MATRIX SCIENCE Mascot Search Results

```
User          : JPROS
Email         : pro@jbios.co.jp
Search title  : D:\JPROS\L015\b_3micro.wiff (sample number 1)
MS data file  : mas8CF.tmp
Database      : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Taxonomy      : Homo sapiens (human) (327411 sequences)
Timestamp     : 13 Feb 2019 at 09:51:30 GMT
Protein hits  : NP_004930.1    ATP-dependent RNA helicase DDX1 [Homo sapiens]
                NP_002477.1    nuclear cap-binding protein subunit 1 isoform 1 [Homo sapiens]
                BAG36698.1     unnamed protein product [Homo sapiens]
                AFA52006.1     keratin 1 [Homo sapiens]
                NP_000412.3    keratin, type I cytoskeletal 10 [Homo sapiens]
                XP_011524076.1 THO complex subunit 1 isoform X3 [Homo sapiens]
                NP_005122.2    THO complex subunit 1 [Homo sapiens]
                NP_000217.2    keratin, type I cytoskeletal 9 [Homo sapiens]
                NP_003669.4    THO complex subunit 5 homolog [Homo sapiens]
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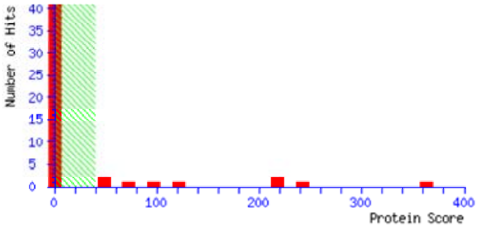
Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 39 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 ●	Display non-significant matches ☑	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**

1. NP_004930.1 **Mass:** 82380 **Score:** 363 **Matches:** 23(11) **Sequences:** 21(11) **emPAI:** 0.61
ATP-dependent RNA helicase DDX1 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	124	418.7112	835.4078	835.4440	-0.0362	0	37	0.31	1	U	K.DGFVALSK.A
☑	168	431.7193	861.4240	861.4596	-0.0356	0	15	23	1	U	K.APDGYIVK.S
☑	195	442.7371	883.4597	883.5127	-0.0530	0	34	0.25	1	U	K.ALIVEPSR.E
☑	225	474.2261	946.4376	946.4971	-0.0595	0	49	0.011	1	U	R.LDDLVSTGK.L
	226	474.2316	946.4486	946.4971	-0.0485	0	(4)	3.3e+02	2	U	R.LDDLVSTGK.L
☑	241	503.2317	1004.4488	1004.4815	-0.0327	0	48	0.01	1	U	K.VPVDEFDGK.V
☑	273	556.3160	1110.6175	1110.6761	-0.0585	0	49	0.0093	1	U	R.ELLIIGGVAAR.D
☑	279	583.2745	1164.5345	1164.5961	-0.0616	0	57	0.0014	1	U	R.FLICTDVAAR.G + Carbamidomethyl (C)
☑	280	585.2599	1168.5053	1168.5369	-0.0316	0	18	12	1	U	K.MDQAIIFCR.T + Carbamidomethyl (C); Oxidation (M
☑	311	624.8170	1247.6194	1247.6795	-0.0601	0	40	0.068	1	U	R.MGLAISLVATEK.E + Oxidation (M)
☑	320	630.8130	1259.6114	1259.6696	-0.0582	0	21	5.7	1	U	K.NQALFPACVLK.N + Carbamidomethyl (C)
☑	324	636.8105	1271.6065	1271.6721	-0.0656	0	75	1.8e-05	1	U	R.ELAEQTLNNIK.Q
☑	378	468.2248	1401.6524	1401.7115	-0.0591	0	12	40	1	U	K.IMHFPTWVDLK.G + Oxidation (M)
☑	423	843.3202	1684.6258	1684.7298	-0.1040	0	33	0.14	1	U	R.GSAFAIGSDGLCCQSR.E + 2 Carbamidomethyl (C)
☑	453	635.3256	1902.9549	1903.0415	-0.0866	0	69	5.6e-05	1	U	K.GHVDILAPTVQELAALEK.E
☑	463	656.6474	1966.9205	1967.0324	-0.1119	0	54	0.0019	1	U	R.DQLSVLENGVDIVVGTPGR.L
☑	467	668.2861	2001.8364	2001.9214	-0.0850	0	41	0.029	1	U	K.DNTRPGANSPEMWSEAIK.I
☑	468	673.6159	2017.8258	2017.9163	-0.0905	0	(18)	4.9	1	U	K.DNTRPGANSPEMWSEAIK.I + Oxidation (M)
☑	469	506.9876	2023.9213	2024.0327	-0.1115	0	17	9.7	1	U	K.GEDSVPDTVHHVVVPVNPK.T
☑	473	693.6772	2078.0098	2078.1048	-0.0950	0	21	3.7	1	U	R.GIDIHGVPYVINVTLPDEK.Q
☑	476	712.0043	2132.9910	2133.1007	-0.1097	0	41	0.039	1	U	K.EAQTSFLHLGYLPNQLFR.T
☑	492	791.3615	2371.0626	2371.1696	-0.1070	0	66	8.2e-05	1	U	R.FLVLDEADGLLSQGYSDFINR.M
☑	497	855.4205	2563.2398	2563.3534	-0.1136	1	39	0.044	1	U	K.TGAFSIPVIQIVYETLKDQQEGK.K

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2. NP_002477.1 **Mass:** 91781 **Score:** 243 **Matches:** 13(5) **Sequences:** 13(5) **emPAI:** 0.21
nuclear cap-binding protein subunit 1 isoform 1 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	285	593.2839	1184.5533	1184.6077	-0.0544	0	67	0.00017	1	U	R.IFANTESYLK.R
☑	286	594.2691	1186.5237	1186.5830	-0.0592	0	38	0.098	1	U	K.DGVLEEQIER.L

☑	313	625.8015	1249.5885	1249.6554	-0.0669	0	63	0.00031	1	U	K.ATNDEIFSILK.D
☑	349	647.7880	1293.5614	1293.6387	-0.0773	0	46	0.018	1	U	K.TCAAQLVSYPGK.N + Carbamidomethyl (C)
☑	358	439.2149	1314.6229	1314.6779	-0.0551	1	17	13	1	U	R.KDGVLEEQIER.L
☑	367	671.2658	1340.5170	1340.5701	-0.0531	0	33	0.23	1	U	R.LDTMNTTCVDR.F + Carbamidomethyl (C); Oxidation
☑	375	463.2423	1386.7050	1386.7693	-0.0643	0	27	1.1	1	U	R.FIMILTEHLVR.C + Oxidation (M)
☑	380	474.8949	1421.6630	1421.7337	-0.0707	1	29	0.66	1	U	R.KTCAAQLVSYPGK.N + Carbamidomethyl (C)
☑	381	713.3167	1424.6188	1424.7048	-0.0860	0	67	0.00012	1	U	K.ANNYNEAVYLVR.F
☑	390	505.5839	1513.7298	1513.7963	-0.0664	0	24	2.2	1	U	R.FVIEENLHCIIK.S + Carbamidomethyl (C)
☑	462	654.5888	1960.7445	1960.8684	-0.1239	0	49	0.0026	1	U	K.TSDANETEDHLESLICK.V + Carbamidomethyl (C)
☑	493	799.9699	2396.8878	2396.9890	-0.1011	0	28	0.12	1	U	R.MFDYTDDPEGPVMPGSHSVER.F + 2 Oxidation (M)
☑	494	830.7225	2489.1458	2489.2698	-0.1241	0	36	0.091	1	U	R.ILDIVPPTFSALCPANPTCIYK.Y + 2 Carbamidomethyl (C

Proteins matching the same set of peptides:
BAG35665.1 **Mass:** 91740 **Score:** 243 **Matches:** 13(5) **Sequences:** 13(5)
unnamed protein product [Homo sapiens]
BAD92470.1 **Mass:** 93151 **Score:** 243 **Matches:** 13(5) **Sequences:** 13(5)
nuclear cap binding protein subunit 1, 80kDa variant, partial [Homo sapiens]

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3. BAG36698.1 **Mass:** 65980 **Score:** 219 **Matches:** 11(6) **Sequences:** 11(6) **emPAI:** 0.38
unnamed protein product [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	181	437.7341	873.4536	873.4920	-0.0383	0	33	0.41	1		R.SLVNLGGSK.S
	251	517.2579	1032.5013	1032.5087	-0.0074	0	19	9.6	2		R.TLLEGEESR.M
☑	263	533.2412	1064.4678	1064.5138	-0.0460	0	22	4.2	1		K.AQYEDIAQK.S
☑	281	590.2789	1178.5433	1178.5931	-0.0498	0	42	0.045	1		K.YEELQITAGR.H
☑	322	633.2941	1264.5737	1264.6299	-0.0562	0	53	0.0032	1		R.TNAENEFVTIK.K
☑	352	651.8273	1301.6401	1301.7078	-0.0677	0	60	0.00067	1	U	R.SLDLDSIIAEVK.A
☑	366	447.5527	1339.6363	1339.6619	-0.0256	1	26	1.6	1		K.SKAEAESLYQSK.Y
☑	369	679.3110	1356.6074	1356.6885	-0.0811	0	0	5.7e+02	1		K.LNDLEDALQQAK.E
☑	372	692.3085	1382.6025	1382.6830	-0.0805	0	78	9.7e-06	1		K.SLNNQFASFIDK.V
☑	377	465.2298	1392.6675	1392.7249	-0.0574	1	53	0.0034	1		R.TNAENEFVTIKK.D
☑	384	738.3549	1474.6953	1474.7780	-0.0827	0	83	3.1e-06	1		R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:
NP_006112.3 **Mass:** 65999 **Score:** 219 **Matches:** 11(6) **Sequences:** 11(6)
keratin, type II cytoskeletal 1 [Homo sapiens]
AAG41947.1 **Mass:** 66027 **Score:** 219 **Matches:** 11(6) **Sequences:** 11(6)
keratin 1 [Homo sapiens]
AFA52002.1 **Mass:** 66013 **Score:** 219 **Matches:** 11(6) **Sequences:** 11(6)
keratin 1 [Homo sapiens]
AFA52004.1 **Mass:** 65930 **Score:** 219 **Matches:** 11(6) **Sequences:** 11(6)
keratin 1 [Homo sapiens]
AFA52005.1 **Mass:** 66086 **Score:** 219 **Matches:** 11(6) **Sequences:** 11(6)
keratin 1 [Homo sapiens]
AFA52007.1 **Mass:** 66071 **Score:** 219 **Matches:** 11(6) **Sequences:** 11(6)
keratin 1 [Homo sapiens]

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4. AFA52006.1 **Mass:** 66026 **Score:** 210 **Matches:** 11(6) **Sequences:** 11(6) **emPAI:** 0.38
keratin 1 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	181	437.7341	873.4536	873.4920	-0.0383	0	33	0.41	1		R.SLVNLGGSK.S
	251	517.2579	1032.5013	1032.5087	-0.0074	0	19	9.6	2		R.TLLEGEESR.M
	263	533.2412	1064.4678	1064.5138	-0.0460	0	22	4.2	1		K.AQYEDIAQK.S
	281	590.2789	1178.5433	1178.5931	-0.0498	0	42	0.045	1		K.YEELQITAGR.H
	322	633.2941	1264.5737	1264.6299	-0.0562	0	53	0.0032	1		R.TNAENEFVTIK.K
☑	361	665.3231	1328.6316	1328.7187	-0.0871	0	44	0.026	1	U	R.NLDLDSIIAEVK.A
	366	447.5527	1339.6363	1339.6619	-0.0256	1	26	1.6	1		K.SKAEAESLYQSK.Y
	369	679.3110	1356.6074	1356.6885	-0.0811	0	0	5.7e+02	1		K.LNDLEDALQQAK.E
	372	692.3085	1382.6025	1382.6830	-0.0805	0	78	9.7e-06	1		K.SLNNQFASFIDK.V
	377	465.2298	1392.6675	1392.7249	-0.0574	1	53	0.0034	1		R.TNAENEFVTIKK.D
	384	738.3549	1474.6953	1474.7780	-0.0827	0	83	3.1e-06	1		R.FLEQQNQVLQTK.W

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5. NP_000412.3 **Mass:** 58766 **Score:** 110 **Matches:** 6(2) **Sequences:** 6(2) **emPAI:** 0.13
keratin, type I cytoskeletal 10 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	91	405.2113	808.4080	808.4330	-0.0251	0	23	2.1	1		R.LASYLDK.V
☑	250	516.2822	1030.5499	1030.5910	-0.0411	0	35	0.24	1	U	R.VLDELTLTK.A
☑	270	545.7352	1089.4559	1089.5237	-0.0678	0	58	0.0011	1	U	K.VTMQNLNDR.L
☑	272	555.2029	1108.3913	1108.4825	-0.0912	0	18	7.9	1	U	K.DAEAWFNEK.S
☑	371	691.2844	1380.5542	1380.6408	-0.0867	0	60	0.00055	1	U	R.ALEESNYELEGK.I
☑	387	498.5559	1492.6457	1492.7270	-0.0812	1	37	0.12	1	U	R.SQYEQLAEQNRK.D

Proteins matching the same set of peptides:
P13645.6 **Mass:** 58792 **Score:** 110 **Matches:** 6(2) **Sequences:** 6(2)
RecName: Full=Keratin, type I cytoskeletal 10; AltName: Full=Cytokeratin-10; Short=CK-10; AltName: Full=Keratin-10; Short=K10
CAA32649.1 **Mass:** 59492 **Score:** 110 **Matches:** 6(2) **Sequences:** 6(2)
unnamed protein product [Homo sapiens]

AAH34697.1 **Mass:** 58792 **Score:** 110 **Matches:** 6(2) **Sequences:** 6(2)
Keratin 10 [Homo sapiens]
EAW60681.1 **Mass:** 63308 **Score:** 110 **Matches:** 6(2) **Sequences:** 6(2)
keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA_b [Homo sapiens]
XP_005257400.1 **Mass:** 63308 **Score:** 110 **Matches:** 6(2) **Sequences:** 6(2)
keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]

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6. XP_011524076.1 **Mass:** 41459 **Score:** 86 **Matches:** 4(2) **Sequences:** 4(2) **emPAI:** 0.18
THO complex subunit 1 isoform X3 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	236	**489.2221**	**976.4297**	**976.4866**	**-0.0568**	**0**	**14**	**29**	**3**		**R.TAPEDFLGK.G**
☑	271	**547.2718**	**1092.5290**	**1092.5889**	**-0.0598**	**0**	**37**	**0.12**	**1**		**K.ILAPYLEMK.D + Oxidation (M)**
☑	287	**596.2780**	**1190.5414**	**1190.5965**	**-0.0551**	**0**	**49**	**0.0074**	**1**		**K.ILMGNEELTR.L + Oxidation (M)**
☑	420	**558.9379**	**1673.7917**	**1673.8624**	**-0.0707**	**0**	**59**	**0.00073**	**1**		**R.DKPVTGEQIEVFANK.L**

Proteins matching the same set of peptides:
XP_024307060.1 **Mass:** 40672 **Score:** 86 **Matches:** 4(2) **Sequences:** 4(2)
THO complex subunit 1 isoform X4 [Homo sapiens]
XP_011524075.1 **Mass:** 61230 **Score:** 86 **Matches:** 4(2) **Sequences:** 4(2)
THO complex subunit 1 isoform X2 [Homo sapiens]

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7. NP_005122.2 **Mass:** 75619 **Score:** 83 **Matches:** 5(2) **Sequences:** 5(2) **emPAI:** 0.10
THO complex subunit 1 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	236	489.2221	976.4297	976.4866	-0.0568	0	14	29	3		R.TAPEDFLGK.G
	271	547.2718	1092.5290	1092.5889	-0.0598	0	37	0.12	1		K.ILAPYLEMK.D + Oxidation (M)
	287	596.2780	1190.5414	1190.5965	-0.0551	0	49	0.0074	1		K.ILMGNEELTR.L + Oxidation (M)
☑	379	**706.3390**	**1410.6634**	**1410.7507**	**-0.0873**	**0**	**14**	**20**	**1**	**U**	**M.SPTPPLFSLPEAR.T**
	420	558.9379	1673.7917	1673.8624	-0.0707	0	59	0.00073	1		R.DKPVTGEQIEVFANK.L

Proteins matching the same set of peptides:
BAG37293.1 **Mass:** 75592 **Score:** 83 **Matches:** 5(2) **Sequences:** 5(2)
unnamed protein product [Homo sapiens]
XP_011524074.1 **Mass:** 76406 **Score:** 83 **Matches:** 5(2) **Sequences:** 5(2)
THO complex subunit 1 isoform X1 [Homo sapiens]

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8. NP_000217.2 **Mass:** 62027 **Score:** 44 **Matches:** 4(1) **Sequences:** 4(1) **emPAI:** 0.06
keratin, type I cytoskeletal 9 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	91	405.2113	808.4080	808.4330	-0.0251	0	23	2.1	1		R.LASYLDK.V
	262	**530.7554**	**1059.4963**	**1059.5560**	**-0.0597**	**0**	**20**	**7.2**	**3**	**U**	**K.TLLDIDNTR.M**
	263	533.2412	1064.4678	1064.4920	-0.0242	0	15	22	2	U	K.STMQELNSR.L
☑	303	**616.7615**	**1231.5084**	**1231.5906**	**-0.0821**	**0**	**44**	**0.025**	**1**	**U**	**R.SGGGGGGGLGSGGSIR.S**

Proteins matching the same set of peptides:
EAW60744.1 **Mass:** 57526 **Score:** 44 **Matches:** 4(1) **Sequences:** 4(1)
keratin 9 (epidermolytic palmoplantar keratoderma) [Homo sapiens]
CAA82315.1 **Mass:** 62092 **Score:** 44 **Matches:** 4(1) **Sequences:** 4(1)
cytokeratin 9 [Homo sapiens]

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9. NP_003669.4 **Mass:** 78458 **Score:** 37 **Matches:** 1(0) **Sequences:** 1(0)
THO complex subunit 5 homolog [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	418	**557.2607**	**1668.7603**	**1668.7890**	**-0.0287**	**0**	**37**	**0.11**	**1**	**U**	**K.AEVTMGDPHQQTLAR.L + Oxidation (M)**

Proteins matching the same set of peptides:
EAW59807.1 **Mass:** 90865 **Score:** 37 **Matches:** 1(0) **Sequences:** 1(0)
hCG2011153, isoform CRA_a [Homo sapiens]
EAW59810.1 **Mass:** 92113 **Score:** 37 **Matches:** 1(0) **Sequences:** 1(0)
hCG2011153, isoform CRA_d [Homo sapiens]
BAG72824.1 **Mass:** 78472 **Score:** 37 **Matches:** 1(0) **Sequences:** 1(0)
THO complex 5, partial [synthetic construct]
XP_005261854.1 **Mass:** 79706 **Score:** 37 **Matches:** 1(0) **Sequences:** 1(0)
THO complex subunit 5 homolog isoform X1 [Homo sapiens]
XP_008962639.1 **Mass:** 78486 **Score:** 37 **Matches:** 1(0) **Sequences:** 1(0)
PREDICTED: THO complex subunit 5 homolog isoform X2 [Pan paniscus]

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

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	268	**538.3105**	**1074.6064**	**1074.5855**	**0.0208**	**1**	**23**	**3.7**	**1**		**MLALSEQKR**
☑	262	530.7554	1059.4963	1059.6176	-0.1212	1	22	5.1	1		LTLTEDKLK
☑	236	489.2221	976.4297	976.4614	-0.0317	1	21	5.9	1		GDPKGDFNK
☑	251	517.2579	1032.5013	1032.5703	-0.0690	0	19	8.5	1		LTLEELSTK
☑	138	**421.7462**	**841.4778**	**841.5022**	**-0.0244**	**0**	**19**	**6.8**	**1**		**GITLSVRP**
☑	157	**428.7453**	**855.4761**	**855.5178**	**-0.0416**	**0**	**19**	**7.5**	**1**		**LASIVTPR**

☑	137	421.7361	841.4577	841.5022	-0.0444	0	18	7.5	1	GITLSVRP
☑	159	428.7457	855.4769	855.5178	-0.0409	0	17	11	1	LASIVTPR
☑	235	487.2488	972.4830	972.5240	-0.0410	0	17	16	1	LLESGAEVR
☑	182	439.2000	876.3854	876.3800	0.0055	0	16	18	1	YFGMSTR + Oxidation (M)
☑	257	523.2614	1044.5082	1044.6179	-0.1097	0	15	21	1	ILAINSSSLK
☑	143	424.2754	846.5362	846.4447	0.0915	0	15	22	1	ESIVNASK
☑	256	523.2613	1044.5080	1044.5564	-0.0483	0	15	22	1	LSSDGLQVAR
☑	172	435.7464	869.4782	869.4971	-0.0189	0	14	22	1	VVDVSVPR
☑	134	420.1000	838.1854	838.3677	-0.1823	0	13	4.6	1	MDAVMTR + Oxidation (M)
☑	259	523.2645	1044.5144	1044.6583	-0.1439	0	13	33	1	LLTTFLPIK
☑	258	523.2637	1044.5129	1044.6583	-0.1454	0	13	34	1	LLTTFLPIK
☑	353	435.1990	1302.5753	1302.6867	-0.1114	1	13	37	1	LWEVATARCVR
☑	112	412.7394	823.4643	823.4262	0.0381	0	12	28	1	VMLGNFK + Oxidation (M)
☑	111	412.7317	823.4488	823.4487	0.0001	1	12	29	1	VPRCPPR
☑	118	414.7382	827.4619	827.5593	-0.0973	1	11	40	1	LLVSLRK
☑	99	409.1419	816.2693	816.4341	-0.1648	0	11	37	1	SLEDVVR
☑	173	435.7532	869.4919	869.4971	-0.0052	0	11	39	1	VVDVSVPR
☑	237	493.2639	984.5132	984.5063	0.0070	0	11	49	1	SVCPVDLPR
☑	128	419.2860	836.5574	836.3884	0.1690	0	11	32	1	DMLMGVR + Oxidation (M)
☑	136	421.2000	840.3854	840.5797	-0.1942	1	11	36	1	AAKVVILK
☑	76	730.3790	729.3718	729.4133	-0.0415	0	11	21	1	GSNALLR
☑	126	419.2812	836.5478	836.3884	0.1594	0	11	35	1	DMLMGVR + Oxidation (M)
☑	440	897.8569	1793.6992	1793.8651	-0.1659	0	10	29	1	LMAEALAMIESTQQAR + 2 Oxidation (M)
☑	155	427.2214	852.4283	852.4818	-0.0534	0	10	44	1	LVTDHLR
☑	140	423.2014	844.3882	844.5018	-0.1136	1	10	85	1	TALGEVKK
☑	103	411.1498	820.2851	820.3320	-0.0469	0	10	49	1	QTPCNCR
☑	255	521.2537	1040.4929	1040.5727	-0.0798	1	10	65	1	VPSRLGQER
☑	167	430.3501	858.6857	858.4923	0.1934	1	10	31	1	AATKQVNK
☑	158	428.7457	855.4769	855.4199	0.0570	0	9	61	1	ISQEHSR
☑	374	463.1158	1386.3255	1386.4890	-0.1635	0	9	0.85	1	CQWMGEDELMG + Carbamidomethyl (C); 2 Oxidation (
☑	161	428.7482	855.4819	855.4199	0.0620	0	9	65	1	ISQEHSR
☑	216	459.2545	916.4945	916.5342	-0.0397	1	9	92	1	NTLKVNTK
☑	94	407.2120	812.4095	812.4102	-0.0007	0	9	47	1	YSVIMGK + Oxidation (M)
☑	296	610.3000	1218.5854	1218.6244	-0.0390	0	9	84	1	YPSESLGNKPK
☑	226	474.2316	946.4486	946.4720	-0.0233	0	9	97	1	NTQNTEIK
☑	162	428.7490	855.4834	855.4199	0.0636	0	9	72	1	ISQEHSR
☑	160	428.7459	855.4772	855.5178	-0.0405	0	9	73	1	LSIIPASR
☑	145	424.2824	846.5503	846.3719	0.1784	0	9	92	1	EAEDVER
☑	82	401.1488	800.2831	800.3929	-0.1098	0	9	64	1	AGSGAWPR
☑	85	402.1785	802.3425	802.4548	-0.1124	1	8	84	1	TKGQEIK
☑	193	442.2707	882.5268	882.5399	-0.0131	1	8	1.1e+02	1	LAPSAIRR
☑	213	453.2591	904.5037	904.4185	0.0852	0	8	1.2e+02	1	QGNIQSCR
☑	92	405.3525	808.6905	808.5170	0.1735	1	8	3.4	1	NLLPPKK
☑	227	474.2432	946.4719	946.5447	-0.0728	0	8	1.2e+02	1	LALSSTVTR
☑	489	761.6891	2282.0455	2282.1278	-0.0823	1	8	86	1	GASSSTNDASVPTTKEFETLIK
☑	183	439.2215	876.4285	876.3946	0.0339	0	8	1.3e+02	1	MALHSMR + 2 Oxidation (M)
☑	175	436.2536	870.4926	870.4746	0.0181	0	7	1.2e+02	1	VHVMLTR + Oxidation (M)
☑	318	420.3000	1257.8782	1257.7082	0.1700	1	7	48	1	HVFGTGTKVTVL
☑	314	419.2710	1254.7913	1254.7044	0.0869	1	7	91	1	GAQTAAATAPRIK
☑	194	442.2935	882.5725	882.4521	0.1204	0	7	1.3e+02	1	TVIEMFK + Oxidation (M)
☑	442	899.3561	1796.6976	1796.8484	-0.1508	1	7	74	1	LCQGRVFCSGNAVVCK + 2 Carbamidomethyl (C)
☑	196	443.2095	884.4045	884.4940	-0.0895	1	7	1.2e+02	1	AGGALARGGR
☑	156	427.2582	852.5019	852.3721	0.1298	0	7	98	1	IEADMMK + Oxidation (M)
☑	121	416.2094	830.4043	830.4359	-0.0315	1	7	1.4e+02	1	GGDLGTRR
☑	459	481.2483	1920.9641	1920.8287	0.1354	0	7	1.1e+02	1	MLESSFTFQCANWWR + Oxidation (M)
☑	443	610.3000	1827.8782	1827.8533	0.0248	1	7	1.1e+02	1	EQPTRTISSPTSCEHR
☑	123	418.2170	834.4195	834.4058	0.0137	0	6	1.4e+02	1	APFLCER
☑	100	409.2035	816.3924	816.3371	0.0553	0	6	1.7e+02	1	ACDHCLR
☑	148	425.2000	848.3854	848.3811	0.0044	0	5	1.9e+02	1	CQGDTIR + Carbamidomethyl (C)
☑	460	481.2561	1920.9954	1920.9581	0.0373	0	5	1.5e+02	1	LPNYNPEESLFTVSGVR
☑	479	1075.4556	2148.8966	2148.9651	-0.0685	1	5	1e+02	1	MEDAAKGMPLICCLWMHK + Carbamidomethyl (C); Oxidat
☑	89	404.3000	806.5854	806.4650	0.1204	0	5	86	1	VSAYVLR
☑	222	468.2566	934.4986	934.4178	0.0808	0	5	2.7e+02	1	MEGGLAGER + Oxidation (M)
☑	214	455.2807	908.5469	908.4385	0.1083	1	5	2.2e+02	1	MSGKANASK + Oxidation (M)
☑	223	471.2887	940.5628	940.4549	0.1079	1	4	2e+02	1	MAGHPKER + Oxidation (M)
☑	465	499.2739	1993.0664	1992.9323	0.1341	1	4	1.6e+02	1	GTPHCKSSQSVLYSSNNK + Carbamidomethyl (C)
☑	129	419.2867	836.5588	836.3923	0.1666	1	4	1.4e+02	1	MGRSSQR + Oxidation (M)
☑	86	402.3000	802.5854	802.4119	0.1735	0	4	1.8e+02	1	KPGTCAAR
☑	425	428.7510	1710.9747	1710.8260	0.1487	1	4	1.5e+02	1	HYGIADPVRNCVPDR
☑	391	760.4475	1518.8804	1518.9749	-0.0944	0	4	2.5e+02	1	LLLGIDILQPAIIK
☑	101	409.2153	816.4161	816.5222	-0.1061	0	4	2.4e+02	1	ILGIFVR
☑	210	450.2304	898.4463	898.4219	0.0244	1	4	2.1e+02	1	QMVGKSSF + Oxidation (M)
☑	132	419.2974	836.5803	836.4868	0.0934	0	4	1.3e+02	1	APQPVVAR
☑	389	505.3000	1512.8782	1512.8082	0.0700	1	4	1.9e+02	1	TIQLHRESALMSK
☑	152	425.7503	849.4860	849.4014	0.0845	0	4	2.8e+02	1	TQMAEVR + Oxidation (M)
☑	197	443.2462	884.4779	884.5192	-0.0413	1	4	2.3e+02	1	KAQLAGAAR
☑	198	443.2477	884.4809	884.4940	-0.0132	1	4	2.3e+02	1	RAAAAGGGVR
☑	189	441.2929	880.5712	880.4324	0.1388	1	4	2.1e+02	1	QMKTETK + Oxidation (M)
☑	299	408.3014	1221.8822	1221.7193	0.1629	1	4	28	1	LNPKTINPGLR
☑	204	446.2281	890.4416	890.4246	0.0170	0	4	3.2e+02	1	VYSNGSHK
☑	359	440.9296	1319.7669	1319.7350	0.0320	0	4	2.6e+02	1	LWSPHIVEALR
☑	130	419.2914	836.5682	836.4868	0.0813	0	4	1.6e+02	1	APQPVVAR
☑	471	509.2587	2033.0057	2033.0074	-0.0017	0	4	1.8e+02	1	MTNNQGILPAGIMLPEFR + 2 Oxidation (M)
☑	315	419.2965	1254.8675	1254.8023	0.0652	1	4	91	1	LKAALSASLLLR
☑	90	405.2083	808.4021	808.3394	0.0628	0	4	1.6e+02	1	AMGMMPR + Oxidation (M)
	221	465.2261	928.4377	928.5164	-0.0787	0	4	3.1e+02	1	ILTCPNLR

☑										
☑	212	450.2545	898.4945	898.3742	0.1202	0	3	2.6e+02	1	LSCEVSDF
☑	188	441.2811	880.5476	880.5130	0.0346	0	3	2.5e+02	1	VPTPQAIR
☑	500	1075.4556	3223.3449	3223.4913	-0.1464	1	3	68	1	YMENLSKEYQTLEQCLQHIPVNEENR + Oxidation (M)
☑	133	419.3057	836.5968	836.4868	0.1099	0	3	1.3e+02	1	APQPVVAR
☑	430	883.8432	1765.6718	1765.7723	-0.1005	1	3	1.4e+02	1	DAVQNCCGISKTEER + 2 Carbamidomethyl (C)
☑	503	835.1429	3336.5424	3336.6305	-0.0881	0	3	1.1e+02	1	MSTGLVLPSLRPSWLSWPMSGLSGVAGSEMR + 3 Oxidation (M
☑	330	639.4000	1276.7854	1276.6268	0.1587	0	3	2.5e+02	1	NVNESLLVMCR
☑	202	445.2120	888.4094	888.4665	-0.0571	0	3	4.1e+02	1	IASTASSPR
☑	464	499.2408	1992.9342	1992.9914	-0.0572	0	3	2.4e+02	1	HVLVHTGEKPFPCLECGK
☑	131	419.2952	836.5759	836.3923	0.1836	1	3	1.7e+02	1	MGRSSQR + Oxidation (M)
☑	84	401.3000	800.5854	800.4141	0.1714	0	3	2.2e+02	1	DNQGVLR
☑	401	401.1369	1600.5184	1600.7007	-0.1824	1	3	53	1	KCISANSNCSMSVK + 2 Carbamidomethyl (C); Oxidatio
☑	215	455.2874	908.5602	908.4650	0.0951	0	3	3.1e+02	1	MHSLHLR + Oxidation (M)
☑	415	411.9094	1643.6086	1643.7622	-0.1537	1	3	1.3e+02	1	GGYFPCCKMTVPLR + Carbamidomethyl (C); Oxidation
☑	363	667.1439	1332.2733	1332.4567	-0.1834	0	3	0.57	1	CMVCGGDGSGCSK + 2 Carbamidomethyl (C); Oxidation
☑	449	465.0267	1856.0778	1855.9111	0.1667	0	3	1.8e+02	1	MLNGYQETHRPAGNIR
☑	242	503.2654	1004.5163	1004.5324	-0.0162	1	3	3.9e+02	1	EREALMLK + Oxidation (M)
☑	368	672.3427	1342.6708	1342.6841	-0.0132	1	2	3.4e+02	1	KPGKEEGDSLQR
☑	125	419.2800	836.5454	836.3884	0.1570	0	2	2.3e+02	1	CAELMVR + Oxidation (M)
☑	106	411.1926	820.3707	820.4364	-0.0657	0	2	2.8e+02	1	ALMTELK + Oxidation (M)
☑	186	441.2000	880.3854	880.4225	-0.0371	0	2	3.3e+02	1	CQYVVGR + Carbamidomethyl (C)
☑	179	437.2182	872.4219	872.4504	-0.0285	0	2	5e+02	1	NPYGPGLR
☑	321	421.2000	1260.5782	1260.6132	-0.0350	0	2	5.5e+02	1	NIIAEMEQASR
☑	165	429.2270	856.4394	856.3935	0.0459	1	2	4.7e+02	1	MCGKAFK + Carbamidomethyl (C); Oxidation (M)
☑	180	437.2331	872.4517	872.4716	-0.0198	1	2	5.2e+02	1	KDLDGLGR
☑	199	444.2158	886.4171	886.4508	-0.0337	1	2	5.6e+02	1	GGSGGEPAKK
☑	275	571.3315	1140.6484	1140.5121	0.1363	1	2	3.7e+02	1	MEKSAGPYDK + Oxidation (M)
☑	187	441.2410	880.4675	880.3531	0.1144	0	2	3.5e+02	1	GSCEGLCR + Carbamidomethyl (C)
☑	357	439.2000	1314.5782	1314.5220	0.0561	0	2	3.9e+02	1	CNLCGEESFGTV + Carbamidomethyl (C)
☑	482	737.6682	2209.9828	2210.1194	-0.1366	1	2	2.7e+02	1	LLENHEVALPNPKIGMWFS + Oxidation (M)
☑	402	401.1401	1600.5314	1600.6221	-0.0907	1	2	87	1	YYCVRGYSCCDGR + Carbamidomethyl (C)
☑	495	637.2676	2545.0412	2545.1795	-0.1383	1	2	1.4e+02	1	GFSIAMDVFGKDGDFDPSTDAVVR
☑	419	419.1482	1672.5637	1672.7562	-0.1925	0	2	80	1	SCTAHLCGLGWGAGAGR + Carbamidomethyl (C)
☑	190	441.2972	880.5798	880.3960	0.1837	0	2	3.4e+02	1	ESIETMR + Oxidation (M)
☑	154	427.1000	852.1854	852.3726	-0.1871	0	2	60	1	EEDAPHR
☑	329	639.4000	1276.7854	1276.7252	0.0603	1	2	3.6e+02	1	AFITSTRQVVR
☑	454	639.4000	1915.1782	1914.9833	0.1949	1	2	1.1e+02	1	TARLIPNAIQVCTDSEK + Carbamidomethyl (C)
☑	238	495.2327	988.4508	988.4872	-0.0364	1	2	4.9e+02	1	QRSTMPNR
☑	319	630.4562	1258.8979	1258.7132	0.1846	1	2	70	1	GLPSSIEKTISK
☑	365	445.1046	1332.2920	1332.4567	-0.1648	0	2	0.95	1	CMVCGGDGSGCSK + 2 Carbamidomethyl (C); Oxidation
☑	244	505.3000	1008.5854	1008.6444	-0.0589	1	1	4.7e+02	1	VIVPQLKGR
☑	201	445.1000	888.1854	888.3461	-0.1607	0	1	24	1	ADPGADGEAS
☑	360	441.2000	1320.5782	1320.6027	-0.0245	1	1	4.6e+02	1	CVSQEGVARCR + 2 Carbamidomethyl (C)
☑	498	673.8371	2691.3193	2691.3043	0.0149	1	1	2.5e+02	1	NTFVGTPFWMAPEVIKQSAYDFK + Oxidation (M)
☑	120	415.1423	828.2700	828.4242	-0.1542	1	1	2.2e+02	1	EGGPWRK
☑	98	408.2918	814.5690	814.3756	0.1934	0	1	3.7e+02	1	MDAHIGR + Oxidation (M)
☑	248	514.1922	1026.3698	1026.3933	-0.0235	0	1	3.3e+02	1	TCTPACSGCK + Carbamidomethyl (C)
☑	139	422.3539	842.6933	842.4974	0.1959	0	1	1.9e+02	1	VLQQLSR
☑	267	538.2988	1074.5831	1074.5128	0.0703	1	1	5.7e+02	1	CTSKSPSTHK
☑	501	1088.7598	3263.2574	3263.3237	-0.0663	0	1	42	1	VEAGDEADYYCQVWDSGSDHPWMFGGGTK + Carbamidomethyl
☑	95	408.2759	814.5372	814.4185	0.1187	0	1	4e+02	1	ANPSTGGVL
☑	200	445.0910	888.1674	888.3544	-0.1869	0	1	12	1	CFICMEK + Oxidation (M)
☑	274	568.2751	1134.5356	1134.5781	-0.0425	1	1	6.5e+02	1	ERYEAAIQR
☑	146	424.2845	846.5545	846.3719	0.1826	0	1	5.5e+02	1	EAEDVER
☑	278	581.3000	1160.5854	1160.5794	0.0060	1	1	5.5e+02	1	GLRSICMHTK + Oxidation (M)
☑	96	408.2840	814.5534	814.4185	0.1349	0	1	4.1e+02	1	ANPSTGGVL
☑	185	439.7066	877.3987	877.4294	-0.0307	0	1	5.8e+02	1	EYSAPGVR
☑	297	408.2896	1221.8471	1221.7193	0.1278	1	1	1.3e+02	1	LNPKTINPGLR
☑	266	1075.4556	1074.4483	1074.5934	-0.1451	1	1	6.2e+02	1	EAFNIIGRR
☑	455	639.4000	1915.1782	1914.9833	0.1949	0	1	1.3e+02	1	NQNLMLELETVQQALR + Oxidation (M)
☑	429	440.9313	1759.6962	1759.8241	-0.1279	1	1	3.1e+02	1	MNCYCNGMTRLLLTK
☑	209	449.3366	896.6586	896.4828	0.1758	1	1	2.4e+02	1	QQPPSGKR
☑	93	406.2246	810.4346	810.3694	0.0652	0	1	2.8e+02	1	FGNQSMK
☑	298	408.2969	1221.8689	1221.7193	0.1495	1	1	86	1	LNPKTINPGLR
☑	437	446.9843	1783.9082	1783.8749	0.0333	1	1	4.5e+02	1	TSGMSAIFVAAMREWK
☑	413	404.9691	1615.8475	1615.8100	0.0375	1	0	4.9e+02	1	TLQRAMETLHASSR + Oxidation (M)
☑	70	639.4000	638.3927	638.3249	0.0678	0	0	8.3	1	GGGHVGR
☑	170	433.3227	864.6308	864.4487	0.1820	1	0	3e+02	1	VTNTMRK + Oxidation (M)
☑	166	430.1000	858.1854	858.3832	-0.1977	0	0	42	1	EGGSHTGSK
☑	245	506.2816	1010.5485	1010.4348	0.1138	0	0	5.4e+02	1	CQGVVCAMK + Carbamidomethyl (C); Oxidation (M)
☑	458	481.2342	1920.9078	1920.8393	0.0685	0	0	4.4e+02	1	AMMGQLSAACSHSHFVR + Carbamidomethyl (C); 2 Oxida
☑	87	403.3000	804.5854	804.4164	0.1691	0	0	3.3e+02	1	GGLLSCQK
☑	456	639.7000	1916.0782	1916.0289	0.0493	1	0	3.2e+02	1	AVDMSGGTVTVLEKVPVSK
☑	102	410.2658	818.5171	818.4511	0.0660	0	0	5.3e+02	1	HAVVHTR
☑	288	599.3441	1196.6737	1196.5860	0.0877	0	0	5.7e+02	1	QMLSDLFTAR + Oxidation (M)
☑	417	831.9117	1661.8089	1661.8447	-0.0358	0	0	5.4e+02	1	LMVYEPNQVLDVSR
☑	326	425.3180	1272.9322	1272.7805	0.1516	0	0	46	1	ILIDGTLIIFR
☑	1	*401.3000*	*400.2927*							
☑	2	*402.3000*	*401.2927*							
☑	3	*403.2074*	*402.2001*							
☑	4	*403.2126*	*402.2054*							
☑	5	*403.3000*	*402.2927*							
☑	6	*404.3000*	*403.2927*							
☑	7	*405.2025*	*404.1952*							
	8	*405.2029*	*404.1956*							

☑			
☑	9	405.2033	404.1960
☑	10	405.2046	404.1974
☑	11	405.2075	404.2002
☑	12	406.2698	405.2626
☑	13	409.2106	408.2033
☑	14	409.2111	408.2038
☑	15	410.2211	409.2138
☑	16	411.2077	410.2004
☑	17	416.2012	415.1939
☑	18	416.2032	415.1959
☑	19	416.2066	415.1993
☑	20	416.2081	415.2008
☑	21	417.1942	416.1869
☑	22	417.3000	416.2927
☑	23	419.2876	418.2803
☑	24	420.1000	419.0927
☑	25	420.2591	419.2518
☑	26	420.3000	419.2927
☑	27	421.2000	420.1927
☑	28	422.2297	421.2224
☑	29	422.2355	421.2282
☑	30	423.4000	422.3927
☑	31	425.2000	424.1927
☑	32	425.2375	424.2302
☑	33	425.2586	424.2513
☑	34	425.2609	424.2536
☑	35	427.1000	426.0927
☑	36	427.2086	426.2013
☑	37	428.2275	427.2202
☑	38	430.1000	429.0927
☑	39	430.2182	429.2109
☑	40	431.1000	430.0927
☑	41	433.2219	432.2146
☑	42	435.1674	434.1601
☑	43	439.2000	438.1927
☑	44	440.3292	439.3219
☑	45	441.1308	440.1235
☑	46	441.2000	440.1927
☑	47	441.3131	440.3058
☑	48	445.1000	444.0927
☑	49	445.2722	444.2649
☑	50	445.2933	444.2860
☑	51	445.2990	444.2917
☑	52	449.2240	448.2167
☑	53	459.4000	458.3927
☑	54	463.3971	462.3898
☑	55	469.3121	468.3048
☑	56	505.3000	504.2927
☑	57	511.2000	510.1927
☑	58	519.1000	518.0927
☑	59	528.3749	527.3676
☑	60	538.1308	537.1236
☑	61	553.4172	552.4099
☑	62	581.3000	580.2927
☑	63	599.3551	598.3478
☑	64	599.5000	598.4927
☑	65	610.3000	609.2927
☑	66	612.1412	611.1339
☑	67	613.1000	612.0927
☑	68	616.6000	615.5927
☑	69	639.4000	638.3927
☑	71	639.5866	638.5794
☑	72	639.7000	638.6927
☑	73	640.7406	639.7333
☑	74	657.4000	656.3927
☑	75	713.3715	712.3642
☑	77	738.8000	737.7927
☑	78	776.1768	775.1695
☑	79	400.0405	798.0665
☑	80	400.0437	798.0729
☑	81	400.5666	799.1187
☑	83	401.3000	800.5854
☑	88	404.0278	806.0411
☑	97	408.2906	814.5667
☑	104	411.1570	820.2995
☑	105	411.1859	820.3572
☑	107	411.2098	820.4051
☑	108	412.2862	822.5578
☑	109	412.3032	822.5918
☑	110	412.3368	822.6590
☑	113	413.2313	824.4480
☑	114	413.2447	824.4748
☑	115	414.1986	826.3825
☑	116	414.5950	827.1755
	117	414.6375	827.2604

☑			
☑	119	415.1072	828.1999
☑	122	417.3000	832.5854
☑	127	419.2837	836.5529
☑	135	420.3000	838.5854
☑	141	423.4000	844.7854
☑	142	424.2739	846.5332
☑	144	424.2765	846.5385
☑	147	424.2880	846.5613
☑	149	425.2313	848.4480
☑	150	425.2861	848.5577
☑	151	425.3761	848.7377
☑	153	426.3517	850.6888
☑	163	429.0618	856.1091
☑	164	429.2170	856.4194
☑	169	433.1392	864.2639
☑	171	434.1831	866.3516
☑	174	435.7548	869.4951
☑	176	436.2776	870.5406
☑	177	436.3144	870.6142
☑	178	437.2093	872.4041
☑	184	439.3559	876.6973
☑	191	441.3000	880.5854
☑	192	441.3229	880.6312
☑	203	445.3594	888.7042
☑	205	446.9700	891.9254
☑	206	449.2273	896.4400
☑	207	449.2332	896.4519
☑	208	449.3129	896.6112
☑	211	450.2509	898.4872
☑	217	459.4000	916.7854
☑	218	459.7879	917.5612
☑	219	461.2257	920.4368
☑	220	462.4236	922.8326
☑	224	472.2500	942.4855
☑	228	477.2376	952.4607
☑	229	477.7989	953.5833
☑	230	477.8096	953.6046
☑	231	479.4056	956.7967
☑	232	482.3984	962.7822
☑	233	483.2310	964.4475
☑	234	484.3522	966.6899
☑	239	499.2855	996.5565
☑	240	499.2985	996.5825
☑	243	504.2655	1006.5165
☑	246	507.2580	1012.5014
☑	247	511.2000	1020.3854
☑	249	514.3091	1026.6036
☑	252	519.0952	1036.1759
☑	253	519.1000	1036.1854
☑	254	521.0889	1040.1633
☑	260	527.5858	1053.1570
☑	261	528.6242	1055.2338
☑	264	537.1373	1072.2601
☑	265	538.1218	1074.2290
☑	269	539.3000	1076.5855
☑	276	571.5209	1141.0272
☑	277	572.5768	1143.1390
☑	282	593.1178	1184.2210
☑	283	593.1209	1184.2271
☑	284	593.1334	1184.2522
☑	289	599.5000	1196.9854
☑	290	401.3000	1200.8782
☑	291	402.3000	1203.8782
☑	292	403.3000	1206.8782
☑	293	404.0149	1209.0230
☑	294	404.3000	1209.8782
☑	295	405.3526	1213.0359
☑	300	613.1000	1224.1854
☑	301	615.4639	1228.9133
☑	302	616.6000	1231.1854
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☑	305	411.9053	1232.6940
☑	306	412.3375	1233.9906
☑	307	412.3530	1234.0370
☑	308	412.3542	1234.0408
☑	309	414.7370	1241.1891
☑	310	415.3613	1243.0620
☑	312	417.3000	1248.8782
☑	316	628.4513	1254.8880
☑	317	420.1000	1257.2782
☑	323	423.4000	1267.1782
☑	325	425.2000	1272.5782
☑	327	425.7587	1274.2542
☑	328	425.7631	1274.2676
	331	639.7000	1277.3854

☑			
☑	332	639.7519	1277.4893
☑	333	427.1000	1278.2782
☑	334	640.7000	1279.3854
☑	335	640.7545	1279.4944
☑	336	428.7380	1283.1922
☑	337	428.7390	1283.1953
☑	338	428.7420	1283.2043
☑	339	428.7451	1283.2134
☑	340	428.7457	1283.2154
☑	341	428.7461	1283.2164
☑	342	428.7463	1283.2171
☑	343	428.7517	1283.2333
☑	344	429.0681	1284.1824
☑	345	429.0712	1284.1917
☑	346	429.0926	1284.2560
☑	347	430.1000	1287.2782
☑	348	431.7279	1292.1619
☑	350	432.3671	1294.0795
☑	351	651.2761	1300.5377
☑	354	435.3277	1302.9613
☑	355	435.3405	1302.9997
☑	356	435.7523	1304.2351
☑	362	667.1355	1332.2565
☑	364	445.1000	1332.2782
☑	370	459.4000	1375.1782
☑	373	463.1090	1386.3053
☑	376	464.0064	1388.9973
☑	382	476.2326	1425.6761
☑	383	480.1347	1437.3822
☑	385	738.8000	1475.5854
☑	386	498.3555	1492.0448
☑	388	503.1052	1506.2938
☑	392	761.6715	1521.3284
☑	393	511.2000	1530.5782
☑	394	769.2820	1536.5494
☑	395	519.1000	1554.2782
☑	396	519.1000	1554.2782
☑	397	519.1265	1554.3577
☑	398	521.0863	1560.2372
☑	399	521.0995	1560.2768
☑	400	522.4681	1564.3825
☑	403	401.3000	1601.1709
☑	404	536.1267	1605.3582
☑	405	536.1434	1605.4083
☑	406	536.1435	1605.4088
☑	407	536.1443	1605.4109
☑	408	537.1251	1608.3535
☑	409	537.1338	1608.3795
☑	410	537.1530	1608.4371
☑	411	538.1263	1611.3570
☑	412	404.9623	1615.8202
☑	414	815.2143	1628.4141
☑	416	554.1471	1659.4196
☑	421	419.9915	1675.9368
☑	422	421.8606	1683.4133
☑	424	425.3153	1697.2321
☑	426	429.0696	1712.2492
☑	427	429.0723	1712.2602
☑	428	581.3000	1740.8782
☑	431	593.1192	1776.3359
☑	432	593.1239	1776.3498
☑	433	593.1249	1776.3529
☑	434	445.0972	1776.3595
☑	435	445.1094	1776.4085
☑	436	594.1303	1779.3690
☑	438	447.0988	1784.3661
☑	439	447.1039	1784.3866
☑	441	599.5000	1795.4782
☑	444	613.1000	1836.2782
☑	445	616.5516	1846.6330
☑	446	616.6000	1846.7782
☑	447	463.1030	1848.3831
☑	448	463.1059	1848.3947
☑	450	930.1000	1858.1854
☑	451	467.4589	1865.8065
☑	452	628.1672	1881.4799
☑	457	480.1392	1916.5277
☑	461	485.0967	1936.3576
☑	466	667.1481	1998.4226
☑	470	509.2553	2032.9920
☑	472	518.0611	2068.2153
☑	474	528.2332	2108.9037
☑	475	704.1774	2109.5104
☑	477	536.1516	2140.5772
	478	538.1078	2148.4021

☑			
☑	480	*539.1140*	*2152.4269*
☑	481	*736.4879*	*2206.4420*
☑	483	*554.1502*	*2212.5717*
☑	484	*738.8000*	*2213.3782*
☑	485	*742.3378*	*2223.9915*
☑	486	*1115.9302*	*2229.8459*
☑	487	*747.0090*	*2238.0051*
☑	488	*566.7318*	*2262.8982*
☑	490	*767.0158*	*2298.0257*
☑	491	*776.1722*	*2325.4946*
☑	496	*639.2842*	*2553.1076*
☑	499	*927.4315*	*2779.2725*
☑	502	*817.1509*	*3264.5746*

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 : ± 0.2 Da
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : Default
Number of queries      : 503
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Mascot: http://www.matrixscience.com/