	1209.6865	1209.6870	-0.40	0	29	0.0014	1	U	K.IQIHPVTVPQK.T
1415	610.8329	1219.6512	1219.6561	-4.01	0	47	8.3e-05	1	U	K.AVVVTGQGFANK.K
1416	610.8372	1219.6599	1219.6561	3.09	0	(36)	0.00092	1	U	K.AVVVTGQGFANK.K
1646	632.3181	1262.6217	1262.6183	2.67	0	47	6.4e-05	1	U	K.YSVIFPGQTK.D
1647	632.3200	1262.6255	1262.6183	5.67	0	(39)	0.00043	1	U	K.YSVIFPGQTK.D
1992	673.8694	1345.7242	1345.7242	0.04	0	32	0.0019	1	U	R.MIPLFVSDVTK.I
1993	673.8700	1345.7254	1345.7242	0.94	0	(31)	0.0022	1	U	R.MIPLFVSDVTK.I
2020	682.3397	1362.6648	1362.6627	1.55	0	(63)	1.3e-06	1	U	K.ASAGLNASSETSVEK.A
2021	682.3401	1362.6657	1362.6627	2.27	0	83	1.3e-08	1	U	K.ASAGLNASSETSVEK.A
2116	701.3947	1400.7748	1400.7776	-2.03	0	83	1.5e-08	1	U	R.IGQNAVADIVIFGR.Q
2117	701.3968	1400.7790	1400.7776	1.02	0	(58)	3.8e-06	1	U	R.IGQNAVADIVIFGR.Q
2492	424.2249	1692.8703	1692.8696	0.41	0	(27)	0.007	1	U	R.THRPHDGSVAGGTLVK.G
2493	424.2265	1692.8769	1692.8696	4.30	0	31	0.0025	1	U	R.THRPHDGSVAGGTLVK.G

4. 2::sp|Q9CEK9|SYN_LACLA Mass: 50865 Score: 189 Matches: 9(9) Sequences: 5(5) emPAI: 0.37

Asparagine--tRNA ligase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=asnS PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
351	459.2810	916.5475	916.5494	-2.08	0	(24)	0.0058	1	U	K.LQFLQLR.D
352	459.2815	916.5484	916.5494	-1.08	0	36	0.00038	1	U	K.LQFLQLR.D
870	542.2855	1082.5564	1082.5549	1.31	0	44	9.3e-05	1	U	R.VDFDGPVFR.A
871	542.2858	1082.5571	1082.5549	1.99	0	(40)	0.00021	1	U	R.VDFDGPVFR.A
2018	454.2393	1359.6960	1359.6969	-0.65	0	23	0.018	1	U	R.MVTFVAGTEHIR.E
2019	454.2398	1359.6975	1359.6969	0.43	0	(23)	0.018	1	U	R.MVTFVAGTEHIR.E
2306	515.2729	1542.7970	1542.7943	1.74	0	(34)	0.0012	1	U	K.FGSPVPHAGFGLGLER.M
2307	515.2733	1542.7981	1542.7943	2.46	0	61	2.6e-06	1	U	K.FGSPVPHAGFGLGLER.M
2446	549.6307	1645.8702	1645.8676	1.61	0	28	0.0052	1	U	K.HLSQETSIVTVGVK.E

5. 2::tr|Q9CJD8|Q9CJD8_LACLA Mass: 49950 Score: 170 Matches: 8(8) Sequences: 4(4) emPAI: 0.29

Dihydroliopyl dehydrogenase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=phdH PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
541	488.2477	974.4809	974.4821	-1.28	0	33	0.0018	1	U	K.LMWSAQK.W
542	488.2486	974.4826	974.4821	0.48	0	(20)	0.03	1	U	K.LMWSAQK.W
654	507.8005	1013.5865	1013.5870	-0.43	0	(44)	5.9e-05	1	U	K.VVNQLTGGVK.M
655	507.8008	1013.5871	1013.5870	0.11	0	49	2.8e-05	1	U	K.VVNQLTGGVK.M
1325	403.5526	1207.6361	1207.6349	0.97	1	(25)	0.0099	1	U	K.ISKFPFPAANGR.A + Deamidated (NQ)
1326	403.5526	1207.6361	1207.6349	0.97	1	43	0.00016	1	U	K.ISKFPFPAANGR.A + Deamidated (NQ)
2474	557.2977	1668.8712	1668.8795	-4.98	0	46	7.2e-05	1	U	R.RPNTDLIGLNNTDVK.L
2475	557.3013	1668.8820	1668.8795	1.50	0	(26)	0.0075	1	U	R.RPNTDLIGLNNTDVK.L

6. 2::tr|Q9CHAD|Q9CHAD_LACLA Mass: 44683 Score: 155 Matches: 8(8) Sequences: 4(4) emPAI: 0.33

30S ribosomal protein S1 OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=rrsA PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
207	421.7583	841.5020	841.5022	-0.14	0	(38)	0.00018	1	U	K.VQGVNVVK.V
210	421.7584	841.5022	841.5022	0.08	0	47	2.1e-05	1	U	K.VQGVNVVK.V

1048	572.8007	1143.586	1143.5884	-1.29	0	(41)	0.00023	1	U	K.IIEVNASENR.F
1049	572.8016	1143.5886	1143.5884	0.20	0	46	7.8e-05	1	U	K.IIEVNASENR.F
1050	572.8136	1143.6126	1143.6136	-0.81	0	41	0.00031	1	U	K.APVGSTVEGTVK.R
1051	572.8143	1143.6141	1143.6136	0.47	0	(33)	0.002	1	U	K.APVGSTVEGTVK.R
1106	385.8831	1154.6274	1154.6295	-1.80	0	26	0.0033	1	U	K.VLDVKPAER.I
1107	385.8843	1154.6310	1154.6295	1.29	0	(23)	0.0067	1	U	K.VLDVKPAER.I

2::tr|Q9CEM3|Q9CEM3_LACLA

Mass: 50509

Score: 131

Matches: 5(5)

Sequences: 3(3)

emPAI: 0.21

Transport protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ysiA PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
976	562.8552	1123.6959	1123.6965	-0.51	0	(36)	0.00026	1	U	R.LAPLLGGTALAK.T
977	562.8582	1123.7018	1123.6965	4.70	0	38	0.00014	1	U	R.LAPLLGGTALAK.T
1410	610.3351	1218.6557	1218.6608	-4.18	0	(52)	2.3e-05	1	U	K.IGENLYVVQGG.M
1411	610.3379	1218.6612	1218.6608	0.33	0	67	6.1e-07	1	U	K.IGENLYVVQGG.M
3111	514.0300	2052.0908	2052.0892	0.79	1	25	0.0097	1	U	R.VPVYDDDDKNILGLHVK.K

2::tr|Q9CGJ6|Q9CGJ6_LACLA

Mass: 56426

Score: 102

Matches: 3(3)

Sequences: 3(3)

emPAI: 0.19

Nicotinate phosphoribosyltransferase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=yiaF PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1221	600.2858	1198.5570	1198.5540	2.51	0	46	2.8e-05	1	U	R.IDSGDMAYISK.K
1369	607.8093	1213.6041	1213.5979	5.12	0	21	0.014	1	U	K.FSETDIATYLR.E
1946	661.8139	1321.6133	1321.6150	-1.32	0	35	0.00077	1	U	R.QQLDEAGFTDAK.I

2::tr|Q9CF08|Q9CF08_LACLA

Mass: 63898

Score: 95

Matches: 4(4)

Sequences: 3(3)

emPAI: 0.16

1-deoxy-D-xylulose-5-phosphate synthase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=dxsB PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
670	510.2606	1018.5067	1018.5083	-1.61	0	31	0.0022	1	U	R.GTQPALENK.E
671	510.2619	1018.5092	1018.5083	0.84	0	(28)	0.0044	1	U	R.GTQPALENK.E
2297	509.9566	1526.8480	1526.8457	1.52	0	34	0.00093	1	U	K.VALLALGGLYSHGEK.V
4036	824.4275	2470.2606	2470.2532	3.00	0	31	0.0037	1	U	R.AYDQFWDLAINEEPAIVTVK.G

2::sp|Q9CD27|SYE_LACLA

Mass: 55427

Score: 90

Matches: 5(5)

Sequences: 3(3)

emPAI: 0.19

Glutamate--tRNA ligase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=gltx PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
26	381.2311	760.4477	760.4483	-0.84	0	35	0.00059	1	U	R.LPLYQK.Y
27	381.2316	760.4486	760.4483	0.37	0	(24)	0.0078	1	U	R.LPLYQK.Y
430	473.7534	945.4923	945.4928	-0.51	0	21	0.028	1	U	K.MLWMPIR.I
1123	388.8957	1163.6653	1163.6662	-0.77	0	(29)	0.0024	1	U	K.VLAHLDAALNK.-
1124	388.8961	1163.6664	1163.6662	0.18	0	34	0.00073	1	U	K.VLAHLDAALNK.-

2::sp|Q9CGD4|POTA_LACLA

Mass: 48455

Score: 86

Matches: 4(4)

Sequences: 3(3)

emPAI: 0.22

Spermidine/putrescine import ATP-binding protein PotA OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=potA PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1453	614.3108	1226.6070	1226.6031	3.24	0	28	0.0029	1	U	K.TIADTDTTVLK.D
3630	728.3779	2182.1120	2182.1092	1.25	0	30	0.0042	1	U	K.AIVGETVGLDFDPEAIIHMR.L
3642	728.3791	2182.1156	2182.1092	2.93	0	(28)	0.0062	1	U	K.AIVGETVGLDFDPEAIIHMR.L
3959	783.3961	2347.1665	2347.1583	3.49	1	29	0.0059	1	U	K.DISFELEGKFTYLLGASGSK.S

2::sp|Q9CDR6|EZRA_LACLA

Mass: 66146

Score: 74

Matches: 4(4)

Sequences: 2(2)

emPAI: 0.10

Septation ring formation regulator EzrA OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ezrA PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1554	621.8364	1241.6583	1241.6615	-2.61	0	37	0.0005	1	U	K.ZLELVEPGAASR.I
1555	621.8398	1241.6651	1241.6615	2.89	0	(27)	0.004	1	U	K.ZLELVEPGAASR.I
1575	623.8545	1245.6944	1245.6969	-1.96	0	(36)	0.0007	1	U	R.ATTEQIPSPFK.T
1576	623.8572	1245.6998	1245.6969	2.36	0	37	0.00054	1	U	R.ATTEQIPSPFK.T

2::tr|Q9CEH2|Q9CEH2_LACLA

Mass: 43961

Score: 57

Matches: 2(2)

Sequences: 1(1)

emPAI: 0.08

Cell division protein FtsZ OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ftsZ PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1542	620.8418	1239.6690	1239.6684	0.52	0	59	1.5e-06	1	U	K.VIGVGGGGGNAIHR.M
1543	620.8424	1239.6703	1239.6684	1.51	0	(40)	0.00014	1	U	K.VIGVGGGGGNAIHR.M

2::tr|Q9CDR3|Q9CDR3_LACLA

Mass: 98331

Score: 55

Matches: 3(3)

Sequences: 2(2)

emPAI: 0.07

Aldehyde-alcohol dehydrogenase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=adhE PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
90	388.2105	774.4064	774.4123	-7.62	0	21	0.031	1	U	K.VLSAEK.A
2696	606.6508	1816.9304	1816.9319	-0.80	0	35	0.0012	1	U	K.NSLSHNLSTYDLLNVK.T
2697	606.6517	1816.9334	1816.9319	0.81	0	(24)	0.013	1	U	K.NSLSHNLSTYDLLNVK.T

2::tr|Q7DAV2|Q7DAV2_LACLA

Mass: 60825

Score: 52

Matches: 3(3)

Sequences: 2(2)

emPAI: 0.11

Alpha-acetolactate synthase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=als PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
518	484.7731	967.5316	967.5338	-2.31	0	(26)	0.0024	1	U	K.AIQPLSDPK.M
519	484.7740	967.5335	967.5338	-0.36	0	28	0.0018	1	U	K.AIQPLSDPK.M
2215	491.5735	1471.6985	1471.6990	-0.33	0	25	0.0082	1	U	R.HEGGAAPMAQAVGR.L

2::sp|Q9CF25|FTSK_LACLA

Mass: 83575

Score: 39

Matches: 2(2)

Sequences: 1(1)

emPAI: 0.04

DNA translocase FtsK OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ftsK PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
824	531.7691	1061.5237	1061.5240	-0.37	0	(29)	0.0039	1	U	R.TLDTTHGAEK.L + Deamidated (NQ)
825	531.7702	1061.5259	1061.5240	1.70	0	39	0.00034	1	U	R.TLDTTHGAEK.L + Deamidated (NQ)

2::sp Q9CI75 PYRG_LACLA		Mass: 59742	Score: 32	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06
CTP synthase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=pyrG PE=3 SV=1						
☐ Check to include this hit in error tolerant search or archive report						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
☒ 25	381.2310	760.4474	760.4483	-1.16	0 34	0.00066 1 U R.LGLIYPAK.L

18. 2::sp|P0A493|RL36_LACLA

Mass: 4589

Score: 30

Matches: 2(2)

Sequences: 1(1)

emPAI: 0.81

50S ribosomal protein L36 OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=rpmJ PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 984	564.7972	1127.5798	1127.5831	-2.93	0 30	0.0015 1 U	R.VHVICPANPK.H
☒ 985	564.7986	1127.5826	1127.5831	-0.44	0 (29)	0.0022 1 U	R.VHVICPANPK.H

19. 2::tr|Q9CE09|Q9CE09_LACLA

Mass: 22096

Score: 29

Matches: 2(2)

Sequences: 1(1)

emPAI: 0.15

Uncharacterized protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=yvca PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 173	417.7373	833.4601	833.4494	12.8	0 29	0.0042 1 U	R.STSAILIJK.R + Deamidated (NQ)
☒ 174	417.7376	833.4607	833.4494	13.5	0 (25)	0.0083 1 U	R.STSAILIJK.R + Deamidated (NQ)

20. 2::tr|Q9CI76|Q9CI76_LACLA

Mass: 42293

Score: 28

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.08

Amino acids and amines aminotransferase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=yeiG PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 3774	556.0229	2220.0627	2220.1103	-21.43	2 28	0.0051 1 U	R.AKATTNPDI LAPYDFYKK.T

21. 2::tr|Q9CGY3|Q9CGY3_LACLA

Mass: 66312

Score: 27

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.05

Fructose-specific PTS system enzyme IIBC component OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=fruA PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 588	495.2500	988.4854	988.4825	2.91	0 27	0.0051 1 U	R.DTEELINR.A

22. 2::sp|Q9CBI6|PNP_LACLA

Mass: 84732

Score: 27

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.04

Polyribonucleotide nucleotidyltransferase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=pnp PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 631	501.7599	1001.5052	1001.5115	-6.29	2 27	0.0056 1 U	R.RKGNGNSNR.G

23. 2::tr|Q9CGA7|Q9CGA7_LACLA

Mass: 55406

Score: 27

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.06

Citrate lyase alpha chain OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=citF PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 1432	408.2017	1221.5832	1221.6023	-15.71	0 27	0.0029 1 U	K.GVVTVITSSGMR.G + Deamidated (NQ)

24. 2::sp|Q9CFV2|CARB_LACLA

Mass: 118270

Score: 25

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.03

Carbamoyl-phosphate synthase large chain OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=carB PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 312	451.2581	900.5017	900.5029	-1.30	0 25	0.0092 1 U	R.DASLNIIIR.A

25. 2::tr|Q9CHF3|Q9CHF3_LACLA

Mass: 49696

Score: 24

Matches: 2(2)

Sequences: 1(1)

emPAI: 0.07

Biotin carboxylase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=accC PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 882	545.3157	1088.6169	1088.6342	-15.86	1 24	0.0093 1 U	M.FMKILIANR.G + Deamidated (NQ)
☒ 885	545.3181	1088.6216	1088.6342	-11.60	1 (21)	0.015 1 U	M.FMKILIANR.G + Deamidated (NQ)

26. 2::tr|Q9CFF6|Q9CFF6_LACLA

Mass: 59782

Score: 23

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.05

ABC transporter ATP binding and permease protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ypgD PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 2304	770.8730	1539.7314	1539.7603	-18.74	1 23	0.014 1 U	R.TMGKFNQLATANVK.L + 2 Deamidated (NQ); Oxidation (M)

27. 2::tr|Q9CJA0|Q9CJA0_LACLA

Mass: 58381

Score: 21

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.06

ABC transporter ATP binding protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ybaB PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 1893	651.8612	1301.7079	1301.7051	2.10	2 21	0.021 1 U	K.KANVATSGQAKAR.E + Deamidated (NQ)

28. 2::sp|P35514|DNAJ_LACLA

Mass: 41102

Score: 21

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.08

Chaperone protein DnaJ OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=dnaJ PE=3 SV=2

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 2218	491.9436	1472.8091	1472.8100	-0.60	1 24	0.013 1 U	K.LKIPAGTQTGANFR.L

29. 2::tr|Q9CHA9|Q9CHA9_LACLA

Mass: 74104

Score: 21

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.04

NADH dehydrogenase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=noxB PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
☒ 338	455.2433	908.4720	908.4504	23.8	0 21	0.016 1 U	K.IWYQGSR.S

30. 2::tr|Q9CDS2|Q9CDS2_LACLA

Mass: 28411

Score: 20

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.12

Uncharacterized protein OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ywba PE=4 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique	Peptide
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☒ [1134](#) 583.8215 1165.6285 1165.6165 10.3 1 20 0.012 1 U R.FLEIVDRMR.A + Oxidation (M)

31. [2::sp|Q9CJ85|SECA_LACLA](#) Mass: 98393 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.03
Protein translocase subunit SecA OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=secA PE=3 SV=1
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☒ 2390	544.2953	1629.8640	1629.8582	3.59	1	20	0.034	1	U	R.LMMKAQIQPQTAIR.Q + 2 Deamidated (NQ)

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Deamidated (NQ), Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Fragment Mass Tolerance: ± 0.8 Da
Max Missed Cleavages : 2
Instrument type : ESI-TRAP
Number of queries : 4554