Mascot Search Results

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User            :
Email           :
Search title    : Winton_26_8_15_LcrVE2_1in5_pt1.raw
Database        : NCBInr 29_1_15 (57851050 sequences; 20740007484 residues)
Timestamp       : 28 Aug 2015 at 09:32:17 GMT
Protein hits    : gi|489191432 MULTISPECIES: type III secretion protein [Pseudomonas]
                  gi|685887085 type III secretion protein [Pseudomonas aeruginosa]
                  gi|62952892  capsule protein fraction 1/virulence antigen fusion protein precursor [synthetic construct]
                  gi|490890815 GTPase CgtA [Acinetobacter sp. ANC 3789]
                  gi|457874719 hypothetical protein PCYB_002770 [Plasmodium cynomolgi strain B]
                  gi|489248865 hypothetical protein [Pseudomonas aeruginosa]
                  gi|50304509  hypothetical protein [Kluyveromyces lactis NRRL Y-1140]
                  gi|700303716 hypothetical protein TEU_09445 [Thermococcus eurythermalis]
                  gi|312207957 Chain A, Crystal Structure Of The Salmonella Type Iii Secretion System Tip Protein Sipd
                  gi|93279729  Chain A, Crystal Structure Of The Putative Transcriptional Regulator, Marr Family From Porphyromonas Gingivalis W83
                  gi|491901269 anaerobic ribonucleoside-triphosphate reductase activating protein [Dethiosulfovibrio peptidovorans]
                  gi|146983    outer membrane protein II, partial [Escherichia fergusonii]
                  gi|489989392 response regulator [Mycobacterium smegmatis]
                  gi|494364767 putative LPS biosynthesis protein WbpG [Hoeflea phototrophica]
                  gi|225733897 Chain A, Solution Structure Of E.Coli Slyd
                  gi|518446942 hypothetical protein [Psychromonas ossibalaenae]
                  gi|118138114 Chain X, Crystal Structure Of Ribosome With Messenger Rna And The Anticodon Stem-Loop Of P-Site Trna. This File Contains The 50s Subunit Of One 70s Ribosome. The Entire Crystal Structure Contains Two 70s Ribosomes And Is Described In Remark 400.
                  gi|136429    RecName: Full=Trypsin; Flags: Precursor [Sus scrofa]
                  gi|493595525 lysyl-tRNA synthetase [Actinomyces urogenitalis]
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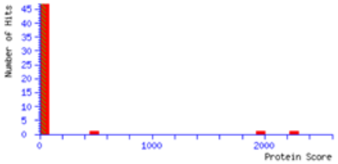
Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 49 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 AUTO

Standard scoring ● MudPIT scoring ○ Ions score or expect cut-off 20 Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○ Sort unassigned Decreasing Score Require bold red ☑

Preferred taxonomy All entries

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. gi|489191432 **Mass:** 32264 **Score:** 2258 **Matches:** 477(187) **Sequences:** 36(24) **emPAI:** 11.99
MULTISPECIES: type III secretion protein [Pseudomonas]
☐ 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
☑	36	358.2086	714.4026	714.4024	0.32	0	34	9.8	1		R.EVLQAR.R
	39	358.2088	714.4030	714.4024	0.88	0	(28)	33	3		R.EVLQAR.R
	40	358.2089	714.4032	714.4024	1.16	0	(23)	1.1e+002	5		R.EVLQAR.R
☑	76	373.2265	744.4384	744.4381	0.43	0	50	0.15	1		K.ALTAELK.V
☑	77	376.6996	751.3846	751.3864	-2.39	0	(36)	2.1	1		K.YDSVLR.D
☑	79	376.7002	751.3858	751.3864	-0.79	0	(34)	3.4	1		K.YDSVLR.D
☑	80	376.7003	751.3860	751.3864	-0.53	0	(27)	16	1		K.YDSVLR.D
☑	81	376.7003	751.3860	751.3864	-0.53	0	(25)	27	1		K.YDSVLR.D
☑	83	376.7004	751.3862	751.3864	-0.26	0	(26)	20	1		K.YDSVLR.D
☑	84	376.7004	751.3862	751.3864	-0.26	0	(34)	3.3	1		K.YDSVLR.D
☑	85	376.7004	751.3862	751.3864	-0.26	0	(25)	27	1		K.YDSVLR.D
☑	88	376.7004	751.3862	751.3864	-0.26	0	(36)	2.3	1		K.YDSVLR.D
☑	90	376.7005	751.3864	751.3864	0.01	0	(25)	25	1		K.YDSVLR.D
☑	91	376.7005	751.3864	751.3864	0.01	0	(23)	48	1		K.YDSVLR.D
☑	92	376.7005	751.3864	751.3864	0.01	0	(28)	12	1		K.YDSVLR.D
☑	93	376.7005	751.3864	751.3864	0.01	0	(34)	3.9	1		K.YDSVLR.D
☑	94	376.7006	751.3866	751.3864	0.27	0	(28)	12	1		K.YDSVLR.D
	95	376.7006	751.3866	751.3864	0.27	0	(23)	48	3		K.YDSVLR.D
☑	96	376.7006	751.3866	751.3864	0.27	0	(25)	25	1		K.YDSVLR.D
☑	97	376.7006	751.3866	751.3864	0.27	0	(38)	1.5	1		K.YDSVLR.D
☑	98	376.7007	751.3868	751.3864	0.54	0	39	1.1	1		K.YDSVLR.D
☑	99	376.7007	751.3868	751.3864	0.54	0	(27)	17	1		K.YDSVLR.D
☑	100	376.7007	751.3868	751.3864	0.54	0	(24)	35	1		K.YDSVLR.D
☑	101	376.7008	751.3870	751.3864	0.80	0	(29)	12	1		K.YDSVLR.D
☑	102	376.7008	751.3870	751.3864	0.80	0	(28)	14	1		K.YDSVLR.D
☑	173	401.2395	800.4644	800.4643	0.13	0	37	1.9	1		K.ALLDELK.A
☑	178	401.2398	800.4650	800.4643	0.88	0	(36)	1.4	1		K.ALLDELK.A
☑	179	401.2400	800.4654	800.4643	1.38	0	(25)	20	1		K.ALLDELK.A

	222	415.2302	828.4458	828.4453	0.61	0	(29)	9.6	2		R.SRPLNDK.V
	223	415.2303	828.4460	828.4453	0.85	0	(31)	6.1	4		R.SRPLNDK.V
	224	415.2303	828.4460	828.4453	0.85	0	(31)	6.6	8		R.SRPLNDK.V
	225	415.2307	828.4468	828.4453	1.82	0	32	5.7	3		R.SRPLNDK.V
☑	254	425.7188	849.4230	849.4232	-0.22	0	(27)	12	1		K.DFLSGSPK.Q
☑	256	425.7193	849.4240	849.4232	0.96	0	42	0.63	1		K.DFLSGSPK.Q
	339	465.2863	928.5580	928.5593	-1.34	1	(32)	3.3	4		R.KALLDELK.A
☑	342	465.2869	928.5592	928.5593	-0.05	1	53	0.029	1		R.KALLDELK.A
☑	343	465.2870	928.5594	928.5593	0.16	1	(50)	0.062	1		R.KALLDELK.A
☑	444	502.2563	1002.4980	1002.4982	-0.15	0	(46)	0.18	1		K.DVLQTQDGK.R
☑	445	502.2565	1002.4984	1002.4982	0.25	0	51	0.07	1		K.DVLQTQDGK.R
☑	559	535.7724	1069.5302	1069.5305	-0.22	0	(29)	7	1		R.QPGAQWDLR.E
☑	560	535.7725	1069.5304	1069.5305	-0.04	0	(36)	1.3	1		R.QPGAQWDLR.E
	561	535.7726	1069.5306	1069.5305	0.15	0	(22)	39	2		R.QPGAQWDLR.E
	562	535.7727	1069.5308	1069.5305	0.34	0	(28)	8.8	2		R.QPGAQWDLR.E
☑	563	535.7728	1069.5310	1069.5305	0.52	0	38	0.62	1		R.QPGAQWDLR.E
☑	565	535.7729	1069.5312	1069.5305	0.71	0	(36)	1.1	1		R.QPGAQWDLR.E
☑	634	554.2853	1106.5560	1106.5568	-0.65	0	(41)	0.35	1		K.TTLLNDTSSR.Y
☑	635	554.2855	1106.5564	1106.5568	-0.28	0	(46)	0.2	1		K.TTLLNDTSSR.Y
☑	636	554.2858	1106.5570	1106.5568	0.26	0	(31)	6.3	1		K.TTLLNDTSSR.Y
☑	637	554.2859	1106.5572	1106.5568	0.44	0	(76)	0.00019	1		K.TTLLNDTSSR.Y
☑	638	554.2859	1106.5572	1106.5568	0.44	0	(49)	0.1	1		K.TTLLNDTSSR.Y
☑	639	554.2860	1106.5574	1106.5568	0.62	0	(49)	0.088	1		K.TTLLNDTSSR.Y
☑	640	554.2861	1106.5576	1106.5568	0.80	0	83	4.3e-005	1		K.TTLLNDTSSR.Y
☑	641	554.2861	1106.5576	1106.5568	0.80	0	(49)	0.095	1		K.TTLLNDTSSR.Y
☑	642	554.2861	1106.5576	1106.5568	0.80	0	(64)	0.0028	1		K.TTLLNDTSSR.Y
☑	643	554.2861	1106.5576	1106.5568	0.80	0	(56)	0.018	1		K.TTLLNDTSSR.Y
☑	644	554.2862	1106.5578	1106.5568	0.98	0	(42)	0.6	1		K.TTLLNDTSSR.Y
☑	645	554.2862	1106.5578	1106.5568	0.98	0	(60)	0.0085	1		K.TTLLNDTSSR.Y
☑	646	554.2863	1106.5580	1106.5568	1.16	0	(74)	0.00038	1		K.TTLLNDTSSR.Y
☑	647	554.2864	1106.5582	1106.5568	1.34	0	(71)	0.00072	1		K.TTLLNDTSSR.Y
☑	648	554.2870	1106.5594	1106.5568	2.43	0	(58)	0.01	1		K.TTLLNDTSSR.Y
☑	710	568.7873	1135.5600	1135.5621	-1.85	0	(64)	0.0021	1		R.YNSAVEALNR.F
☑	712	568.7881	1135.5616	1135.5621	-0.44	0	(44)	0.25	1		R.YNSAVEALNR.F
☑	713	568.7882	1135.5618	1135.5621	-0.27	0	(53)	0.035	1		R.YNSAVEALNR.F
☑	714	568.7885	1135.5624	1135.5621	0.26	0	79	0.00011	1		R.YNSAVEALNR.F
☑	715	568.7886	1135.5626	1135.5621	0.44	0	(76)	0.00017	1		R.YNSAVEALNR.F
☑	716	568.7888	1135.5630	1135.5621	0.79	0	(70)	0.00064	1		R.YNSAVEALNR.F
☑	717	568.7888	1135.5630	1135.5621	0.79	0	(51)	0.05	1		R.YNSAVEALNR.F
☑	718	568.7888	1135.5630	1135.5621	0.79	0	(58)	0.01	1		R.YNSAVEALNR.F
☑	719	568.7889	1135.5632	1135.5621	0.97	0	(45)	0.2	1		R.YNSAVEALNR.F
☑	720	568.7889	1135.5632	1135.5621	0.97	0	(46)	0.19	1		R.YNSAVEALNR.F
☑	721	568.7890	1135.5634	1135.5621	1.14	0	(47)	0.13	1		R.YNSAVEALNR.F
☑	722	568.7891	1135.5636	1135.5621	1.32	0	(51)	0.047	1		R.YNSAVEALNR.F
☑	723	568.7891	1135.5636	1135.5621	1.32	0	(59)	0.0084	1		R.YNSAVEALNR.F
☑	724	568.7897	1135.5648	1135.5621	2.38	0	(57)	0.014	1		R.YNSAVEALNR.F
☑	760	575.8026	1149.5906	1149.5918	-0.96	0	(61)	0.0049	1		R.LDEDVIGVYK.D
☑	761	575.8034	1149.5922	1149.5918	0.43	0	(61)	0.0058	1		R.LDEDVIGVYK.D
☑	762	575.8038	1149.5930	1149.5918	1.13	0	(39)	1	1		R.LDEDVIGVYK.D
☑	763	575.8042	1149.5938	1149.5918	1.82	0	62	0.0035	1		R.LDEDVIGVYK.D
☑	779	580.3071	1158.5996	1158.5993	0.30	1	(34)	3.5	1		K.DVLQTQDGKR.K
	783	580.3074	1158.6002	1158.5993	0.81	1	(27)	15	2		K.DVLQTQDGKR.K
	784	580.3074	1158.6002	1158.5993	0.81	1	(25)	24	2		K.DVLQTQDGKR.K
☑	786	580.3074	1158.6002	1158.5993	0.81	1	(47)	0.16	1		K.DVLQTQDGKR.K
☑	787	580.3075	1158.6004	1158.5993	0.99	1	54	0.034	1		K.DVLQTQDGKR.K
☑	788	387.2082	1158.6028	1158.5993	2.99	1	(36)	2.6	1		K.DVLQTQDGKR.K
☑	849	592.7778	1183.5410	1183.5397	1.14	0	61	0.0028	1	U	K.GLSDEYPFEK.D
☑	963	409.5509	1225.6309	1225.6316	-0.59	1	(24)	23	1		R.RQPGAQWDLR.E
☑	964	409.5510	1225.6312	1225.6316	-0.34	1	(32)	3.3	1		R.RQPGAQWDLR.E
☑	965	409.5510	1225.6312	1225.6316	-0.34	1	(40)	0.52	1		R.RQPGAQWDLR.E
☑	966	409.5510	1225.6312	1225.6316	-0.34	1	(27)	12	1		R.RQPGAQWDLR.E
	971	613.8230	1225.6314	1225.6316	-0.12	1	(25)	17	7		R.RQPGAQWDLR.E
☑	972	409.5511	1225.6315	1225.6316	-0.10	1	(40)	0.61	1		R.RQPGAQWDLR.E
☑	973	409.5511	1225.6315	1225.6316	-0.10	1	(38)	0.99	1		R.RQPGAQWDLR.E
☑	974	409.5511	1225.6315	1225.6316	-0.10	1	53	0.028	1		R.RQPGAQWDLR.E
☑	975	409.5511	1225.6315	1225.6316	-0.10	1	(41)	0.4	1		R.RQPGAQWDLR.E
☑	976	409.5511	1225.6315	1225.6316	-0.10	1	(42)	0.39	1		R.RQPGAQWDLR.E
☑	977	409.5511	1225.6315	1225.6316	-0.10	1	(39)	0.63	1		R.RQPGAQWDLR.E
☑	978	409.5511	1225.6315	1225.6316	-0.10	1	(40)	0.58	1		R.RQPGAQWDLR.E
☑	979	613.8231	1225.6316	1225.6316	0.05	1	(41)	0.45	1		R.RQPGAQWDLR.E
☑	981	409.5512	1225.6318	1225.6316	0.15	1	(39)	0.72	1		R.RQPGAQWDLR.E
☑	982	409.5512	1225.6318	1225.6316	0.15	1	(36)	1.5	1		R.RQPGAQWDLR.E
☑	983	409.5512	1225.6318	1225.6316	0.15	1	(40)	0.58	1		R.RQPGAQWDLR.E
☑	984	409.5512	1225.6318	1225.6316	0.15	1	(36)	1.3	1		R.RQPGAQWDLR.E
☑	988	613.8232	1225.6318	1225.6316	0.21	1	(22)	35	1		R.RQPGAQWDLR.E
	990	613.8233	1225.6320	1225.6316	0.37	1	(32)	4	2		R.RQPGAQWDLR.E
☑	991	409.5513	1225.6321	1225.6316	0.39	1	(47)	0.11	1		R.RQPGAQWDLR.E
☑	992	409.5513	1225.6321	1225.6316	0.39	1	(38)	0.98	1		R.RQPGAQWDLR.E
☑	993	409.5513	1225.6321	1225.6316	0.39	1	(26)	12	1		R.RQPGAQWDLR.E
☑	994	409.5513	1225.6321	1225.6316	0.39	1	(27)	11	1		R.RQPGAQWDLR.E
☑	995	409.5513	1225.6321	1225.6316	0.39	1	(36)	1.3	1		R.RQPGAQWDLR.E
☑	996	409.5513	1225.6321	1225.6316	0.39	1	(31)	4.8	1		R.RQPGAQWDLR.E
☑	997	409.5513	1225.6321	1225.6316	0.39	1	(34)	2.2	1		R.RQPGAQWDLR.E
☑	998	409.5513	1225.6321	1225.6316	0.39	1	(41)	0.45	1		R.RQPGAQWDLR.E
☑	999	409.5513	1225.6321	1225.6316	0.39	1	(35)	1.7	1		R.RQPGAQWDLR.E
☑	1000	409.5513	1225.6321	1225.6316	0.39	1	(43)	0.27	1		R.RQPGAQWDLR.E
☑	1001	409.5513	1225.6321	1225.6316	0.39	1	(44)	0.23	1		R.RQPGAQWDLR.E
☑	1002	409.5513	1225.6321	1225.6316	0.39	1	(31)	4.2	1		R.RQPGAQWDLR.E

	1006	613.8234	1225.6322	1225.6316	0.54	1	(21)	44	6	R.RQPGAQWDLR.E
☑	1007	409.5514	1225.6324	1225.6316	0.64	1	(34)	2.5	1	R.RQPGAQWDLR.E
☑	1008	409.5514	1225.6324	1225.6316	0.64	1	(35)	1.7	1	R.RQPGAQWDLR.E
☑	1009	409.5514	1225.6324	1225.6316	0.64	1	(45)	0.19	1	R.RQPGAQWDLR.E
☑	1010	409.5514	1225.6324	1225.6316	0.64	1	(38)	0.86	1	R.RQPGAQWDLR.E
☑	1018	409.5515	1225.6327	1225.6316	0.88	1	(47)	0.11	1	R.RQPGAQWDLR.E
☑	1019	409.5515	1225.6327	1225.6316	0.88	1	(45)	0.14	1	R.RQPGAQWDLR.E
☑	1020	409.5515	1225.6327	1225.6316	0.88	1	(39)	0.59	1	R.RQPGAQWDLR.E
☑	1022	613.8240	1225.6334	1225.6316	1.51	1	(31)	4.3	1	R.RQPGAQWDLR.E
☑	1024	409.5519	1225.6339	1225.6316	1.86	1	(39)	0.7	1	R.RQPGAQWDLR.E
☑	1025	613.8243	1225.6340	1225.6316	2.00	1	(32)	4	1	R.RQPGAQWDLR.E
☑	1169	634.8540	1267.6934	1267.6925	0.78	1	42	0.27	1	R.FIQKYDSVLR.D
☑	1238	646.3661	1290.7176	1290.7183	-0.53	1	(51)	0.033	1	K.LSIKDFLSGSPK.Q
☑	1239	431.2465	1290.7177	1290.7183	-0.52	1	(23)	18	1	K.LSIKDFLSGSPK.Q
☑	1240	646.3662	1290.7178	1290.7183	-0.38	1	(44)	0.14	1	K.LSIKDFLSGSPK.Q
☑	1241	646.3663	1290.7180	1290.7183	-0.22	1	(50)	0.048	1	K.LSIKDFLSGSPK.Q
☑	1242	431.2467	1290.7183	1290.7183	-0.05	1	(28)	7.3	1	K.LSIKDFLSGSPK.Q
☑	1243	646.3665	1290.7184	1290.7183	0.09	1	(67)	0.00084	1	K.LSIKDFLSGSPK.Q
☑	1244	646.3665	1290.7184	1290.7183	0.09	1	(22)	29	1	K.LSIKDFLSGSPK.Q
☑	1245	646.3665	1290.7184	1290.7183	0.09	1	(64)	0.0017	1	K.LSIKDFLSGSPK.Q
☑	1248	431.2468	1290.7186	1290.7183	0.18	1	(28)	7.1	1	K.LSIKDFLSGSPK.Q
☑	1249	431.2468	1290.7186	1290.7183	0.18	1	(28)	6.5	1	K.LSIKDFLSGSPK.Q
☑	1251	646.3666	1290.7186	1290.7183	0.24	1	(43)	0.21	1	K.LSIKDFLSGSPK.Q
☑	1252	646.3666	1290.7186	1290.7183	0.24	1	(65)	0.0015	1	K.LSIKDFLSGSPK.Q
☑	1253	646.3666	1290.7186	1290.7183	0.24	1	(46)	0.1	1	K.LSIKDFLSGSPK.Q
☑	1254	646.3666	1290.7186	1290.7183	0.24	1	(65)	0.0013	1	K.LSIKDFLSGSPK.Q
☑	1255	646.3667	1290.7188	1290.7183	0.40	1	(65)	0.0012	1	K.LSIKDFLSGSPK.Q
☑	1256	431.2469	1290.7189	1290.7183	0.41	1	(21)	32	1	K.LSIKDFLSGSPK.Q
☑	1258	646.3668	1290.7190	1290.7183	0.55	1	(43)	0.23	1	K.LSIKDFLSGSPK.Q
☑	1259	646.3668	1290.7190	1290.7183	0.55	1	(71)	0.00038	1	K.LSIKDFLSGSPK.Q
☑	1260	431.2470	1290.7192	1290.7183	0.65	1	(25)	12	1	K.LSIKDFLSGSPK.Q
☑	1261	646.3669	1290.7192	1290.7183	0.71	1	(68)	0.00069	1	K.LSIKDFLSGSPK.Q
☑	1262	646.3670	1290.7194	1290.7183	0.86	1	(68)	0.00062	1	K.LSIKDFLSGSPK.Q
☑	1263	431.2471	1290.7195	1290.7183	0.88	1	(37)	0.85	1	K.LSIKDFLSGSPK.Q
☑	1264	646.3671	1290.7196	1290.7183	1.01	1	(55)	0.013	1	K.LSIKDFLSGSPK.Q
☑	1265	646.3671	1290.7196	1290.7183	1.01	1	(60)	0.0038	1	K.LSIKDFLSGSPK.Q
☑	1266	646.3671	1290.7196	1290.7183	1.01	1	(45)	0.14	1	K.LSIKDFLSGSPK.Q
☑	1267	431.2472	1290.7198	1290.7183	1.11	1	(30)	4.1	1	K.LSIKDFLSGSPK.Q
☑	1268	646.3672	1290.7198	1290.7183	1.17	1	(42)	0.25	1	K.LSIKDFLSGSPK.Q
☑	1269	646.3672	1290.7198	1290.7183	1.17	1	(58)	0.0074	1	K.LSIKDFLSGSPK.Q
☑	1270	646.3672	1290.7198	1290.7183	1.17	1	75	0.00014	1	K.LSIKDFLSGSPK.Q
☑	1271	646.3674	1290.7202	1290.7183	1.48	1	(47)	0.089	1	K.LSIKDFLSGSPK.Q
☑	1287	650.3521	1298.6896	1298.6942	-3.53	1	(36)	1.6	1	R.SRPLNDKVNEK.T
	1288	650.3528	1298.6910	1298.6942	-2.45	1	(25)	21	5	R.SRPLNDKVNEK.T
☑	1289	433.9044	1298.6914	1298.6942	-2.20	1	(21)	48	1	R.SRPLNDKVNEK.T
☑	1291	650.3532	1298.6918	1298.6942	-1.83	1	(47)	0.12	1	R.SRPLNDKVNEK.T
☑	1293	433.9047	1298.6923	1298.6942	-1.51	1	(33)	2.5	1	R.SRPLNDKVNEK.T
☑	1295	433.9048	1298.6926	1298.6942	-1.28	1	(33)	2.3	1	R.SRPLNDKVNEK.T
☑	1296	433.9049	1298.6929	1298.6942	-1.04	1	(33)	2.4	1	R.SRPLNDKVNEK.T
☑	1297	433.9049	1298.6929	1298.6942	-1.04	1	(26)	13	1	R.SRPLNDKVNEK.T
☑	1298	433.9050	1298.6932	1298.6942	-0.81	1	(26)	16	1	R.SRPLNDKVNEK.T
☑	1299	433.9051	1298.6935	1298.6942	-0.58	1	(27)	12	1	R.SRPLNDKVNEK.T
☑	1300	433.9051	1298.6935	1298.6942	-0.58	1	(39)	0.72	1	R.SRPLNDKVNEK.T
☑	1302	433.9051	1298.6935	1298.6942	-0.58	1	(37)	1.4	1	R.SRPLNDKVNEK.T
☑	1303	433.9051	1298.6935	1298.6942	-0.58	1	(28)	11	1	R.SRPLNDKVNEK.T
☑	1304	433.9051	1298.6935	1298.6942	-0.58	1	(43)	0.33	1	R.SRPLNDKVNEK.T
☑	1305	433.9052	1298.6938	1298.6942	-0.35	1	(27)	12	1	R.SRPLNDKVNEK.T
☑	1306	433.9052	1298.6938	1298.6942	-0.35	1	(29)	8.5	1	R.SRPLNDKVNEK.T
☑	1307	433.9052	1298.6938	1298.6942	-0.35	1	(35)	2.1	1	R.SRPLNDKVNEK.T
☑	1308	433.9052	1298.6938	1298.6942	-0.35	1	(31)	4.7	1	R.SRPLNDKVNEK.T
	1309	433.9052	1298.6938	1298.6942	-0.35	1	(23)	31	2	R.SRPLNDKVNEK.T
☑	1310	433.9052	1298.6938	1298.6942	-0.35	1	(29)	7.6	1	R.SRPLNDKVNEK.T
☑	1313	433.9053	1298.6941	1298.6942	-0.12	1	(24)	22	1	R.SRPLNDKVNEK.T
☑	1314	433.9053	1298.6941	1298.6942	-0.12	1	(34)	2.4	1	R.SRPLNDKVNEK.T
☑	1315	433.9053	1298.6941	1298.6942	-0.12	1	(25)	20	1	R.SRPLNDKVNEK.T
☑	1316	433.9053	1298.6941	1298.6942	-0.12	1	(31)	4.6	1	R.SRPLNDKVNEK.T
☑	1317	433.9054	1298.6944	1298.6942	0.11	1	(20)	61	1	R.SRPLNDKVNEK.T
	1318	433.9054	1298.6944	1298.6942	0.11	1	(26)	16	2	R.SRPLNDKVNEK.T
☑	1319	433.9054	1298.6944	1298.6942	0.11	1	(30)	5.9	1	R.SRPLNDKVNEK.T
☑	1320	433.9054	1298.6944	1298.6942	0.11	1	(36)	1.5	1	R.SRPLNDKVNEK.T
☑	1321	433.9054	1298.6944	1298.6942	0.11	1	(32)	4.2	1	R.SRPLNDKVNEK.T
☑	1322	433.9054	1298.6944	1298.6942	0.11	1	(27)	11	1	R.SRPLNDKVNEK.T
☑	1323	433.9054	1298.6944	1298.6942	0.11	1	(28)	10	1	R.SRPLNDKVNEK.T
☑	1324	433.9054	1298.6944	1298.6942	0.11	1	(31)	5	1	R.SRPLNDKVNEK.T
	1325	433.9054	1298.6944	1298.6942	0.11	1	(26)	15	2	R.SRPLNDKVNEK.T
☑	1326	650.3546	1298.6946	1298.6942	0.32	1	(57)	0.011	1	R.SRPLNDKVNEK.T
	1327	433.9055	1298.6947	1298.6942	0.34	1	(22)	40	2	R.SRPLNDKVNEK.T
☑	1328	433.9055	1298.6947	1298.6942	0.34	1	(31)	5.6	1	R.SRPLNDKVNEK.T
☑	1329	433.9055	1298.6947	1298.6942	0.34	1	(26)	16	1	R.SRPLNDKVNEK.T
☑	1330	433.9055	1298.6947	1298.6942	0.34	1	(31)	5	1	R.SRPLNDKVNEK.T
☑	1331	433.9055	1298.6947	1298.6942	0.34	1	(34)	2.7	1	R.SRPLNDKVNEK.T
☑	1332	433.9055	1298.6947	1298.6942	0.34	1	(28)	11	1	R.SRPLNDKVNEK.T
	1333	433.9055	1298.6947	1298.6942	0.34	1	(23)	34	2	R.SRPLNDKVNEK.T
☑	1334	433.9055	1298.6947	1298.6942	0.34	1	(29)	7.7	1	R.SRPLNDKVNEK.T
☑	1335	650.3547	1298.6948	1298.6942	0.48	1	(57)	0.012	1	R.SRPLNDKVNEK.T
☑	1336	433.9056	1298.6950	1298.6942	0.57	1	(34)	2.5	1	R.SRPLNDKVNEK.T
☑	1337	433.9056	1298.6950	1298.6942	0.57	1	(32)	3.5	1	R.SRPLNDKVNEK.T
☑	1338	433.9056	1298.6950	1298.6942	0.57	1	(40)	0.59	1	R.SRPLNDKVNEK.T

☑	1339	433.9056	1298.6950	1298.6942	0.57	1	(37)	1.1	1	R.SRPLNDKVNEK.T
☑	1340	433.9056	1298.6950	1298.6942	0.57	1	(29)	8.2	1	R.SRPLNDKVNEK.T
☑	1342	650.3549	1298.6952	1298.6942	0.78	1	(44)	0.28	1	R.SRPLNDKVNEK.T
☑	1343	650.3550	1298.6954	1298.6942	0.94	1	(24)	28	1	R.SRPLNDKVNEK.T
☑	1344	433.9058	1298.6956	1298.6942	1.03	1	(40)	0.59	1	R.SRPLNDKVNEK.T
☑	1345	433.9058	1298.6956	1298.6942	1.03	1	(24)	25	1	R.SRPLNDKVNEK.T
☑	1346	650.3551	1298.6956	1298.6942	1.09	1	59	0.0077	1	R.SRPLNDKVNEK.T
☑	1347	650.3553	1298.6960	1298.6942	1.40	1	(36)	1.6	1	R.SRPLNDKVNEK.T
☑	1348	650.3553	1298.6960	1298.6942	1.40	1	(51)	0.046	1	R.SRPLNDKVNEK.T
☑	1349	650.3554	1298.6962	1298.6942	1.55	1	(43)	0.31	1	R.SRPLNDKVNEK.T
☑	1350	650.3554	1298.6962	1298.6942	1.55	1	(58)	0.0093	1	R.SRPLNDKVNEK.T
☑	1351	650.3555	1298.6964	1298.6942	1.71	1	(44)	0.27	1	R.SRPLNDKVNEK.T
☑	1579	682.8749	1363.7352	1363.7347	0.39	1	(39)	0.57	1	K.YDSVLRDILSAI.-
☑	1580	682.8752	1363.7358	1363.7347	0.83	1	(37)	1	1	K.YDSVLRDILSAI.-
☑	1581	682.8752	1363.7358	1363.7347	0.83	1	51	0.039	1	K.YDSVLRDILSAI.-
☑	1582	682.8755	1363.7364	1363.7347	1.27	1	(47)	0.091	1	K.YDSVLRDILSAI.-
☑	1796	763.3928	1524.7710	1524.7725	-0.96	0	(46)	0.13	1	R.EFLVSAYFSLHGR.L
☑	1797	763.3929	1524.7712	1524.7725	-0.83	0	(64)	0.002	1	R.EFLVSAYFSLHGR.L
☑	1798	763.3932	1524.7718	1524.7725	-0.43	0	90	5.3e-006	1	R.EFLVSAYFSLHGR.L
☑	1799	763.3934	1524.7722	1524.7725	-0.17	0	(74)	0.00019	1	R.EFLVSAYFSLHGR.L
☑	1800	763.3934	1524.7722	1524.7725	-0.17	0	(67)	0.0011	1	R.EFLVSAYFSLHGR.L
☑	1802	763.3936	1524.7726	1524.7725	0.09	0	(80)	5.8e-005	1	R.EFLVSAYFSLHGR.L
☑	1803	509.2650	1524.7732	1524.7725	0.44	0	(54)	0.024	1	R.EFLVSAYFSLHGR.L
☑	1804	509.2650	1524.7732	1524.7725	0.44	0	(34)	2.4	1	R.EFLVSAYFSLHGR.L
☑	1806	509.2651	1524.7735	1524.7725	0.63	0	(40)	0.56	1	R.EFLVSAYFSLHGR.L
☑	1807	509.2651	1524.7735	1524.7725	0.63	0	(27)	12	1	R.EFLVSAYFSLHGR.L
☑	1808	509.2651	1524.7735	1524.7725	0.63	0	(47)	0.13	1	R.EFLVSAYFSLHGR.L
☑	1809	509.2651	1524.7735	1524.7725	0.63	0	(39)	0.82	1	R.EFLVSAYFSLHGR.L
☑	1810	509.2651	1524.7735	1524.7725	0.63	0	(39)	0.71	1	R.EFLVSAYFSLHGR.L
☑	1811	509.2651	1524.7735	1524.7725	0.63	0	(33)	3.1	1	R.EFLVSAYFSLHGR.L
☑	1812	509.2651	1524.7735	1524.7725	0.63	0	(49)	0.07	1	R.EFLVSAYFSLHGR.L
☑	1813	509.2651	1524.7735	1524.7725	0.63	0	(44)	0.25	1	R.EFLVSAYFSLHGR.L
☑	1814	509.2651	1524.7735	1524.7725	0.63	0	(48)	0.1	1	R.EFLVSAYFSLHGR.L
☑	1815	509.2651	1524.7735	1524.7725	0.63	0	(50)	0.063	1	R.EFLVSAYFSLHGR.L
☑	1817	509.2652	1524.7738	1524.7725	0.83	0	(40)	0.71	1	R.EFLVSAYFSLHGR.L
☑	1818	509.2652	1524.7738	1524.7725	0.83	0	(39)	0.84	1	R.EFLVSAYFSLHGR.L
☑	1819	509.2652	1524.7738	1524.7725	0.83	0	(43)	0.33	1	R.EFLVSAYFSLHGR.L
☑	1820	509.2652	1524.7738	1524.7725	0.83	0	(29)	8.9	1	R.EFLVSAYFSLHGR.L
☑	1821	509.2652	1524.7738	1524.7725	0.83	0	(43)	0.36	1	R.EFLVSAYFSLHGR.L
☑	1822	509.2652	1524.7738	1524.7725	0.83	0	(28)	11	1	R.EFLVSAYFSLHGR.L
☑	1823	509.2652	1524.7738	1524.7725	0.83	0	(27)	13	1	R.EFLVSAYFSLHGR.L
☑	1824	763.3942	1524.7738	1524.7725	0.88	0	(60)	0.0059	1	R.EFLVSAYFSLHGR.L
☑	1825	763.3943	1524.7740	1524.7725	1.01	0	(68)	0.0011	1	R.EFLVSAYFSLHGR.L
☑	1826	763.3943	1524.7740	1524.7725	1.01	0	(64)	0.0025	1	R.EFLVSAYFSLHGR.L
☑	1827	509.2653	1524.7741	1524.7725	1.03	0	(41)	0.54	1	R.EFLVSAYFSLHGR.L
☑	1829	763.3945	1524.7744	1524.7725	1.27	0	(60)	0.0068	1	R.EFLVSAYFSLHGR.L
☑	1830	763.3945	1524.7744	1524.7725	1.27	0	(56)	0.017	1	R.EFLVSAYFSLHGR.L
☑	1831	763.3946	1524.7746	1524.7725	1.40	0	(69)	0.0006	1	R.EFLVSAYFSLHGR.L
☑	1832	763.3946	1524.7746	1524.7725	1.40	0	(72)	0.00035	1	R.EFLVSAYFSLHGR.L
☑	1833	763.3947	1524.7748	1524.7725	1.54	0	(67)	0.00091	1	R.EFLVSAYFSLHGR.L
☑	1834	763.3947	1524.7748	1524.7725	1.54	0	(66)	0.0013	1	R.EFLVSAYFSLHGR.L
☑	1835	763.3948	1524.7750	1524.7725	1.67	0	(73)	0.00024	1	R.EFLVSAYFSLHGR.L
☑	1836	763.3948	1524.7750	1524.7725	1.67	0	(49)	0.066	1	R.EFLVSAYFSLHGR.L
☑	1840	764.4536	1526.8926	1526.8919	0.49	1	45	0.036	1	K.ALLDELKALTAELK.V
☑	1918	526.6100	1576.8082	1576.8056	1.60	1	35	2.6	1	K.VNEKTTLLNDTSSR.Y
☑	1965	803.8762	1605.7378	1605.7383	-0.30	0	(63)	0.0017	1	K.DNNPVGNFATTVSDR.S
☑	1966	803.8762	1605.7378	1605.7383	-0.30	0	(61)	0.003	1	K.DNNPVGNFATTVSDR.S
☑	1967	803.8766	1605.7386	1605.7383	0.20	0	96	8.1e-007	1	K.DNNPVGNFATTVSDR.S
☑	1968	803.8773	1605.7400	1605.7383	1.07	0	(74)	0.00017	1	K.DNNPVGNFATTVSDR.S
☑	2057	846.4699	1690.9252	1690.9254	-0.06	0	(92)	1.8e-006	1	K.VYSVIQSQINAALSAK.Q
☑	2059	846.4701	1690.9256	1690.9254	0.17	0	(77)	5.2e-005	1	K.VYSVIQSQINAALSAK.Q
☑	2060	564.6492	1690.9258	1690.9254	0.25	0	(35)	0.89	1	K.VYSVIQSQINAALSAK.Q
☑	2061	564.6492	1690.9258	1690.9254	0.25	0	(55)	0.0073	1	K.VYSVIQSQINAALSAK.Q
☑	2062	564.6493	1690.9261	1690.9254	0.42	0	(46)	0.073	1	K.VYSVIQSQINAALSAK.Q
☑	2063	564.6493	1690.9261	1690.9254	0.42	0	(46)	0.082	1	K.VYSVIQSQINAALSAK.Q
☑	2064	846.4704	1690.9262	1690.9254	0.53	0	120	2.8e-009	1	K.VYSVIQSQINAALSAK.Q
☑	2065	564.6494	1690.9264	1690.9254	0.60	0	(66)	0.00076	1	K.VYSVIQSQINAALSAK.Q
☑	2066	846.4705	1690.9264	1690.9254	0.65	0	(75)	9.1e-005	1	K.VYSVIQSQINAALSAK.Q
☑	2067	846.4705	1690.9264	1690.9254	0.65	0	(119)	4e-009	1	K.VYSVIQSQINAALSAK.Q
☑	2068	846.4705	1690.9264	1690.9254	0.65	0	(108)	4.2e-008	1	K.VYSVIQSQINAALSAK.Q
☑	2069	846.4706	1690.9266	1690.9254	0.77	0	(112)	1.7e-008	1	K.VYSVIQSQINAALSAK.Q
☑	2070	564.6495	1690.9267	1690.9254	0.78	0	(53)	0.014	1	K.VYSVIQSQINAALSAK.Q
☑	2071	564.6495	1690.9267	1690.9254	0.78	0	(50)	0.029	1	K.VYSVIQSQINAALSAK.Q
☑	2072	564.6495	1690.9267	1690.9254	0.78	0	(48)	0.047	1	K.VYSVIQSQINAALSAK.Q
☑	2073	564.6495	1690.9267	1690.9254	0.78	0	(62)	0.0019	1	K.VYSVIQSQINAALSAK.Q
☑	2074	564.6495	1690.9267	1690.9254	0.78	0	(51)	0.025	1	K.VYSVIQSQINAALSAK.Q
☑	2075	564.6495	1690.9267	1690.9254	0.78	0	(52)	0.018	1	K.VYSVIQSQINAALSAK.Q
☑	2076	846.4707	1690.9268	1690.9254	0.88	0	(95)	8.6e-007	1	K.VYSVIQSQINAALSAK.Q
☑	2077	846.4707	1690.9268	1690.9254	0.88	0	(102)	1.9e-007	1	K.VYSVIQSQINAALSAK.Q
☑	2078	846.4707	1690.9268	1690.9254	0.88	0	(99)	3.2e-007	1	K.VYSVIQSQINAALSAK.Q
☑	2079	564.6496	1690.9270	1690.9254	0.96	0	(51)	0.023	1	K.VYSVIQSQINAALSAK.Q
☑	2080	564.6496	1690.9270	1690.9254	0.96	0	(76)	7.6e-005	1	K.VYSVIQSQINAALSAK.Q
☑	2081	564.6496	1690.9270	1690.9254	0.96	0	(66)	0.00081	1	K.VYSVIQSQINAALSAK.Q
☑	2082	564.6496	1690.9270	1690.9254	0.96	0	(67)	0.0006	1	K.VYSVIQSQINAALSAK.Q
☑	2083	564.6496	1690.9270	1690.9254	0.96	0	(51)	0.024	1	K.VYSVIQSQINAALSAK.Q
☑	2084	846.4708	1690.9270	1690.9254	1.00	0	(106)	8e-008	1	K.VYSVIQSQINAALSAK.Q
☑	2085	846.4709	1690.9272	1690.9254	1.12	0	(95)	8.1e-007	1	K.VYSVIQSQINAALSAK.Q
☑	2086	846.4709	1690.9272	1690.9254	1.12	0	(92)	1.8e-006	1	K.VYSVIQSQINAALSAK.Q

☑	2087	564.6497	1690.9273	1690.9254	1.13	0	(52)	0.019	1		K.VYSVIQSQINAALSAK.Q
☑	2088	846.4710	1690.9274	1690.9254	1.24	0	(106)	8e-008	1		K.VYSVIQSQINAALSAK.Q
☑	2089	846.4710	1690.9274	1690.9254	1.24	0	(102)	1.8e-007	1		K.VYSVIQSQINAALSAK.Q
☑	2090	564.6498	1690.9276	1690.9254	1.31	0	(59)	0.004	1		K.VYSVIQSQINAALSAK.Q
☑	2091	564.6498	1690.9276	1690.9254	1.31	0	(65)	0.00093	1		K.VYSVIQSQINAALSAK.Q
☑	2092	564.6498	1690.9276	1690.9254	1.31	0	(58)	0.0047	1		K.VYSVIQSQINAALSAK.Q
☑	2093	846.4711	1690.9276	1690.9254	1.36	0	(96)	6.9e-007	1		K.VYSVIQSQINAALSAK.Q
☑	2094	846.4711	1690.9276	1690.9254	1.36	0	(92)	2.1e-006	1		K.VYSVIQSQINAALSAK.Q
☑	2095	846.4711	1690.9276	1690.9254	1.36	0	(98)	5.1e-007	1		K.VYSVIQSQINAALSAK.Q
☑	2096	846.4711	1690.9276	1690.9254	1.36	0	(104)	1.1e-007	1		K.VYSVIQSQINAALSAK.Q
☑	2097	846.4712	1690.9278	1690.9254	1.47	0	(101)	2.4e-007	1		K.VYSVIQSQINAALSAK.Q
☑	2098	846.4712	1690.9278	1690.9254	1.47	0	(106)	7.2e-008	1		K.VYSVIQSQINAALSAK.Q
☑	2099	846.4713	1690.9280	1690.9254	1.59	0	(104)	1.1e-007	1		K.VYSVIQSQINAALSAK.Q
☑	2100	846.4713	1690.9280	1690.9254	1.59	0	(108)	4.6e-008	1		K.VYSVIQSQINAALSAK.Q
☑	2101	846.4713	1690.9280	1690.9254	1.59	0	(110)	2.7e-008	1		K.VYSVIQSQINAALSAK.Q
☑	2102	846.4714	1690.9282	1690.9254	1.71	0	(102)	1.9e-007	1		K.VYSVIQSQINAALSAK.Q
☑	2103	564.6502	1690.9288	1690.9254	2.02	0	(53)	0.014	1		K.VYSVIQSQINAALSAK.Q
☑	2105	564.6508	1690.9306	1690.9254	3.09	0	(30)	3.5	1		K.VYSVIQSQINAALSAK.Q
☑	2277	592.0109	1773.0109	1773.0148	-2.24	0	(45)	0.037	1		R.IVLAHAGQPLSEAQVLK.A
☑	2278	592.0117	1773.0133	1773.0148	-0.89	0	(44)	0.043	1		R.IVLAHAGQPLSEAQVLK.A
☑	2280	592.0118	1773.0136	1773.0148	-0.72	0	(42)	0.066	1		R.IVLAHAGQPLSEAQVLK.A
☑	2281	592.0120	1773.0142	1773.0148	-0.38	0	(33)	0.57	1		R.IVLAHAGQPLSEAQVLK.A
☑	2282	592.0120	1773.0142	1773.0148	-0.38	0	(28)	1.8	1		R.IVLAHAGQPLSEAQVLK.A
☑	2283	887.5146	1773.0146	1773.0148	-0.11	0	(69)	0.00014	1		R.IVLAHAGQPLSEAQVLK.A
☑	2284	887.5146	1773.0146	1773.0148	-0.11	0	(60)	0.0011	1		R.IVLAHAGQPLSEAQVLK.A
☑	2285	592.0122	1773.0148	1773.0148	-0.04	0	(28)	1.8	1		R.IVLAHAGQPLSEAQVLK.A
☑	2286	592.0122	1773.0148	1773.0148	-0.04	0	(37)	0.18	1		R.IVLAHAGQPLSEAQVLK.A
☑	2287	887.5148	1773.0150	1773.0148	0.11	0	(42)	0.067	1		R.IVLAHAGQPLSEAQVLK.A
☑	2288	592.0123	1773.0151	1773.0148	0.13	0	(49)	0.012	1		R.IVLAHAGQPLSEAQVLK.A
☑	2289	592.0123	1773.0151	1773.0148	0.13	0	(45)	0.029	1		R.IVLAHAGQPLSEAQVLK.A
☑	2290	592.0123	1773.0151	1773.0148	0.13	0	(35)	0.29	1		R.IVLAHAGQPLSEAQVLK.A
☑	2291	592.0123	1773.0151	1773.0148	0.13	0	(24)	3.5	1		R.IVLAHAGQPLSEAQVLK.A
☑	2292	592.0124	1773.0154	1773.0148	0.30	0	(30)	1.1	1		R.IVLAHAGQPLSEAQVLK.A
☑	2293	592.0124	1773.0154	1773.0148	0.30	0	(37)	0.24	1		R.IVLAHAGQPLSEAQVLK.A
☑	2294	592.0124	1773.0154	1773.0148	0.30	0	(32)	0.69	1		R.IVLAHAGQPLSEAQVLK.A
☑	2295	592.0125	1773.0157	1773.0148	0.47	0	(42)	0.07	1		R.IVLAHAGQPLSEAQVLK.A
☑	2296	592.0126	1773.0160	1773.0148	0.63	0	(29)	1.2	1		R.IVLAHAGQPLSEAQVLK.A
☑	2297	592.0126	1773.0160	1773.0148	0.63	0	(28)	1.8	1		R.IVLAHAGQPLSEAQVLK.A
☑	2298	592.0126	1773.0160	1773.0148	0.63	0	(42)	0.065	1		R.IVLAHAGQPLSEAQVLK.A
☑	2299	592.0126	1773.0160	1773.0148	0.63	0	(39)	0.12	1		R.IVLAHAGQPLSEAQVLK.A
☑	2300	887.5153	1773.0160	1773.0148	0.68	0	(51)	0.0084	1		R.IVLAHAGQPLSEAQVLK.A
☑	2301	887.5153	1773.0160	1773.0148	0.68	0	74	3.9e-005	1		R.IVLAHAGQPLSEAQVLK.A
☑	2302	887.5154	1773.0162	1773.0148	0.79	0	(54)	0.0038	1		R.IVLAHAGQPLSEAQVLK.A
☑	2303	592.0127	1773.0163	1773.0148	0.80	0	(40)	0.1	1		R.IVLAHAGQPLSEAQVLK.A
☑	2304	592.0127	1773.0163	1773.0148	0.80	0	(38)	0.18	1		R.IVLAHAGQPLSEAQVLK.A
☑	2305	887.5156	1773.0166	1773.0148	1.02	0	(54)	0.0045	1		R.IVLAHAGQPLSEAQVLK.A
☑	2306	592.0129	1773.0169	1773.0148	1.14	0	(39)	0.15	1		R.IVLAHAGQPLSEAQVLK.A
☑	2307	887.5160	1773.0174	1773.0148	1.47	0	(68)	0.00018	1		R.IVLAHAGQPLSEAQVLK.A
☑	2308	592.0131	1773.0175	1773.0148	1.48	0	(25)	3.7	1		R.IVLAHAGQPLSEAQVLK.A
☑	2309	592.0132	1773.0178	1773.0148	1.65	0	(30)	1.1	1		R.IVLAHAGQPLSEAQVLK.A
☑	2310	592.0132	1773.0178	1773.0148	1.65	0	(29)	1.4	1		R.IVLAHAGQPLSEAQVLK.A
☑	2311	887.5170	1773.0194	1773.0148	2.60	0	(43)	0.066	1		R.IVLAHAGQPLSEAQVLK.A
☑	2312	592.0138	1773.0196	1773.0148	2.66	0	(46)	0.029	1		R.IVLAHAGQPLSEAQVLK.A
☑	2313	887.5171	1773.0196	1773.0148	2.71	0	(29)	1.7	1		R.IVLAHAGQPLSEAQVLK.A
☑	2462	928.9492	1855.8838	1855.8840	-0.06	0	(58)	0.0082	1	U	K.DSPEYALLSNLDTFSGK.L
☑	2463	619.6356	1855.8850	1855.8840	0.55	0	(27)	9.1	1	U	K.DSPEYALLSNLDTFSGK.L
☑	2464	928.9503	1855.8860	1855.8840	1.13	0	106	1.4e-007	1	U	K.DSPEYALLSNLDTFSGK.L
☑	2465	619.6360	1855.8862	1855.8840	1.19	0	(72)	0.00035	1	U	K.DSPEYALLSNLDTFSGK.L
☑	2711	712.3669	2134.0789	2134.0794	-0.24	1	(52)	0.04	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2712	712.3671	2134.0795	2134.0794	0.04	1	(23)	27	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2713	712.3672	2134.0798	2134.0794	0.18	1	(56)	0.014	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2714	712.3674	2134.0804	2134.0794	0.46	1	(33)	3.2	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2715	712.3676	2134.0810	2134.0794	0.74	1	(33)	3.4	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2716	712.3676	2134.0810	2134.0794	0.74	1	(34)	2.4	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2717	712.3676	2134.0810	2134.0794	0.74	1	(58)	0.009	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2718	1068.0480	2134.0814	2134.0794	0.96	1	(46)	0.14	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2719	1068.0480	2134.0814	2134.0794	0.96	1	95	1.7e-006	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2720	1068.0480	2134.0814	2134.0794	0.96	1	(91)	4.6e-006	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2721	712.3679	2134.0819	2134.0794	1.16	1	(37)	0.99	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2722	712.3679	2134.0819	2134.0794	1.16	1	(52)	0.038	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2723	712.3680	2134.0822	2134.0794	1.30	1	(29)	6.7	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2724	712.3680	2134.0822	2134.0794	1.30	1	(53)	0.03	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2725	712.3680	2134.0822	2134.0794	1.30	1	(40)	0.64	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2726	712.3681	2134.0825	2134.0794	1.44	1	(60)	0.005	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2727	712.3682	2134.0828	2134.0794	1.58	1	(53)	0.03	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2728	712.3685	2134.0837	2134.0794	2.01	1	(60)	0.0065	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2729	712.3688	2134.0846	2134.0794	2.43	1	(20)	56	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2730	712.3690	2134.0852	2134.0794	2.71	1	(27)	13	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2731	712.3698	2134.0876	2134.0794	3.83	1	(35)	1.9	1		R.LDEDVIGVYKDVLQTQDGK.R
☑	2740	716.0714	2145.1924	2145.1906	0.84	1	37	0.29	1		K.VYSVIQSQINAALSAKQGIR.I
☑	2784	1086.0350	2170.0554	2170.0582	-1.28	1	(100)	5.2e-007	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2785	1086.0360	2170.0574	2170.0582	-0.36	1	(65)	0.0018	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2786	724.3598	2170.0576	2170.0582	-0.30	1	(48)	0.087	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2787	724.3602	2170.0588	2170.0582	0.25	1	(56)	0.014	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2788	724.3604	2170.0594	2170.0582	0.53	1	(50)	0.051	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2789	1086.0370	2170.0594	2170.0582	0.56	1	(54)	0.024	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2790	1086.0370	2170.0594	2170.0582	0.56	1	(71)	0.00045	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2791	1086.0370	2170.0594	2170.0582	0.56	1	(48)	0.096	1	U	R.WKDSPEYALLSNLDTFSGK.L

☑	2792	1086.0370	2170.0594	2170.0582	0.56	1	(92)	3.7e-006	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2793	724.3605	2170.0597	2170.0582	0.67	1	(44)	0.22	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2794	724.3607	2170.0603	2170.0582	0.94	1	(43)	0.31	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2795	724.3607	2170.0603	2170.0582	0.94	1	(48)	0.099	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2796	724.3608	2170.0606	2170.0582	1.08	1	(56)	0.014	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2797	724.3608	2170.0606	2170.0582	1.08	1	(41)	0.4	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2798	724.3608	2170.0606	2170.0582	1.08	1	(53)	0.029	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2799	724.3608	2170.0606	2170.0582	1.08	1	(36)	1.3	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2800	724.3608	2170.0606	2170.0582	1.08	1	(46)	0.13	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2801	724.3608	2170.0606	2170.0582	1.08	1	(46)	0.13	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2802	724.3608	2170.0606	2170.0582	1.08	1	(42)	0.34	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2803	724.3610	2170.0612	2170.0582	1.36	1	(51)	0.042	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2804	724.3610	2170.0612	2170.0582	1.36	1	(41)	0.47	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2805	1086.0380	2170.0614	2170.0582	1.48	1	(69)	0.00075	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2806	1086.0380	2170.0614	2170.0582	1.48	1	112	3.4e-008	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2807	724.3613	2170.0621	2170.0582	1.77	1	(41)	0.5	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2808	724.3617	2170.0633	2170.0582	2.32	1	(46)	0.12	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2809	1086.0390	2170.0634	2170.0582	2.41	1	(79)	7.5e-005	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2810	1086.0390	2170.0634	2170.0582	2.41	1	(67)	0.0012	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2811	724.3620	2170.0642	2170.0582	2.74	1	(36)	1.4	1	U	R.WKDSPEYALLSNLDTFSGK.L
☑	2924	742.3766	2224.1080	2224.1084	-0.17	1	43	0.3	1		K.TTLLNDTSSRYNSAVEALNR.F
☑	2969	1122.6290	2243.2434	2243.2426	0.38	0	(48)	0.024	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2970	1122.6290	2243.2434	2243.2426	0.38	0	(46)	0.039	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2971	1122.6290	2243.2434	2243.2426	0.38	0	(58)	0.0025	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2972	1122.6290	2243.2434	2243.2426	0.38	0	(67)	0.00034	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2973	748.7555	2243.2447	2243.2426	0.92	0	(31)	1.4	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2974	1122.6300	2243.2454	2243.2426	1.27	0	88	2.6e-006	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2975	1122.6300	2243.2454	2243.2426	1.27	0	(46)	0.041	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2976	1122.6300	2243.2454	2243.2426	1.27	0	(45)	0.048	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2977	1122.6300	2243.2454	2243.2426	1.27	0	(58)	0.0026	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2978	1122.6300	2243.2454	2243.2426	1.27	0	(58)	0.0023	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2979	1122.6300	2243.2454	2243.2426	1.27	0	(68)	0.00022	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2980	748.7558	2243.2456	2243.2426	1.33	0	(31)	1.3	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2981	748.7558	2243.2456	2243.2426	1.33	0	(49)	0.018	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2982	748.7558	2243.2456	2243.2426	1.33	0	(51)	0.012	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2983	748.7558	2243.2456	2243.2426	1.33	0	(58)	0.0028	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2984	748.7560	2243.2462	2243.2426	1.59	0	(28)	2.2	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2985	748.7560	2243.2462	2243.2426	1.59	0	(52)	0.01	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2986	748.7562	2243.2468	2243.2426	1.86	0	(55)	0.0051	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2987	748.7562	2243.2468	2243.2426	1.86	0	(35)	0.48	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2988	748.7563	2243.2471	2243.2426	1.99	0	(30)	1.6	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2989	748.7563	2243.2471	2243.2426	1.99	0	(62)	0.00093	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	2990	748.7573	2243.2501	2243.2426	3.33	0	(53)	0.0072	1		K.ALAWLLAANPSAPPGQGLEVLR.E
☑	3055	1139.0710	2276.1274	2276.1325	-2.22	0	93	3.3e-006	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3056	1139.0730	2276.1314	2276.1325	-0.46	0	(61)	0.0054	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3057	1139.0730	2276.1314	2276.1325	-0.46	0	(74)	0.00024	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3058	759.7184	2276.1334	2276.1325	0.39	0	(21)	56	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3059	1139.0740	2276.1334	2276.1325	0.42	0	(56)	0.016	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3060	1139.0740	2276.1334	2276.1325	0.42	0	(52)	0.039	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3061	759.7186	2276.1340	2276.1325	0.65	0	(29)	8.8	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3062	759.7187	2276.1343	2276.1325	0.78	0	(25)	20	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3063	759.7187	2276.1343	2276.1325	0.78	0	(38)	1	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3064	759.7189	2276.1349	2276.1325	1.05	0	(26)	15	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3065	759.7189	2276.1349	2276.1325	1.05	0	(29)	7.8	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3066	1139.0750	2276.1354	2276.1325	1.30	0	(65)	0.0022	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3067	1139.0750	2276.1354	2276.1325	1.30	0	(86)	1.5e-005	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3068	1139.0750	2276.1354	2276.1325	1.30	0	(74)	0.00028	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3069	1139.0750	2276.1354	2276.1325	1.30	0	(80)	6.4e-005	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3070	759.7191	2276.1355	2276.1325	1.31	0	(28)	10	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3071	759.7191	2276.1355	2276.1325	1.31	0	(28)	11	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3072	759.7192	2276.1358	2276.1325	1.44	0	(34)	2.7	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3073	759.7194	2276.1364	2276.1325	1.70	0	(21)	55	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3074	1139.0760	2276.1374	2276.1325	2.18	0	(37)	1.2	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3075	1139.0760	2276.1374	2276.1325	2.18	0	(60)	0.0071	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3076	1139.0760	2276.1374	2276.1325	2.18	0	(70)	0.00064	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3077	759.7199	2276.1379	2276.1325	2.36	0	(36)	1.6	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3078	759.7202	2276.1388	2276.1325	2.76	0	(46)	0.18	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3079	1139.0770	2276.1394	2276.1325	3.06	0	(67)	0.0013	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
☑	3344	806.7914	2417.3524	2417.3529	-0.23	1	47	0.022	1		K.ALTAELKVYSVIQSQINAALSAK.Q
☑	3346	806.7927	2417.3563	2417.3529	1.39	1	(44)	0.037	1		K.ALTAELKVYSVIQSQINAALSAK.Q
☑	3412	911.1422	2730.4048	2730.3977	2.59	1	60	0.0043	1		K.QGIRIDAGGIDLVDPTLYGYAVGDPR.W
☑	3420	1386.6390	2771.2634	2771.2675	-1.45	1	60	0.0026	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3421	924.7623	2771.2651	2771.2675	-0.87	1	(35)	0.88	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3422	924.7626	2771.2660	2771.2675	-0.54	1	(42)	0.18	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3423	924.7630	2771.2672	2771.2675	-0.11	1	(29)	3.6	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3424	924.7635	2771.2687	2771.2675	0.43	1	(39)	0.36	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3425	924.7635	2771.2687	2771.2675	0.43	1	(46)	0.08	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3426	924.7636	2771.2690	2771.2675	0.54	1	(38)	0.48	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3427	924.7636	2771.2690	2771.2675	0.54	1	(36)	0.8	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3428	924.7636	2771.2690	2771.2675	0.54	1	(37)	0.58	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3429	924.7637	2771.2693	2771.2675	0.65	1	(39)	0.39	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3430	924.7637	2771.2693	2771.2675	0.65	1	(47)	0.055	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3431	924.7638	2771.2696	2771.2675	0.76	1	(46)	0.077	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3432	924.7639	2771.2699	2771.2675	0.87	1	(39)	0.37	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3433	924.7639	2771.2699	2771.2675	0.87	1	(41)	0.22	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3435	924.7640	2771.2702	2771.2675	0.97	1	(37)	0.59	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3436	924.7640	2771.2702	2771.2675	0.97	1	(45)	0.084	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3437	924.7640	2771.2702	2771.2675	0.97	1	(46)	0.077	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S

☑	3438	924.7641	2771.2705	2771.2675	1.08	1	(40)	0.29	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3439	924.7642	2771.2708	2771.2675	1.19	1	(44)	0.13	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3440	924.7643	2771.2711	2771.2675	1.30	1	(34)	1.2	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3441	924.7645	2771.2717	2771.2675	1.52	1	(50)	0.028	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3442	924.7645	2771.2717	2771.2675	1.52	1	(49)	0.038	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3443	924.7646	2771.2720	2771.2675	1.62	1	(48)	0.045	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3444	924.7648	2771.2726	2771.2675	1.84	1	(41)	0.23	1	U	K.GLSDEYPFEKDNNPVGNFATTVSDR.S
☑	3528	1442.2730	2882.5314	2882.5276	1.33	0	65	0.00075	1	U	R.ELFLDELLAASAAPASAEQEELLALLR.S
☑	3529	961.8517	2882.5333	2882.5276	1.96	0	(51)	0.021	1	U	R.ELFLDELLAASAAPASAEQEELLALLR.S

Proteins matching the same set of peptides:
gi|730481600 **Mass:** 32292 **Score:** 2258 **Matches:** 477(187) **Sequences:** 36(24)
type III secretion protein [Pseudomonas aeruginosa]
gi|734477586 **Mass:** 32234 **Score:** 2258 **Matches:** 477(187) **Sequences:** 36(24)
type III secretion protein PcrV [Pseudomonas aeruginosa]

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2. gi|685887085 **Mass:** 32277 **Score:** 1952 **Matches:** 385(153) **Sequences:** 32(20) **emPAI:** 7.47
type III secretion protein [Pseudomonas aeruginosa]
☐ 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
36	358.2086	714.4026	714.4024	0.32	0	34	9.8	1		R.EVLQAR.R
39	358.2088	714.4030	714.4024	0.88	0	(28)	33	3		R.EVLQAR.R
40	358.2089	714.4032	714.4024	1.16	0	(23)	1.1e+002	5		R.EVLQAR.R
76	373.2265	744.4384	744.4381	0.43	0	50	0.15	1		K.ALTAELK.V
77	376.6996	751.3846	751.3864	-2.39	0	(36)	2.1	1		K.YDSVLR.D
79	376.7002	751.3858	751.3864	-0.79	0	(34)	3.4	1		K.YDSVLR.D
80	376.7003	751.3860	751.3864	-0.53	0	(27)	16	1		K.YDSVLR.D
81	376.7003	751.3860	751.3864	-0.53	0	(25)	27	1		K.YDSVLR.D
83	376.7004	751.3862	751.3864	-0.26	0	(26)	20	1		K.YDSVLR.D
84	376.7004	751.3862	751.3864	-0.26	0	(34)	3.3	1		K.YDSVLR.D
85	376.7004	751.3862	751.3864	-0.26	0	(25)	27	1		K.YDSVLR.D
88	376.7004	751.3862	751.3864	-0.26	0	(36)	2.3	1		K.YDSVLR.D
90	376.7005	751.3864	751.3864	0.01	0	(25)	25	1		K.YDSVLR.D
91	376.7005	751.3864	751.3864	0.01	0	(23)	48	1		K.YDSVLR.D
92	376.7005	751.3864	751.3864	0.01	0	(28)	12	1		K.YDSVLR.D
93	376.7005	751.3864	751.3864	0.01	0	(34)	3.9	1		K.YDSVLR.D
94	376.7006	751.3866	751.3864	0.27	0	(28)	12	1		K.YDSVLR.D
95	376.7006	751.3866	751.3864	0.27	0	(23)	48	3		K.YDSVLR.D
96	376.7006	751.3866	751.3864	0.27	0	(25)	25	1		K.YDSVLR.D
97	376.7006	751.3866	751.3864	0.27	0	(38)	1.5	1		K.YDSVLR.D
98	376.7007	751.3868	751.3864	0.54	0	39	1.1	1		K.YDSVLR.D
99	376.7007	751.3868	751.3864	0.54	0	(27)	17	1		K.YDSVLR.D
100	376.7007	751.3868	751.3864	0.54	0	(24)	35	1		K.YDSVLR.D
101	376.7008	751.3870	751.3864	0.80	0	(29)	12	1		K.YDSVLR.D
102	376.7008	751.3870	751.3864	0.80	0	(28)	14	1		K.YDSVLR.D
173	401.2395	800.4644	800.4643	0.13	0	37	1.9	1		K.ALLDELK.A
178	401.2398	800.4650	800.4643	0.88	0	(36)	1.4	1		K.ALLDELK.A
179	401.2400	800.4654	800.4643	1.38	0	(25)	20	1		K.ALLDELK.A
222	415.2302	828.4458	828.4453	0.61	0	(29)	9.6	2		R.SRPLNDK.V
223	415.2303	828.4460	828.4453	0.85	0	(31)	6.1	4		R.SRPLNDK.V
224	415.2303	828.4460	828.4453	0.85	0	(31)	6.6	8		R.SRPLNDK.V
225	415.2307	828.4468	828.4453	1.82	0	32	5.7	3		R.SRPLNDK.V
254	425.7188	849.4230	849.4232	-0.22	0	(27)	12	1		K.DFLSGSPK.Q
256	425.7193	849.4240	849.4232	0.96	0	42	0.63	1		K.DFLSGSPK.Q
339	465.2863	928.5580	928.5593	-1.34	1	(32)	3.3	4		R.KALLDELK.A
342	465.2869	928.5592	928.5593	-0.05	1	53	0.029	1		R.KALLDELK.A
343	465.2870	928.5594	928.5593	0.16	1	(50)	0.062	1		R.KALLDELK.A
444	502.2563	1002.4980	1002.4982	-0.15	0	(46)	0.18	1		K.DVLQTQDGK.R
445	502.2565	1002.4984	1002.4982	0.25	0	51	0.07	1		K.DVLQTQDGK.R
559	535.7724	1069.5302	1069.5305	-0.22	0	(29)	7	1		R.QPGAQWDLR.E
560	535.7725	1069.5304	1069.5305	-0.04	0	(36)	1.3	1		R.QPGAQWDLR.E
561	535.7726	1069.5306	1069.5305	0.15	0	(22)	39	2		R.QPGAQWDLR.E
562	535.7727	1069.5308	1069.5305	0.34	0	(28)	8.8	2		R.QPGAQWDLR.E
563	535.7728	1069.5310	1069.5305	0.52	0	38	0.62	1		R.QPGAQWDLR.E
565	535.7729	1069.5312	1069.5305	0.71	0	(36)	1.1	1		R.QPGAQWDLR.E
634	554.2853	1106.5560	1106.5568	-0.65	0	(41)	0.35	1		K.TTLLNDTSSR.Y
635	554.2855	1106.5564	1106.5568	-0.28	0	(46)	0.2	1		K.TTLLNDTSSR.Y
636	554.2858	1106.5570	1106.5568	0.26	0	(31)	6.3	1		K.TTLLNDTSSR.Y
637	554.2859	1106.5572	1106.5568	0.44	0	(76)	0.00019	1		K.TTLLNDTSSR.Y
638	554.2859	1106.5572	1106.5568	0.44	0	(49)	0.1	1		K.TTLLNDTSSR.Y
639	554.2860	1106.5574	1106.5568	0.62	0	(49)	0.088	1		K.TTLLNDTSSR.Y
640	554.2861	1106.5576	1106.5568	0.80	0	83	4.3e-005	1		K.TTLLNDTSSR.Y
641	554.2861	1106.5576	1106.5568	0.80	0	(49)	0.095	1		K.TTLLNDTSSR.Y
642	554.2861	1106.5576	1106.5568	0.80	0	(64)	0.0028	1		K.TTLLNDTSSR.Y
643	554.2861	1106.5576	1106.5568	0.80	0	(56)	0.018	1		K.TTLLNDTSSR.Y
644	554.2862	1106.5578	1106.5568	0.98	0	(42)	0.6	1		K.TTLLNDTSSR.Y
645	554.2862	1106.5578	1106.5568	0.98	0	(60)	0.0085	1		K.TTLLNDTSSR.Y
646	554.2863	1106.5580	1106.5568	1.16	0	(74)	0.00038	1		K.TTLLNDTSSR.Y
647	554.2864	1106.5582	1106.5568	1.34	0	(71)	0.00072	1		K.TTLLNDTSSR.Y
648	554.2870	1106.5594	1106.5568	2.43	0	(58)	0.01	1		K.TTLLNDTSSR.Y
710	568.7873	1135.5600	1135.5621	-1.85	0	(64)	0.0021	1		R.YNSAVEALNR.F
712	568.7881	1135.5616	1135.5621	-0.44	0	(44)	0.25	1		R.YNSAVEALNR.F
713	568.7882	1135.5618	1135.5621	-0.27	0	(53)	0.035	1		R.YNSAVEALNR.F
714	568.7885	1135.5624	1135.5621	0.26	0	79	0.00011	1		R.YNSAVEALNR.F
715	568.7886	1135.5626	1135.5621	0.44	0	(76)	0.00017	1		R.YNSAVEALNR.F
716	568.7888	1135.5630	1135.5621	0.79	0	(70)	0.00064	1		R.YNSAVEALNR.F
717	568.7888	1135.5630	1135.5621	0.79	0	(51)	0.05	1		R.YNSAVEALNR.F
718	568.7888	1135.5630	1135.5621	0.79	0	(58)	0.01	1		R.YNSAVEALNR.F

719	568.7889	1135.5632	1135.5621	0.97	0	(45)	0.2	1	R.YNSAVEALNR.F
720	568.7889	1135.5632	1135.5621	0.97	0	(46)	0.19	1	R.YNSAVEALNR.F
721	568.7890	1135.5634	1135.5621	1.14	0	(47)	0.13	1	R.YNSAVEALNR.F
722	568.7891	1135.5636	1135.5621	1.32	0	(51)	0.047	1	R.YNSAVEALNR.F
723	568.7891	1135.5636	1135.5621	1.32	0	(59)	0.0084	1	R.YNSAVEALNR.F
724	568.7897	1135.5648	1135.5621	2.38	0	(57)	0.014	1	R.YNSAVEALNR.F
760	575.8026	1149.5906	1149.5918	-0.96	0	(61)	0.0049	1	R.LDEDVIGVYK.D
761	575.8034	1149.5922	1149.5918	0.43	0	(61)	0.0058	1	R.LDEDVIGVYK.D
762	575.8038	1149.5930	1149.5918	1.13	0	(39)	1	1	R.LDEDVIGVYK.D
763	575.8042	1149.5938	1149.5918	1.82	0	62	0.0035	1	R.LDEDVIGVYK.D
779	580.3071	1158.5996	1158.5993	0.30	1	(34)	3.5	1	K.DVLQTQDGKR.K
783	580.3074	1158.6002	1158.5993	0.81	1	(27)	15	2	K.DVLQTQDGKR.K
784	580.3074	1158.6002	1158.5993	0.81	1	(25)	24	2	K.DVLQTQDGKR.K
786	580.3074	1158.6002	1158.5993	0.81	1	(47)	0.16	1	K.DVLQTQDGKR.K
787	580.3075	1158.6004	1158.5993	0.99	1	54	0.034	1	K.DVLQTQDGKR.K
788	387.2082	1158.6028	1158.5993	2.99	1	(36)	2.6	1	K.DVLQTQDGKR.K
963	409.5509	1225.6309	1225.6316	-0.59	1	(24)	23	1	R.RQPGAQWDLR.E
964	409.5510	1225.6312	1225.6316	-0.34	1	(32)	3.3	1	R.RQPGAQWDLR.E
965	409.5510	1225.6312	1225.6316	-0.34	1	(40)	0.52	1	R.RQPGAQWDLR.E
966	409.5510	1225.6312	1225.6316	-0.34	1	(27)	12	1	R.RQPGAQWDLR.E
971	613.8230	1225.6314	1225.6316	-0.12	1	(25)	17	7	R.RQPGAQWDLR.E
972	409.5511	1225.6315	1225.6316	-0.10	1	(40)	0.61	1	R.RQPGAQWDLR.E
973	409.5511	1225.6315	1225.6316	-0.10	1	(38)	0.99	1	R.RQPGAQWDLR.E
974	409.5511	1225.6315	1225.6316	-0.10	1	53	0.028	1	R.RQPGAQWDLR.E
975	409.5511	1225.6315	1225.6316	-0.10	1	(41)	0.4	1	R.RQPGAQWDLR.E
976	409.5511	1225.6315	1225.6316	-0.10	1	(42)	0.39	1	R.RQPGAQWDLR.E
977	409.5511	1225.6315	1225.6316	-0.10	1	(39)	0.63	1	R.RQPGAQWDLR.E
978	409.5511	1225.6315	1225.6316	-0.10	1	(40)	0.58	1	R.RQPGAQWDLR.E
979	613.8231	1225.6316	1225.6316	0.05	1	(41)	0.45	1	R.RQPGAQWDLR.E
981	409.5512	1225.6318	1225.6316	0.15	1	(39)	0.72	1	R.RQPGAQWDLR.E
982	409.5512	1225.6318	1225.6316	0.15	1	(36)	1.5	1	R.RQPGAQWDLR.E
983	409.5512	1225.6318	1225.6316	0.15	1	(40)	0.58	1	R.RQPGAQWDLR.E
984	409.5512	1225.6318	1225.6316	0.15	1	(36)	1.3	1	R.RQPGAQWDLR.E
988	613.8232	1225.6318	1225.6316	0.21	1	(22)	35	1	R.RQPGAQWDLR.E
990	613.8233	1225.6320	1225.6316	0.37	1	(32)	4	2	R.RQPGAQWDLR.E
991	409.5513	1225.6321	1225.6316	0.39	1	(47)	0.11	1	R.RQPGAQWDLR.E
992	409.5513	1225.6321	1225.6316	0.39	1	(38)	0.98	1	R.RQPGAQWDLR.E
993	409.5513	1225.6321	1225.6316	0.39	1	(26)	12	1	R.RQPGAQWDLR.E
994	409.5513	1225.6321	1225.6316	0.39	1	(27)	11	1	R.RQPGAQWDLR.E
995	409.5513	1225.6321	1225.6316	0.39	1	(36)	1.3	1	R.RQPGAQWDLR.E
996	409.5513	1225.6321	1225.6316	0.39	1	(31)	4.8	1	R.RQPGAQWDLR.E
997	409.5513	1225.6321	1225.6316	0.39	1	(34)	2.2	1	R.RQPGAQWDLR.E
998	409.5513	1225.6321	1225.6316	0.39	1	(41)	0.45	1	R.RQPGAQWDLR.E
999	409.5513	1225.6321	1225.6316	0.39	1	(35)	1.7	1	R.RQPGAQWDLR.E
1000	409.5513	1225.6321	1225.6316	0.39	1	(43)	0.27	1	R.RQPGAQWDLR.E
1001	409.5513	1225.6321	1225.6316	0.39	1	(44)	0.23	1	R.RQPGAQWDLR.E
1002	409.5513	1225.6321	1225.6316	0.39	1	(31)	4.2	1	R.RQPGAQWDLR.E
1006	613.8234	1225.6322	1225.6316	0.54	1	(21)	44	6	R.RQPGAQWDLR.E
1007	409.5514	1225.6324	1225.6316	0.64	1	(34)	2.5	1	R.RQPGAQWDLR.E
1008	409.5514	1225.6324	1225.6316	0.64	1	(35)	1.7	1	R.RQPGAQWDLR.E
1009	409.5514	1225.6324	1225.6316	0.64	1	(45)	0.19	1	R.RQPGAQWDLR.E
1010	409.5514	1225.6324	1225.6316	0.64	1	(38)	0.86	1	R.RQPGAQWDLR.E
1018	409.5515	1225.6327	1225.6316	0.88	1	(47)	0.11	1	R.RQPGAQWDLR.E
1019	409.5515	1225.6327	1225.6316	0.88	1	(45)	0.14	1	R.RQPGAQWDLR.E
1020	409.5515	1225.6327	1225.6316	0.88	1	(39)	0.59	1	R.RQPGAQWDLR.E
1022	613.8240	1225.6334	1225.6316	1.51	1	(31)	4.3	1	R.RQPGAQWDLR.E
1024	409.5519	1225.6339	1225.6316	1.86	1	(39)	0.7	1	R.RQPGAQWDLR.E
1025	613.8243	1225.6340	1225.6316	2.00	1	(32)	4	1	R.RQPGAQWDLR.E
1169	634.8540	1267.6934	1267.6925	0.78	1	42	0.27	1	R.FIQKYDSVLR.D
1238	646.3661	1290.7176	1290.7183	-0.53	1	(51)	0.033	1	K.LSIKDFLSGSPK.Q
1239	431.2465	1290.7177	1290.7183	-0.52	1	(23)	18	1	K.LSIKDFLSGSPK.Q
1240	646.3662	1290.7178	1290.7183	-0.38	1	(44)	0.14	1	K.LSIKDFLSGSPK.Q
1241	646.3663	1290.7180	1290.7183	-0.22	1	(50)	0.048	1	K.LSIKDFLSGSPK.Q
1242	431.2467	1290.7183	1290.7183	-0.05	1	(28)	7.3	1	K.LSIKDFLSGSPK.Q
1243	646.3665	1290.7184	1290.7183	0.09	1	(67)	0.00084	1	K.LSIKDFLSGSPK.Q
1244	646.3665	1290.7184	1290.7183	0.09	1	(22)	29	1	K.LSIKDFLSGSPK.Q
1245	646.3665	1290.7184	1290.7183	0.09	1	(64)	0.0017	1	K.LSIKDFLSGSPK.Q
1248	431.2468	1290.7186	1290.7183	0.18	1	(28)	7.1	1	K.LSIKDFLSGSPK.Q
1249	431.2468	1290.7186	1290.7183	0.18	1	(28)	6.5	1	K.LSIKDFLSGSPK.Q
1251	646.3666	1290.7186	1290.7183	0.24	1	(43)	0.21	1	K.LSIKDFLSGSPK.Q
1252	646.3666	1290.7186	1290.7183	0.24	1	(65)	0.0015	1	K.LSIKDFLSGSPK.Q
1253	646.3666	1290.7186	1290.7183	0.24	1	(46)	0.1	1	K.LSIKDFLSGSPK.Q
1254	646.3666	1290.7186	1290.7183	0.24	1	(65)	0.0013	1	K.LSIKDFLSGSPK.Q
1255	646.3667	1290.7188	1290.7183	0.40	1	(65)	0.0012	1	K.LSIKDFLSGSPK.Q
1256	431.2469	1290.7189	1290.7183	0.41	1	(21)	32	1	K.LSIKDFLSGSPK.Q
1258	646.3668	1290.7190	1290.7183	0.55	1	(43)	0.23	1	K.LSIKDFLSGSPK.Q
1259	646.3668	1290.7190	1290.7183	0.55	1	(71)	0.00038	1	K.LSIKDFLSGSPK.Q
1260	431.2470	1290.7192	1290.7183	0.65	1	(25)	12	1	K.LSIKDFLSGSPK.Q
1261	646.3669	1290.7192	1290.7183	0.71	1	(68)	0.00069	1	K.LSIKDFLSGSPK.Q
1262	646.3670	1290.7194	1290.7183	0.86	1	(68)	0.00062	1	K.LSIKDFLSGSPK.Q
1263	431.2471	1290.7195	1290.7183	0.88	1	(37)	0.85	1	K.LSIKDFLSGSPK.Q
1264	646.3671	1290.7196	1290.7183	1.01	1	(55)	0.013	1	K.LSIKDFLSGSPK.Q
1265	646.3671	1290.7196	1290.7183	1.01	1	(60)	0.0038	1	K.LSIKDFLSGSPK.Q
1266	646.3671	1290.7196	1290.7183	1.01	1	(45)	0.14	1	K.LSIKDFLSGSPK.Q
1267	431.2472	1290.7198	1290.7183	1.11	1	(30)	4.1	1	K.LSIKDFLSGSPK.Q
1268	646.3672	1290.7198	1290.7183	1.17	1	(42)	0.25	1	K.LSIKDFLSGSPK.Q
1269	646.3672	1290.7198	1290.7183	1.17	1	(58)	0.0074	1	K.LSIKDFLSGSPK.Q
1270	646.3672	1290.7198	1290.7183	1.17	1	75	0.00014	1	K.LSIKDFLSGSPK.Q
1271	646.3674	1290.7202	1290.7183	1.48	1	(47)	0.089	1	K.LSIKDFLSGSPK.Q
1287	650.3521	1298.6896	1298.6942	-3.53	1	(36)	1.6	1	R.SRPLNDKVNEK.T

1288	650.3528	1298.6910	1298.6942	-2.45	1	(25)	21	5	R.SRPLNDKVNEK.T
1289	433.9044	1298.6914	1298.6942	-2.20	1	(21)	48	1	R.SRPLNDKVNEK.T
1291	650.3532	1298.6918	1298.6942	-1.83	1	(47)	0.12	1	R.SRPLNDKVNEK.T
1293	433.9047	1298.6923	1298.6942	-1.51	1	(33)	2.5	1	R.SRPLNDKVNEK.T
1295	433.9048	1298.6926	1298.6942	-1.28	1	(33)	2.3	1	R.SRPLNDKVNEK.T
1296	433.9049	1298.6929	1298.6942	-1.04	1	(33)	2.4	1	R.SRPLNDKVNEK.T
1297	433.9049	1298.6929	1298.6942	-1.04	1	(26)	13	1	R.SRPLNDKVNEK.T
1298	433.9050	1298.6932	1298.6942	-0.81	1	(26)	16	1	R.SRPLNDKVNEK.T
1299	433.9051	1298.6935	1298.6942	-0.58	1	(27)	12	1	R.SRPLNDKVNEK.T
1300	433.9051	1298.6935	1298.6942	-0.58	1	(39)	0.72	1	R.SRPLNDKVNEK.T
1302	433.9051	1298.6935	1298.6942	-0.58	1	(37)	1.4	1	R.SRPLNDKVNEK.T
1303	433.9051	1298.6935	1298.6942	-0.58	1	(28)	11	1	R.SRPLNDKVNEK.T
1304	433.9051	1298.6935	1298.6942	-0.58	1	(43)	0.33	1	R.SRPLNDKVNEK.T
1305	433.9052	1298.6938	1298.6942	-0.35	1	(27)	12	1	R.SRPLNDKVNEK.T
1306	433.9052	1298.6938	1298.6942	-0.35	1	(29)	8.5	1	R.SRPLNDKVNEK.T
1307	433.9052	1298.6938	1298.6942	-0.35	1	(35)	2.1	1	R.SRPLNDKVNEK.T
1308	433.9052	1298.6938	1298.6942	-0.35	1	(31)	4.7	1	R.SRPLNDKVNEK.T
1309	433.9052	1298.6938	1298.6942	-0.35	1	(23)	31	2	R.SRPLNDKVNEK.T
1310	433.9052	1298.6938	1298.6942	-0.35	1	(29)	7.6	1	R.SRPLNDKVNEK.T
1313	433.9053	1298.6941	1298.6942	-0.12	1	(24)	22	1	R.SRPLNDKVNEK.T
1314	433.9053	1298.6941	1298.6942	-0.12	1	(34)	2.4	1	R.SRPLNDKVNEK.T
1315	433.9053	1298.6941	1298.6942	-0.12	1	(25)	20	1	R.SRPLNDKVNEK.T
1316	433.9053	1298.6941	1298.6942	-0.12	1	(31)	4.6	1	R.SRPLNDKVNEK.T
1317	433.9054	1298.6944	1298.6942	0.11	1	(20)	61	1	R.SRPLNDKVNEK.T
1318	433.9054	1298.6944	1298.6942	0.11	1	(26)	16	2	R.SRPLNDKVNEK.T
1319	433.9054	1298.6944	1298.6942	0.11	1	(30)	5.9	1	R.SRPLNDKVNEK.T
1320	433.9054	1298.6944	1298.6942	0.11	1	(36)	1.5	1	R.SRPLNDKVNEK.T
1321	433.9054	1298.6944	1298.6942	0.11	1	(32)	4.2	1	R.SRPLNDKVNEK.T
1322	433.9054	1298.6944	1298.6942	0.11	1	(27)	11	1	R.SRPLNDKVNEK.T
1323	433.9054	1298.6944	1298.6942	0.11	1	(28)	10	1	R.SRPLNDKVNEK.T
1324	433.9054	1298.6944	1298.6942	0.11	1	(31)	5	1	R.SRPLNDKVNEK.T
1325	433.9054	1298.6944	1298.6942	0.11	1	(26)	15	2	R.SRPLNDKVNEK.T
1326	650.3546	1298.6946	1298.6942	0.32	1	(57)	0.011	1	R.SRPLNDKVNEK.T
1327	433.9055	1298.6947	1298.6942	0.34	1	(22)	40	2	R.SRPLNDKVNEK.T
1328	433.9055	1298.6947	1298.6942	0.34	1	(31)	5.6	1	R.SRPLNDKVNEK.T
1329	433.9055	1298.6947	1298.6942	0.34	1	(26)	16	1	R.SRPLNDKVNEK.T
1330	433.9055	1298.6947	1298.6942	0.34	1	(31)	5	1	R.SRPLNDKVNEK.T
1331	433.9055	1298.6947	1298.6942	0.34	1	(34)	2.7	1	R.SRPLNDKVNEK.T
1332	433.9055	1298.6947	1298.6942	0.34	1	(28)	11	1	R.SRPLNDKVNEK.T
1333	433.9055	1298.6947	1298.6942	0.34	1	(23)	34	2	R.SRPLNDKVNEK.T
1334	433.9055	1298.6947	1298.6942	0.34	1	(29)	7.7	1	R.SRPLNDKVNEK.T
1335	650.3547	1298.6948	1298.6942	0.48	1	(57)	0.012	1	R.SRPLNDKVNEK.T
1336	433.9056	1298.6950	1298.6942	0.57	1	(34)	2.5	1	R.SRPLNDKVNEK.T
1337	433.9056	1298.6950	1298.6942	0.57	1	(32)	3.5	1	R.SRPLNDKVNEK.T
1338	433.9056	1298.6950	1298.6942	0.57	1	(40)	0.59	1	R.SRPLNDKVNEK.T
1339	433.9056	1298.6950	1298.6942	0.57	1	(37)	1.1	1	R.SRPLNDKVNEK.T
1340	433.9056	1298.6950	1298.6942	0.57	1	(29)	8.2	1	R.SRPLNDKVNEK.T
1342	650.3549	1298.6952	1298.6942	0.78	1	(44)	0.28	1	R.SRPLNDKVNEK.T
1343	650.3550	1298.6954	1298.6942	0.94	1	(24)	28	1	R.SRPLNDKVNEK.T
1344	433.9058	1298.6956	1298.6942	1.03	1	(40)	0.59	1	R.SRPLNDKVNEK.T
1345	433.9058	1298.6956	1298.6942	1.03	1	(24)	25	1	R.SRPLNDKVNEK.T
1346	650.3551	1298.6956	1298.6942	1.09	1	59	0.0077	1	R.SRPLNDKVNEK.T
1347	650.3553	1298.6960	1298.6942	1.40	1	(36)	1.6	1	R.SRPLNDKVNEK.T
1348	650.3553	1298.6960	1298.6942	1.40	1	(51)	0.046	1	R.SRPLNDKVNEK.T
1349	650.3554	1298.6962	1298.6942	1.55	1	(43)	0.31	1	R.SRPLNDKVNEK.T
1350	650.3554	1298.6962	1298.6942	1.55	1	(58)	0.0093	1	R.SRPLNDKVNEK.T
1351	650.3555	1298.6964	1298.6942	1.71	1	(44)	0.27	1	R.SRPLNDKVNEK.T
1579	682.8749	1363.7352	1363.7347	0.39	1	(39)	0.57	1	K.YDSVLRDILSAI.-
1580	682.8752	1363.7358	1363.7347	0.83	1	(37)	1	1	K.YDSVLRDILSAI.-
1581	682.8752	1363.7358	1363.7347	0.83	1	51	0.039	1	K.YDSVLRDILSAI.-
1582	682.8755	1363.7364	1363.7347	1.27	1	(47)	0.091	1	K.YDSVLRDILSAI.-
1796	763.3928	1524.7710	1524.7725	-0.96	0	(46)	0.13	1	R.EFLVSAYFSLHGR.L
1797	763.3929	1524.7712	1524.7725	-0.83	0	(64)	0.002	1	R.EFLVSAYFSLHGR.L
1798	763.3932	1524.7718	1524.7725	-0.43	0	90	5.3e-006	1	R.EFLVSAYFSLHGR.L
1799	763.3934	1524.7722	1524.7725	-0.17	0	(74)	0.00019	1	R.EFLVSAYFSLHGR.L
1800	763.3934	1524.7722	1524.7725	-0.17	0	(67)	0.0011	1	R.EFLVSAYFSLHGR.L
1802	763.3936	1524.7726	1524.7725	0.09	0	(80)	5.8e-005	1	R.EFLVSAYFSLHGR.L
1803	509.2650	1524.7732	1524.7725	0.44	0	(54)	0.024	1	R.EFLVSAYFSLHGR.L
1804	509.2650	1524.7732	1524.7725	0.44	0	(34)	2.4	1	R.EFLVSAYFSLHGR.L
1806	509.2651	1524.7735	1524.7725	0.63	0	(40)	0.56	1	R.EFLVSAYFSLHGR.L
1807	509.2651	1524.7735	1524.7725	0.63	0	(27)	12	1	R.EFLVSAYFSLHGR.L
1808	509.2651	1524.7735	1524.7725	0.63	0	(47)	0.13	1	R.EFLVSAYFSLHGR.L
1809	509.2651	1524.7735	1524.7725	0.63	0	(39)	0.82	1	R.EFLVSAYFSLHGR.L
1810	509.2651	1524.7735	1524.7725	0.63	0	(39)	0.71	1	R.EFLVSAYFSLHGR.L
1811	509.2651	1524.7735	1524.7725	0.63	0	(33)	3.1	1	R.EFLVSAYFSLHGR.L
1812	509.2651	1524.7735	1524.7725	0.63	0	(49)	0.07	1	R.EFLVSAYFSLHGR.L
1813	509.2651	1524.7735	1524.7725	0.63	0	(44)	0.25	1	R.EFLVSAYFSLHGR.L
1814	509.2651	1524.7735	1524.7725	0.63	0	(48)	0.1	1	R.EFLVSAYFSLHGR.L
1815	509.2651	1524.7735	1524.7725	0.63	0	(50)	0.063	1	R.EFLVSAYFSLHGR.L
1817	509.2652	1524.7738	1524.7725	0.83	0	(40)	0.71	1	R.EFLVSAYFSLHGR.L
1818	509.2652	1524.7738	1524.7725	0.83	0	(39)	0.84	1	R.EFLVSAYFSLHGR.L
1819	509.2652	1524.7738	1524.7725	0.83	0	(43)	0.33	1	R.EFLVSAYFSLHGR.L
1820	509.2652	1524.7738	1524.7725	0.83	0	(29)	8.9	1	R.EFLVSAYFSLHGR.L
1821	509.2652	1524.7738	1524.7725	0.83	0	(43)	0.36	1	R.EFLVSAYFSLHGR.L
1822	509.2652	1524.7738	1524.7725	0.83	0	(28)	11	1	R.EFLVSAYFSLHGR.L
1823	509.2652	1524.7738	1524.7725	0.83	0	(27)	13	1	R.EFLVSAYFSLHGR.L
1824	763.3942	1524.7738	1524.7725	0.88	0	(60)	0.0059	1	R.EFLVSAYFSLHGR.L
1825	763.3943	1524.7740	1524.7725	1.01	0	(68)	0.0011	1	R.EFLVSAYFSLHGR.L
1826	763.3943	1524.7740	1524.7725	1.01	0	(64)	0.0025	1	R.EFLVSAYFSLHGR.L
1827	509.2653	1524.7741	1524.7725	1.03	0	(41)	0.54	1	R.EFLVSAYFSLHGR.L

	1829	763.3945	1524.7744	1524.7725	1.27	0	(60)	0.0068	1		R.EFLVSAYFSLHGR.L
	1830	763.3945	1524.7744	1524.7725	1.27	0	(56)	0.017	1		R.EFLVSAYFSLHGR.L
	1831	763.3946	1524.7746	1524.7725	1.40	0	(69)	0.0006	1		R.EFLVSAYFSLHGR.L
	1832	763.3946	1524.7746	1524.7725	1.40	0	(72)	0.00035	1		R.EFLVSAYFSLHGR.L
	1833	763.3947	1524.7748	1524.7725	1.54	0	(67)	0.00091	1		R.EFLVSAYFSLHGR.L
	1834	763.3947	1524.7748	1524.7725	1.54	0	(66)	0.0013	1		R.EFLVSAYFSLHGR.L
	1835	763.3948	1524.7750	1524.7725	1.67	0	(73)	0.00024	1		R.EFLVSAYFSLHGR.L
	1836	763.3948	1524.7750	1524.7725	1.67	0	(49)	0.066	1		R.EFLVSAYFSLHGR.L
	1840	764.4536	1526.8926	1526.8919	0.49	1	45	0.036	1		K.ALLDELKALTAELK.V
	1918	526.6100	1576.8082	1576.8056	1.60	1	35	2.6	1		K.VNEKTTLLNDTSSR.Y
	1965	803.8762	1605.7378	1605.7383	-0.30	0	(63)	0.0017	1		K.DNNPVGNFATTVSDR.S
	1966	803.8762	1605.7378	1605.7383	-0.30	0	(61)	0.003	1		K.DNNPVGNFATTVSDR.S
	1967	803.8766	1605.7386	1605.7383	0.20	0	96	8.1e-007	1		K.DNNPVGNFATTVSDR.S
	1968	803.8773	1605.7400	1605.7383	1.07	0	(74)	0.00017	1		K.DNNPVGNFATTVSDR.S
	2057	846.4699	1690.9252	1690.9254	-0.06	0	(92)	1.8e-006	1		K.VYSVIQSQINAALSAK.Q
	2059	846.4701	1690.9256	1690.9254	0.17	0	(77)	5.2e-005	1		K.VYSVIQSQINAALSAK.Q
	2060	564.6492	1690.9258	1690.9254	0.25	0	(35)	0.89	1		K.VYSVIQSQINAALSAK.Q
	2061	564.6492	1690.9258	1690.9254	0.25	0	(55)	0.0073	1		K.VYSVIQSQINAALSAK.Q
	2062	564.6493	1690.9261	1690.9254	0.42	0	(46)	0.073	1		K.VYSVIQSQINAALSAK.Q
	2063	564.6493	1690.9261	1690.9254	0.42	0	(46)	0.082	1		K.VYSVIQSQINAALSAK.Q
	2064	846.4704	1690.9262	1690.9254	0.53	0	120	2.8e-009	1		K.VYSVIQSQINAALSAK.Q
	2065	564.6494	1690.9264	1690.9254	0.60	0	(66)	0.00076	1		K.VYSVIQSQINAALSAK.Q
	2066	846.4705	1690.9264	1690.9254	0.65	0	(75)	9.1e-005	1		K.VYSVIQSQINAALSAK.Q
	2067	846.4705	1690.9264	1690.9254	0.65	0	(119)	4e-009	1		K.VYSVIQSQINAALSAK.Q
	2068	846.4705	1690.9264	1690.9254	0.65	0	(108)	4.2e-008	1		K.VYSVIQSQINAALSAK.Q
	2069	846.4706	1690.9266	1690.9254	0.77	0	(112)	1.7e-008	1		K.VYSVIQSQINAALSAK.Q
	2070	564.6495	1690.9267	1690.9254	0.78	0	(53)	0.014	1		K.VYSVIQSQINAALSAK.Q
	2071	564.6495	1690.9267	1690.9254	0.78	0	(50)	0.029	1		K.VYSVIQSQINAALSAK.Q
	2072	564.6495	1690.9267	1690.9254	0.78	0	(48)	0.047	1		K.VYSVIQSQINAALSAK.Q
	2073	564.6495	1690.9267	1690.9254	0.78	0	(62)	0.0019	1		K.VYSVIQSQINAALSAK.Q
	2074	564.6495	1690.9267	1690.9254	0.78	0	(51)	0.025	1		K.VYSVIQSQINAALSAK.Q
	2075	564.6495	1690.9267	1690.9254	0.78	0	(52)	0.018	1		K.VYSVIQSQINAALSAK.Q
	2076	846.4707	1690.9268	1690.9254	0.88	0	(95)	8.6e-007	1		K.VYSVIQSQINAALSAK.Q
	2077	846.4707	1690.9268	1690.9254	0.88	0	(102)	1.9e-007	1		K.VYSVIQSQINAALSAK.Q
	2078	846.4707	1690.9268	1690.9254	0.88	0	(99)	3.2e-007	1		K.VYSVIQSQINAALSAK.Q
	2079	564.6496	1690.9270	1690.9254	0.96	0	(51)	0.023	1		K.VYSVIQSQINAALSAK.Q
	2080	564.6496	1690.9270	1690.9254	0.96	0	(76)	7.6e-005	1		K.VYSVIQSQINAALSAK.Q
	2081	564.6496	1690.9270	1690.9254	0.96	0	(66)	0.00081	1		K.VYSVIQSQINAALSAK.Q
	2082	564.6496	1690.9270	1690.9254	0.96	0	(67)	0.0006	1		K.VYSVIQSQINAALSAK.Q
	2083	564.6496	1690.9270	1690.9254	0.96	0	(51)	0.024	1		K.VYSVIQSQINAALSAK.Q
	2084	846.4708	1690.9270	1690.9254	1.00	0	(106)	8e-008	1		K.VYSVIQSQINAALSAK.Q
	2085	846.4709	1690.9272	1690.9254	1.12	0	(95)	8.1e-007	1		K.VYSVIQSQINAALSAK.Q
	2086	846.4709	1690.9272	1690.9254	1.12	0	(92)	1.8e-006	1		K.VYSVIQSQINAALSAK.Q
	2087	564.6497	1690.9273	1690.9254	1.13	0	(52)	0.019	1		K.VYSVIQSQINAALSAK.Q
	2088	846.4710	1690.9274	1690.9254	1.24	0	(106)	8e-008	1		K.VYSVIQSQINAALSAK.Q
	2089	846.4710	1690.9274	1690.9254	1.24	0	(102)	1.8e-007	1		K.VYSVIQSQINAALSAK.Q
	2090	564.6498	1690.9276	1690.9254	1.31	0	(59)	0.004	1		K.VYSVIQSQINAALSAK.Q
	2091	564.6498	1690.9276	1690.9254	1.31	0	(65)	0.00093	1		K.VYSVIQSQINAALSAK.Q
	2092	564.6498	1690.9276	1690.9254	1.31	0	(58)	0.0047	1		K.VYSVIQSQINAALSAK.Q
	2093	846.4711	1690.9276	1690.9254	1.36	0	(96)	6.9e-007	1		K.VYSVIQSQINAALSAK.Q
	2094	846.4711	1690.9276	1690.9254	1.36	0	(92)	2.1e-006	1		K.VYSVIQSQINAALSAK.Q
	2095	846.4711	1690.9276	1690.9254	1.36	0	(98)	5.1e-007	1		K.VYSVIQSQINAALSAK.Q
	2096	846.4711	1690.9276	1690.9254	1.36	0	(104)	1.1e-007	1		K.VYSVIQSQINAALSAK.Q
	2097	846.4712	1690.9278	1690.9254	1.47	0	(101)	2.4e-007	1		K.VYSVIQSQINAALSAK.Q
	2098	846.4712	1690.9278	1690.9254	1.47	0	(106)	7.2e-008	1		K.VYSVIQSQINAALSAK.Q
	2099	846.4713	1690.9280	1690.9254	1.59	0	(104)	1.1e-007	1		K.VYSVIQSQINAALSAK.Q
	2100	846.4713	1690.9280	1690.9254	1.59	0	(108)	4.6e-008	1		K.VYSVIQSQINAALSAK.Q
	2101	846.4713	1690.9280	1690.9254	1.59	0	(110)	2.7e-008	1		K.VYSVIQSQINAALSAK.Q
	2102	846.4714	1690.9282	1690.9254	1.71	0	(102)	1.9e-007	1		K.VYSVIQSQINAALSAK.Q
	2103	564.6502	1690.9288	1690.9254	2.02	0	(53)	0.014	1		K.VYSVIQSQINAALSAK.Q
	2105	564.6508	1690.9306	1690.9254	3.09	0	(30)	3.5	1		K.VYSVIQSQINAALSAK.Q
☑	2367	**899.9454**	**1797.8762**	**1797.8785**	**-1.24**	**0**	**74**	**0.00025**	**1**		**K.GSPEYALLSNLDTFSGK.L**
☑	2693	**1059.5810**	**2117.1474**	**2117.1480**	**-0.28**	**0**	**98**	**4.3e-007**	**1**	**U**	**R.SEQIVLAHAGQPLSEAQVLK.A**
☑	2694	**706.7238**	**2117.1496**	**2117.1480**	**0.72**	**0**	**(52)**	**0.016**	**1**	**U**	**R.SEQIVLAHAGQPLSEAQVLK.A**
	2711	712.3669	2134.0789	2134.0794	-0.24	1	(52)	0.04	1		R.LDEDVIGVYKDVLQTQDGK.R
	2712	712.3671	2134.0795	2134.0794	0.04	1	(23)	27	1		R.LDEDVIGVYKDVLQTQDGK.R
	2713	712.3672	2134.0798	2134.0794	0.18	1	(56)	0.014	1		R.LDEDVIGVYKDVLQTQDGK.R
	2714	712.3674	2134.0804	2134.0794	0.46	1	(33)	3.2	1		R.LDEDVIGVYKDVLQTQDGK.R
	2715	712.3676	2134.0810	2134.0794	0.74	1	(33)	3.4	1		R.LDEDVIGVYKDVLQTQDGK.R
	2716	712.3676	2134.0810	2134.0794	0.74	1	(34)	2.4	1		R.LDEDVIGVYKDVLQTQDGK.R
	2717	712.3676	2134.0810	2134.0794	0.74	1	(58)	0.009	1		R.LDEDVIGVYKDVLQTQDGK.R
	2718	1068.0480	2134.0814	2134.0794	0.96	1	(46)	0.14	1		R.LDEDVIGVYKDVLQTQDGK.R
	2719	1068.0480	2134.0814	2134.0794	0.96	1	95	1.7e-006	1		R.LDEDVIGVYKDVLQTQDGK.R
	2720	1068.0480	2134.0814	2134.0794	0.96	1	(91)	4.6e-006	1		R.LDEDVIGVYKDVLQTQDGK.R
	2721	712.3679	2134.0819	2134.0794	1.16	1	(37)	0.99	1		R.LDEDVIGVYKDVLQTQDGK.R
	2722	712.3679	2134.0819	2134.0794	1.16	1	(52)	0.038	1		R.LDEDVIGVYKDVLQTQDGK.R
	2723	712.3680	2134.0822	2134.0794	1.30	1	(29)	6.7	1		R.LDEDVIGVYKDVLQTQDGK.R
	2724	712.3680	2134.0822	2134.0794	1.30	1	(53)	0.03	1		R.LDEDVIGVYKDVLQTQDGK.R
	2725	712.3680	2134.0822	2134.0794	1.30	1	(40)	0.64	1		R.LDEDVIGVYKDVLQTQDGK.R
	2726	712.3681	2134.0825	2134.0794	1.44	1	(60)	0.005	1		R.LDEDVIGVYKDVLQTQDGK.R
	2727	712.3682	2134.0828	2134.0794	1.58	1	(53)	0.03	1		R.LDEDVIGVYKDVLQTQDGK.R
	2728	712.3685	2134.0837	2134.0794	2.01	1	(60)	0.0065	1		R.LDEDVIGVYKDVLQTQDGK.R
	2729	712.3688	2134.0846	2134.0794	2.43	1	(20)	56	1		R.LDEDVIGVYKDVLQTQDGK.R
	2730	712.3690	2134.0852	2134.0794	2.71	1	(27)	13	1		R.LDEDVIGVYKDVLQTQDGK.R
	2731	712.3698	2134.0876	2134.0794	3.83	1	(35)	1.9	1		R.LDEDVIGVYKDVLQTQDGK.R
	2740	716.0714	2145.1924	2145.1906	0.84	1	37	0.29	1		K.VYSVIQSQINAALSAKQGIR.I
	2924	742.3766	2224.1080	2224.1084	-0.17	1	43	0.3	1		K.TTLLNDTSSRYNSAVEALNR.F
	2969	1122.6290	2243.2434	2243.2426	0.38	0	(48)	0.024	1		K.ALAWLLAANPSAPPGQGLEVLR.E
	2970	1122.6290	2243.2434	2243.2426	0.38	0	(46)	0.039	1		K.ALAWLLAANPSAPPGQGLEVLR.E
	2971	1122.6290	2243.2434	2243.2426	0.38	0	(58)	0.0025	1		K.ALAWLLAANPSAPPGQGLEVLR.E

2972	1122.6290	2243.2434	2243.2426	0.38	0	(67)	0.00034	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2973	748.7555	2243.2447	2243.2426	0.92	0	(31)	1.4	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2974	1122.6300	2243.2454	2243.2426	1.27	0	88	2.6e-006	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2975	1122.6300	2243.2454	2243.2426	1.27	0	(46)	0.041	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2976	1122.6300	2243.2454	2243.2426	1.27	0	(45)	0.048	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2977	1122.6300	2243.2454	2243.2426	1.27	0	(58)	0.0026	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2978	1122.6300	2243.2454	2243.2426	1.27	0	(58)	0.0023	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2979	1122.6300	2243.2454	2243.2426	1.27	0	(68)	0.00022	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2980	748.7558	2243.2456	2243.2426	1.33	0	(31)	1.3	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2981	748.7558	2243.2456	2243.2426	1.33	0	(49)	0.018	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2982	748.7558	2243.2456	2243.2426	1.33	0	(51)	0.012	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2983	748.7558	2243.2456	2243.2426	1.33	0	(58)	0.0028	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2984	748.7560	2243.2462	2243.2426	1.59	0	(28)	2.2	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2985	748.7560	2243.2462	2243.2426	1.59	0	(52)	0.01	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2986	748.7562	2243.2468	2243.2426	1.86	0	(55)	0.0051	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2987	748.7562	2243.2468	2243.2426	1.86	0	(35)	0.48	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2988	748.7563	2243.2471	2243.2426	1.99	0	(30)	1.6	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2989	748.7563	2243.2471	2243.2426	1.99	0	(62)	0.00093	1		K.ALAWLLAANPSAPPGQGLEVLR.E
2990	748.7573	2243.2501	2243.2426	3.33	0	(53)	0.0072	1		K.ALAWLLAANPSAPPGQGLEVLR.E
3055	1139.0710	2276.1274	2276.1325	-2.22	0	93	3.3e-006	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3056	1139.0730	2276.1314	2276.1325	-0.46	0	(61)	0.0054	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3057	1139.0730	2276.1314	2276.1325	-0.46	0	(74)	0.00024	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3058	759.7184	2276.1334	2276.1325	0.39	0	(21)	56	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3059	1139.0740	2276.1334	2276.1325	0.42	0	(56)	0.016	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3060	1139.0740	2276.1334	2276.1325	0.42	0	(52)	0.039	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3061	759.7186	2276.1340	2276.1325	0.65	0	(29)	8.8	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3062	759.7187	2276.1343	2276.1325	0.78	0	(25)	20	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3063	759.7187	2276.1343	2276.1325	0.78	0	(38)	1	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3064	759.7189	2276.1349	2276.1325	1.05	0	(26)	15	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3065	759.7189	2276.1349	2276.1325	1.05	0	(29)	7.8	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3066	1139.0750	2276.1354	2276.1325	1.30	0	(65)	0.0022	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3067	1139.0750	2276.1354	2276.1325	1.30	0	(86)	1.5e-005	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3068	1139.0750	2276.1354	2276.1325	1.30	0	(74)	0.00028	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3069	1139.0750	2276.1354	2276.1325	1.30	0	(80)	6.4e-005	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3070	759.7191	2276.1355	2276.1325	1.31	0	(28)	10	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3071	759.7191	2276.1355	2276.1325	1.31	0	(28)	11	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3072	759.7192	2276.1358	2276.1325	1.44	0	(34)	2.7	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3073	759.7194	2276.1364	2276.1325	1.70	0	(21)	55	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3074	1139.0760	2276.1374	2276.1325	2.18	0	(37)	1.2	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3075	1139.0760	2276.1374	2276.1325	2.18	0	(60)	0.0071	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3076	1139.0760	2276.1374	2276.1325	2.18	0	(70)	0.00064	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3077	759.7199	2276.1379	2276.1325	2.36	0	(36)	1.6	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3078	759.7202	2276.1388	2276.1325	2.76	0	(46)	0.18	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3079	1139.0770	2276.1394	2276.1325	3.06	0	(67)	0.0013	1		R.IDAGGIDLVDPTLYGYAVGDPR.W
3344	806.7914	2417.3524	2417.3529	-0.23	1	47	0.022	1		K.ALTAELKVYSVIQSQINAALSAK.Q
3346	806.7927	2417.3563	2417.3529	1.39	1	(44)	0.037	1		K.ALTAELKVYSVIQSQINAALSAK.Q
3412	911.1422	2730.4048	2730.3977	2.59	1	60	0.0043	1		K.QGIRIDAGGIDLVDPTLYGYAVGDPR.W

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3. gi|62952892 **Mass:** 53160 **Score:** 559 **Matches:** 13(4) **Sequences:** 12(4) **emPAI:** 0.30

capsule protein fraction 1/virulence antigen fusion protein precursor [synthetic construct]

☐ 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
☑	137	387.2290	772.4434	772.4443	-1.09	0	30	24	1	U	R.TGALGNLK.N
☑	233	418.7126	835.4106	835.4109	-0.34	0	31	7	1	U	K.SINL<u>M</u>DK.N + Oxidation (M)
	542	533.2698	1064.5250	1064.5251	-0.01	1	40	0.75	3	U	K.DFLGSENKR.T
☑	543	533.2700	1064.5254	1064.5251	0.37	1	55	0.025	1	U	R.KDSEVFANR.V
☑	778	579.8334	1157.6522	1157.6543	-1.81	0	35	2	1	U	R.VITDDIELLK.K
☑	1699	470.2430	1407.7072	1407.7106	-2.46	0	49	0.086	1	U	K.HLSSSGTINIHDK.S
☑	1700	704.8631	1407.7116	1407.7106	0.72	0	(35)	1.8	1	U	K.HLSSSGTINIHDK.S
☑	1750	725.3500	1448.6854	1448.6817	2.58	0	64	0.0019	1	U	K.<u>M</u>PQTTIQVDGSEK.K + Oxidation (M)
☑	1773	746.3544	1490.6942	1490.6929	0.90	0	59	0.0058	1	U	K.NLYGYTDEEIFK.A
☑	1790	757.9247	1513.8348	1513.8351	-0.18	1	67	0.00076	1	U	K.LREELAELTAELK.I
☑	2475	620.9637	1859.8693	1859.8690	0.17	0	35	1.3	1	U	R.AYEQNPQHFIEDLEK.V
☑	2579	981.9999	1961.9852	1961.9847	0.30	1	50	0.07	1	U	R.VKEFLESSPNTQWELR.A
☑	2774	722.4001	2164.1785	2164.1739	2.09	0	46	0.067	1	U	R.VEQLTGHGSSVLEELVQLVK.D

Proteins matching the same set of peptides:

gi|115394488 **Mass:** 37471 **Score:** 559 **Matches:** 13(4) **Sequences:** 12(4)
V antigen [synthetic construct]
gi|488141773 **Mass:** 37217 **Score:** 559 **Matches:** 13(4) **Sequences:** 12(4)
virulence factor [Yersinia pestis]
gi|499485355 **Mass:** 37101 **Score:** 559 **Matches:** 13(4) **Sequences:** 12(4)
virulence factor [Yersinia pestis]

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4. gi|490890815 **Mass:** 44141 **Score:** 105 **Matches:** 2(1) **Sequences:** 2(1) **emPAI:** 0.08

GTPase CgtA [Acinetobacter sp. ANC 3789]

☐ 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
	76	373.2265	744.4384	744.4381	0.43	0	50	0.15	1	U	K.AITAELK.K
☑	270	437.2737	872.5328	872.5331	-0.27	1	55	0.016	1	U	K.AITAELKK.F

Proteins matching the same set of peptides:

gi|740190021 **Mass:** 35946 **Score:** 105 **Matches:** 2(1) **Sequences:** 2(1)
hypothetical protein [Thermonema rossianum]

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5. gi|457874719 **Mass:** 42464 **Score:** 105 **Matches:** 3(1) **Sequences:** 3(1) **emPAI:** 0.09
hypothetical protein PCYB_002770 [Plasmodium cynomolgi strain B]
☐ 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
☑	59	365.7208	729.4270	729.4272	-0.25	0	32	10	1	U	K.IIDELK.R
	289	443.7715	885.5284	885.5283	0.13	1	21	1.1e+002	2	U	K.IIDELKR.H
	342	465.2869	928.5592	928.5593	-0.05	1	52	0.034	8	U	K.AKIIDELK.R

Proteins matching the same set of peptides:
gi|457877872 **Mass:** 40177 **Score:** 105 **Matches:** 3(1) **Sequences:** 3(1)
hypothetical protein PCYB_006250 [Plasmodium cynomolgi strain B]

6. gi|489248865 **Mass:** 36677 **Score:** 93 **Matches:** 3(0) **Sequences:** 2(0)
hypothetical protein [Pseudomonas aeruginosa]
☐ 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
☑	263	429.7504	857.4862	857.4858	0.51	0	45	0.35	1	U	K.ALLDELGK.V
	425	493.7973	985.5800	985.5808	-0.73	1	(40)	0.63	6	U	R.KALLDELGK.V
	426	493.7973	985.5800	985.5808	-0.73	1	48	0.11	2	U	R.KALLDELGK.V

Proteins matching the same set of peptides:
gi|489379926 **Mass:** 36693 **Score:** 93 **Matches:** 3(0) **Sequences:** 2(0)
hypothetical protein [Pseudomonas stutzeri]
gi|497299350 **Mass:** 36337 **Score:** 93 **Matches:** 3(0) **Sequences:** 2(0)
protein Ssg [Pseudomonas sp. M1]
gi|501025578 **Mass:** 37964 **Score:** 93 **Matches:** 3(0) **Sequences:** 2(0)
hypothetical protein [Pseudomonas aeruginosa]
gi|505292099 **Mass:** 36578 **Score:** 93 **Matches:** 3(0) **Sequences:** 2(0)
hypothetical protein [Pseudomonas denitrificans]
gi|516089869 **Mass:** 36389 **Score:** 93 **Matches:** 3(0) **Sequences:** 2(0)
protein Ssg [Pseudomonas nitroreducens]
gi|664811807 **Mass:** 36612 **Score:** 93 **Matches:** 3(0) **Sequences:** 2(0)
glycosyltransferase [Pseudomonas sp. AAC]
gi|730722014 **Mass:** 36649 **Score:** 93 **Matches:** 3(0) **Sequences:** 2(0)
glycosyltransferase [Pseudomonas aeruginosa]

7. gi|50304509 **Mass:** 57260 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1) **emPAI:** 0.06
hypothetical protein [Kluyveromyces lactis NRRL Y-1140]
☐ 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
☑	172	401.2392	800.4638	800.4643	-0.61	0	(35)	3.2	1	U	K.AIIDELK.V
	173	401.2395	800.4644	800.4643	0.13	0	37	1.9	1	U	K.AIIDELK.V
☑	174	401.2395	800.4644	800.4643	0.13	0	(36)	2.8	1	U	K.AIIDELK.V
☑	175	401.2397	800.4648	800.4643	0.63	0	(34)	3.6	1	U	K.AIIDELK.V
☑	176	401.2398	800.4650	800.4643	0.88	0	(35)	1.9	1	U	K.AIIDELK.V
	178	401.2398	800.4650	800.4643	0.88	0	(36)	1.4	1	U	K.AIIDELK.V
	179	401.2400	800.4654	800.4643	1.38	0	(25)	20	1	U	K.AIIDELK.V
	339	465.2863	928.5580	928.5593	-1.34	1	(32)	3.3	4	U	K.KAIIDELK.V
☑	340	465.2868	928.5590	928.5593	-0.27	1	54	0.021	1	U	K.KAIIDELK.V
	341	465.2868	928.5590	928.5593	-0.27	1	(35)	1.8	3	U	K.KAIIDELK.V
	342	465.2869	928.5592	928.5593	-0.05	1	(53)	0.029	1	U	K.KAIIDELK.V
	343	465.2870	928.5594	928.5593	0.16	1	(50)	0.062	1	U	K.KAIIDELK.V
☑	344	465.2870	928.5594	928.5593	0.16	1	(52)	0.04	1	U	K.KAIIDELK.V
	345	465.2873	928.5600	928.5593	0.81	1	(39)	0.71	7	U	K.KAIIDELK.V

Proteins matching the same set of peptides:
gi|491932069 **Mass:** 39667 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
mannonate oxidoreductase [Bacteroides caccae]
gi|491940013 **Mass:** 39717 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
mannonate oxidoreductase [Bacteroides caccae]
gi|496035219 **Mass:** 39975 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
mannonate oxidoreductase [Bacteroides sp. 1_1_14]
gi|496039455 **Mass:** 39965 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
MULTISPECIES: mannonate oxidoreductase [Bacteroides]
gi|499030058 **Mass:** 14602 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
PREDICTED: protein C19orf12-like [Maylandia zebra]
gi|503589086 **Mass:** 138576 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
subtilisin [Desulfotomaculum kuznetsovii]
gi|511014227 **Mass:** 39961 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
hypothetical protein [Bacteroides thetaiotaomicron]
gi|517451928 **Mass:** 50687 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
hypothetical protein [Gardnerella vaginalis]
gi|518091175 **Mass:** 50617 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
hypothetical protein [Gardnerella vaginalis]
gi|547309708 **Mass:** 39701 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
uncharacterized protein [Bacteroides caccae CAG:21]
gi|548252685 **Mass:** 39974 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
putative DNA mismatch repair protein [Bacteroides thetaiotaomicron CAG:40]
gi|548348266 **Mass:** 11621 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
PREDICTED: protein C19orf12 homolog [Pundamilia nyererei]
gi|554826909 **Mass:** 11522 **Score:** 92 **Matches:** 14(3) **Sequences:** 2(1)
PREDICTED: protein C19orf12 homolog [Haplochromis burtoni]

8. gi|700303716 **Mass:** 46160 **Score:** 80 **Matches:** 3(1) **Sequences:** 2(1) **emPAI:** 0.08
hypothetical protein TEU_09445 [Thermococcus eurythermalis]
☐ 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
☑	**262**	**429.7502**	**857.4858**	**857.4858**	**0.05**	**0**	**30**	**11**	**1**	**U**	**K.ALLDGELK.K**
☑	425	493.7973	985.5800	985.5808	-0.73	1	52	0.046	1	U	K.KALLDGELK.K
☑	426	493.7973	985.5800	985.5808	-0.73	1	(49)	0.089	1	U	K.KALLDGELK.K

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9. gi|312207957 **Mass:** 33418 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1) **emPAI:** 0.11
Chain A, Crystal Structure Of The Salmonella Type Iii Secretion System Tip Protein Sipd
☐ 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
☑	**1721**	**711.8887**	**1421.7628**	**1421.7613**	**1.07**	**0**	**76**	**0.00012**	**1**	**U**	**K.VLSSTISSSLETAK.S**

Proteins matching the same set of peptides:
gi|312207959 **Mass:** 33402 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Chain A, Crystal Structure Of The Salmonella Type Iii Secretion System Tip Protein Sipd-C244s
gi|343781050 **Mass:** 25459 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Chain A, Truncated Sipd From Salmonella Typhimurium
gi|343781052 **Mass:** 37371 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Chain A, Sipd From Salmonella Typhimurium
gi|343781317 **Mass:** 33113 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Chain A, Prgi-Sipd From Salmonella Typhimurium
gi|353568350 **Mass:** 25469 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD, partial [Salmonella enterica subsp. enterica serovar Gaminara str. A4-567]
gi|353569572 **Mass:** 4450 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD, partial [Salmonella enterica subsp. enterica serovar Alachua str. R6-377]
gi|353579414 **Mass:** 25207 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD, partial [Salmonella enterica subsp. enterica serovar Adelaide str. A4-669]
gi|353596252 **Mass:** 30642 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD, partial [Salmonella enterica subsp. enterica serovar Inverness str. R8-3668]
gi|353606539 **Mass:** 24527 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD, partial [Salmonella enterica subsp. enterica serovar Johannesburg str. S5-703]
gi|353610102 **Mass:** 24155 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD, partial [Salmonella enterica subsp. enterica serovar Minnesota str. A4-603]
gi|353637485 **Mass:** 23622 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD [Salmonella enterica subsp. enterica serovar Rubislaw str. A4-653]
gi|353638021 **Mass:** 24221 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD [Salmonella enterica subsp. enterica serovar Senftenberg str. A4-543]
gi|353661026 **Mass:** 24266 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
Cell invasion protein SipD [Salmonella enterica subsp. enterica serovar Wandsworth str. A4-580]
gi|381307082 **Mass:** 28189 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica subsp. enterica serovar Heidelberg str. 41573]
gi|435339085 **Mass:** 26967 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD, partial [Salmonella enterica subsp. enterica serovar Enteritidis str. 6.0562-1]
gi|445990657 **Mass:** 23666 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell division protein FtsQ [Salmonella enterica]
gi|446854984 **Mass:** 36483 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854985 **Mass:** 37047 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854986 **Mass:** 37020 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854987 **Mass:** 36526 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854988 **Mass:** 36523 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854989 **Mass:** 37049 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854990 **Mass:** 37090 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854992 **Mass:** 37095 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854993 **Mass:** 37081 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854994 **Mass:** 36480 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854995 **Mass:** 36508 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446854999 **Mass:** 36522 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446855000 **Mass:** 36466 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446855001 **Mass:** 36510 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446855002 **Mass:** 36383 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella bongori]
gi|446855003 **Mass:** 36542 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446855004 **Mass:** 36374 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446855005 **Mass:** 36454 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|446975728 **Mass:** 11598 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)

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hypothetical protein [Salmonella enterica]
gi|486164633    Mass: 36510    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|486185730    Mass: 37110    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|486381881    Mass: 25128    Score: 76     Matches: 1(1)  Sequences: 1(1)
Cell invasion protein SipD, partial [Salmonella enterica]
gi|487364299    Mass: 21953    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell division protein FtsQ [Salmonella enterica]
gi|487366748    Mass: 21951    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell division protein FtsQ [Salmonella enterica]
gi|487381055    Mass: 22533    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell division protein FtsQ [Salmonella enterica]
gi|487525687    Mass: 15697    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD, partial [Salmonella enterica]
gi|487580045    Mass: 24755    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD, partial [Salmonella enterica]
gi|487595947    Mass: 36522    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|489044084    Mass: 36498    Score: 76     Matches: 1(1)  Sequences: 1(1)
Cell invasion protein sipD [Salmonella enterica]
gi|501175654    Mass: 33700    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|513037986    Mass: 36514    Score: 76     Matches: 1(1)  Sequences: 1(1)
pathogenicity island 1 effector protein [Salmonella enterica]
gi|515086747    Mass: 37097    Score: 76     Matches: 1(1)  Sequences: 1(1)
type III effector protein IpaD/SipD/SspD [Salmonella enterica]
gi|516010559    Mass: 37039    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|526088020    Mass: 37111    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|526248995    Mass: 36491    Score: 76     Matches: 1(1)  Sequences: 1(1)
Cell invasion protein SipD [Salmonella bongori]
gi|527085191    Mass: 37067    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|549798998    Mass: 37061    Score: 76     Matches: 1(1)  Sequences: 1(1)
pathogenicity island 1 effector protein [Salmonella enterica]
gi|554669518    Mass: 37117    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|554679405    Mass: 36388    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|554684193    Mass: 36487    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|554691169    Mass: 36561    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|554922742    Mass: 37036    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|554957115    Mass: 36996    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|554957557    Mass: 37033    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|554960691    Mass: 37022    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|554961919    Mass: 37093    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|555219359    Mass: 36436    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|555221720    Mass: 36450    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|555236228    Mass: 36706    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|555243630    Mass: 37085    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|555248189    Mass: 37063    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|555251163    Mass: 37123    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|555267895    Mass: 36958    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|555272257    Mass: 12774    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD, partial [Salmonella enterica]
gi|555275751    Mass: 6358     Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD, partial [Salmonella enterica]
gi|555283842    Mass: 14523    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD, partial [Salmonella enterica]
gi|599840902    Mass: 4823     Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD, partial [Salmonella enterica subsp. enterica serovar Heidelberg str. SARA32]
gi|640127303    Mass: 36437    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|677859281    Mass: 14750    Score: 76     Matches: 1(1)  Sequences: 1(1)
hypothetical protein SEEB0208_21740, partial [Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000208]
gi|685251667    Mass: 21721    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD, partial [Salmonella enterica]
gi|694275216    Mass: 36790    Score: 76     Matches: 1(1)  Sequences: 1(1)
sipD [Salmonella enterica]
gi|740606894    Mass: 36907    Score: 76     Matches: 1(1)  Sequences: 1(1)
cell invasion protein SipD [Salmonella bongori]
gi|740609153    Mass: 36478    Score: 76     Matches: 1(1)  Sequences: 1(1)
```

cell invasion protein SipD [Salmonella enterica]
gi|740609973 **Mass:** 37056 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]
gi|740662518 **Mass:** 37116 **Score:** 76 **Matches:** 1(1) **Sequences:** 1(1)
cell invasion protein SipD [Salmonella enterica]

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10. gi|93279729 **Mass:** 12276 **Score:** 71 **Matches:** 4(0) **Sequences:** 2(0)
Chain A, Crystal Structure Of The Putative Transcriptional Regualator, Marr Family From Porphyromonas Gingivalis W83
☐ 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	401.2395	800.4644	800.4643	0.13	0	37	1.9	1	U	K.ALIDELK.F
	178	401.2398	800.4650	800.4643	0.88	0	(36)	1.4	1	U	K.ALIDELK.F
	179	401.2400	800.4654	800.4643	1.38	0	(25)	20	1	U	K.ALIDELK.F
☑	**210**	**414.2472**	**826.4798**	**826.4800**	**-0.18**	**0**	**33**	**1.8**	**1**	**U**	**K.PLIDELK.F**

Proteins matching the same set of peptides:
gi|657962441 **Mass:** 133330 **Score:** 71 **Matches:** 4(0) **Sequences:** 2(0)
PREDICTED: uncharacterized protein LOC103436169 [Malus domestica]

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11. gi|491901269 **Mass:** 25867 **Score:** 69 **Matches:** 8(0) **Sequences:** 2(0)
anaerobic ribonucleoside-triphosphate reductase activating protein [Dethiosulfovibrio peptidovorans]
☐ 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
	637	554.2859	1106.5572	1106.5608	-3.19	0	(29)	11	4	U	K.TTLIDYPER.I
	640	554.2861	1106.5576	1106.5608	-2.83	0	(32)	5.5	4	U	K.TTLIDYPER.I
	642	554.2861	1106.5576	1106.5608	-2.83	0	(30)	8.8	4	U	K.TTLIDYPER.I
	643	554.2861	1106.5576	1106.5608	-2.83	0	(25)	27	6	U	K.TTLIDYPER.I
	646	554.2863	1106.5580	1106.5608	-2.47	0	32	5	4	U	K.TTLIDYPER.I
	647	554.2864	1106.5582	1106.5608	-2.28	0	(31)	7.2	4	U	K.TTLIDYPER.I
	648	554.2870	1106.5594	1106.5608	-1.20	0	(25)	24	6	U	K.TTLIDYPER.I
☑	**1048**	**618.3334**	**1234.6522**	**1234.6557**	**-2.82**	**1**	**36**	**2**	**1**	**U**	**R.KTTLIDYPER.I**

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12. gi|146983 **Mass:** 26114 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
outer membrane protein II, partial [Escherichia fergusonii]
☐ 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
☑	**2014**	**827.9200**	**1653.8254**	**1653.8250**	**0.27**	**0**	**35**	**1.5**	**1**	**U**	**K.LGYPITDDLDIYTR.L**
☑	**2948**	**744.7275**	**2231.1607**	**2231.1586**	**0.92**	**0**	**32**	**2.8**	**1**	**U**	**R.FGQGEAAPVVAPAPAPAPEVQTK.H**

Proteins matching the same set of peptides:
gi|229485743 **Mass:** 26128 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
RecName: Full=Outer membrane protein A; AltName: Full=Outer membrane protein II, partial [Escherichia fergusonii]
gi|300397206 **Mass:** 38387 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
OmpA-like transmembrane domain protein [Escherichia coli MS 69-1]
gi|300412048 **Mass:** 38359 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
OmpA-like transmembrane domain protein [Escherichia coli MS 115-1]
gi|300528219 **Mass:** 38091 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
outer membrane protein A [Escherichia coli MS 107-1]
gi|323462898 **Mass:** 37213 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
Chain A, The Host Outer Membrane Proteins Ompa And Ompc Are Packed At Specific Sites In The Shigella Phage Sf6 Virion As Structural Components
gi|324113719 **Mass:** 38610 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
OmpA transmembrane domain-containing protein [Escherichia fergusonii B253]
gi|326346124 **Mass:** 29481 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
Outer membrane protein A precursor [Escherichia coli O157:H7 str. 1044]
gi|331038284 **Mass:** 40182 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
outer membrane protein A [Escherichia coli H736]
gi|338771000 **Mass:** 39904 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
Outer membrane protein A [Escherichia coli PCN033]
gi|386138203 **Mass:** 38399 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
outer membrane protein A [Escherichia coli 1.2741]
gi|388392255 **Mass:** 28265 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
outer membrane protein A, partial [Escherichia coli KD2]
gi|446237587 **Mass:** 36790 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
membrane protein, partial [Escherichia coli]
gi|446264697 **Mass:** 38109 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
membrane protein [Escherichia coli]
gi|446553514 **Mass:** 36080 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
membrane protein, partial [Escherichia coli]
gi|446673069 **Mass:** 37468 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
MULTISPECIES: membrane protein [Escherichia]
gi|446673070 **Mass:** 37178 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
MULTISPECIES: outer membrane protein A (3a;II*;G;d) [Enterobacteriaceae]
gi|446673071 **Mass:** 25817 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
membrane protein, partial [Escherichia coli]
gi|446673072 **Mass:** 37456 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
membrane protein [Escherichia coli]
gi|446673074 **Mass:** 37208 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
membrane protein [Escherichia coli]
gi|446875567 **Mass:** 39626 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
membrane protein [Escherichia coli]
gi|446875573 **Mass:** 39918 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)
membrane protein [Escherichia coli]
gi|481041560 **Mass:** 38401 **Score:** 68 **Matches:** 2(0) **Sequences:** 2(0)

```
        membrane protein [Escherichia coli]
        gi|485664529    Mass: 37469    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|485666433    Mass: 37428    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|485670686    Mass: 40474    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|485707694    Mass: 37120    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|485714280    Mass: 37470    Score: 68     Matches: 2(0)  Sequences: 2(0)
        MULTISPECIES: membrane protein [Escherichia]
        gi|485728443    Mass: 36282    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Shigella sonnei]
        gi|485776803    Mass: 37177    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|485786575    Mass: 37442    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|485815280    Mass: 37165    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|485829345    Mass: 37196    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|485830522    Mass: 37236    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|485906836    Mass: 37174    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|485935400    Mass: 37130    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|486142546    Mass: 37497    Score: 68     Matches: 2(0)  Sequences: 2(0)
        MULTISPECIES: outer membrane protein A [Escherichia]
        gi|486648058    Mass: 37226    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|487363100    Mass: 37226    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|487566161    Mass: 37424    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|491126837    Mass: 37182    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Shigella boydii]
        gi|498062767    Mass: 37527    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia sp. TW09308]
        gi|499697891    Mass: 37472    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Shigella dysenteriae]
        gi|506433598    Mass: 40683    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia fergusonii]
        gi|507087281    Mass: 37467    Score: 68     Matches: 2(0)  Sequences: 2(0)
        MULTISPECIES: outer membrane protein A [Escherichia]
        gi|510913438    Mass: 37455    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|519077113    Mass: 37484    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|545246159    Mass: 37177    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|545297005    Mass: 37446    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A [Escherichia coli]
        gi|559186956    Mass: 25901    Score: 68     Matches: 2(0)  Sequences: 2(0)
        outer membrane protein A, partial [Escherichia coli]
        gi|564932452    Mass: 41001    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli LAU-EC7]
        gi|585182969    Mass: 37483    Score: 68     Matches: 2(0)  Sequences: 2(0)
        MULTISPECIES: membrane protein [Escherichia]
        gi|585319840    Mass: 37148    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|585350225    Mass: 37528    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|585374859    Mass: 37679    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia fergusonii]
        gi|692968399    Mass: 37415    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|693229516    Mass: 37120    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|729992633    Mass: 37459    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|740534776    Mass: 39945    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia sp. HT073016]
        gi|742917886    Mass: 37192    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Escherichia coli]
        gi|745761649    Mass: 37178    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Shigella boydii]
        gi|745768689    Mass: 37206    Score: 68     Matches: 2(0)  Sequences: 2(0)
        membrane protein [Shigella boydii]
```

```
13.     gi|489989392    Mass: 27079    Score: 64     Matches: 1(1)  Sequences: 1(1)  emPAI: 0.14
        response regulator [Mycobacterium smegmatis]
      ☐ 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  542.8218  1083.6290  1083.6288  0.26   0    64  0.0017   1     U    R.EQEILALLR.S
```

```
     Proteins matching the same set of peptides:
     gi|491440118    Mass: 39341    Score: 64     Matches: 1(1)  Sequences: 1(1)
     MULTISPECIES: carbohydrate kinase [Aeromonas]
     gi|491460055    Mass: 39388    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas salmonicida]
     gi|491477571    Mass: 39254    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas veronii]
     gi|491490576    Mass: 39132    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas veronii]
     gi|491496540    Mass: 39215    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas veronii]
     gi|491504920    Mass: 39157    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas veronii]
     gi|492578278    Mass: 38750    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas molluscorum]
     gi|498318877    Mass: 39461    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas dhakensis]
     gi|498361290    Mass: 39315    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas caviae]
     gi|500046678    Mass: 27111    Score: 64     Matches: 1(1)  Sequences: 1(1)
     response regulator [Mycobacterium smegmatis]
     gi|504689859    Mass: 26766    Score: 64     Matches: 1(1)  Sequences: 1(1)
     response regulator [Mycobacterium smegmatis]
     gi|511291535    Mass: 39285    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas hydrophila]
     gi|515978774    Mass: 39292    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas hydrophila]
     gi|515982402    Mass: 39424    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas salmonicida]
     gi|516376331    Mass: 39330    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas hydrophila]
     gi|516391647    Mass: 39358    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas hydrophila]
     gi|516394754    Mass: 39392    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas hydrophila]
     gi|516398962    Mass: 39376    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas hydrophila]
     gi|518274823    Mass: 39227    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas sp. 159]
     gi|544709421    Mass: 39348    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas salmonicida]
     gi|544814183    Mass: 39199    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas veronii]
     gi|569546803    Mass: 39358    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas hydrophila 4AK4]
     gi|610710855    Mass: 39347    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas hydrophila AD9]
     gi|612335732    Mass: 39376    Score: 64     Matches: 1(1)  Sequences: 1(1)
     pseudouridine kinase [Aeromonas salmonicida subsp. masoucida NBRC 13784]
     gi|615550753    Mass: 39283    Score: 64     Matches: 1(1)  Sequences: 1(1)
     carbohydrate kinase [Aeromonas media WS]
     gi|640504956    Mass: 39362    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas hydrophila]
     gi|640507207    Mass: 39361    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas hydrophila]
     gi|651304789    Mass: 39329    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas sp. HZM]
     gi|657056466    Mass: 39423    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas hydrophila]
     gi|657061848    Mass: 39389    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas hydrophila]
     gi|662016601    Mass: 39345    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas caviae]
     gi|663466793    Mass: 39331    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas hydrophila]
     gi|675524491    Mass: 39275    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas salmonicida]
     gi|696588558    Mass: 39228    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas sp. AE122]
     gi|696628400    Mass: 39269    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas sp. AE235]
     gi|696651748    Mass: 39144    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas sp. 4287D]
     gi|721526397    Mass: 39285    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas caviae]
     gi|721535650    Mass: 39358    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas hydrophila]
     gi|743523061    Mass: 39300    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas caviae]
     gi|746153448    Mass: 39289    Score: 64     Matches: 1(1)  Sequences: 1(1)
     kinase [Aeromonas hydrophila]
```

```
14.  gi|494364767    Mass: 41662    Score: 63     Matches: 13(0)  Sequences: 2(0)
     putative LPS biosynthesis protein WbpG [Hoeflea phototrophica]
   ☐ 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
       80  376.7003  751.3860  751.3864  -0.53   0   (25)     25   5     U    R.YDLVSR.T
```

```
       81  376.7003  751.3860  751.3864  -0.53   0   (25)     27   1     U    R.YDLVSR.T
☑      82  376.7003  751.3860  751.3864  -0.53   0   (24)     33   1     U    R.YDLVSR.T
       90  376.7005  751.3864  751.3864   0.01   0    25      25   1     U    R.YDLVSR.T
       91  376.7005  751.3864  751.3864   0.01   0   (23)     48   1     U    R.YDLVSR.T
       94  376.7006  751.3866  751.3864   0.27   0   (25)     27   5     U    R.YDLVSR.T
       99  376.7007  751.3868  751.3864   0.54   0   (25)     31   3     U    R.YDLVSR.T
      100  376.7007  751.3868  751.3864   0.54   0   (24)     35   1     U    R.YDLVSR.T
      172  401.2392  800.4638  800.4643  -0.61   0   (35)    3.2   1          K.ALIDEIK.A
      173  401.2395  800.4644  800.4643   0.13   0    37     1.9   1          K.ALIDEIK.A
      176  401.2398  800.4650  800.4643   0.88   0   (35)    1.9   1          K.ALIDEIK.A
      178  401.2398  800.4650  800.4643   0.88   0   (36)    1.4   1          K.ALIDEIK.A
      179  401.2400  800.4654  800.4643   1.38   0   (25)     20   1          K.ALIDEIK.A
```

```
      Proteins matching the same set of peptides:
      gi|685804020    Mass: 42570    Score: 63     Matches: 13(0)  Sequences: 2(0)
      N-acetyl sugar amidotransferase [Hoeflea phototrophica DFL-43]
```

```
15.   gi|225733897    Mass: 18808    Score: 59     Matches: 1(1)  Sequences: 1(1)  emPAI: 0.20
      Chain A, Solution Structure Of E.Coli Slyd
    ☐ 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
☑      510  523.8039  1045.5932  1045.5920   1.17   0    59  0.0089   1     U    K.FNVEVVAIR.E
```

```
      Proteins matching the same set of peptides:
      gi|353566445    Mass: 8811     Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase SlyD, partial [Salmonella enterica subsp. enterica serovar Alachua str. R6-377]
      gi|353593590    Mass: 10479    Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase SlyD, partial [Salmonella enterica subsp. enterica serovar Inverness str. R8-3668]
      gi|353633808    Mass: 10811    Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [Salmonella enterica subsp. enterica serovar Rubislaw str. A4-653]
      gi|353658866    Mass: 11767    Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase SlyD, partial [Salmonella enterica subsp. enterica serovar Urbana str. R8-2977]
      gi|446225023    Mass: 6787     Score: 59     Matches: 1(1)  Sequences: 1(1)
      hypothetical protein, partial [Escherichia sp. TW14182]
      gi|446784059    Mass: 20852    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784060    Mass: 20761    Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase [Salmonella enterica]
      gi|446784062    Mass: 20854    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784063    Mass: 20882    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784064    Mass: 20787    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784065    Mass: 19493    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784070    Mass: 20854    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784071    Mass: 20296    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Shigella dysenteriae]
      gi|446784074    Mass: 20336    Score: 59     Matches: 1(1)  Sequences: 1(1)
      MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacteriaceae]
      gi|446784075    Mass: 20588    Score: 59     Matches: 1(1)  Sequences: 1(1)
      MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Escherichia]
      gi|446784076    Mass: 20826    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784077    Mass: 20898    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784078    Mass: 20840    Score: 59     Matches: 1(1)  Sequences: 1(1)
      MULTISPECIES: FKBP-type peptidyl prolyl cis-trans isomerase (rotamase) [Enterobacteriaceae]
      gi|446784079    Mass: 20866    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784080    Mass: 20870    Score: 59     Matches: 1(1)  Sequences: 1(1)
      MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [Escherichia]
      gi|446784081    Mass: 20602    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia albertii]
      gi|446784082    Mass: 20866    Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase [Escherichia sp. TW15838]
      gi|446784083    Mass: 20854    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Escherichia coli]
      gi|446784084    Mass: 20978    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Salmonella bongori]
      gi|446784085    Mass: 20775    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Salmonella enterica]
      gi|446784086    Mass: 20968    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Salmonella enterica]
      gi|446784087    Mass: 20348    Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase, partial [Salmonella enterica]
      gi|446784088    Mass: 20538    Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase, partial [Salmonella enterica]
      gi|446784089    Mass: 20835    Score: 59     Matches: 1(1)  Sequences: 1(1)
      peptidyl-prolyl cis-trans isomerase [Salmonella enterica]
      gi|446784090    Mass: 20789    Score: 59     Matches: 1(1)  Sequences: 1(1)
      FKBP-type peptidyl-prolyl cis-trans isomerase [Salmonella enterica]
      gi|446784091    Mass: 20854    Score: 59     Matches: 1(1)  Sequences: 1(1)
      MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacteriaceae]
```

gi|446784092 **Mass:** 20870 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Escherichia fergusonii]
gi|485758914 **Mass:** 20800 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|485770871 **Mass:** 20800 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|485890455 **Mass:** 20870 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|486158291 **Mass:** 20805 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Salmonella enterica]
gi|486258340 **Mass:** 20824 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|486343313 **Mass:** 20836 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|487139208 **Mass:** 20764 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|487370191 **Mass:** 20798 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|487374260 **Mass:** 20798 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|487400797 **Mass:** 20909 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|487442612 **Mass:** 20798 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|487561721 **Mass:** 20798 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|487629456 **Mass:** 18549 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase, partial [Salmonella enterica]
gi|487759610 **Mass:** 17540 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase, partial [Salmonella enterica]
gi|488366938 **Mass:** 20471 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Escherichia hermannii]
gi|488375476 **Mass:** 22014 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Shimwellia blattae]
gi|489009580 **Mass:** 20731 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Klebsiella]
gi|489044308 **Mass:** 20581 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
hypothetical protein [Salmonella enterica]
gi|489113781 **Mass:** 21169 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacteriaceae]
gi|489924421 **Mass:** 21393 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Citrobacter freundii]
gi|489958384 **Mass:** 20832 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacter cloacae complex]
gi|490227601 **Mass:** 20708 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Klebsiella]
gi|490307143 **Mass:** 20983 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: FKBP-type peptidylprolyl isomerase [Klebsiella]
gi|490993116 **Mass:** 20708 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Klebsiella]
gi|491006678 **Mass:** 20795 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacteriaceae]
gi|491010846 **Mass:** 20983 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Klebsiella pneumoniae]
gi|493178713 **Mass:** 20924 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Enterobacter cancerogenus]
gi|493738191 **Mass:** 21112 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Citrobacter youngae]
gi|493865507 **Mass:** 21530 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Enterobacter hormaechei]
gi|493871002 **Mass:** 20860 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Yokenella regensburgei]
gi|493947984 **Mass:** 20694 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [Salmonella enterica]
gi|494611549 **Mass:** 20766 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Kosakonia radicincitans]
gi|495732519 **Mass:** 20894 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Enterobacter sp. Ag1]
gi|495778431 **Mass:** 20845 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacter]
gi|496061787 **Mass:** 21363 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Citrobacter]
gi|496082532 **Mass:** 20917 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Klebsiella]
gi|498122142 **Mass:** 20934 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Enterobacter mori]
gi|501084960 **Mass:** 20709 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Citrobacter koseri]
gi|501534380 **Mass:** 21169 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Klebsiella pneumoniae]
gi|502326197 **Mass:** 21245 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Dickeya]
gi|502345515 **Mass:** 20560 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Dickeya]
gi|502650076 **Mass:** 21518 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Dickeya]
gi|502672597 **Mass:** 21111 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidyl-prolyl cis-trans isomerase [Citrobacter rodentium]

```
gi|502864061    Mass: 20651    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacter]
gi|503084857    Mass: 21078    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase [Dickeya dadantii]
gi|503937918    Mass: 20889    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacter cloacae complex]
gi|503993048    Mass: 20766    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase [Klebsiella oxytoca]
gi|504646419    Mass: 20903    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacter]
gi|504698389    Mass: 20890    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacter]
gi|506486182    Mass: 20687    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase [Enterobacteriaceae bacterium strain FGI 57]
gi|510920819    Mass: 21092    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|514235830    Mass: 22538    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase, FKBP-type SlyD [Cedecea davisae]
gi|515509734    Mass: 21726    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase [Dickeya zeae]
gi|515953591    Mass: 21084    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Enterobacter cloacae complex]
gi|516029309    Mass: 20792    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase [Enterobacter sp. R4-368]
gi|518683492    Mass: 21712    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase [Dickeya zeae]
gi|519080133    Mass: 20600    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase [Escherichia coli]
gi|537687563    Mass: 20638    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase, partial [Salmonella enterica]
gi|545158424    Mass: 20888    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|545166487    Mass: 20830    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|545171560    Mass: 20816    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|545259459    Mass: 20830    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|545297806    Mass: 20676    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Escherichia coli]
gi|550653409    Mass: 20771    Score: 59     Matches: 1(1)  Sequences: 1(1)
Peptidyl-prolyl cis-trans isomerase [Dickeya solani]
gi|550711947    Mass: 20284    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Klebsiella pneumoniae]
gi|550766236    Mass: 20580    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Enterobacteriaceae]
gi|553728158    Mass: 19512    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [Escherichia coli]
gi|554434547    Mass: 20018    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase, partial [Salmonella enterica subsp. enterica serovar London str. CFSAN001081]
gi|554925606    Mass: 20803    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase [Salmonella enterica]
gi|556370622    Mass: 20925    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Klebsiella pneumoniae]
gi|556479878    Mass: 20638    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Enterobacter cloacae complex]
gi|556490163    Mass: 20638    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Enterobacter cloacae complex]
gi|558090270    Mass: 20986    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Enterobacter cloacae]
gi|568603461    Mass: 20830    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase [Dickeya dianthicola]
gi|585374055    Mass: 18363    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidylprolyl isomerase, partial [Escherichia coli]
gi|603584086    Mass: 18298    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidylprolyl isomerase, partial [Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121004]
gi|627377118    Mass: 22492    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase [Salmonella enterica subsp. enterica serovar Cerro FSL R8-0235]
gi|635729852    Mass: 20918    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase slyD [Citrobacter sp. MGH 55]
gi|640460397    Mass: 20903    Score: 59     Matches: 1(1)  Sequences: 1(1)
MULTISPECIES: peptidylprolyl isomerase [Enterobacter]
gi|647263924    Mass: 20745    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidylprolyl isomerase [Klebsiella sp. 10982]
gi|654659164    Mass: 20646    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidylprolyl isomerase [Escherichia coli]
gi|657899497    Mass: 20479    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidylprolyl isomerase [Klebsiella pneumoniae]
gi|667711461    Mass: 20789    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidyl-prolyl cis-trans isomerase [Klebsiella pneumoniae subsp. pneumoniae PittNDM01]
gi|671538017    Mass: 20682    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidylprolyl isomerase [Cronobacter sp. 1383]
gi|673535480    Mass: 20903    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase [Citrobacter koseri]
gi|685392227    Mass: 16260    Score: 59     Matches: 1(1)  Sequences: 1(1)
peptidylprolyl isomerase, partial [Salmonella enterica]
gi|689828010    Mass: 20733    Score: 59     Matches: 1(1)  Sequences: 1(1)
FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [Escherichia vulneris NBRC 102420]
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gi|692981311 **Mass:** 20856 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Escherichia coli]
gi|693024543 **Mass:** 20313 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Escherichia coli]
gi|693059073 **Mass:** 20394 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Escherichia coli]
gi|693190736 **Mass:** 20854 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Escherichia coli]
gi|695625249 **Mass:** 20819 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidylprolyl isomerase [Enterobacter cloacae complex]
gi|695639476 **Mass:** 20637 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Leclercia adecarboxylata]
gi|695669145 **Mass:** 20008 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Enterobacter sp. MGH 4]
gi|695767461 **Mass:** 20989 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Raoultella ornithinolytica]
gi|695770781 **Mass:** 20960 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
MULTISPECIES: peptidylprolyl isomerase [Klebsiella]
gi|723056706 **Mass:** 20830 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Escherichia coli]
gi|723115247 **Mass:** 20440 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase, partial [Escherichia coli]
gi|723593051 **Mass:** 20632 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Dickeya sp. 2B12]
gi|727387042 **Mass:** 20859 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Escherichia coli]
gi|729877603 **Mass:** 20898 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Escherichia coli]
gi|737362387 **Mass:** 20555 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Dickeya sp. DW 0440]
gi|737929391 **Mass:** 21240 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Kluyvera ascorbata]
gi|740321464 **Mass:** 20617 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Trabulsiella guamensis]
gi|740692890 **Mass:** 21181 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Cedecea neteri]
gi|740879765 **Mass:** 20812 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Dickeya solani]
gi|742423129 **Mass:** 20826 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Dickeya dadantii]
gi|742463569 **Mass:** 20798 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Dickeya sp. MK7]
gi|742925505 **Mass:** 20844 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Enterobacter asburiae]
gi|743514001 **Mass:** 20795 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Leclercia adecarboxylata]
gi|745758440 **Mass:** 20729 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Enterobacter sp. Bisph1]
gi|746239832 **Mass:** 20880 **Score:** 59 **Matches:** 1(1) **Sequences:** 1(1)
peptidylprolyl isomerase [Cedecea neteri]

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16. gi|518446942 **Mass:** 82781 **Score:** 52 **Matches:** 2(0) **Sequences:** 2(0)
hypothetical protein [Psychromonas ossibalaenae]
☐ 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
☑	198	**407.2391**	**812.4636**	**812.4644**	**-0.87**	**0**	**32**	**3.2**	**1**	**U**	**K.VPIDELK.I**
	355	**471.2871**	**940.5596**	**940.5593**	**0.36**	**1**	**20**	**32**	**8**	**U**	**K.KVPIDELK.I**

Proteins matching the same set of peptides:
gi|655483392 **Mass:** 85976 **Score:** 52 **Matches:** 2(0) **Sequences:** 2(0)
hypothetical protein [Psychromonas aquimarina]

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17. gi|118138114 **Mass:** 8870 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
Chain X, Crystal Structure Of Ribosome With Messenger Rna And The Anticodon Stem-Loop Of P-Site Trna. This File Contains The 50s Subunit Of One 70s Ribosome. The Entire Crystal Structure Contains Two 70s Ribosomes And Is Described In Remark 400.
☐ 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
☑	597	**543.8116**	**1085.6086**	**1085.6081**	**0.54**	**0**	**50**	**0.086**	**1**	**U**	**K.GIDTVLAELR.A**

Proteins matching the same set of peptides:
gi|208726602 **Mass:** 10012 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
ribosomal protein L28 [Escherichia coli O157:H7 str. EC4206]
gi|446014100 **Mass:** 9001 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
MULTISPECIES: 50S ribosomal protein L28 [Enterobacteriaceae]
gi|446069563 **Mass:** 7690 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
MULTISPECIES: 50S ribosomal protein L28 [Enterobacteriaceae]
gi|446069564 **Mass:** 7720 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
50S ribosomal protein L28 [Shigella flexneri]
gi|476083841 **Mass:** 7676 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
ribosomal protein L28 [Escherichia coli MP021017.11]
gi|476107273 **Mass:** 7686 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
ribosomal protein L28 [Escherichia coli BCE002_MS12]
gi|476112070 **Mass:** 7610 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
ribosomal protein L28 [Escherichia coli 2875000]
gi|476262192 **Mass:** 7650 **Score:** 50 **Matches:** 1(0) **Sequences:** 1(0)
ribosomal protein L28 [Escherichia coli 2747800]

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      gi|476774490    Mass: 7650     Score: 50     Matches: 1(0)  Sequences: 1(0)
      ribosomal protein L28 [Escherichia coli 2730350]
      gi|485866674    Mass: 8961     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia coli]
      gi|487428382    Mass: 8961     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia coli]
      gi|488390981    Mass: 9029     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia albertii]
      gi|490009682    Mass: 8987     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia coli]
      gi|490247109    Mass: 8914     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Klebsiella pneumoniae]
      gi|491128996    Mass: 9031     Score: 50     Matches: 1(0)  Sequences: 1(0)
      MULTISPECIES: 50S ribosomal protein L28 [Shigella]
      gi|494076066    Mass: 8973     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Bermanella marisrubri]
      gi|494440852    Mass: 9119     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [marine gamma proteobacterium HTCC2080]
      gi|497262153    Mass: 9107     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [gamma proteobacterium IMCC3088]
      gi|497817924    Mass: 9041     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Microbulbifer agarilyticus]
      gi|498912430    Mass: 9015     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Xenorhabdus nematophila]
      gi|499789415    Mass: 9025     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Saccharophagus degradans]
      gi|517453253    Mass: 8963     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Kangiella aquimarina]
      gi|545243968    Mass: 9013     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia coli]
      gi|551347959    Mass: 9003     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Pseudomonas caeni]
      gi|557804075    Mass: 9112     Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain X, E. Coli 70s-fmetval-trnaval-trnafmet Complex In Classic Pre- Translocation State (pre1b, 50s Subunit)
      gi|585234621    Mass: 8961     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia coli]
      gi|585279289    Mass: 8997     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia coli]
      gi|585280544    Mass: 8921     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia coli]
      gi|654839673    Mass: 9010     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Oceanobacter kriegii]
      gi|661559608    Mass: 9001     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Xenorhabdus doucetiae]
      gi|727408157    Mass: 8948     Score: 50     Matches: 1(0)  Sequences: 1(0)
      50S ribosomal protein L28 [Escherichia coli]
      gi|740406308    Mass: 8987     Score: 50     Matches: 1(0)  Sequences: 1(0)
      MULTISPECIES: 50S ribosomal protein L28 [Xenorhabdus]
```

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18.   gi|136429    Mass: 24394    Score: 50     Matches: 1(0)  Sequences: 1(0)
      RecName: Full=Trypsin; Flags: Precursor [Sus scrofa]
    ☐ 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
    ☑  239   421.7583  841.5020  841.5022  -0.12  0    50     0.1   1     U    R.VATVSLPR.S


      Proteins matching the same set of peptides:
      gi|494360    Mass: 23458    Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain A, The Refined 1.6 Angstroms Resolution Crystal Structure Of The Complex Formed Between Porcine Beta-trypsin And Mcti-a, A Trypsin Inhibitor Of Squash Family
      gi|999627    Mass: 8814     Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain B, Refined 1.8 Angstroms Resolution Crystal Structure Of Porcine Epsilon-Trypsin
      gi|1942351    Mass: 13284    Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain A, Crystal Structure Of The First Active Autolysate Form Of The Porcine Alpha Trypsin
      gi|2914482    Mass: 23460    Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain A, Complex Of The Second Kunitz Domain Of Tissue Factor Pathway Inhibitor With Porcine Trypsin
      gi|3318722    Mass: 23457    Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain E, Leech-Derived Tryptase InhibitorTRYPSIN COMPLEX
      gi|110590762    Mass: 23458    Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain A, Trypsin In Complex With Borate
      gi|157878102    Mass: 24157    Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain E, Complex Of Eeti-Ii With Porcine Trypsin
      gi|242253868    Mass: 25865    Score: 50     Matches: 1(0)  Sequences: 1(0)
      trypsinogen precursor [Sus scrofa]
      gi|315583496    Mass: 23430    Score: 50     Matches: 1(0)  Sequences: 1(0)
      Chain A, The Bowman-Birk Type Inhibitor From Mung Bean In Ternary Complex With Porcine Trypsin
      gi|338819392    Mass: 842      Score: 50     Matches: 1(0)  Sequences: 1(0)
      RecName: Full=Sarcoplasmic calcium-binding protein, partial [Chionoecetes opilio]
      gi|545882044    Mass: 25922    Score: 50     Matches: 1(0)  Sequences: 1(0)
      PREDICTED: trypsinogen isoform X1 [Sus scrofa]
      gi|731509157    Mass: 26287    Score: 50     Matches: 1(0)  Sequences: 1(0)
      PREDICTED: LOW QUALITY PROTEIN: cationic trypsin-3-like [Loxodonta africana]
      gi|731509159    Mass: 26239    Score: 50     Matches: 1(0)  Sequences: 1(0)
      PREDICTED: cationic trypsin-3-like [Loxodonta africana]
```

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19.   gi|493595525    Mass: 61671    Score: 49     Matches: 1(0)  Sequences: 1(0)
      lysyl-tRNA synthetase [Actinomyces urogenitalis]
    ☐ 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
☑	1972	804.9125	1607.8104	1607.8090	0.92	1	49	0.09	1	U	R.SSGKLCFVALADGAGR.T + Carbamidomethyl (C)

Proteins matching the same set of peptides:
gi|736103835 **Mass:** 61657 **Score:** 49 **Matches:** 1(0) **Sequences:** 1(0)
lysyl-tRNA synthetase [Actinomyces urogenitalis]

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	294	448.7273	895.4400	895.4400	0.10	0	49	0.072	1		FATTVSDR
☑	542	533.2698	1064.5250	1064.5251	-0.02	0	48	0.12	1		DFISGNGLSR
☑	429	494.2896	986.5646	986.5648	-0.14	0	48	0.096	1		VSALDLELK
☑	401	486.2924	970.5702	970.5699	0.39	0	47	0.098	1		AAVILDELK
☑	181	401.7372	801.4598	801.4596	0.32	0	47	0.29	1		ALTAEIGK
☑	403	487.2568	972.4990	972.4988	0.23	0	47	0.19	1		NSGLEALNR
☑	192	405.2115	808.4084	808.4079	0.66	0	47	0.21	1		YGDSVLR
☑	374	478.2949	954.5752	954.5750	0.31	1	46	0.074	1		IKEVPEIK
☑	2536	954.9847	1907.9548	1907.9564	-0.81	0	45	0.19	1		CFGFVTGSQQVLDALPAR
☑	214	415.2072	828.3998	828.3977	2.55	0	45	0.14	1		QDPLNDK
☑	1612	689.3249	1376.6352	1376.6354	-0.13	0	45	0.13	1		VDQLSNDVNAMR + Oxidation (M)
☑	264	430.2354	858.4562	858.4559	0.40	0	43	0.71	1		SAELGLNR
☑	189	405.2113	808.4080	808.4079	0.17	0	43	0.47	1		YGDSVLR
☑	417	492.7896	983.5646	983.5651	-0.48	0	43	0.17	1		IPSEIGQLK
☑	2162	862.4653	1722.9160	1722.9192	-1.84	1	43	0.22	1		FFADLGADVIKIESAK
☑	219	415.2300	828.4454	828.4453	0.13	1	43	0.43	1		QPTKNNK
☑	1870	776.4022	1550.7898	1550.7875	1.52	1	43	0.38	1		NFGNISDMASVLKR
☑	478	514.8027	1027.5908	1027.5913	-0.48	0	42	0.29	1		VAAIIDEAVK
☑	1352	650.8516	1299.6886	1299.6856	2.32	1	42	0.44	1		MKNNLPPTLEK + Oxidation (M)
☑	399	486.2923	970.5700	970.5699	0.18	0	42	0.3	1		GIAILDELK
☑	548	533.3064	1064.5982	1064.5978	0.40	0	42	0.22	1		IHEGLEVIR
☑	577	540.2962	1078.5778	1078.5771	0.71	1	42	0.38	1		GKSYQEVLR
☑	819	586.3062	1170.5978	1170.5993	-1.23	0	42	0.26	1		DSIRPNVQDK
☑	1975	537.6298	1609.8676	1609.8675	0.04	0	42	0.28	1		GPIGSDDAAELIALLR
☑	480	514.8032	1027.5918	1027.5913	0.50	0	42	0.35	1		VAAIIDEAVK
☑	1986	812.9094	1623.8042	1623.8039	0.22	1	41	0.43	1		ISCKGYDVNVLSGGR + Carbamidomethyl (C)
☑	323	458.7457	915.4768	915.4774	-0.57	0	41	0.75	1		ASVEGALNR
☑	2319	887.9890	1773.9634	1773.9658	-1.35	1	41	0.25	1		VINMKELQNTLNTIK + Oxidation (M)
☑	226	415.2307	828.4468	828.4453	1.82	1	41	0.71	1		QPTKNNK
☑	1480	671.3597	1340.7048	1340.7010	2.89	0	41	0.38	1		EIMVHVEVLEK + Oxidation (M)
☑	1483	671.3609	1340.7072	1340.7088	-1.18	1	41	0.45	1		LLYNDPHVKDK
☑	345	465.2873	928.5600	928.5593	0.81	1	41	0.47	1		KAIDIEIK
☑	225	415.2307	828.4468	828.4453	1.82	1	41	0.79	1		KDARPDK
☑	547	533.3061	1064.5976	1064.5978	-0.17	0	41	0.33	1		IHEGLEVIR
☑	232	418.2499	834.4852	834.4851	0.19	0	41	0.33	1		ISIIFDK
☑	220	415.2301	828.4456	828.4453	0.37	0	40	0.74	1		KPTNQNK
☑	599	544.2785	1086.5424	1086.5418	0.63	0	40	0.63	1		DLSAVQANNR
☑	222	415.2302	828.4458	828.4453	0.61	1	40	0.78	1		QPTKNNK
☑	404	487.2568	972.4990	972.4988	0.23	0	40	1	1		SNAVAEINR
☑	224	415.2303	828.4460	828.4453	0.85	1	40	0.88	1		QPTKNNK
☑	1011	613.8235	1225.6324	1225.6277	3.85	1	39	0.63	1		RDIPMYYLR
☑	506	522.7948	1043.5750	1043.5723	2.59	1	39	1	1		VLQTDKANR
☑	777	579.8280	1157.6414	1157.6404	0.88	0	39	0.91	1		DASIQVVSAIR
☑	550	533.3065	1064.5984	1064.6025	-3.84	1	39	0.42	1		MRVPPGRPR
☑	1859	776.4009	1550.7872	1550.7909	-2.34	1	39	0.65	1		NVSMGRSMASVIGVK + Oxidation (M)
☑	182	401.7373	801.4600	801.4596	0.57	0	39	1.8	1		ALTAEIGK
☑	346	466.2289	930.4432	930.4407	2.78	0	39	0.58	1		GNATEAGSPK
☑	1909	785.8431	1569.6716	1569.6696	1.33	0	39	0.21	1		EGVNDNEEGFFSAR
☑	1419	662.8228	1323.6310	1323.6306	0.32	1	39	0.75	1		ENSVDYKVNEK
☑	298	450.2688	898.5230	898.5236	-0.64	0	38	1.2	1		GVATVSLPR
☑	453	505.7491	1009.4836	1009.4862	-2.56	0	38	0.79	1		SSMAGTITSR
☑	379	478.7993	955.5840	955.5814	2.73	1	38	1.4	1		AIAALDRVK
☑	1778	501.2589	1500.7549	1500.7572	-1.56	0	38	1.1	1		FAAALAAAPEDEGLR
☑	943	608.8183	1215.6220	1215.6208	1.06	1	38	1.1	1		VGDLESGRDLR
☑	2117	852.4706	1702.9266	1702.9253	0.77	0	38	0.64	1		ISFIINNISAANVEAK
☑	698	566.2865	1130.5584	1130.5567	1.50	0	38	1.2	1		EPLSPASTSSR
☑	2155	859.9711	1717.9276	1717.9250	1.51	1	38	0.65	1		LFDVDIGGNIEKIGTK
☑	479	514.8030	1027.5914	1027.5913	0.11	0	38	0.89	1		GLAILEDGLK
☑	931	607.3427	1212.6708	1212.6714	-0.42	0	38	0.8	1		EAGEIELALLR
☑	1407	660.8505	1319.6864	1319.6834	2.35	0	37	1.4	1		AAPFSQASSSVLR
☑	860	595.7936	1189.5726	1189.5761	-2.89	0	37	1.5	1		AAMEADIANIR + Oxidation (M)
☑	136	386.7195	771.4244	771.4239	0.72	0	37	2.6	1		EVIGAAGR
☑	1780	501.2599	1500.7579	1500.7532	3.10	0	37	1.2	1		EASVSGGSPLQLSNR
☑	562	535.7727	1069.5308	1069.5339	-2.82	0	37	0.96	1		ICHQVSDIR
☑	1110	626.8307	1251.6468	1251.6459	0.73	0	37	1.1	1		SVTPTSGSFTLR
☑	67	367.6960	733.3774	733.3792	-2.45	0	37	3.6	1		SDIMIR
☑	382	479.2842	956.5538	956.5542	-0.38	0	37	1.3	1		LNIEVEIK
☑	743	569.2834	1136.5522	1136.5495	2.38	1	37	0.85	1		SSGEKNVASMK
☑	1674	699.3874	1396.7602	1396.7562	2.92	0	37	0.78	1		ADTLAVEEPLAIR
☑	852	594.2942	1186.5738	1186.5764	-2.18	0	37	1	1		APSQCVEALNR
☑	400	486.2924	970.5702	970.5699	0.39	0	37	1.1	1		IGAIIEDIK
☑	545	533.3056	1064.5966	1064.5978	-1.10	0	37	0.64	1		IHEGLEVIR
☑	177	401.2398	800.4650	800.4643	0.88	0	37	1.2	1		AIIIDEK
☑	1148	632.3367	1262.6588	1262.6540	3.83	1	37	1.7	1		MLAAKAIDTSDK
☑	558	535.7656	1069.5166	1069.5152	1.34	0	37	0.82	1		NPSADPSNLR
☑	2050	841.4607	1680.9068	1680.9120	-3.07	0	37	0.77	1		MNLPLIEPDLELLR + Oxidation (M)
☑	1868	776.4019	1550.7892	1550.7909	-1.05	1	37	1.5	1		NVSMGRSMASVIGVK + Oxidation (M)

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☑  961  613.8222 1225.6298 1225.6302 -0.31  0   37     1  1      EASPPGLSAELR
☑  532  530.7672 1059.5198 1059.5197  0.18  1   37   1.4  1      GTPEQTKDGK
☑  868  597.2996 1192.5846 1192.5832  1.25  0   37   1.3  1      ECLEALVTGMK
☑  410  489.7659  977.5172  977.5182 -0.98  1   37   1.9  1      KDFTSVGPK
☑ 1156  633.3408 1264.6670 1264.6663  0.59  0   36   1.4  1      LAISNYSVVDGK
☑  288  443.7405  885.4664  885.4668 -0.43  1   36   1.2  1      QDVRSPGK
☑  156  395.2090  788.4034  788.4028  0.78  0   36     4  1      IGATQDGK
☑  341  465.2868  928.5590  928.5593 -0.27  1   36   1.3  1      KAIEVEIK
☑  281  441.7499  881.4852  881.4858 -0.64  0   36  0.89  1      AIPDPELK
☑  318  458.2610  914.5074  914.5073  0.19  0   36   2.2  1      ALLDELGGK
☑  261  429.7501  857.4856  857.4858 -0.19  0   36   2.5  1      AIIDEGIK
☑ 1123  629.2945 1256.5744 1256.5794 -3.96  0   36  0.89  1      GACFAFMNALR + Carbamidomethyl (C)
☑ 1210  641.8425 1281.6704 1281.6717 -1.01  0   36   1.6  1      QTLGWEPVQPK
☑  277  440.2197  878.4248  878.4246  0.26  0   36   2.2  1      FQSNEVR
☑  600  544.3167 1086.6188 1086.6219 -2.84  1   36   2.1  1      IPSLVTRCAK
☑ 1517  675.3680 1348.7214 1348.7238 -1.74  1   36   1.6  1      EAIEGDIFSIKK
☑ 2380  901.5097 1801.0048 1801.0084 -1.98  1   36  0.69  1      LIGEVEELTETIKSLK
☑ 2254  880.4834 1758.9522 1758.9590 -3.82  0   36     1  1      LITMLQLWDIGLAEK + Oxidation (M)
☑  948  610.3079 1218.6012 1218.5993  1.61  0   36   1.9  1      VDADAFGAALNR
☑   55  364.2224  726.4302  726.4276  3.69  0   35   1.1  1      AIGPELK
☑  250  424.2125  846.4104  846.4083  2.54  0   35   2.8  1      DNAGITEK
☑   68  367.6962  733.3778  733.3759  2.70  0   35   5.5  1      YDPAIR
☑  874  597.7906 1193.5666 1193.5710 -3.66  0   35   1.6  1      SMTSALEGINR + Oxidation (M)
☑   35  358.1964  714.3782  714.3773  1.36  0   35   1.1  1      NIGGGAAR
☑ 1561  679.3583 1356.7020 1356.6997  1.70  1   35   2.3  1      GDEAVLRQVGEGK
☑  796  582.2888 1162.5630 1162.5587  3.77  0   35   2.7  1      ACGLAAMAINR + Carbamidomethyl (C); Oxidation (M)
☑ 1730  715.4044 1428.7942 1428.7936  0.44  1   35   1.5  1      SVLQSKLNGEGGLK
☑  212  414.7453  827.4760  827.4752  0.96  0   35   1.3  1      APVTAEIK
☑  272  438.2587  874.5028  874.5058 -3.43  1   35   2.2  1      IVICSGRK
☑  223  415.2303  828.4460  828.4453  0.85  0   34   2.9  1      KPTNQNK
☑ 1510  674.8777 1347.7408 1347.7398  0.78  1   34   1.7  1      QIKEDLFSIQK
☑  435  499.2405  996.4664  996.4665 -0.04  0   34   2.2  1      YGYAVPDGR
☑ 1467  670.3640 1338.7134 1338.7143 -0.66  0   34   1.8  1      QQVIPDGDINIK
☑  339  465.2863  928.5580  928.5593 -1.34  1   34   2.1  1      KIALDEIK
☑ 1553  678.8655 1355.7164 1355.7157  0.56  1   34   2.2  1      NERNLIVGANEK
☑ 2049  561.3088 1680.9046 1680.9046 -0.03  0   34   1.6  1      DSLAESNGPLSPILIR
☑  215  415.2291  828.4436  828.4453 -2.05  1   34     3  1      QPTKNNK
☑  385  480.2619  958.5092  958.5083  0.96  1   34   5.5  1      INDVKNEK
☑ 1283  649.8486 1297.6826 1297.6878 -3.95  0   34   2.3  1      LDELTGLVEGPR
☑  191  405.2115  808.4084  808.4079  0.66  0   34   3.8  1      YDGSVIR
☑  246  423.2170  844.4194  844.4191  0.36  0   34   2.1  1      QAGWDIR
☑  221  415.2301  828.4456  828.4453  0.37  1   34   3.2  1      QPTKNNK
☑  455  505.7977 1009.5808 1009.5808  0.08  0   34  0.73  1      LKPPEGELK
☑  443  501.7831 1001.5516 1001.5505  1.11  0   34     5  1      NTLQQIASK
☑  820  586.3071 1170.5996 1170.5993  0.32  1   34   2.3  1      RSDLPDEALR
☑  360  471.7742  941.5338  941.5334  0.44  0   34  0.83  1      SWPIAIAGK
☑  297  450.2322  898.4498  898.4508 -1.10  0   34   1.4  1      AGAGGPINDK
☑  459  506.8055 1011.5964 1011.5964  0.03  1   34   1.2  1      LKEVDPALK
☑  370  477.2644  952.5142  952.5164 -2.25  1   34   1.5  1      EMKHPAIK
☑  699  566.3043 1130.5940 1130.5932  0.79  1   34     4  1      DVLKTVDADR
☑  549  533.3065 1064.5984 1064.5978  0.59  0   33   1.6  1      IHEGLEVIR
☑ 1381  657.3535 1312.6924 1312.6874  3.82  0   33   2.2  1      SLIQDGVIDEPK
☑ 2190  867.9684 1733.9222 1733.9200  1.31  0   33     2  1      YVLIAGGDGTIDSVINK
☑  491  519.2606 1036.5066 1036.5090 -2.27  0   33   2.7  1      ASYYIHAGR
☑  990  613.8233 1225.6320 1225.6316  0.37  0   33   2.7  1      QRPQWQDLR
☑   56  364.6881  727.3616  727.3613  0.52  0   33   1.4  1      AEPNAAR
☑ 2447  920.5207 1839.0268 1839.0254  0.79  1   33     1  1      NAELITTIQANLWPKK
☑ 1860  776.4009 1550.7872 1550.7913 -2.63  1   33   2.7  1      DPERRPAGAGELAGR
☑ 2269  590.3200 1767.9382 1767.9342  2.27  1   33   1.8  1      MFRVFTEQEIALLR + Oxidation (M)
☑  110  379.2138  756.4130  756.4130  0.09  0   33   3.3  1      IPAETAR
☑  902  603.2992 1204.5838 1204.5805  2.81  1   33   3.6  1      RMNALDAMQR
☑  416  491.7698  981.5250  981.5284 -3.38  0   33   2.4  1      AFFTEVIR
☑  211  414.7447  827.4748  827.4752 -0.49  0   33     3  1      APVTAEIK
☑ 1453  667.3720 1332.7294 1332.7289  0.41  1   33   2.7  1      KILFPESSTSPK
☑ 1120  628.8107 1255.6068 1255.6091 -1.82  1   33   3.2  1      RMENVHSDIR
☑  701  566.7999 1131.5852 1131.5812  3.58  0   33   4.6  1      IPEDVIDGFK
☑ 1084  625.3332 1248.6518 1248.6471  3.79  1   33   2.8  1      MLGAKVCWLR + Carbamidomethyl (C); Oxidation (M)
☑ 1208  428.2287 1281.6643 1281.6677 -2.67  1   33   3.1  1      KDARPDQDPIK
☑   54  364.2212  726.4278  726.4276  0.39  0   33     2  1      AIGPELK
☑  248  423.7200  845.4254  845.4243  1.39  0   33   6.9  1      EAITNGNK
☑ 2122  853.4791 1704.9436 1704.9484 -2.78  1   33   1.5  1      MKLPLNYTAIVDSLK
☑ 1858  776.3983 1550.7820 1550.7875 -3.51  1   32     5  1      NFGNISDMASVLKR
☑  188  405.2103  808.4060  808.4079 -2.31  0   32   5.4  1      YDGSVIR
☑ 1190  637.8160 1273.6174 1273.6125  3.89  0   32   3.6  1      SMALDWAPDIR
☑  153  394.2371  786.4596  786.4599 -0.34  0   32    14  1      INAAIASK
☑ 1511  674.8781 1347.7416 1347.7398  1.38  1   32   2.8  1      LAEKDLSFIQGK
☑ 1897  784.3992 1566.7838 1566.7831  0.51  0   32   4.2  1      YAEPFSALAWLSGR
☑  835  589.7942 1177.5738 1177.5761 -1.92  0   32   4.6  1      MAAINTTGDLR + Oxidation (M)
☑ 2213  874.4667 1746.9188 1746.9120  3.90  1   32   3.2  1      CISLSIEAGQKIGICGR
☑ 1657  695.8837 1389.7528 1389.7504  1.80  1   32   3.1  1      EILKDIFDIER
☑ 2243  877.9757 1753.9368 1753.9397 -1.60  1   32   2.8  1      TMTVLSGAKNISTLFR + Oxidation (M)
☑  670  560.7669 1119.5192 1119.5230 -3.37  0   32   3.7  1      ADCEVTVLDR
☑ 1430  663.3640 1324.7134 1324.7139 -0.35  1   32     3  1      FIAGQEKYITR
☑  628  551.7682 1101.5218 1101.5203  1.40  0   32   2.2  1      ESADAFHGLR
☑  446  502.7469 1003.4792 1003.4822 -2.93  0   32   4.8  1      SGALLDEDGK
☑ 1026  614.3192 1226.6238 1226.6190  3.99  0   32     3  1      CAIIAAANPNGGR
☑  859  595.7762 1189.5378 1189.5397 -1.55  0   32     2  1      EMAEQEAINR
☑ 1004  613.8234 1225.6322 1225.6343 -1.66  0   32   3.7  1      TADVLFEYLR
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☑	413	490.7379	979.4612	979.4644	-3.25	0	32	4.9	1	TGSAAMEAVK + Oxidation (M)
☑	621	549.7706	1097.5266	1097.5288	-1.94	0	32	2.9	1	GVLCHGEDLR
☑	867	398.5350	1192.5832	1192.5870	-3.20	1	32	4.4	1	SLNSAVSKCER
☑	2010	827.4327	1652.8508	1652.8562	-3.26	1	32	4.4	1	GKADYWLVGEFLQK
☑	141	388.7009	775.3872	775.3865	1.02	1	32	8	1	WTADKVG
☑	953	611.3035	1220.5924	1220.5958	-2.78	0	31	5	1	LDLSLSLCDDK
☑	315	456.2815	910.5484	910.5487	-0.32	0	31	1.2	1	QALIPELK
☑	2156	859.9715	1717.9284	1717.9250	1.98	1	31	2.6	1	KAVVDGFEVVSVAEAAK
☑	833	589.7939	1177.5732	1177.5728	0.42	0	31	5.7	1	DGFSAGELGGLR
☑	941	608.8182	1215.6218	1215.6248	-2.42	0	31	5.2	1	GDVIEVFPANR
☑	273	438.7263	875.4380	875.4348	3.66	0	31	7.3	1	NSSVDLNK
☑	1074	622.3533	1242.6920	1242.6931	-0.88	1	31	4.1	1	EAKQALNALSAK
☑	42	359.1880	716.3614	716.3639	-3.45	0	31	6.7	1	CSPAAIR
☑	1873	778.4509	1554.8872	1554.8868	0.26	0	31	1.7	1	EIALTPGLSLTAEIK
☑	1050	618.3354	1234.6562	1234.6557	0.42	1	31	5.9	1	YPRTLETDLK
☑	1866	776.4017	1550.7888	1550.7875	0.88	1	31	5.5	1	NFGNISDMASVLKR
☑	573	538.2495	1074.4844	1074.4885	-3.78	1	31	2.5	1	GVMPPCGRCR
☑	1521	676.3532	1350.6918	1350.6966	-3.50	1	31	6.3	1	MGNSKVVFVDQK
☑	531	530.7663	1059.5180	1059.5196	-1.49	1	31	4.8	1	GELKEENGGK
☑	685	565.2732	1128.5318	1128.5281	3.36	1	31	3.5	1	RMPHTGGMSR
☑	810	584.2970	1166.5794	1166.5754	3.48	0	31	7.1	1	ATDGIMSGFLR
☑	1360	436.5580	1306.6522	1306.6486	2.76	1	31	6.1	1	MLCRAQVSDLR + Oxidation (M)
☑	580	541.2806	1080.5466	1080.5451	1.41	0	31	5.6	1	LNSLESFSGK
☑	790	580.7881	1159.5616	1159.5621	-0.43	1	31	6.1	1	DWKEEALNR
☑	348	467.2374	932.4602	932.4610	-0.84	1	31	4.9	1	AIGCSRGGR + Carbamidomethyl (C)
☑	299	450.2815	898.5484	898.5487	-0.32	1	31	3.2	1	AITKELPK
☑	2316	887.9858	1773.9570	1773.9546	1.37	1	31	3.7	1	VMDILKQISALIGDDK + Oxidation (M)
☑	2222	875.4720	1748.9294	1748.9243	2.93	0	31	4.1	1	YVVSIGACATAGGLQALR
☑	1106	625.8282	1249.6418	1249.6376	3.38	0	31	6.3	1	YILPNMINEK + Oxidation (M)
☑	2212	873.4965	1744.9784	1744.9763	1.21	1	31	2.2	1	FKNIIYYSTIVVSAK
☑	537	531.7581	1061.5016	1061.4989	2.59	1	31	3.9	1	ASPKNDTSDK
☑	1554	452.9128	1355.7166	1355.7157	0.63	1	30	5.2	1	RSLNPDGLDLTR
☑	378	478.7925	955.5704	955.5702	0.25	1	30	3.8	1	KITAEPIGK
☑	1625	691.3298	1380.6450	1380.6456	-0.38	1	30	4.8	1	CEAQQYKEVQR
☑	1505	450.2536	1347.7390	1347.7432	-3.11	0	30	4.1	1	ISCILSSIQSIK + Carbamidomethyl (C)
☑	1414	662.3326	1322.6506	1322.6507	-0.00	0	30	6.3	1	ENEFGIQVYPK
☑	200	407.7246	813.4346	813.4344	0.25	1	30	5.3	1	DPDIKAR
☑	1013	613.8235	1225.6324	1225.6350	-2.07	1	30	5.4	1	CALPGGVGRGSPR
☑	1767	739.3801	1476.7456	1476.7460	-0.24	1	30	6.8	1	ADGKPVDEYLDKK
☑	306	453.2378	904.4610	904.4614	-0.38	0	30	6.2	1	LLNDTSSR
☑	1924	790.4513	1578.8880	1578.8842	2.45	1	30	2	1	QAQGQKHQLTTVLK
☑	546	533.3061	1064.5976	1064.5978	-0.17	0	30	3.8	1	IHEGLEVIR
☑	1971	804.9081	1607.8016	1607.8016	0.04	0	30	6.2	1	HVDDAVANGASVLAGGR
☑	1446	666.8217	1331.6288	1331.6292	-0.27	1	30	5.4	1	TRFPCPSNPEK + Carbamidomethyl (C)
☑	41	358.2095	714.4044	714.4024	2.84	1	30	23	1	NNIKAVG
☑	561	535.7726	1069.5306	1069.5338	-2.99	1	30	5.6	1	CLHKGEDLR
☑	784	580.3074	1158.6002	1158.5993	0.83	1	30	8	1	VDLSRDELGR
☑	697	566.2860	1130.5574	1130.5567	0.62	0	30	6.9	1	EPLSPASTSSR
☑	753	574.7702	1147.5258	1147.5292	-2.89	0	30	5.1	1	VQELNMQDR + Oxidation (M)
☑	45	361.2038	720.3930	720.3918	1.67	0	30	14	1	YAIAGAR
☑	2154	859.9708	1717.9270	1717.9219	3.01	1	30	3.8	1	MVDIISLGIMRGLER + Oxidation (M)
☑	754	574.7709	1147.5272	1147.5292	-1.67	0	30	4.2	1	TLGDCEANLR + Carbamidomethyl (C)
☑	533	530.7673	1059.5200	1059.5197	0.37	1	30	6.6	1	GTPEQTKDGK
☑	352	469.7817	937.5488	937.5457	3.32	1	30	2.4	1	HALRGSGLK
☑	2121	853.4786	1704.9426	1704.9484	-3.40	1	30	2.7	1	EFKAVVLGMGVLVDTK
☑	1083	625.3196	1248.6246	1248.6284	-3.04	1	30	8.1	1	AEANAPMVRYK
☑	1589	684.8796	1367.7446	1367.7408	2.78	1	30	4.2	1	KPDIEEIRGSPK
☑	571	537.7698	1073.5250	1073.5254	-0.35	0	30	7	1	DATTGFGHLR
☑	748	571.3024	1140.5902	1140.5928	-2.20	0	30	5	1	VDIAWLPDGR
☑	1608	688.3740	1374.7334	1374.7354	-1.44	1	30	7.2	1	SSLDKEIESVLR
☑	794	581.7965	1161.5784	1161.5778	0.54	0	30	9.3	1	SAGWAEVSSLR
☑	1280	649.8474	1297.6802	1297.6765	2.88	0	30	5.3	1	LEEIIEVDNPK
☑	1005	613.8234	1225.6322	1225.6350	-2.23	1	30	5.9	1	RMDVGGLGHLR + Oxidation (M)
☑	1477	671.3575	1340.7004	1340.7048	-3.25	0	30	5.7	1	IANGVDAVEAINR
☑	677	562.2835	1122.5524	1122.5557	-2.88	0	30	8.6	1	SDEISFLANK
☑	276	439.7223	877.4300	877.4327	-3.07	0	30	15	1	MAEISVGR + Oxidation (M)
☑	853	594.3046	1186.5946	1186.5942	0.37	1	30	6.9	1	VDIAGEGDQRK
☑	618	548.7907	1095.5668	1095.5673	-0.38	0	30	5.2	1	SPINPGQDLR
☑	319	458.2611	914.5076	914.5073	0.42	0	30	10	1	SPLAASEIK
☑	171	400.7168	799.4190	799.4188	0.30	0	30	5.8	1	TPGEIAGR
☑	807	583.2884	1164.5622	1164.5662	-3.41	0	29	7.7	1	DEEIAAYLNK
☑	980	613.8231	1225.6316	1225.6350	-2.71	1	29	6.3	1	RMSHSVSGPIR
☑	1353	434.2369	1299.6889	1299.6863	1.97	0	29	8.4	1	FLQTKPFYEK
☑	667	560.2858	1118.5570	1118.5529	3.72	0	29	7.9	1	TILIEMEEAA
☑	1533	677.8798	1353.7450	1353.7504	-3.92	1	29	4.7	1	LDELAKIVNPDK
☑	1400	659.3767	1316.7388	1316.7340	3.70	1	29	3.7	1	KIPEDFLNTIK
☑	394	484.7795	967.5444	967.5451	-0.65	1	29	4.3	1	PGKLSDVPR
☑	1147	421.8934	1262.6584	1262.6619	-2.79	0	29	9.4	1	YNATTGALTPVR
☑	1224	642.8506	1283.6866	1283.6834	2.55	0	29	6.4	1	VVGQEPTGQTIR
☑	830	589.7933	1177.5720	1177.5761	-3.42	0	29	8.6	1	NSSLASELAMR
☑	64	366.6983	731.3820	731.3814	0.94	1	29	24	1	KDGGIDK
☑	419	492.7901	983.5656	983.5651	0.52	0	29	4.2	1	PLTDGQLLK
☑	39	358.2088	714.4030	714.4024	0.88	0	29	27	1	IAGVEAR
☑	1596	457.9210	1370.7412	1370.7380	2.31	0	29	7.1	1	AIAEWCLPSLLR
☑	1033	410.8828	1229.6266	1229.6252	1.14	1	29	9.6	1	VPSDKETDAIR
☑	1592	685.8668	1369.7190	1369.7201	-0.78	0	29	7.8	1	KPTDSNNALVSPK
☑	481	515.2509	1028.4872	1028.4887	-1.38	0	29	3.7	1	GTENPEINR
☑	971	613.8230	1225.6314	1225.6303	0.97	0	29	7	1	ESAVVGSPDPIR

☑	52	364.2082	726.4018	726.4024	-0.79	0	29	8.3	1	SAISPPR
☑	495	521.7507	1041.4868	1041.4880	-1.07	0	29	3.3	1	YFGADAGSVR
☑	1865	776.4017	1550.7888	1550.7875	0.88	1	29	9	1	NFGNISDMASVLKR
☑	821	586.3074	1170.6002	1170.6033	-2.61	0	29	6.8	1	PELDNFAPLR
☑	802	582.7961	1163.5776	1163.5782	-0.49	0	29	10	1	TSAILDNTSSR
☑	414	490.7917	979.5688	979.5702	-1.40	0	29	2.9	1	QIGVPPELK
☑	800	582.7845	1163.5544	1163.5539	0.44	1	29	6.3	1	MLQGRGLDCR + Oxidation (M)
☑	1046	618.3039	1234.5932	1234.5976	-3.52	0	29	7.5	1	GSTGVAPSTTAMR
☑	759	575.7826	1149.5506	1149.5522	-1.35	1	29	6.2	1	MPLLDDMKR + 2 Oxidation (M)
☑	1236	645.8444	1289.6742	1289.6768	-1.99	0	29	10	1	TWADYGPLVLR
☑	1325	433.9054	1298.6944	1298.6983	-3.02	1	29	8.2	1	GIFNGPPKVDQK
☑	834	589.7941	1177.5736	1177.5761	-2.08	0	29	10	1	SMTSALEGINR
☑	439	500.2958	998.5770	998.5760	1.03	0	29	8.4	1	LILDEAVAR
☑	1904	784.4001	1566.7856	1566.7831	1.66	0	29	8.3	1	YAEPFSALAWLSGR
☑	500	522.3088	1042.6030	1042.6022	0.78	1	29	9.5	1	KGAIDLADLK
☑	517	527.2593	1052.5040	1052.4999	3.95	0	29	7.3	1	AAHANADDLR
☑	607	545.7730	1089.5314	1089.5302	1.12	0	29	9.8	1	TTLETGPDTR
☑	530	529.3343	1056.6540	1056.6543	-0.21	1	29	2.8	1	KAIISDLIGK
☑	2124	854.4677	1706.9208	1706.9252	-2.53	1	29	4.5	1	IAMVFQKLALMPWK + 2 Oxidation (M)
☑	43	359.6902	717.3658	717.3657	0.20	0	29	24	1	QSADIGK
☑	1412	661.8506	1321.6866	1321.6878	-0.85	0	29	7.2	1	IAVTNLHTPDEI
☑	390	482.7408	963.4670	963.4635	3.68	1	29	12	1	GGGFGGSGRGR
☑	284	442.7579	883.5012	883.5015	-0.25	0	29	5	1	AVPLDEIK
☑	1735	717.3911	1432.7676	1432.7674	0.17	1	29	8.1	1	SNRFVGELPSSLK
☑	1901	784.3996	1566.7846	1566.7831	1.02	0	29	11	1	YAEPFSALAWLSGR
☑	363	473.2592	944.5038	944.5039	-0.09	0	29	12	1	TSGNILGQR
☑	2459	928.0249	1854.0352	1854.0397	-2.38	1	28	3.1	1	IISNMGSANPLAAGKAVLK
☑	366	475.2351	948.4556	948.4526	3.24	1	28	10	1	RSGSGGWSR
☑	1359	436.2380	1305.6922	1305.6929	-0.52	0	28	9.2	1	LDGADVIYLATR
☑	1157	633.3408	1264.6670	1264.6663	0.59	0	28	9.1	1	LAISNYSVVDGK
☑	2993	1123.1250	2244.2354	2244.2338	0.72	0	28	2.8	1	SAGGNPAQIAAQLAAAVALPQGIR
☑	139	388.7007	775.3868	775.3898	-3.85	0	28	17	1	VNQMLGV + Oxidation (M)
☑	603	545.2823	1088.5500	1088.5509	-0.79	1	28	14	1	MAQGSQVGRR
☑	1318	433.9054	1298.6944	1298.6942	0.10	0	28	9.1	1	GALSSAVPAGNLSR
☑	1388	658.3302	1314.6458	1314.6503	-3.36	0	28	7.6	1	ACLHSYAPQGLR
☑	2268	884.9761	1767.9376	1767.9366	0.57	0	28	5.8	1	VDANDAQEIDLIALLR
☑	1036	616.3139	1230.6132	1230.6105	2.20	1	28	10	1	DHGRIVDTYR
☑	2349	895.9866	1789.9586	1789.9574	0.71	1	28	5.9	1	TDPAYLQELVSRLASK
☑	1141	629.8189	1257.6232	1257.6201	2.50	0	28	7.1	1	GVDEQVVEDLR
☑	2358	898.5049	1794.9952	1794.9914	2.16	1	28	3.3	1	LLNKSSGTSFVGMVVLK + Oxidation (M)
☑	2610	1012.4980	2022.9814	2022.9820	-0.26	0	28	8.3	1	LQTALDLVNSTVTMEFEP + Oxidation (M)
☑	2158	860.4680	1718.9214	1718.9216	-0.10	0	28	6	1	AGLGSAHWPALAAALTGR
☑	229	417.2321	832.4496	832.4476	2.40	0	28	15	1	AIMAATGAK
☑	2182	867.4760	1732.9374	1732.9393	-1.09	1	28	5.2	1	SIGCTGVILTKLDGTAK + Carbamidomethyl (C)
☑	904	603.7693	1205.5240	1205.5207	2.75	0	28	3.4	1	CAGGGSSRPDSR + Carbamidomethyl (C)
☑	245	423.2155	844.4164	844.4191	-3.19	0	28	12	1	GAAGDWLR
☑	795	581.7966	1161.5786	1161.5812	-2.16	1	28	13	1	MKIAEQASER
☑	1080	624.8154	1247.6162	1247.6180	-1.41	0	28	13	1	CSVDVVVSDLR + Carbamidomethyl (C)
☑	418	492.7897	983.5648	983.5651	-0.27	0	28	5.4	1	SLPENIALK
☑	259	426.7448	851.4750	851.4727	2.70	1	28	9.3	1	KMFWIK
☑	1853	515.2634	1542.7684	1542.7638	2.95	0	28	8.2	1	SGGQSGPVIGDDSVIR
☑	1519	675.8381	1349.6616	1349.6609	0.56	0	28	11	1	GSTAATLMEAINR + Oxidation (M)
☑	285	442.7579	883.5012	883.5015	-0.25	0	28	5.9	1	IPIEGDLK
☑	1137	420.2147	1257.6223	1257.6176	3.74	1	28	9.3	1	YMAQKAFLDR + Oxidation (M)
☑	858	595.7751	1189.5356	1189.5397	-3.42	0	28	5.5	1	MPSASDPSLNR + Oxidation (M)
☑	186	403.6879	805.3612	805.3640	-3.41	0	28	6.8	1	CSPVDSAK
☑	2318	887.9888	1773.9630	1773.9658	-1.57	1	28	6.4	1	SLCNILEKITAGNGTLK
☑	2143	859.4779	1716.9412	1716.9444	-1.83	0	28	5.8	1	MLDLLNSIGVSASLLR + Oxidation (M)
☑	1695	469.5848	1405.7326	1405.7275	3.60	0	28	10	1	MQFSTEIALAAPK
☑	1526	677.3599	1352.7052	1352.7009	3.18	1	28	9.3	1	KFMSSIEAALEK
☑	1650	464.2573	1389.7501	1389.7537	-2.64	0	28	9.6	1	VMDIISAGTINIK + Oxidation (M)
☑	519	527.2593	1052.5040	1052.4999	3.95	0	28	9.2	1	AAHANADDLR
☑	253	425.7186	849.4226	849.4201	3.05	0	28	10	1	MMLVNSR
☑	832	589.7938	1177.5730	1177.5727	0.29	0	28	14	1	NYEAIDALNR
☑	1894	784.3990	1566.7834	1566.7831	0.25	0	28	11	1	YAEPFSALAWLSGR
☑	307	454.2295	906.4444	906.4481	-3.98	0	28	18	1	ATMLSPSGK + Oxidation (M)
☑	1563	679.3704	1356.7262	1356.7249	1.01	0	28	11	1	SQVNILDLSGSPK
☑	350	467.2541	932.4936	932.4927	1.03	0	28	16	1	DSLLAASTR
☑	1862	776.4014	1550.7882	1550.7875	0.50	1	28	12	1	NMGLGYSLNEGLRK
☑	1221	642.8331	1283.6516	1283.6470	3.65	0	28	11	1	EGDNPAVSLLNR
☑	783	580.3074	1158.6002	1158.6033	-2.65	0	28	14	1	DVLAGTEWLR
☑	498	522.3087	1042.6028	1042.6022	0.59	1	27	13	1	QKILDEIGK
☑	806	583.2870	1164.5594	1164.5631	-3.13	0	27	14	1	SDLLSMIGCAR
☑	438	500.2891	998.5636	998.5648	-1.14	0	27	11	1	TAPLEVELK
☑	1987	812.9094	1623.8042	1623.8039	0.22	1	27	11	1	ISCKGYDVNVLSGGR + Carbamidomethyl (C)
☑	2322	888.4821	1774.9496	1774.9433	3.57	1	27	7.3	1	KASMINNLMVAIVSER
☑	1064	414.8825	1241.6257	1241.6227	2.41	1	27	10	1	SFFQKEVCVR
☑	516	527.2563	1052.4980	1052.4961	1.87	0	27	10	1	CALDVETFR
☑	237	421.7346	841.4546	841.4545	0.16	0	27	7	1	AGIPDEIK
☑	328	461.7659	921.5172	921.5171	0.14	0	27	7.7	1	LSLTLVNY
☑	197	407.2109	812.4072	812.4068	0.50	0	27	8.9	1	FLAGYDK
☑	676	561.8113	1121.6080	1121.6080	0.00	0	27	11	1	LEAGISYTLR
☑	1758	730.3706	1458.7266	1458.7314	-3.29	0	27	14	1	LAQITDLDVDGSGR
☑	1923	790.3993	1578.7840	1578.7824	1.04	1	27	14	1	MDFEEARAVSLVGR
☑	74	372.6980	743.3814	743.3813	0.13	0	27	9.3	1	SPNGEIK
☑	1863	517.9368	1550.7886	1550.7875	0.70	1	27	13	1	VRILSMYSPADQR + Oxidation (M)
☑	513	526.7673	1051.5200	1051.5199	0.11	0	27	13	1	DTAWPGHIR
☑	1911	785.9019	1569.7892	1569.7933	-2.60	0	27	11	1	LSPQTAVTAMTTGHR

☑	451	505.2283	1008.4420	1008.4434	-1.30	0	27	3.7	1	CIETDETAK
☑	2346	895.9860	1789.9574	1789.9509	3.68	1	27	8.6	1	TMQNLSQQLFIAPRK + Oxidation (M)
☑	487	516.3014	1030.5882	1030.5845	3.68	1	27	12	1	AIKCLNELK
☑	1105	625.8097	1249.6048	1249.6051	-0.20	0	27	13	1	YNVGTNAAEVGR
☑	2159	860.4689	1718.9232	1718.9203	1.73	1	27	8.2	1	NKSFIDIGEQLGLSAK
☑	140	388.7008	775.3870	775.3898	-3.57	0	27	23	1	MPGSIQK + Oxidation (M)
☑	1273	646.8151	1291.6156	1291.6116	3.12	1	27	11	1	SSDSSRAEANLR
☑	190	405.2114	808.4082	808.4079	0.41	0	27	20	1	YDGSVIR
☑	499	522.3088	1042.6030	1042.6022	0.80	0	27	15	1	QAIISEAIAK
☑	1288	650.3528	1298.6910	1298.6942	-2.46	1	27	12	1	GIGNETIRNTPK
☑	231	417.7091	833.4036	833.4032	0.56	0	27	26	1	FVSGGDPR
☑	241	422.2448	842.4750	842.4749	0.16	0	27	20	1	LLLDELQ
☑	1404	660.3643	1318.7140	1318.7166	-1.96	0	27	12	1	LSLGLTTDMGALK
☑	1409	660.8672	1319.7198	1319.7198	0.07	0	27	10	1	SPAPPVTQPTAVR
☑	1501	674.3567	1346.6988	1346.7016	-2.07	1	27	18	1	EMQPLFKEGIR
☑	1425	663.3629	1324.7112	1324.7099	1.02	0	27	9.9	1	NERPVIQVDQK
☑	529	529.3125	1056.6104	1056.6114	-0.86	1	27	6.8	1	LPLVNKSMR
☑	1142	629.8190	1257.6234	1257.6201	2.69	0	27	9.9	1	SLSDNIPEDLR
☑	2108	846.9627	1691.9108	1691.9094	0.87	1	27	7.2	1	DIFEGLIGLSNTKSAK
☑	70	368.2060	734.3974	734.3996	-2.99	1	27	30	1	MLKNLT + Oxidation (M)
☑	454	505.7977	1009.5808	1009.5808	0.08	0	27	3.8	1	LKPPEGELK
☑	1543	452.9124	1355.7154	1355.7197	-3.22	0	27	12	1	FLEGLNHVNVSK
☑	1546	452.9125	1355.7157	1355.7197	-3.00	0	27	12	1	FLEGLNHVNVSK
☑	1988	812.9097	1623.8048	1623.8039	0.61	1	27	14	1	KTAMVSAYAGQLNDR
☑	551	533.3065	1064.5984	1064.5978	0.59	0	27	7.8	1	IHEGLEVIR
☑	2211	873.4960	1744.9774	1744.9763	0.64	1	27	5.4	1	FKNIIYYSTIVVSAK
☑	552	533.7924	1065.5702	1065.5706	-0.33	1	27	11	1	LSLKDFSEK
☑	1731	715.4048	1428.7950	1428.7936	0.99	1	27	10	1	GIEGTGKVVGANISK
☑	2332	890.9833	1779.9520	1779.9553	-1.82	1	27	9.4	1	VLTMEYIGGTKISNVR
☑	591	543.2659	1084.5172	1084.5189	-1.53	1	27	8.3	1	EYLDDRFK
☑	34	358.1961	714.3776	714.3773	0.50	0	27	7.6	1	QVGAGGAR
☑	286	442.7579	883.5012	883.5015	-0.25	0	27	8.1	1	AVPLDEIK
☑	402	487.2512	972.4878	972.4876	0.23	0	27	16	1	VDIQDDLR
☑	805	582.7967	1163.5788	1163.5757	2.71	0	27	18	1	MANSAFPLASR
☑	816	585.8160	1169.6174	1169.6153	1.87	1	27	9.8	1	LNDGGINKSPR
☑	1541	452.9124	1355.7154	1355.7157	-0.25	0	27	13	1	QILQQEAGVASGR
☑	309	454.7364	907.4582	907.4611	-3.10	0	27	10	1	AGASSSSTLK
☑	2259	881.4743	1760.9340	1760.9342	-0.08	1	27	11	1	MANSVLEIKNASLDIK + Oxidation (M)
☑	3288	791.4530	2371.3372	2371.3297	3.15	0	27	1.9	1	YGAIATVVSLSMNVALNLALVPR
☑	2586	989.5010	1976.9874	1976.9843	1.57	0	26	14	1	EGDAAYAVGTLYPDLAPVR
☑	365	473.7502	945.4858	945.4879	-2.22	0	26	19	1	IQTLNDSR
☑	989	613.8232	1225.6318	1225.6349	-2.53	1	26	13	1	RLDLSNCHLR
☑	458	506.8052	1011.5958	1011.5964	-0.57	0	26	6.2	1	KPIIDADIK
☑	69	368.2054	734.3962	734.3963	-0.05	0	26	15	1	FIINQT
☑	1952	530.9754	1589.9044	1589.9001	2.66	1	26	3.7	1	ALLHGLGRVLGEEAR
☑	624	367.8898	1100.6476	1100.6454	1.93	1	26	8.1	1	TRAPPPPPLR
☑	1176	637.3611	1272.7076	1272.7078	-0.10	0	26	15	1	IAEAGFGAVTLPK
☑	322	458.2792	914.5438	914.5437	0.21	0	26	16	1	ALTAELLGK
☑	625	551.7676	1101.5206	1101.5203	0.31	0	26	12	1	HSQEDAFLR
☑	1734	715.8997	1429.7848	1429.7816	2.24	0	26	8.7	1	VEYIPLVEEALR
☑	1420	663.3391	1324.6636	1324.6596	3.07	1	26	12	1	ISSDNHNNRIR
☑	369	477.2380	952.4614	952.4648	-3.48	0	26	11	1	MSTISSTAR
☑	935	608.7661	1215.5176	1215.5190	-1.10	0	26	2.4	1	EMDPSSPSNPR
☑	310	455.2550	908.4954	908.4967	-1.38	0	26	14	1	ASTYINLK
☑	1138	629.8185	1257.6224	1257.6201	1.89	0	26	14	1	SLSDNIPEDLR
☑	1309	433.9052	1298.6938	1298.6904	2.60	0	26	15	1	MNIELPGITAPK + Oxidation (M)
☑	1654	695.8833	1389.7520	1389.7504	1.21	1	26	13	1	LGKIENDVLFDK
☑	1455	667.3721	1332.7296	1332.7249	3.59	1	26	13	1	DKSGSLASLASVAK
☑	1372	655.3415	1308.6684	1308.6674	0.83	1	26	15	1	SAESFAKVSDLR
☑	2047	841.4192	1680.8238	1680.8254	-0.90	1	26	15	1	CSGAIAKTFTGQEVGR + Carbamidomethyl (C)
☑	1999	821.9601	1641.9056	1641.9050	0.41	0	26	8.1	1	ALTNLTNNVQGVLSAK
☑	608	364.4911	1090.4515	1090.4536	-1.91	0	26	2	1	HDMMDSAIR + Oxidation (M)
☑	447	503.7618	1005.5090	1005.5091	-0.05	0	26	14	1	VDITQTSSR
☑	610	546.3087	1090.6028	1090.6022	0.58	1	26	18	1	LKNYESLPK
☑	1861	776.4012	1550.7878	1550.7882	-0.20	1	26	17	1	PSVVWFAYSPDRK
☑	1574	682.3526	1362.6906	1362.6887	1.44	0	26	17	1	LEMVMQLLGGEK + Oxidation (M)
☑	2040	838.8820	1675.7494	1675.7472	1.36	0	26	7.4	1	LANDCAVPGTDSVSDR + Carbamidomethyl (C)
☑	789	580.7860	1159.5574	1159.5582	-0.61	1	26	10	1	DDTGAVAERAR
☑	1793	760.3687	1518.7228	1518.7283	-3.58	1	26	15	1	VGECTPGRMDSVLR
☑	29	351.2008	700.3870	700.3868	0.38	1	26	51	1	QGIRID
☑	1984	812.3688	1622.7230	1622.7246	-0.95	0	26	8.4	1	NIICYQENSEEPK + Carbamidomethyl (C)
☑	862	595.8045	1189.5944	1189.5979	-2.89	0	26	19	1	IDLLYHDSSK
☑	3277	1180.5930	2359.1714	2359.1665	2.11	1	26	15	1	VLMFQGTGSDVGKSVLTAAFCR + Carbamidomethyl (C); Oxidation (M)
☑	598	543.8297	1085.6448	1085.6444	0.38	1	26	12	1	IKDTILIDR
☑	629	551.7682	1101.5218	1101.5237	-1.65	1	26	9	1	RMDAEDPLR
☑	1207	641.3527	1280.6908	1280.6877	2.45	1	26	11	1	KWNAVDPVQPK
☑	1974	805.9409	1609.8672	1609.8675	-0.17	0	26	13	1	ADDAPDLVATGLALIR
☑	489	518.7449	1035.4752	1035.4767	-1.43	1	26	11	1	GRMSDADLR + Oxidation (M)
☑	882	599.3352	1196.6558	1196.6513	3.78	0	26	14	1	QTEVPLAANVR
☑	2572	975.4888	1948.9630	1948.9577	2.72	1	26	16	1	VACLGPWNYEGRIGATSR
☑	2123	853.9506	1705.8866	1705.8821	2.66	0	26	18	1	MNPHQPITLDAALASK
☑	2196	868.9617	1735.9088	1735.9039	2.84	1	26	14	1	ACYVLQSRAGNIVSAK + Carbamidomethyl (C)
☑	490	518.7457	1035.4768	1035.4767	0.10	0	26	15	1	AGCTGSGASLR + Carbamidomethyl (C)
☑	556	534.7644	1067.5142	1067.5103	3.67	1	26	17	1	ACETMKTLR + Oxidation (M)
☑	649	554.7793	1107.5440	1107.5482	-3.71	0	26	16	1	TTLLAEMDSK
☑	1494	672.3932	1342.7718	1342.7708	0.81	1	26	8	1	VEEISPKTVTLK
☑	1743	482.2313	1443.6721	1443.6776	-3.85	0	26	13	1	GAETCGPIVQEQR + Carbamidomethyl (C)
☑	2257	881.4718	1760.9290	1760.9342	-2.93	1	26	16	1	AMINASDKVVLLADSAK + Oxidation (M)

☑	397	485.2847	968.5548	968.5542	0.65	0	26	6.6	1	AGIEPLELK
☑	525	528.7886	1055.5626	1055.5611	1.46	1	26	17	1	IPNDKGPTSK
☑	866	596.8134	1191.6122	1191.6104	1.58	1	26	21	1	MINNMKSAGVK
☑	567	535.7775	1069.5404	1069.5404	0.08	0	26	14	1	QINPDINEK
☑	1132	629.8179	1257.6212	1257.6255	-3.35	0	26	16	1	SSIHFFHDLR
☑	1159	633.3411	1264.6676	1264.6663	1.06	0	26	17	1	AIISYQTDQVK
☑	194	405.7397	809.4648	809.4647	0.21	1	26	8.4	1	AYTSKIK
☑	2030	834.9097	1667.8048	1667.8114	-3.95	1	25	16	1	TDEEEAHRILAEQK
☑	557	535.2567	1068.4988	1068.4948	3.78	0	25	13	1	HAQGAESNQK
☑	1434	664.3521	1326.6896	1326.6891	0.38	1	25	15	1	NEPVSREVLER
☑	1591	685.3580	1368.7014	1368.6997	1.25	0	25	14	1	SGLTSAHVQVNEK
☑	696	565.7651	1129.5156	1129.5152	0.37	0	25	9.6	1	FPNAGPQEDR
☑	300	450.2818	898.5490	898.5487	0.35	1	25	11	1	ALETPLKK
☑	331	463.7296	925.4446	925.4480	-3.62	0	25	7.8	1	FYMNPVR
☑	1163	634.8275	1267.6404	1267.6417	-0.99	0	25	15	1	GMVTLFMQGLR + Oxidation (M)
☑	1663	697.3714	1392.7282	1392.7283	-0.03	1	25	18	1	DKMVVVTGLSGSGK + Oxidation (M)
☑	652	557.2973	1112.5800	1112.5839	-3.47	1	25	17	1	QRSWPGNIR
☑	854	594.3053	1186.5960	1186.5942	1.58	0	25	18	1	QNLQEASIER
☑	1215	642.3337	1282.6528	1282.6558	-2.27	0	25	17	1	TVSIDFFEGIR
☑	1432	663.8384	1325.6622	1325.6575	3.58	0	25	19	1	AEAPDAVAEANLR
☑	336	464.7458	927.4770	927.4774	-0.33	0	25	11	1	KPAANNADK
☑	432	496.2630	990.5114	990.5134	-2.00	0	25	21	1	PAAYSVDLR
☑	666	560.2769	1118.5392	1118.5390	0.23	0	25	22	1	EMTVGEALNR
☑	700	566.7981	1131.5816	1131.5812	0.43	0	25	29	1	ASPPLLDEYK
☑	2109	846.9630	1691.9114	1691.9062	3.10	1	25	11	1	AIGRLSSMAMISGLSAK
☑	216	415.2293	828.4440	828.4454	-1.58	1	25	24	1	QRILGDQ
☑	1468	670.3657	1338.7168	1338.7183	-1.10	1	25	18	1	ISLKYEFGAPSK
☑	1133	420.2145	1257.6217	1257.6201	1.27	0	25	18	1	ALVDEQAEDLR
☑	398	485.7455	969.4764	969.4767	-0.24	1	25	8.5	1	KENPEPEK
☑	249	423.7213	845.4280	845.4283	-0.30	0	25	8.1	1	YPEVNPK
☑	1205	640.8287	1279.6428	1279.6408	1.57	0	25	21	1	TFLGGATTEDLR
☑	468	509.2646	1016.5146	1016.5138	0.79	0	25	31	1	LQVETAGDGK
☑	1652	695.8831	1389.7516	1389.7551	-2.45	1	25	18	1	ELIQFACRLAAR
☑	151	394.2318	786.4490	786.4487	0.44	0	25	41	1	LLTEAGLA
☑	255	425.7190	849.4234	849.4201	3.99	0	25	37	1	MMLVNSR
☑	329	462.7737	923.5328	923.5328	0.09	0	25	8.2	1	SSITYILK
☑	1538	452.9122	1355.7148	1355.7157	-0.69	1	25	19	1	RSLNPDGLDLTR
☑	1402	440.5782	1318.7128	1318.7092	2.70	1	25	19	1	ISNSNTSLDKIK
☑	1174	425.2307	1272.6703	1272.6674	2.29	0	25	24	1	LSINELEGVGSR
☑	373	477.7791	953.5436	953.5447	-1.08	1	25	11	1	SHGWVKIK
☑	690	377.1954	1128.5644	1128.5638	0.54	0	25	14	1	SFNCYVVLK + Carbamidomethyl (C)
☑	1524	677.3034	1352.5922	1352.5887	2.63	1	25	8.9	1	AGMDVVMDRCPK + 2 Oxidation (M)
☑	460	506.8059	1011.5972	1011.5964	0.82	0	25	9.9	1	KPIIDADIK
☑	1165	423.5548	1267.6426	1267.6449	-1.80	1	25	18	1	FFEKQIADGIT
☑	38	358.2087	714.4028	714.4024	0.60	0	25	73	1	VEIQAR
☑	2439	917.9761	1833.9376	1833.9441	-3.51	1	25	21	1	SCGQIVNVASMAGKIGTAK
☑	1373	655.8327	1309.6508	1309.6523	-1.08	0	25	17	1	SSFMPGVLMGIR + Oxidation (M)
☑	1506	450.2536	1347.7390	1347.7432	-3.11	0	25	15	1	ISCILSSIQSIK + Carbamidomethyl (C)
☑	828	589.7921	1177.5696	1177.5728	-2.64	0	25	19	1	GFDSVAAGDALR
☑	815	585.8157	1169.6168	1169.6180	-0.94	0	25	15	1	ILLVEDEDPK
☑	2180	867.4759	1732.9372	1732.9393	-1.20	1	25	12	1	SIGCTGVILTKLDGTAK + Carbamidomethyl (C)
☑	138	387.2423	772.4700	772.4695	0.75	0	25	16	1	LATVLTVG
☑	1059	620.8477	1239.6808	1239.6823	-1.16	1	25	12	1	KQPINDIDGIK
☑	1027	409.8829	1226.6269	1226.6255	1.13	0	25	19	1	LNGPEQAETLR
☑	2119	569.3092	1704.9058	1704.9086	-1.69	0	25	15	1	APFFLPSIDSAAAISAK
☑	501	522.7520	1043.4894	1043.4883	1.06	1	25	14	1	SHLDAATSKD
☑	217	415.2294	828.4442	828.4415	3.30	0	25	27	1	IMDLPPK + Oxidation (M)
☑	942	608.8182	1215.6218	1215.6208	0.90	0	25	24	1	ANSSGDQVLIGR
☑	1508	450.2539	1347.7399	1347.7398	0.05	1	25	17	1	ELGADFQLTVKK
☑	2251	879.4339	1756.8532	1756.8596	-3.59	0	25	19	1	MLMGVLCTSLLLSGCK + Carbamidomethyl (C); 2 Oxidation (M)
☑	1281	649.8478	1297.6810	1297.6765	3.48	0	25	18	1	VEEVDLPAGIEK
☑	1158	633.3408	1264.6670	1264.6663	0.59	0	25	22	1	LAISNYSVVDGK
☑	757	575.2906	1148.5666	1148.5682	-1.32	0	25	19	1	LNELINMMR + Oxidation (M)
☑	421	493.2516	984.4886	984.4876	1.02	1	25	21	1	VDITKGTDH
☑	3278	1180.5930	2359.1714	2359.1656	2.49	1	25	20	1	VPDAGEVLVDGYPVSRLSDSER
☑	2176	867.4749	1732.9352	1732.9393	-2.34	1	24	14	1	DIAKLTCAVQSSVLSAK
☑	584	542.3409	1082.6672	1082.6699	-2.47	0	24	4.9	1	VLSILLNPSK
☑	1166	634.8286	1267.6426	1267.6383	3.41	1	24	19	1	WTTKGEMFIR
☑	1006	613.8234	1225.6322	1225.6302	1.64	0	24	20	1	AESAAPEVSPLR
☑	1375	656.8327	1311.6508	1311.6493	1.21	0	24	21	1	IMLEHPSVNEK + Oxidation (M)
☑	312	455.7413	909.4680	909.4668	1.36	0	24	19	1	LNPEPGQR
☑	593	543.7702	1085.5258	1085.5288	-2.69	1	24	17	1	SCPDKNPGLR
☑	766	576.7849	1151.5552	1151.5571	-1.59	1	24	15	1	GKSIGEEYGGR
☑	1620	690.8315	1379.6484	1379.6463	1.54	1	24	19	1	DRSTGSSCLAEVR
☑	1275	648.3332	1294.6518	1294.6492	2.03	0	24	19	1	TWMHELPPLR + Oxidation (M)
☑	358	471.7434	941.4722	941.4753	-3.22	1	24	16	1	GPGCPKDIR
☑	1487	448.2358	1341.6856	1341.6888	-2.40	0	24	21	1	KPINASNEVENK
☑	1278	649.8227	1297.6308	1297.6349	-3.16	0	24	22	1	ANCIASLWQHR
☑	1068	621.8213	1241.6280	1241.6252	2.33	0	24	19	1	GTEEEGLAPALR
☑	3097	1146.0660	2290.1174	2290.1086	3.88	1	24	21	1	VISNLNKCYAMAELVDGGEHK
☑	40	358.2089	714.4032	714.4024	1.16	0	24	83	1	VEIQAR
☑	1708	707.3767	1412.7388	1412.7334	3.89	0	24	21	1	NEGGMLPLVPGSVK + Oxidation (M)
☑	1610	459.2532	1374.7378	1374.7354	1.71	1	24	22	1	ATDKATALESQIK
☑	955	611.3075	1220.6004	1220.6005	-0.08	0	24	32	1	MAILNTAGMQR + Oxidation (M)
☑	2414	911.5142	1821.0138	1821.0108	1.65	1	24	7.7	1	TSVNGTLPVHGAKNSVLK
☑	305	451.2242	900.4338	900.4341	-0.28	1	24	9	1	KDYYANK
☑	1214	428.5582	1282.6528	1282.6517	0.82	0	24	22	1	LLDPAGADGADLR
☑	813	585.2744	1168.5342	1168.5369	-2.25	0	24	11	1	CLANAMFLDR + Oxidation (M)

☑	1557	678.8661	1355.7176	1355.7157	1.42	1	24	20	1	ELGRVGAAGGVDAGK
☑	1864	776.4016	1550.7886	1550.7909	-1.44	1	24	26	1	NVSMGRSMASVIGVK + Oxidation (M)
☑	2120	853.4604	1704.9062	1704.9086	-1.41	0	24	17	1	APFFLPSIDSAAAISAK
☑	1161	423.5536	1267.6390	1267.6349	3.19	1	24	21	1	KFFEHYEIR
☑	1410	661.3452	1320.6758	1320.6748	0.80	0	24	29	1	VMVLFQDVDGAK
☑	3365	1224.7060	2447.3974	2447.4012	-1.54	0	24	2.5	1	NALVAGSLLLLAANLAALGGVAWNR
☑	505	522.7939	1043.5732	1043.5764	-3.01	1	24	36	1	VIKTFDGHK
☑	135	386.2340	770.4534	770.4538	-0.43	0	24	26	1	IPTAEIK
☑	1218	642.8246	1283.6346	1283.6398	-3.98	0	24	20	1	FYLETEVDLR
☑	755	383.5328	1147.5766	1147.5808	-3.68	1	24	33	1	GFCRLEAQPK
☑	1237	645.8510	1289.6874	1289.6874	0.05	1	24	26	1	QAMTASLLSGRR
☑	1139	629.8188	1257.6230	1257.6201	2.37	0	24	19	1	SLSDNIPEDLR
☑	1675	699.8356	1397.6566	1397.6575	-0.61	0	24	17	1	NEIYESFNINR
☑	769	576.8024	1151.5902	1151.5935	-2.79	1	24	22	1	DIGSSLNYKR
☑	1047	618.3046	1234.5946	1234.5976	-2.37	0	24	27	1	MATSAATLGSPGR + Oxidation (M)
☑	623	550.7604	1099.5062	1099.5047	1.42	0	24	12	1	WTGHDTDLR
☑	457	506.8051	1011.5956	1011.5964	-0.78	0	24	11	1	QIEVPVSIK
☑	2866	1100.6080	2199.2014	2199.2025	-0.46	1	24	9.5	1	LINWPAANRVVEAAALHAQR
☑	122	382.7007	763.3868	763.3865	0.51	0	24	62	1	FDIVDR
☑	168	399.7271	797.4396	797.4395	0.13	0	24	21	1	DPVLGAAR
☑	756	574.8188	1147.6230	1147.6237	-0.57	0	24	32	1	DIQIILYDR
☑	985	613.8232	1225.6318	1225.6350	-2.54	1	24	23	1	RMTANPVQGPR
☑	1892	784.3989	1566.7832	1566.7790	2.69	1	24	27	1	SVPREFYSGLAEGR
☑	888	600.7741	1199.5336	1199.5306	2.56	0	24	10	1	EQEPSQEPEK
☑	183	401.7555	801.4964	801.4960	0.56	0	24	24	1	ITAVLTGK
☑	2125	854.4680	1706.9214	1706.9203	0.67	1	24	14	1	YLVAIGGSPGSGKTTTAK
☑	617	548.3048	1094.5950	1094.5972	-1.92	1	24	16	1	VTASKADYIK
☑	2337	893.4788	1784.9430	1784.9380	2.81	1	24	23	1	ENLSGGNQAQLQKSALK
☑	463	507.2977	1012.5808	1012.5804	0.40	0	24	27	1	ILGLLDEAGL
☑	864	596.8081	1191.6016	1191.5996	1.69	0	24	26	1	LNVGDDPHLGR
☑	1160	633.8419	1265.6692	1265.6728	-2.80	0	24	23	1	LQGSEHLAVGGAK
☑	1333	433.9055	1298.6947	1298.6904	3.29	0	24	27	1	MNIELPGITAPK + Oxidation (M)
☑	1219	642.8263	1283.6380	1283.6405	-1.88	0	24	29	1	ISSQCGVHAGLR + Carbamidomethyl (C)
☑	827	589.7866	1177.5586	1177.5628	-3.56	0	24	26	1	FNSQHYNLR
☑	149	394.2314	786.4482	786.4487	-0.59	1	24	57	1	IITDKTP
☑	1518	450.5823	1348.7251	1348.7238	0.94	1	24	24	1	LSEADVFLAKEK
☑	1451	445.2503	1332.7291	1332.7249	3.16	1	24	23	1	LSQESNSLISKK
☑	2148	573.3216	1716.9430	1716.9410	1.14	0	24	14	1	SLASFLPSQLLGSIER
☑	507	523.2623	1044.5100	1044.5087	1.25	0	23	29	1	VDIDELEGR
☑	2226	875.4735	1748.9324	1748.9308	0.92	1	23	17	1	LNYDIKVETQGATGIK
☑	1426	442.5778	1324.7116	1324.7139	-1.77	1	23	18	1	FIAGQEKYITR
☑	482	515.2524	1028.4902	1028.4895	0.68	0	23	20	1	CSMIGHPIR + Oxidation (M)
☑	152	394.2319	786.4492	786.4487	0.68	1	23	38	1	IITDKTP
☑	768	576.7861	1151.5576	1151.5539	3.22	1	23	26	1	SCMRVTLNR + Carbamidomethyl (C); Oxidation (M)
☑	906	603.8019	1205.5892	1205.5928	-2.95	0	23	31	1	DEGIIFDLER
☑	2237	876.5000	1750.9854	1750.9804	2.90	1	23	7.9	1	KVFKPAPVEMLDHIK
☑	2637	1031.0260	2060.0374	2060.0295	3.84	1	23	27	1	CFLKCDNVLSNLAIGHTR + Carbamidomethyl (C)
☑	2027	832.3882	1662.7618	1662.7672	-3.20	0	23	19	1	AQSGGPVEDAVFAEMR
☑	836	589.7946	1177.5746	1177.5761	-1.23	0	23	32	1	SMTSALEGINR
☑	1640	693.3759	1384.7372	1384.7422	-3.60	1	23	27	1	EALANEILGSGRR
☑	2224	875.4731	1748.9316	1748.9308	0.47	0	23	18	1	AAPEPAVTPQLEQLSAK
☑	115	380.6951	759.3756	759.3763	-0.81	0	23	54	1	QEGGELK
☑	121	382.7002	763.3858	763.3865	-0.80	0	23	35	1	FDDVIR
☑	1500	673.3724	1344.7302	1344.7323	-1.51	0	23	29	1	GLIVIDMSSIGPK + Oxidation (M)
☑	2193	867.9703	1733.9260	1733.9312	-2.94	1	23	24	1	FIAASNTNIQEKIASK
☑	765	576.2830	1150.5514	1150.5553	-3.35	1	23	35	1	MRDFAENLR
☑	958	408.8791	1223.6155	1223.6146	0.73	0	23	26	1	SSAASYAAIDLR
☑	1429	442.5784	1324.7134	1324.7173	-2.97	1	23	23	1	MLSLKFGTSGLR + Oxidation (M)
☑	987	613.8232	1225.6318	1225.6350	-2.55	1	23	27	1	VDGGRGIMHLR + Oxidation (M)
☑	962	613.8227	1225.6308	1225.6350	-3.36	1	23	28	1	CALRDHGVSLR
☑	2185	867.4764	1732.9382	1732.9359	1.35	1	23	17	1	YVELVQQSLELEKR
☑	355	471.2871	940.5596	940.5593	0.36	1	23	17	1	KLDPVELK
☑	1842	765.9072	1529.7998	1529.8024	-1.66	1	23	33	1	WNDAMKNLNLAIK
☑	664	559.7659	1117.5172	1117.5186	-1.20	1	23	16	1	SCPDNKADLR
☑	260	426.7450	851.4754	851.4752	0.23	0	23	29	1	AITASVYK
☑	494	521.3008	1040.5870	1040.5866	0.45	1	23	20	1	LPADDAAKLK
☑	856	594.8164	1187.6182	1187.6146	3.08	1	23	44	1	KDLPSASLSDR
☑	95	376.7006	751.3866	751.3864	0.27	0	23	43	1	YDVSIR
☑	1104	625.8094	1249.6042	1249.6085	-3.38	0	23	33	1	SGSGLQSSAGLMR
☑	116	380.6955	759.3764	759.3763	0.24	0	23	57	1	NISEGIQ
☑	1277	649.7986	1297.5826	1297.5835	-0.65	0	23	17	1	MHPSFYMLEK + Oxidation (M)
☑	527	528.7891	1055.5636	1055.5611	2.40	1	23	28	1	IPDNQVDKK
☑	968	613.8229	1225.6312	1225.6349	-3.02	1	23	29	1	HMEQLAGRIR + Oxidation (M)
☑	448	503.7618	1005.5090	1005.5091	-0.05	0	23	29	1	VDITQTSSR
☑	1900	784.3995	1566.7844	1566.7831	0.89	0	23	39	1	YAEPFSALAWLSGR
☑	1550	452.9127	1355.7163	1355.7197	-2.56	1	23	30	1	LRSLFGNDPLPQ
☑	1867	517.9369	1550.7889	1550.7940	-3.31	1	23	36	1	ELATVSDYLDAAKR
☑	662	559.7646	1117.5146	1117.5152	-0.53	0	23	22	1	SHFQTDDLR
☑	1131	420.2142	1257.6208	1257.6176	2.55	0	23	30	1	VLAPEGAMWER
☑	1312	650.3542	1298.6938	1298.6942	-0.30	1	23	32	1	SSNLSPRSGIGPK
☑	1898	523.2686	1566.7840	1566.7790	3.15	1	23	36	1	SVPREFYSGLAEGR
☑	1448	445.2502	1332.7288	1332.7323	-2.61	1	23	27	1	ELIMSVGLAKEK + Oxidation (M)
☑	1023	613.8242	1225.6338	1225.6349	-0.90	1	23	30	1	MHSARLQDLR
☑	2502	943.4734	1884.9322	1884.9345	-1.20	0	23	30	1	SVTLFSAAFCAWQIWR
☑	1016	613.8236	1225.6326	1225.6302	1.97	0	23	28	1	ENLQEIDPIR
☑	1082	625.3190	1248.6234	1248.6211	1.89	0	23	32	1	DHGVGIAPEAQR
☑	251	424.2416	846.4686	846.4712	-2.97	0	23	19	1	AIEHHLK
☑	737	568.7969	1135.5792	1135.5768	2.17	1	23	27	1	TRSQSSVLCR

☑	1164	634.8280	1267.6414	1267.6455	-3.20	1	23	29	1	MRLAAHDEGLR
☑	702	566.8041	1131.5936	1131.5924	1.10	1	23	43	1	QSKVEEWVK
☑	2642	1033.5100	2065.0054	2065.0078	-1.13	0	23	37	1	IMPDYYDSLSNLPDVPVK
☑	725	568.7955	1135.5764	1135.5729	3.11	1	23	41	1	ACKDVLASAMK
☑	1121	628.8109	1255.6072	1255.6091	-1.49	1	23	27	1	RHADSAMAEIR
☑	371	477.2867	952.5588	952.5593	-0.47	1	23	7.8	1	KLPEPEIK
☑	1186	637.8155	1273.6164	1273.6150	1.14	0	23	32	1	NDLLATDEDLR
☑	616	547.8148	1093.6150	1093.6131	1.74	0	23	19	1	EHGLEGIVIK
☑	2008	825.9084	1649.8022	1649.8051	-1.74	0	23	39	1	AIMQSGACAALLAAMR + Carbamidomethyl (C); Oxidation (M)
☑	738	568.7970	1135.5794	1135.5768	2.36	1	23	28	1	SSCTRNSLLR
☑	1112	418.2234	1251.6484	1251.6493	-0.71	1	23	39	1	SSLITSQNMKK + Oxidation (M)
☑	1449	445.2502	1332.7288	1332.7249	2.93	0	23	28	1	VSNSSALSLSQIK
☑	1622	690.8443	1379.6740	1379.6721	1.41	0	23	37	1	IIYPNGFENGEK
☑	1403	660.3639	1318.7132	1318.7180	-3.58	1	23	32	1	MVRFVLASGSPR
☑	913	604.8101	1207.6056	1207.6084	-2.32	0	23	47	1	EFSSDLIIER
☑	1587	684.8622	1367.7098	1367.7045	3.92	0	23	33	1	GDPAVDLLNADLR
☑	1454	667.3721	1332.7296	1332.7257	2.95	1	23	28	1	NQLKMAGSMLIK
☑	945	406.5551	1216.6435	1216.6411	1.91	0	23	40	1	QSDLILGASSAR
☑	2220	874.9822	1747.9498	1747.9542	-2.50	0	23	21	1	VAMIGFAAALLGEAITGK + Oxidation (M)
☑	308	454.2297	906.4448	906.4420	3.14	1	23	60	1	NGFNSGRR
☑	1220	642.8321	1283.6496	1283.6470	2.10	0	23	32	1	EGDNPAVSLLNR
☑	1779	751.3862	1500.7578	1500.7572	0.40	0	23	35	1	GITYPIPGNDDAIR
☑	925	606.7928	1211.5710	1211.5683	2.26	0	23	25	1	VASDEAHAWAR
☑	1209	428.2301	1281.6685	1281.6717	-2.55	1	22	35	1	EKVPDPGAWGVK
☑	2147	859.4785	1716.9424	1716.9410	0.85	1	22	18	1	ARVALIYEETPGISAK
☑	601	545.2811	1088.5476	1088.5502	-2.35	0	22	47	1	SPIIPDYER
☑	109	379.2138	756.4130	756.4130	0.07	0	22	37	1	PLVSDAR
☑	477	514.7595	1027.5044	1027.5022	2.24	0	22	19	1	CWHSILNR
☑	569	537.3036	1072.5926	1072.5917	0.91	0	22	24	1	AGITNPYIPK
☑	596	543.7708	1085.5270	1085.5301	-2.82	0	22	22	1	CHLNHGHLR
☑	1869	776.4022	1550.7898	1550.7909	-0.66	1	22	40	1	NVSMGRSMASVIGVK + Oxidation (M)
☑	1063	621.8197	1241.6248	1241.6227	1.77	1	22	27	1	KCNLYEFIR + Carbamidomethyl (C)
☑	1070	621.8215	1241.6284	1241.6252	2.65	0	22	29	1	ESAPDILNIDR
☑	632	551.7689	1101.5232	1101.5203	2.67	0	22	20	1	ADGQQWELR
☑	675	561.7798	1121.5450	1121.5474	-2.09	1	22	26	1	ACLCSVWRK + Carbamidomethyl (C)
☑	486	516.2542	1030.4938	1030.4931	0.75	0	22	32	1	NVIEENEGK
☑	785	580.3074	1158.6002	1158.5993	0.84	1	22	46	1	EGSAIIKDNGR
☑	1628	691.8744	1381.7342	1381.7314	2.07	1	22	29	1	KDGIQTHDVLTR
☑	2359	898.5078	1795.0010	1794.9953	3.18	0	22	14	1	AYFSSAIMIIAIPTGIK
☑	242	422.2452	842.4758	842.4749	1.11	0	22	12	1	LLLDELQ
☑	2275	886.9809	1771.9472	1771.9428	2.52	1	22	31	1	NTKLNAEASGLSGELLR
☑	2392	905.4310	1808.8474	1808.8468	0.34	0	22	28	1	SEPASADSDGPLYLPYK
☑	1460	667.8398	1333.6650	1333.6626	1.81	1	22	45	1	TVDAGKVYNDPR
☑	1527	451.9092	1352.7058	1352.7048	0.72	1	22	33	1	GSSLGSQIYARSK
☑	609	546.3082	1090.6018	1090.6022	-0.37	0	22	44	1	IQDFTLNLK
☑	1125	629.3767	1256.7388	1256.7340	3.88	0	22	15	1	SILQDLLGSLAK
☑	24	350.6906	699.3666	699.3664	0.36	0	22	18	1	VGGPGSAR
☑	960	613.8222	1225.6298	1225.6303	-0.34	0	22	28	1	ESAVVGSPDPIR
☑	1961	534.2657	1599.7753	1599.7740	0.79	0	22	38	1	QNTDEQLPSIQEAK
☑	891	601.3091	1200.6036	1200.6026	0.83	1	22	28	1	KYIDDTGVYK
☑	1032	615.8203	1229.6260	1229.6265	-0.36	1	22	46	1	RQNNGEFPIR
☑	1134	629.8182	1257.6218	1257.6201	1.40	0	22	35	1	DLPSDQSLDLR
☑	750	572.2805	1142.5464	1142.5502	-3.31	0	22	31	1	QQDAVNPCLR
☑	362	472.2948	942.5750	942.5749	0.12	1	22	20	1	KIAIEEIK
☑	1484	671.3613	1340.7080	1340.7088	-0.60	0	22	32	1	QSLPVPYDGLPR
☑	2181	867.4760	1732.9374	1732.9359	0.87	1	22	20	1	INDIFAGKGVTEAIGTK
☑	2321	888.4817	1774.9488	1774.9474	0.84	0	22	25	1	FIPMAAVICLGANLASK + Carbamidomethyl (C)
☑	440	500.7867	999.5588	999.5600	-1.18	0	22	39	1	AQALVEEIK
☑	2149	859.4796	1716.9446	1716.9410	2.13	1	22	19	1	ARVALIYEETPGISAK
☑	3168	771.3803	2311.1191	2311.1274	-3.59	1	22	32	1	NRPGPGAEPSCARCGTVLSQVR + Carbamidomethyl (C)
☑	1575	455.2518	1362.7336	1362.7329	0.46	1	22	38	1	FAIIKMPSGEVR + Oxidation (M)
☑	2146	859.4784	1716.9422	1716.9410	0.72	0	22	19	1	SLASFLPSQLLGSIER
☑	3166	1155.6130	2309.2114	2309.2056	2.53	0	22	25	1	NAPAASFPDPPYTVVPTTPVIR
☑	73	371.2173	740.4200	740.4181	2.66	0	22	49	1	QVEIPR
☑	869	597.2996	1192.5846	1192.5837	0.83	0	22	37	1	DFASSVAGGLGGR
☑	1522	676.8112	1351.6078	1351.6111	-2.44	0	22	23	1	ELSNMAAMVENK + Oxidation (M)
☑	2191	867.9687	1733.9228	1733.9199	1.69	1	22	28	1	VEIIRYLDELGESAK
☑	289	443.7715	885.5284	885.5284	0.11	0	22	80	1	LSVVALER
☑	1472	670.8279	1339.6412	1339.6408	0.33	1	22	38	1	KSDLEAFYDPR
☑	2023	831.8868	1661.7590	1661.7528	3.76	0	22	23	1	DMISMYESEISTLK + Oxidation (M)
☑	2173	865.9770	1729.9394	1729.9461	-3.87	1	22	24	1	SEAVTGELSKLLNEIK
☑	1327	433.9055	1298.6947	1298.6983	-2.77	0	22	40	1	LFNNAGDVKPPK
☑	123	383.2038	764.3930	764.3929	0.18	1	22	40	1	GNYGKAR
☑	758	575.7763	1149.5380	1149.5414	-2.94	1	22	39	1	KDDNEFNIR
☑	408	489.2852	976.5558	976.5593	-3.56	0	22	33	1	ATIDAVFIK
☑	441	501.7699	1001.5252	1001.5254	-0.16	0	22	45	1	LGASSAVGAGGR
☑	2902	738.3654	2212.0744	2212.0802	-2.66	1	22	34	1	GFCAAGRVIEALSLSQMMQK + Carbamidomethyl (C); Oxidation (M)
☑	462	507.2976	1012.5806	1012.5804	0.22	0	22	40	1	ALPTELEIK
☑	2198	870.4678	1738.9210	1738.9213	-0.15	1	22	33	1	STLEENAAHAKAVLSAK
☑	940	406.2145	1215.6217	1215.6208	0.75	0	22	50	1	VTAVAASAGEAGGR
☑	1189	637.8160	1273.6174	1273.6197	-1.77	1	22	40	1	RQQDLCADLR + Carbamidomethyl (C)
☑	185	403.2215	804.4284	804.4276	1.08	1	22	43	1	AKSCAGLR
☑	1369	654.8331	1307.6516	1307.6503	1.01	1	22	51	1	SIAGRMSDSIGAK + Oxidation (M)
☑	265	430.2479	858.4812	858.4810	0.23	0	22	96	1	NAITAELK
☑	746	571.3013	1140.5880	1140.5887	-0.58	0	22	23	1	VLPQAASEGNR
☑	1766	493.2556	1476.7450	1476.7460	-0.70	1	22	55	1	ADGKPVDEYLDKK
☑	1072	621.8231	1241.6316	1241.6364	-3.81	0	22	35	1	NNISDNISPIR
☑	1439	665.8732	1329.7318	1329.7292	1.96	1	22	33	1	KLGASITFDGPPK

☑	1193	425.5467	1273.6183	1273.6203	-1.63	1	22	32	1	GFAYAKYGNQR
☑	939	406.2144	1215.6214	1215.6248	-2.81	0	22	51	1	PDGSPPPSLPPR
☑	585	542.7626	1083.5106	1083.5131	-2.30	0	22	26	1	GDDLCVHLR + Carbamidomethyl (C)
☑	1529	677.8550	1353.6954	1353.7001	-3.41	1	22	40	1	KEHTTVGELANR
☑	959	613.2937	1224.5728	1224.5748	-1.61	1	22	28	1	DHGRTWNSPR
☑	3085	1143.0770	2284.1394	2284.1448	-2.33	1	22	39	1	RNLIVTHDESEEVLDFVNR
☑	166	398.7190	795.4234	795.4239	-0.55	1	22	24	1	SSAKTFR
☑	928	404.8957	1211.6653	1211.6622	2.53	1	22	34	1	KNRPVEINDK
☑	1958	798.3975	1594.7804	1594.7773	1.96	0	22	45	1	MGSALPQADPAPLDGR
☑	2114	851.9636	1701.9126	1701.9124	0.17	1	22	32	1	MIVNPEATKLLWGSK + Oxidation (M)
☑	771	577.3013	1152.5880	1152.5887	-0.58	1	22	37	1	TAAYTSRDIR
☑	1476	671.3558	1340.6970	1340.6983	-0.92	1	22	38	1	RVVQQEPCINR
☑	415	491.7413	981.4680	981.4702	-2.19	1	22	33	1	DGSFCRLK + Carbamidomethyl (C)
☑	823	586.7927	1171.5708	1171.5721	-1.03	1	22	28	1	LDEDEAPQKK
☑	2428	916.0247	1830.0348	1830.0363	-0.81	1	22	9.8	1	QTYLVGGAVRDQLLGLK
☑	1520	451.2369	1350.6889	1350.6853	2.64	0	22	44	1	MEEVLNFAIASK
☑	1659	696.3748	1390.7350	1390.7344	0.48	1	22	42	1	LDPSEDFLSLKK
☑	1433	664.3512	1326.6878	1326.6853	1.91	0	22	31	1	AMGIIEVQPEPK + Oxidation (M)
☑	1728	477.2716	1428.7930	1428.7936	-0.46	1	22	34	1	SVLQSKLNGEGGLK
☑	602	545.2820	1088.5494	1088.5462	2.99	0	22	65	1	SDILNPTSSR
☑	1461	668.3548	1334.6950	1334.6942	0.60	1	22	44	1	SRAQGLYGIDAGK
☑	1962	801.4103	1600.8060	1600.8070	-0.58	1	22	43	1	NFSENSTLLRHQR
☑	1739	479.2238	1434.6496	1434.6496	-0.04	0	22	21	1	YMSGAQCVNHLR + Carbamidomethyl (C)
☑	2019	828.9395	1655.8644	1655.8631	0.82	0	22	40	1	LLFVLDEHATNAASR
☑	705	378.5607	1132.6603	1132.6604	-0.13	1	22	25	1	SLDIFIKAAR
☑	1955	796.9349	1591.8552	1591.8491	3.88	1	21	32	1	MALPSSALKSETLTK + Oxidation (M)
☑	2345	597.6596	1789.9570	1789.9574	-0.25	0	21	32	1	DTLSEQGLFIVNLVSR
☑	2770	1082.0470	2162.0794	2162.0750	2.08	1	21	46	1	ETECLKTARPNVSASTQATR
☑	2217	874.9807	1747.9468	1747.9403	3.73	1	21	27	1	RFLSNLLQCSVDVVR
☑	37	358.2087	714.4028	714.4024	0.60	1	21	1.6e+002	1	LRAEAGV
☑	389	482.7403	963.4660	963.4662	-0.11	1	21	69	1	DFGGKEPSK
☑	878	598.2958	1194.5770	1194.5768	0.20	1	21	48	1	IDEDGYLDKK
☑	1152	422.2264	1263.6574	1263.6571	0.20	1	21	50	1	QKYGSLDALNR
☑	1569	681.3694	1360.7242	1360.7238	0.33	0	21	44	1	ELLAFLSAEGPSK
☑	970	613.8230	1225.6314	1225.6302	0.98	0	21	41	1	VGEAELQDPLR
☑	1066	621.8209	1241.6272	1241.6227	3.70	1	21	42	1	RMELFYDIR
☑	2384	902.0114	1802.0082	1802.0050	1.80	1	21	15	1	RVLQQLSYEGLVEIR
☑	2022	830.9717	1659.9288	1659.9308	-1.16	1	21	18	1	TYRAQLLGAQAEVLK
☑	2107	564.9771	1691.9095	1691.9094	0.06	1	21	33	1	EELSESIQYLRVVK
☑	327	461.7474	921.4802	921.4807	-0.54	0	21	53	1	EDVLVGYK
☑	1980	540.2852	1617.8338	1617.8402	-4.00	0	21	61	1	IIVHESIFDAFAEK
☑	2376	901.0197	1800.0248	1800.0179	3.87	1	21	11	1	KPDVKTLIAMGAATGAIK + Oxidation (M)
☑	1639	693.3757	1384.7368	1384.7350	1.31	1	21	40	1	NEIPVPEAKNFK
☑	1653	695.8832	1389.7518	1389.7537	-1.35	1	21	43	1	ELLKMIENTGVK + Oxidation (M)
☑	1515	675.3663	1348.7180	1348.7198	-1.30	0	21	45	1	LSSVSTATESVLR
☑	2134	857.9523	1713.8900	1713.8897	0.21	1	21	40	1	ASIEEVRAAIDQAVDK
☑	326	461.2555	920.4964	920.4935	3.15	1	21	80	1	LAIAMCRK + Oxidation (M)
☑	1630	461.5945	1381.7617	1381.7605	0.83	0	21	29	1	VEPEQVLLAWAK
☑	583	542.2468	1082.4790	1082.4828	-3.50	0	21	18	1	HAQQHFGCR
☑	1707	471.9194	1412.7364	1412.7372	-0.55	1	21	44	1	ENAAALGLEDRVR
☑	2589	992.9970	1983.9794	1983.9758	1.86	1	21	46	1	IARPTDNLSTIKDMYCK + Oxidation (M)
☑	1431	663.3647	1324.7148	1324.7139	0.71	1	21	36	1	FIAGQEKYITR
☑	71	370.1869	738.3592	738.3595	-0.34	1	21	21	1	ARYCAR
☑	933	608.2940	1214.5734	1214.5761	-2.15	1	21	29	1	AHQQCRMLR + Carbamidomethyl (C); Oxidation (M)
☑	3088	1143.6350	2285.2554	2285.2565	-0.47	1	21	15	1	LTLRLLAATQFPELACAGEIR
☑	2682	703.3403	2106.9991	2106.9979	0.54	1	21	37	1	LHSGEKPFVCDDCGKAFVR
☑	1488	448.2495	1341.7267	1341.7252	1.09	0	21	44	1	LSLAQEILDQGR
☑	303	450.7450	899.4754	899.4726	3.19	1	21	27	1	ARFVDHR
☑	1129	629.8174	1257.6202	1257.6201	0.14	0	21	42	1	SLSDNIPEDLR
☑	683	564.2769	1126.5392	1126.5407	-1.33	0	21	23	1	DYFVGSGLGGR
☑	695	565.2899	1128.5652	1128.5676	-2.08	1	21	31	1	TEGDPRWLR
☑	631	551.7684	1101.5222	1101.5203	1.76	0	21	26	1	ESADAFHGLR
☑	2231	876.0081	1750.0016	1749.9989	1.60	1	21	8.2	1	VEELVSLKLASGQHLK
☑	2244	585.6530	1753.9372	1753.9362	0.53	1	21	35	1	HDINAIIKDIAEQFK
☑	692	565.2897	1128.5648	1128.5676	-2.43	0	21	34	1	HAYGQVGEIR
☑	2317	887.9884	1773.9622	1773.9625	-0.14	1	21	29	1	VKLFLDGDNAGINATVK
☑	2328	890.0046	1777.9946	1777.9978	-1.78	1	21	13	1	YIRTILPFVDSDVIK
☑	3087	1143.6340	2285.2534	2285.2604	-3.04	1	21	15	1	DTGIPLIQLNNIRDGQHILR
☑	1450	667.3718	1332.7290	1332.7289	0.12	0	21	41	1	LELSYIADGKPK
☑	1694	703.3889	1404.7632	1404.7612	1.43	1	21	44	1	NLSLKDFEALQK
☑	368	475.7460	949.4774	949.4770	0.48	0	21	41	1	YAFISHGR
☑	1671	698.8722	1395.7298	1395.7292	0.43	0	21	36	1	MASLSVHASQIPR
☑	2420	457.4891	1825.9273	1825.9250	1.23	0	21	47	1	FPAFGELHDELVDPIK
☑	2411	607.3465	1819.0177	1819.0131	2.50	0	21	15	1	VYSVASLADLPIISFPK
☑	1444	444.5748	1330.7026	1330.6994	2.42	0	21	61	1	FLQGSSNPGGVLR
☑	518	527.2593	1052.5040	1052.4999	3.95	0	21	44	1	AAHANADDLR
☑	1180	637.8137	1273.6128	1273.6150	-1.68	0	21	48	1	AESDVQEIVER
☑	3009	1129.0360	2256.0574	2256.0647	-3.21	1	21	33	1	HHLKSFFFDCNNIDNLHR
☑	595	543.7704	1085.5262	1085.5288	-2.33	1	21	32	1	DCHKTVDIR
☑	522	528.7114	1055.4082	1055.4099	-1.59	1	21	2.8	1	KCCWCSGR + 2 Carbamidomethyl (C)
☑	1415	662.3336	1322.6526	1322.6579	-3.96	1	21	56	1	DAGKTFTNVNTR
☑	1548	678.8654	1355.7162	1355.7197	-2.58	1	21	47	1	QFGGRDELPLPK
☑	1457	667.3723	1332.7300	1332.7289	0.86	1	21	42	1	IELKDINVDFK
☑	2184	578.6533	1732.9381	1732.9359	1.23	0	21	29	1	IYTPGLSQSILDGITR
☑	2819	726.3715	2176.0927	2176.0980	-2.44	0	21	47	1	SNALVSQIDLLGSMAGMLNAR + Oxidation (M)
☑	703	567.2939	1132.5732	1132.5724	0.76	0	21	63	1	IDLENSISSR
☑	658	559.2783	1116.5420	1116.5411	0.84	0	21	53	1	TGILNQDDNK
☑	1065	414.8829	1241.6269	1241.6252	1.38	0	21	48	1	EPTAQELADLR

☑	1719	711.3862	1420.7578	1420.7530	3.40	1	21	44	1	MLMTVSLSRLDR
☑	592	543.7701	1085.5256	1085.5214	3.95	1	21	43	1	SSNDSPAPRR
☑	65	366.6983	731.3820	731.3813	0.96	1	21	1.7e+002	1	SSAKDPK
☑	619	366.1963	1095.5671	1095.5681	-0.95	0	21	57	1	LMHGAMAPLR
☑	1234	644.8475	1287.6804	1287.6823	-1.44	1	21	55	1	VDLKQEGFAGPK
☑	1021	613.8237	1225.6328	1225.6303	2.11	0	21	49	1	SSTTSASFVALR
☑	1387	439.2225	1314.6457	1314.6424	2.48	1	21	44	1	MYGSAKSVMSVR
☑	2590	662.3344	1983.9814	1983.9758	2.82	0	21	47	1	EAVMHTEGPLLLMAGAGSGK + Oxidation (M)
☑	496	521.7619	1041.5092	1041.5091	0.16	0	21	39	1	DVLGQEEPR
☑	2151	859.4804	1716.9462	1716.9522	-3.49	1	21	32	1	IVDFALSNALNSGIRK
☑	1536	678.8019	1355.5892	1355.5841	3.79	0	21	17	1	TTLADYDSNGGDK
☑	680	563.3050	1124.5954	1124.5978	-2.13	0	21	38	1	GWPLTPAQAGK
☑	1774	746.3631	1490.7116	1490.7114	0.19	1	21	41	1	NDFSLEPGRVSDR
☑	1054	619.8037	1237.5928	1237.5907	1.74	1	21	38	1	TMMSANANKVR + Oxidation (M)
☑	2038	558.9767	1673.9083	1673.9135	-3.09	1	21	39	1	MSRGLLIVVSGPSGTGK + Oxidation (M)
☑	2167	865.4415	1728.8684	1728.8716	-1.82	0	21	53	1	LEGMNIISIAQDPNAK + Oxidation (M)
☑	1053	618.8257	1235.6368	1235.6332	2.92	1	21	71	1	MPTITAGDFRK
☑	1282	649.8483	1297.6820	1297.6779	3.22	0	21	42	1	IDEAHQFLGLR
☑	1929	528.2719	1581.7939	1581.7999	-3.78	0	21	48	1	GAGADVNAGVDPAVIEK
☑	916	605.2971	1208.5796	1208.5786	0.91	0	21	42	1	NTADFTSALNR
☑	655	557.7965	1113.5784	1113.5778	0.56	0	21	53	1	GNQEVLADIR
☑	840	590.2926	1178.5706	1178.5714	-0.61	1	21	50	1	VASDEVTMRR + Oxidation (M)
☑	1067	621.8210	1241.6274	1241.6299	-1.95	1	21	50	1	RMDGLHSSAIR
☑	2398	907.0204	1812.0262	1812.0258	0.27	0	21	13	1	VLLLSSPPLHDAAQPVR
☑	2015	827.9217	1653.8288	1653.8297	-0.52	0	21	46	1	MVLNHGGATSIPSWGK
☑	2958	748.0461	2241.1165	2241.1207	-1.89	0	21	48	1	EVMLVLQPCIHQMESVELK + Oxidation (M)
☑	745	381.2029	1140.5869	1140.5887	-1.64	0	21	33	1	GGVLQQADTPR
☑	1216	428.5585	1282.6537	1282.6517	1.52	0	21	48	1	DLPPSQADATIR
☑	2611	1012.4980	2022.9814	2022.9820	-0.26	0	21	49	1	LQTALDLVNSTVTMEFEP + Oxidation (M)
☑	3271	1179.5850	2357.1554	2357.1616	-2.60	0	21	52	1	GVMLPVVIMTGHGDVDMAVAAMK + Oxidation (M)
☑	1222	642.8333	1283.6520	1283.6470	3.97	0	21	55	1	EGDNPAVSLLNR
☑	731	568.7964	1135.5782	1135.5768	1.30	1	20	45	1	SASRSLVACSR
☑	1680	467.2424	1398.7054	1398.7038	1.14	1	20	54	1	HEGGVGQALRTMK + Oxidation (M)
☑	824	587.7595	1173.5044	1173.5084	-3.39	0	20	14	1	SSNDGCEPIPR
☑	730	568.7963	1135.5780	1135.5808	-2.42	1	20	46	1	FLCLGKENR + Carbamidomethyl (C)
☑	1028	410.2109	1227.6109	1227.6104	0.40	0	20	50	1	SCPLCSGALHIK
☑	2221	583.9837	1748.9293	1748.9322	-1.68	1	20	42	1	ALHPQTVSKLHDTFR
☑	1062	621.8193	1241.6240	1241.6265	-2.00	1	20	35	1	RGGHGFVDEIR
☑	903	603.3097	1204.6048	1204.6048	0.07	1	20	71	1	SGRLLASGSDDK
☑	1651	464.2574	1389.7504	1389.7538	-2.43	0	20	53	1	IVSLDMAGIVAGTK + Oxidation (M)
☑	1140	420.2150	1257.6232	1257.6201	2.47	0	20	43	1	EPTAQELSDLR
☑	128	384.6974	767.3802	767.3788	1.83	0	20	38	1	YMIWR
☑	278	440.7282	879.4418	879.4450	-3.59	0	20	95	1	GAGSANYIK
☑	921	605.8127	1209.6108	1209.6142	-2.79	1	20	67	1	VFLFDNDGKR
☑	467	509.2431	1016.4716	1016.4709	0.70	0	20	27	1	GEICPGQTGR
☑	1185	425.5460	1273.6162	1273.6203	-3.28	1	20	55	1	GFAYAKYGNQR
☑	3377	1241.1510	2480.2874	2480.2832	1.71	1	20	37	1	EVARSVLITCEYDLAQTVETLK
☑	1456	667.3723	1332.7300	1332.7249	3.90	1	20	48	1	LELKTSSAELSR
☑	2582	987.0417	1972.0688	1972.0742	-2.70	1	20	31	1	SSLIAVSVPTSSWVVERR
☑	689	377.1953	1128.5641	1128.5676	-3.12	0	20	55	1	AHHLSGAPPDK
☑	751	572.2807	1142.5468	1142.5502	-2.97	0	20	48	1	HTGADAVMIGR + Oxidation (M)
☑	1756	486.2929	1455.8569	1455.8523	3.13	1	20	11	1	IIQLPFKMPIEK
☑	1366	654.8327	1307.6508	1307.6557	-3.71	1	20	73	1	LWSGPQPRHCK
☑	266	435.7503	869.4860	869.4858	0.26	0	20	29	1	VPGIDELK
☑	469	509.8059	1017.5972	1017.5971	0.14	1	20	40	1	LVIAFDKGR
☑	1073	621.8253	1241.6360	1241.6364	-0.29	0	20	49	1	GSSGQPVNVELR
☑	861	595.8020	1189.5894	1189.5939	-3.72	0	20	68	1	STPIASSPTSSR
☑	51	364.1963	726.3780	726.3773	1.09	0	20	28	1	APQNAAR
☑	693	565.2898	1128.5650	1128.5636	1.32	1	20	38	1	NNSIPESGRR
☑	2677	1054.4960	2106.9774	2106.9748	1.25	0	20	38	1	VCPLCEATCGLELTLDTGR + 2 Carbamidomethyl (C)
☑	814	585.3304	1168.6462	1168.6452	0.89	0	20	45	1	QGIPVVSDGGIK
☑	2183	867.4763	1732.9380	1732.9393	-0.74	1	20	34	1	SIGCTGVILTKLDGTAK + Carbamidomethyl (C)
☑	384	479.7465	957.4784	957.4767	1.81	0	20	43	1	AGGPQSISIE
☑	2223	875.4724	1748.9302	1748.9342	-2.27	1	20	44	1	TMVTNAISELLKSGTGK
☑	1377	656.8365	1311.6584	1311.6605	-1.57	0	20	45	1	DATHATSLMPLR
☑	1693	703.3887	1404.7628	1404.7659	-2.20	1	20	51	1	MAANAAYLVVRAR
☑	1837	763.8618	1525.7090	1525.7116	-1.67	1	20	39	1	ADSMSMDLASLKNK + Oxidation (M)
☑	155	395.2088	788.4030	788.4028	0.29	0	20	1.7e+002	1	QTASAPSK
☑	1747	723.8774	1445.7402	1445.7449	-3.22	1	20	68	1	ECGKSFAHISVLR
☑	240	422.2446	842.4746	842.4763	-1.91	0	20	96	1	IAISHFR
☑	1122	628.8170	1255.6194	1255.6197	-0.18	0	20	53	1	ESAQAAFTYIR
☑	1723	476.6035	1426.7887	1426.7854	2.30	0	20	44	1	QIPDVIGVMIQAK + Oxidation (M)
☑	1539	452.9123	1355.7151	1355.7157	-0.46	1	20	57	1	QDIAVRLNGNEK
☑	526	352.8615	1055.5627	1055.5611	1.48	1	20	59	1	DKENVQPVK
☑	1150	632.8242	1263.6338	1263.6380	-3.32	1	20	63	1	DLETKVIDMGK + Oxidation (M)
☑	1191	637.8160	1273.6174	1273.6150	1.92	0	20	61	1	TADDEPATVSLR
☑	1130	420.2141	1257.6205	1257.6176	2.31	1	20	57	1	YMAQKAFLDR + Oxidation (M)
☑	2323	888.4838	1774.9530	1774.9577	-2.62	1	20	47	1	ISAEALYVRAGILDER
☑	1482	671.3604	1340.7062	1340.7010	3.93	0	20	50	1	MPLNVITPSEPK + Oxidation (M)
☑	1493	672.3654	1342.7162	1342.7205	-3.15	1	20	59	1	GTNSDLIVRGSPK
☑	663	559.7647	1117.5148	1117.5186	-3.34	1	20	45	1	SCPDNKADLR
☑	728	568.7961	1135.5776	1135.5768	0.76	1	20	65	1	TRSQSSVLCR
☑	900	602.3308	1202.6470	1202.6442	2.41	0	20	77	1	VVQLVGSAQMR + Oxidation (M)
☑	2360	898.9973	1795.9800	1795.9767	1.87	0	20	35	1	HIAIIGGGAAGCFAAINIK
☑	822	586.7729	1171.5312	1171.5339	-2.26	1	20	25	1	TCRHPGCSVR + Carbamidomethyl (C)
☑	31	352.1850	702.3554	702.3548	0.93	0	20	1e+002	1	AGEGEIK
☑	3051	1138.0670	2274.1194	2274.1274	-3.50	1	20	55	1	DLAGVADVLQQTLGKMSNQDR + Oxidation (M)
☑	911	604.3127	1206.6108	1206.6132	-1.97	0	20	77	1	AVDPTESVVYK

☑	1418	662.3668	1322.7190	1322.7194	-0.28	0	20	39	1	TTHPSIVDNVLK
☑	2568	973.0135	1944.0124	1944.0098	1.35	1	20	51	1	MADLVQEASNITIQRGAK
☑	199	407.2403	812.4660	812.4644	2.08	0	20	32	1	PVIDELK
☑	3350	1213.1180	2424.2214	2424.2148	2.75	0	20	50	1	MQPVATIIDDPVAPFDFPAPQR
☑	464	507.7242	1013.4338	1013.4301	3.65	0	20	19	1	DSEYASTNK
☑	804	582.7965	1163.5784	1163.5791	-0.54	1	20	82	1	MAIICRADSK + Carbamidomethyl (C)
☑	1843	766.4428	1530.8710	1530.8770	-3.88	1	20	91	1	TSVVVELGLFSPRK
☑	1135	629.8184	1257.6222	1257.6248	-2.02	1	20	60	1	RGPEAAGGMSGIR
☑	909	604.2946	1206.5746	1206.5703	3.59	0	20	60	1	GPMLFDGEGIR + Oxidation (M)
☑	1182	425.5456	1273.6150	1273.6163	-1.08	0	20	57	1	TPGRPGAQDGYR
☑	1849	512.5796	1534.7170	1534.7198	-1.87	0	20	46	1	FGAPGAVGMSPSATGGR + Oxidation (M)
☑	150	394.2315	786.4484	786.4460	3.09	1	20	1.3e+002	1	AIRAGGSR
☑	615	547.7717	1093.5288	1093.5264	2.20	1	20	60	1	SAYSSNPRGR
☑	3298	1188.1120	2374.2094	2374.2128	-1.42	0	20	50	1	AAIGDAPDAADTAPGLSPPLSALAGR
☑	626	551.7676	1101.5206	1101.5203	0.31	0	20	53	1	AHDASDAFIR
☑	1015	613.8235	1225.6324	1225.6349	-2.04	1	20	58	1	RLDLSNCHLR
☑	2255	587.3248	1758.9526	1758.9549	-1.34	1	20	38	1	IEITSAGKMLQIEAQK
☑	2421	914.5213	1827.0280	1827.0241	2.18	1	20	24	1	EALEIVTVEKIEDVLK
☑	2461	619.6350	1855.8832	1855.8840	-0.42	0	20	53	1	DSPEYALLSNLDTFSGK
☑	1794	761.8802	1521.7458	1521.7497	-2.55	0	20	75	1	TVADFASLLMADPR + Oxidation (M)
☑	1038	617.3091	1232.6036	1232.6071	-2.78	0	20	87	1	TLNIINDDGMK
☑	103	376.7015	751.3884	751.3864	2.67	0	20	96	1	YDSVIR
☑	1301	433.9051	1298.6935	1298.6942	-0.58	1	20	68	1	SRPLNDKVNEK
☑	2686	1055.0640	2108.1134	2108.1113	1.01	1	20	39	1	LASEVALRVDPLIDDPETR
☑	1411	661.8218	1321.6290	1321.6310	-1.44	1	20	92	1	GMRNPVAHGDPR + Oxidation (M)
☑	1656	695.8835	1389.7524	1389.7537	-0.92	1	20	59	1	ISVIKDMEQAIK + Oxidation (M)
☑	1143	629.8238	1257.6330	1257.6288	3.35	1	20	66	1	TLVMWGKHDR + Oxidation (M)
☑	957	408.8790	1223.6152	1223.6146	0.49	0	20	59	1	SSAASYAAIDLR
☑	1213	642.3328	1282.6510	1282.6517	-0.52	0	20	54	1	VGGAAEELPDGLR
☑	1532	677.8723	1353.7300	1353.7292	0.61	1	20	49	1	KNYTLLAGSYPK
☑	812	585.2725	1168.5304	1168.5295	0.82	1	20	30	1	RDLATCYDR + Carbamidomethyl (C)
☑	1107	625.8480	1249.6814	1249.6853	-3.05	1	20	60	1	LMQGAQKLFAK + Oxidation (M)
☑	1499	673.3550	1344.6954	1344.6932	1.69	1	20	75	1	MASSSSPRAAKPR
☑	2133	857.4625	1712.9104	1712.9057	2.77	1	20	57	1	VQGADLTELTNKTAPR
☑	865	596.8083	1191.6020	1191.6037	-1.35	1	20	66	1	HDFDRVIYK
☑	1045	618.3039	1234.5932	1234.5976	-3.50	0	20	64	1	ASQANGATGAMIK + Oxidation (M)
☑	1041	617.3273	1232.6400	1232.6369	2.53	1	20	1.1e+002	1	LSCLCGGSKIPR
☑	452	505.2446	1008.4746	1008.4764	-1.72	0	20	54	1	DLAEGVYDK
☑	3021	1130.6290	2259.2434	2259.2409	1.13	1	20	21	1	MLQTPPAPAAAEPVLVVDRLR + Oxidation (M)
☑	898	602.3214	1202.6282	1202.6295	-1.06	1	20	1.1e+002	1	DFLGEKEIPR
☑	3174	772.0912	2313.2518	2313.2441	3.32	1	20	29	1	HVADAVTDDAAALDLPPVVRLR
☑	157	395.2477	788.4808	788.4830	-2.69	0	20	17	1	ISICILK
☑	799	582.7670	1163.5194	1163.5241	-3.98	0	20	37	1	DSGIGIGEMNR + Oxidation (M)
☑	826	588.8113	1175.6080	1175.6081	-0.04	1	20	99	1	LNRDVMGVTR + Oxidation (M)
☑	1607	459.2508	1374.7306	1374.7354	-3.52	1	20	88	1	SALANKDSSELLK
☑	2433	916.4996	1830.9846	1830.9839	0.38	1	20	48	1	IIDFIEKNVEVGNSVR
☑	287	442.7580	883.5014	883.5015	-0.02	0	20	41	1	IPIDEIGK
☑	915	605.2953	1208.5760	1208.5795	-2.82	1	20	56	1	MTGKGFPCVGGR
☑	2052	843.9577	1685.9008	1685.8995	0.79	1	20	58	1	LSNVASRIMGGNGVVGR
☑	922	605.8137	1209.6128	1209.6176	-3.93	0	19	79	1	LDMPVIVHDR + Oxidation (M)
☑	434	496.7924	991.5702	991.5702	0.04	1	19	60	1	IKNTFELK
☑	1655	695.8834	1389.7522	1389.7537	-1.06	1	19	63	1	AAVLKETCSEVLK
☑	497	521.7870	1041.5594	1041.5567	2.62	0	19	61	1	DGALVGGIGAGR
☑	1957	797.9042	1593.7938	1593.7929	0.62	1	19	73	1	DIVMVSVMPCTAKK + Carbamidomethyl (C); Oxidation (M)
☑	2130	857.4576	1712.9006	1712.8945	3.61	0	19	67	1	AQAIADGVLVDVSEQAK
☑	1212	642.3219	1282.6292	1282.6306	-1.04	0	19	64	1	NYDGVAAASFLR
☑	1399	439.9183	1316.7331	1316.7373	-3.24	0	19	50	1	IIMELINNTIK + Oxidation (M)
☑	1223	642.8334	1283.6522	1283.6510	1.00	0	19	57	1	SAFYLTEAINR
☑	1199	638.8167	1275.6188	1275.6142	3.63	1	19	47	1	EACRQIASWR + Carbamidomethyl (C)
☑	1903	784.4001	1566.7856	1566.7831	1.66	0	19	71	1	YAEPFSALAWLSGR
☑	2432	611.0203	1830.0391	1830.0325	3.62	0	19	15	1	LEIHTYLNMILLTIK + Oxidation (M)
☑	1229	644.3568	1286.6990	1286.7016	-2.02	0	19	95	1	QAQKPTVSMVAK
☑	2377	601.0160	1800.0262	1800.0244	0.98	1	19	14	1	VETIDELLSVTKNVLK
☑	209	413.2396	824.4646	824.4643	0.37	0	19	40	1	IEPPELK
☑	2659	1041.5060	2080.9974	2081.0027	-2.52	0	19	64	1	IMPDYYDSLSNLPDVPVK + Oxidation (M)
☑	1200	638.8564	1275.6982	1275.6935	3.72	1	19	72	1	SPLTRLAAEYR
☑	2542	957.4605	1912.9064	1912.9088	-1.22	1	19	64	1	MAETFNLSDLKGTSAAEL + Oxidation (M)
☑	782	387.2073	1158.6001	1158.6033	-2.80	0	19	98	1	DVLSLPWSSR
☑	1509	674.8775	1347.7404	1347.7432	-2.02	1	19	57	1	SGVMEKIISQIK + Oxidation (M)
☑	302	450.7448	899.4750	899.4721	3.27	0	19	41	1	MPVVAPMR
☑	359	471.7510	941.4874	941.4905	-3.27	0	19	42	1	AHPFAMLR
☑	1365	654.8320	1307.6494	1307.6470	1.88	0	19	94	1	NLDTVPGPGADPR
☑	304	450.7552	899.4958	899.4964	-0.58	0	19	97	1	EPLETAIK
☑	893	601.3127	1200.6108	1200.6098	0.83	1	19	79	1	RVLELDDDAR
☑	1416	662.3551	1322.6956	1322.6904	3.97	0	19	66	1	LLMLQYGVNEK + Oxidation (M)
☑	2200	871.4362	1740.8578	1740.8539	2.29	1	19	62	1	KQGSIELICGSMFSGK + Carbamidomethyl (C)
☑	28	351.1829	700.3512	700.3504	1.21	0	19	51	1	DGPVSAR
☑	879	598.3253	1194.6360	1194.6357	0.33	1	19	69	1	NEKLPPENVR
☑	2246	878.4643	1754.9140	1754.9124	0.94	1	19	60	1	EFMSSVILEKSALSAK + Oxidation (M)
☑	1438	665.8715	1329.7284	1329.7252	2.45	0	19	77	1	LSLNQLSSNNLK
☑	252	425.7185	849.4224	849.4201	2.81	0	19	83	1	MMLVNSR
☑	735	568.7968	1135.5790	1135.5768	2.01	1	19	61	1	SASRSLVACSR
☑	733	568.7966	1135.5786	1135.5808	-1.89	0	19	60	1	APPPPAVAASCR
☑	1679	699.8854	1397.7562	1397.7588	-1.82	1	19	53	1	KLAENMLEPLKP + Oxidation (M)
☑	1788	755.4485	1508.8824	1508.8813	0.73	1	19	13	1	EAIEVIKALGLPEK
☑	3213	1164.5800	2327.1454	2327.1546	-3.94	1	19	70	1	HTDHSDVLDTRYLTWLDLK
☑	3476	939.0987	2814.2743	2814.2663	2.83	0	19	31	1	ENCPHPVSFTGMLNMGSSFLTVTEK + Carbamidomethyl (C); 2 Oxidation (M)
☑	793	581.2916	1160.5686	1160.5673	1.13	0	19	87	1	QAGLIDGDGSTK

☑	811	584.2978	1166.5810	1166.5792	1.56	0	19	55	1	TTNNHQPSLR
☑	1172	636.8089	1271.6032	1271.6040	-0.63	1	19	55	1	REGATGEMHIR + Oxidation (M)
☑	3149	1152.6200	2303.2254	2303.2307	-2.29	0	19	39	1	DTHSILGMIHAEEALLVSIVR
☑	1740	718.3369	1434.6592	1434.6627	-2.40	0	19	46	1	FSGEEGQPTAGEVK
☑	1183	425.5459	1273.6159	1273.6125	2.65	1	19	73	1	MSQFKSDFLR + Oxidation (M)
☑	2145	859.4783	1716.9420	1716.9484	-3.71	1	19	38	1	FDPKMPISTLIGSLAK
☑	275	439.7158	877.4170	877.4182	-1.26	0	19	63	1	DFDLGSPK
☑	120	382.6826	763.3506	763.3534	-3.66	0	19	1.2e+002	1	MDDVIR + Oxidation (M)
☑	1686	467.9157	1400.7253	1400.7259	-0.47	1	19	84	1	AGDVLRQAVEESK
☑	282	441.7500	881.4854	881.4858	-0.41	0	19	46	1	APPIDLEK
☑	1568	680.8777	1359.7408	1359.7398	0.78	1	19	74	1	VANPEDFLKSLK
☑	1658	464.5820	1390.7242	1390.7205	2.67	1	19	94	1	HSYTLNSSGGKIK
☑	741	568.7975	1135.5804	1135.5768	3.24	1	19	79	1	SASRSLVACSR
☑	1888	784.3986	1566.7826	1566.7791	2.28	1	19	75	1	GGFGLVYKGDLNDGR
☑	604	545.2880	1088.5614	1088.5648	-3.07	0	19	1.5e+002	1	DAMAALASAIR
☑	321	458.2790	914.5434	914.5437	-0.26	0	19	88	1	IAGVVDTLK
☑	919	404.2105	1209.6097	1209.6064	2.74	0	19	92	1	LVFMTDQAAAK + Oxidation (M)
☑	1947	792.9641	1583.9136	1583.9134	0.16	1	19	17	1	LIDAEIKSLVEGGLK
☑	954	611.3073	1220.6000	1220.5972	2.35	1	19	1e+002	1	ASTGWRLMGDK
☑	1604	686.8782	1371.7418	1371.7405	0.99	1	19	78	1	RPVIGLDMSGRR + Oxidation (M)
☑	1896	784.3992	1566.7838	1566.7790	3.07	1	19	91	1	SVPREFYSGLAEGR
☑	1537	452.9117	1355.7133	1355.7157	-1.80	1	19	73	1	RSLNPDGLDLTR
☑	1902	784.3998	1566.7850	1566.7831	1.27	0	19	92	1	YAEPFSALAWLSGR
☑	72	371.2164	740.4182	740.4181	0.23	0	19	95	1	QVEIPR
☑	2955	746.6982	2237.0728	2237.0722	0.27	1	19	67	1	VFSMLDSMGFVPKQQSQHR + Oxidation (M)
☑	1394	658.3666	1314.7186	1314.7157	2.28	1	19	90	1	HSISATFRAGIR
☑	1435	664.3647	1326.7148	1326.7143	0.39	0	19	65	1	KPLGSSPVSSGSPK
☑	2488	625.3612	1873.0618	1873.0614	0.18	0	19	18	1	LVGGYHFPLFLLTLQR
☑	1716	709.8815	1417.7484	1417.7453	2.24	0	19	68	1	ENEGSAFTIILPK
☑	1729	715.4041	1428.7936	1428.7936	0.03	0	19	62	1	ISVGASSAAVNAALAK
☑	2144	859.4780	1716.9414	1716.9410	0.26	1	19	39	1	GNILEFNITKIVDNK
☑	1311	650.3542	1298.6938	1298.6942	-0.30	1	19	83	1	GERVIIQNQDK
☑	1153	632.8369	1263.6592	1263.6605	-0.98	1	19	80	1	TNTTALRAASMK
☑	2405	606.0167	1815.0283	1815.0215	3.71	0	19	20	1	ELIEAYIPILCALGGIK
☑	2427	611.0175	1830.0307	1830.0285	1.19	1	19	26	1	GKMVVVLSGGPTTISGALK + Oxidation (M)
☑	1408	660.8666	1319.7186	1319.7237	-3.86	1	19	68	1	SPAYIFEPKIR
☑	986	613.8232	1225.6318	1225.6302	1.30	0	19	76	1	EDIITETHIR
☑	268	436.7388	871.4630	871.4651	-2.32	0	19	89	1	AIISDEPK
☑	651	556.8201	1111.6256	1111.6277	-1.87	1	19	60	1	YFDIKSVLK
☑	1030	614.8180	1227.6214	1227.6248	-2.71	0	19	75	1	VAPEDFNALPR
☑	2192	578.9821	1733.9245	1733.9200	2.60	1	19	63	1	SFEVIVGKSIPDTGASK
☑	1551	452.9127	1355.7163	1355.7157	0.42	1	19	79	1	QDIAVRLNGNEK
☑	428	494.2893	986.5640	986.5661	-2.11	1	19	84	1	QAWVRSLK
☑	1507	450.2538	1347.7396	1347.7398	-0.15	1	19	67	1	EAVLYKLEIDR
☑	2418	913.0206	1824.0266	1824.0293	-1.48	0	19	23	1	MVVELFCFLAVVVVLK + Oxidation (M)
☑	1893	523.2684	1566.7834	1566.7791	2.76	0	19	91	1	VAVFGYNQEQLGSR
☑	2436	611.3492	1831.0258	1831.0203	2.98	1	19	30	1	IVFSNVNLNNKSELIK
☑	1437	665.3738	1328.7330	1328.7374	-3.24	0	19	82	1	IIIMVDLNASPK + Oxidation (M)
☑	503	522.7644	1043.5142	1043.5108	3.29	1	19	80	1	DPSRQTQGR
☑	1144	632.3125	1262.6104	1262.6078	2.13	1	19	81	1	DWLIGCRTGDK
☑	1225	643.3425	1284.6704	1284.6721	-1.28	1	19	79	1	MTRIIAGTHGGR + Oxidation (M)
☑	1627	691.8732	1381.7318	1381.7275	3.15	1	19	66	1	ILYLMENAGSKK + Oxidation (M)
☑	2400	907.0220	1812.0294	1812.0357	-3.44	1	19	23	1	KIQTVLDSVQGVEGVLK
☑	514	526.7675	1051.5204	1051.5233	-2.70	1	19	88	1	MRNDFTLR
☑	2179	578.6530	1732.9372	1732.9359	0.73	1	19	47	1	YILQDVQSLEKLER
☑	3248	1173.1340	2344.2534	2344.2539	-0.19	1	19	40	1	AAEYGQYAIKQPAVISNVGLPR
☑	671	561.2732	1120.5318	1120.5295	2.11	1	19	73	1	DSLMERNTR
☑	3367	818.4281	2452.2625	2452.2607	0.74	0	19	64	1	ALAAELIHFVTMHPDAAMITLR + 2 Oxidation (M)
☑	2131	857.4608	1712.9070	1712.9057	0.79	1	19	72	1	ISDDLVVVRDLANER
☑	1069	621.8214	1241.6282	1241.6299	-1.29	1	18	72	1	MRANPADQAIR
☑	1489	448.2503	1341.7291	1341.7252	2.89	1	18	88	1	ENLTPAERATLK
☑	1503	674.8593	1347.7040	1347.7003	2.81	0	18	1.1e+002	1	MMGGIVSSIALNR
☑	672	561.2758	1120.5370	1120.5369	0.15	0	18	95	1	MAGMLDQALR + Oxidation (M)
☑	1885	523.2681	1566.7825	1566.7791	2.18	0	18	85	1	VAVFGYNQEQLGSR
☑	1272	646.7951	1291.5756	1291.5721	2.77	0	18	43	1	YGIFSDEYGNK
☑	1423	442.5772	1324.7098	1324.7099	-0.11	1	18	67	1	TVSQAVPGREGPK
☑	780	387.2072	1158.5998	1158.5993	0.42	0	18	1.2e+002	1	SQDGSLVAINR
☑	1632	692.3657	1382.7168	1382.7201	-2.35	1	18	77	1	MSGNVVNLRTHR
☑	2188	867.4785	1732.9424	1732.9359	3.75	1	18	60	1	INDIFAGKGVTEAIGTK
☑	885	599.8018	1197.5890	1197.5850	3.35	1	18	78	1	SHAEGGTRDLR
☑	1188	425.5463	1273.6171	1273.6197	-2.08	1	18	86	1	DTHRQTITMR + Oxidation (M)
☑	2157	860.4664	1718.9182	1718.9203	-1.18	1	18	70	1	VAGGYLIIENKGTAADK
☑	3323	1196.6720	2391.3294	2391.3260	1.43	1	18	20	1	SLDEALAIKNSAIAEELALPPVK
☑	1364	436.5788	1306.7146	1306.7132	1.02	1	18	68	1	LSLFDSGLAKEK
☑	773	577.3023	1152.5900	1152.5887	1.17	0	18	72	1	EIHQSNALNK
☑	1076	623.3275	1244.6404	1244.6361	3.51	0	18	1.4e+002	1	IQNTLTGEVDR
☑	2375	900.5239	1799.0332	1799.0305	1.53	1	18	20	1	EYLGPAAGLLQVTRLAK
☑	3321	1196.0950	2390.1754	2390.1801	-1.94	1	18	79	1	MKRPIIISQHSSYSYGHADGK + Oxidation (M)
☑	1109	626.8307	1251.6468	1251.6459	0.74	0	18	83	1	TSVGGYTIADIR
☑	1851	514.5966	1540.7680	1540.7636	2.86	0	18	89	1	AFLEWPYMVLEK + Oxidation (M)
☑	1795	509.2634	1524.7684	1524.7725	-2.71	0	18	77	1	EFLVSAYFSLHGR
☑	2110	848.4104	1694.8062	1694.8080	-1.01	1	18	87	1	SLRGNEMNCLSGIGTK + Oxidation (M)
☑	2503	472.2409	1884.9345	1884.9363	-0.97	0	18	85	1	GDLDIANNMAVADINALR
☑	78	376.7001	751.3856	751.3864	-1.06	0	18	1.3e+002	1	YDVSIR
☑	2262	882.4792	1762.9438	1762.9425	0.76	1	18	57	1	LTGTTTVAKEQITTSGR
☑	2906	739.3530	2215.0372	2215.0368	0.16	0	18	60	1	HPGEMEHGFINVTDLTFGSK
☑	3234	1168.0770	2334.1394	2334.1452	-2.47	0	18	82	1	GGDTLIGGVAADTLSGGSGADALFGR
☑	335	464.2845	926.5544	926.5549	-0.47	1	18	85	1	AITPELKR

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☑   58   365.1972   728.3798   728.3817  -2.54  0   18    1e+002  1        DIPGTAR
☑ 1749   483.5999  1447.7779  1447.7745   2.35  0   18        71  1        GDLYLLPVMNSVK
☑ 2504   629.6981  1886.0725  1886.0724   0.04  0   18        17  1        LLLNTSAIASQSIILSDK
☑ 1691   469.2610  1404.7612  1404.7572   2.82  1   18        81  1        SSRESTLISANLK
☑ 2613  1012.5540  2023.0934  2023.0884   2.48  1   18        43  1        NGVTLTKEQDHLICALIR
☑ 1558   678.8668  1355.7190  1355.7157   2.47  1   18        98  1        DQALIKAQEAGGR
☑ 2028   832.3884  1662.7622  1662.7631  -0.54  1   18        64  1        MTGDATTAPSPSSERR
☑ 2141   859.4776  1716.9406  1716.9444  -2.17  1   18        55  1        LSLISAMDKNGLIGTGK
☑ 2844  1094.0340  2186.0534  2186.0599  -2.95  1   18        85  1        TDNPLLCDPKEGLCELPTTK
☑ 1504   450.2530  1347.7372  1347.7371   0.04  1   18        78  1        KAHIHSSLGGVSR
☑  582   361.5331  1081.5775  1081.5768   0.67  1   18        76  1        KYGASSQTIK
☑  687   377.1947  1128.5623  1128.5636  -1.15  0   18        65  1        QQRPQTSER
☑ 2357   898.4599  1794.9052  1794.9040   0.72  1   18        89  1        AYKSLITDVDEDWIK
☑  142   389.7085   777.4024   777.4055  -3.87  0   18  2.3e+002  1        ACLVSASK
☑   75   372.7043   743.3940   743.3966  -3.44  0   18    2e+002  1        FHAEIK
☑ 3029  1133.6180  2265.2214  2265.2270  -2.44  1   18        43  1        LPAPFGDRSVWTPDAALALLR
☑ 1201   639.3100  1276.6054  1276.6008   3.68  1   18        94  1        RSLDGSGEVSDR
☑ 2585   988.4979  1974.9812  1974.9759   2.71  0   18        94  1        WGTEAAVALAAAGSAASGATSR
☑ 2900   738.3646  2212.0720  2212.0648   3.25  1   18        85  1        NKAIVQEGQYDELTGEFGSK
☑  484   515.2647  1028.5148  1028.5185  -3.59  1   18        92  1        CHIKQTSGR
☑ 2136   429.7286  1714.8853  1714.8825   1.64  1   18        89  1        VMEGHGIFRVTAVGDK
☑ 1111   626.8308  1251.6470  1251.6459   0.93  0   18        91  1        SSLGQYLSELR
☑ 1940   528.2725  1581.7957  1581.7895   3.92  1   18    1e+002  1        VCCVKNIYDVLEK + Carbamidomethyl (C)
☑  934   608.3023  1214.5900  1214.5891   0.76  1   18        78  1        TSFKTNSSTSR
☑ 1406   660.8315  1319.6484  1319.6438   3.52  1   18  1.1e+002  1        ARMVNAMGGIER + Oxidation (M)
☑ 2104   564.6504  1690.9294  1690.9254   2.38  0   18        47  1        VYSVIQSQINAALSAK
☑  193   405.7030   809.3914   809.3919  -0.59  0   18        91  1        YDGSVAAK
☑  736   568.7968  1135.5790  1135.5833  -3.77  0   18        84  1        GQSVTSSTTLR
☑ 1246   431.2468  1290.7186  1290.7143   3.30  1   18        70  1        TKSASALTGLTNK
☑ 3155  1154.0580  2306.1014  2306.0995   0.86  1   18        87  1        QPNADQLAMLQKDITSTCSSR
☑  354   471.2689   940.5232   940.5229   0.33  0   18        56  1        GPLLDDALK
☑ 1177   637.3616  1272.7086  1272.7038   3.85  0   18  1.1e+002  1        NLTLQINSVGSK
☑  587   542.7677  1083.5208  1083.5239  -2.80  1   18        85  1        TLIKMCGMR + 2 Oxidation (M)
☑  244   422.7135   843.4124   843.4095   3.51  0   18        37  1        MPAAAPMR
☑  627   551.7680  1101.5214  1101.5203   1.03  0   18        60  1        ESADAFHGLR
☑  660   559.7645  1117.5144  1117.5186  -3.72  1   18        69  1        MTEHVSKDR + Oxidation (M)
☑ 2054   845.4670  1688.9194  1688.9209  -0.89  1   18        68  1        VRLAANTYDALIVDR
☑  372   477.2871   952.5596   952.5593   0.34  0   18        24  1        LPPGDITLK
☑ 2175   867.4741  1732.9336  1732.9359  -1.32  1   18        64  1        INDIFAGKGVTEAIGTK
☑ 1688   702.8724  1403.7302  1403.7330  -1.94  1   18  1.2e+002  1        AELLKQLAEMDK + Oxidation (M)
☑  897   602.2979  1202.5812  1202.5832  -1.65  0   18        79  1        WGAWSADALAR
☑ 2002   823.4675  1644.9204  1644.9198   0.37  1   18        38  1        LEKPASYDAIKAAIR
☑ 1250   646.3666  1290.7186  1290.7183   0.24  1   18        72  1        LSIKDFLSGSPK
☑ 1374   437.9045  1310.6917  1310.6904   0.97  0   18        90  1        LMEILLDSHPK + Oxidation (M)
☑   89   376.7004   751.3862   751.3864  -0.26  0   18  1.4e+002  1        YDSVIR
☑ 1136   420.2147  1257.6223  1257.6176   3.74  1   18        97  1        YMAQKAFLDR + Oxidation (M)
☑ 2150   859.4799  1716.9452  1716.9444   0.50  0   18        50  1        TNLQLVGITCLSIASK + Carbamidomethyl (C)
☑ 2851   731.3740  2191.1002  2191.0943   2.69  0   18        91  1        LDDINIFVAIADNASMTAAAR
☑ 1395   658.3669  1314.7192  1314.7183   0.69  1   18  1.2e+002  1        KLLEPVLGEFNG
☑  132   385.2262   768.4378   768.4382  -0.40  0   18        33  1        PTPDVLK
☑ 1631   461.9122  1382.7148  1382.7154  -0.43  0   18        95  1        LLAEQPDNTNIR
☑  144   389.7139   777.4132   777.4133  -0.09  0   18  1.1e+002  1        AGYIQAR
☑ 3153  1153.0880  2304.1614  2304.1685  -3.06  1   18        92  1        IDWKVLITSVCNQYSGHVSR
☑  917   605.2990  1208.5834  1208.5794   3.33  0   18        96  1        CQNIAFMGGLR
☑  594   543.7704  1085.5262  1085.5288  -2.32  0   18        69  1        SLSMHQDLR
☑  873   597.7903  1193.5660  1193.5677  -1.35  0   18        72  1        YGGSGLEGGEIR
☑ 1513   675.3638  1348.7130  1348.7108   1.69  1   18  1.3e+002  1        LQFRCLPGMLR + Oxidation (M)
☑  117   380.6956   759.3766   759.3763   0.50  0   18    2e+002  1        QEEGLGK
☑  566   535.7731  1069.5316  1069.5338  -2.05  0   18        75  1        MRPAPDDLR
☑  908   604.2905  1206.5664  1206.5663   0.16  1   18        95  1        EDLLERCSSR
☑ 1151   632.8250  1263.6354  1263.6380  -2.04  0   18  1.4e+002  1        LTAEISACTDLK
☑ 1969   804.3698  1606.7250  1606.7236   0.87  1   18        59  1        TQNREHFDGNYAR
☑ 3197   773.7328  2318.1766  2318.1796  -1.32  0   18        96  1        LCVQVLGMSTADLEVLLAQCR + Carbamidomethyl (C)
☑  691   565.2895  1128.5644  1128.5636   0.79  1   18        77  1        DLAGARAANDR
☑   46   361.6967   721.3788   721.3792  -0.55  1   18        65  1        SSLRML + Oxidation (M)
☑  450   504.7779  1007.5412  1007.5400   1.28  1   18  1.1e+002  1        KAGYTAEIR
☑ 1203   639.8258  1277.6370  1277.6404  -2.63  1   18  1.4e+002  1        EYFLQHADKK
☑ 1167   634.8292  1267.6438  1267.6455  -1.32  1   18  1.1e+002  1        MRDHIVDNLR
☑ 3209  1163.0250  2324.0354  2324.0325   1.25  0   18        42  1        QSSSDESDPLVLNEMLSNDTK + Oxidation (M)
☑ 1562   453.2420  1356.7042  1356.7072  -2.20  0   18  1.3e+002  1        AGVPMIVSGVGQDK
☑  337   464.7459   927.4772   927.4774  -0.15  1   17        60  1        REDGKPVGA
☑  889   400.8825  1199.6257  1199.6294  -3.10  0   17  1.2e+002  1        TLGMYVMLLK + 2 Oxidation (M)
☑ 1458   667.3723  1332.7300  1332.7289   0.87  1   17        92  1        EILKDNTIYPK
☑ 1502   674.3614  1346.7082  1346.7042   3.03  1   17  1.2e+002  1        KSDGSLGTPSTAVK
☑ 3192  1160.0800  2318.1454  2318.1439   0.67  1   17    1e+002  1        MKNQKPLFSGEFVIDMAFGK + 2 Oxidation (M)
☑   25   350.6910   699.3674   699.3664   1.53  0   17        54  1        NGPVSAR
☑ 1187   425.5462  1273.6168  1273.6203  -2.81  1   17  1.1e+002  1        GFAYAKYGNQR
☑  311   455.7294   909.4442   909.4412   3.34  0   17        89  1        MMITGTTR
☑  937   608.8067  1215.5988  1215.5956   2.70  1   17  1.1e+002  1        SRNQEEIANR
☑ 1495   672.8168  1343.6190  1343.6140   3.79  1   17        69  1        KGPADACTPGENK + Carbamidomethyl (C)
☑  809   583.8007  1165.5868  1165.5914  -3.89  0   17  1.4e+002  1        IDPVNVGPCPR
☑  936   608.7724  1215.5302  1215.5255   3.90  0   17        35  1        ADGEDVQEPEK
☑ 1003   613.8234  1225.6322  1225.6302   1.63  0   17    1e+002  1        AEGSATDLPPIR
☑ 1497   672.8206  1343.6266  1343.6317  -3.76  0   17        76  1        ESNNSNTAPVSPK
☑   61   365.7216   729.4286   729.4272   1.92  0   17  1.4e+002  1        ILLPSTS
☑ 2205   872.4730  1742.9314  1742.9275   2.28  1   17        84  1        DQNAATTKTINNIAIR
☑ 2497   628.0232  1881.0478  1881.0472   0.30  1   17        34  1        DQLINEGKPIKAVFPGR
☑ 2209   873.4760  1744.9374  1744.9433  -3.35  1   17        77  1        YPELISKAMPLLQDK
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☑	1616	689.3808	1376.7470	1376.7486	-1.11	1	17	75	1	QMVKANFEAVIK
☑	2530	634.7113	1901.1121	1901.1098	1.19	1	17	7.9	1	KILTHILVTQSAPDPLR
☑	1029	614.8168	1227.6190	1227.6207	-1.38	1	17	79	1	IEDIDPQRSR
☑	740	568.7974	1135.5802	1135.5808	-0.48	0	17	1.1e+002	1	APPPPAVAASCR
☑	899	602.3254	1202.6362	1202.6407	-3.73	1	17	1.6e+002	1	RYADLEAPLR
☑	1916	788.9273	1575.8400	1575.8369	2.00	1	17	95	1	SSAGLRTTNPPPPPGK
☑	2142	859.4779	1716.9412	1716.9345	3.93	1	17	66	1	GCPLPPVIPAQLRGDK + Carbamidomethyl (C)
☑	2164	862.9562	1723.8978	1723.8927	2.99	1	17	1.1e+002	1	LTAFCSEQILRTGTK + Carbamidomethyl (C)
☑	1891	523.2683	1566.7831	1566.7831	0.00	0	17	1.2e+002	1	LTPFAAEAVYWSGR
☑	1362	436.5782	1306.7128	1306.7133	-0.37	0	17	88	1	LDYQTVLSQIK
☑	1759	731.3787	1460.7428	1460.7414	0.97	0	17	1.6e+002	1	MTVGRPIVQACMR
☑	2005	824.8823	1647.7500	1647.7457	2.62	0	17	65	1	ECSVRPGCSVGVENR + Carbamidomethyl (C)
☑	2845	729.6927	2186.0563	2186.0565	-0.12	0	17	1e+002	1	YEVDMVQSLIEEFVTVNR + Oxidation (M)
☑	1124	629.3353	1256.6560	1256.6547	1.08	1	17	1.1e+002	1	AHQKMVTEVAK + Oxidation (M)
☑	801	582.7946	1163.5746	1163.5744	0.25	0	17	1.2e+002	1	IDEESLAMLK + Oxidation (M)
☑	1531	452.2501	1353.7285	1353.7252	2.40	0	17	83	1	LAQGLHLSETTGK
☑	1565	453.9196	1358.7370	1358.7405	-2.61	1	17	1.3e+002	1	DKNTLLSDLVNK
☑	2552	960.9883	1919.9620	1919.9611	0.50	0	17	1.2e+002	1	TSVVGMVCYRPGWRPR + Carbamidomethyl (C)
☑	1615	459.9208	1376.7406	1376.7412	-0.48	0	17	98	1	SATVLGGQITFAGR
☑	1973	804.9143	1607.8140	1607.8123	1.07	1	17	1.3e+002	1	IASGSCQTTMNVIKR
☑	1516	675.3666	1348.7186	1348.7238	-3.82	0	17	1.4e+002	1	LSLETAAEPPPPK
☑	271	437.6967	873.3788	873.3763	2.94	1	17	17	1	ERHCSDK
☑	2340	894.4875	1786.9604	1786.9537	3.77	1	17	2e+002	1	EISAVTAALRSGDLATGR
☑	2395	604.6843	1811.0311	1811.0379	-3.76	1	17	30	1	MKIIVINPILFTHEK + Oxidation (M)
☑	349	467.2375	932.4604	932.4577	2.99	1	17	1.1e+002	1	SRSGAGGWR
☑	803	582.7964	1163.5782	1163.5791	-0.71	1	17	1.5e+002	1	MLKGCSAEIGR
☑	131	384.6982	767.3818	767.3788	3.91	0	17	73	1	YMWIR
☑	1445	666.3591	1330.7036	1330.7027	0.69	0	17	1.3e+002	1	MGGVAQQVASVLR + Oxidation (M)
☑	1915	788.9270	1575.8394	1575.8409	-0.92	1	17	1e+002	1	FYSNPKLNLPVER
☑	2126	569.9811	1706.9215	1706.9178	2.17	1	17	66	1	MFSVQAEKLWSILR
☑	541	532.2982	1062.5818	1062.5822	-0.32	1	17	1.3e+002	1	SWSTIKSVR
☑	2413	911.5126	1821.0106	1821.0036	3.87	0	17	47	1	ALLLFSSLGFAAAENGLK
☑	511	524.2568	1046.4990	1046.4992	-0.18	0	17	95	1	EQAVSDAATR
☑	492	520.2747	1038.5348	1038.5346	0.28	0	17	84	1	VAENPVGPEK
☑	2409	909.4183	1816.8220	1816.8214	0.37	0	17	61	1	EEAETPEESEEVQALK
☑	236	421.7219	841.4292	841.4294	-0.16	0	17	71	1	SLPTDGPR
☑	347	466.2296	930.4446	930.4447	-0.06	0	17	46	1	HVGYVIDE
☑	2487	937.5105	1873.0064	1873.0098	-1.77	1	17	85	1	LSTVYPLPEPFALRDR
☑	325	459.7609	917.5072	917.5083	-1.13	1	17	86	1	SPFRNGLK
☑	967	613.8229	1225.6312	1225.6302	0.82	0	17	1.1e+002	1	GLPAAGEDIDLR
☑	2551	640.3461	1918.0165	1918.0090	3.92	1	17	94	1	ILMMPVAISKECLELR + Carbamidomethyl (C); Oxidation (M)
☑	2756	718.6893	2153.0461	2153.0423	1.77	1	17	1.1e+002	1	SYKEQLNNIVVMASEDGTR
☑	1118	419.5423	1255.6051	1255.6091	-3.24	0	17	1e+002	1	AMVHAQASATGGR
☑	2199	870.4680	1738.9214	1738.9254	-2.25	1	17	90	1	NTFIDAAGFSGLIKSAK
☑	767	576.7850	1151.5554	1151.5539	1.32	1	17	81	1	QMSMGIARAR + 2 Oxidation (M)
☑	3358	811.7521	2432.2345	2432.2257	3.60	0	17	98	1	LQGDIVEVTANTNMSPEVFIQK
☑	1922	526.9373	1577.7901	1577.7950	-3.15	0	17	1.4e+002	1	VRPPDNGSFPLDHK
☑	3584	1162.2090	3483.6052	3483.5936	3.33	1	17	48	1	ADCATRHDSPDADLVEANLLWWQEMGGNITR
☑	930	607.3011	1212.5876	1212.5921	-3.66	0	17	1e+002	1	EPKPVCSPSNR
☑	1294	650.3535	1298.6924	1298.6942	-1.38	1	17	97	1	TAAARPVADGDKK
☑	1712	472.2486	1413.7240	1413.7212	1.98	1	17	1.3e+002	1	IIDGLNDEQNKR
☑	1119	419.5427	1255.6063	1255.6084	-1.73	0	17	1e+002	1	YEQVVQEYAK
☑	622	549.7941	1097.5736	1097.5717	1.79	0	17	1e+002	1	TEGSEIVVHK
☑	3148	768.7477	2303.2213	2303.2134	3.43	1	17	71	1	ADAAAQEAAARAAALAALPAWAPR
☑	3090	1143.6360	2285.2574	2285.2646	-3.14	0	17	38	1	IVGTIFGMFVAAVGYIYPVLR
☑	1678	466.9254	1397.7544	1397.7528	1.15	1	17	94	1	ATALGPNWLSGRR
☑	159	396.6765	791.3384	791.3410	-3.17	0	17	36	1	DSDSNVR
☑	202	409.2451	816.4756	816.4745	1.38	0	17	34	1	ISPPLYK
☑	1473	670.8458	1339.6770	1339.6806	-2.63	0	17	1.3e+002	1	ESALAFSVTMLR + Oxidation (M)
☑	3011	753.4153	2257.2241	2257.2179	2.76	1	17	51	1	QQILQVIANSPGARTELYTR
☑	1040	617.3221	1232.6296	1232.6262	2.83	0	17	1.7e+002	1	AVNNAQGLYQR
☑	1162	634.8273	1267.6400	1267.6408	-0.60	1	17	93	1	VSTYKEDSALR
☑	2878	735.0244	2202.0514	2202.0600	-3.91	1	17	1.1e+002	1	GHNSNVTPSNNISNIGKMFR + Oxidation (M)
☑	630	551.7684	1101.5222	1101.5237	-1.30	0	17	69	1	QCDPNSLLR + Carbamidomethyl (C)
☑	1647	694.8536	1387.6926	1387.6943	-1.19	0	17	1.4e+002	1	GLSDETLQAVAER
☑	2996	1124.6270	2247.2394	2247.2335	2.64	1	17	33	1	LVRIALEHSGEDNVTVQVLR
☑	1942	528.2728	1581.7966	1581.7999	-2.07	0	17	1e+002	1	GAGADVNAGVDPAVIEK
☑	62	366.1775	730.3404	730.3398	0.83	1	17	78	1	KFEGGGH
☑	1341	650.3548	1298.6950	1298.6951	-0.06	1	17	1.3e+002	1	CKTVILCIGHR + Carbamidomethyl (C)
☑	2344	597.3445	1789.0117	1789.0098	1.05	1	17	27	1	TDKGVSSVGQVIALFLR
☑	1884	523.2681	1566.7825	1566.7790	2.19	1	17	1.2e+002	1	SVPREFYSGLAEGR
☑	2562	484.2704	1933.0525	1933.0489	1.88	1	17	64	1	SMVILISGRGSNMQALLK + Oxidation (M)
☑	2592	663.0529	1986.1369	1986.1302	3.36	0	17	21	1	TAPLAILTSVLAALGAWYR
☑	515	526.7678	1051.5210	1051.5233	-2.14	0	17	1.3e+002	1	QQPGCPPLR + Carbamidomethyl (C)
☑	890	601.3040	1200.5934	1200.5921	1.12	0	17	1.1e+002	1	ISSCHTIDIR + Carbamidomethyl (C)
☑	1443	666.3486	1330.6826	1330.6802	1.82	0	17	1.2e+002	1	NEEMIVLGGLEK
☑	2258	881.4734	1760.9322	1760.9308	0.80	1	17	99	1	NLFEKQSQLVLEDAK
☑	3144	1152.0850	2302.1554	2302.1475	3.47	1	17	1.2e+002	1	MSPDVADLVETSNNVARVELK + Oxidation (M)
☑	2106	846.4734	1690.9322	1690.9328	-0.32	1	17	54	1	GSWIISMIVKLVTTQ + Oxidation (M)
☑	817	586.2801	1170.5456	1170.5451	0.44	1	17	90	1	FEMRSASTSR
☑	2899	1107.0430	2212.0714	2212.0647	3.03	1	17	1.1e+002	1	SSYDSLLSNYDSILKENHK
☑	1014	613.8235	1225.6324	1225.6276	3.96	1	17	1.2e+002	1	RGGSAAVGGGQGPR
☑	2744	717.0279	2148.0619	2148.0674	-2.55	1	17	1.2e+002	1	IGGIPWFNAMEAGIKSQGEK + Oxidation (M)
☑	764	575.8148	1149.6150	1149.6142	0.74	0	17	1.3e+002	1	YLASNGVASLR
☑	1257	431.2469	1290.7189	1290.7217	-2.18	1	17	92	1	ISMIENIKSIK + Oxidation (M)
☑	2279	887.5140	1773.0134	1773.0148	-0.79	0	17	25	1	IVLAHAGQPLSEAQVLK
☑	2625	683.6827	2048.0263	2048.0248	0.70	0	17	1.3e+002	1	GEEILQLGEVCDYVGIVR + Carbamidomethyl (C)
☑	727	568.7959	1135.5772	1135.5729	3.80	0	17	1.6e+002	1	SLLCIGGASMK + Carbamidomethyl (C)

☑	654	557.7692	1113.5238	1113.5237	0.16	0	17	90	1	AHINVEEMR + Oxidation (M)
☑	3159	769.7338	2306.1796	2306.1794	0.06	1	17	1.1e+002	1	ILDKDFTVVDEISFEVGAGPR
☑	1058	414.2110	1239.6112	1239.6142	-2.46	0	17	1.1e+002	1	MHLQQGNVSAR
☑	291	446.7241	891.4336	891.4338	-0.16	0	17	1.6e+002	1	DFPDLASK
☑	1970	804.3712	1606.7278	1606.7236	2.61	1	17	78	1	TQNREHFDGNYAR
☑	2564	970.4696	1938.9246	1938.9204	2.18	0	17	1.2e+002	1	SDALITLNGSSNIDMTGSK + Oxidation (M)
☑	3245	1172.1460	2342.2774	2342.2794	-0.82	1	17	48	1	LPIWRTAANMAIAHPVNGVGVR
☑	204	412.2247	822.4348	822.4348	0.08	1	17	91	1	SASFGKAR
☑	3447	925.0927	2772.2563	2772.2656	-3.38	1	17	56	1	DVETIDMPDSVELIGTKAFQCCTK + 2 Carbamidomethyl (C); Oxidation (M)
☑	706	567.7621	1133.5096	1133.5070	2.35	1	17	79	1	RSHMTCDLR + Oxidation (M)
☑	1985	541.9254	1622.7544	1622.7536	0.48	1	17	84	1	TRVADQDEEEYLR
☑	2163	575.3133	1722.9181	1722.9226	-2.64	1	17	92	1	ALDVKFMDIGTVATVK + Oxidation (M)
☑	2831	1092.0200	2182.0254	2182.0295	-1.84	1	17	1e+002	1	EWKPLCVLKMDIDCMTGK + Carbamidomethyl (C); Oxidation (M)
☑	1603	686.8781	1371.7416	1371.7411	0.37	1	17	1.3e+002	1	SHLYHLFRTAK
☑	1906	784.4020	1566.7894	1566.7923	-1.82	1	17	1.1e+002	1	MSGSTKESAAVSLATK
☑	2048	841.4212	1680.8278	1680.8327	-2.92	0	17	1.4e+002	1	VMLAMQGDGNVVLYR + Oxidation (M)
☑	381	479.2373	956.4600	956.4572	2.99	0	17	1.2e+002	1	HCTQLMPK
☑	280	441.2579	880.5012	880.5018	-0.63	0	17	49	1	LALDGAPPK
☑	2354	897.4866	1792.9586	1792.9570	0.89	0	17	80	1	QLVELLGGHLELESEK
☑	1354	652.3656	1302.7166	1302.7143	1.77	0	17	1.3e+002	1	TATGGTVELVSLR
☑	2228	875.4758	1748.9370	1748.9308	3.55	1	17	96	1	FETQLAKLQSDLASAK
☑	1805	509.2650	1524.7732	1524.7725	0.44	0	17	1.4e+002	1	EFLVSAYFSLHGR
☑	1578	682.8748	1363.7350	1363.7347	0.24	0	17	1.1e+002	1	TTSLSDLYVPLR
☑	1646	694.3836	1386.7526	1386.7541	-1.02	0	17	1.2e+002	1	LLLSGSPMQNSLK
☑	3008	1128.0880	2254.1614	2254.1593	0.93	1	16	1e+002	1	ASEVTAVLEALERWGGVEPGGK
☑	2460	619.3540	1855.0402	1855.0468	-3.58	1	16	44	1	DKPVKANIFAAGAVLWR
☑	3139	1151.1400	2300.2654	2300.2641	0.60	1	16	38	1	QDSNLRPLAPSGAAIFLYVRL
☑	1211	642.2936	1282.5726	1282.5720	0.54	0	16	67	1	VAVCMSLAACGDK + Oxidation (M)
☑	1382	657.3587	1312.7028	1312.7027	0.13	1	16	1.2e+002	1	YTKADIFSAIGK
☑	1875	779.8897	1557.7648	1557.7675	-1.67	0	16	1.3e+002	1	KPPIENINDFEDK
☑	1997	546.6661	1636.9765	1636.9763	0.08	1	16	11	1	TEVVLKLQTPALPTK
☑	1905	784.4010	1566.7874	1566.7824	3.24	1	16	1.7e+002	1	AMKALNYALSGEAGR + Oxidation (M)
☑	841	590.3102	1178.6058	1178.6044	1.25	1	16	1.5e+002	1	ATDRYVDALR
☑	1545	452.9125	1355.7157	1355.7119	2.79	0	16	1.3e+002	1	CDLGEVNVLLPK + Carbamidomethyl (C)
☑	3119	1146.0990	2290.1834	2290.1814	0.92	0	16	1.1e+002	1	IVFLGAGSAGCGIAEMIIAQTPR + Oxidation (M)
☑	3338	803.0734	2406.1984	2406.2035	-2.14	1	16	1.3e+002	1	VMLGQRLGLPELNDSMYSIDR
☑	938	406.2143	1215.6211	1215.6207	0.28	1	16	1.7e+002	1	TLANRDEAAQK
☑	3341	806.1159	2415.3259	2415.3196	2.62	0	16	40	1	LADLVSLLPVLAMPLAVADEHGR + Oxidation (M)
☑	442	501.7822	1001.5498	1001.5505	-0.69	1	16	2.4e+002	1	SKLNGDAVAK
☑	1052	618.7963	1235.5780	1235.5782	-0.12	0	16	1.4e+002	1	TFEEQEAINR
☑	86	376.7004	751.3862	751.3864	-0.26	0	16	2e+002	1	YDVISR
☑	1279	649.8465	1297.6784	1297.6739	3.54	1	16	1.3e+002	1	QSNDVLVPDRR
☑	104	377.7132	753.4118	753.4133	-1.95	0	16	1.5e+002	1	DKPAPAR
☑	875	597.8224	1193.6302	1193.6292	0.88	0	16	1.5e+002	1	LISNSTDVAFK
☑	2342	894.5055	1786.9964	1786.9975	-0.57	1	16	48	1	VLLACTKLATSAEAIAR + Carbamidomethyl (C)
☑	2565	970.5119	1939.0092	1939.0024	3.54	0	16	1.2e+002	1	ASSSLARPPADPHDLLHR
☑	437	499.7797	997.5448	997.5444	0.45	0	16	76	1	IDDPAQVIK
☑	1421	442.5754	1324.7044	1324.7027	1.29	1	16	98	1	ISYENPFIKSK
☑	2034	837.4653	1672.9160	1672.9182	-1.27	1	16	87	1	QLSKLSEVVNAMVQK
☑	950	610.7995	1219.5844	1219.5833	0.94	0	16	1.6e+002	1	DAFDADLANLR
☑	2396	604.6851	1811.0335	1811.0265	3.86	1	16	40	1	GTLNANSAVVGANGKVVLK
☑	2451	922.5181	1843.0216	1843.0204	0.70	0	16	52	1	GQGFATGQINLGEIVVLK
☑	301	450.7448	899.4750	899.4726	2.74	1	16	83	1	AFRVDHR
☑	1645	694.3832	1386.7518	1386.7541	-1.59	1	16	1.6e+002	1	IATSLIHTMEKK + Oxidation (M)
☑	2638	687.9828	2060.9266	2060.9190	3.67	1	16	72	1	IDAADGGDRNHMMLSVCTR
☑	590	543.2545	1084.4944	1084.4938	0.62	0	16	76	1	HDPDAFDLR
☑	1669	465.9160	1394.7262	1394.7307	-3.21	1	16	1.5e+002	1	SRVSFFSQNVPK
☑	1571	454.9071	1361.6995	1361.6980	1.12	0	16	1.5e+002	1	FTFGVQPAAEAPK
☑	1542	452.9124	1355.7154	1355.7157	-0.24	1	16	1.4e+002	1	QDIAVRLNGNEK
☑	1566	680.3800	1358.7454	1358.7405	3.62	1	16	1.4e+002	1	ERTVDELSVLAK
☑	2747	717.0422	2148.1048	2148.1103	-2.58	1	16	1.3e+002	1	KEGFDVIVAGDGPTALVEFGK
☑	243	422.2457	842.4768	842.4749	2.29	0	16	70	1	IILVEGEA
☑	3335	802.4171	2404.2295	2404.2274	0.84	0	16	1.3e+002	1	GTLDAFATGFDPLLNGVVAEEIR
☑	2225	875.4734	1748.9322	1748.9309	0.78	1	16	91	1	FLAVEDVVTTGESVRK
☑	1179	425.2438	1272.7096	1272.7111	-1.22	0	16	90	1	IELMKPATINK + Oxidation (M)
☑	1848	768.3656	1534.7166	1534.7160	0.45	0	16	1.1e+002	1	CYLNLLGTNYSMK + Oxidation (M)
☑	2189	578.9810	1733.9212	1733.9199	0.71	1	16	1e+002	1	VSVTPYAETKAGIAEAK
☑	3126	1147.0700	2292.1254	2292.1242	0.53	1	16	1.6e+002	1	YDCMLLVDEAHSLGVLGKTGR + Oxidation (M)
☑	831	393.5316	1177.5730	1177.5736	-0.53	1	16	2e+002	1	AGMWMEAVKR
☑	1950	795.3640	1588.7134	1588.7191	-3.59	0	16	73	1	VMYSVNEVTNYDR
☑	3086	1143.6340	2285.2534	2285.2604	-3.04	1	16	46	1	DTGIPLIQLNNIRDGQHILR
☑	969	613.8229	1225.6312	1225.6303	0.80	0	16	1.4e+002	1	GTEALPPTDGLR
☑	1196	637.8486	1273.6826	1273.6819	0.59	0	16	2e+002	1	SSIPFPPNFLR
☑	392	484.7379	967.4612	967.4644	-3.31	0	16	1.1e+002	1	SLGTATMSGK + Oxidation (M)
☑	1887	523.2681	1566.7825	1566.7791	2.18	0	16	1.5e+002	1	VAVFGYNQEQLGSR
☑	2356	897.9128	1793.8110	1793.8101	0.51	1	16	1e+002	1	EMSVDESKQAGTQADAK
☑	2775	723.0170	2166.0292	2166.0328	-1.68	0	16	1.2e+002	1	EAESLGAGELFINSIDTDGTK
☑	2341	894.5049	1786.9952	1786.9975	-1.25	1	16	52	1	LVLAMSLDGRIALSSGGK
☑	1146	632.3197	1262.6248	1262.6295	-3.71	0	16	1.9e+002	1	VPGPWDPEPAAK
☑	1228	644.3552	1286.6958	1286.6983	-1.88	0	16	1.5e+002	1	TVSIENAVWIR
☑	1247	431.2468	1290.7186	1290.7217	-2.41	1	16	1.1e+002	1	ISLMNELSKIK + Oxidation (M)
☑	3012	753.4359	2257.2859	2257.2769	3.97	1	16	24	1	RNGLLLQAAGVVIWCIISFK + Carbamidomethyl (C)
☑	791	580.7991	1159.5836	1159.5833	0.30	0	16	1.9e+002	1	SAPILNSTDSR
☑	1577	682.8702	1363.7258	1363.7282	-1.72	0	16	1.4e+002	1	MTVGFAALNATLR
☑	742	568.7976	1135.5806	1135.5808	-0.13	0	16	1.3e+002	1	MANLFGTLNR
☑	1055	619.8043	1237.5940	1237.5986	-3.66	1	16	1.4e+002	1	RMDADPQHLR
☑	1660	696.3749	1390.7352	1390.7317	2.56	1	16	1.5e+002	1	APNANGTSHKLGPK
☑	1475	670.8643	1339.7140	1339.7095	3.36	1	16	1.3e+002	1	EPKGVIDEANIR

☑	1662	465.2485	1392.7237	1392.7283	-3.29	1	16	1.9e+002	1	LDTMAGKLTGTAAK + Oxidation (M)
☑	926	606.8389	1211.6632	1211.6662	-2.46	0	16	1.1e+002	1	QFNLLHALEK
☑	1752	725.8802	1449.7458	1449.7464	-0.35	1	16	1.5e+002	1	QYGVNKIVTEGDK
☑	411	489.7667	977.5188	977.5182	0.68	0	16	2.8e+002	1	QFGEVLSAK
☑	424	493.2867	984.5588	984.5604	-1.54	0	16	1.8e+002	1	NLLPINSSK
☑	1417	662.3554	1322.6962	1322.6983	-1.53	0	16	1e+002	1	LLYNFSPVNTR
☑	1512	450.2610	1347.7612	1347.7649	-2.78	1	16	60	1	LIEEEFISKLK
☑	2177	867.4750	1732.9354	1732.9359	-0.27	1	16	1e+002	1	YVELVQQSLELEKR
☑	2606	1006.9940	2011.9734	2011.9698	1.81	0	16	1.4e+002	1	NLPLTNESDPLQNSDLDK
☑	406	488.2447	974.4748	974.4781	-3.34	0	16	1.6e+002	1	GASLAADGSAR
☑	1838	764.3339	1526.6532	1526.6493	2.57	1	16	42	1	ICRESNCYEPEK + Carbamidomethyl (C)
☑	2033	558.6279	1672.8619	1672.8632	-0.77	1	16	1.8e+002	1	TESAVPGKSTASAKPDK
☑	1882	522.5935	1564.7587	1564.7602	-0.99	1	16	1.6e+002	1	IWCAARASNSMVTR
☑	678	562.2848	1122.5550	1122.5525	2.24	1	16	1.5e+002	1	KMEVMGVSSR
☑	781	387.2072	1158.5998	1158.5993	0.43	1	16	2.2e+002	1	EGETKIAAQGR
☑	47	361.7080	721.4014	721.4010	0.58	1	16	2.1e+002	1	LSLKDF
☑	1376	656.8364	1311.6582	1311.6531	3.92	1	16	1.4e+002	1	IDENRLPQDGR
☑	2416	609.0156	1824.0250	1824.0291	-2.29	1	16	52	1	LVVVGGMGKQDRPDIIK
☑	1128	629.8173	1257.6200	1257.6214	-1.09	1	16	1.4e+002	1	RGADAWEAIGGR
☑	2470	619.9636	1856.8690	1856.8625	3.46	1	16	1.2e+002	1	VCVTAQRMVCCLMLCK + Carbamidomethyl (C)
☑	2749	717.3626	2149.0660	2149.0725	-3.04	0	16	1.6e+002	1	ISLSFVEQDEVNLQQCLK + Carbamidomethyl (C)
☑	1890	523.2682	1566.7828	1566.7790	2.38	1	16	1.7e+002	1	SVPREFYSGLAEGR
☑	589	543.2513	1084.4880	1084.4897	-1.55	1	16	66	1	SSSSGDRAYR
☑	367	475.7458	949.4770	949.4770	0.06	0	16	1.4e+002	1	YAFISHGR
☑	534	530.7873	1059.5600	1059.5634	-3.16	0	16	2.9e+002	1	LCSLPESALK
☑	1368	654.8328	1307.6510	1307.6470	3.10	0	16	2e+002	1	NLDTVPGPGADPR
☑	1886	523.2681	1566.7825	1566.7790	2.19	1	16	1.6e+002	1	SVPREFYSGLAEGR
☑	2943	743.6971	2228.0695	2228.0685	0.46	1	16	1.4e+002	1	GMTPFVPETGDWKLHNLDR + Oxidation (M)
☑	2363	599.9985	1796.9737	1796.9793	-3.14	1	16	1.1e+002	1	AIAMHKQHILLMYTK
☑	3154	769.0611	2304.1615	2304.1705	-3.94	0	16	1.4e+002	1	IIVVTMQGLQGGEMSVVGDDIK + Oxidation (M)
☑	383	479.3027	956.5908	956.5906	0.22	0	16	56	1	VVLIDTGIK
☑	420	493.2509	984.4872	984.4876	-0.37	0	16	82	1	VNIEPNDGK
☑	686	565.2792	1128.5438	1128.5411	2.43	0	16	1e+002	1	SHLLGDSSADK
☑	1204	640.2810	1278.5474	1278.5510	-2.77	0	16	47	1	SEAEIQSDMNR
☑	1590	457.2407	1368.7003	1368.7038	-2.54	1	16	1.5e+002	1	FVLEKDTAYQR
☑	2388	602.6758	1805.0056	1805.0047	0.48	1	16	46	1	FLKADTVIISTGVTANR
☑	2945	743.6974	2228.0704	2228.0651	2.38	1	16	1.4e+002	1	AYSRGFTPHFPNSLDAGTYK
☑	2966	748.6999	2243.0779	2243.0780	-0.04	1	16	1.4e+002	1	QIIENCEYLLSNETKDFK + Carbamidomethyl (C)
☑	850	593.3141	1184.6136	1184.6149	-1.08	0	16	1e+002	1	QKPGATDAEIR
☑	1071	621.8218	1241.6290	1241.6299	-0.66	1	16	1.5e+002	1	VGSARHEAMLR + Oxidation (M)
☑	1556	678.8661	1355.7176	1355.7157	1.45	0	16	1.4e+002	1	AGGGAAAAAVAAAAAASK
☑	2169	865.4707	1728.9268	1728.9233	2.07	1	16	1.1e+002	1	MEIQEGPKGPVFLIR + Oxidation (M)
☑	2260	881.9711	1761.9276	1761.9220	3.18	1	16	1.3e+002	1	ATASSTISADAAARALASK
☑	290	444.2586	886.5026	886.5058	-3.61	1	16	1.5e+002	1	LPVMSGKR
☑	1367	654.8327	1307.6508	1307.6503	0.38	1	16	2.1e+002	1	ITGNIDTMRSGK + Oxidation (M)
☑	508	523.2628	1044.5110	1044.5134	-2.29	0	16	1.4e+002	1	QQLCQQAAR
☑	2230	875.9760	1749.9374	1749.9310	3.70	1	16	94	1	MPRYLSLMFPPLSAK
☑	770	577.2768	1152.5390	1152.5411	-1.77	1	16	1.4e+002	1	DEASAKVYDR
☑	1921	789.9023	1577.7900	1577.7897	0.24	0	16	1.9e+002	1	LTETTQSLSEQVSR
☑	2435	916.5198	1831.0250	1831.0203	2.58	1	16	61	1	VEYNVLVGIRTAEQIK
☑	1154	633.3212	1264.6278	1264.6268	0.85	1	16	2.2e+002	1	VGKAMIMDTQR + Oxidation (M)
☑	26	350.6912	699.3678	699.3664	2.10	1	16	1.6e+002	1	RAGGPDK
☑	2827	1092.0180	2182.0214	2182.0212	0.11	0	16	1.2e+002	1	NICDNNEADLILTTGGTGFSK
☑	3037	757.3779	2269.1119	2269.1082	1.60	1	16	1.5e+002	1	YMIILDGTNMVLEDRLEGR + 2 Oxidation (M)
☑	1194	637.8171	1273.6196	1273.6237	-3.20	0	16	1.6e+002	1	QGCAALAAWDLR
☑	2833	728.3611	2182.0615	2182.0549	3.03	0	16	1.5e+002	1	SAQSNCNQVLINHLAAAESR + Carbamidomethyl (C)
☑	1776	498.2595	1491.7567	1491.7569	-0.15	0	16	1.9e+002	1	DFLIVASSEEINR
☑	227	415.2369	828.4592	828.4593	-0.03	0	16	3.3e+002	1	IVLLEDQ
☑	818	586.2806	1170.5466	1170.5452	1.27	0	16	79	1	DSGHIVLCDR + Carbamidomethyl (C)
☑	1012	613.8235	1225.6324	1225.6349	-2.04	1	16	1.5e+002	1	RMEVSGAHALR
☑	540	532.2735	1062.5324	1062.5346	-2.02	0	16	1.6e+002	1	VGDLNDFVGK
☑	2368	899.9897	1797.9648	1797.9585	3.55	0	16	1.2e+002	1	SLPGSGASGGLGAGLAGALSAK
☑	2006	824.8830	1647.7514	1647.7563	-2.93	1	16	1e+002	1	GTLGYGYMKSDVSDR
☑	3020	754.0877	2259.2413	2259.2429	-0.72	1	16	55	1	QWPLPFGLAGQAWLARLHAK
☑	555	534.2494	1066.4842	1066.4825	1.60	1	16	82	1	SMTESQRGR + Oxidation (M)
☑	1459	667.3726	1332.7306	1332.7289	1.31	1	16	1.3e+002	1	KIEGIIYGTDPK
☑	2320	592.3419	1774.0039	1774.0063	-1.34	1	16	49	1	VVLGYKILDPSCNLLK
☑	2250	586.3378	1755.9916	1755.9917	-0.06	1	16	50	1	CSILGQNDVVAIKVIK + Carbamidomethyl (C)
☑	1785	754.9326	1507.8506	1507.8511	-0.29	1	16	56	1	TVLDLLRHPNLFA
☑	2508	630.0267	1887.0583	1887.0540	2.29	0	16	47	1	PDYVGSVLLLLCALQVK + Carbamidomethyl (C)
☑	3236	1170.5790	2339.1434	2339.1362	3.10	1	16	1.5e+002	1	MSTNRDVLDPPEIVMVNTHR + Oxidation (M)
☑	707	567.7630	1133.5114	1133.5135	-1.80	0	16	92	1	NQEQMEALR + Oxidation (M)
☑	2178	867.4752	1732.9358	1732.9359	-0.06	1	16	1.1e+002	1	INDIFAGKGVTEAIGTK
☑	218	415.2295	828.4444	828.4454	-1.10	1	15	2.2e+002	1	LPRGSGDK
☑	855	594.7954	1187.5762	1187.5791	-2.38	1	15	1.8e+002	1	KHADINLMCK + Oxidation (M)
☑	752	573.2570	1144.4994	1144.5005	-0.94	0	15	48	1	CASSFVTMQR + Oxidation (M)
☑	3351	1213.1200	2424.2254	2424.2206	1.99	1	15	1.4e+002	1	TGILEVIKNMGGQVTIENYDSK + Oxidation (M)
☑	1292	650.3533	1298.6920	1298.6956	-2.73	1	15	1.7e+002	1	AHLHTPAPGSRR
☑	1485	671.3746	1340.7346	1340.7347	-0.00	1	15	1.3e+002	1	HSIIAASMLARR + Oxidation (M)
☑	1599	458.2540	1371.7402	1371.7432	-2.18	0	15	2e+002	1	DQALLPLVASMAK + Oxidation (M)
☑	1828	509.2653	1524.7741	1524.7797	-3.71	1	15	1.9e+002	1	AFVDHPEQGRLTR
☑	3000	1125.0720	2248.1294	2248.1218	3.38	0	15	1.6e+002	1	LIVADLTDEMVDDVIIPSMK + 2 Oxidation (M)
☑	313	455.7656	909.5166	909.5146	2.23	1	15	97	1	KMFPLFK
☑	586	362.1776	1083.5110	1083.5131	-1.99	0	15	1.1e+002	1	GDVMEAHGLR
☑	1126	629.8167	1257.6188	1257.6200	-0.95	0	15	1.3e+002	1	NLELEEENLR
☑	2013	827.9185	1653.8224	1653.8218	0.37	1	15	1.6e+002	1	FCTPTSLMSISPSKR
☑	2219	583.6566	1747.9480	1747.9468	0.65	1	15	1.1e+002	1	FVLDAAGGLERLSSSVK
☑	568	536.7667	1071.5188	1071.5171	1.61	0	15	93	1	MAINYFASR

☑	1371	437.2294	1308.6664	1308.6707	-3.34	1	15	1.6e+002	1	TSMTTAKDSVLR
☑	2399	605.0163	1812.0271	1812.0244	1.47	0	15	43	1	SEIVTSIPVISQAEVLK
☑	380	479.2306	956.4466	956.4505	-3.98	0	15	1.2e+002	1	FHQIFEH
☑	1605	687.8022	1373.5898	1373.5890	0.60	0	15	48	1	QCEHMCVGLPK + 2 Carbamidomethyl (C); Oxidation (M)
☑	1995	545.6506	1633.9300	1633.9264	2.20	1	15	42	1	PSLQTKAPTPVRPSR
☑	2166	864.4703	1726.9260	1726.9213	2.73	1	15	1.4e+002	1	IGASLDEKDQQALALR
☑	2535	636.9713	1907.8921	1907.8903	0.93	1	15	1.3e+002	1	GSINEMMKMKPQDVER + Oxidation (M)
☑	2873	734.3514	2200.0324	2200.0346	-1.02	0	15	1.3e+002	1	DIYAHHHVFINNAMMPFK + Oxidation (M)
☑	267	435.7737	869.5328	869.5334	-0.69	0	15	1.9e+002	1	VSIVSLPR
☑	2266	883.4716	1764.9286	1764.9258	1.62	1	15	1.3e+002	1	AIGTEDSAGTKVFALTGK
☑	1672	698.8851	1395.7556	1395.7582	-1.85	1	15	1.5e+002	1	TRAAELGIAGPNAR
☑	1677	699.8717	1397.7288	1397.7263	1.84	1	15	1.7e+002	1	IDPNSGGIRVNEK
☑	1692	469.2615	1404.7627	1404.7647	-1.42	1	15	1.6e+002	1	LGSVVCDVTSIKK + Carbamidomethyl (C)
☑	2382	901.5117	1801.0088	1801.0097	-0.50	1	15	65	1	TLDGFANALKLNGINLK
☑	2455	616.6838	1847.0296	1847.0265	1.67	1	15	55	1	TRPTYNISVTAVNVKGK
☑	1097	625.3384	1248.6622	1248.6648	-2.08	1	15	1.8e+002	1	GLRIAFCEAAAK
☑	2236	876.4851	1750.9556	1750.9577	-1.17	1	15	93	1	KLSHIELLQQATNEK
☑	1197	637.8492	1273.6838	1273.6812	2.04	1	15	2.2e+002	1	RMVGLVSEDLR
☑	2897	1106.0330	2210.0514	2210.0563	-2.20	1	15	1.4e+002	1	NGVSDKEASEIAQNNEHIQK
☑	694	565.2898	1128.5650	1128.5676	-2.26	1	15	1.2e+002	1	GDDWAKGKPR
☑	1039	617.3216	1232.6286	1232.6296	-0.74	1	15	2.5e+002	1	GRGLDGVISGMR + Oxidation (M)
☑	2025	831.9581	1661.9016	1661.8988	1.71	1	15	1.1e+002	1	APGYEAALTLQTKATK
☑	847	592.2850	1182.5554	1182.5525	2.46	0	15	1.4e+002	1	MSLGMSISWR + Oxidation (M)
☑	2053	845.3959	1688.7772	1688.7716	3.35	0	15	1.1e+002	1	SGADVTMNAFGFSELK + Oxidation (M)
☑	1233	430.2340	1287.6802	1287.6823	-1.64	0	15	2e+002	1	VNLQYLAAGPDK
☑	1286	650.3365	1298.6584	1298.6540	3.40	1	15	1.6e+002	1	KDVSALTSFMGK + Oxidation (M)
☑	2992	1123.0870	2244.1594	2244.1637	-1.90	1	15	1.6e+002	1	ENLHEELSLEKLAALSSFSK
☑	1689	469.2601	1404.7585	1404.7534	3.62	0	15	1.7e+002	1	ILMSSLDIEISGK
☑	2434	916.5184	1831.0222	1831.0165	3.14	1	15	58	1	MISEPDTPLFTLKVLK
☑	1226	643.7940	1285.5734	1285.5721	1.05	0	15	63	1	NTTASTNVYCR + Carbamidomethyl (C)
☑	1623	460.9120	1379.7142	1379.7119	1.68	1	15	1.6e+002	1	KLFEVNIMENK + Oxidation (M)
☑	66	366.6985	731.3824	731.3854	-4.00	0	15	6.2e+002	1	DYPIPK
☑	1284	649.8555	1297.6964	1297.6931	2.57	1	15	1.6e+002	1	YYHLHPVNKK
☑	407	489.2307	976.4468	976.4470	-0.15	0	15	1.3e+002	1	LMPNEMAR + Oxidation (M)
☑	1392	439.2468	1314.7186	1314.7152	2.57	1	15	2.2e+002	1	IMVMAPVVDGRK
☑	1552	452.9127	1355.7163	1355.7157	0.40	1	15	1.8e+002	1	ELGRVGAAGGVDAGK
☑	2595	996.4940	1990.9734	1990.9670	3.24	0	15	1.7e+002	1	FLSEYSTSLMAVGVQTSR + Oxidation (M)
☑	1784	503.2623	1506.7651	1506.7678	-1.81	0	15	2.2e+002	1	LEEVASSYNLQVR
☑	2187	578.6537	1732.9393	1732.9433	-2.34	0	15	1.1e+002	1	FPTALQMVLSVALAEK + Oxidation (M)
☑	2940	1114.5490	2227.0834	2227.0838	-0.15	1	15	1.8e+002	1	NELHGCINDVVAMRGTLVDR + Oxidation (M)
☑	1701	705.3218	1408.6290	1408.6326	-2.53	1	15	98	1	QTAEEMMAEKGGK
☑	1149	632.7960	1263.5774	1263.5803	-2.29	0	15	1.4e+002	1	SSNTATNANGATR
☑	1155	633.3401	1264.6656	1264.6663	-0.50	1	15	1.7e+002	1	ALNEALDKYTK
☑	2165	862.9578	1723.9010	1723.9005	0.29	1	15	1.5e+002	1	GSQHALKWAADNLVSK
☑	2327	889.4896	1776.9646	1776.9621	1.41	1	15	1e+002	1	FDVIISGLSITEERAK
☑	504	522.7900	1043.5654	1043.5651	0.31	0	15	1.1e+002	1	LDDLIWAAK
☑	1878	781.4381	1560.8616	1560.8624	-0.47	1	15	97	1	DNYGQVIGIVKISR
☑	476	513.3021	1024.5896	1024.5917	-1.98	1	15	75	1	RIETPLSLP
☑	2450	922.0262	1842.0378	1842.0397	-0.99	1	15	53	1	MNLLSNVAIGGKAGLQLK + Oxidation (M)
☑	161	397.7057	793.3968	793.3938	3.79	1	15	3.4e+002	1	CAKCTIR
☑	2036	558.9736	1673.8990	1673.9022	-1.92	1	15	1.7e+002	1	DMIINALVTAGVKDAK + Oxidation (M)
☑	3586	1167.8930	3500.6572	3500.6461	3.15	1	15	1e+002	1	MNPARAMSHFAGLLDAFEHGCLPDLEAVMLGR + 2 Oxidation (M)
☑	684	564.2841	1126.5536	1126.5553	-1.48	1	15	1.4e+002	1	CHLKGELGDR
☑	1588	456.9214	1367.7424	1367.7409	1.09	1	15	1.3e+002	1	LSDVATPPADRVK
☑	3359	610.5743	2438.2681	2438.2628	2.19	0	15	1.4e+002	1	TSGLLHLENMPIISPGFLESQR
☑	124	383.7018	765.3890	765.3882	1.15	0	15	1.8e+002	1	HTPAANR
☑	613	547.2632	1092.5118	1092.5101	1.57	0	15	1.6e+002	1	GGFGGGPGGGAFR
☑	657	372.8210	1115.4412	1115.4376	3.22	0	15	23	1	SMFDADACTR
☑	2922	742.3644	2224.0714	2224.0802	-3.97	1	15	1.9e+002	1	NYIMMLSNNICRAPGISEAK
☑	3050	759.0468	2274.1186	2274.1161	1.08	1	15	1.9e+002	1	DALNEALKNVVINASEAMDNK + Oxidation (M)
☑	2692	706.3637	2116.0693	2116.0656	1.73	0	15	2e+002	1	IDMLVQENNQISMILEAR
☑	2952	1117.5640	2233.1134	2233.1161	-1.18	1	15	2e+002	1	IENNTALEMVYRINIGDPR + Oxidation (M)
☑	2898	1107.0240	2212.0334	2212.0405	-3.19	0	15	1.4e+002	1	TVMWIDADAIICNPNHDIR + Oxidation (M)
☑	3551	984.1126	2949.3160	2949.3228	-2.32	0	15	60	1	ALSSGANAAITGDFLMTGGMSIDSDMAMAK + Oxidation (M)
☑	1385	439.2139	1314.6199	1314.6204	-0.41	1	15	1.4e+002	1	YSAEVQKDYGR
☑	1462	668.3553	1334.6960	1334.6983	-1.66	1	15	1.7e+002	1	NEPKEFHLPPK
☑	1845	511.9356	1532.7850	1532.7868	-1.22	0	15	2.4e+002	1	DMLSVLQSGLADIR + Oxidation (M)
☑	3108	573.5525	2290.1809	2290.1892	-3.63	1	15	1.6e+002	1	VEETLCSIVDAAPWLRHPVR
☑	180	401.7362	801.4578	801.4596	-2.20	0	15	5e+002	1	GGIDLSLK
☑	1560	453.2393	1356.6961	1356.6997	-2.69	1	15	2.1e+002	1	ENVEGAGRAVDLK
☑	1964	803.4082	1604.8018	1604.8014	0.27	1	15	2.5e+002	1	MQKESLPIQTTACR
☑	3156	1154.0600	2306.1054	2306.1082	-1.20	1	15	1.8e+002	1	FRMGAMINQLCDVLGPGQQR + Carbamidomethyl (C); Oxidation (M)
☑	808	583.7733	1165.5320	1165.5285	3.07	1	15	1.4e+002	1	IGSDKEMNEK + Oxidation (M)
☑	2865	734.0268	2199.0586	2199.0524	2.79	1	15	1.8e+002	1	TMSAPAMNAGDAIPAERGQVGR
☑	3002	751.7027	2252.0863	2252.0808	2.43	1	15	1.8e+002	1	SEAEQVREELLSGGDYETIK
☑	3207	775.4205	2323.2397	2323.2430	-1.44	1	15	1e+002	1	AGVVVAAAARAPSALGLCTAPASSR + Carbamidomethyl (C)
☑	2210	582.6652	1744.9738	1744.9757	-1.09	1	15	69	1	SCNLSLTILGKQLIDK
☑	2227	583.9849	1748.9329	1748.9308	1.17	1	15	1.4e+002	1	ITGSLKLENLDLYDR
☑	1949	794.8711	1587.7276	1587.7239	2.36	0	15	1.1e+002	1	FLQDEFMTISSDR
☑	2812	724.6883	2171.0431	2171.0490	-2.72	0	15	1.8e+002	1	YMEITLDSMQISDAIGAAVK + Oxidation (M)
☑	2942	1115.0420	2228.0694	2228.0671	1.07	1	15	1.9e+002	1	VAWAEPLNEPDEDEMLKVK + Oxidation (M)
☑	257	425.7363	849.4580	849.4596	-1.84	0	15	3.8e+002	1	VYIVNDK
☑	3018	1130.6270	2259.2394	2259.2409	-0.65	1	15	66	1	MLQTPPAPAAAEPVLVVDRLR + Oxidation (M)
☑	1850	513.2648	1536.7726	1536.7759	-2.15	0	15	2.4e+002	1	CPPPTFAIPPDLNR
☑	661	559.7646	1117.5146	1117.5152	-0.52	0	15	1.4e+002	1	EHSQSDFLR
☑	2204	871.9764	1741.9382	1741.9322	3.47	1	15	1.6e+002	1	LARELAANQTDAALSAK
☑	3040	757.4283	2269.2631	2269.2542	3.90	0	15	55	1	IVAIALLADGHLNSSELAAVHR
☑	2138	858.4714	1714.9282	1714.9287	-0.27	1	15	1.3e+002	1	IAGVDKAIMAAALEQAK + Oxidation (M)

☑	2750	1076.0450	2150.0754	2150.0752	0.13	1	15	2.2e+002	1	DTMTVKLVDFGMAALQPEGK
☑	3019	1130.6270	2259.2394	2259.2409	-0.65	1	15	67	1	MLQTPPAPAAAEPVLVVDRLR + Oxidation (M)
☑	2024	554.9739	1661.8999	1661.9062	-3.80	1	15	1.3e+002	1	VLEKCIAEEQLLFK
☑	164	397.7060	793.3974	793.4004	-3.69	0	15	4.1e+002	1	SSLVSACK
☑	2348	597.6601	1789.9585	1789.9574	0.59	0	15	1.4e+002	1	ELSHLPIIVDPSQGTGK
☑	2860	732.3607	2194.0603	2194.0616	-0.61	1	15	1.9e+002	1	RYEGFDLSILEPDGLMPDK
☑	3112	764.4011	2290.1815	2290.1847	-1.43	0	15	1.7e+002	1	MGLICATPTAGSAGVLAGVLMAVR + 2 Oxidation (M)
☑	1959	798.8943	1595.7740	1595.7766	-1.61	1	14	2.3e+002	1	KFALGGHGDMYGLSK + Oxidation (M)
☑	107	379.2081	756.4016	756.4018	-0.15	0	14	1.1e+002	1	AIDPDVK
☑	1889	784.3986	1566.7826	1566.7831	-0.26	0	14	2.2e+002	1	YAEPFSALAWLSGR
☑	3137	1151.1390	2300.2634	2300.2674	-1.74	0	14	61	1	LAQELGIAIGVGSQRPMIIYR + Oxidation (M)
☑	2829	1092.0190	2182.0234	2182.0220	0.65	0	14	1.5e+002	1	MDYLIMTAIMSLHNEAAAR + 2 Oxidation (M)
☑	1481	447.9093	1340.7061	1340.7048	0.95	1	14	1.8e+002	1	ERLDNPQGATIK
☑	3092	763.4146	2287.2220	2287.2284	-2.81	1	14	1.2e+002	1	EGQAAAALADILVYGLSQSRVR
☑	1937	528.2723	1581.7951	1581.7933	1.13	0	14	2.3e+002	1	EIMVGAAQAAHAEIR + Oxidation (M)
☑	3322	1196.0960	2390.1774	2390.1756	0.77	1	14	2.1e+002	1	LTAGTVVNLVPDRAEMLMECR + Carbamidomethyl (C); Oxidation (M)
☑	905	603.8015	1205.5884	1205.5928	-3.61	0	14	2.3e+002	1	LPFGNSLESDK
☑	2026	832.3857	1662.7568	1662.7598	-1.75	0	14	1.2e+002	1	ASTFVQSHNEETSAR
☑	1478	447.9081	1340.7025	1340.7048	-1.75	1	14	2e+002	1	SRSSVAAPPSPTGK
☑	1492	672.3363	1342.6580	1342.6551	2.20	1	14	2e+002	1	KDLLNHVDMDK + Oxidation (M)
☑	2336	892.4843	1782.9540	1782.9588	-2.64	1	14	2.7e+002	1	ALANVLSIAEQNAADRK
☑	775	579.2728	1156.5310	1156.5342	-2.73	1	14	90	1	CRHACGQIR + 2 Carbamidomethyl (C)
☑	2218	874.9808	1747.9470	1747.9509	-2.19	0	14	1.4e+002	1	FTAADIVTGGVLLWASK
☑	877	598.2822	1194.5498	1194.5525	-2.25	0	14	1.8e+002	1	CGALALWSCSK + Carbamidomethyl (C)
☑	947	609.7844	1217.5542	1217.5524	1.54	0	14	1.2e+002	1	TEEEQEIANR
☑	2473	929.5256	1857.0366	1857.0295	3.87	1	14	77	1	LQMNGKKPAPVTPHPVK + Oxidation (M)
☑	2624	1025.0180	2048.0214	2048.0249	-1.66	0	14	2.4e+002	1	VLCAPEAAIGETGPGVSPQPV + Carbamidomethyl (C)
☑	2593	664.3650	1990.0732	1990.0735	-0.15	1	14	1.2e+002	1	YSVIQVKTEQQANEILK
☑	1127	420.2137	1257.6193	1257.6214	-1.70	1	14	1.8e+002	1	RQLEEFGHSR
☑	2859	1098.0370	2194.0594	2194.0663	-3.13	1	14	1.9e+002	1	LHCKGMANVSLWQLGSYSK + Carbamidomethyl (C); Oxidation (M)
☑	1816	509.2651	1524.7735	1524.7792	-3.78	1	14	2.2e+002	1	EIFVMRSGAIQMK + Oxidation (M)
☑	2272	885.9703	1769.9260	1769.9199	3.45	1	14	2e+002	1	DFVSLYENLKSTINK
☑	3291	594.2973	2373.1601	2373.1551	2.11	1	14	2e+002	1	WTHQFMKCPFVFYIANLR + Carbamidomethyl (C); Oxidation (M)
☑	466	508.7835	1015.5524	1015.5525	-0.01	0	14	4.2e+002	1	FAPPLVMNK
☑	1103	417.5355	1249.5847	1249.5800	3.77	0	14	1.6e+002	1	HNHATTDADLR
☑	2335	892.4828	1782.9510	1782.9450	3.37	1	14	1.5e+002	1	HPKNIQQSLYPAMLK + Oxidation (M)
☑	880	399.2203	1194.6391	1194.6357	2.84	1	14	2.3e+002	1	KSGYVTAVQSR
☑	3194	773.7232	2318.1478	2318.1424	2.31	0	14	2.1e+002	1	SGTEASSGGMSIPTAVVIETPVGR + Oxidation (M)
☑	386	480.7531	959.4916	959.4924	-0.75	0	14	3.4e+002	1	IDPTASTQK
☑	2891	1104.1160	2206.2174	2206.2209	-1.55	1	14	68	1	SLSITALSANDFTLNTIGIKK
☑	1681	467.2433	1398.7081	1398.7065	1.15	0	14	2.1e+002	1	AITLATDVMTYGK + Oxidation (M)
☑	2947	558.2595	2229.0089	2229.0008	3.61	0	14	1.1e+002	1	MDDDPPGALVLDSVSHAFGDR + Oxidation (M)
☑	2137	572.6497	1714.9273	1714.9213	3.47	1	14	1.7e+002	1	LRSVEESAGVSLNNIK
☑	2248	878.5101	1755.0056	1755.0043	0.79	1	14	49	1	ALRIALEPVLEASAFR
☑	2453	615.6903	1844.0491	1844.0560	-3.75	1	14	43	1	LVGEYIVNNFPVKPKK
☑	2706	711.6964	2132.0674	2132.0610	2.98	1	14	2.3e+002	1	EDPTAAGAQYQLGRTAALSGR
☑	118	382.2198	762.4250	762.4276	-3.32	1	14	3.2e+002	1	YVPVKSA
☑	1989	542.2758	1623.8056	1623.8039	1.04	1	14	2.7e+002	1	TAMRNDFEIVLSGR + Oxidation (M)
☑	3096	1146.0630	2290.1114	2290.1151	-1.58	0	14	2.1e+002	1	MLAYNEDDNEIILVPLEQR + Oxidation (M)
☑	3261	783.4086	2347.2040	2347.1981	2.51	0	14	1.9e+002	1	IDEIVMFNSLSPDSINAIIEK
☑	871	597.3120	1192.6094	1192.6121	-2.25	1	14	3.7e+002	1	EMSELTAKLR + Oxidation (M)
☑	1175	425.2426	1272.7060	1272.7038	1.73	0	14	2.1e+002	1	SIQGNVSLGVATK
☑	2366	899.5162	1797.0178	1797.0247	-3.83	1	14	75	1	LTDDLALEIGKAAVLQK
☑	1782	753.4069	1504.7992	1504.7997	-0.33	1	14	2e+002	1	AIANAYGADLAATKR
☑	1895	523.2685	1566.7837	1566.7790	2.96	1	14	2.7e+002	1	SVPREFYSGLAEGR
☑	2838	729.0187	2184.0343	2184.0265	3.56	0	14	1.9e+002	1	MGNILCLMVENSLPDGFSTK + Oxidation (M)
☑	27	350.7164	699.4182	699.4167	2.23	0	14	1.3e+002	1	IEVVIQ
☑	553	534.2490	1066.4834	1066.4832	0.25	0	14	1.2e+002	1	DYWNSNIR
☑	1697	704.8184	1407.6222	1407.6188	2.47	0	14	98	1	MDDVDSALADNVK + Oxidation (M)
☑	842	590.3298	1178.6450	1178.6421	2.50	1	14	2.2e+002	1	ARGGHQVWLR
☑	2549	638.6990	1913.0752	1913.0734	0.90	1	14	58	1	LPSVTYLRLDGSVPAGLR
☑	1232	644.8387	1287.6628	1287.6605	1.83	1	14	3.1e+002	1	RDAMAVLEDIR
☑	1787	503.9677	1508.8813	1508.8787	1.70	1	14	43	1	ALAGLAGTGRVTVPAR
☑	2021	553.8913	1658.6521	1658.6521	-0.01	0	14	12	1	MAEGLGCSAMAVDGCR + Carbamidomethyl (C); 2 Oxidation (M)
☑	2533	636.3306	1905.9700	1905.9684	0.83	0	14	2.2e+002	1	TTDTEGALQTVLTQPFGK
☑	3300	1188.5890	2375.1634	2375.1555	3.35	0	14	2.2e+002	1	VINSNGVVLVEFFAPWCGHCK + Carbamidomethyl (C)
☑	1941	528.2726	1581.7960	1581.7933	1.68	1	14	2.2e+002	1	CLLHEGREVVGGEK + Carbamidomethyl (C)
☑	2584	494.5271	1974.0793	1974.0860	-3.38	0	14	1.1e+002	1	LYDIIVVAEGIGNVMQIK
☑	2813	1086.5310	2171.0474	2171.0425	2.28	1	14	2.1e+002	1	VAVVAVDDCDISMAIRFGMK + 2 Oxidation (M)
☑	2329	890.4974	1778.9802	1778.9791	0.63	1	14	89	1	SNLDQLLHPFRAQLK
☑	887	600.2933	1198.5720	1198.5691	2.49	1	14	1.7e+002	1	QPNDGSKSPGGR
☑	1555	452.9128	1355.7166	1355.7157	0.63	0	14	2.2e+002	1	QILQQEAGVASGR
☑	1427	442.5781	1324.7125	1324.7173	-3.63	0	14	1.9e+002	1	ILKPSSTHSPMK
☑	2998	750.3810	2248.1212	2248.1257	-1.99	1	14	2.2e+002	1	MSAKVTDLITETDLQDLAER
☑	3314	797.4109	2389.2109	2389.2020	3.73	1	14	2.1e+002	1	VQNNQSIGSSSGLGDTIINKMAR
☑	2020	552.9689	1655.8849	1655.8883	-2.05	1	14	1.7e+002	1	FLLGDKNVPDSPLNK
☑	2201	581.2933	1740.8581	1740.8530	2.92	1	14	2.1e+002	1	TSKDNDLSDIITTYR
☑	2426	610.6911	1829.0515	1829.0451	3.49	1	14	37	1	IGTIFKNLPAWLDLTK
☑	3269	1178.5730	2355.1314	2355.1239	3.21	1	14	1.9e+002	1	NLSAGYGKMEILHDFDLCVSK + Oxidation (M)
☑	108	379.2137	756.4128	756.4130	-0.19	0	14	2.6e+002	1	VIPSDAR
☑	2545	957.4609	1912.9072	1912.9088	-0.81	0	14	2.1e+002	1	DIIGSATLSMPSSSEFGSK
☑	1617	459.9252	1376.7538	1376.7551	-0.96	0	14	1.8e+002	1	EEYLATLSKPVK
☑	2194	868.4499	1734.8852	1734.8788	3.71	1	14	2.7e+002	1	KTGSSTISWIENVDAK
☑	2263	882.4810	1762.9474	1762.9474	0.05	0	14	1.4e+002	1	ILMGAIMLASWLVSSR + Oxidation (M)
☑	2457	927.0161	1852.0176	1852.0207	-1.63	1	14	1.1e+002	1	GAIVIHGVINNKDFVEK
☑	3048	1137.6160	2273.2174	2273.2168	0.27	0	14	1.2e+002	1	LGPVVNGAFPISNAPPGVNGTPAK
☑	351	467.7292	933.4438	933.4403	3.78	0	14	2.5e+002	1	SATATLQEN
☑	1613	689.3424	1376.6702	1376.6659	3.14	0	14	2.2e+002	1	ASWHFTAISAMR

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☑  1855   774.3853  1546.7560  1546.7601  -2.59  1   14  2.1e+002  1        SSGSPRHENVHVGGK
☑   146   392.6953   783.3760   783.3736   3.13  1   14        78  1        RGDGSHR
☑  1178   425.2436  1272.7090  1272.7111  -1.69  0   14  1.5e+002  1        LSIEQLIQMAK
☑  3101   573.5523  2290.1801  2290.1838  -1.63  1   14    2e+002  1        MDTLDKTDLQILSILQSNAR + Oxidation (M)
☑  1042   617.3516  1232.6886  1232.6877   0.78  1   14    2e+002  1        LDANGRYALLK
☑   845   591.7985  1181.5824  1181.5789   3.03  1   14  2.7e+002  1        LDIHERDER
☑  1549   452.9127  1355.7163  1355.7119   3.24  1   14  2.3e+002  1        QPDMEGVPVKLK + Oxidation (M)
☑  2578   654.6902  1961.0488  1961.0438   2.54  1   14  1.4e+002  1        GKVLLMENVASLQGTMVR + Oxidation (M)
☑  2739  1072.9990  2143.9834  2143.9883  -2.25  0   14  1.4e+002  1        GDTAAGPGAGAGPGPGAGAAAEPDPR
☑  1696   703.8803  1405.7460  1405.7421   2.80  1   14  2.7e+002  1        MSAITAKMVADLR
☑  2641  1033.5030  2064.9914  2064.9898   0.78  0   14  2.1e+002  1        DGGPELNNVNIMAVAHGETK
☑  1945   791.9061  1581.7976  1581.7972   0.30  1   14  2.4e+002  1        NPNRSGGSPVLGGTGGR
☑  1358   436.2099  1305.6079  1305.6095  -1.28  1   14  1.5e+002  1        MASTSTGHQRSK + Oxidation (M)
☑   472   513.2269  1024.4392  1024.4383   0.95  1   14        67  1        SEEKTAMVD + Oxidation (M)
☑  3080  1139.0810  2276.1474  2276.1397   3.41  1   14  2.5e+002  1        AVDQLLVDGSNVSFSDDARLR
☑   665   560.2311  1118.4476  1118.4476   0.03  0   14        17  1        DDGDGDAADLR
☑  2438   917.4662  1832.9178  1832.9129   2.69  1   14  2.6e+002  1        GVHIETTIDNQAKDHR
☑  2514   947.9261  1893.8376  1893.8381  -0.22  1   14        98  1        GIQSDFARYEDESSYK
☑   949   610.3175  1218.6204  1218.6213  -0.68  0   14  3.1e+002  1        CSINAICAVIR + Carbamidomethyl (C)
☑  2140   572.9854  1715.9344  1715.9359  -0.88  1   14  1.6e+002  1        SAFAWGLASRVVPLDK
☑  1031   615.3301  1228.6456  1228.6485  -2.36  0   14  3.5e+002  1        DQLEMLVPIR + Oxidation (M)
☑  2569   649.0328  1944.0766  1944.0754   0.59  0   14        92  1        VAVLVSGGVDSSLALWIMK
☑   148   393.7397   785.4648   785.4647   0.18  0   14    4e+002  1        GAPTVTLK
☑   581   541.7958  1081.5770  1081.5768   0.27  0   14  1.8e+002  1        IPNDAVPASAK
☑  1594   457.9123  1370.7151  1370.7162  -0.86  1   14  2.4e+002  1        HVLCKNLSCVQK
☑  2039   838.3882  1674.7618  1674.7632  -0.78  0   14  1.4e+002  1        EGCSLSTSPTNVSTHR
☑  1611   459.5811  1375.7215  1375.7169   3.29  1   14  2.7e+002  1        ILHSDMEKIFK + Oxidation (M)
☑  1523   676.8116  1351.6086  1351.6112  -1.86  1   14  1.5e+002  1        KMMQTENDLDK
☑  1547   452.9126  1355.7160  1355.7157   0.19  0   14  2.4e+002  1        LVQINDGAGNSIR
☑  1643   694.3829  1386.7512  1386.7507   0.38  0   14  2.9e+002  1        VIDAYLGHGLTTK
☑  2042   839.9288  1677.8430  1677.8429   0.07  1   14  2.5e+002  1        ISENIISQMKEQMK
☑   356   471.7429   941.4712   941.4719  -0.70  0   14  1.5e+002  1        WTPPQASR
☑  3324  1196.6750  2391.3354  2391.3308   1.96  1   14        53  1        SPLSSILMGAHILNSGKLSGKPGK
☑  1755   728.3704  1454.7262  1454.7300  -2.58  1   14  2.2e+002  1        ARGVHGDVIDAAMK + Oxidation (M)
☑  1635   692.8388  1383.6630  1383.6639  -0.59  1   14  2.1e+002  1        MALLYKDQSGCR
☑  1357   653.3251  1304.6356  1304.6394  -2.91  1   14  3.2e+002  1        KLPMAGDVTSDR + Oxidation (M)
☑  2511   630.3560  1888.0462  1888.0418   2.33  1   14  1.1e+002  1        STVIPYLLQAETRELR
☑  2751   717.6991  2150.0755  2150.0790  -1.63  0   14  2.7e+002  1        LNQTIEHEATPQIQGMVNK
☑   918   605.3022  1208.5898  1208.5893   0.43  0   14  3.3e+002  1        QGMMQSLLTGK + Oxidation (M)
☑  1614   689.3774  1376.7402  1376.7452  -3.60  1   14  2.2e+002  1        AKLYGFLSEPPR
☑  2506   944.5342  1887.0538  1887.0466   3.86  0   14    1e+002  1        SAPTLSNGSILQNVFVLK
☑  2331   890.9058  1779.7970  1779.7985  -0.84  0   14  1.3e+002  1        VDGVECVDLETEYPR + Carbamidomethyl (C)
☑  2946   743.6993  2228.0761  2228.0830  -3.13  1   14  2.3e+002  1        NMGYVGGPALGGLLYGMAGRSR + 2 Oxidation (M)
☑  2135   857.9539  1713.8932  1713.8971  -2.25  0   14  2.5e+002  1        MAEVPGLLISAPSSGTGK
☑  2923  1113.0450  2224.0754  2224.0795  -1.84  0   14  2.4e+002  1        EFLTANLSIMEYLLSFCSK + Oxidation (M)
☑   544   533.2888  1064.5630  1064.5615   1.49  1   14  2.5e+002  1        KGTDQFTIR
☑  1491   672.2999  1342.5852  1342.5897  -3.31  0   14        91  1        IYEMAMEDGIR + Oxidation (M)
☑  2456   927.0151  1852.0156  1852.0094   3.37  0   14  1.2e+002  1        LPEPEIILVDEAHHIK
☑  3400   869.7757  2606.3053  2606.3050   0.09  0   14  2.1e+002  1        LGQDLLDLLTFNLSLSLDDCWR + Carbamidomethyl (C)
☑  1535   678.3644  1354.7142  1354.7092   3.69  0   14  2.3e+002  1        APAQVVEVVSDNK
☑  1609   688.3752  1374.7358  1374.7330   2.10  0   14  2.4e+002  1        SMQTAFVLTIHK
☑   611   546.3090  1090.6034  1090.6056  -1.99  1   14  3.1e+002  1        IKGCTDIITK
☑   247   423.7193   845.4240   845.4243  -0.28  0   14  5.4e+002  1        NSVGVENK
☑  2688  1056.5100  2111.0054  2111.0027   1.29  0   14    2e+002  1        QNNSPIIVTGGMAEMVYQK + 2 Oxidation (M)
☑  1666   697.3820  1392.7494  1392.7473   1.51  1   14    2e+002  1        DKADIQIHGIQR
☑  2523   475.7485  1898.9649  1898.9585   3.35  0   14  2.5e+002  1        VSVEDATAVTLAGPDALDR
☑  1744   482.2612  1443.7618  1443.7582   2.46  1   14  2.8e+002  1        NRPAAKGEFEIGR
☑  2364   450.2507  1796.9737  1796.9785  -2.65  1   14  1.9e+002  1        FKDKPNLTIHSADALK
☑  1544   452.9125  1355.7157  1355.7157  -0.03  1   14  2.6e+002  1        RSLNPDGLDLTR
☑  2927  1114.0340  2226.0534  2226.0483   2.31  0   14    2e+002  1        MASDTIMASFVCQVHSGIIK + Carbamidomethyl (C); 2 Oxidation (M)
☑  1397   658.8210  1315.6274  1315.6237   2.81  1   14  2.3e+002  1        ASNTVCHRCLR + Carbamidomethyl (C)
☑  2538   956.0228  1910.0310  1910.0334  -1.21  0   14  1.6e+002  1        SPSTARPSTPTSRPLLSR
☑  3334   602.0645  2404.2289  2404.2346  -2.39  1   14  2.2e+002  1        ETAGRNIPLLPDLPGDGDTANLR
☑  2735   715.0363  2142.0871  2142.0786   3.98  1   14  2.2e+002  1        IHETVIYHYLAKYYDSK
☑  1436   665.3731  1328.7316  1328.7308   0.60  0   13  2.5e+002  1        LLSGVCCLIVPR + Carbamidomethyl (C)
☑  2270   884.9843  1767.9540  1767.9593  -2.98  1   13  1.8e+002  1        TFMVEISFATKIPLR + Oxidation (M)
☑   894   601.3132  1200.6118  1200.6098   1.68  0   13    3e+002  1        QAGIESAALDAR
☑  1990   542.2762  1623.8068  1623.8039   1.78  1   13  2.8e+002  1        GNFLCSNTSVKELR + Carbamidomethyl (C)
☑    53   364.2086   726.4026   726.4024   0.31  0   13    3e+002  1        AISAHTK
☑  1192   637.8163  1273.6180  1273.6163   1.33  1   13  2.2e+002  1        RQVEWTADGGR
☑  3173  1157.6320  2313.2494  2313.2514  -0.86  1   13  1.3e+002  1        VLKNAWLAVALAAIAASQESCK + Carbamidomethyl (C)
☑  3084   571.7930  2283.1429  2283.1495  -2.90  0   13  2.5e+002  1        LLATFAGEGEPAGGATAPAAGADLR
☑  3312   797.4055  2389.1947  2389.1887   2.50  1   13  2.4e+002  1        AFNGTYAQDILDRGRPQGTPGR
☑   650   554.7991  1107.5836  1107.5812   2.25  0   13  2.7e+002  1        GEEILSYLGK
☑  3463   932.7635  2795.2687  2795.2717  -1.08  1   13  1.2e+002  1        FMGPQRDCLAQLAQGPMWLDEETK + 2 Oxidation (M)
☑   870   398.5358  1192.5856  1192.5836   1.64  1   13  2.6e+002  1        SKNFDEAINR
☑  2406   908.5215  1815.0284  1815.0215   3.80  0   13        67  1        ELIEAYIPILCALGGIK
☑   857   595.2422  1188.4698  1188.4726  -2.30  0   13        22  1        LSCPSCSFSCR
☑  2558   965.5422  1929.0698  1929.0758  -3.06  0   13        89  1        TVGAPLLTGGCAAGAFLLLGK
☑   332   463.7631   925.5116   925.5134  -1.86  1   13  1.7e+002  1        WSHQKLK
☑  2602  1003.9990  2005.9834  2005.9819   0.78  1   13  2.6e+002  1        AQYQYLFDTCIIKSEK + Carbamidomethyl (C)
☑  1447   666.8308  1331.6470  1331.6478  -0.58  0   13  3.2e+002  1        ACNSCLLPWLR + Carbamidomethyl (C)
☑  2458   927.9402  1853.8658  1853.8652   0.36  1   13  2.2e+002  1        HTFCVESLVKMSESGK + Carbamidomethyl (C); Oxidation (M)
☑  2689   704.6763  2111.0071  2111.0027   2.06  1   13  2.5e+002  1        QMLDTSIDWMNTQLKSGK + Oxidation (M)
☑  2362   899.4576  1796.9006  1796.9057  -2.79  1   13  2.8e+002  1        EPAAEGLEAQGLGWKNK
☑   739   568.7970  1135.5794  1135.5808  -1.17  1   13  2.4e+002  1        YRTPEAIMR
☑  1928   528.2719  1581.7939  1581.7973  -2.19  1   13  2.6e+002  1        FKAYSGIQIMPDGR
☑   119   382.6816   763.3486   763.3501  -1.86  0   13  1.5e+002  1        TADWSGK
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☑	2471	929.4424	1856.8702	1856.8702	0.04	0	13	2.1e+002	1	GQLCPPYPICHPNQYK
☑	3123	1146.6210	2291.2274	2291.2281	-0.27	1	13	1.3e+002	1	AVQSARQQAGIVKPATCHTLR + Carbamidomethyl (C)
☑	3142	768.0905	2301.2497	2301.2485	0.51	0	13	1.1e+002	1	LIVPPLMMLGATIAMSFLMPR
☑	1452	667.3719	1332.7292	1332.7258	2.62	1	13	2.4e+002	1	QIVVGICAMSKK + Carbamidomethyl (C)
☑	3320	797.7324	2390.1754	2390.1722	1.32	1	13	2.5e+002	1	MIPGKQMTSENISGPYSQAVPR
☑	391	484.2770	966.5394	966.5359	3.67	1	13	2e+002	1	GRHDLTIR
☑	2754	1077.0330	2152.0514	2152.0583	-3.17	1	13	2.8e+002	1	ADRVVHLLPTMDDTPAETR + Oxidation (M)
☑	2742	1074.0940	2146.1734	2146.1718	0.75	1	13	1.1e+002	1	SQAAAAAAAAARPKPKANSPAAR
☑	2926	1113.5540	2225.0934	2225.0998	-2.84	0	13	2.6e+002	1	MLLDLDGTLVDHEAAAESGLR
☑	1075	622.8454	1243.6762	1243.6714	3.93	0	13	3.2e+002	1	TWWAVVVLDR
☑	1479	447.9086	1340.7040	1340.7048	-0.61	1	13	2.5e+002	1	ENPASVAIAGREK
☑	2839	729.0193	2184.0361	2184.0409	-2.20	0	13	2.3e+002	1	YEVDMVQSLIEEFVTPNR + Oxidation (M)
☑	1769	741.8663	1481.7180	1481.7184	-0.25	1	13	2.7e+002	1	AVTEKVSMDEFAR
☑	2253	879.9988	1757.9830	1757.9887	-3.20	0	13	1.2e+002	1	ISAASQSLLNSVASAVIK
☑	1871	777.3260	1552.6374	1552.6326	3.09	0	13	40	1	CFPDQMPEWESK + Carbamidomethyl (C)
☑	320	458.2660	914.5174	914.5185	-1.16	1	13	8.5e+002	1	NEGLKAVGK
☑	910	604.3010	1206.5874	1206.5914	-3.29	1	13	3.7e+002	1	LTKDEMDALR + Oxidation (M)
☑	1854	773.3959	1544.7772	1544.7731	2.68	0	13	2.8e+002	1	VMVVNGLGSYLCYK
☑	612	546.3091	1090.6036	1090.6056	-1.81	1	13	3.4e+002	1	IKEGTTVCIK
☑	1925	790.4518	1578.8890	1578.8869	1.39	1	13	1e+002	1	YLEVSSSKVVVEIK
☑	2526	634.6948	1901.0626	1901.0622	0.21	1	13	92	1	KIEFQQLPQITSAIASK
☑	956	408.2111	1221.6115	1221.6102	1.07	1	13	2.7e+002	1	INYNTGEGKAR
☑	1405	660.8314	1319.6482	1319.6503	-1.58	1	13	3.4e+002	1	CRIAAASDLGDTK
☑	376	478.7764	955.5382	955.5352	3.22	0	13	94	1	HLPHPSLR
☑	2486	937.0316	1872.0486	1872.0509	-1.20	0	13	81	1	ATIPTIPHPAAVSPYPLK
☑	3183	1159.1040	2316.1934	2316.1896	1.65	0	13	2.4e+002	1	NQVVIRPCSSSTNVFDPLNVK
☑	521	352.8094	1055.4064	1055.4086	-2.08	0	13	15	1	LMECSECGK + Carbamidomethyl (C)
☑	1390	439.2370	1314.6892	1314.6853	2.92	0	13	3.4e+002	1	QVLEIVGPGMEK + Oxidation (M)
☑	1789	757.9202	1513.8258	1513.8286	-1.85	1	13	2.3e+002	1	IVLATKVGSEMGPGR
☑	2381	601.3434	1801.0084	1801.0132	-2.65	1	13	1.1e+002	1	IVETCQGAITVTVARLK
☑	1601	686.8780	1371.7414	1371.7398	1.19	0	13	2e+002	1	TPTPPPPPISGSPK
☑	3116	573.5529	2290.1825	2290.1734	3.95	1	13	2.3e+002	1	MLIAKPCTSMKAINITPEEK + Carbamidomethyl (C); Oxidation (M)
☑	283	441.7509	881.4872	881.4872	0.11	1	13	1.4e+002	1	HKIHGYK
☑	2835	728.6819	2183.0239	2183.0317	-3.58	1	13	2.3e+002	1	FDEFDSDILDNRLCAAALR
☑	129	384.6978	767.3810	767.3788	2.87	0	13	2.1e+002	1	YMWIR
☑	1356	652.8536	1303.6926	1303.6884	3.22	1	13	3.8e+002	1	LFGRDETPTLR
☑	2708	1067.5320	2133.0494	2133.0491	0.18	1	13	3.2e+002	1	NLKAEQGYQVDLVYGHDGK
☑	2877	734.6848	2201.0326	2201.0276	2.24	1	13	2.1e+002	1	EEFSPPANPPAPSFEEKSNK
☑	3145	768.4013	2302.1821	2302.1813	0.32	0	13	2.6e+002	1	LHVAVLLNVIMDAYEQCISR + Oxidation (M)
☑	405	487.2591	972.5036	972.5062	-2.67	0	13	3e+002	1	SNAVAPGMVK
☑	892	401.2106	1200.6100	1200.6098	0.10	1	13	3.4e+002	1	DVEAAEKQVGR
☑	1370	654.8335	1307.6524	1307.6557	-2.49	1	13	2.8e+002	1	LWSGPQPRHCK
☑	2571	973.5125	1945.0104	1945.0057	2.42	0	13	2.5e+002	1	GQQVQLANELLASFWNK
☑	1687	468.2346	1401.6820	1401.6785	2.50	1	13	2.5e+002	1	MFVCSKNEFIK + Carbamidomethyl (C)
☑	2672	700.6779	2099.0119	2099.0131	-0.57	0	13	2.6e+002	1	DQIASHTQSIQQSLTDAEK
☑	292	447.7690	893.5234	893.5222	1.41	1	13	77	1	YIETKIK
☑	1670	698.3716	1394.7286	1394.7302	-1.11	0	13	2.6e+002	1	MFMVSVTVLPQK + Oxidation (M)
☑	1979	809.8770	1617.7394	1617.7392	0.16	0	13	1.9e+002	1	VHTGEKPFECNVCR
☑	3241	781.7346	2342.1820	2342.1749	3.01	0	13	4.2e+002	1	TGFMIESMTTAIVENILSLEK + Oxidation (M)
☑	1170	635.3461	1268.6776	1268.6738	3.02	1	13	1.6e+002	1	TWHRLVSTGGR
☑	2822	1089.0550	2176.0954	2176.0980	-1.18	1	13	3e+002	1	RDLEVLDVCTGSGCIAVSLAR
☑	2933	743.3668	2227.0786	2227.0844	-2.62	1	13	2.8e+002	1	RILNSYTWLLSDWSTCNR
☑	395	484.7920	967.5694	967.5702	-0.78	0	13	97	1	LAGPAAVELK
☑	3083	762.0532	2283.1378	2283.1342	1.56	1	13	2.8e+002	1	LNSSAEVLPDANNRVELADEK
☑	2904	738.7115	2213.1127	2213.1111	0.73	0	13	2.8e+002	1	EGDVNVMGVSPAVAVQSLVGNR + Oxidation (M)
☑	3081	761.7307	2282.1703	2282.1754	-2.25	1	13	2.6e+002	1	DIQITLDEPELVTRDATTPR
☑	1290	650.3531	1298.6916	1298.6911	0.44	0	13	3.1e+002	1	FIEPPPFDLPK
☑	3384	1254.1580	2506.3014	2506.2998	0.67	0	13	2.2e+002	1	TFSLMAAINGIAPVGAPVLGGIMMK + 3 Oxidation (M)
☑	143	389.7086	777.4026	777.4021	0.73	0	13	7.6e+002	1	YIPTER
☑	423	493.2700	984.5254	984.5280	-2.59	1	13	3.1e+002	1	SKIPYYSK
☑	2815	1087.5540	2173.0934	2173.1015	-3.71	1	13	2.8e+002	1	EVTIGALRDQDWTELTQAK
☑	1017	613.8236	1225.6326	1225.6349	-1.88	1	13	2.8e+002	1	RMDHNIATLR
☑	3190	773.7211	2318.1415	2318.1390	1.05	0	13	3e+002	1	SEAVGGLAVAPDADAVVADTTSFR
☑	3127	765.3693	2293.0861	2293.0806	2.38	1	13	2.7e+002	1	GGCYIDGLMVFLSMRQAGFR + Carbamidomethyl (C); Oxidation (M)
☑	829	589.7928	1177.5710	1177.5728	-1.45	0	13	2.4e+002	1	GFDSVAAGDALR
☑	920	605.8123	1209.6100	1209.6064	3.04	1	13	3.8e+002	1	DQFTKVTMPK + Oxidation (M)
☑	2853	731.3746	2191.1020	2191.1017	0.13	1	13	3e+002	1	INGEDCFILKLCAEPQTLK + Carbamidomethyl (C)
☑	3135	767.7611	2300.2615	2300.2675	-2.61	1	13	1e+002	1	QVQAIVVVSPTAVDVGMRYLR
☑	393	484.7380	967.4614	967.4611	0.39	0	13	2.3e+002	1	LSNSTDFGK
☑	1540	452.9124	1355.7154	1355.7119	2.57	0	13	3e+002	1	CDLGEVNVLLPK + Carbamidomethyl (C)
☑	2468	929.0336	1856.0526	1856.0506	1.10	1	13	78	1	TASLSEPISLKIEEVLK
☑	3014	1130.0690	2258.1234	2258.1219	0.67	0	13	3e+002	1	QLQILEGHSDTVDGVEFFPK
☑	1391	658.3658	1314.7170	1314.7157	1.06	0	13	3.7e+002	1	HSLDQPLPRPR
☑	2245	585.9710	1754.8912	1754.8911	0.03	1	13	2.8e+002	1	DPALQASIDRTDGQLR
☑	2469	619.6915	1856.0527	1856.0520	0.38	0	13	79	1	VLTTSILGQQISWLAAR
☑	726	568.7959	1135.5772	1135.5808	-3.11	1	13	4e+002	1	RAYVNPASMK
☑	1727	715.3829	1428.7512	1428.7460	3.69	1	13	3.3e+002	1	LLIDENKGEEAAK
☑	412	489.7848	977.5550	977.5546	0.49	0	13	3.4e+002	1	LSLSNLFGK
☑	3001	751.3666	2251.0780	2251.0806	-1.15	1	13	2.8e+002	1	FAKMYSENSIISFQWLCK + Carbamidomethyl (C)
☑	2481	623.6901	1868.0485	1868.0447	2.00	0	13	99	1	QLLNAFSILDIYLAFK
☑	2539	638.0195	1911.0367	1911.0360	0.35	1	13	1.8e+002	1	ATVRLADGMPLLVSAQNR
☑	2560	965.5654	1929.1162	1929.1160	0.15	0	13	45	1	LHIGIAGAGPAGLATSIALAR
☑	1711	472.2361	1413.6865	1413.6888	-1.68	0	13	2.6e+002	1	GVSDPILDQWER
☑	1583	683.3432	1364.6718	1364.6684	2.50	0	13	4e+002	1	EAGATAVAFTGSQR
☑	3025	755.0659	2262.1759	2262.1831	-3.19	1	13	2.5e+002	1	MLDIVFLGGGGGRWESITQVK
☑	2893	737.0325	2208.0757	2208.0699	2.63	0	13	3e+002	1	NLNLGADLIGFISDDQFNDK
☑	111	379.2140	756.4134	756.4130	0.60	0	13	3.6e+002	1	VSPLADR
☑	1726	715.3413	1428.6680	1428.6707	-1.87	1	13	2.3e+002	1	EEFIRYSCSAPK

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☑ 3366 1227.1380 2452.2614 2452.2519  3.88  1   13 2.6e+002  1        LYIDGDSIAVLLMTSGTTSDPKR
☑   17  631.3663  630.3590  630.3588  0.31  0   13    7e+002  1        ALISVE
☑ 2521  949.9635 1897.9124 1897.9066  3.07  0   13 2.7e+002  1        CSMSISSILPAPYSWTR
☑ 2615  676.3386 2025.9940 2026.0014 -3.68  1   13    4e+002  1        MNVHGDGEAGLLVRTSQSR
☑ 3189 1160.0780 2318.1414 2318.1464 -2.15  1   13 3.1e+002  1        DDCYEKTLLLGDVVLQHSTI + Carbamidomethyl (C)
☑ 2743 1075.0370 2148.0594 2148.0600 -0.24  1   13 3.4e+002  1        WEPTGNGLYNIVDRASGATK
☑ 1593  685.8699 1369.7252 1369.7275 -1.65  0   13 2.8e+002  1        EALLAGMVENVPK
☑ 1698  704.8562 1407.6978 1407.6929  3.55  1   13    4e+002  1        EGNFATCLIRER
☑ 3170 1157.1370 2312.2594 2312.2674 -3.46  0   13 1.3e+002  1        MVAGAALALAPVALADEHGAPVLR
☑ 1498  672.8668 1343.7190 1343.7197 -0.52  0   13 4.3e+002  1        INAVAPGYVSTPR
☑ 2474  620.3635 1858.0687 1858.0717 -1.61  0   13        48  1        LVIGIHDVPLDLVAAWK
☑ 2949  745.3614 2233.0624 2233.0548  3.40  0   13 2.7e+002  1        SLPSCFQGLYIECVVTDFR + Carbamidomethyl (C)
☑  539  532.2675 1062.5204 1062.5247 -3.98  0   13 4.4e+002  1        WSDAFKPGR
☑ 1559  679.3348 1356.6550 1356.6521  2.18  0   13 2.5e+002  1        QSAPLADEEELR
☑  749  572.2727 1142.5308 1142.5325 -1.42  0   13 1.5e+002  1        MHSAVGAPMAR + Oxidation (M)
☑ 2370  600.6841 1799.0305 1799.0339 -1.91  1   12        71  1        GMLGKAAGGGIVTAGTVVLK
☑ 2936  743.3676 2227.0810 2227.0880 -3.15  0   12 3.1e+002  1        MEFLLACSLSIFMTFVFR + Carbamidomethyl (C); Oxidation (M)
☑  881  599.3107 1196.6068 1196.6037  2.63  0   12 3.2e+002  1        SSDASLYLVSR
☑  776  579.2736 1156.5326 1156.5360 -2.92  0   12 2.1e+002  1        SSGLSEFSSTR
☑ 1079  624.2820 1246.5494 1246.5540 -3.62  1   12 1.2e+002  1        VKYEYECEK + Carbamidomethyl (C)
☑ 1992  816.8845 1631.7544 1631.7582 -2.30  1   12 1.8e+002  1        MSASVRSMSLTFCR + Carbamidomethyl (C)
☑ 2276  886.9816 1771.9486 1771.9468  1.03  1   12 2.6e+002  1        VEDFLPRLEALEVSR
☑ 2871 1101.0210 2200.0274 2200.0194  3.66  1   12 2.3e+002  1        HSRPYSCTFPPCTKTFGSK + Carbamidomethyl (C)
☑ 3547  980.8596 2939.5570 2939.5525  1.51  0   12 1.4e+002  1        LLAEGCGETVTAAAPVEVVETEVLTLLR + Carbamidomethyl (C)
☑ 1742  481.9407 1442.8003 1442.7980  1.55  0   12 2.3e+002  1        ALEVSGLSLDQLAK
☑ 1960  534.2657 1599.7753 1599.7754 -0.06  1   12 3.6e+002  1        GDRFGAQPPSDGLQR
☑ 3313  598.3099 2389.2105 2389.2026  3.30  1   12 3.1e+002  1        TAVQWTIDLKNGSGEVYQGPAR
☑  364  473.7349  945.4552  945.4556 -0.35  0   12 4.5e+002  1        NAGPFKPSE
☑ 3569 1137.1960 3408.5662 3408.5616  1.35  0   12 1.5e+002  1        QDQAVQHQASIGMYCGAGNNGGDGWLLAAYLK + Carbamidomethyl (C); Oxidation (M)
☑ 1839  764.3735 1526.7324 1526.7287  2.49  0   12 2.8e+002  1        TTSPSDYLLMDLR + Oxidation (M)
☑ 2596  997.4642 1992.9138 1992.9072  3.35  1   12 2.3e+002  1        DASCDLRVASHDDHPLSR
☑ 3326  800.0807 2397.2203 2397.2145  2.42  1   12 3.1e+002  1        MSHLSGKVQTVLGLMDPDQLGR + Oxidation (M)
☑  564  535.7729 1069.5312 1069.5338 -2.43  1   12 2.5e+002  1        CLHKGEDLR
☑ 1664  465.2567 1392.7483 1392.7500 -1.27  1   12 3.2e+002  1        TLSDDVKFLDLK
☑ 1786  755.3289 1508.6432 1508.6379  3.53  0   12        92  1        DAADIDDEGASFGAR
☑ 2385  601.9817 1802.9233 1802.9212  1.17  1   12 4.1e+002  1        VYRFMTTILMYPPR + Oxidation (M)
☑ 2495  627.6911 1880.0515 1880.0493  1.15  1   12 1.1e+002  1        DHRGQHVGLLAPLVVNR
☑ 2410  455.5071 1817.9993 1818.0033 -2.18  1   12 1.5e+002  1        RISTILLMAAASELASR + Oxidation (M)
☑  520  527.7619 1053.5092 1053.5091  0.16  0   12 2.6e+002  1        LTLQDEHQA
☑ 2752 1076.5090 2151.0034 2151.0015  0.91  1   12 2.5e+002  1        MAPTPPETDAGGAPSTDPRQR
☑ 1754  727.3889 1452.7632 1452.7646 -0.94  1   12 3.2e+002  1        IAADCIAGIKSTYK
☑ 2934 1114.5470 2227.0794 2227.0732  2.81  0   12 3.2e+002  1        YQSAFGIQADLATCWQQLK + Carbamidomethyl (C)
☑ 3256  783.4067 2347.1983 2347.1954  1.21  1   12 2.9e+002  1        LGNACDAADLVQDTFVRVITAR
☑ 1440  666.2845 1330.5544 1330.5533  0.84  0   12        59  1        MATFDMSDEIR + Oxidation (M)
☑ 3327  800.7090 2399.1052 2399.1041  0.46  1   12 2.3e+002  1        CVLGGLSMGGQIVMECCARFPGR + Oxidation (M)
☑ 3150 1153.0530 2304.0914 2304.0917 -0.09  0   12 2.8e+002  1        EVGGLANMLANHLDIENADHR + Oxidation (M)
☑ 3046  758.0877 2271.2413 2271.2409  0.16  1   12 1.3e+002  1        GFEVTRALVSEGCAIAILPGLR
☑   63  366.6981  731.3816  731.3814  0.39  1   12 1.2e+003  1        KDLSNVG
☑  456  506.2467 1010.4788 1010.4781  0.75  1   12 2.4e+002  1        YSNSQEKR
☑ 2261  881.9712 1761.9278 1761.9220  3.29  1   12    3e+002  1        ATASSTISADAAARALASK
☑ 1181  425.5455 1273.6147 1273.6163 -1.32  0   12 3.2e+002  1        TPGRPGAQDGYR
☑ 2843  729.4164 2185.2274 2185.2219  2.50  1   12        71  1        QVAVDVPDLAGRVEILGVHAK
☑ 1441  666.3262 1330.6378 1330.6340  2.91  0   12 3.1e+002  1        MIEDFHVDGLR
☑ 2437  916.5206 1831.0266 1831.0277 -0.60  0   12 1.3e+002  1        EEVIVGGMGLLLAFLVR + Oxidation (M)
☑ 2651 1036.9920 2071.9694 2071.9666  1.35  1   12 2.6e+002  1        SLGMEIYMITGDNERTAR + Oxidation (M)
☑ 2626 1025.5060 2048.9974 2048.9949  1.22  1   12 3.4e+002  1        VRTMIDAGASTDEVVAGWR + Oxidation (M)
☑ 3537  970.5226 2908.5460 2908.5545 -2.94  0   12 1.5e+002  1        SSLLALLAVQVFGAPAQSDEAAAAAPAELK
☑ 1857  775.8937 1549.7728 1549.7745 -1.07  1   12 4.3e+002  1        MADPVSQCFVLKR + Carbamidomethyl (C)
☑  792  580.8185 1159.6224 1159.6271 -3.99  1   12 5.4e+002  1        VEKLQLDMGK
☑ 1217  642.8111 1283.6076 1283.6027  3.84  0   12 2.9e+002  1        SNSTSTTIGSMAK
☑ 1899  523.2687 1566.7843 1566.7864 -1.38  1   12 4.6e+002  1        SNKNPPTLFAGFMK + Oxidation (M)
☑ 2171  865.9752 1729.9358 1729.9397 -2.20  0   12 2.6e+002  1        TELLAAVVAAGACVTSVR
☑ 2671 1050.5130 2099.0114 2099.0067  2.25  0   12 3.4e+002  1        YFDLDIPVEAMSACLLAR + Carbamidomethyl (C); Oxidation (M)
☑ 2517  633.6393 1897.8961 1897.8958  0.12  0   12 3.1e+002  1        LFYEHYDLLSQNNSR
☑ 1496  672.8177 1343.6208 1343.6247 -2.89  0   12 2.4e+002  1        MVMLMTGASSIR + 3 Oxidation (M)
☑  838  589.8244 1177.6342 1177.6376 -2.88  1   12 3.9e+002  1        AKQMTLTELK + Oxidation (M)
☑  951  610.8246 1219.6346 1219.6343  0.29  1   12 4.9e+002  1        NIGSSVCLKSR + Carbamidomethyl (C)
☑ 1714  709.3295 1416.6444 1416.6490 -3.18  1   12    2e+002  1        MRDMPDTDALPR
☑ 2051  562.0009 1682.9809 1682.9818 -0.56  0   12        64  1        VDSLLQAEATLVLAIK
☑ 3227  778.4203 2332.2391 2332.2362  1.25  1   12 2.1e+002  1        LTLDQKLPANACPIHPPTFTR
☑ 1641  462.8865 1385.6377 1385.6384 -0.53  0   12 2.3e+002  1        YEEMTEISAGLK + Oxidation (M)
☑ 1665  465.2570 1392.7492 1392.7474  1.30  1   12 2.7e+002  1        GYGRTLTKPSTGR
☑ 3195  773.7232 2318.1478 2318.1511 -1.45  1   12 3.5e+002  1        MMDGWDATAAGVLALPSGRLVR + 2 Oxidation (M)
☑ 1474  670.8531 1339.6916 1339.6918 -0.13  0   12 3.3e+002  1        IPCSGVLDNPIR + Carbamidomethyl (C)
☑ 2547  957.4631 1912.9116 1912.9135 -0.97  0   12 3.1e+002  1        HILNNECSILDIGCGAGK + Carbamidomethyl (C)
☑ 3028  756.0789 2265.2149 2265.2117  1.41  0   12 1.9e+002  1        LAEQILLLLHEAYVENNQR
☑  201  408.2059  814.3972  814.3973 -0.11  0   12 1.6e+002  1        EPDWIR
☑  704 1133.6110 1132.6037 1132.6063 -2.27  0   12    3e+002  1        SANMVFPLVR
☑ 2113  849.9344 1697.8542 1697.8598 -3.24  1   12 3.7e+002  1        SFIVASRDHAGAASPGR
☑ 1428  442.5781 1324.7125 1324.7139 -1.09  1   12    3e+002  1        LGFDYLKNSLR
☑ 2828  728.3480 2182.0222 2182.0187  1.59  0   12 2.9e+002  1        AGYDVMVEAEFGLMHITGAR + Oxidation (M)
☑  353  470.2247  938.4348  938.4314  3.73  0   12 2.9e+002  1        SMASSMGIR
☑  772  577.3021 1152.5896 1152.5887  0.81  0   12 3.1e+002  1        QENVPDARPK
☑ 2599 1002.9930 2003.9714 2003.9636  3.93  1   12 3.4e+002  1        ECGQGFTWKSNLITHQR
☑ 2855 1096.5590 2191.1034 2191.0977  2.63  1   12 3.5e+002  1        MEGIDVDITQSMARIVVNGK + Oxidation (M)
☑ 1943  528.2728 1581.7966 1581.7967 -0.07  1   12    3e+002  1        MSAIRMTSISVASGR + Oxidation (M)
☑ 1471  670.8278 1339.6410 1339.6368  3.17  1   12 3.9e+002  1        KDSETGEGPPAPR
☑ 1709  707.3918 1412.7690 1412.7735 -3.18  1   12    3e+002  1        KLQQLNQNAQTK
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☑	1881	781.9321	1561.8496	1561.8498	-0.07	1	12	2.8e+002	1	AGGSKIVMNASGITIK + Oxidation (M)
☑	2528	476.2849	1901.1105	1901.1098	0.34	1	12	29	1	GQLKHIVVTGPGDLLGGLK
☑	2630	1028.4940	2054.9734	2054.9666	3.32	1	12	3.4e+002	1	AADRLGMPAGVFNMVFGDR + 2 Oxidation (M)
☑	2929	1114.1080	2226.2014	2226.2008	0.27	1	12	1.8e+002	1	VIGLRDGQILFDLPTEAVDR
☑	2965	1122.5440	2243.0734	2243.0721	0.59	1	12	3.2e+002	1	KYTFIDLFAGCGGLSEGFYR
☑	1525	677.3365	1352.6584	1352.6612	-2.05	0	12	3.3e+002	1	LPDWSPSTPEPK
☑	2603	1004.0000	2005.9854	2005.9779	3.76	0	12	4.1e+002	1	VEAMTHGVTIFTEAETVR + Oxidation (M)
☑	2510	630.2987	1887.8743	1887.8673	3.70	1	12	2.6e+002	1	TTSTSSTSKGFWMQDPK
☑	3237	781.0391	2340.0955	2340.1031	-3.28	0	12	2.7e+002	1	HKPVPTVVMDWGPTNFPCDK + Carbamidomethyl (C); Oxidation (M)
☑	863	596.2906	1190.5666	1190.5713	-3.95	0	12	3.5e+002	1	QCLSLSNQNK + Carbamidomethyl (C)
☑	2995	750.0861	2247.2365	2247.2409	-1.97	1	12	1.1e+002	1	GKEAILSLRPAPAPDQVVQMK
☑	3299	792.7280	2375.1622	2375.1620	0.08	1	12	3.5e+002	1	EYEFDVLAVCAPAYAGGRFLK + Carbamidomethyl (C)
☑	3118	573.5530	2290.1829	2290.1741	3.83	1	12	3.2e+002	1	MPMLATGTASFPFPPIEDLKK
☑	235	420.7451	839.4756	839.4752	0.47	0	12	1.3e+002	1	SPAPLVEK
☑	3328	800.7892	2399.3458	2399.3372	3.57	1	12	62	1	ARPRMVIALGAQAAQAFLGVGFR
☑	3319	797.7320	2390.1742	2390.1649	3.89	1	12	3.8e+002	1	QTVRACGGTDVNELFSLVNDPR
☑	207	413.2166	824.4186	824.4214	-3.38	1	12	4.7e+002	1	ALEKMHP
☑	2168	577.2972	1728.8698	1728.8696	0.11	0	12	4e+002	1	ALHDLLAGHAADPWSR
☑	1644	694.3832	1386.7518	1386.7541	-1.59	1	12	4.5e+002	1	ENLKPVLMDGKK + Oxidation (M)
☑	293	448.6999	895.3852	895.3883	-3.38	0	12	1.4e+002	1	SSNSASSEK
☑	1168	634.8442	1267.6738	1267.6772	-2.66	0	12	2.9e+002	1	DAGIGGVEINPVK
☑	1597	457.9260	1370.7562	1370.7517	3.23	1	12	4e+002	1	EIVLRGEEASLR
☑	2876	1101.0970	2200.1794	2200.1852	-2.61	1	12	2.3e+002	1	VPGVTATPSAALSSAVSPSAFRK
☑	2887	736.0346	2205.0820	2205.0888	-3.10	1	12	4e+002	1	ILECILRFANDEFEHTQK
☑	3164	1155.0680	2308.1214	2308.1237	-0.96	0	12	4.2e+002	1	YPQSASYGFIGQGVDLTHVNR
☑	2011	551.9579	1652.8519	1652.8459	3.64	1	12	3.4e+002	1	VACFYYFKLAGLMK
☑	338	465.2395	928.4644	928.4623	2.35	0	12	3.4e+002	1	QLHCAVMK
☑	3129	766.0348	2295.0826	2295.0763	2.74	0	12	3.5e+002	1	EGALLADEIDGFDMVSVDIMR
☑	2441	613.0159	1836.0259	1836.0244	0.79	0	12	1.4e+002	1	ILEGIVTEEPVQVVAQL
☑	2830	1092.0190	2182.0234	2182.0286	-2.35	1	12	2.8e+002	1	LVPLDESYKVASMEDPMAR + 2 Oxidation (M)
☑	1733	477.6017	1429.7833	1429.7790	2.97	1	12	4e+002	1	RVFGGGLDGGVQIR
☑	3093	1145.0120	2288.0094	2288.0098	-0.15	0	12	1.3e+002	1	MFTNIEYADMLLVMGECHR + Oxidation (M)
☑	1702	471.2565	1410.7477	1410.7428	3.44	0	12	3.2e+002	1	YISELLSMSIQK
☑	2684	1054.9880	2107.9614	2107.9588	1.26	1	12	2.1e+002	1	MKTPCKPCDEDEVAIQTK + Carbamidomethyl (C); Oxidation (M)
☑	2634	1029.9960	2057.9774	2057.9841	-3.21	1	12	3.3e+002	1	YGTGVTRELGMDVQNFGSK
☑	2445	920.5153	1839.0160	1839.0214	-2.91	1	12	1.8e+002	1	ALRGVDVQTLLNAGDGLK
☑	2574	978.4681	1954.9216	1954.9232	-0.79	0	12	3.1e+002	1	DAPQQEALDLTVEANADR
☑	474	513.2718	1024.5290	1024.5263	2.68	0	12	3.1e+002	1	IAMDGYVIK + Oxidation (M)
☑	711	568.7878	1135.5610	1135.5656	-3.97	0	12	4.1e+002	1	GLSSGSIVASCR
☑	2621	1021.9910	2041.9674	2041.9700	-1.24	0	12	3.5e+002	1	LSPAAQMLMDINSIESYK + 2 Oxidation (M)
☑	2834	1092.5150	2183.0154	2183.0137	0.78	0	12	2.6e+002	1	DLSGINGNGQIMSNNNNHIR + Oxidation (M)
☑	1202	639.3388	1276.6630	1276.6664	-2.59	0	12	4.9e+002	1	VDGDVLTQGFVK
☑	3010	753.0866	2256.2380	2256.2300	3.54	1	12	1.3e+002	1	LAYMLDDSGVKLLLTQAHLR
☑	2872	734.3508	2200.0306	2200.0293	0.59	0	12	2.9e+002	1	SGNDCVVCLNLLPGTYQYK + 2 Carbamidomethyl (C)
☑	3232	1167.5870	2333.1594	2333.1533	2.65	1	12	4.2e+002	1	VVESVNALVDSTISAMEEERR
☑	130	384.6982	767.3818	767.3789	3.89	0	12	2.6e+002	1	FMWIR + Oxidation (M)
☑	1235	645.8127	1289.6108	1289.6140	-2.41	0	12	3.5e+002	1	GVEYVTDAPDPK
☑	2654	1038.0160	2074.0174	2074.0194	-0.92	1	12	3.8e+002	1	KYSVWCGGSILASLSTFQQ
☑	2635	1030.5680	2059.1214	2059.1136	3.82	1	12	2e+002	1	TALTPAEMFLSNVGKVPLR + Oxidation (M)
☑	2009	551.6301	1651.8685	1651.8682	0.19	1	12	3e+002	1	YNSAVEALNRFIQK
☑	3160	769.7597	2306.2573	2306.2634	-2.67	0	12	1.5e+002	1	APVTPTEQQLAAIFGELLGVPR
☑	3316	1196.0920	2390.1694	2390.1714	-0.80	1	12	3.8e+002	1	RDALLENVGVLANGDVDYADGSK
☑	3525	960.4377	2878.2913	2878.2949	-1.27	1	12	1.5e+002	1	NFDAITCTAIRTCSGCYQGQGGFPVR + 2 Carbamidomethyl (C)
☑	2555	963.9547	1925.8948	1925.8950	-0.10	1	12	3.1e+002	1	FSVCTFDAPIICRHCSK
☑	3262	783.4088	2347.2046	2347.2053	-0.31	1	12	3.5e+002	1	LADTDLTTRIGMVIEANISNGK + Oxidation (M)
☑	1748	482.9334	1445.7784	1445.7739	3.09	0	12	3.7e+002	1	QAQPVNLHGVDIR
☑	2783	1085.5310	2169.0474	2169.0484	-0.46	1	12	3.7e+002	1	TNQTLPSGMRVSTQDTYVR + Oxidation (M)
☑	2373	600.6849	1799.0329	1799.0345	-0.92	1	12	88	1	TLGLQGVFPAIKEWIK
☑	2484	937.0313	1872.0480	1872.0444	1.96	0	12	1.2e+002	1	FLMALGAAVTLAAFLAHR
☑	2518	949.9554	1897.8962	1897.8945	0.90	0	12	3.5e+002	1	SEFDILLDFLDTDGNGK
☑	3122	1146.6200	2291.2254	2291.2281	-1.14	1	12	2e+002	1	AVQSARQQAGIVKPATCHTLR + Carbamidomethyl (C)
☑	554	534.2493	1066.4840	1066.4866	-2.35	0	12	2.1e+002	1	DMAFSLNNR
☑	895	601.7863	1201.5580	1201.5550	2.57	0	12	2.8e+002	1	WALMEPANDR
☑	2928	743.0366	2226.0880	2226.0880	-0.03	1	12	3.9e+002	1	NSSIAELLGAVRVLCSTMMLC + Oxidation (M)
☑	3130	766.3843	2296.1311	2296.1369	-2.54	1	12	3.9e+002	1	HLLDEEGLDPTQTLMIGDRK + Oxidation (M)
☑	3242	781.7650	2342.2732	2342.2668	2.73	1	12	1.5e+002	1	LAYNISTPTIMAIPVQVKDPR + Oxidation (M)
☑	3247	781.7665	2342.2777	2342.2706	3.01	1	12	1.5e+002	1	LELVRSAPSILVDAGHNPEGIR
☑	1951	795.3915	1588.7684	1588.7747	-3.91	1	11	4.5e+002	1	TGRGTFEHFGLDPR
☑	2816	725.7304	2174.1694	2174.1630	2.94	1	11	2.2e+002	1	CALLERLHVVNDEPIALGR + Carbamidomethyl (C)
☑	932	608.2884	1214.5622	1214.5649	-2.14	0	11	2.1e+002	1	VCHILGNSCGR + Carbamidomethyl (C)
☑	3226	778.4050	2332.1932	2332.1886	1.98	0	11	3.7e+002	1	GGSLLSAFAGNMTLYTALVAGFR + Oxidation (M)
☑	1621	460.8980	1379.6722	1379.6755	-2.41	0	11	4.7e+002	1	QEITIFVNECK + Carbamidomethyl (C)
☑	3141	768.0905	2301.2497	2301.2441	2.42	0	11	1.7e+002	1	LGDGVRPGQVADAVGIEPPSLVR
☑	1636	462.2441	1383.7105	1383.7106	-0.09	1	11	3.7e+002	1	AAHSESGKIESLR
☑	2746	717.0410	2148.1012	2148.1063	-2.37	0	11	3.6e+002	1	AVNADTIETGGAFVSESVLLR
☑	2997	750.3808	2248.1206	2248.1191	0.65	1	11	4.1e+002	1	LTAEGRLLLCLGEENSLDMR + Oxidation (M)
☑	536	531.7567	1061.4988	1061.4998	-0.88	0	11	3.2e+002	1	MEVVMGQPR + Oxidation (M)
☑	668	560.3405	1118.6664	1118.6699	-3.11	0	11	1.4e+002	1	LILTPPAAPLN
☑	1470	670.7808	1339.5470	1339.5497	-1.94	0	11	58	1	MQNVQADTDMR + 2 Oxidation (M)
☑	3105	764.4008	2290.1806	2290.1879	-3.19	0	11	3.5e+002	1	MTDLFVAVDPASVLSLTELNR
☑	1363	436.5783	1306.7131	1306.7132	-0.13	1	11	3.4e+002	1	LSLFDSGLAKEK
☑	1573	681.8672	1361.7198	1361.7190	0.59	0	11	5.1e+002	1	LAAEAGAQIEYVK
☑	1801	509.2647	1524.7723	1524.7725	-0.15	0	11	4e+002	1	EFLVSAYFSLHGR
☑	1618	689.3863	1376.7580	1376.7551	2.13	0	11	2.1e+002	1	DEILSYLGIAGVK
☑	87	376.7004	751.3862	751.3864	-0.22	0	11	6.3e+002	1	YAASAAAK
☑	2622	1023.4870	2044.9594	2044.9636	-2.04	0	11	3.2e+002	1	DNVCNYLDIALQHISDR + Carbamidomethyl (C)
☑	1764	737.3656	1472.7166	1472.7154	0.85	1	11	3.8e+002	1	HSSAQRCDITLSR
☑	2607	673.0376	2016.0910	2016.0892	0.90	0	11	2.1e+002	1	QILEGIFGSGQTTSLPGAIK

☑	2895	1105.0460	2208.0774	2208.0844	-3.17	1	11	4.2e+002	1	ASPPNSSICIISASDKNSYVR
☑	3379	1248.1390	2494.2634	2494.2672	-1.50	1	11	3.5e+002	1	LVRICMTPEDITAAAVEIAEHR + Carbamidomethyl (C)
☑	1184	425.5460	1273.6162	1273.6197	-2.77	1	11	4.4e+002	1	AGREDGCIGALR + Carbamidomethyl (C)
☑	1856	774.8748	1547.7350	1547.7290	3.91	0	11	4.7e+002	1	AGFNSTMYQVSSLK + Oxidation (M)
☑	1930	528.2720	1581.7942	1581.7999	-3.59	0	11	4.1e+002	1	DLGNDPESGLPVTLR
☑	2216	874.4847	1746.9548	1746.9516	1.88	1	11	2.2e+002	1	NSTALAGFAKLIESTPK
☑	3369	1231.6940	2461.3734	2461.3693	1.69	0	11	79	1	TPPAYRPPNAPILSTLPTTTVVR
☑	2757	1078.0990	2154.1834	2154.1866	-1.46	1	11	1.6e+002	1	SDKFMIIISMLILLAAMTK + Oxidation (M)
☑	774	578.2849	1154.5552	1154.5567	-1.29	0	11	2.5e+002	1	EPAEEPTNIR
☑	2417	609.0159	1824.0259	1824.0311	-2.87	1	11	1.3e+002	1	LFRHIASLPLAFFHR
☑	575	359.8277	1076.4613	1076.4572	3.80	0	11	98	1	CSYWCFLR
☑	674	561.3217	1120.6288	1120.6314	-2.31	0	11	1.3e+002	1	GLAAGMLFTLK
☑	2493	940.0227	1878.0308	1878.0350	-2.19	1	11	1.9e+002	1	IDYAILKATTTAEEVLK
☑	3161	770.0448	2307.1126	2307.1131	-0.23	0	11	3.9e+002	1	AVAEAYAAGYDAGLAEGAPVSAQR
☑	2556	643.3223	1926.9451	1926.9507	-2.94	1	11	4.3e+002	1	DTAGGAVRGAAGDAGEAAALAR
☑	3143	768.3908	2302.1506	2302.1562	-2.45	1	11	4.3e+002	1	LGFSEGVLNGMRVPCSIVGPDR
☑	3258	587.8079	2347.2025	2347.2094	-2.92	1	11	3.6e+002	1	IPITDQDDVGTMFEKLSLLGR
☑	3399	1304.1580	2606.3014	2606.3050	-1.37	1	11	3.7e+002	1	TALQNNPNAPLFIMDGYEVKIDK + Oxidation (M)
☑	1061	621.2963	1240.5780	1240.5796	-1.24	0	11	2.9e+002	1	ENHSSEQAALR
☑	357	471.7431	941.4716	941.4753	-3.84	0	11	3.9e+002	1	HADLAMLR + Oxidation (M)
☑	1713	708.8152	1415.6158	1415.6138	1.46	1	11	1.6e+002	1	NEDAQEGGGRGGGGR
☑	848	395.1928	1182.5566	1182.5604	-3.23	1	11	3.3e+002	1	WRDGMLYSR
☑	1113	626.8317	1251.6488	1251.6506	-1.40	1	11	4.9e+002	1	GETPLHRACIR
☑	1933	528.2722	1581.7948	1581.7895	3.33	1	11	4.7e+002	1	MVEGVDLFMGGKVGK + Oxidation (M)
☑	3263	1174.6100	2347.2054	2347.2067	-0.54	1	11	3.7e+002	1	MTTRGVVQGGGGGDGGLFNGILIR + Oxidation (M)
☑	1081	625.3187	1248.6228	1248.6211	1.40	0	11	4.6e+002	1	DHGVGIAPEAQR
☑	2018	552.6702	1654.9888	1654.9878	0.59	0	11	27	1	AINCCVVLLLVVVLK + Carbamidomethyl (C)
☑	3353	809.4609	2425.3609	2425.3515	3.86	0	11	82	1	LSLGPLLAAAAVGALAGAQCGYLLGR
☑	1910	785.9013	1569.7880	1569.7859	1.37	1	11	5.5e+002	1	AKVEGGANQSGSAAPAR
☑	2186	578.6534	1732.9384	1732.9359	1.41	1	11	2.7e+002	1	FSVLIDAGLSGKELER
☑	1944	528.2731	1581.7975	1581.8007	-2.04	1	11	3.6e+002	1	FIVMAREGIDMLR + 2 Oxidation (M)
☑	3283	787.7353	2360.1841	2360.1868	-1.17	1	11	4.5e+002	1	AVKEMNPSVTMEVLIPDFQGR
☑	2734	1072.0500	2142.0854	2142.0918	-2.98	0	11	4.4e+002	1	ETSFDIAFASEIMAILALGK + Oxidation (M)
☑	15	631.3661	630.3588	630.3588	-0.00	0	11	9.8e+002	1	EVIASL
☑	3179	773.0521	2316.1345	2316.1274	3.07	0	11	4.8e+002	1	AFYETQINNSLTVLFEGENK
☑	2423	915.0189	1828.0232	1828.0281	-2.63	1	11	1.6e+002	1	SIMKLQSTFGIIPHIK + Oxidation (M)
☑	1935	528.2723	1581.7951	1581.7998	-3.00	1	11	4.8e+002	1	TIKEDNQHEVEIK
☑	22	687.4020	686.3947	686.3963	-2.25	1	11	1.3e+003	1	EAKVVAA
☑	2045	560.6702	1678.9888	1678.9923	-2.09	1	11	50	1	KFFHLNPILVGPGIK
☑	3107	764.4009	2290.1809	2290.1805	0.18	0	11	3.7e+002	1	LDETLLDAPEALAGADTHGLLR
☑	3217	1166.1450	2330.2754	2330.2668	3.73	0	11	1.6e+002	1	MTHTLLLAALIAAAPTLHAEEK + Oxidation (M)
☑	3034	1135.5530	2269.0914	2269.0988	-3.24	0	11	4.2e+002	1	NNGQALIFSGWNNSNIIHDR
☑	203	411.7039	821.3932	821.3919	1.60	0	11	5.7e+002	1	GVAGDEFK
☑	1227	643.8398	1285.6650	1285.6700	-3.86	0	11	6.1e+002	1	MPTSSPTIAPLR + Oxidation (M)
☑	1976	807.4109	1612.8072	1612.8097	-1.50	1	11	4.3e+002	1	GYQTGYEKGELAGLK
☑	2614	1013.4990	2024.9834	2024.9846	-0.55	1	11	4.6e+002	1	YGLPRAEMLSPVSTMCVR + Oxidation (M)
☑	1086	625.3376	1248.6606	1248.6575	2.52	0	11	5.4e+002	1	PGSAVVGGAPAPGGR
☑	2505	944.4658	1886.9170	1886.9156	0.78	0	11	4.6e+002	1	LLDINNQMANATNQEAK
☑	1737	717.8881	1433.7616	1433.7667	-3.52	1	11	4.6e+002	1	KVAAFGDIVYHSK
☑	2430	611.0197	1830.0373	1830.0403	-1.68	1	11	1e+002	1	YTLHLTGTPFKALALGK
☑	461	507.2971	1012.5796	1012.5804	-0.79	0	11	4.9e+002	1	ILGLLDEAGL
☑	3229	778.7254	2333.1544	2333.1469	3.18	0	11	4.7e+002	1	GVDDLAACAPLMCAGITLFDPIK
☑	1534	678.3607	1354.7068	1354.7101	-2.39	1	11	4.3e+002	1	LMAEMVKAPPPR + Oxidation (M)
☑	2483	936.9467	1871.8788	1871.8724	3.47	1	11	4.2e+002	1	LASSASWSDMKFGTPSGK + Oxidation (M)
☑	3032	567.8088	2267.2061	2267.2130	-3.03	1	11	2.9e+002	1	LAAMDCRLIVTPNIQPEVIR + Oxidation (M)
☑	2489	938.0038	1873.9930	1873.9871	3.18	1	11	3.9e+002	1	AQAQALGVATGPDVQRHR
☑	3389	1269.6610	2537.3074	2537.3060	0.56	1	11	3.7e+002	1	SAGAPASPAPPILGDIPGDIPGRMHK + Oxidation (M)
☑	2386	903.4913	1804.9680	1804.9618	3.48	1	11	3.1e+002	1	ASMNAALRFLDQTIVR
☑	3023	754.7079	2261.1019	2261.0998	0.92	0	11	4.3e+002	1	TTAPEMAYSITTEPVLHGATR + Oxidation (M)
☑	1198	638.7516	1275.4886	1275.4900	-1.08	0	11	19	1	IDEFGFCACGSAG
☑	2507	944.5358	1887.0570	1887.0578	-0.39	1	11	1.4e+002	1	GIVLSFTPQSAATKKPSR
☑	574	538.2915	1074.5684	1074.5709	-2.32	0	11	6.7e+002	1	LSSGIPPNYK
☑	1087	625.3377	1248.6608	1248.6649	-3.23	0	11	5.6e+002	1	LVNFIGSVGGMR
☑	1936	528.2723	1581.7951	1581.7933	1.11	1	11	5.1e+002	1	GGLEHCEPLTVSKR + Carbamidomethyl (C)
☑	2544	638.6429	1912.9069	1912.9088	-1.01	0	11	4.2e+002	1	AMEFDANATTALLDTVSK + Oxidation (M)
☑	2707	711.7145	2132.1217	2132.1268	-2.41	1	11	3.6e+002	1	MRVAIIGSGPVGMTAAMLLGR + 2 Oxidation (M)
☑	1908	523.6464	1567.9174	1567.9120	3.44	1	11	1e+002	1	ALPMRVVLAGLDVSK
☑	3106	764.4008	2290.1806	2290.1813	-0.33	1	11	4e+002	1	LPFDVAVEAMSADLRMSLVAR
☑	1422	442.5770	1324.7092	1324.7139	-3.58	0	11	3.9e+002	1	FLPPNRPVEEK
☑	1720	711.8782	1421.7418	1421.7402	1.17	1	11	5.4e+002	1	EFGTKINETISAL
☑	2884	735.7040	2204.0902	2204.0936	-1.54	1	11	5e+002	1	IFASIHMPNEFELKTDQGK
☑	3109	573.5525	2290.1809	2290.1885	-3.32	1	11	4e+002	1	LIVDDVYPYAVKYYTEALR
☑	1037	616.7415	1231.4684	1231.4705	-1.68	0	11	15	1	NCSMSMPTSMK + Oxidation (M)
☑	2821	1089.0540	2176.0934	2176.0946	-0.55	1	11	4.8e+002	1	RNDMLVSTLQHYIESLGGK + Oxidation (M)
☑	3548	980.8870	2939.6392	2939.6379	0.44	1	11	64	1	LNVNGGAIALGHPLGGSGTKLMTTLVHALK
☑	3169	578.7871	2311.1193	2311.1154	1.68	1	11	4.4e+002	1	EVCAAKVLPHAAEADETGEFPK
☑	2675	1054.0050	2105.9954	2105.9899	2.63	0	11	4.1e+002	1	MNSNTLEDNVTAAQTSVSPK
☑	2485	625.0234	1872.0484	1872.0430	2.86	0	11	1.4e+002	1	ELIEAYIPILCALGGIK + Carbamidomethyl (C)
☑	2881	735.0770	2202.2092	2202.2122	-1.39	1	11	1.9e+002	1	VWYIAGDIDLPATLGLKMVK
☑	1413	441.8900	1322.6482	1322.6461	1.53	0	11	4.9e+002	1	LLVIEDEMMSK + Oxidation (M)
☑	1389	439.2306	1314.6700	1314.6714	-1.08	0	11	4.2e+002	1	SRPSAAGMNPLSK
☑	3114	573.5527	2290.1817	2290.1780	1.62	1	11	4.1e+002	1	MPVLEIFGPTFQGEGRSIGQK
☑	3163	770.3810	2308.1212	2308.1183	1.24	0	11	5.3e+002	1	TGLDGIGGVSVLASETFDETQGR
☑	196	406.7474	811.4802	811.4803	-0.12	0	11	2.7e+002	1	GVPGIELK
☑	160	397.6592	793.3038	793.3033	0.65	0	11	65	1	MPCCGAR + Carbamidomethyl (C)
☑	688	565.2891	1128.5636	1128.5638	-0.10	0	11	5e+002	1	GETMIFFIR + Oxidation (M)
☑	3052	1138.5840	2275.1534	2275.1459	3.30	1	11	4.7e+002	1	YSRYALTAHGMGLTLAAGIYF
☑	3113	573.5527	2290.1817	2290.1726	3.98	1	11	4.1e+002	1	ESLAQSIDASMAGVKLIDDALK + Oxidation (M)

☑	872	398.8403	1193.4991	1193.5023	-2.68	0	11	1.1e+002	1	FPDPEESMAR + Oxidation (M)
☑	3378	832.1196	2493.3370	2493.3380	-0.41	1	11	2.1e+002	1	SDIGGPGIGISVVLAQIFEYFRR
☑	1977	808.8691	1615.7236	1615.7235	0.08	1	11	2.7e+002	1	GYCALCRTGPFASDR
☑	2271	885.4335	1768.8524	1768.8494	1.71	0	11	4.9e+002	1	AYENVFPFIMPLGASN
☑	427	494.2531	986.4916	986.4920	-0.41	0	11	4.3e+002	1	GEQLVVEVD
☑	2944	743.6974	2228.0704	2228.0644	2.68	1	11	4.5e+002	1	MLSPEHPDEPKSGLGDHLNR
☑	2962	1122.0300	2242.0454	2242.0423	1.41	0	11	3.4e+002	1	IQPEADIDAELADMAAAVDER
☑	3303	792.7296	2375.1670	2375.1652	0.76	1	11	5e+002	1	ARTILATCHQGAASPSSSFLDSR
☑	3333	802.4167	2404.2283	2404.2234	2.02	0	11	4.2e+002	1	QHIIPLENVTIDSIQDEGDLR
☑	2007	825.8585	1649.7024	1649.7073	-2.92	0	11	1.1e+002	1	GTRPDCPACGGMGVTGR + Oxidation (M)
☑	3136	767.7616	2300.2630	2300.2569	2.65	1	11	1.5e+002	1	YPSIITDQFVAKAAIFIFTR
☑	2032	836.9750	1671.9354	1671.9341	0.79	1	11	2.8e+002	1	MANNLKQVIINISAK + Oxidation (M)
☑	679	563.2990	1124.5834	1124.5826	0.77	0	11	5e+002	1	GPIQIDPETR
☑	1683	700.3836	1398.7526	1398.7514	0.91	1	11	4.6e+002	1	RSAPRPAGMTSLR
☑	2153	573.3289	1716.9649	1716.9597	3.04	1	11	1.7e+002	1	GTVAPLMLFAGRIVEK + Oxidation (M)
☑	2444	614.0124	1839.0154	1839.0115	2.12	1	11	2.3e+002	1	ARQQLIQTLINYHNK
☑	113	379.7059	757.3972	757.3970	0.30	0	11	3.4e+002	1	GNVEIVAG
☑	1847	512.2840	1533.8302	1533.8263	2.50	1	11	3.7e+002	1	SLISAGGGVFSRQQK
☑	2174	577.9852	1730.9338	1730.9349	-0.63	1	11	3.7e+002	1	MGILELIENTLARSR + Oxidation (M)
☑	708	568.2716	1134.5286	1134.5305	-1.65	1	11	3.1e+002	1	IYSAPENERG
☑	2519	949.9556	1897.8966	1897.8956	0.53	0	11	4.3e+002	1	CMGVGLLAMMLVVGCGSK + 2 Carbamidomethyl (C); Oxidation (M)
☑	1956	796.9371	1591.8596	1591.8604	-0.44	1	11	3.7e+002	1	MSNKVLVITGATGTGK + Oxidation (M)
☑	2912	740.0483	2217.1231	2217.1286	-2.48	1	11	4.7e+002	1	AQVADVAAYILSKHGPMTAMK + Oxidation (M)
☑	1049	618.3348	1234.6550	1234.6531	1.61	1	11	6.1e+002	1	HNLPRVTGDAR
☑	2870	1101.0210	2200.0274	2200.0252	1.02	1	11	3.6e+002	1	METIVKINSNANSNFNNMK + 2 Oxidation (M)
☑	3049	758.7603	2273.2591	2273.2644	-2.36	1	11	1.3e+002	1	IPGRNFLAVPGPTNIPDQVLR
☑	238	421.7530	841.4914	841.4909	0.66	0	11	4.4e+002	1	KPIDEIK
☑	1998	546.9474	1637.8204	1637.8161	2.58	1	11	5.7e+002	1	SYGKAGSQSWLLEGR
☑	2863	1100.0100	2198.0054	2197.9970	3.85	1	11	3.3e+002	1	EFFDIDWHHHYPENKGK
☑	2591	497.0229	1984.0625	1984.0589	1.81	0	11	4.3e+002	1	IVAAIISQVEGSLQANDTR
☑	2892	553.0095	2208.0089	2208.0039	2.27	1	11	3.1e+002	1	SLPCDVKASEDTVTVDCVDR + Carbamidomethyl (C)
☑	114	379.7062	757.3978	757.3970	1.12	0	11	3e+002	1	EAAPSGVK
☑	3115	573.5528	2290.1821	2290.1773	2.08	1	11	4.2e+002	1	KTACLAISGLAGLGMVSDAVAGGR + Carbamidomethyl (C); Oxidation (M)
☑	3231	1167.5860	2333.1574	2333.1539	1.50	0	10	5.2e+002	1	TIEVSGGSIEYDGDPAWIGVLR
☑	1983	811.8709	1621.7272	1621.7307	-2.15	0	10	2.7e+002	1	NTLQHMWGYVSDR + Oxidation (M)
☑	2256	881.4569	1760.8992	1760.8978	0.81	1	10	5.7e+002	1	EVECSVLGNLDIKASK + Carbamidomethyl (C)
☑	3016	754.0305	2259.0697	2259.0624	3.24	0	10	4.3e+002	1	HIDCGIAESNMAGIGAGIATTGK + Carbamidomethyl (C); Oxidation (M)
☑	2832	728.3492	2182.0258	2182.0299	-1.90	1	10	4.2e+002	1	IGWRMSKPEDSEVNLFCR + Oxidation (M)
☑	2394	906.4405	1810.8664	1810.8706	-2.28	1	10	4.8e+002	1	RVAQYLISTACPSCDGK
☑	2852	1096.5580	2191.1014	2191.0943	3.27	1	10	5.1e+002	1	DKNNSLCIDIYNGLLSPQK + Carbamidomethyl (C)
☑	2991	749.0266	2244.0580	2244.0667	-3.90	0	10	4.5e+002	1	DYGNTIGCSVPLMLAEPVHR + Carbamidomethyl (C); Oxidation (M)
☑	682	564.2679	1126.5212	1126.5189	2.07	0	10	2.7e+002	1	AEHPTAAQMR + Oxidation (M)
☑	3349	1212.1140	2422.2134	2422.2203	-2.81	1	10	4.5e+002	1	VVDDVLRGDIPTTFFEAELMR
☑	2858	549.5125	2194.0209	2194.0187	1.00	0	10	3.7e+002	1	EAPYLAVPCLVMDGSHTYR + Carbamidomethyl (C); Oxidation (M)
☑	2548	957.5444	1913.0742	1913.0774	-1.67	1	10	1.4e+002	1	REVGIYLFIHISPELK
☑	375	478.7763	955.5380	955.5385	-0.50	1	10	1.8e+002	1	ACLPQRLR
☑	1057	620.7659	1239.5172	1239.5159	1.11	0	10	90	1	MGVCSSCLGGGR + 2 Carbamidomethyl (C)
☑	1274	646.8396	1291.6646	1291.6667	-1.55	1	10	5.4e+002	1	TGTASICARLSR + Carbamidomethyl (C)
☑	1704	706.8912	1411.7678	1411.7671	0.54	0	10	3.9e+002	1	AVEAATAGGIGTIPGK
☑	1724	714.4286	1426.8426	1426.8395	2.19	1	10	1.4e+002	1	SVGKIDDLLAVLGK
☑	3138	767.7623	2300.2651	2300.2740	-3.89	0	10	1.7e+002	1	KPDGGVELATPPLGDLVLPGVTR
☑	1145	632.3126	1262.6106	1262.6111	-0.37	0	10	5.6e+002	1	VIANADGIMGMR + Oxidation (M)
☑	3402	874.4628	2620.3666	2620.3717	-1.95	0	10	3.5e+002	1	HIALVDPDLLVIMGNISCDALLGR + Carbamidomethyl (C); Oxidation (M)
☑	3030	1134.0200	2266.0254	2266.0259	-0.20	0	10	2.8e+002	1	MEAALVSYAEPHQHHVMER + 2 Oxidation (M)
☑	1195	637.8408	1273.6670	1273.6666	0.33	1	10	8.8e+002	1	ESAIPREFTPK
☑	1934	528.2722	1581.7948	1581.7998	-3.20	0	10	5.7e+002	1	LQDLIAHVSSEGGEK
☑	1514	450.5790	1348.7152	1348.7173	-1.57	1	10	6.9e+002	1	EMVGLFKAEGIR
☑	2172	577.6526	1729.9360	1729.9362	-0.16	1	10	3.9e+002	1	TEVNLKGYLNIPQNK
☑	2206	873.4177	1744.8208	1744.8195	0.75	0	10	4.2e+002	1	GIPYEYIEEDLYNK
☑	3224	778.4041	2332.1905	2332.1959	-2.34	1	10	5e+002	1	FAPTSPSSWAQMPIEIVCKIK
☑	274	439.2551	876.4956	876.4957	-0.00	0	10	4.4e+002	1	IELVQYI
☑	1927	528.2717	1581.7933	1581.7973	-2.58	0	10	4.9e+002	1	CVEVPISIHEFPR + Carbamidomethyl (C)
☑	2910	740.0438	2217.1096	2217.1113	-0.79	1	10	5.4e+002	1	QPGPDCRLDLDHHLVLSFR
☑	1116	418.9051	1253.6935	1253.6980	-3.60	0	10	3.1e+002	1	SGVLVVGGDPGIGK
☑	1676	466.9161	1397.7265	1397.7224	2.89	0	10	4.7e+002	1	LLYASAVSSISCK + Carbamidomethyl (C)
☑	2655	692.3469	2074.0189	2074.0266	-3.70	1	10	5.9e+002	1	MAHLRLTEEQFTQLGER + Oxidation (M)
☑	2968	1122.6030	2243.1914	2243.1957	-1.90	1	10	3.5e+002	1	NVLGGALAVQVRVNNASVCFR + Carbamidomethyl (C)
☑	2058	564.6491	1690.9255	1690.9254	0.07	0	10	2.9e+002	1	VYSVIQSQINAALSAK
☑	3481	942.0952	2823.2638	2823.2586	1.83	1	10	2e+002	1	EACATPTTVTTVNSAPRGCCGGIGEGDTR
☑	470	512.7805	1023.5464	1023.5461	0.31	0	10	4.5e+002	1	IDTAHAQLR
☑	2353	598.6599	1792.9579	1792.9645	-3.68	1	10	3.3e+002	1	VKFMESLVVGDIAELK + Oxidation (M)
☑	1626	691.8463	1381.6780	1381.6734	3.37	0	10	4.9e+002	1	MNVLNIFVCADK + Oxidation (M)
☑	1948	528.9788	1583.9146	1583.9134	0.74	0	10	1.2e+002	1	AILDLAISDSLQVVK
☑	2583	659.0336	1974.0790	1974.0720	3.51	1	10	2.6e+002	1	STCLSGIAHALPELKHLK + Carbamidomethyl (C)
☑	2454	616.3386	1845.9940	1845.9883	3.06	1	10	3.9e+002	1	RGMVLARPDILGTFER + Oxidation (M)
☑	1667	697.3828	1392.7510	1392.7473	2.66	1	10	4.3e+002	1	SGVTRSAFLASAAR
☑	1171	636.7602	1271.5058	1271.5055	0.29	0	10	56	1	DDGENPFDHAVG
☑	1703	706.8422	1411.6698	1411.6666	2.27	1	10	4.9e+002	1	RMYWSSEQGLR
☑	2604	1004.9850	2007.9554	2007.9538	0.83	0	10	4.7e+002	1	DEFHVVEIVPAEDGEAPR
☑	2961	748.0792	2241.2158	2241.2159	-0.08	1	10	2.4e+002	1	MKALIGIGLCAALLGGCAALPGR + Carbamidomethyl (C); Oxidation (M)
☑	57	365.1858	728.3570	728.3565	0.70	0	10	1.5e+002	1	QGSNAPR
☑	2666	1047.0160	2092.0174	2092.0194	-0.92	1	10	4.9e+002	1	DVVGTWTGRSACLLQEAMR
☑	1361	654.3627	1306.7108	1306.7092	1.23	1	10	5.2e+002	1	TSALTGVSTNTKK
☑	1939	528.2725	1581.7957	1581.7926	1.92	0	10	6e+002	1	LSFPDASYDVVLEK
☑	2365	600.0125	1797.0157	1797.0108	2.70	1	10	1.6e+002	1	IRLSSVSASVASSPAPLR
☑	886	599.8185	1197.6224	1197.6255	-2.51	0	10	3.5e+002	1	QQHSFVPSLR
☑	2629	1027.9980	2053.9814	2053.9738	3.71	0	10	5.5e+002	1	EIAAEQPAATVIACPDENR + Carbamidomethyl (C)
☑	3225	584.0555	2332.1929	2332.1845	3.60	1	10	4.7e+002	1	WKDLTENVNTMALNLTSQVR

☑	1378	657.2800	1312.5454	1312.5452	0.16	1	10	92	1	ESKMSESQEDK + Oxidation (M)
☑	2868	734.0755	2199.2047	2199.2124	-3.51	1	10	2.1e+002	1	LQADHAPRIITPLGNDTVIR
☑	2918	741.7457	2222.2153	2222.2205	-2.35	1	10	1.8e+002	1	MLAHRLDLVAGVSALTAEALR + Oxidation (M)
☑	471	512.7808	1023.5470	1023.5461	0.90	1	10	4.7e+002	1	NARDQPVPK
☑	2355	897.4875	1792.9604	1792.9584	1.15	1	10	3.4e+002	1	LAHNLKVQGNWLDSAK
☑	570	537.7559	1073.4972	1073.4989	-1.55	0	10	3.3e+002	1	TIDTDEQPR
☑	1034	615.8509	1229.6872	1229.6914	-3.38	1	10	5.4e+002	1	IMIVASRSTPR
☑	1401	440.2335	1317.6787	1317.6776	0.83	1	10	7.1e+002	1	ESEIKNLDGSVK
☑	3307	1191.5800	2381.1454	2381.1533	-3.31	0	10	5e+002	1	LGVTFTEKPNGDMLVSTQDGTR + Oxidation (M)
☑	3578	1150.8750	3449.6032	3449.5951	2.35	0	10	2.8e+002	1	SGMFMSCVPDVPCITPGTYAFLGAAAALSGVMR + 2 Carbamidomethyl (C); Oxidation (M)
☑	112	379.6955	757.3764	757.3793	-3.71	0	10	2.7e+002	1	SPCPQVK
☑	884	599.7954	1197.5762	1197.5738	2.05	0	10	3e+002	1	ASGAAPDQAASPR
☑	2402	605.6880	1814.0422	1814.0374	2.62	1	10	98	1	VNSTGVRTLGTQLLTVR
☑	2880	1102.1090	2202.2034	2202.2121	-3.92	1	10	2.3e+002	1	RTPGGAPITVAVTVDAASGLPPR
☑	2543	957.4607	1912.9068	1912.9135	-3.48	0	10	5.1e+002	1	HILNNECSILDIGCGAGK + Carbamidomethyl (C)
☑	579	541.2673	1080.5200	1080.5240	-3.69	0	10	5.5e+002	1	VTGDWQTFK
☑	729	568.7961	1135.5776	1135.5734	3.73	1	10	6.5e+002	1	YGGSIDNRVR
☑	1710	707.8038	1413.5930	1413.5943	-0.86	1	10	1.1e+002	1	RTDEYGGSMENR
☑	170	400.6928	799.3710	799.3725	-1.85	0	10	1.4e+002	1	SSGWHAR
☑	433	496.7922	991.5698	991.5702	-0.36	1	10	5.4e+002	1	SGIKAFELK
☑	1379	438.5647	1312.6723	1312.6697	1.98	0	10	4.4e+002	1	STLMPTPPSASPK
☑	524	528.7885	1055.5624	1055.5652	-2.56	0	10	6.2e+002	1	DLPSPFGPVK
☑	1572	681.8662	1361.7178	1361.7190	-0.88	0	10	7.8e+002	1	LAAEAGAQIEYVK
☑	2823	726.6998	2177.0776	2177.0739	1.67	1	10	5.5e+002	1	AKAEDILDTFEIVGGVDEEK
☑	839	589.8254	1177.6362	1177.6343	1.66	0	10	6.5e+002	1	TVSPSVNSFIK
☑	3518	1436.1560	2870.2974	2870.3062	-3.05	0	10	2.4e+002	1	YIANDTAEAVELQCTLAETQCNAASK + 2 Carbamidomethyl (C)
☑	572	537.8058	1073.5970	1073.5982	-1.05	1	10	4.3e+002	1	VSGWTKAAVR
☑	2745	717.0287	2148.0643	2148.0674	-1.43	0	10	6.1e+002	1	IDAFIVAEPFNAAGEMLAGGR
☑	3272	786.7270	2357.1592	2357.1539	2.22	1	10	6.2e+002	1	EEFEQEVKNVLPEFPVGDPR
☑	3331	1202.0220	2402.0294	2402.0276	0.76	1	10	1.1e+002	1	CPVCSHEVDPRDPVCPTCGFK + 2 Carbamidomethyl (C)
☑	3267	786.0490	2355.1252	2355.1205	1.97	0	10	5.2e+002	1	DGIPFTGFLYAGLMIDSNGDPR
☑	3446	1387.1350	2772.2554	2772.2591	-1.31	1	10	2.6e+002	1	GMMSDPNFLRVLQEMNCDEITLK + Carbamidomethyl (C); 2 Oxidation (M)
☑	1424	442.5773	1324.7101	1324.7139	-2.92	0	10	4.8e+002	1	QITLHDAPGVFK
☑	2492	939.9393	1877.8640	1877.8656	-0.84	1	10	3.9e+002	1	NAAGDFSLGKEGGHSEFR
☑	2326	889.4560	1776.8974	1776.8923	2.92	1	10	6.4e+002	1	FWFLCQHWLVDRK
☑	3158	769.7331	2306.1775	2306.1828	-2.30	1	10	5.6e+002	1	IDDEVIGPMLSVSGYRGIEIK + Oxidation (M)
☑	1092	625.3382	1248.6618	1248.6649	-2.41	1	10	6.8e+002	1	SAPIMQRVGYK
☑	2653	1037.9950	2073.9754	2073.9789	-1.69	1	10	5.1e+002	1	HSTPCGVALGDNVEEAYKK + Carbamidomethyl (C)
☑	1393	658.3666	1314.7186	1314.7197	-0.79	1	10	7.2e+002	1	SSIVPPFWARR
☑	1783	503.2618	1506.7636	1506.7637	-0.12	1	10	8e+002	1	AARATSASAAISSSEK
☑	3184	580.0557	2316.1937	2316.1936	0.03	1	10	5.1e+002	1	RVSFTLVGLAQSPEFIYSMR + Oxidation (M)
☑	3361	814.7934	2441.3584	2441.3563	0.83	0	10	1.3e+002	1	VIAVTLIVVVASLGAALAADAMSDR + Oxidation (M)
☑	2111	848.9290	1695.8434	1695.8477	-2.49	1	10	6.6e+002	1	GRVGEFPMTPIFAMK + Oxidation (M)
☑	2274	886.4466	1770.8786	1770.8723	3.60	1	10	6e+002	1	LMQEYTQNYIRAGGK
☑	3567	1133.1970	3396.5692	3396.5813	-3.57	0	10	2.7e+002	1	SNATLEMMQEIEQAAQGVIASYEDQVEQIR + Oxidation (M)
☑	2618	1020.9950	2039.9754	2039.9688	3.28	0	10	5.5e+002	1	AELPSAEAFVGSDVTESGFK
☑	2901	738.3646	2212.0720	2212.0794	-3.34	1	10	5.6e+002	1	MNQLTQANNTISQLDSKYK + Oxidation (M)
☑	2956	747.3555	2239.0447	2239.0427	0.89	0	10	4.6e+002	1	NICDNNEADLILTTGGTGFSK + Carbamidomethyl (C)
☑	3128	765.3922	2293.1548	2293.1550	-0.10	1	10	6e+002	1	TNKISPDEIAGATFTLTNTGSR
☑	1760	732.8138	1463.6130	1463.6133	-0.18	0	10	1.1e+002	1	DAACQGVAAGSVAACN + Carbamidomethyl (C)
☑	2676	1054.0160	2106.0174	2106.0238	-3.00	1	10	5.8e+002	1	MSVYLDPDVMKALSAHAAR + 2 Oxidation (M)
☑	3287	790.7386	2369.1940	2369.2015	-3.19	0	10	5.4e+002	1	LAFKPYETNVLSQQNQNTFK
☑	2195	868.9431	1735.8716	1735.8774	-3.34	1	10	6.4e+002	1	QKSAPALTCTVSSTSAK + Carbamidomethyl (C)
☑	2273	885.9718	1769.9290	1769.9345	-3.09	0	10	5.8e+002	1	QPSALLATLSKPCEANK
☑	2390	603.3413	1807.0021	1807.0026	-0.30	0	10	2.5e+002	1	VGLPEVGLGMIPGAGGIVR + Oxidation (M)
☑	3398	652.5824	2606.3005	2606.3051	-1.75	1	10	5.4e+002	1	GFQSSVSPILHFGLGKEDMVDSLK + Oxidation (M)
☑	734	568.7966	1135.5786	1135.5808	-1.88	1	10	5.4e+002	1	RAYVNPASMK
☑	1931	528.2721	1581.7945	1581.7998	-3.38	1	10	6.5e+002	1	LTYDEAKTLSANTR
☑	2467	619.6908	1856.0506	1856.0441	3.49	1	10	1.8e+002	1	VIMEGATLEPLKIVSTR
☑	2541	956.9438	1911.8730	1911.8785	-2.84	1	10	3.7e+002	1	GHPVKEAIWEAEEDMR + Oxidation (M)
☑	1442	444.5674	1330.6804	1330.6778	1.97	0	10	6.8e+002	1	MLPQVVWAMPK + 2 Oxidation (M)
☑	2431	611.0200	1830.0382	1830.0403	-1.18	1	10	1.3e+002	1	GLIFNKTLPLLDPYAR
☑	732	568.7965	1135.5784	1135.5803	-1.64	1	10	5.4e+002	1	IMIPMEKMK + Oxidation (M)
☑	2559	483.2863	1929.1161	1929.1155	0.32	0	10	90	1	LAAAIVCTMTIALLLSIR + Carbamidomethyl (C)
☑	2765	720.7272	2159.1598	2159.1613	-0.70	0	10	3.4e+002	1	DTAVILLEEIDLISDPYLK
☑	3235	1170.1230	2338.2314	2338.2290	1.05	1	10	4e+002	1	AFGPSMRVLGCGSITLIAGLFR + Carbamidomethyl (C); Oxidation (M)
☑	1982	810.7968	1619.5790	1619.5803	-0.78	0	10	3.9	1	DPYCAWDGMSCSR + 2 Carbamidomethyl (C); Oxidation (M)
☑	2849	1095.5170	2189.0194	2189.0205	-0.47	0	10	4.4e+002	1	FADDSYVDSYISTIGVYFK
☑	3175	579.5274	2314.0805	2314.0825	-0.87	0	10	5e+002	1	DIQWAAQNAIAEQVEESAADR
☑	3383	835.0952	2502.2638	2502.2577	2.44	1	10	5.4e+002	1	EGESMVLPLFLNGWLAVNKDDR
☑	2480	623.6350	1867.8832	1867.8873	-2.23	1	10	5.2e+002	1	FTKLQTADSEIPMEDK + Oxidation (M)
☑	1115	627.7689	1253.5232	1253.5268	-2.82	0	10	1.6e+002	1	EMSDMSAPSGVK + Oxidation (M)
☑	1938	528.2725	1581.7957	1581.8007	-3.19	1	10	6.8e+002	1	APGMSVGSKIITFCR + Oxidation (M)
☑	105	378.7225	755.4304	755.4290	1.96	0	10	7.2e+002	1	ATPVAAAR
☑	2499	941.9584	1881.9022	1881.8998	1.29	0	10	5.8e+002	1	AMLINMILADSIQMDR + 3 Oxidation (M)
☑	3215	1165.6300	2329.2454	2329.2538	-3.57	1	10	3.6e+002	1	AIVMPNLVPPVTTIEMAKAYR + Oxidation (M)
☑	269	436.7751	871.5356	871.5378	-2.52	1	10	3.6e+002	1	VLLKIESA
☑	3131	1150.0620	2298.1094	2298.1123	-1.26	0	10	5.5e+002	1	DMLITNGFTEGLDIVLSAMDK + Oxidation (M)
☑	2616	1014.4990	2026.9834	2026.9895	-2.97	1	10	6e+002	1	SPHGCDVSPDGRYIIIGGK + Carbamidomethyl (C)
☑	837	589.8237	1177.6328	1177.6356	-2.35	1	10	5.9e+002	1	DKHPVQWLR
☑	2778	723.0307	2166.0703	2166.0692	0.52	1	10	6.5e+002	1	VEEKLLEAGTITYEEEASR
☑	3488	943.7700	2828.2882	2828.2892	-0.35	1	10	2.9e+002	1	CSETVTAGRSGTMGDIDAMAVGLTAWR + Carbamidomethyl (C); Oxidation (M)
☑	2701	1063.9920	2125.9694	2125.9700	-0.26	1	10	3.8e+002	1	DLYMVKDSELYAAFSQCK + Oxidation (M)
☑	3302	1188.5900	2375.1654	2375.1613	1.73	1	10	6e+002	1	HAEMVGLKSDFTILGMDDQLR
☑	2886	736.0341	2205.0805	2205.0736	3.13	0	10	6.7e+002	1	DLDDLSAGLFGQANIMVAEAR
☑	3054	759.4218	2275.2436	2275.2497	-2.70	1	10	2.4e+002	1	LIFPTIATAIIIACGGSTEEKK
☑	3152	577.0472	2304.1597	2304.1532	2.82	1	10	6.2e+002	1	AVGDESMPGAANRLAFLETALR + Oxidation (M)
☑	2600	668.9991	2003.9755	2003.9808	-2.68	0	10	6.4e+002	1	AVHGQPYEEVLSMMLLR + 2 Oxidation (M)

☑	3555	992.8141	2975.4205	2975.4126	2.66	0	10	4.5e+002	1	YSHVMHIVSNVEGMLKPGMSNMDVLR + 2 Oxidation (M)
☑	1098	625.3386	1248.6626	1248.6649	-1.77	1	10	4.9e+002	1	TAGMSPALFRAK
☑	614	547.3022	1092.5898	1092.5927	-2.65	0	10	7.2e+002	1	AFTSQSLALR
☑	2160	862.4102	1722.8058	1722.8029	1.71	1	9	5.4e+002	1	ALGLDMDASGGGMGTRSK
☑	2612	1012.5000	2022.9854	2022.9793	3.05	0	9	6.7e+002	1	MSATSGVPARPDLPDDAPAR
☑	3372	824.1249	2469.3529	2469.3591	-2.51	1	9	1.9e+002	1	AVLIPINTYQNISQELIKQER
☑	2905	1108.0120	2214.0094	2214.0087	0.32	1	9	3.8e+002	1	MAIGLLTPCLDCRICSSSCR + Carbamidomethyl (C); Oxidation (M)
☑	2771	1082.0470	2162.0794	2162.0790	0.21	1	9	7.2e+002	1	VCDAVGKPVYIAGSIDREDR
☑	3296	792.0809	2373.2209	2373.2151	2.44	1	9	5.2e+002	1	TARFDAIGLVVADMAASLAFYR + Oxidation (M)
☑	2161	862.4573	1722.9000	1722.9053	-3.06	1	9	6.7e+002	1	NSYAVGERVIVVFDR
☑	2882	1102.5610	2203.1074	2203.1155	-3.64	1	9	6.3e+002	1	ADLEIVVAGTRDGITMVEGGGK + Oxidation (M)
☑	656	558.3369	1114.6592	1114.6598	-0.46	0	9	2.7e+002	1	LSEQVVSILK
☑	1567	680.8774	1359.7402	1359.7411	-0.65	1	9	6.9e+002	1	LNWPSLRTFAR
☑	2001	548.9030	1643.6872	1643.6919	-2.89	1	9	1.3e+002	1	GYQKAMEEMSSPDR + Oxidation (M)
☑	1060	621.2873	1240.5600	1240.5580	1.64	0	9	3.4e+002	1	MTEASWTMLR + Oxidation (M)
☑	2252	586.6395	1756.8967	1756.9029	-3.54	1	9	6.8e+002	1	EEIELICTAPVKEQR
☑	1606	687.8858	1373.7570	1373.7555	1.15	0	9	4.8e+002	1	DLLNITTVNFKP
☑	2448	921.4337	1840.8528	1840.8492	1.96	1	9	4.8e+002	1	YHQYDPGRYLSEGTR
☑	2491	938.9201	1875.8256	1875.8196	3.21	1	9	2.5e+002	1	FTIYAQEMDDEENKK + Oxidation (M)
☑	2639	688.3641	2062.0705	2062.0735	-1.46	1	9	6.3e+002	1	FPVLNASFDEERGEIVLK
☑	1094	625.3383	1248.6620	1248.6601	1.53	1	9	7e+002	1	LKEYQVEVIE
☑	1089	625.3380	1248.6614	1248.6615	-0.04	0	9	7.7e+002	1	TGLAHYALFTR
☑	1602	686.8781	1371.7416	1371.7398	1.34	1	9	7e+002	1	ELGYPVVADKGPK
☑	3038	1135.6360	2269.2574	2269.2543	1.41	1	9	1.8e+002	1	SVTVHLTPAGDELRAAALPVPR
☑	44	361.1907	720.3668	720.3667	0.19	0	9	8.1e+002	1	PGPSHAR
☑	1585	683.8522	1365.6898	1365.6889	0.72	0	9	6.7e+002	1	TADGDTPGPLPAVR
☑	1996	818.9788	1635.9430	1635.9382	2.98	1	9	1.4e+002	1	KSLHTCLPPSLISIK
☑	2401	907.5311	1813.0476	1813.0495	-1.03	0	9	1e+002	1	MIGLISLGLSAIAGAAVTR
☑	3047	758.7443	2273.2111	2273.2168	-2.51	1	9	3.9e+002	1	SLYFEAAAVLSGPLHAGSLKSR
☑	2383	601.3562	1801.0468	1801.0461	0.36	1	9	75	1	LVIALGYAKASDSLRPK
☑	2524	950.9265	1899.8384	1899.8455	-3.71	0	9	2.8e+002	1	MSTDIPQPNPQPGMAER + 2 Oxidation (M)
☑	3103	573.5523	2290.1801	2290.1735	2.89	1	9	5.7e+002	1	TKQPINSMPIIVNLDVMMAK + 3 Oxidation (M)
☑	3407	884.4418	2650.3036	2650.2973	2.35	1	9	6e+002	1	EKITSPNGTTQAAIETLDEYNVEK
☑	3457	697.8240	2787.2669	2787.2633	1.30	0	9	3.1e+002	1	TMQEFRPDGWFITGDIVTMAEDGR + Oxidation (M)
☑	1738	717.8888	1433.7630	1433.7626	0.28	1	9	6.2e+002	1	GALGAETLDIYRR
☑	1736	717.8776	1433.7406	1433.7435	-2.01	0	9	8e+002	1	LIASNSMIIESEK
☑	2700	1063.9910	2125.9674	2125.9674	0.04	1	9	3.9e+002	1	NGLTSYGAYGCHCGVGGKGTPK
☑	673	561.3194	1120.6242	1120.6240	0.20	1	9	5.9e+002	1	SLSAAFKEIR
☑	2687	1056.4860	2110.9574	2110.9511	3.02	0	9	3.6e+002	1	STLTDAQLGNADMEMTLER + Oxidation (M)
☑	3348	808.4061	2422.1965	2422.1879	3.55	1	9	6.7e+002	1	YAVQEVTFEACTLSYKGIWSK
☑	2512	945.9789	1889.9432	1889.9371	3.26	0	9	7.3e+002	1	IVPATPTTSDTGVYPESR
☑	2680	703.3400	2106.9982	2106.9939	2.05	1	9	6e+002	1	LMEMNNLRSAQDLWAGSR + Oxidation (M)
☑	169	400.2189	798.4232	798.4236	-0.42	0	9	5.8e+002	1	SGITVSVH
☑	1777	750.3598	1498.7050	1498.7099	-3.27	1	9	4.9e+002	1	DFRVNTCTPHPR + Carbamidomethyl (C)
☑	2352	896.9230	1791.8314	1791.8250	3.60	1	9	5.2e+002	1	GAYDDDFLMRLAAYR + Oxidation (M)
☑	2772	721.7006	2162.0800	2162.0864	-2.98	1	9	7.3e+002	1	VQNSVFECVVDPGQCKLLK + Carbamidomethyl (C)
☑	2914	740.3566	2218.0480	2218.0510	-1.38	0	9	5.8e+002	1	GYPHAELSLILENNTMMNR + Oxidation (M)
☑	2378	901.0207	1800.0268	1800.0257	0.61	1	9	1.4e+002	1	IGALISQLERDVFLAR
☑	2466	619.6907	1856.0503	1856.0519	-0.90	1	9	2e+002	1	NIPEYQGALGALRTILK
☑	2697	1063.5000	2124.9854	2124.9820	1.63	1	9	5.1e+002	1	DLDPKYANITMQMPSDVR + 2 Oxidation (M)
☑	3053	759.4177	2275.2313	2275.2358	-2.01	1	9	3.1e+002	1	LSGPLPISRGSTPGLDMLVHTK
☑	2930	1114.5440	2227.0734	2227.0790	-2.51	0	9	6.3e+002	1	LLQQMLKPGSDPDEGDEALR + Oxidation (M)
☑	3133	767.4308	2299.2706	2299.2702	0.16	1	9	2e+002	1	TVGPARALLWGGLTVVYHHPR
☑	3041	757.4300	2269.2682	2269.2695	-0.58	0	9	1.5e+002	1	LLNVGPWATLALANPSLLHNR
☑	2446	920.5159	1839.0172	1839.0115	3.14	1	9	3.3e+002	1	ARQQLIQTLINYHNK
☑	2857	1097.0270	2192.0394	2192.0321	3.37	1	9	6.3e+002	1	IISDRGTSFTSNAFQNFCK + Carbamidomethyl (C)
☑	2404	908.5202	1815.0258	1815.0241	0.98	1	9	1.9e+002	1	TSIVIDELIKDITVEK
☑	3362	816.1240	2445.3502	2445.3494	0.31	0	9	2e+002	1	MIVEALLFLVWLVVLSWGADR + Oxidation (M)
☑	1914	788.8718	1575.7290	1575.7311	-1.28	1	9	5.4e+002	1	QMAAEREAAAEDIR + Oxidation (M)
☑	3527	721.3070	2881.1989	2881.1890	3.43	0	9	64	1	CIADPMMCPYYHSQCPFSTTVTGTGV + Carbamidomethyl (C); Oxidation (M)
☑	1102	625.3395	1248.6644	1248.6649	-0.35	1	9	6.4e+002	1	MPVAQGRFTVK + Oxidation (M)
☑	3140	1151.1400	2300.2654	2300.2739	-3.69	1	9	2.1e+002	1	ERLPGDQALAEIGLEPLALAPK
☑	1661	464.9290	1391.7652	1391.7660	-0.61	0	9	4.6e+002	1	TLTLGAYPQTSLK
☑	3031	756.4149	2266.2229	2266.2182	2.04	1	9	3.5e+002	1	AFVDATGQVDVVAHSRGGLIVR
☑	512	525.7889	1049.5632	1049.5618	1.38	1	9	7.3e+002	1	RSDGTVFLR
☑	32	352.6890	703.3634	703.3653	-2.67	0	9	1.6e+003	1	GGGSWLK
☑	2429	611.0189	1830.0349	1830.0325	1.32	0	9	1.8e+002	1	LEIHTYLNMILLTIK + Oxidation (M)
☑	2657	1041.0070	2079.9994	2080.0014	-0.94	1	9	6.1e+002	1	DIKWVVIGDWNYGEGSSR
☑	3043	757.7580	2270.2522	2270.2562	-1.79	0	9	2e+002	1	VVGYYAIATGAVELVDVPPPLK
☑	2931	743.3657	2227.0753	2227.0799	-2.08	1	9	6.7e+002	1	RMEVLDASNNLIVCLCAGYK + Oxidation (M)
☑	2314	887.8767	1773.7388	1773.7419	-1.71	0	9	1.3e+002	1	EEPRPGACPMGCAPMR + Carbamidomethyl (C); Oxidation (M)
☑	317	456.7718	911.5290	911.5301	-1.14	1	9	2.5e+002	1	VRRPQVSA
☑	3418	920.0944	2757.2614	2757.2704	-3.28	1	9	3.6e+002	1	ENQEKLFQFMDSGNFRPIGEDEK
☑	2374	600.6850	1799.0332	1799.0339	-0.41	1	9	1.6e+002	1	MRGAVVVSAPLSGVTVLK + Oxidation (M)
☑	1706	707.3113	1412.6080	1412.6024	4.00	1	9	2.6e+002	1	KQSSMSMTDPNR + 2 Oxidation (M)
☑	2490	469.5225	1874.0609	1874.0625	-0.86	1	9	1.4e+002	1	AIQLFSERAATVLNLTK
☑	3375	825.8004	2474.3794	2474.3744	2.01	1	9	1.4e+002	1	GDISSTILQSLELAKQIINYLR
☑	314	455.7660	909.5174	909.5144	3.31	1	9	4.4e+002	1	GHKNIVSR
☑	2848	1094.5030	2186.9914	2186.9949	-1.60	1	9	4.2e+002	1	SCQQGSWPTHNTECVNLKR
☑	1953	796.3636	1590.7126	1590.7097	1.87	0	9	3.2e+002	1	DVNPVQPDMGNFSR + Oxidation (M)
☑	1035	616.2488	1230.4830	1230.4823	0.63	0	9	64	1	MTAENDTYDR + Oxidation (M)
☑	1173	637.2814	1272.5482	1272.5470	1.01	0	9	2.5e+002	1	GEAESPGSEPEGK
☑	3381	1249.1300	2496.2454	2496.2496	-1.68	1	9	6.9e+002	1	NVEVSIIDKAWDTGDVAPSVPER
☑	578	540.7600	1079.5054	1079.5029	2.32	0	9	5.5e+002	1	MSQSTQINR + Oxidation (M)
☑	2576	979.0339	1956.0532	1956.0602	-3.54	1	9	4.9e+002	1	ADDIKDLLSMVGGAPVVIK + Oxidation (M)
☑	1595	457.9128	1370.7166	1370.7154	0.88	1	9	7.8e+002	1	AEAAKPVTKADDR
☑	3246	781.7665	2342.2777	2342.2706	3.03	1	9	2.7e+002	1	ALEPEIGLQAALARQHEELVR
☑	2908	739.3756	2215.1050	2215.1096	-2.07	1	9	7.8e+002	1	LGGYREIVFVGFNALNSCEK

☑	3165	770.7161	2309.1265	2309.1355	-3.92	1	9	7e+002	1	NRLNTSECLTLGDVTTVNMTK
☑	2482	935.9390	1869.8634	1869.8680	-2.41	0	9	5.2e+002	1	NCYTFALNPLGTQTDR + Carbamidomethyl (C)
☑	3276	787.3970	2359.1692	2359.1604	3.72	0	9	7.1e+002	1	ATVDARPGLDCQRPSPHTPWR
☑	2241	876.9747	1751.9348	1751.9305	2.49	1	9	5.8e+002	1	ALIEHDVEIEEISKK
☑	3125	764.7548	2291.2426	2291.2381	1.95	0	9	3.2e+002	1	ATATTMCTLYLALPLGAALALR + Carbamidomethyl (C)
☑	2534	954.9529	1907.8912	1907.8903	0.49	1	9	6e+002	1	GSINEMMKMKPQDVER + Oxidation (M)
☑	2925	1113.5400	2225.0654	2225.0604	2.26	0	9	7.1e+002	1	MMSSISMLISVAFYTIMER + Oxidation (M)
☑	851	395.8795	1184.6167	1184.6124	3.57	1	9	6.9e+002	1	RFQYTCLVR
☑	1085	625.3376	1248.6606	1248.6570	2.90	0	9	9.2e+002	1	VITTGGGGMILCK
☑	2214	583.3247	1746.9523	1746.9529	-0.38	0	9	3.9e+002	1	VAPTDHRPVAPTIAFR
☑	2762	720.3680	2158.0822	2158.0881	-2.75	1	9	7.7e+002	1	MKQERPLYFTGVDVYQGK
☑	3208	775.6856	2324.0350	2324.0373	-0.99	1	9	3.1e+002	1	QGDSGELAKCSGQMTDQVADLR + Oxidation (M)
☑	2472	929.4429	1856.8712	1856.8653	3.21	1	9	6e+002	1	NAVSGYAGGKADTAQYER
☑	1398	658.8453	1315.6760	1315.6772	-0.88	1	9	1e+003	1	DKFSYSSLTIR
☑	3219	1167.0790	2332.1434	2332.1477	-1.81	1	9	8.6e+002	1	AQPCLLDLDKAPTSQTLCLCLS
☑	538	531.8177	1061.6208	1061.6233	-2.32	1	9	5e+002	1	VKSGAAFLAAK
☑	2670	700.6761	2099.0065	2098.9993	3.40	1	9	7.7e+002	1	MFIDVGNQNNATIEDYKK
☑	1649	464.2571	1389.7495	1389.7537	-3.06	1	9	6.9e+002	1	DAMLQELSVLKK + Oxidation (M)
☑	3017	754.0870	2259.2392	2259.2348	1.92	0	9	2.6e+002	1	QAVRPHIQPPAAQEIQHIAR
☑	3264	783.7390	2348.1952	2348.1868	3.55	1	9	7e+002	1	LPYVVMELVDGQSLDDMLRR
☑	912	403.5070	1207.4992	1207.4961	2.51	0	9	1.4e+002	1	CEACIAVDDNR
☑	1101	625.3392	1248.6638	1248.6687	-3.89	1	9	6.7e+002	1	PQTLARQNGHK
☑	2597	998.0324	1994.0502	1994.0506	-0.19	0	9	5.7e+002	1	MIINAVEDLVEGINALHK + Oxidation (M)
☑	2957	747.7091	2240.1055	2240.1048	0.30	0	9	7.3e+002	1	SNILCEFPYNGHEHIALVK + Carbamidomethyl (C)
☑	3172	772.0594	2313.1564	2313.1497	2.88	1	9	7.5e+002	1	NPFVLNDIFTSCSCLQLSKK + Carbamidomethyl (C)
☑	3506	948.4318	2842.2736	2842.2803	-2.36	1	9	2.7e+002	1	TNPSGEATMWGDYHMREVALYVQR + 2 Oxidation (M)
☑	316	456.6906	911.3666	911.3663	0.35	0	9	1.7e+002	1	VCCTSMPR + Oxidation (M)
☑	154	394.7186	787.4226	787.4228	-0.24	0	9	3.9e+002	1	DILGGWK
☑	2419	913.0214	1824.0282	1824.0298	-0.84	1	9	2.3e+002	1	VLFSSAQGLYFLVPKR
☑	2540	956.5259	1911.0372	1911.0327	2.40	0	9	4.7e+002	1	QLQTVVLQNGIWTQQR
☑	1464	668.8124	1335.6102	1335.6055	3.57	1	9	5.7e+002	1	DAVEQAYAERGQ
☑	502	522.7642	1043.5138	1043.5135	0.32	1	9	5.9e+002	1	DDLVGSPKDV
☑	3410	908.7512	2723.2318	2723.2254	2.33	1	9	3.6e+002	1	RNAWCGSVGYISFCGNMDTSITIR + Carbamidomethyl (C); Oxidation (M)
☑	927	404.8951	1211.6635	1211.6662	-2.28	1	9	5.8e+002	1	KKPHEIGFEK
☑	3045	758.0483	2271.1231	2271.1280	-2.15	0	9	8e+002	1	LDVTGFSMTGKPGIICVEGFK + Carbamidomethyl (C); Oxidation (M)
☑	3205	581.5508	2322.1741	2322.1712	1.26	1	9	7.4e+002	1	LSVAVVVNYCLNADGKAQPMSK + Oxidation (M)
☑	2003	824.8816	1647.7486	1647.7497	-0.66	1	9	4.4e+002	1	CHPSLSADCRDLFK + Carbamidomethyl (C)
☑	2315	887.8988	1773.7830	1773.7880	-2.78	0	9	3.3e+002	1	ETGCGSLEFDISVFDR
☑	3531	962.7766	2885.3080	2885.2974	3.67	1	9	3.5e+002	1	GERTDGHCYVSNVFQQGASWVMVSR + Carbamidomethyl (C); Oxidation (M)
☑	475	513.2724	1024.5302	1024.5342	-3.82	0	9	9.8e+002	1	VEGFAAIYR
☑	3250	1173.5880	2345.1614	2345.1646	-1.36	1	9	7.4e+002	1	YISYLAEMGMAEIVNNSKLAL + Oxidation (M)
☑	473	513.2546	1024.4946	1024.4938	0.85	0	9	5.7e+002	1	DGDPAAGPGLR
☑	1093	625.3382	1248.6618	1248.6575	3.49	0	9	9.3e+002	1	DRPVLGPDGAPR
☑	2264	882.5006	1762.9866	1762.9869	-0.15	1	9	2.3e+002	1	ETELWVLVPKEPVPK
☑	1619	689.8194	1377.6242	1377.6194	3.50	1	8	4.7e+002	1	DGQEKNAVECTK + Carbamidomethyl (C)
☑	1722	476.2469	1425.7189	1425.7174	1.06	1	8	8e+002	1	MLEVKGLDTGYGK + Oxidation (M)
☑	167	399.6818	797.3490	797.3490	0.04	0	8	1.8e+002	1	EMTHHK + Oxidation (M)
☑	2527	476.2846	1901.1093	1901.1019	3.87	1	8	67	1	MTTLAIKNIGILVSGNIK + Oxidation (M)
☑	3100	573.5522	2290.1797	2290.1805	-0.34	0	8	7.1e+002	1	AITADVLALHGIEPDEETIQR
☑	2741	716.3682	2146.0828	2146.0836	-0.40	1	8	8e+002	1	CPKVVSPSVCSILSDTPVMK + Carbamidomethyl (C)
☑	2874	734.3520	2200.0342	2200.0430	-3.99	1	8	5.9e+002	1	PELDQALAEVAAEMAERSDR
☑	2907	739.3741	2215.1005	2215.0952	2.39	1	8	8.1e+002	1	CDGPCALPLHQLKAFLSQMK + Oxidation (M)
☑	1490	671.8884	1341.7622	1341.7616	0.47	0	8	5.8e+002	1	QLVEATGSGVLLR
☑	3260	587.8082	2347.2037	2347.2060	-0.97	1	8	6.8e+002	1	DPFPYLTTKQPLDLQISTDR
☑	1386	658.3287	1314.6428	1314.6424	0.33	0	8	7.5e+002	1	SLDPMPMQQLR
☑	1994	817.8755	1633.7364	1633.7406	-2.56	0	8	4.2e+002	1	SGYGCLEVGDLPDPR + Carbamidomethyl (C)
☑	2748	717.0663	2148.1771	2148.1725	2.14	1	8	3.2e+002	1	VRLSITSAALAATMFSGLPAR + Oxidation (M)
☑	2764	1080.0510	2158.0874	2158.0915	-1.87	1	8	8.9e+002	1	HVIDMLVGDMQRVIEYPK + Oxidation (M)
☑	2443	919.5118	1837.0090	1837.0131	-2.23	0	8	3.8e+002	1	LGLPADLINTGMPQIIR + Oxidation (M)
☑	2608	1010.4810	2018.9474	2018.9415	2.97	1	8	6.9e+002	1	IPHCKMSPSQVDNQNHK + Carbamidomethyl (C)
☑	633	552.3026	1102.5906	1102.5883	2.11	0	8	1.2e+003	1	ILAEDHLHR
☑	747	571.3023	1140.5900	1140.5927	-2.36	0	8	6.9e+002	1	NEVIPEVWR
☑	2573	978.4679	1954.9212	1954.9153	3.03	0	8	6.9e+002	1	ELSQSESGIINTTSSQMK + Oxidation (M)
☑	3252	1174.0780	2346.1414	2346.1496	-3.47	0	8	7.9e+002	1	SFILALLCLMVAGVMDMFDGK + Carbamidomethyl (C); Oxidation (M)
☑	3317	797.7309	2390.1709	2390.1675	1.40	0	8	8.3e+002	1	ALQEADVQLIGGDLDEAPMVYK + Oxidation (M)
☑	3091	1144.6090	2287.2034	2287.1954	3.51	1	8	6e+002	1	RTVTVALLLAAASAGCGEPTSSGR
☑	2422	610.0285	1827.0637	1827.0652	-0.82	1	8	94	1	MSSVKLVAPLSGSIVALR
☑	2501	471.7445	1882.9489	1882.9425	3.41	0	8	8.6e+002	1	KPTPDFLGAEEEQPGLR
☑	3274	786.7693	2357.2861	2357.2856	0.21	1	8	3.2e+002	1	QDPVEVLRQAIAGGITLFQFR
☑	163	397.7060	793.3974	793.3970	0.54	0	8	1.7e+003	1	YGGVPSSK
☑	1841	764.8267	1527.6388	1527.6399	-0.67	0	8	1.8e+002	1	YEPMQDEESGSLK + Oxidation (M)
☑	3228	778.7159	2333.1259	2333.1243	0.69	0	8	7.4e+002	1	DLGEAMVGINEQEIALLMAER + 2 Oxidation (M)
☑	3387	1262.1550	2522.2954	2522.2864	3.60	1	8	6.1e+002	1	QAELTKGNAQSGLELSVIDAYTSK
☑	1117	628.3825	1254.7504	1254.7547	-3.39	0	8	2.2e+002	1	SAEALAALLGVLK
☑	1715	473.2239	1416.6499	1416.6521	-1.57	0	8	5.4e+002	1	YDTESQATIYAR
☑	2681	703.3403	2106.9991	2107.0010	-0.93	1	8	7.2e+002	1	NSKSFNANFGLEYFLNDK
☑	2704	710.0092	2127.0058	2127.0089	-1.45	0	8	7.4e+002	1	CLLTMLGESDPSNLGHQGAGK
☑	896	401.8419	1202.5039	1202.5051	-1.04	0	8	1.6e+002	1	IDDSSPDSDPR
☑	3124	1146.6240	2291.2334	2291.2307	1.19	1	8	4.2e+002	1	NNAAPILLIKSCSGLGPAVTAPQ + Carbamidomethyl (C)
☑	3405	878.4470	2632.3192	2632.3167	0.96	1	8	8e+002	1	VQPGGLRFEITESLIMEDIDQAR + Oxidation (M)
☑	944	609.2515	1216.4884	1216.4852	2.63	0	8	1.1e+002	1	SECMDYIGSR + Carbamidomethyl (C)
☑	1781	752.8578	1503.7010	1503.6987	1.54	0	8	6.9e+002	1	AAPGNDALICSTSER
☑	2017	552.6696	1654.9870	1654.9909	-2.38	1	8	86	1	LEYPELKLLPVTLK
☑	3211	1164.1480	2326.2814	2326.2896	-3.50	0	8	2.7e+002	1	LIVIAAALAAAGAVLSAAAFAQASDA
☑	2665	698.0128	2091.0166	2091.0246	-3.85	1	8	8.9e+002	1	GALGTGGPADGVRAAAWQHDGK
☑	2890	736.3625	2206.0657	2206.0650	0.32	0	8	8.8e+002	1	EYQSLMILSASSCSGIGLFK + Carbamidomethyl (C); Oxidation (M)
☑	2767	1081.0560	2160.0974	2160.0963	0.51	1	8	7.5e+002	1	AAVAPYDTVGPDYRAPSLAAR
☑	1771	744.9085	1487.8024	1487.7984	2.74	1	8	7.4e+002	1	DLYEKLLPVADGR

☑	2498	628.3076	1881.9010	1881.8956	2.86	0	8	8.3e+002	1	SISDQAISEADIFGNTSK
☑	2425	610.6884	1829.0434	1829.0370	3.47	1	8	1.6e+002	1	AITEAIQTRLTLISGSR
☑	3196	1160.0820	2318.1494	2318.1511	-0.72	0	8	8.8e+002	1	DQCLHNLSLLPPPTELVCNR + Carbamidomethyl (C)
☑	2139	572.9629	1715.8669	1715.8690	-1.23	0	8	9.8e+002	1	SSQAADQVEIQQVSVK
☑	2500	471.7438	1882.9461	1882.9458	0.14	0	8	8.7e+002	1	IDPAALAVSNTPAEVEMR
☑	3099	573.5520	2290.1789	2290.1726	2.75	1	8	7.8e+002	1	DMVLDTLASTELSEADKALLR
☑	3558	997.4744	2989.4014	2989.3949	2.18	1	8	6.2e+002	1	IMSQGTDGEVAGVVNSHDDKDHVHGTIR + Oxidation (M)
☑	2035	837.4655	1672.9164	1672.9195	-1.83	0	8	5.7e+002	1	NTALAMGVIAGLIHHR
☑	2636	687.6863	2060.0371	2060.0394	-1.14	1	8	9e+002	1	AASPKAIESGIMVGMVAADAR + Oxidation (M)
☑	2994	750.0356	2247.0850	2247.0875	-1.13	1	8	8.1e+002	1	GVPEGNLVSLDCPMTSEISRK + Oxidation (M)
☑	3380	832.4516	2494.3330	2494.3391	-2.46	1	8	3.9e+002	1	TEERAIDALAPVSVVTLEQIQGR
☑	2847	729.7465	2186.2177	2186.2212	-1.60	1	8	2.3e+002	1	ITSFTIDHLRLLPGVYVSR
☑	3098	573.5515	2290.1769	2290.1780	-0.47	1	8	7.8e+002	1	EVILNAKQHDVQFIFMGASK + Oxidation (M)
☑	3408	888.7836	2663.3290	2663.3224	2.46	0	8	8e+002	1	NAIVTEAGNCRPINEIAEEEPPLK + Carbamidomethyl (C)
☑	2372	600.6846	1799.0320	1799.0347	-1.53	1	8	1.9e+002	1	MGRVMLLAPVLMLLAR + Oxidation (M)
☑	3201	1162.0590	2322.1034	2322.1031	0.14	1	8	7.8e+002	1	FRMGAMINQLCDVLGPGQQR + Carbamidomethyl (C); 2 Oxidation (M)
☑	3370	821.4658	2461.3756	2461.3832	-3.09	1	8	1.6e+002	1	LFPSPEAPLIAGILVGDEAKIPSK
☑	2755	718.6741	2153.0005	2152.9960	2.08	1	8	6.3e+002	1	MFNLDNELPTPDAHPDRR + Oxidation (M)
☑	1732	477.6013	1429.7821	1429.7830	-0.65	1	8	7.9e+002	1	ALGFKLLNDHFR
☑	2777	1084.0230	2166.0314	2166.0350	-1.65	0	8	8.1e+002	1	VFVMGHSAGAYNAAMVALDAR + Oxidation (M)
☑	3243	1172.1450	2342.2754	2342.2715	1.69	1	8	3.6e+002	1	NRLIGGGVAAALAGGAFALMPMLR + Oxidation (M)
☑	206	412.7106	823.4066	823.4076	-1.13	0	8	1.1e+003	1	SVAAPPPAD
☑	1383	657.8199	1313.6252	1313.6286	-2.52	0	8	8.9e+002	1	ITGLDMPDGPNGK
☑	2780	723.0322	2166.0748	2166.0766	-0.83	0	8	9.1e+002	1	GAVEEILSICSYIEIDGEVK
☑	208	413.2395	824.4644	824.4617	3.37	1	8	5.4e+002	1	AHSVKQR
☑	2247	878.4777	1754.9408	1754.9427	-1.08	1	8	7.2e+002	1	VSVAHNTADFIALNRK
☑	449	504.2675	1006.5204	1006.5191	1.34	0	8	1.2e+003	1	LIAMDMLGK + Oxidation (M)
☑	2575	652.7177	1955.1313	1955.1237	3.85	1	8	1.1e+002	1	LTRVTGAGCALGALIAALLAT
☑	2953	745.3786	2233.1140	2233.1226	-3.89	1	8	9e+002	1	DNDGYSKHQVTTVLETSVLK
☑	1043	617.7532	1233.4918	1233.4940	-1.77	1	8	66	1	GMCYGMEGKSR + Oxidation (M)
☑	3230	778.7259	2333.1559	2333.1474	3.64	1	8	1e+003	1	AAEPMVARETAYYEAHIGQVK
☑	19	631.3667	630.3594	630.3588	0.95	0	8	2e+003	1	LSAVLE
☑	1775	497.9113	1490.7121	1490.7100	1.39	1	8	7.6e+002	1	LDKEEEESGQTVK
☑	3121	573.5538	2290.1861	2290.1917	-2.45	1	8	7.2e+002	1	LTEDNTAGKILGYNGGVVNSLR
☑	3290	792.0588	2373.1546	2373.1576	-1.27	0	8	8.8e+002	1	GLYQGFNVSSGYYHLPSCLLR
☑	1078	623.7543	1245.4940	1245.4979	-3.08	0	8	76	1	QMQSDHCANR + Carbamidomethyl (C)
☑	1673	699.3541	1396.6936	1396.6987	-3.59	0	8	9.9e+002	1	LLDAVFGADYASR
☑	2840	1093.5120	2185.0094	2185.0031	2.91	1	8	5.9e+002	1	DDNLEVAMSLLDKAMEYGR + Oxidation (M)
☑	3472	703.3112	2809.2157	2809.2153	0.14	0	8	1.8e+002	1	NCTTTAMGSAAAQTPVHCPGCGTPHAPR + Carbamidomethyl (C); Oxidation (M)
☑	2683	703.3410	2107.0012	2107.0069	-2.73	0	8	8.5e+002	1	ADLVPGSLASEVYGATSADER
☑	1705	706.8924	1411.7702	1411.7745	-2.99	1	8	6.7e+002	1	MTKSLFIITGASK + Oxidation (M)
☑	2696	1062.4930	2122.9714	2122.9710	0.19	1	8	5.7e+002	1	MDCCARHPAVQEIPLGDPR + Oxidation (M)
☑	3462	1398.6410	2795.2674	2795.2702	-0.97	1	8	4.3e+002	1	MAQEGTSTSPGSLEVTAAELAECRADR + Oxidation (M)
☑	2197	869.9011	1737.7876	1737.7888	-0.67	0	8	5.3e+002	1	HCINMMDEAFTLLGK + Oxidation (M)
☑	1642	693.8654	1385.7162	1385.7150	0.87	0	8	9.8e+002	1	LQQPAGPSSSISSK
☑	2239	876.9346	1751.8546	1751.8512	1.96	1	8	1e+003	1	VNTNNKLMTEYGPQK + Oxidation (M)
☑	1465	669.3448	1336.6750	1336.6735	1.15	1	8	8e+002	1	SSLNGKLDFSNR
☑	334	464.2543	926.4940	926.4934	0.72	1	8	8.9e+002	1	PSGTKGPQR
☑	2867	734.0751	2199.2035	2199.2007	1.27	1	8	3.2e+002	1	VIPIQITEAAVEMVKAGMGVK + Oxidation (M)
☑	205	412.6900	823.3654	823.3680	-3.15	0	8	5.7e+002	1	SAMTVCR + Carbamidomethyl (C)
☑	1993	545.2827	1632.8263	1632.8327	-3.96	0	8	1.2e+003	1	MSVLSTGINNPILCR + Oxidation (M)
☑	2202	581.3053	1740.8941	1740.8941	0.01	1	8	8.7e+002	1	SAMSAKAHLNNVVNAAK + Oxidation (M)
☑	2361	899.4574	1796.9002	1796.8992	0.59	1	8	9.8e+002	1	FVNGMVNVASKFANQR + Oxidation (M)
☑	2999	750.3822	2248.1248	2248.1191	2.51	1	8	9.2e+002	1	VGSNVNVPSKLNMAEMSKPSK + 2 Oxidation (M)
☑	2238	876.8870	1751.7594	1751.7542	3.02	1	8	3.3e+002	1	MNYECPHCGKTLAR + 2 Carbamidomethyl (C); Oxidation (M)
☑	3233	1167.5870	2333.1594	2333.1612	-0.74	1	8	1e+003	1	SGALRDLVVDPDDHSPSSITPR
☑	147	392.6954	783.3762	783.3736	3.39	1	8	3.2e+002	1	GHDGRSR
☑	2673	1051.9980	2101.9814	2101.9739	3.60	0	8	7.5e+002	1	GTDFLIMDAPAGTHGAEIDR + Oxidation (M)
☑	3221	584.0543	2332.1881	2332.1870	0.47	1	8	8.4e+002	1	EIQEATATLGGNRISSLSATADK
☑	3580	864.9104	3455.6125	3455.6206	-2.35	1	8	4.8e+002	1	NFFTNLRMPLNMLNNALQGNAEGTMNDLMR + Oxidation (M)
☑	2170	577.3167	1728.9283	1728.9258	1.46	1	8	7.4e+002	1	ESVDAIVEATRAVLEK
☑	3588	1238.2650	3711.7732	3711.7648	2.26	1	8	5.7e+002	1	DYAQVKADGEITAAIADAALSMLDVDPVGFDLMDR + Oxidation (M)
☑	2710	712.3669	2134.0789	2134.0794	-0.24	1	8	9.4e+002	1	LDEDVIGVYKDVLQTQDGK
☑	3024	566.5511	2262.1753	2262.1817	-2.84	0	8	7.6e+002	1	DVYEEAVETVLKPLAQTMVK
☑	2885	736.0339	2205.0799	2205.0736	2.86	0	8	9.7e+002	1	DLDDLSAGLFGQANIMVAEAR
☑	3180	773.0521	2316.1345	2316.1428	-3.61	0	8	1e+003	1	SYMQALASMRPIVIMDEPHK
☑	1637	692.8778	1383.7410	1383.7358	3.80	0	8	8.1e+002	1	LLPNGTLSGGVNDK
☑	2702	709.6641	2125.9705	2125.9700	0.21	0	8	6e+002	1	GMTYEADSIIYATGFMTQK
☑	3401	1308.5910	2615.1674	2615.1587	3.35	1	8	3.7e+002	1	SAEMTEVMMSTPSMEEIGLNPRK + 3 Oxidation (M)
☑	3502	947.1000	2838.2782	2838.2741	1.43	0	8	4e+002	1	AAYSNWGDSIAVCAPSNNAPPGMSFPAK + Oxidation (M)
☑	523	528.7881	1055.5616	1055.5658	-3.96	1	8	1e+003	1	MGITRHAVR + Oxidation (M)
☑	907	603.8219	1205.6292	1205.6326	-2.74	0	8	1.4e+003	1	MTNDILTIAAK + Oxidation (M)
☑	3279	787.3978	2359.1716	2359.1656	2.55	1	8	9.6e+002	1	DNASAKFDETVEVAINLGVDPR
☑	2339	894.4868	1786.9590	1786.9611	-1.13	1	8	1.7e+003	1	DLATGLAMLAAKEGAALR + Oxidation (M)
☑	798	582.3536	1162.6926	1162.6935	-0.69	1	8	2.4e+002	1	ARLVLIGHER
☑	2387	602.6633	1804.9681	1804.9611	3.87	1	8	6.5e+002	1	TVSYSVIGGDLLKYYK
☑	2685	1054.9890	2107.9634	2107.9559	3.58	1	8	6.2e+002	1	SDWDAIARLTGDSSWSADR
☑	2403	606.0148	1815.0226	1815.0182	2.41	0	8	3e+002	1	ALPVSAFEIVWTIIEK
☑	2617	1019.4870	2036.9594	2036.9514	3.97	0	8	8.5e+002	1	FAVHNDAVTLSDVTLCFE + Carbamidomethyl (C)
☑	1981	809.9490	1617.8834	1617.8813	1.31	1	8	5.7e+002	1	MHFSGASKPLIKFR
☑	1629	461.5854	1381.7344	1381.7388	-3.18	1	8	8.6e+002	1	MTRLLTTLFDR + Oxidation (M)
☑	2864	1100.5020	2198.9894	2198.9936	-1.88	1	8	4.9e+002	1	LAEESGGCVADSLEMARFGNK + Oxidation (M)
☑	3253	1174.5730	2347.1314	2347.1379	-2.77	0	8	9.2e+002	1	VYSGNSWACVTIVGDHTNIVR + Carbamidomethyl (C)
☑	528	529.3116	1056.6086	1056.6113	-2.55	1	8	5.6e+002	1	AKMNKPKPK + Oxidation (M)
☑	1932	528.2721	1581.7945	1581.8007	-3.92	1	8	1.1e+003	1	ALMRQIICYSAEK + Carbamidomethyl (C)
☑	3459	1395.1310	2788.2474	2788.2574	-3.56	0	8	3.7e+002	1	ALAMSCGVGSGSMLAACTGSLATVMPENK + 2 Oxidation (M)
☑	1920	789.8806	1577.7466	1577.7476	-0.61	1	8	8.7e+002	1	LMAASMRHSTGMAAK + Oxidation (M)
☑	1638	692.9064	1383.7982	1383.7973	0.68	0	8	4.2e+002	1	QILELILSPSSGK

☑	2325	889.4549	1776.8952	1776.8975	-1.25	1	8	1.2e+003	1	RIALVDVMNSGNGMLR + 2 Oxidation (M)
☑	2732	1069.4990	2136.9834	2136.9858	-1.10	1	8	6.4e+002	1	LDIVAIDDNKCNNNSNYR + Carbamidomethyl (C)
☑	3294	594.3112	2373.2157	2373.2063	3.94	0	8	8.7e+002	1	VQDIVYELEDQLLPLSEQSR
☑	3244	1172.1450	2342.2754	2342.2821	-2.83	0	8	4e+002	1	NSAVPGGIPMLIAGVLFAVDVFR
☑	2768	721.0399	2160.0979	2160.1063	-3.88	1	8	9.2e+002	1	VNDVAVIGVYSKDDATELPR
☑	3146	768.4330	2302.2772	2302.2685	3.78	1	8	2.7e+002	1	TKPNNKTALLFPLPSIETYR
☑	2658	1041.0090	2080.0034	2080.0007	1.31	0	8	9.5e+002	1	QVLAELEAAQQHCDELQR
☑	3363	816.4191	2446.2355	2446.2448	-3.80	0	8	9.1e+002	1	NDLIAGSIGGIMGTVLNTPMDVVK + 2 Oxidation (M)
☑	230	417.6959	833.3772	833.3775	-0.34	0	8	4.5e+002	1	MPCLQDK
☑	1466	669.3518	1336.6890	1336.6847	3.22	1	8	1.2e+003	1	NAPSPRGGLESPR
☑	2407	606.3438	1816.0096	1816.0110	-0.77	0	8	4.2e+002	1	LLLFMYGFGAFIGLVR
☑	659	559.7635	1117.5124	1117.5161	-3.27	1	8	5.7e+002	1	MIGFYGRCR + Oxidation (M)
☑	2334	594.9959	1781.9659	1781.9710	-2.86	0	8	6.5e+002	1	VPALTPEGTLAGVIGMTR
☑	3485	943.7689	2828.2849	2828.2892	-1.52	1	8	4.6e+002	1	CSETVTAGRSGTMGDIDAMAVGLTAWR + Carbamidomethyl (C); Oxidation (M)
☑	1600	686.8777	1371.7408	1371.7358	3.71	1	8	1.2e+003	1	LKENEVADSVLR
☑	3015	753.7155	2258.1247	2258.1300	-2.34	0	8	1e+003	1	EVLEGLCAMAPAPRPHPAVER + Oxidation (M)
☑	49	363.6708	725.3270	725.3274	-0.50	1	8	1.2e+002	1	LMKGMM + Oxidation (M)
☑	2234	584.6570	1750.9492	1750.9438	3.07	0	8	5.5e+002	1	VRPRPAGTENANLATGK
☑	2118	852.4708	1702.9270	1702.9254	0.97	0	7	6.8e+002	1	QNTVTWSVTNLLTVK
☑	2674	1053.5290	2105.0434	2105.0483	-2.30	1	7	1.2e+003	1	VKVWLGDHAEHYYVFSR
☑	1090	625.3380	1248.6614	1248.6575	3.20	0	7	1.2e+003	1	HASGPAELAAGIR
☑	2546	638.6432	1912.9078	1912.9088	-0.52	1	7	9.1e+002	1	MKDQSNLIIAYEEDTK + Oxidation (M)
☑	1096	625.3384	1248.6622	1248.6602	1.68	0	7	1.1e+003	1	EFVLESISPTK
☑	1576	455.2532	1362.7378	1362.7368	0.73	1	7	9.4e+002	1	NANSSILSRVFR
☑	2763	720.3681	2158.0825	2158.0841	-0.76	0	7	1e+003	1	ATVAMEGLGGDGLFHAVQTLR + Oxidation (M)
☑	1684	700.9044	1399.7942	1399.7922	1.44	0	7	5.8e+002	1	VVEATSASLSPVIK
☑	3004	1127.5580	2253.1014	2253.0994	0.92	1	7	1e+003	1	RGDEAALLSLMIHCENPVNR + Oxidation (M)
☑	3082	761.7314	2282.1724	2282.1754	-1.33	1	7	8.7e+002	1	DIQITLDEPELVTRDATTPR
☑	3397	868.0620	2601.1642	2601.1693	-1.99	1	7	4.1e+002	1	AFETVFAKDGVDPASAAMFEDDPR + Oxidation (M)
☑	2594	498.5258	1990.0741	1990.0769	-1.40	0	7	5.7e+002	1	GTNVSGGSISVAGSIIMVLTK
☑	3039	1135.6380	2269.2614	2269.2695	-3.54	0	7	2.9e+002	1	WAPVQLAALAAHGIGGAGLIAANK
☑	3191	773.7219	2318.1439	2318.1390	2.10	1	7	1e+003	1	DRLDEELPGGSFLLEDTGSLR
☑	1991	814.4625	1626.9104	1626.9093	0.70	1	7	5.5e+002	1	LPALDVVAERFELR
☑	2000	822.4603	1642.9060	1642.9004	3.43	0	7	6.7e+002	1	EVYGIPMDIVAVPIK
☑	2964	748.4218	2242.2436	2242.2355	3.61	1	7	3.1e+002	1	QSMLVTTIPAALEKGAQLISR + Oxidation (M)
☑	3451	930.0941	2787.2605	2787.2669	-2.31	1	7	4.3e+002	1	DTPQHSHSIQHSPERSGSGSVGNGSSR
☑	3456	697.8237	2787.2657	2787.2757	-3.58	1	7	4.4e+002	1	DCSLDASTNGDSSTPSTSSGIEVKLIF + Carbamidomethyl (C)
☑	493	520.7091	1039.4036	1039.4029	0.71	0	7	1.3e+002	1	ECPYSDGGGR
☑	3110	573.5526	2290.1813	2290.1879	-2.87	1	7	8.8e+002	1	IWVESLADSMKEVVDATLLR + Oxidation (M)
☑	3499	944.1009	2829.2809	2829.2918	-3.86	1	7	4.6e+002	1	ECVSMGFADQVTPSLQAMACIQSKR + 2 Carbamidomethyl (C); Oxidation (M)
☑	1753	727.3392	1452.6638	1452.6602	2.51	1	7	7e+002	1	RCTAYGSLCHTK + 2 Carbamidomethyl (C)
☑	1913	787.9277	1573.8408	1573.8464	-3.52	1	7	1.2e+003	1	RALIVSFSDPVNEK
☑	3035	757.3720	2269.0942	2269.0970	-1.25	1	7	1e+003	1	MTLKMTVSPALIGGDADEGYGK + Oxidation (M)
☑	3483	707.0531	2824.1833	2824.1738	3.35	0	7	1.1e+002	1	SNSTWLLNGPDMGAMMNGSDEAEPPR + 3 Oxidation (M)
☑	2753	718.3565	2152.0477	2152.0412	3.03	1	7	1.1e+003	1	QPCPQASFAGTWSAKEAVFK
☑	844	591.7717	1181.5288	1181.5247	3.48	0	7	5.7e+002	1	ALNCAEGHDPR
☑	2656	1038.9490	2075.8834	2075.8858	-1.14	1	7	2.3e+002	1	KLDGLYECILCACCSTACPA
☑	3132	767.3696	2299.0870	2299.0790	3.45	1	7	8.5e+002	1	EVCAAKVTPHAAEADETGEFPK
☑	3505	1421.6460	2841.2774	2841.2756	0.64	0	7	4.4e+002	1	DIVDEITVYDTNIEDYVEYDQYK
☑	2577	653.7187	1958.1343	1958.1393	-2.58	0	7	1.1e+002	1	DPWFLILATLFVAALLR
☑	2846	1094.1110	2186.2074	2186.2059	0.71	1	7	3.1e+002	1	VGLVIKADIRPGYESGQLSGK
☑	2667	1047.0200	2092.0254	2092.0324	-3.33	0	7	1.2e+003	1	DSTAELGQEALDLSVEFIR
☑	465	508.7723	1015.5300	1015.5298	0.23	0	7	2.1e+003	1	LADDLGAVSR
☑	1926	528.2715	1581.7927	1581.7933	-0.42	1	7	1e+003	1	DCLVRVYLGSTSGR + Carbamidomethyl (C)
☑	3044	1136.1340	2270.2534	2270.2457	3.42	0	7	2.9e+002	1	DGNLLLAIGTVPTGLAMVFVNR
☑	3492	1415.1530	2828.2914	2828.2997	-2.91	0	7	5.1e+002	1	SFAGLTMELGLEMPGEEANGSFGPLSR + 2 Oxidation (M)
☑	3503	947.7717	2840.2933	2840.2853	2.80	0	7	5.2e+002	1	ENLCHGVPIVMVTANDSAMDGTMYLK + 2 Oxidation (M)
☑	1751	725.8257	1449.6368	1449.6405	-2.55	0	7	4.4e+002	1	IQDSIDADMEAAR + Oxidation (M)
☑	2776	1084.0220	2166.0294	2166.0263	1.46	0	7	9e+002	1	VILVMPNNSSVFSDSSDNNK
☑	2896	737.3641	2209.0705	2209.0759	-2.43	1	7	1e+003	1	IAVDMFNEGLIDEKEALMR + Oxidation (M)
☑	3157	577.5516	2306.1773	2306.1689	3.66	1	7	1e+003	1	EAEIVAQAGKYGAVTVATNMAGR
☑	2132	857.4612	1712.9078	1712.9057	1.27	1	7	1e+003	1	RAIGEAQIELDAQTAK
☑	2633	1029.9620	2057.9094	2057.9147	-2.53	0	7	4.2e+002	1	VSQGLVETFSTTCEACNGR + Carbamidomethyl (C)
☑	2640	688.3642	2062.0708	2062.0630	3.79	1	7	1e+003	1	GETLGVFQLDGNGMRSLLR
☑	2826	728.3474	2182.0204	2182.0212	-0.37	1	7	8.3e+002	1	ADVEAMEVRTLLSGEYDER
☑	158	395.7323	789.4500	789.4497	0.41	0	7	1.8e+003	1	IVAAFGGR
☑	2937	743.3677	2227.0813	2227.0725	3.93	1	7	1e+003	1	QIMDDSMDIHAGRAIQLGPK + 2 Oxidation (M)
☑	3268	1178.5710	2355.1274	2355.1265	0.42	0	7	9.3e+002	1	GVEGVLFGECGLTPSSTTTTTNK + Carbamidomethyl (C)
☑	1846	767.9221	1533.8296	1533.8337	-2.65	0	7	8.4e+002	1	NSHLIQSPVPAMLK
☑	2889	736.3486	2206.0240	2206.0212	1.26	1	7	7.8e+002	1	EGRLHDLFISATDEEDTMK
☑	2915	1111.5250	2221.0354	2221.0355	-0.02	0	7	8e+002	1	TCGSPSSSSSSPMGSLGSGKPPVK
☑	1088	625.3378	1248.6610	1248.6570	3.24	0	7	1.3e+003	1	MALNVVIMAAGK + 2 Oxidation (M)
☑	3120	573.5535	2290.1849	2290.1814	1.55	1	7	8.8e+002	1	VEILHMLSGRADGQVLVYMK + 2 Oxidation (M)
☑	1598	457.9260	1370.7562	1370.7591	-2.17	0	7	1.2e+003	1	LKPLGIDLESMR
☑	2031	835.8718	1669.7290	1669.7307	-1.01	0	7	3.9e+002	1	MWGTGHAYEQYVGR + Oxidation (M)
☑	3187	773.4224	2317.2454	2317.2518	-2.75	1	7	5.8e+002	1	IPPPFGPGMRPPLGLREFAPR + Oxidation (M)
☑	744	569.7758	1137.5370	1137.5349	1.88	1	7	9.7e+002	1	QRMEAAFGGR + Oxidation (M)
☑	2781	1084.0980	2166.1814	2166.1757	2.65	0	7	4.5e+002	1	SSTINTVAVLGGTGNIGTHIVR
☑	2820	726.3717	2176.0933	2176.0980	-2.16	1	7	1.1e+003	1	RLAAEAGDAEAMSVLGAMLLR + 2 Oxidation (M)
☑	3376	827.0997	2478.2773	2478.2732	1.66	1	7	9.3e+002	1	EVRCRPAVMYCVLAVLCSVVPR + Oxidation (M)
☑	2203	581.3071	1740.8995	1740.8947	2.72	0	7	1.1e+003	1	VAAWANGGADLWIIER
☑	2415	912.5153	1823.0160	1823.0094	3.65	1	7	3.6e+002	1	RVNGFWGIEALVAPPVV
☑	1570	454.5936	1360.7590	1360.7636	-3.38	1	7	7.3e+002	1	LLVSMLVDAKEK + Oxidation (M)
☑	2129	571.6769	1712.0089	1712.0097	-0.50	0	7	1.3e+002	1	TTLALAVLHHPVIATR
☑	2648	691.6608	2071.9606	2071.9545	2.91	1	7	8.3e+002	1	KTAHDDEELTDEAAATVEK
☑	396	484.7924	967.5702	967.5702	0.01	0	7	3.7e+002	1	QPVGVDLIK
☑	483	515.2582	1028.5018	1028.4999	1.89	1	7	7.8e+002	1	DPTQQERR
☑	2235	876.4822	1750.9498	1750.9478	1.15	1	7	6.2e+002	1	SRLAHIESAAVQVWGK

☑	436	499.3001	996.5856	996.5855	0.12	1	7	4.4e+002	1	LEPEVKIIG
☑	145	392.1993	782.3840	782.3819	2.75	1	7	8.9e+002	1	KCCIIF + Carbamidomethyl (C)
☑	2619	1021.0110	2040.0074	2040.0000	3.67	1	7	1.1e+003	1	NWYLEHCPTNQPVKVR + Carbamidomethyl (C)
☑	3210	1163.0680	2324.1214	2324.1293	-3.38	1	7	1.2e+003	1	QNELSFNIATGNPICPKMFK + Carbamidomethyl (C); Oxidation (M)
☑	3251	1174.0600	2346.1054	2346.1096	-1.78	1	7	9e+002	1	TSGLMALAQQQYGKCDIYQR + Carbamidomethyl (C); Oxidation (M)
☑	3013	1130.0690	2258.1234	2258.1291	-2.49	0	7	1.1e+003	1	VATPEAAPPVEAAPAEESRPNR
☑	2012	551.9583	1652.8531	1652.8481	2.98	1	7	1.1e+003	1	YNSASLEASLSSRLR
☑	127	384.6972	767.3798	767.3814	-1.97	0	7	8.6e+002	1	NSSSVFK
☑	2761	540.5173	2158.0401	2158.0472	-3.30	1	7	1.1e+003	1	AKASQCSLSLSLSTPFSLCLC
☑	3388	635.0938	2536.3461	2536.3368	3.66	1	7	5.9e+002	1	MNIFRFAGDMTHLCSIVVLLLK + Oxidation (M)
☑	2627	1026.5140	2051.0134	2051.0133	0.08	0	7	1.2e+003	1	VTSISPGLVDTEMVPEAYK + Oxidation (M)
☑	2733	1070.4890	2138.9634	2138.9613	1.02	1	7	5.6e+002	1	FVTLMDTCASSYARDASTK + Carbamidomethyl (C); Oxidation (M)
☑	2128	571.3121	1710.9145	1710.9161	-0.94	0	7	9.4e+002	1	IGVTSMPPLGCLPAAIR + Oxidation (M)
☑	2412	911.0106	1820.0066	1820.0044	1.25	1	7	4.6e+002	1	SVNLTNKDLSVVFTVGK
☑	2678	703.3388	2106.9946	2107.0000	-2.56	0	7	9.5e+002	1	MLVGCEIVSVSAMTSHVDLT + Oxidation (M)
☑	3266	1178.0950	2354.1754	2354.1763	-0.34	1	7	1.1e+003	1	MAQVAIAAKGSISAWVNTMFDK + Oxidation (M)
☑	3561	998.1464	2991.4174	2991.4075	3.31	1	7	8.5e+002	1	VCIPCQIKVENQHDYQDITSMVAMAR
☑	3089	1143.6350	2285.2554	2285.2631	-3.34	0	7	4.1e+002	1	ILSILQTSLPLFAQEGLEGTR
☑	3403	875.1071	2622.2995	2622.3087	-3.51	1	7	1.1e+003	1	RYAICFTPPMADPLSTVAASWLGR
☑	3465	934.0956	2799.2650	2799.2563	3.10	0	7	4.7e+002	1	VTLPCGFMLVAAMNPCPCGYLGDPK + 3 Carbamidomethyl (C); 2 Oxidation (M)
☑	2913	1110.0270	2218.0394	2218.0371	1.04	1	7	9.2e+002	1	CLGNYLSAAAAQPGDMPGGRGR + Carbamidomethyl (C)
☑	2935	743.3671	2227.0795	2227.0772	1.02	1	7	1.2e+003	1	FPGYASMLTYISRTWQYK + Oxidation (M)
☑	825	587.8043	1173.5940	1173.5965	-2.05	1	7	9.4e+002	1	VECKNGHIFK
☑	924	606.7637	1211.5128	1211.5097	2.61	0	7	4e+002	1	CMQVLMANDR + 2 Oxidation (M)
☑	3117	573.5529	2290.1825	2290.1879	-2.35	0	7	9.9e+002	1	TLIGWNMVSSDISTEQIGVLK
☑	1584	683.3646	1364.7146	1364.7122	1.80	0	7	1.5e+003	1	INLAAVCNYSAVK
☑	3026	1133.0580	2264.1014	2264.1033	-0.81	1	7	1.1e+003	1	ATDLNELPDKPTDTDHRQAK
☑	2515	632.7001	1895.0785	1895.0736	2.56	1	7	3.1e+002	1	GKAIIILNPVTPPMIMR + 2 Oxidation (M)
☑	3315	797.4112	2389.2118	2389.2060	2.41	1	7	1.2e+003	1	FEVVRGEQDGLVCLDLVTNQR
☑	1469	670.4061	1338.7976	1338.7983	-0.48	0	7	3.8e+002	1	LLLAAITAGNLNR
☑	3239	1171.0680	2340.1214	2340.1276	-2.63	1	7	1.2e+003	1	CTGYKPLIDAVMDAAAVMRGDK + Oxidation (M)
☑	3473	937.7696	2810.2870	2810.2934	-2.28	0	7	6.4e+002	1	SMCCIVSVSWISNMGITAFATGIMTR + 2 Oxidation (M)
☑	2854	731.3747	2191.1023	2191.1055	-1.48	1	7	1.2e+003	1	LDVAINYERNGNMVINTQK
☑	1880	781.4391	1560.8636	1560.8698	-3.91	0	7	7.1e+002	1	MIAELGALLGFSAIR
☑	1682	467.2573	1398.7501	1398.7507	-0.45	1	7	1.3e+003	1	GAQYSSAFVTKIK
☑	3171	771.7631	2312.2675	2312.2715	-1.74	0	7	4.5e+002	1	IPVEQLGWAAAIAGGVMFILTR
☑	3281	1180.6570	2359.2994	2359.3012	-0.75	1	7	3.3e+002	1	VRPSLADVDLRPYLFVTKDR
☑	2587	990.5201	1979.0256	1979.0251	0.25	1	7	1.1e+003	1	LQKYVEDPTYTPDLVAK
☑	2647	1036.4940	2070.9734	2070.9722	0.58	1	7	9.9e+002	1	MELNNRIGIPAMCTYMAK + Oxidation (M)
☑	2760	720.3520	2158.0342	2158.0398	-2.63	1	7	1e+003	1	IVSCPRDSAPELTCVDPATGK
☑	1912	786.4344	1570.8542	1570.8501	2.65	1	7	9.6e+002	1	SLHLLSKADTAMLR + Oxidation (M)
☑	2442	919.4148	1836.8150	1836.8182	-1.70	0	7	5.2e+002	1	MPSCAVHGQGSAHLACPR + Oxidation (M)
☑	3357	1217.1040	2432.1934	2432.1927	0.31	0	7	1.1e+003	1	IVDGKPITEQMQDQNIALMEK + 2 Oxidation (M)
☑	485	516.2363	1030.4580	1030.4542	3.73	1	7	5.8e+002	1	FYGMDRDK
☑	2044	840.5013	1678.9880	1678.9869	0.71	1	7	1.4e+002	1	QLKNLPELEILLEK
☑	3111	573.5526	2290.1813	2290.1818	-0.22	0	7	1e+003	1	EAVHDYAEVNARPVQPLNLR
☑	2703	1064.5070	2126.9994	2126.9976	0.87	1	7	9.4e+002	1	ELTDMEKVTANNCYEIVR
☑	3337	802.7377	2405.1913	2405.1897	0.67	0	7	1.3e+003	1	LINDTLEQTICTAFNSVHSTAK
☑	3413	684.1068	2732.3981	2732.3949	1.15	0	7	9.8e+002	1	ISVEGLTVEFGGFTLFDDISFVVNK
☑	1564	679.8701	1357.7256	1357.7242	1.10	0	7	9e+002	1	AEIDAVVEPIFR
☑	2522	633.9779	1898.9119	1898.9118	0.05	1	7	1.2e+003	1	LVKSMLCGTSDIDFENK
☑	60	365.7209	729.4272	729.4272	0.00	0	7	3.3e+003	1	IIGVSEL
☑	2525	634.6840	1901.0302	1901.0267	1.83	1	7	8.8e+002	1	MAIVTNKAHCFTVPLLK + Oxidation (M)
☑	3355	811.4171	2431.2295	2431.2203	3.77	1	7	1.3e+003	1	SAAAPAAETAPAAEAAAEPAERPRR
☑	2668	1049.5210	2097.0274	2097.0248	1.28	1	7	1.4e+003	1	MIPTRAAPLGHASAACYPDR
☑	1095	625.3384	1248.6622	1248.6602	1.68	0	6	1.3e+003	1	LAVSFEVVEEK
☑	2967	748.7377	2243.1913	2243.1990	-3.46	1	6	8.3e+002	1	YPDITASFLGIFLRAVDAFK
☑	3409	895.1193	2682.3361	2682.3397	-1.34	1	6	1.1e+003	1	NFASEGAAKVFITDEIIAQLMCAPK + Oxidation (M)
☑	1384	658.2875	1314.5604	1314.5584	1.56	0	6	2.9e+002	1	QMMEIGYNADK + Oxidation (M)
☑	1668	698.3068	1394.5990	1394.6024	-2.38	0	6	4.1e+002	1	NDEGLCVYEEPK
☑	2769	721.0404	2160.0994	2160.1051	-2.66	1	6	1.3e+003	1	IRAVHVIVGFNYSFGCHGK + Carbamidomethyl (C)
☑	1919	789.8415	1577.6684	1577.6681	0.22	0	6	2.9e+002	1	NISYNCNNGGFYR + Carbamidomethyl (C)
☑	3513	953.1016	2856.2830	2856.2742	3.09	0	6	4.6e+002	1	GENAGASVSPAPKPFADHLCNCAAAGCK + 3 Carbamidomethyl (C)
☑	3373	824.1320	2469.3742	2469.3743	-0.07	0	6	2.5e+002	1	NTLNVPPPPPPPLAPPLINENLR
☑	3582	1157.8790	3470.6152	3470.6123	0.84	0	6	6.5e+002	1	MPPTTPVGDEASLPQSQQVGDDAPAPPAYTFMR
☑	3347	807.0989	2418.2749	2418.2790	-1.70	1	6	8e+002	1	VLFEETCLPSKDVIMPIDLLK + Oxidation (M)
☑	923	606.3696	1210.7246	1210.7285	-3.18	1	6	3.5e+002	1	LPLLDANTKVK
☑	3003	1127.5400	2253.0654	2253.0729	-3.32	0	6	1.1e+003	1	MSSSSCASVQSAAASSVTVALGPR
☑	3134	576.0319	2300.0985	2300.0995	-0.42	1	6	1.2e+003	1	KSPLTEEYIVFDAGSGGMIDR + Oxidation (M)
☑	2644	1034.4750	2066.9354	2066.9435	-3.89	0	6	7.1e+002	1	LTAMGSSVPMSNEACAQVAK + Carbamidomethyl (C); Oxidation (M)
☑	3212	1164.1480	2326.2814	2326.2870	-2.37	1	6	4.1e+002	1	GEPVAGVVTAVARQVAALHAASPR
☑	3571	1138.8760	3413.6062	3413.6126	-1.89	1	6	7.3e+002	1	QEVGTRTGQAMGHLAQSGPGGMIEVLDTMPASR + 2 Oxidation (M)
☑	1757	729.8167	1457.6188	1457.6245	-3.90	1	6	4e+002	1	VDEGSYQPSRCFA
☑	1230	644.3613	1286.7080	1286.7082	-0.10	0	6	1.3e+003	1	EISLSPSLVGGTK
☑	3339	1207.5610	2413.1074	2413.1114	-1.66	1	6	7.9e+002	1	GMTACGKDSGNTTLGVFSNRPER + Oxidation (M)
☑	2004	550.2571	1647.7495	1647.7432	3.79	1	6	6.8e+002	1	CRCLHGFVAAPDMR + Carbamidomethyl (C); Oxidation (M)
☑	162	397.7059	793.3972	793.4004	-3.92	1	6	2.7e+003	1	EKSATMK
☑	3223	778.4040	2332.1902	2332.1984	-3.54	1	6	1.2e+003	1	SLTGTMPKSLYVEAIEQLLSH + Oxidation (M)
☑	3509	949.1022	2844.2848	2844.2868	-0.70	1	6	5.4e+002	1	ESCAEVIKFVGSTSMDPMPDTGVLDK + Carbamidomethyl (C); 2 Oxidation (M)
☑	3352	809.0837	2424.2293	2424.2372	-3.28	1	6	1.1e+003	1	DVGDRNLLVLPRPFDWMPER
☑	3455	930.0956	2787.2650	2787.2757	-3.84	1	6	5.6e+002	1	DCSLDASTNGDSSTPSTSSGIEVKLIF + Carbamidomethyl (C)
☑	3460	932.4200	2794.2382	2794.2320	2.20	1	6	4.1e+002	1	EMNEILDGRGGGKPDMAQGGCQSLDK + Carbamidomethyl (C); 2 Oxidation (M)
☑	3539	974.1274	2919.3604	2919.3570	1.16	1	6	8.1e+002	1	DTMHQSPPPTPHAPRTVSVTYAGGDER + Oxidation (M)
☑	2758	1078.5130	2155.0114	2155.0182	-3.12	0	6	1.1e+003	1	TAELSGPAGQLYSAGFSADGTR
☑	2664	1045.9950	2089.9754	2089.9739	0.75	0	6	1e+003	1	TDDGHSMLTPSEFLQIAGR + Oxidation (M)
☑	2570	973.4920	1944.9694	1944.9649	2.35	0	6	1.5e+003	1	NSSIPCPMDIGETILVTR
☑	3545	976.7968	2927.3686	2927.3746	-2.07	0	6	8.7e+002	1	SQLFADVMEGDALAGGSLTAEDLAALFAE + Oxidation (M)
☑	3579	1152.2070	3453.5992	3453.5902	2.60	1	6	6.3e+002	1	YDLFREADGTPGFHLFEIYDDEQALEAHR

☑	133	385.2269	768.4392	768.4382	1.40	0	6	92	1	VVDVLPQ
☑	2939	743.3680	2227.0822	2227.0864	-1.92	0	6	1.3e+003	1	LLSVQIFMTDISEIDSMNR + Oxidation (M)
☑	2232	584.3412	1750.0018	1749.9964	3.09	1	6	2.5e+002	1	ILHAGFKVEHMLLVK + Oxidation (M)
☑	3102	573.5523	2290.1801	2290.1852	-2.24	1	6	1.2e+003	1	VVTTAMTVGAVWSGAATRATGAGR
☑	106	378.7289	755.4432	755.4442	-1.30	1	6	2.4e+002	1	KIPGWR
☑	1877	780.4713	1558.9280	1558.9235	2.89	0	6	1.1e+002	1	LQPVTPAVFIPHLK
☑	2581	658.0491	1971.1255	1971.1265	-0.53	1	6	2.4e+002	1	ELNQLHPPLARLLATTGK
☑	3526	961.1007	2880.2803	2880.2912	-3.80	0	6	4.5e+002	1	LLEWHGSPFQMLDYTNISNEDDEK
☑	576	539.7018	1077.3890	1077.3896	-0.49	0	6	23	1	GYFSCCNEV + Carbamidomethyl (C)
☑	952	610.8303	1219.6460	1219.6422	3.20	0	6	1.8e+003	1	HDASPLARPTR
☑	3188	1159.6530	2317.2914	2317.2940	-1.11	1	6	3.2e+002	1	IVVMSPRPGRITDVIDSPLPR
☑	2643	1034.0180	2066.0214	2066.0181	1.61	0	6	1.6e+003	1	STSAPQGPTAAPLSFHDLNR
☑	2911	1109.5670	2217.1194	2217.1199	-0.19	0	6	1.3e+003	1	LDDADVAVVSATVNVICEISK + Carbamidomethyl (C)
☑	3007	752.3712	2254.0918	2254.0939	-0.97	1	6	1.3e+003	1	ISNPQDFQPMLYNESKLSK + Oxidation (M)
☑	2479	623.3510	1867.0312	1867.0277	1.85	1	6	5.8e+002	1	VIVLDHPLLFEAKMDK
☑	3318	797.7313	2390.1721	2390.1776	-2.31	1	6	1.3e+003	1	WLRCAAWIQGAAMVGYAVGPDR
☑	3364	816.7466	2447.2180	2447.2179	0.02	1	6	1.5e+003	1	SVITNSINKAILEPENEYEER
☑	3289	791.7392	2372.1958	2372.1933	1.02	0	6	1.4e+003	1	DGFVMGEGSAILVLEELEHALK + Oxidation (M)
☑	946	609.7753	1217.5360	1217.5346	1.16	0	6	5.5e+002	1	MQQSPNSDPSK
☑	2875	551.0197	2200.0497	2200.0504	-0.32	0	6	1.2e+003	1	SGMIPLEGQTLVSVSSACSYR + Oxidation (M)
☑	3385	837.4181	2509.2325	2509.2384	-2.35	1	6	1.4e+003	1	GGPLAEEAFAVLRDVCDGLGIDHR
☑	3176	772.3997	2314.1773	2314.1735	1.64	0	6	1.4e+003	1	LLSLDTLAQLSGAFMMMITSR + Oxidation (M)
☑	2932	743.3668	2227.0786	2227.0837	-2.32	1	6	1.3e+003	1	ASAQTGAGRIAYISCNVATMAR + Oxidation (M)
☑	3095	1145.6310	2289.2474	2289.2440	1.48	1	6	5.4e+002	1	AEEIEGRPLPLDADARAVLVR
☑	3501	946.0954	2835.2644	2835.2725	-2.85	0	6	5e+002	1	MEGAAPGPLGTAEELMKPGMSAETDSAR + 2 Oxidation (M)
☑	3285	1182.5950	2363.1754	2363.1758	-0.13	1	6	1.4e+003	1	ERVPLDDGGELDTGLAFLSFGR
☑	3530	962.7761	2885.3065	2885.3026	1.36	0	6	6.1e+002	1	APLPPGIGCLVSTGWVESDDSNDDDAAK + Carbamidomethyl (C)
☑	2449	615.0197	1842.0373	1842.0363	0.53	1	6	4.2e+002	1	FGIAKEQLPSGSLIINR
☑	3493	943.7711	2828.2915	2828.2826	3.13	1	6	6.8e+002	1	ELNICTGCGPGAMEGPMKGAAIGHAQQR + 2 Oxidation (M)
☑	165	397.7064	793.3982	793.4004	-2.68	0	6	2.9e+003	1	SSLVSACK
☑	1954	796.3989	1590.7832	1590.7838	-0.32	1	6	1.6e+003	1	WGPGAAAPPPARACGR + Carbamidomethyl (C)
☑	3259	587.8081	2347.2033	2347.2068	-1.51	0	6	1.2e+003	1	TCILYFACSAFGLLASILTGAR + Carbamidomethyl (C)
☑	422	493.2693	984.5240	984.5253	-1.30	1	6	1.1e+003	1	AFVREAHR
☑	3186	773.0941	2316.2605	2316.2689	-3.64	0	6	5.3e+002	1	VAQVAGVAVSSLALAFAASADATVK
☑	3461	699.8149	2795.2305	2795.2209	3.43	1	6	4.2e+002	1	ECMASVPEASYRAMMLALMGFDQR + Carbamidomethyl (C); 2 Oxidation (M)
☑	3249	782.7267	2345.1583	2345.1611	-1.20	1	6	1.3e+003	1	NQENGAPEKSVEKPHEKPEAK
☑	3392	856.1026	2565.2860	2565.2863	-0.14	0	6	1.3e+003	1	EDSLWNQIIAQDFTLIGGNYLR
☑	2371	600.6846	1799.0320	1799.0345	-1.42	1	6	3.2e+002	1	TLGLQGVFPAIKEWIK
☑	2605	1006.0160	2010.0174	2010.0120	2.69	1	6	1.6e+003	1	LWNPFFSRKPVWMMR + Oxidation (M)
☑	2699	709.3376	2124.9910	2124.9981	-3.36	0	6	1e+003	1	LFVTLEPCAMCLGAMFHAR + Oxidation (M)
☑	3416	919.0905	2754.2497	2754.2443	1.96	0	6	7.1e+002	1	SNVHNILETFQQMGYVEQDEETK + Oxidation (M)
☑	1717	710.3293	1418.6440	1418.6395	3.23	1	6	8.2e+002	1	LVRGECSGPCDAR + Carbamidomethyl (C)
☑	2037	558.9749	1673.9029	1673.8988	2.42	0	6	9.7e+002	1	WELLQTTILQTNSK
☑	1648	695.3776	1388.7406	1388.7412	-0.41	0	6	2.4e+003	1	GPIGPAGPQGKPGEK
☑	3536	1455.2770	2908.5394	2908.5367	0.95	1	6	6.8e+002	1	VVVTGGPGETSLTATVAGPSARNLGGGTNLR
☑	3517	955.8474	2864.5204	2864.5131	2.53	0	6	6.3e+002	1	GGVGDDLPTLTLDAGELGEGISLAQLVVR
☑	2679	703.3397	2106.9973	2106.9957	0.75	1	6	1.4e+003	1	ESTTSKDAPAPTPSYEIDAK
☑	2883	1103.0310	2204.0474	2204.0393	3.71	1	6	1.4e+003	1	CATSAGGGGARIGDPAFQAVADR + Carbamidomethyl (C)
☑	2888	1104.0190	2206.0234	2206.0252	-0.79	0	6	1e+003	1	LYEVYETNNLSACDYKPK + Carbamidomethyl (C)
☑	3185	773.0729	2316.1969	2316.1961	0.33	1	6	1.2e+003	1	IKSNEIFVLNSSQDIVEEPR
☑	3542	976.4532	2926.3378	2926.3324	1.82	1	6	7.4e+002	1	GGAPYMTMLVSPNNAKGEALGDGATTDEK + 2 Oxidation (M)
☑	2529	951.5632	1901.1118	1901.1138	-1.03	1	6	1.1e+002	1	LIPQKLYQANVLNFIK
☑	1883	523.2681	1566.7825	1566.7824	0.05	0	6	1.6e+003	1	CLSNSLSVAGNLAYR
☑	3394	1286.6110	2571.2074	2571.2097	-0.88	1	6	1.2e+003	1	MDINQIFNMIDDRYIANNDLK + Oxidation (M)
☑	1530	677.8586	1353.7026	1353.7041	-1.06	1	6	1.5e+003	1	EPKVYHPSGNVK
☑	2055	563.9821	1688.9245	1688.9250	-0.29	1	6	9.2e+002	1	EEIFGPILPIRSYR
☑	2609	1011.9900	2021.9654	2021.9694	-1.96	1	6	1.5e+003	1	ELNDLGIPTTDDSWKYR
☑	3275	787.3969	2359.1689	2359.1651	1.61	0	6	1.5e+003	1	EAEMEITLPTVEVIPLGAMER + 2 Oxidation (M)
☑	2818	726.3713	2176.0921	2176.0868	2.43	1	6	1.6e+003	1	ANAVKLGAGMETGTEMGPLVSK + Oxidation (M)
☑	2861	1098.0590	2194.1034	2194.0973	2.79	1	6	1.4e+003	1	TAEAAIRIMVDMVNEGTITK + 2 Oxidation (M)
☑	3382	834.3878	2500.1416	2500.1337	3.14	1	6	8.9e+002	1	EMLSNFLFDIAKCHQNWNMK + 2 Oxidation (M)
☑	1978	809.4288	1616.8430	1616.8444	-0.81	0	6	1.8e+003	1	TLAMLADLPVDVSTR + Oxidation (M)
☑	18	631.3664	630.3591	630.3588	0.47	0	6	3.4e+003	1	AILSDI
☑	2343	597.3438	1789.0096	1789.0098	-0.11	1	6	3.9e+002	1	KGISITTSVIQIPYNR
☑	1231	644.7604	1287.5062	1287.5080	-1.33	0	6	1.7e+002	1	CLSCNTMANCTK
☑	2623	683.3220	2046.9442	2046.9429	0.64	0	6	1e+003	1	ELGAEVAYCQGNIANPADR + Carbamidomethyl (C)
☑	2869	1101.0160	2200.0174	2200.0107	3.09	1	6	1.1e+003	1	NFVEGCLNGTPTSSDFEKAGK
☑	3419	920.7653	2759.2741	2759.2708	1.17	1	6	8.9e+002	1	MSSATPTPPSPFPEDPTADGSLTERR + Oxidation (M)
☑	1285	649.8881	1297.7616	1297.7605	0.89	1	6	6.7e+002	1	KNAAIAVLEELK
☑	1741	480.5915	1438.7527	1438.7490	2.57	0	6	1.4e+003	1	LIVLDPHSSEMAK
☑	1091	625.3381	1248.6616	1248.6649	-2.57	1	6	1.8e+003	1	REMLILDFGR
☑	1874	778.8518	1555.6890	1555.6867	1.53	1	6	7.4e+002	1	GVMQCLQMEMKDK + Oxidation (M)
☑	3033	757.0402	2268.0988	2268.1031	-1.91	1	6	1.6e+003	1	FNTMANLPPADIATFSVRCK + Carbamidomethyl (C); Oxidation (M)
☑	3511	951.7662	2852.2768	2852.2849	-2.84	1	6	5.2e+002	1	RQNEHEDEPAGDVLPVGETFAEEER
☑	3557	992.8182	2975.4328	2975.4343	-0.53	0	6	1.1e+003	1	LGISWSAQTCAIVGLAFLGGSYMAEAMR + Carbamidomethyl (C); Oxidation (M)
☑	653	557.7542	1113.4938	1113.4947	-0.76	1	6	6.7e+002	1	MSERTFCPK + Oxidation (M)
☑	3368	820.4678	2458.3816	2458.3736	3.24	1	6	2.5e+002	1	DFAIINLAAKVSSFIPALNWLR
☑	3556	992.8155	2975.4247	2975.4299	-1.75	0	6	1.1e+003	1	DAAFSGVMMLPMTLSMVVGGMLGGALISR + 4 Oxidation (M)
☑	3532	962.7773	2885.3101	2885.3039	2.15	0	6	6.9e+002	1	SQNGQSFFQEEPVHMSIQESGPASHK
☑	3199	1161.5890	2321.1634	2321.1620	0.61	1	6	1.6e+003	1	SNLVGMGVLPLQFTDGMTRNR + Oxidation (M)
☑	3475	938.7670	2813.2792	2813.2848	-1.99	0	6	7.3e+002	1	LVAAGMLTACADDDDPEAQPTPSAPTTR
☑	3162	770.0759	2307.2059	2307.2005	2.34	1	6	1.3e+003	1	ALLAALDDPSNEAGQRAMPIVR
☑	2652	692.0041	2072.9905	2072.9945	-1.92	0	6	1.5e+003	1	FMQEISMTMTSLLGTEVR
☑	3564	1018.1140	3051.3202	3051.3096	3.47	1	6	2.7e+002	1	FCDSMTCIPQGFEQECTGAARRPEFR + Carbamidomethyl (C); Oxidation (M)
☑	3414	914.7766	2741.3080	2741.3045	1.27	1	5	1.2e+003	1	AADLVGALGQENNPEWKTVAWDDSR
☑	3305	793.4032	2377.1878	2377.1947	-2.93	0	5	1.5e+003	1	EAYEADVLVVGSGIAGCATALAAAR
☑	2903	1107.5010	2212.9874	2212.9848	1.20	0	5	7e+002	1	QGFLGMAVPEEYGGGGNPDFR + Oxidation (M)
☑	387	480.7760	959.5374	959.5361	1.37	0	5	1.7e+003	1	ETIPMLIK + Oxidation (M)

☑	2127	856.4100	1710.8054	1710.8029	1.52	1	5	1.5e+003	1	QQAASSMELAKSSMAR + Oxidation (M)
☑	3434	693.8248	2771.2701	2771.2611	3.24	1	5	8.4e+002	1	WIPEDKDCLKPPPFSYNGTYTPM + Carbamidomethyl (C); Oxidation (M)
☑	3489	943.7702	2828.2888	2828.2927	-1.40	0	5	7.9e+002	1	MVCVDPHDIPVVAVVDPEMMSTMPK + Carbamidomethyl (C); 2 Oxidation (M)
☑	3516	955.1074	2862.3004	2862.2986	0.61	1	5	7.2e+002	1	ERLSDVAISLQNCNNMFFCETVEK + Carbamidomethyl (C); Oxidation (M)
☑	3500	945.0939	2832.2599	2832.2622	-0.82	1	5	5.8e+002	1	AKAMGADYLINYENTPEWDEEVMK + Oxidation (M)
☑	1056	620.3099	1238.6052	1238.6078	-2.03	0	5	1.8e+003	1	LDGSAGCPPPGLR
☑	2532	953.4769	1904.9392	1904.9448	-2.91	1	5	1.8e+003	1	AQSLEDCVGMARELLVR + Oxidation (M)
☑	2773	722.3468	2164.0186	2164.0148	1.72	1	5	1.4e+003	1	MPEKIELPITGMSCAACAAR + Carbamidomethyl (C); Oxidation (M)
☑	330	463.2296	924.4446	924.4413	3.59	0	5	7.3e+002	1	GDDAAAHLR
☑	2862	733.3432	2197.0078	2197.0058	0.91	1	5	1.1e+003	1	SSCLGCPFHENAQWRHIR + Carbamidomethyl (C)
☑	3309	597.8187	2387.2457	2387.2519	-2.58	1	5	1.3e+003	1	NGSHSEKAVLGIVAFEVATLMSK
☑	2408	606.3510	1816.0312	1816.0319	-0.39	1	5	3.9e+002	1	DPNLAGLSRIIPPANLR
☑	2738	715.6679	2143.9819	2143.9844	-1.19	1	5	1e+003	1	VGDSPGVSYSDIAAKAYECGR
☑	2116	852.4111	1702.8076	1702.8130	-3.17	1	5	1.6e+003	1	LGLENPMDMRDQIR + Oxidation (M)
☑	2152	859.4841	1716.9536	1716.9518	1.10	0	5	7.4e+002	1	DSICIIIIILNCLSK + Carbamidomethyl (C)
☑	2347	895.9865	1789.9584	1789.9621	-2.05	1	5	1.2e+003	1	LRSQPIDIPGLSVCHR
☑	2476	621.3448	1861.0126	1861.0170	-2.37	1	5	1e+003	1	VAVVHNGIIDNAADVRAK
☑	2477	621.6875	1862.0407	1862.0374	1.77	1	5	4.9e+002	1	AGQPATIEVDALPGVRLR
☑	3478	940.7531	2819.2375	2819.2427	-1.86	0	5	4.2e+002	1	NMMTWWGEAMGSVVLMDGELFAANK + 2 Oxidation (M)
☑	3238	1171.0660	2340.1174	2340.1130	1.90	0	5	1.6e+003	1	YVQPMTSPLYNNVISPVCDK + Carbamidomethyl (C); Oxidation (M)
☑	3533	967.4625	2899.3657	2899.3667	-0.35	0	5	1.2e+003	1	VSTNQHGLSMGAGANVNAFFGIMTMIIS + 2 Oxidation (M)
☑	2207	582.6144	1744.8214	1744.8243	-1.67	0	5	1.4e+003	1	CNAYLTTHGIQPIEW
☑	3454	697.8235	2787.2649	2787.2553	3.43	1	5	7.2e+002	1	SEIYPYDMAKIIELGEHCSMTER + Carbamidomethyl (C); Oxidation (M)
☑	2779	1084.0440	2166.0734	2166.0739	-0.20	1	5	1.7e+003	1	NQSSINQLFGREASLLMDK + Oxidation (M)
☑	2766	720.7280	2159.1622	2159.1635	-0.62	1	5	9.2e+002	1	RTFALALWSMTVIIAPICGP
☑	1633	692.4188	1382.8230	1382.8245	-1.08	1	5	5.1e+002	1	GKDIVLANLVSVR
☑	1690	469.2610	1404.7612	1404.7613	-0.06	0	5	1.6e+003	1	IDNLSQFINLTK
☑	2229	875.4779	1748.9412	1748.9421	-0.47	0	5	1.1e+003	1	EGAIHLVLADGNAAISAK
☑	3292	792.0729	2373.1969	2373.1924	1.87	1	5	1.6e+003	1	ADIEQRQQLVEAFVNDTELR
☑	2663	1045.4670	2088.9194	2088.9270	-3.60	0	5	5.8e+002	1	QSLENSNTNFSATMSTVDK + Oxidation (M)
☑	2233	584.6565	1750.9477	1750.9539	-3.56	0	5	8.7e+002	1	TFQALLLETQVMLTK + Oxidation (M)
☑	2661	1042.0160	2082.0174	2082.0139	1.70	1	5	2e+003	1	MGLPADAVLVGGCGHAEWRK + Oxidation (M)
☑	1852	771.9329	1541.8512	1541.8525	-0.83	1	5	1.5e+003	1	TRALTPAQQSSALAK
☑	2709	1067.5350	2133.0554	2133.0524	1.42	1	5	1.9e+003	1	KWGAELSTMSELEQLQQR
☑	2814	544.0150	2172.0309	2172.0382	-3.35	1	5	1.6e+003	1	NNMHLSSSVHEEARFISAK + Oxidation (M)
☑	3104	573.5523	2290.1801	2290.1780	0.92	0	5	1.5e+003	1	LVEFLDGRPTPAVGFAMGIER + Oxidation (M)
☑	3570	854.4084	3413.6045	3413.6068	-0.66	1	5	9.8e+002	1	EMWIVHHSLEGMRGASTGPASGGVICFTPGTR + Carbamidomethyl (C); Oxidation (M)
☑	2921	742.0380	2223.0922	2223.0915	0.30	1	5	1.8e+003	1	EKVIEPMYETKPVNDIMR + 2 Oxidation (M)
☑	2632	1028.9900	2055.9654	2055.9578	3.71	1	5	1.5e+003	1	IADEKPGQAPRCPSCSQGR + Carbamidomethyl (C)
☑	2836	1093.0140	2184.0134	2184.0078	2.57	0	5	1.3e+003	1	LLCDLEPPEALPSLDECDR + Carbamidomethyl (C)
☑	3559	997.4760	2989.4062	2989.3990	2.39	1	5	1.2e+003	1	NATDMEMARQLCTVACAGSGHRPGLIAK + Carbamidomethyl (C); 2 Oxidation (M)
☑	2557	965.5169	1929.0192	1929.0207	-0.77	1	5	1.5e+003	1	SVAYDVLQTVSKSYTLR
☑	2215	874.4836	1746.9526	1746.9489	2.16	1	5	9.3e+002	1	KHRPELLGAGAGGSLER
☑	2631	686.3276	2055.9610	2055.9571	1.86	1	5	1.5e+003	1	EEWTSEVFDMELLRTR + Oxidation (M)
☑	2736	536.7501	2142.9713	2142.9793	-3.73	1	5	9.6e+002	1	EVQSGFECGIGSNKFNNWK
☑	125	384.2354	766.4562	766.4589	-3.41	0	5	4.3e+002	1	LEPKPAL
☑	2960	1121.6120	2241.2094	2241.2013	3.62	1	5	9.3e+002	1	LPNLSLLNGRVPLFECMTPK
☑	3448	929.0786	2784.2140	2784.2160	-0.71	0	5	4.2e+002	1	ILAAFESDETWSDGPDTLCYHAMR + Carbamidomethyl (C)
☑	2563	970.4684	1938.9222	1938.9258	-1.82	1	5	1.8e+003	1	ERAGENAVYFIMGGPGSGK
☑	3514	954.4322	2860.2748	2860.2648	3.49	0	5	5.9e+002	1	LAYGIGGLMDGGGVSMMSCVMLAYMTK + Carbamidomethyl (C); 3 Oxidation (M)
☑	2531	952.5008	1902.9870	1902.9880	-0.52	1	5	1.9e+003	1	KQSVVVFGFPGTTFFDK
☑	3167	771.1022	2310.2848	2310.2882	-1.49	1	5	4.4e+002	1	MRVLVTGHDGYIGSVLVPILR + Oxidation (M)
☑	1624	690.8723	1379.7300	1379.7271	2.11	1	5	1.5e+003	1	KGVAFGMLFPGEK
☑	3006	752.3685	2254.0837	2254.0834	0.11	1	5	1.7e+003	1	EIPGHLLQVQGDMSVNDCRK + Oxidation (M)
☑	3396	866.8046	2597.3920	2597.3966	-1.78	1	5	8.3e+002	1	AVVLPVGTFLDGKIHIGLDNYSGGR
☑	3345	605.3463	2417.3561	2417.3484	3.17	1	5	3.3e+002	1	KWFILVALFGLGLAQHNPHTR
☑	2782	1084.5910	2167.1674	2167.1612	2.88	0	5	1e+003	1	GAIVVPLACWWGALELVASR + Carbamidomethyl (C)
☑	3286	789.0678	2364.1816	2364.1817	-0.06	1	5	1.8e+003	1	CELQLAAQNEMIVKLDDFLR + Oxidation (M)
☑	2265	882.9909	1763.9672	1763.9716	-2.47	1	5	9.7e+002	1	LSIALIGMGSAGSRFLR + Oxidation (M)
☑	2496	941.0336	1880.0526	1880.0488	2.03	1	5	6.3e+002	1	MGRPAVKVIMTVLHAGGK + Oxidation (M)
☑	3482	1412.6410	2823.2674	2823.2689	-0.52	1	5	7.2e+002	1	MVASSTPNNETANSAADNSLATDGASRR + Oxidation (M)
☑	2333	891.5043	1780.9940	1780.9948	-0.41	1	5	6.9e+002	1	FQHILRILNTNIDGK
☑	2850	1096.0960	2190.1774	2190.1731	1.97	1	5	9.3e+002	1	EVNATLLMRNHAPWLANIK
☑	2959	748.0466	2241.1180	2241.1171	0.37	1	5	1.8e+003	1	LAVHRALADALTSSAAMDAADR + Oxidation (M)
☑	361	472.2880	942.5614	942.5651	-3.85	1	5	2.5e+003	1	GYHKVVLK
☑	3343	806.4062	2416.1968	2416.1996	-1.18	1	5	1.8e+003	1	SWNTGHPGGVATVHADSAAKGLQR
☑	2698	1063.5010	2124.9874	2124.9939	-3.03	0	5	1.3e+003	1	EDGHTQQWCVPYLPIDPK
☑	279	441.1998	880.3850	880.3861	-1.24	0	5	5.6e+002	1	GQCSSFPR
☑	1879	781.4390	1560.8634	1560.8664	-1.89	1	5	9e+002	1	RIFYGTPAEPAVLK
☑	2338	596.3234	1785.9484	1785.9481	0.16	0	5	1.6e+003	1	LQALMGQVMQNPALIK + 2 Oxidation (M)
☑	3534	725.8489	2899.3665	2899.3631	1.18	1	5	1.4e+003	1	NAAQQGHNGMLLRDNIFGSIEEDAQR + Oxidation (M)
☑	2963	1122.1090	2242.2034	2242.2004	1.34	1	5	1.1e+003	1	LGHLLRTMPGEDGAKPPGVAAR
☑	3512	951.7723	2852.2951	2852.2865	3.02	1	5	8.5e+002	1	MNMEPLDHASHGRPGSSGGVRTMADSR
☑	2249	586.0096	1755.0070	1755.0043	1.53	1	5	4.4e+002	1	LVSFRLPEDLLQGLR
☑	2520	633.6395	1897.8967	1897.9013	-2.42	0	5	1.7e+003	1	TTIEMKPATTLAMDSEK + 2 Oxidation (M)
☑	2894	737.0326	2208.0760	2208.0766	-0.28	0	5	1.9e+003	1	LGLSGMTGSIAANCTLIAAEGDK + Oxidation (M)
☑	3265	784.4003	2350.1791	2350.1852	-2.62	1	5	1.9e+003	1	HETLPGRFTGSLTAVVGPHSCK + Carbamidomethyl (C)
☑	2393	905.5140	1809.0134	1809.0108	1.44	1	5	6.6e+002	1	SARTATVLLPDSGGLVPR
☑	3415	1377.6300	2753.2454	2753.2346	3.93	0	5	8.8e+002	1	ELGFGNINMDLIMGLPEENMDDVR + 2 Oxidation (M)
☑	876	597.8566	1193.6986	1193.6993	-0.54	1	5	3.8e+002	1	GRQKPGTPVVR
☑	2041	839.4058	1676.7970	1676.8005	-2.08	1	5	1.6e+003	1	GKPDQAPKESESNYK
☑	2916	1111.5980	2221.1814	2221.1817	-0.11	1	5	1.2e+003	1	TAVAPDGMLWVSLYGTGKLVK + Oxidation (M)
☑	3521	957.7752	2870.3038	2870.3082	-1.54	1	5	9.1e+002	1	HRYGYSAACAEFTLAYLSPDGNPPDR
☑	2056	563.9937	1688.9593	1688.9574	1.14	1	5	5.4e+002	1	NLFITGGAGSGKSLVIR
☑	3574	857.9037	3427.5857	3427.5929	-2.11	1	5	9.3e+002	1	IMCFCPCFHVVLLMKQGLSPNDACESVIK + 3 Carbamidomethyl (C); 2 Oxidation (M)
☑	2691	1058.0110	2114.0074	2114.0038	1.75	1	5	1.8e+003	1	VRPSVVVACGYFDDSCRK + 2 Carbamidomethyl (C)
☑	2029	556.8919	1667.6539	1667.6490	2.89	1	5	1.1e+002	1	CDTCGHRSECFSLNP
☑	3042	757.6947	2270.0623	2270.0534	3.91	1	5	1.5e+003	1	EMVGDYLKMHGFAVTLCDGGK

☑	1463	668.7369	1335.4592	1335.4563	2.24	0	5	8.1	1	YNNVXXXXQVR
☑	1100	625.3391	1248.6636	1248.6609	2.23	1	5	1.6e+003	1	LTARTSMTVGGR
☑	3310	797.0692	2388.1858	2388.1809	2.04	1	5	1.9e+003	1	DKEPDDKPGVEDPVTPAQPVQK
☑	3497	944.0981	2829.2725	2829.2805	-2.85	1	5	7.8e+002	1	AGDADLVMAAGMENMSASPFLMPGKVR + 4 Oxidation (M)
☑	2208	873.4563	1744.8980	1744.9029	-2.79	1	5	2.4e+003	1	VLNREESLQLMDLLG + Oxidation (M)
☑	2628	685.3648	2053.0726	2053.0653	3.55	1	5	1.5e+003	1	TEKVMDLISQLYDLLEK + Oxidation (M)
☑	3470	935.4286	2803.2640	2803.2714	-2.66	0	5	7.9e+002	1	YPSVDTLSMGMSGDMEAAIEAGSTIVR + Oxidation (M)
☑	1586	684.8203	1367.6260	1367.6252	0.65	1	5	1.2e+003	1	KNGEAASGAMYNR
☑	2954	1117.5660	2233.1174	2233.1147	1.21	0	5	2e+003	1	DLEAQIAVVTSESNLQELMK + Oxidation (M)
☑	2909	1109.5110	2217.0074	2217.0160	-3.87	1	4	1.1e+003	1	MTENAWFAARPSGTEDKYK + Oxidation (M)
☑	1528	677.3958	1352.7770	1352.7776	-0.39	0	4	8.8e+002	1	ATPGAAILAGTAALR
☑	3203	775.0629	2322.1669	2322.1638	1.34	1	4	2e+003	1	AALAPRTPASPADDCIVEEALR + Carbamidomethyl (C)
☑	3293	792.0790	2373.2152	2373.2236	-3.57	1	4	1.7e+003	1	DAVAAAVRLHGEPMVHAHVTHR
☑	1380	438.5647	1312.6723	1312.6735	-0.95	1	4	1.6e+003	1	DGAPLQTPSGSKR
☑	3282	1180.6600	2359.3054	2359.2987	2.86	1	4	5.3e+002	1	MLRHIAFGLGGLAVLAAAFEFR
☑	3393	857.4106	2569.2100	2569.2083	0.67	0	4	1.8e+003	1	MMSCVTSSGAASIPDVILPMCVIR + Carbamidomethyl (C); 2 Oxidation (M)
☑	3458	697.8241	2787.2673	2787.2729	-2.01	1	4	9.1e+002	1	RRPSQAQAEEEIEDEAAEATELCR + Carbamidomethyl (C)
☑	3538	974.1271	2919.3595	2919.3704	-3.75	1	4	1.2e+003	1	AFEQIMEALKDDSIDMIGLYGMGGVGK + 2 Oxidation (M)
☑	2424	610.6877	1829.0413	1829.0485	-3.94	0	4	4.3e+002	1	ATLLIAGAAVMTVWVLGK + Oxidation (M)
☑	3182	580.0555	2316.1929	2316.1961	-1.38	1	4	1.8e+003	1	KGVAAFIENLIGSEQAEEAVNK
☑	2856	731.3758	2191.1056	2191.1055	0.01	0	4	2.1e+003	1	DISAAICGGDTPHIGAVALASPR
☑	3524	720.3364	2877.3165	2877.3136	1.02	0	4	1e+003	1	YSEPASLWDLAEAVLCPMTHMGLDR + Carbamidomethyl (C); Oxidation (M)
☑	2391	904.9221	1807.8296	1807.8267	1.64	1	4	1.5e+003	1	KCEAGAVNTACPVCVTDK
☑	3507	948.4326	2842.2760	2842.2816	-2.00	1	4	7.9e+002	1	WGSHTNEHCFIQMPDNHHQPVKK + Carbamidomethyl (C); Oxidation (M)
☑	3546	733.5938	2930.3461	2930.3361	3.41	1	4	1e+003	1	CTSTGVIKCQQGGQPMSAENISWYAAK + Carbamidomethyl (C); Oxidation (M)
☑	1765	738.8839	1475.7532	1475.7555	-1.50	0	4	2.7e+003	1	QYQMGLANPLLGR + Oxidation (M)
☑	3486	943.7696	2828.2870	2828.2892	-0.78	1	4	9.7e+002	1	CSETVTAGRSGTMGDIDAMAVGLTAWR + Carbamidomethyl (C); Oxidation (M)
☑	1051	618.7771	1235.5396	1235.5386	0.82	1	4	7.1e+002	1	RMAMEAEENR
☑	2016	827.9265	1653.8384	1653.8362	1.34	0	4	2.2e+003	1	ELVPEGQTPETWLR
☑	3329	600.8438	2399.3461	2399.3552	-3.79	1	4	3.6e+002	1	RTLVMAVAAAVVLFLVGGFFYR
☑	3240	781.0536	2340.1390	2340.1341	2.08	1	4	2e+003	1	EQEVIRCYLEGMTVTEIAEK
☑	3297	792.4068	2374.1986	2374.1991	-0.21	0	4	1.9e+003	1	FEETSIIASWPELMGKPVANR
☑	1768	741.8166	1481.6186	1481.6205	-1.25	0	4	4.1e+002	1	SEPPGQDQAAAMQH + Oxidation (M)
☑	3332	801.6840	2402.0302	2402.0253	2.02	0	4	4.1e+002	1	LNANDDAASDAEFDEMLSALMK + 2 Oxidation (M)
☑	3573	1141.1990	3420.5752	3420.5853	-2.97	1	4	9.5e+002	1	EAFFEEQTQSLCIIMEFADNGDLQTKIER + Oxidation (M)
☑	1044	412.2203	1233.6391	1233.6387	0.27	1	4	3.5e+003	1	TRVLDGTVDMK
☑	2690	1057.4980	2112.9814	2112.9879	-3.03	0	4	1.6e+003	1	HASHVDVFWPGQADPTHGR
☑	3572	854.4108	3413.6141	3413.6200	-1.73	1	4	1.3e+003	1	LMGLLMTDGEHGTCRVVAAACTIGEAIEHEVR + 2 Oxidation (M)
☑	3284	788.0634	2361.1684	2361.1708	-1.04	1	4	2.3e+003	1	VWEVMPIENLQMRLEDSLK + 2 Oxidation (M)
☑	2842	1093.6190	2185.2234	2185.2299	-2.97	0	4	4.5e+002	1	WLILIIPTVTNGIWEYVR
☑	2553	961.9209	1921.8272	1921.8298	-1.35	0	4	6.7e+002	1	NEAIDMGPVMDASSWQR + Oxidation (M)
☑	3214	1165.5240	2329.0334	2329.0348	-0.58	0	4	8.4e+002	1	AAALLSSGCNDMGGSIMNESITR + 2 Oxidation (M)
☑	2817	726.3691	2176.0855	2176.0933	-3.61	0	4	2.3e+003	1	GNDVIVVLSAMGDTTDELIAK + Oxidation (M)
☑	3391	854.0959	2559.2659	2559.2673	-0.55	0	4	2.1e+003	1	GPSMTIDTACSSSLVAVHQAISALK + Carbamidomethyl (C); Oxidation (M)
☑	3565	1038.8980	3113.6722	3113.6608	3.64	1	4	7.2e+002	1	AIAGTVGGEVTEELPGSALQKHPDVVIIADK
☑	324	459.6917	917.3688	917.3661	2.96	0	4	1.7e+002	1	SATCTHNQ + Carbamidomethyl (C)
☑	2043	840.4150	1678.8154	1678.8097	3.42	1	4	2.7e+003	1	MTQAEFATHRGVSTK + Oxidation (M)
☑	3177	772.4014	2314.1824	2314.1813	0.45	0	4	2.2e+003	1	LGCKPPIQAPSTEPSGIVAMYR
☑	2267	884.4103	1766.8060	1766.8113	-2.99	0	4	1.5e+003	1	QAITAAGSGCMAAMLAER + Oxidation (M)
☑	1396	439.5494	1315.6264	1315.6230	2.53	0	4	2.1e+003	1	MAYDAQLYGLR + Oxidation (M)
☑	2440	918.0087	1834.0028	1833.9989	2.16	1	4	1.3e+003	1	IAPGFEPSGGPLVPSPKGK
☑	3255	1174.5940	2347.1734	2347.1703	1.36	1	4	2.2e+003	1	ANVQLLPDPSIPTNESGMRHR + Oxidation (M)
☑	2350	895.9871	1789.9596	1789.9542	3.02	1	4	1.7e+003	1	QGIRNSMVMLNTSVIK
☑	3216	1166.0800	2330.1454	2330.1545	-3.88	1	4	2.3e+003	1	LGILAHMGAETVGKQIAMDMGR + 2 Oxidation (M)
☑	3147	1152.1470	2302.2794	2302.2831	-1.60	1	4	5.7e+002	1	SKVLIAISGGVDSVVLAHLCHK + Carbamidomethyl (C)
☑	228	416.2522	830.4898	830.4902	-0.39	0	4	3.7e+002	1	ITPPYLK
☑	377	478.7857	955.5568	955.5563	0.58	1	4	3e+003	1	AIPRASVSR
☑	2737	1072.6130	2143.2114	2143.2041	3.42	0	4	4.5e+002	1	QFVILNQIVVPLQDYINK
☑	3519	957.7743	2870.3011	2870.3111	-3.49	1	4	1e+003	1	QICMTEEEYSCMLAIILFRSDYR + Carbamidomethyl (C)
☑	2917	741.4018	2221.1836	2221.1796	1.78	1	4	1.3e+003	1	NSAQVFIAAYGLAWIQRWK
☑	2240	876.9385	1751.8624	1751.8625	-0.01	1	4	2.3e+003	1	GGRAEVVNADSMLVYR + Oxidation (M)
☑	3273	1179.6500	2357.2854	2357.2777	3.29	1	4	8.2e+002	1	MELGTRTIFNILGPLTNPAGVK + Oxidation (M)
☑	3280	1180.5940	2359.1734	2359.1736	-0.07	1	4	2.2e+003	1	EAEIVANAGQRGMVTIATNMAGR
☑	3356	811.7379	2432.1919	2432.1981	-2.56	0	4	2.4e+003	1	CVVVFHGGEPLLMGSGEIAAFAR + Carbamidomethyl (C); Oxidation (M)
☑	3484	707.3024	2825.1805	2825.1805	-0.02	0	4	2.4e+002	1	CQDNFFLVDGDTGCQECPTCYALVK + Carbamidomethyl (C)
☑	2825	728.3463	2182.0171	2182.0160	0.47	0	4	1.8e+003	1	HNTVSLGMLHSGGFSAMHAGR + Oxidation (M)
☑	3390	1276.6470	2551.2794	2551.2815	-0.80	1	4	2.2e+003	1	VPVDKWPDPGAVLPVLVAMDDMR + 2 Oxidation (M)
☑	3522	957.7765	2870.3077	2870.3116	-1.36	1	4	1.2e+003	1	QWWADNKPGMTFGIGATMTRNEAEK + 2 Oxidation (M)
☑	3342	1209.1020	2416.1894	2416.1814	3.34	1	4	2.4e+003	1	SHGMSIDSRHVMLLADLMTFR
☑	1077	623.7542	1245.4938	1245.4940	-0.16	0	4	2.1e+002	1	GACEAVFSCMR + Carbamidomethyl (C); Oxidation (M)
☑	3306	794.0322	2379.0748	2379.0696	2.19	1	4	1.3e+003	1	DGLNEAGFAITNPNAQRSCGCGK + Carbamidomethyl (C)
☑	3374	825.7590	2474.2552	2474.2475	3.10	0	4	2e+003	1	MAILPQNPESAGGLTVGELVSYGR + Oxidation (M)
☑	2919	556.7501	2222.9713	2222.9676	1.65	0	4	8.2e+002	1	QPPDTGGQPSETGGQPSDTDPR
☑	2841	729.3730	2185.0972	2185.1029	-2.60	1	4	2.5e+003	1	QRFLQQHDQVLGLGFDER
☑	3474	1407.6440	2813.2734	2813.2789	-1.92	1	4	1e+003	1	LEQKWQEWETTMEGAEMFLNAAR + Oxidation (M)
☑	3178	1158.5800	2315.1454	2315.1468	-0.57	0	4	2.6e+003	1	ADLSDLTVVHEMPGIDYAVVR + Oxidation (M)
☑	2650	1036.9910	2071.9674	2071.9608	3.22	0	4	2.1e+003	1	HANEYLEHMTFCLPPVR + Oxidation (M)
☑	3515	954.4333	2860.2781	2860.2718	2.21	0	4	8.3e+002	1	GCILVDEYMQTNLPDVYAAGDCAEVR + Oxidation (M)
☑	2242	876.9794	1751.9442	1751.9458	-0.87	1	4	1.5e+003	1	FSLFDLLGLGEAAGKSK
☑	3295	594.3115	2373.2169	2373.2117	2.18	1	4	2.2e+003	1	GYENVRLGVLVSNTSAFSFWK
☑	2938	743.3680	2227.0822	2227.0790	1.41	1	4	2.4e+003	1	MASGSGKTLPSYESGEGIATLR + Oxidation (M)
☑	3445	924.7672	2771.2798	2771.2796	0.07	1	4	1.5e+003	1	CRSSPVSPPPQELLDVSGSECWWR + Carbamidomethyl (C)
☑	2513	632.0238	1893.0496	1893.0506	-0.54	1	4	9.6e+002	1	IVGLHENGTVIDMLRVK
☑	3453	930.0952	2787.2638	2787.2731	-3.35	1	4	1.1e+003	1	NEEMQTNAKMVDDLFEIDANGFIK + Oxidation (M)
☑	3568	850.1527	3396.5817	3396.5735	2.42	1	4	1.3e+003	1	QKMCEETSLVNSEQQPLPVTSDAMSTVSTEK
☑	2561	965.9710	1929.9274	1929.9214	3.13	1	4	2.3e+003	1	IINKGSDSLMESEQSHR
☑	2509	944.9379	1887.8612	1887.8607	0.27	1	3	1.6e+003	1	FEVCTAAMNKQFEASGR
☑	3543	976.7811	2927.3215	2927.3311	-3.27	1	3	1.1e+003	1	EIVQDCEISKVSEGSCSLSAGSGEMIGR + Carbamidomethyl (C)

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☑ 3354  811.0875 2430.2407 2430.2503 -3.96  1     3  2.2e+003  1         IGLVNDVFDDQDALLAAARSTAR
☑ 3477  939.7714 2816.2924 2816.2891  1.16  1     3  1.4e+003  1         LQASEMESYQRSQALVMLNDMANR + 2 Oxidation (M)
☑  430  494.3012  986.5878  986.5873  0.58  1     3  1.7e+003  1         KGGVVASITR
☑ 2695 1060.9320 2119.8494 2119.8510 -0.72  1     3  1.5e+002  1         MDRGYESYNVMAHCQER + 2 Oxidation (M)
☑ 3464  933.4357 2797.2853 2797.2793  2.13  1     3  1.4e+003  1         CTDGSGGIANLVNAGSTNVVRDMDIMR + 2 Oxidation (M)
☑ 1844  511.6506 1531.9300 1531.9238  4.00  1     3        91  1         KNIGAGLAFLLLFR
☑ 3151 1153.0730 2304.1314 2304.1240  3.22  1     3  2.5e+003  1         EAARNAVSNIATNTGQVCSAATR
☑ 3562 1007.4660 3019.3762 3019.3759  0.10  1     3  1.2e+003  1         LKMAIQMGNQETGGSVIEMGEAEYMVR + 3 Oxidation (M)
☑ 3301 1188.5900 2375.1654 2375.1647  0.32  1     3  2.5e+003  1         VEMAKEQNSQGLTSLHLICMK + Oxidation (M)
☑ 2588  992.9890 1983.9634 1983.9684 -2.49  0     3  2.5e+003  1         NIHVVDMDTIDISNLNR + Oxidation (M)
☑ 3336  802.7357 2405.1853 2405.1935 -3.43  1     3  2.7e+003  1         EKLPNSTVVSSPADGAAGAPHSGTR
☑ 3022  754.4303 2260.2691 2260.2692 -0.03  1     3    5e+002  1         AAQKQEKPSVQGLIHIWLSK
☑ 3550  981.7875 2942.3407 2942.3298  3.71  1     3  1.2e+003  1         RMESFCMFFSVSFCISVMLSLAYR + Carbamidomethyl (C); 2 Oxidation (M)
☑ 3204  581.5505 2322.1729 2322.1712  0.74  0     3  2.7e+003  1         NLCQLGSCLLVIQGDYESVLR
☑ 2649 1036.9910 2071.9674 2071.9732 -2.76  0     3  2.3e+003  1         LTIGAVDDPLEAEADAMADR
☑ 3198 1161.5520 2321.0894 2321.0818  3.27  0     3  2.1e+003  1         ASNGQNTVAGGFNINVNEMNVR + Oxidation (M)
☑ 3360  610.5746 2438.2693 2438.2699 -0.26  0     3    2e+003  1         ALLGAAALGASGLALMQNAAGAAANDR
☑ 3469  935.4263 2803.2571 2803.2654 -2.96  1     3  9.9e+002  1         EDISHSFLPGEAQGAVDRETCQMAR + Carbamidomethyl (C)
☑ 3450  929.7595 2786.2567 2786.2541  0.92  1     3  1.2e+003  1         NMPACFSGQSGTVDLGSVFFNGDKHR + Oxidation (M)
☑ 3583  868.6632 3470.6237 3470.6302 -1.88  1     3  1.4e+003  1         MDTQYQLLERVCDAAANQTILCVGDIMLDR + Carbamidomethyl (C); Oxidation (M)
☑   23  350.1825  698.3504  698.3500  0.63  0     3  1.2e+002  1         TWAGHK
☑  295  449.2739  896.5332  896.5304  3.16  1     3    1e+003  1         RAKPGVNR
☑ 3270  786.7245 2357.1517 2357.1508  0.38  1     3  3.1e+003  1         MPPPPPPMTSSPSSLFGSLSRR + 2 Oxidation (M)
☑ 3449  929.7572 2786.2498 2786.2454  1.57  0     3  1.1e+003  1         AFGTGLEGGVMDQQSVFSVETNGDADR
☑ 3552  986.5334 2956.5784 2956.5797 -0.46  0     3    1e+003  1         ADDAGTQLTLLITFLAAVFTSSYAVQIK
☑   16  631.3662  630.3589  630.3588  0.13  0     3  6.3e+003  1         VTAIVE
☑ 3452  697.8232 2787.2637 2787.2633  0.15  0     3  1.2e+003  1         TMQEFRPDGWFITGDIVTMAEDGR + Oxidation (M)
☑ 2601 1003.4910 2004.9674 2004.9752 -3.88  1     3    3e+003  1         IKEQSAADYVPQTGENAGK
☑ 3587  911.2186 3640.8453 3640.8519 -1.81  1     3  1.5e+003  1         QVKPSHRGELEITTLNEMYLNDGSLNVELLGR + Oxidation (M)
☑ 1872  778.3097 1554.6048 1554.6110 -3.98  0     3  1.2e+002  1         EQWVDPSESDSYN
☑  709  568.3505 1134.6864 1134.6873 -0.75  0     3  6.6e+002  1         HLIATIGALAR
☑ 3340  805.3773 2413.1101 2413.1172 -2.97  0     3  1.9e+003  1         DLQYDYVPVELAIENSSSATEA
☑ 2759 1079.0360 2156.0574 2156.0507  3.14  0     3    3e+003  1         NLNVAAGHAMMGWSLGPITGK + 2 Oxidation (M)
☑ 2837 1093.0140 2184.0134 2184.0197 -2.88  1     3  2.1e+003  1         LSAAYFLDSFCNSEVYRSI
☑ 3386  841.1242 2520.3508 2520.3522 -0.58  1     3  1.5e+003  1         ARAAEVLLGADAWLMPTVSIAPPR + Oxidation (M)
☑ 3576  860.6518 3438.5781 3438.5742  1.14  0     3  1.2e+003  1         VPMDPSELIIGTICGGSDGTSGMTGNPAAGLAFDR + 2 Oxidation (M)
☑ 2369  900.4472 1798.8798 1798.8785  0.77  0     3  3.1e+003  1         DMLDLPVDGGHPRPHK + Oxidation (M)
☑ 2452  923.0139 1844.0132 1844.0077  3.00  1     3  1.6e+003  1         QIVKLMGGAIGVESELGK + Oxidation (M)
☑ 2951 1117.5630 2233.1114 2233.1123 -0.38  1     3  3.3e+003  1         GTSGGSIKFNITCSVLEMVFK + Oxidation (M)
☑ 3202  775.0434 2322.1084 2322.1087 -0.16  1     3  2.7e+003  1         RTELADSPPEPGSASAGLPADER
☑ 3560  998.1318 2991.3736 2991.3623  3.75  1     3  1.5e+003  1         LSHCQLEADVKAESIVVDMAANDSDMK + Carbamidomethyl (C); Oxidation (M)
☑ 2662 1044.4930 2086.9714 2086.9782 -3.25  1     3  2.2e+003  1         IFVGYDPREDVAYEVCR + Carbamidomethyl (C)
☑ 3206 1162.1310 2322.2474 2322.2430  1.90  1     3  1.5e+003  1         APPSEVLTAERILEATEEVLR
☑ 3222  778.4035 2332.1887 2332.1845  1.79  1     3  2.8e+003  1         AGAAQTIVASSQRWALMTETPK + Oxidation (M)
☑ 2705 1066.0980 2130.1814 2130.1758  2.64  1     3  9.1e+002  1         LKTGVMEILDYLDALAIPR
☑ 3479  940.7580 2819.2522 2819.2459  2.22  1     3    1e+003  1         LHSRASTVVPSDSCMHLDMSAVCER + Carbamidomethyl (C); 2 Oxidation (M)
☑ 1761  491.2994 1470.8764 1470.8745  1.31  1     3  4.4e+002  1         MANPLFVGLLRLK
☑ 3490  943.7706 2828.2900 2828.2984 -2.96  1     2  1.6e+003  1         NLLVQPGCEHCFRTAEHDHQQPR + 2 Carbamidomethyl (C)
☑ 3540  974.1277 2919.3613 2919.3544  2.34  1     2  1.9e+003  1         EINKATGTQMCSHWFSASQWQLPNR
☑ 2580  493.7883 1971.1241 1971.1261 -1.01  0     2  5.8e+002  1         SLAMLPMGLTVLVGVLVAR + 2 Oxidation (M)
☑ 2824  726.7069 2177.0989 2177.1006 -0.79  1     2  3.1e+003  1         DLMMMALADRIASELAAALR + Oxidation (M)
☑  184  403.1561  804.2976  804.3007 -3.78  0     2  1.5e+002  1         CDMSGHR
☑ 3467  935.0861 2802.2365 2802.2386 -0.78  1     2  9.9e+002  1         PIGSYCPSCRYPCFPTDLMNPVR + 3 Carbamidomethyl (C); Oxidation (M)
☑ 3200 1161.6500 2321.2854 2321.2856 -0.07  1     2  8.2e+002  1         LTVVGRVPAGSVFPGTVGPGEAVR
☑ 3218  778.3808 2332.1206 2332.1265 -2.56  1     2    3e+003  1         MAWSKMNSLLLVSGGLGMFDK + 3 Oxidation (M)
☑ 2941 1114.5730 2227.1314 2227.1233  3.66  1     2  3.1e+003  1         TAVAAIEVVSRSNPDNDWVGK
☑   33  356.1408  710.2670  710.2662  1.19  0     2  1.2e+002  1         QACCMR
☑   50  363.6711  725.3276  725.3266  1.51  0     2    4e+002  1         SMVSISS + Oxidation (M)
☑ 3036 1135.5570 2269.0994 2269.0911  3.67  0     2  3.4e+003  1         VLNYCLYGSPQAMAPWIAEK + Oxidation (M)
☑  258  426.2461  850.4776  850.4773  0.38  0     2  1.8e+003  1         AGHSKPVR
☑ 3498  944.0986 2829.2740 2829.2673  2.36  1     2  1.4e+003  1         SHKAWMIEHTMYVTSQEGGTCVFR + 2 Oxidation (M)
☑ 3549  981.7827 2942.3263 2942.3175  3.00  1     2  1.4e+003  1         EQAAAYSGPETTIDCRSMVPEGASPGFR + Oxidation (M)
☑ 1946  792.7858 1583.5570 1583.5552  1.19  0     2        21  1         DGGHDQDVCNYCCR
☑ 3330 1201.7050 2401.3954 2401.3919  1.47  1     2  2.1e+002  1         SALLACLAVTLLLGGVWAYARLK
☑ 3466  935.0765 2802.2077 2802.2171 -3.38  1     2  6.8e+002  1         ATTTTTTTAEPESGEGAQEMMEVDKR + 2 Oxidation (M)
☑ 3487  943.7700 2828.2882 2828.2976 -3.34  0     2  1.6e+003  1         MHTLFDNHNHDNLEEIIYPAYAR + Oxidation (M)
☑ 2516  948.5474 1895.0802 1895.0777  1.37  0     2  9.2e+002  1         NMIFITSILCFLLIVR
☑ 3585 1166.2120 3495.6142 3495.6181 -1.12  1     2  1.7e+003  1         MARLSFQTGLPSGPSCENEANACGQLTIDSLR + 2 Carbamidomethyl (C); Oxidation (M)
☑  669  560.3426 1118.6706 1118.6672  3.05  1     2    1e+003  1         PVRAHSLALR
☑ 2950  745.3701 2233.0885 2233.0844  1.81  1     2  3.8e+003  1         QGERAHISIDPLHQMICGR + Carbamidomethyl (C); Oxidation (M)
☑ 3577  862.4070 3445.5989 3445.5952  1.07  1     2  1.7e+003  1         AAYDMGQVVNPRAAEGQIEGGIAMGMGYALTEK + 3 Oxidation (M)
☑ 3535  967.5259 2899.5559 2899.5639 -2.75  0     2  1.5e+003  1         RPLLALLVACLLAGVCVATGMVWDPFR + Oxidation (M)
☑ 3544  976.7886 2927.3440 2927.3463 -0.81  0     2  1.8e+003  1         GLGMGSTSGFVAAQLDALGMDTIGADDAMR
☑ 3480  940.7596 2819.2570 2819.2643 -2.60  1     2  1.3e+003  1         FDYAPHQAHATGMLELVGMDDKSDR + Oxidation (M)
☑ 2389  903.5102 1805.0058 1805.0047  0.65  1     2  1.1e+003  1         LDEVTLEALLNRLIGH
☑  843  591.7304 1181.4462 1181.4506 -3.70  1     2  1.7e+002  1         REEEDDDMK + Oxidation (M)
☑ 3575 1146.8720 3437.5942 3437.6038 -2.81  0     2  1.8e+003  1         ELTQGANVQANSLQESAAAVEQMSSSMNAISQK + Oxidation (M)
☑ 3523  959.4498 2875.3276 2875.3215  2.10  1     2  2.2e+003  1         GDLDRQIGEALCEITSIDPPMEGGSEK + Oxidation (M)
☑  187  404.2325  806.4504  806.4473  3.93  0     2  1.9e+003  1         AFCVVIR
☑ 3257  783.4069 2347.1989 2347.2059 -3.01  1     2  3.2e+003  1         YKLALENGVGTSEWNDIPTLK
☑ 2554  963.4983 1924.9820 1924.9750  3.64  1     2  3.9e+003  1         KFSLGASCLLELVDSGMR
☑ 2645 1035.0280 2068.0414 2068.0338  3.72  1     2  4.4e+003  1         QRDNGLGGESIWDILNPGK
☑ 2046  841.3236 1680.6326 1680.6297  1.77  0     2        78  1         YYNNGDPYACECR + 2 Carbamidomethyl (C)
☑ 3553  989.5306 2965.5700 2965.5761 -2.05  1     2  1.8e+003  1         RSTDSELHVVEQINVDFVVEISILPK
☑  213  414.7617  827.5088  827.5116 -3.38  1     2    3e+003  1         LAVLLKGD
☑ 3417  919.7573 2756.2501 2756.2543 -1.53  1     2  1.8e+003  1         VWLSCAFCCLPTGESLSPSCGAAKR + 3 Carbamidomethyl (C)
☑ 3541 1463.2770 2924.5394 2924.5396 -0.07  1     2  2.1e+003  1         QRFVGTVSDPGEIEWTTGLPVIATVPR
☑ 3496  943.7746 2828.3020 2828.3127 -3.78  1     2  2.1e+003  1         ICCFLPSHSCNPIMCFLRCLLGSQK + Oxidation (M)
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☑	2478	933.5240	1865.0334	1865.0384	-2.64	1	2	1.3e+003	1	VKPDNKPRLRPQDFR
☑	2660	1042.0140	2082.0134	2082.0090	2.14	0	2	4.5e+003	1	GNVAALSNSASSGPVSNNPSPR
☑	2550	640.2731	1917.7975	1917.8044	-3.62	1	1	5.6e+002	1	KAMTSSDGATADAMSGETR + 2 Oxidation (M)
☑	2397	906.9569	1811.8992	1811.9014	-1.19	1	1	4.1e+003	1	GVDAGLGDVLVADGGRGVDA
☑	3563	1011.8230	3032.4472	3032.4510	-1.25	1	1	2.9e+003	1	TTSVSPRSPVAGGPPPTASTTESGDCGFTIR
☑	30	351.6677	701.3208	701.3232	-3.33	0	1	9.6e+002	1	EQTPDL
☑	3094	1145.0580	2288.1014	2288.1073	-2.56	0	1	3.6e+003	1	HQEEYFDIPTSNLTPTQIR
☑	3554	989.7902	2966.3488	2966.3547	-2.01	1	1	1.8e+003	1	MSTLAPFGTVRSMGSSTLDWCYLACGR + Carbamidomethyl (C)
☑	2494	627.3640	1879.0702	1879.0680	1.17	1	1	7.8e+002	1	VAFSVSAFRVVITSQLR
☑	3468	1402.6350	2803.2554	2803.2471	2.97	1	1	1.5e+003	1	AICCFDCLPCAAGEISNLTDSTKCIR + Carbamidomethyl (C)
☑	3510	949.4296	2845.2670	2845.2600	2.45	0	1	1.4e+003	1	ETTYIGGTDNCYVEYTQATSSAAATTK
☑	2920	1112.4930	2222.9714	2222.9711	0.14	0	1	1.5e+003	1	DYTSQMEPLASLTASECFSK + Oxidation (M)
☑	1876	780.4696	1558.9246	1558.9307	-3.91	1	1	5.4e+002	1	RTPSLGHQVIVKPK
☑	3193	1160.0810	2318.1474	2318.1506	-1.37	0	1	4.3e+003	1	MLLMIAVETPGMNCILRPDL + Carbamidomethyl (C); 2 Oxidation (M)
☑	3581	864.9119	3455.6185	3455.6198	-0.38	1	1	2.4e+003	1	DEVPAPDNLTIRVYVNGECMQENHTGNLVR + Carbamidomethyl (C); Oxidation (M)
☑	1634	692.4191	1382.8236	1382.8245	-0.63	1	1	1.3e+003	1	NLVAALKGIVTER
☑	12	543.3152	542.3079	542.3064	2.79	0	1	5.3e+003	1	VALGPS
☑	1108	626.3782	1250.7418	1250.7459	-3.21	1	1	1.5e+003	1	LIELRANPAVR
☑	846	592.2240	1182.4334	1182.4355	-1.75	0	1	82	1	GGGMSPMMEAAE + Oxidation (M)
☑	3308	1194.0380	2386.0614	2386.0641	-1.13	1	1	1.9e+003	1	MLAPSGEMPAGNESLSRDTHDR + Oxidation (M)
☑	1791	758.4579	1514.9012	1514.9072	-3.92	1	1	4.6e+002	1	IIVSTKPPKEYLK
☑	3494	943.7714	2828.2924	2828.3006	-2.90	1	1	2.4e+003	1	EGDKFTGLMAFAGATMIMGSFCTAIAR + 2 Oxidation (M)
☑	1725	714.4286	1426.8426	1426.8408	1.27	1	1	1.3e+003	1	AALPAPPPLTAPRR
☑	3254	1174.5780	2347.1414	2347.1419	-0.20	1	1	4.5e+003	1	NLSRNGVMHEGYYSYLFGLK
☑	2379	901.4627	1800.9108	1800.9046	3.45	0	1	5.7e+003	1	YFGLGLENGNYTVNLK
☑	1486	671.7493	1341.4840	1341.4887	-3.45	0	1	46	1	LMCMEDDPNDK + 2 Oxidation (M)
☑	3520	957.7745	2870.3017	2870.3046	-1.03	1	1	2.1e+003	1	AVKQTFASLCEGCICPPEFPVCVCGR + 2 Carbamidomethyl (C)
☑	388	480.8014	959.5882	959.5916	-3.52	0	1	9.3e+002	1	RPVPPPVAK
☑	2879	1102.1090	2202.2034	2202.2055	-0.95	1	0	2e+003	1	LGQPGSILALVSPSGGMAVRHR
☑	1772	496.9750	1487.9032	1487.8977	3.71	1	0	2.2e+002	1	VPRLVPSPFLHVK
☑	2669	1049.5220	2097.0294	2097.0235	2.86	1	0	5.1e+003	1	LVLGGEEREMTIMFSDVR + Oxidation (M)
☑	3508	949.1016	2844.2830	2844.2926	-3.37	1	0	1.9e+003	1	FHDYWGSAPSIEQASYMAVGRAETR + Oxidation (M)
☑	3495	943.7717	2828.2933	2828.2892	1.45	1	0	2.6e+003	1	CSETVTAGRSGTMGDIDAMAVGLTAWR + Carbamidomethyl (C); Oxidation (M)
☑	2646	1035.9370	2069.8594	2069.8621	-1.29	1	0	6.6e+002	1	DEGNDSRSSSIDGSESVDSK
☑	3311	797.0707	2388.1903	2388.1948	-1.90	0	0	5.3e+003	1	VLEIESPLVVDNTFVDLDDEK
☑	1685	467.6240	1399.8502	1399.8551	-3.52	0	0	4.1e+002	1	LAAPPPPVALVISR
☑	1355	652.4095	1302.8044	1302.8023	1.63	0	0	2.7e+002	1	LPLTPLPLAAAAR
☑	1099	625.3389	1248.6632	1248.6615	1.40	1	0	4.3e+003	1	SFGDRPPFKAK
☑	620	549.3354	1096.6562	1096.6604	-3.80	0	0	2.4e+003	1	APLTALATALR
☑	3491	943.7709	2828.2909	2828.2957	-1.71	0	0	2.6e+003	1	TGTLTTNEMTVVTVSTFHATGEACER + Carbamidomethyl (C); Oxidation (M)
☑	2324	889.3506	1776.6866	1776.6841	1.44	0	0	2.1e+002	1	GVCVNGTCYCMDGWR + 2 Carbamidomethyl (C)
☑	3566	1067.6100	3199.8082	3199.8164	-2.57	1	0	4.9e+002	1	VCTGPTPWVAVVHIMMIPTIIIRAIVVVR + Oxidation (M)
☑	3304	1189.1070	2376.1994	2376.2004	-0.39	1	0	5.2e+003	1	TLAPLAPEMMPGAQVVASKFMR + 2 Oxidation (M)
☑	3504	948.0921	2841.2545	2841.2512	1.16	1	0	1.6e+003	1	GWFTSGSSTALPAPNPSTMDSGSGDKDR + Oxidation (M)
☑	883	599.7703	1197.5260	1197.5223	3.11	0	0	2.4e+003	1	GDYCELELEK
☑	1	*419.3155*	*418.3082*							
☑	2	*419.3156*	*418.3083*							
☑	3	*419.3156*	*418.3083*							
☑	4	*419.3156*	*418.3083*							
☑	5	*419.3156*	*418.3083*							
☑	6	*419.3156*	*418.3083*							
☑	7	*419.3157*	*418.3084*							
☑	8	*419.3157*	*418.3084*							
☑	9	*493.2525*	*492.2452*							
☑	10	*510.2779*	*509.2706*							
☑	11	*538.3273*	*537.3200*							
☑	13	*557.2977*	*556.2904*							
☑	14	*568.3514*	*567.3441*							
☑	20	*653.3500*	*652.3427*							
☑	21	*671.3620*	*670.3547*							
☑	48	*362.2225*	*722.4304*							
☑	126	*384.6514*	*767.2882*							
☑	134	*385.2269*	*768.4392*							
☑	195	*406.2487*	*810.4828*							
☑	234	*419.3155*	*836.6164*							
☑	296	*449.6311*	*897.2476*							
☑	333	*464.1079*	*926.2012*							
☑	409	*489.3141*	*976.6136*							
☑	431	*495.8337*	*989.6528*							
☑	488	*516.3146*	*1030.6146*							
☑	509	*523.3036*	*1044.5926*							
☑	535	*531.6996*	*1061.3846*							
☑	605	*545.3168*	*1088.6190*							
☑	606	*545.3177*	*1088.6208*							
☑	681	*564.1767*	*1126.3388*							
☑	797	*582.3516*	*1162.6886*							
☑	901	*602.7225*	*1203.4304*							
☑	914	*605.0281*	*1208.0416*							
☑	929	*607.1976*	*1212.3806*							
☑	1114	*627.5749*	*1253.1352*							
☑	1206	*641.2153*	*1280.4160*							
☑	1276	*648.3960*	*1294.7774*							
☑	1718	*711.2332*	*1420.4518*							
☑	1745	*482.2994*	*1443.8764*							
☑	1746	*723.4388*	*1444.8630*							
☑	1762	*736.4461*	*1470.8776*							
☑	1763	*736.4472*	*1470.8798*							
☑	1770	*495.7504*	*1484.2294*							

☑	1792	*758.4592*	*1514.9038*
☑	1907	*784.7799*	*1567.5452*
☑	1917	*526.3254*	*1575.9544*
☑	1963	*802.4857*	*1602.9568*
☑	2112	*849.5836*	*1697.1526*
☑	2115	*852.2592*	*1702.5038*
☑	2330	*890.5331*	*1779.0516*
☑	2351	*896.5020*	*1790.9894*
☑	2537	*955.4037*	*1908.7928*
☑	2566	*972.9239*	*1943.8332*
☑	2567	*973.0016*	*1943.9886*
☑	2598	*998.4896*	*1994.9646*
☑	2620	*1021.0130*	*2040.0114*
☑	3005	*1128.0370*	*2254.0594*
☑	3027	*1133.5350*	*2265.0554*
☑	3181	*1159.0750*	*2316.1354*
☑	3220	*1167.0860*	*2332.1574*
☑	3325	*1197.1050*	*2392.1954*
☑	3371	*824.1049*	*2469.2929*
☑	3395	*861.4869*	*2581.4389*
☑	3404	*878.4066*	*2632.1980*
☑	3406	*878.7282*	*2633.1628*
☑	3411	*910.1669*	*2727.4789*
☑	3471	*936.0983*	*2805.2731*

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Variable modifications : Carbamidomethyl (C),Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 4 ppm
Fragment Mass Tolerance: ± 0.4 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-TRAP
Number of queries      : 3588
```

Mascot: http://www.matrixscience.com/