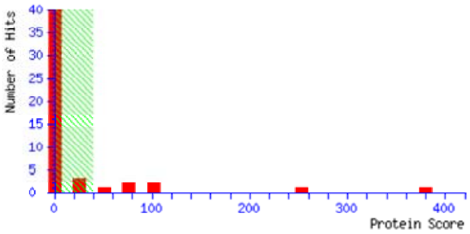
MATRIX SCIENCE Mascot Search Results

```
User           : JPROS
Email          : pro@jbios.co.jp
Search title   : D:\JPROS\L015\f_3micro.wiff (sample number 1)
MS data file   : mas8BB.tmp
Database       : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Taxonomy       : Homo sapiens (human) (327411 sequences)
Timestamp      : 13 Feb 2019 at 09:41:55 GMT
Protein hits   : AAG41947.1  keratin 1 [Homo sapiens]
                 NP_149073.1 SAP domain-containing ribonucleoprotein [Homo sapiens]
                 NP_005773.3 THO complex subunit 4 [Homo sapiens]
                 NP_000412.3 keratin, type I cytoskeletal 10 [Homo sapiens]
                 NP_000414.2 keratin, type II cytoskeletal 2 epidermal [Homo sapiens]
                 BAB14489.1  unnamed protein product [Homo sapiens]
                 NP_000217.2 keratin, type I cytoskeletal 9 [Homo sapiens]
                 NP_055285.1 rho-related GTP-binding protein Rho6 precursor [Homo sapiens]
                 NP_000996.2 40S ribosomal protein S3 isoform 1 [Homo sapiens]
                 Q8IZ52.2    RecName: Full=Chondroitin sulfate synthase 2; AltName: Full=Chondroitin glucuronyltransferase 2; AltName
```

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.     AAG41947.1     Mass: 66027     Score: 379     Matches: 16(10)   Sequences: 16(10)   emPAI: 0.72
       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
    ☑  255  487.2480   972.4814   972.5240 -0.0426  0    48    0.011   1          K.IEISELNR.V
    ☑  265  517.2310  1032.4474  1032.5087 -0.0613  0    47    0.014   1     U    R.TLLEGEESR.M
       282  533.2460  1064.4775  1064.5138 -0.0363  0    11       54   3     U    K.AQYEDIAQK.S
    ☑  297  563.2451  1124.4756  1124.5349 -0.0593  0    35     0.19   1     U    K.AEAESLYQSK.Y
    ☑  308  590.2715  1178.5284  1178.5931 -0.0648  0    66  0.00016   1     U    K.YEELQITAGR.H
    ☑  346  633.2893  1264.5640  1264.6299 -0.0659  0    64  0.00021   1     U    R.TNAENEFVTIK.K
    ☑  374  650.7356  1299.4567  1299.5224 -0.0656  0    34     0.14   1     U    K.NMQDMVEDYR.N
    ☑  375  651.8273  1301.6401  1301.7078 -0.0677  0    82  3.6e-06   1     U    R.SLDLDSIIAEVK.A
    ☑  392  447.5407  1339.6002  1339.6619 -0.0617  1    18      9.3   1     U    K.SKAEAESLYQSK.Y
    ☑  394  679.3175  1356.6205  1356.6885 -0.0679  0    91  4.6e-07   1     U    K.LNDLEDALQQAK.E
    ☑  398  692.3059  1382.5972  1382.6830 -0.0858  0    82  3.3e-06   1     U    K.SLNNQFASFIDK.V
    ☑  401  465.2366  1392.6879  1392.7249 -0.0370  1    37     0.14   1     U    R.TNAENEFVTIKK.D
    ☑  412  738.3346  1474.6547  1474.7416 -0.0869  0    46    0.014   1     U    K.WELLQQVDTSTR.T
    ☑  413  738.3529  1474.6912  1474.7780 -0.0868  0    69  8.8e-05   1          R.FLEQQNQVLQTK.W
    ☑  438  829.3301  1656.6457  1656.7856 -0.1399  0    21      2.9   1     U    R.SGGGFSSGSAGIINYQR.R
    ☑  491  665.2982  1992.8727  1992.9693 -0.0967  0    53    0.002   1     U    R.THNLEPYFESFINNLR.R


       Proteins matching the same set of peptides:
       NP_006112.3     Mass: 65999     Score: 379     Matches: 16(10)   Sequences: 16(10)
       keratin, type II cytoskeletal 1 [Homo sapiens]
       AFA52002.1     Mass: 66013     Score: 379     Matches: 16(10)   Sequences: 16(10)
       keratin 1 [Homo sapiens]
       AFA52003.1     Mass: 66029     Score: 379     Matches: 16(10)   Sequences: 16(10)
       keratin 1 [Homo sapiens]
       AFA52004.1     Mass: 65930     Score: 379     Matches: 16(10)   Sequences: 16(10)
       keratin 1 [Homo sapiens]
       AFA52005.1     Mass: 66086     Score: 379     Matches: 16(10)   Sequences: 16(10)
       keratin 1 [Homo sapiens]
       AFA52007.1     Mass: 66071     Score: 379     Matches: 16(10)   Sequences: 16(10)
       keratin 1 [Homo sapiens]
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2. NP_149073.1 **Mass:** 23656 **Score:** 254 **Matches:** 16(7) **Sequences:** 8(6) **emPAI:** 1.42
SAP domain-containing ribonucleoprotein [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	238	468.2388	934.4631	934.5124	-0.0493	0	48	0.011	1	U	R.FGISSVPTK.G
☑	239	468.2498	934.4850	934.5124	-0.0274	0	(41)	0.061	1	U	R.FGISSVPTK.G
☑	289	540.2571	1078.4996	1078.5771	-0.0775	0	57	0.0014	1	U	R.FGLNVSSISR.K
	291	540.2788	1078.5431	1078.5771	-0.0340	0	(6)	1.9e+02	2	U	R.FGLNVSSISR.K
☑	295	560.2768	1118.5391	1118.5972	-0.0581	0	58	0.0012	1	U	R.FNVPVSLESK.K
☑	296	560.2859	1118.5573	1118.5972	-0.0399	0	(11)	63	1	U	R.FNVPVSLESK.K
☑	303	587.2647	1172.5149	1172.6037	-0.0888	0	(17)	15	1	U	K.ITSEIPQTER.M
☑	304	587.2778	1172.5411	1172.6037	-0.0626	0	42	0.049	1	U	K.ITSEIPQTER.M
☑	305	587.2794	1172.5442	1172.6037	-0.0595	0	(30)	0.79	1	U	K.ITSEIPQTER.M
☑	306	587.2852	1172.5558	1172.6037	-0.0479	0	(16)	21	1	U	K.ITSEIPQTER.M
☑	307	587.2867	1172.5588	1172.6037	-0.0449	0	(38)	0.12	1	U	K.ITSEIPQTER.M
☑	383	444.2247	1329.6522	1329.7074	-0.0553	1	41	0.057	1	U	K.LAELKQECLAR.G + Carbamidomethyl (C)
☑	417	511.8731	1532.5975	1532.7504	-0.1530	0	(21)	3.3	1	U	K.GLSSDNKPMVNLDK.L + Oxidation (M)
☑	418	511.9073	1532.7001	1532.7504	-0.0504	0	32	0.42	1	U	K.GLSSDNKPMVNLDK.L + Oxidation (M)
☑	475	936.3922	1870.7699	1870.8796	-0.1097	0	104	1.7e-08	1	U	R.FGIVTSSAGTGTTEDTEAK.K
☑	493	667.3034	1998.8884	1998.9746	-0.0862	1	58	0.00065	1	U	R.FGIVTSSAGTGTTEDTEAKK.R

Proteins matching the same set of peptides:
EAW96835.1 **Mass:** 51750 **Score:** 254 **Matches:** 16(7) **Sequences:** 8(6)
hCG2016179, isoform CRA_c [Homo sapiens]
EAW96839.1 **Mass:** 99837 **Score:** 254 **Matches:** 16(7) **Sequences:** 8(6)
hCG2016179, isoform CRA_f [Homo sapiens]

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3. NP_005773.3 **Mass:** 27541 **Score:** 112 **Matches:** 6(2) **Sequences:** 6(2) **emPAI:** 0.29
THO complex subunit 4 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	316	606.7478	1211.4811	1211.5414	-0.0603	0	32	0.33	1	U	K.MDMSLDDIIK.L + 2 Oxidation (M)
☑	327	411.1910	1230.5513	1230.5993	-0.0481	0	34	0.31	1	U	R.SLGTADVHFER.K
☑	497	678.9597	2033.8574	2033.9654	-0.1080	0	59	0.0005	1	U	K.QQLSAEELDAQLDAYNAR.M
☑	509	737.9548	2210.8425	2210.9745	-0.1320	1	15	5.3	1	U	M.PDSAPAMADKMDMSLDDIIK.L + 3 Oxidation (M)
☑	522	676.5479	2702.1626	2702.2725	-0.1100	1	25	1	1	U	K.QLPDKWQHDLFDSGFGGGAGVETGGK.L
☑	526	943.7616	2828.2630	2828.4239	-0.1609	0	47	0.0062	1	U	K.QYNGVPLDGRPMNIQLVTSQIDAQR.R + Oxidation (M)

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4. NP_000412.3 **Mass:** 58766 **Score:** 92 **Matches:** 7(3) **Sequences:** 7(3) **emPAI:** 0.20
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
☑	97	405.2014	808.3883	808.4330	-0.0448	0	40	0.04	1		R.LASYLDK.V
	155	424.2605	846.5064	846.4447	0.0617	0	10	64	7	U	K.SEITELR.R
☑	264	516.2706	1030.5266	1030.5910	-0.0644	0	40	0.066	1	U	R.VLDELTLTK.A
☑	292	545.7461	1089.4777	1089.5237	-0.0460	0	43	0.04	1	U	K.VTMQNLNDR.L
☑	302	583.2630	1164.5115	1164.5775	-0.0659	0	21	5.3	1	U	R.LENEIQTYR.S
☑	397	691.2879	1380.5612	1380.6408	-0.0796	0	59	0.00073	1	U	R.ALEESNYELEGK.I
☑	414	498.5586	1492.6541	1492.7270	-0.0729	1	35	0.21	1	U	R.SQYEQLAEQNRK.D

Proteins matching the same set of peptides:
P13645.6 **Mass:** 58792 **Score:** 92 **Matches:** 7(3) **Sequences:** 7(3)
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:** 92 **Matches:** 7(3) **Sequences:** 7(3)
unnamed protein product [Homo sapiens]
AAH34697.1 **Mass:** 58792 **Score:** 92 **Matches:** 7(3) **Sequences:** 7(3)
Keratin 10 [Homo sapiens]
EAW60681.1 **Mass:** 63308 **Score:** 92 **Matches:** 7(3) **Sequences:** 7(3)
keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA_b [Homo sapiens]
XP_005257400.1 **Mass:** 63308 **Score:** 92 **Matches:** 7(3) **Sequences:** 7(3)
keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]

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5. NP_000414.2 **Mass:** 65393 **Score:** 87 **Matches:** 3(2) **Sequences:** 3(2) **emPAI:** 0.12
keratin, type II cytoskeletal 2 epidermal [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	255	487.2480	972.4814	972.5240	-0.0426	0	48	0.011	1		K.IEISELNR.V
☑	309	597.2898	1192.5650	1192.6088	-0.0438	0	36	0.16	1	U	K.YEELQVTVGR.H
	413	738.3529	1474.6912	1474.7780	-0.0868	0	69	8.8e-05	1		R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:
AAC83410.1 **Mass:** 65825 **Score:** 87 **Matches:** 3(2) **Sequences:** 3(2)
epidermal cytokeratin 2 [Homo sapiens]

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6. BAB14489.1 **Mass:** 44345 **Score:** 77 **Matches:** 3(2) **Sequences:** 3(2) **emPAI:** 0.17
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

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   ☑ 301  579.8244 1157.6343 1157.6808 -0.0466  0    63 0.00038   1     U    R.TPGGVFLNLLK.N
   ☑ 336  623.3010 1244.5874 1244.6248 -0.0374  0    28       1   1     U    K.NTPSISEEQIK.D
   ☑ 379  656.7648 1311.5151 1311.5830 -0.0679  0    41   0.033   1     U    R.YEITAEDSQEK.V


     Proteins matching the same set of peptides:
     EAW48850.1     Mass: 46023     Score: 77     Matches: 3(2)  Sequences: 3(2)
     RNA U, small nuclear RNA export adaptor (phosphorylation regulated), partial [Homo sapiens]
     NP_115553.2     Mass: 44375     Score: 77     Matches: 3(2)  Sequences: 3(2)
     phosphorylated adapter RNA export protein [Homo sapiens]
─────────────────────────────────────────────────────────────────────────────────────────────
7.   NP_000217.2     Mass: 62027     Score: 54     Matches: 6(1)  Sequences: 6(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
       97  405.2014   808.3883   808.4330  -0.0448   0    40    0.04   1          R.LASYLDK.V
   ☑  222  449.1791   896.3436   896.4062  -0.0626   0    26     1.2   1     U    R.MTLDDFR.I
   ☑  279  530.7586  1059.5027  1059.5560  -0.0534   0    28     1.2   1     U    K.TLLDIDNTR.M
   ☑  282  533.2460  1064.4775  1064.4920  -0.0145   0    18     9.9   1     U    K.STMQELNSR.L
   ☑  329  616.7812  1231.5478  1231.5906  -0.0427   0    30    0.67   1     U    R.SGGGGGGGLGSGGSIR.S
   ☑  470  613.2874  1836.8404  1836.9581  -0.1177   0    37   0.088   1     U    R.HGVQELEIELQSQLSK.K


     Proteins matching the same set of peptides:
     EAW60744.1     Mass: 57526     Score: 54     Matches: 6(1)  Sequences: 6(1)
     keratin 9 (epidermolytic palmoplantar keratoderma) [Homo sapiens]
     CAA82315.1     Mass: 62092     Score: 54     Matches: 6(1)  Sequences: 6(1)
     cytokeratin 9 [Homo sapiens]
─────────────────────────────────────────────────────────────────────────────────────────────
8.   NP_055285.1     Mass: 26039     Score: 23     Matches: 7(0)  Sequences: 1(0)
     rho-related GTP-binding protein Rho6 precursor [Homo sapiens]
   ☐ Check to include this hit in error tolerant search

    Query  Observed  Mr(expt)  Mr(calc)   Delta Miss Score   Expect Rank Unique  Peptide
   ☑  136  419.2869  836.5592  836.4868  0.0724   0    (4) 1.7e+02   1     U    R.APQPVVAR.C
      137  419.2876  836.5606  836.4868  0.0738   0    (3) 1.9e+02   2     U    R.APQPVVAR.C
      138  419.2946  836.5746  836.4868  0.0878   0    (3) 1.5e+02   2     U    R.APQPVVAR.C
   ☑  140  419.2999  836.5853  836.4868  0.0985   0    (4) 1.4e+02   1     U    R.APQPVVAR.C
   ☑  143  419.3054  836.5963  836.4868  0.1094   0    23       1.5   1     U    R.APQPVVAR.C
   ☑  144  419.3068  836.5990  836.4868  0.1122   0    (5)       98   1     U    R.APQPVVAR.C
   ☑  145  419.3076  836.6006  836.4868  0.1138   0    (2) 1.6e+02   1     U    R.APQPVVAR.C

─────────────────────────────────────────────────────────────────────────────────────────────
9.   NP_000996.2     Mass: 26671     Score: 22     Matches: 1(0)  Sequences: 1(0)
     40S ribosomal protein S3 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
   ☑  411  735.8334  1469.6523  1469.7613  -0.1090   0    22     3.4   1     U    K.DEILPTTPISEQK.G


     Proteins matching the same set of peptides:
     AAH03577.1     Mass: 26540     Score: 22     Matches: 1(0)  Sequences: 1(0)
     Unknown (protein for IMAGE:3544292), partial [Homo sapiens]
     AAB19349.2     Mass: 26699     Score: 22     Matches: 1(0)  Sequences: 1(0)
     S3 ribosomal protein [Homo sapiens]
     CAA39248.1     Mass: 26703     Score: 22     Matches: 1(0)  Sequences: 1(0)
     unnamed protein product [Homo sapiens]
     EAW78297.1     Mass: 12460     Score: 22     Matches: 1(0)  Sequences: 1(0)
     hCG2022018 [Homo sapiens]
     AAF82383.1     Mass: 17099     Score: 22     Matches: 1(0)  Sequences: 1(0)
     ribosomal protein S3, partial [Homo sapiens]
     NP_001127020.1     Mass: 26672     Score: 22     Matches: 1(0)  Sequences: 1(0)
     40S ribosomal protein S3 [Pongo abelii]
     NP_001247435.1     Mass: 28468     Score: 22     Matches: 1(0)  Sequences: 1(0)
     40S ribosomal protein S3 isoform 2 [Homo sapiens]
     NP_001247436.1     Mass: 12606     Score: 22     Matches: 1(0)  Sequences: 1(0)
     40S ribosomal protein S3 isoform 3 [Homo sapiens]
─────────────────────────────────────────────────────────────────────────────────────────────
10.  Q8IZ52.2     Mass: 85414     Score: 22     Matches: 1(0)  Sequences: 1(0)
     RecName: Full=Chondroitin sulfate synthase 2; AltName: Full=Chondroitin glucuronyltransferase 2; AltName: Full=Chondroitin-polym
   ☐ Check to include this hit in error tolerant search

    Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score Expect Rank Unique  Peptide
   ☑  287  538.2733  1074.5321  1074.6298  -0.0977   1    22     4.7   1     U    R.VVFLTGARGR.R


     Proteins matching the same set of peptides:
     NP_078812.2     Mass: 85442     Score: 22     Matches: 1(0)  Sequences: 1(0)
     chondroitin sulfate synthase 2 isoform 1 [Homo sapiens]
     AAQ88769.1     Mass: 85428     Score: 22     Matches: 1(0)  Sequences: 1(0)
     RASL651 [Homo sapiens]
─────────────────────────────────────────────────────────────────────────────────────────────
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
   ☑  451   577.2767  1728.8082  1728.9015  -0.0933   1    22        3    1         ACNTVLKSMNLPPLGR + Oxidation (M)
```

☑	298	565.7793	1129.5440	1129.6455	-0.1016	0	19	7.6	1	VLTSTVQQVR
☑	149	421.7413	841.4681	841.5022	-0.0341	0	19	7.2	1	GITLSVRP
☑	263	516.2237	1030.4329	1030.5295	-0.0966	0	18	11	1	ASGVEGADVVK
☑	155	424.2605	846.5064	846.4447	0.0617	0	18	12	1	ESIVNASK
☑	273	523.2675	1044.5205	1044.5716	-0.0511	0	17	14	1	LSSAHVYLR
☑	286	535.2652	1068.5158	1068.6543	-0.1384	1	17	13	1	LTPLELKQK
☑	271	523.2646	1044.5146	1044.6583	-0.1437	0	16	15	1	LLTTFLPIK
☑	150	421.7417	841.4688	841.5022	-0.0334	0	16	12	1	GITLSVRP
☑	112	409.2281	816.4417	816.4065	0.0353	0	16	17	1	LMGFGHR
☑	419	776.8239	1551.6332	1551.7710	-0.1379	0	15	15	1	DLAMVASDMMVLLK + Oxidation (M)
☑	283	535.2451	1068.4757	1068.5564	-0.0806	1	15	19	1	QDTEIAKHK
☑	284	535.2597	1068.5048	1068.6543	-0.1495	1	15	19	1	LTPLELKQK
☑	272	523.2664	1044.5182	1044.5703	-0.0521	0	15	23	1	LSEDIDLLK
☑	192	435.7575	869.5005	869.5157	-0.0152	1	15	18	1	VVKMHLK + Oxidation (M)
☑	191	435.7554	869.4963	869.5335	-0.0372	0	14	20	1	VTVLVSPR
☑	338	416.8689	1247.5849	1247.5023	0.0825	0	14	24	1	CGGDGGGACIPER + Carbamidomethyl (C)
☑	395	682.2868	1362.5591	1362.6013	-0.0422	0	14	25	1	YSEVSFMELDK + Oxidation (M)
☑	270	523.2627	1044.5109	1044.6583	-0.1474	0	13	32	1	LLTTFLPIK
☑	153	423.1994	844.3843	844.4767	-0.0924	0	13	44	1	TIGSLQAR
☑	130	416.2088	830.4030	830.4610	-0.0580	1	13	36	1	AQSIERK
☑	403	469.2000	1404.5782	1404.7184	-0.1402	0	12	30	1	TNAALGFAQMLPR + Oxidation (M)
☑	146	420.2283	838.4421	838.3677	0.0744	0	12	26	1	MDAVMTR + Oxidation (M)
☑	268	520.6756	1039.3367	1039.5298	-0.1931	0	12	22	1	QGPPAAEAATK
☑	200	439.2872	876.5599	876.4851	0.0748	1	12	44	1	KMVGTLGR + Oxidation (M)
☑	434	403.2078	1608.8023	1608.8947	-0.0924	1	12	37	1	LRAGPGEIALALGESR
☑	396	687.3040	1372.5934	1372.6557	-0.0623	1	12	39	1	NYSFSLACNAKR
☑	152	422.2361	842.4576	842.5226	-0.0650	0	12	41	1	LGTTVKPK
☑	378	436.8620	1307.5642	1307.6371	-0.0729	0	12	43	1	GAPHFPDGVAGQR
☑	219	446.2276	890.4406	890.5199	-0.0792	1	12	50	1	IPHVGRGR
☑	256	493.2688	984.5231	984.6219	-0.0988	0	12	40	1	GISEILILK
☑	294	559.7662	1117.5178	1117.5914	-0.0736	1	12	46	1	MTGRVAGGIEK
☑	344	419.3000	1254.8782	1254.7044	0.1738	1	12	12	1	GAQTAAATAPRIK
☑	190	435.7526	869.4907	869.4971	-0.0064	0	12	36	1	VVDVSVPR
☑	299	570.7575	1139.5005	1139.6563	-0.1559	1	11	44	1	ALRLDHFLR
☑	234	463.2000	924.3854	924.3946	-0.0091	1	11	48	1	RMEGWCK + Oxidation (M)
☑	157	424.2737	846.5328	846.4157	0.1171	0	11	57	1	EVVPEMK + Oxidation (M)
☑	274	523.2699	1044.5253	1044.6192	-0.0940	1	11	59	1	AVLGFGGRLR
☑	135	419.2831	836.5516	836.3884	0.1631	0	11	35	1	DMLMGVR + Oxidation (M)
☑	428	792.8114	1583.6082	1583.7501	-0.1419	1	10	35	1	KDLSVFEVDGNMSK + Oxidation (M)
☑	321	408.3105	1221.9097	1221.7193	0.1904	1	10	3.2	1	LNPKTINPGLR
☑	339	627.7532	1253.4919	1253.5558	-0.0639	0	10	53	1	GISSDGTANMTGK + Oxidation (M)
☑	154	423.2056	844.3967	844.4542	-0.0575	0	10	94	1	EELEVVK
☑	122	412.7308	823.4471	823.4487	-0.0016	1	9	49	1	VPRCPPR
☑	241	469.2000	936.3854	936.4335	-0.0480	0	9	80	1	TANMELSR + Oxidation (M)
☑	110	409.2102	816.4058	816.4276	-0.0218	0	9	80	1	MGGVAQVR
☑	347	425.2063	1272.5970	1272.5955	0.0016	1	9	88	1	CKISSLSYCR + 2 Carbamidomethyl (C)
☑	407	470.2508	1407.7305	1407.5983	0.1321	1	8	82	1	VESCSCRSGGGGPR + Carbamidomethyl (C)
☑	400	463.2000	1386.5782	1386.6503	-0.0721	1	8	76	1	RFWAETMGFSR
☑	310	400.2000	1197.5782	1197.5673	0.0109	1	8	88	1	GGSCPSGPQPRR
☑	425	784.8165	1567.6185	1567.7660	-0.1475	0	8	70	1	DLAMVASDMMVLLK + 2 Oxidation (M)
☑	230	459.7794	917.5443	917.4429	0.1013	0	8	1.2e+02	1	MGWVAGPGK + Oxidation (M)
☑	217	445.2387	888.4628	888.4739	-0.0111	1	8	1.3e+02	1	CENIKLL + Carbamidomethyl (C)
☑	179	429.2143	856.4141	856.5130	-0.0990	1	8	1.2e+02	1	NEVLRVK
☑	116	411.1960	820.3775	820.4443	-0.0668	0	8	79	1	VTAIDFR
☑	123	413.2329	824.4512	824.4215	0.0297	0	8	64	1	VGSFMIR + Oxidation (M)
☑	181	430.3589	858.7032	858.5035	0.1997	1	8	18	1	SAGLRSLR
☑	121	412.7197	823.4248	823.3317	0.0931	0	8	70	1	VMCEGGR + Carbamidomethyl (C); Oxidation (M)
☑	148	421.2199	840.4253	840.5797	-0.1543	1	8	71	1	AAKVVILK
☑	337	416.2081	1245.6024	1245.6717	-0.0694	0	8	1.2e+02	1	AFINLEAAGVGGK
☑	462	897.8686	1793.7227	1793.9193	-0.1966	1	8	68	1	MSVSEEIIISRATQSK + Oxidation (M)
☑	108	408.3088	814.6030	814.4912	0.1117	1	7	79	1	ATVTKAPK
☑	151	421.7467	841.4789	841.5022	-0.0232	0	7	95	1	GITLSVRP
☑	244	472.2566	942.4986	942.5359	-0.0373	1	7	1.2e+02	1	RQAGGSLVR
☑	115	411.1954	820.3762	820.4443	-0.0681	0	7	93	1	VTAIDFR
☑	158	424.2760	846.5374	846.4447	0.0927	1	7	1.3e+02	1	EENKSLK
☑	164	425.7541	849.4936	849.4127	0.0810	1	7	1.4e+02	1	MAGRGGSAK + Oxidation (M)
☑	139	419.2990	836.5834	836.3884	0.1950	0	7	65	1	CAELMVR + Oxidation (M)
☑	281	533.2444	1064.4742	1064.6091	-0.1348	1	7	1.4e+02	1	INVKVGGNHK
☑	196	437.2492	872.4839	872.5080	-0.0241	1	7	1.7e+02	1	EVTAAVRK
☑	102	407.1815	812.3484	812.3738	-0.0254	0	6	83	1	FVCSSSAL
☑	171	427.2886	852.5626	852.4891	0.0734	0	6	96	1	IIMVHPK + Oxidation (M)
☑	357	427.2188	1278.6345	1278.8024	-0.1679	0	6	1.4e+02	1	LVTTGIPVVKPR
☑	223	449.1883	896.3620	896.3698	-0.0078	0	6	1.3e+02	1	NQPYCSSV
☑	361	640.7695	1279.5244	1279.6013	-0.0769	0	6	1.3e+02	1	LSSIANAMCGTR + Carbamidomethyl (C)
☑	134	419.2000	836.3854	836.3884	-0.0030	0	6	1e+02	1	DMLMGVR + Oxidation (M)
☑	360	640.7554	1279.4962	1279.6013	-0.1050	0	6	1.2e+02	1	LSSIANAMCGTR + Carbamidomethyl (C)
☑	100	406.2322	810.4498	810.3946	0.0553	0	6	78	1	GFLAEMK + Oxidation (M)
☑	291	540.2788	1078.5431	1078.5845	-0.0415	0	6	1.7e+02	1	CGTGIVGVFVK
☑	342	419.2800	1254.8182	1254.7044	0.1138	1	6	97	1	GAQTAAATAPRIK
☑	204	441.2472	880.4798	880.4079	0.0719	1	6	1.5e+02	1	ENFWGKT
☑	107	408.2948	814.5750	814.4046	0.1705	1	6	1.2e+02	1	GDPGRGTR
☑	514	756.0185	2265.0338	2264.9495	0.0842	1	6	1e+02	1	KMEDLTMQMFNMEDDMLK + Oxidation (M)
☑	275	524.2712	1046.5278	1046.5179	0.0099	0	6	1.9e+02	1	LSPAVCGTSR + Carbamidomethyl (C)
☑	118	411.3000	820.5854	820.4364	0.1490	0	6	95	1	MSILVDK + Oxidation (M)
☑	343	419.3000	1254.8782	1254.6820	0.1962	0	6	49	1	LTLTAVDGGSPPK
	194	437.2054	872.3963	872.4868	-0.0905	0	6	2.3e+02	1	SLQWIAR

☑										
☑	242	471.2263	940.4381	940.5202	-0.0821	1	5	1.6e+02	1	NPANTRLR
☑	86	400.2000	798.3854	798.4170	-0.0316	1	5	1.1e+02	1	KACVHGGK
☑	254	487.2000	972.3854	972.4600	-0.0745	0	5	2.2e+02	1	HPPSPHCAK
☑	252	484.2000	966.3854	966.4415	-0.0561	0	5	1.8e+02	1	GMCVSWIR + Oxidation (M)
☑	215	445.1000	888.1854	888.3825	-0.1970	0	5	10	1	GDQEEPSK
☑	127	414.2353	826.4560	826.4661	-0.0100	1	5	1.4e+02	1	SNLTKHK
☑	174	428.7439	855.4733	855.5178	-0.0444	0	5	1.8e+02	1	LSIIPASR
☑	106	408.2854	814.5563	814.4046	0.1518	1	5	1.6e+02	1	GDPGRGTR
☑	175	428.7615	855.5084	855.4273	0.0812	0	5	1.9e+02	1	ICLQDHK
☑	478	477.2276	1904.8814	1904.9149	-0.0336	0	5	1.8e+02	1	SLMEQGTQEDEQLLLR + Oxidation (M)
☑	212	444.2275	886.4404	886.3967	0.0437	0	5	3.2e+02	1	GEPGSMGPR
☑	88	401.2541	800.4937	800.4181	0.0756	0	5	1.9e+02	1	YTAPPPR
☑	173	428.7420	855.4695	855.5178	-0.0483	0	4	2e+02	1	LSIIPASR
☑	111	409.2251	816.4357	816.4527	-0.0171	1	4	2.4e+02	1	MRLDLGI
☑	463	598.9593	1793.8562	1793.8003	0.0559	0	4	2e+02	1	CPHAPDETEGTAAPVSR + Carbamidomethyl (C)
☑	430	401.1395	1600.5290	1600.6502	-0.1212	0	4	48	1	DQGEDPPDDSHPHR
☑	170	427.2390	852.4635	852.4011	0.0624	0	4	1.8e+02	1	ITMTTDR + Oxidation (M)
☑	105	408.2830	814.5514	814.4661	0.0854	0	4	1.9e+02	1	LLQTANR
☑	237	467.2775	932.5405	932.4902	0.0503	0	4	3e+02	1	MFHTLLR + Oxidation (M)
☑	319	408.2823	1221.8252	1221.6288	0.1963	0	4	1e+02	1	MVGGVHPEAAVR
☑	165	425.7551	849.4957	849.4232	0.0725	0	4	2.9e+02	1	TNIPYDK
☑	457	444.4715	1773.8567	1773.9308	-0.0740	1	4	2.2e+02	1	LNARCSVLAAANPVYGR
☑	226	450.2425	898.4705	898.3855	0.0850	0	4	2.4e+02	1	CEYSVGNK
☑	161	425.1987	848.3828	848.4538	-0.0710	1	4	2.7e+02	1	TIRNAMK + Oxidation (M)
☑	415	506.2864	1515.8375	1515.8331	0.0044	0	4	2.3e+02	1	GLLGSVMLDLDVLR + Oxidation (M)
☑	477	628.3000	1881.8782	1881.9737	-0.0956	1	4	2.4e+02	1	SGIPISWYRDLHDVPK
☑	131	417.1975	832.3804	832.4589	-0.0785	1	4	2.7e+02	1	GSKCLIR + Carbamidomethyl (C)
☑	293	553.3134	1104.6123	1104.5855	0.0267	0	4	3.1e+02	1	LAFLYTYSK
☑	410	487.2000	1458.5782	1458.6128	-0.0346	0	4	2.8e+02	1	ICGMQMSFGKPGM + Carbamidomethyl (C); Oxidation (
☑	285	535.2611	1068.5077	1068.6179	-0.1102	0	4	2.6e+02	1	TLEIPLDLR
☑	138	419.2946	836.5746	836.3923	0.1823	1	4	1.5e+02	1	MGRSSQR + Oxidation (M)
☑	169	427.1000	852.1854	852.3726	-0.1871	0	3	40	1	EEDAPHR
☑	481	479.2177	1912.8415	1912.8389	0.0027	0	3	1.9e+02	1	SYPLCPYCYNHPPFR + Carbamidomethyl (C)
☑	280	531.3000	1060.5854	1060.5302	0.0553	0	3	3.1e+02	1	TNGGAFPQAAK
☑	225	449.2840	896.5534	896.3732	0.1803	0	3	2.7e+02	1	LADMMER + 2 Oxidation (M)
☑	183	432.2335	862.4524	862.4735	-0.0211	0	3	3.2e+02	1	MAFILPR + Oxidation (M)
☑	137	419.2876	836.5606	836.3923	0.1683	1	3	1.8e+02	1	MGRSSQR + Oxidation (M)
☑	227	450.2567	898.4988	898.4218	0.0770	1	3	2.9e+02	1	NKMATTAF + Oxidation (M)
☑	99	405.3540	808.6934	808.5170	0.1764	1	3	4.2	1	NLLPPKK
☑	513	747.0064	2237.9974	2238.1864	-0.1891	1	3	2.2e+02	1	QKEQSPHVVQSVISLIMGMK
☑	101	407.1530	812.2915	812.4327	-0.1412	0	3	1.5e+02	1	MGLALHR + Oxidation (M)
☑	96	405.1927	808.3707	808.4443	-0.0736	0	3	2e+02	1	GLPGPPGSK
☑	260	511.2000	1020.3854	1020.5352	-0.1498	0	3	3.4e+02	1	LAPDPAGPQR
☑	473	463.9863	1851.9159	1851.7992	0.1167	0	3	2.6e+02	1	SACQSAVCGPQSSTWAR + 2 Carbamidomethyl (C)
☑	224	449.2309	896.4473	896.3667	0.0807	1	2	3.3e+02	1	CPSGCRMK + Oxidation (M)
☑	228	450.2675	898.5204	898.5124	0.0080	0	2	3.2e+02	1	ATVTPSPVK
☑	406	470.2390	1407.6951	1407.6962	-0.0011	1	2	3.3e+02	1	NRSLLVGCMQSK + Carbamidomethyl (C); Oxidation (M
☑	124	413.2428	824.4710	824.3738	0.0972	0	2	2.3e+02	1	YTPCVDK
☑	466	450.2412	1796.9356	1796.8185	0.1170	0	2	3.3e+02	1	MGEFAQLAAAGLGCETR + Carbamidomethyl (C); Oxidati
☑	341	628.3000	1254.5854	1254.5914	-0.0060	0	2	3.6e+02	1	DGFCISGSITAK + Carbamidomethyl (C)
☑	512	742.3381	2223.9925	2224.0807	-0.0883	1	2	2.5e+02	1	VGMAHKADAWPATLSGGQQQR + Oxidation (M)
☑	516	761.6925	2282.0557	2282.1278	-0.0720	1	2	3.2e+02	1	GASSSTNDASVPTTKEFETLIK
☑	328	411.3000	1230.8782	1230.6972	0.1810	0	2	56	1	LGIINYNPSLK
☑	523	685.1538	2736.5860	2736.4810	0.1050	1	2	51	1	EKPAYPPGTEAEGSTRAVVIVPVLTR
☑	520	852.1000	2553.2782	2553.0862	0.1920	0	2	2.7e+02	1	SGHENLALEMYTDLCMFEYAK + Carbamidomethyl (C); 2 O
☑	508	737.6756	2210.0049	2210.0249	-0.0200	0	2	2.8e+02	1	ASSVSPTFCPPTTSHHPVCAK + Carbamidomethyl (C)
☑	525	938.0918	2811.2535	2811.1535	0.1000	0	2	1.9e+02	1	SSVDNCTIPCTGNTTFSYNSQACER + 2 Carbamidomethyl (C
☑	186	433.3225	864.6305	864.5181	0.1124	0	2	2.2e+02	1	VIHLVER
☑	500	519.2427	2072.9418	2072.9614	-0.0197	1	2	2.9e+02	1	MSQMDTIIMAPATGTKAMK + 3 Oxidation (M)
☑	484	639.7000	1916.0782	1915.9487	0.1295	1	2	2.3e+02	1	AERDSALETLQGQLEEK
☑	128	414.2477	826.4809	826.4661	0.0148	1	2	3e+02	1	SNLTKHK
☑	240	468.2687	934.5229	934.5236	-0.0007	0	2	5.5e+02	1	ATILAAGYR
☑	486	481.2486	1920.9655	1920.8029	0.1626	0	1	3.5e+02	1	TEHKPCTYQQCPCNR + 2 Carbamidomethyl (C)
☑	147	420.3139	838.6133	838.4773	0.1360	1	1	1.8e+02	1	APRVGSPR
☑	189	435.7517	869.4888	869.4429	0.0458	0	1	3.8e+02	1	TPCPSLPR
☑	495	506.0060	2019.9951	2019.8714	0.1237	1	1	3.3e+02	1	FNLGGRGCGELGSCHCTPV + 2 Carbamidomethyl (C)
☑	494	1009.4236	2016.8327	2017.0231	-0.1903	0	1	2.4e+02	1	MGVDVVSEYVFANAFILK + Oxidation (M)
☑	492	500.0595	1996.2090	1996.0209	0.1881	0	1	1.2e+02	1	VCRPACVAINGCLPPGLWK
☑	87	401.1489	800.2833	800.3374	-0.0542	0	1	3.5e+02	1	TYTCDAK
☑	208	441.3271	880.6396	880.4510	0.1886	1	1	2.1e+02	1	MQKMLSK + Oxidation (M)
☑	399	463.1163	1386.3271	1386.5050	-0.1779	1	1	5.5	1	GSCCGRCGNCWK + 2 Carbamidomethyl (C)
☑	385	445.1000	1332.2782	1332.4567	-0.1785	0	1	0.82	1	CMVCGGDGSGCSK + 2 Carbamidomethyl (C); Oxidation
☑	95	404.3000	806.5854	806.4035	0.1820	0	1	2e+02	1	VHHASEK
☑	267	519.1588	1036.3031	1036.4673	-0.1642	0	1	2.1e+02	1	LENGSDTSSK
☑	482	639.4000	1915.1782	1915.0666	0.1116	0	1	1.2e+02	1	DLKPANIFISTEDLVLK
☑	214	445.1000	888.1854	888.2784	-0.0930	0	1	25	1	CCMGMCGK + Carbamidomethyl (C)
☑	503	704.0498	2109.1277	2109.0234	0.1042	1	1	3e+02	1	LQKMEEACGTIAVYQGPQK + Oxidation (M)
☑	488	481.2555	1920.9928	1921.0064	-0.0136	1	1	3.8e+02	1	AAAAQSLQPSPCRPRVGR + Carbamidomethyl (C)
☑	210	442.2821	882.5496	882.4447	0.1049	0	1	5.6e+02	1	DVEPAAGPK
☑	404	704.3000	1406.5854	1406.6687	-0.0832	0	1	4.2e+02	1	CPPVTPSPPCQPK + Carbamidomethyl (C)
☑	193	435.7580	869.5014	869.4171	0.0844	0	1	4.4e+02	1	YEGIEFI
☑	109	409.1000	816.1854	816.3613	-0.1759	0	1	48	1	ETNDNPK
☑	221	447.2000	892.3854	892.4589	-0.0734	0	1	5.6e+02	1	AANMALFR
☑	104	407.3000	812.5854	812.4504	0.1350	1	1	2.7e+02	1	KQSHVSK
	163	425.3261	848.6376	848.4426	0.1950	0	1	2.5e+02	1	CATGLSLK + Carbamidomethyl (C)

☑										
☑	195	437.2379	872.4612	872.3772	0.0840	0	1	7.3e+02	1	MDFLGMK + 2 Oxidation (M)
☑	251	483.2464	964.4783	964.4688	0.0095	0	1	8.9e+02	1	GEMKPYPK + Oxidation (M)
☑	261	513.2439	1024.4733	1024.4583	0.0151	0	1	5.6e+02	1	GQICFMNR + Carbamidomethyl (C)
☑	243	471.2989	940.5832	940.5454	0.0378	1	1	4.8e+02	1	KAQAGGKPGK
☑	345	421.9852	1262.9337	1262.7347	0.1991	0	1	25	1	LHVELSLISPR
☑	330	411.9087	1232.7044	1232.5828	0.1216	0	0	7.5e+02	1	ACLALLPCCNR + Carbamidomethyl (C)
☑	496	509.2551	2032.9913	2032.9863	0.0050	1	0	4.1e+02	1	CPPPRPPTSPYPPCPKDK + Carbamidomethyl (C)
☑	515	760.4420	2278.3041	2278.2871	0.0170	1	0	1.9e+02	1	LLRALIGVSLFAAAYMAEVVR + Oxidation (M)
☑	405	470.2221	1407.6446	1407.6962	-0.0516	1	0	5.3e+02	1	NRSLLVGCMQSK + Carbamidomethyl (C); Oxidation (M
☑	504	704.3000	2109.8782	2109.7947	0.0834	0	0	3.2e+02	1	IHYNYMCNSSCMGGMNR + 2 Carbamidomethyl (C); Oxida
☑	456	883.8594	1765.7042	1765.7723	-0.0681	1	0	5.1e+02	1	DAVQNCCGISKTEER + 2 Carbamidomethyl (C)
☑	490	495.2468	1976.9581	1976.8985	0.0595	1	0	4.8e+02	1	GWDWTSGVNKCPAGALCR + Carbamidomethyl (C)
☑	176	429.1000	856.1854	856.3823	-0.1968	0	0	44	1	MDFLGMK + Oxidation (M)
☑	89	401.3000	800.5854	800.4868	0.0986	1	0	4.5e+02	1	RSGLLQK
☑	352	639.4000	1276.7854	1276.6710	0.1144	1	0	5.2e+02	1	TYRSLMTHLR
☑	324	613.2000	1224.3854	1224.5808	-0.1954	0	0	1.8e+02	1	GLQAMYEELR + Oxidation (M)
☑	276	526.2846	1050.5547	1050.4375	0.1172	0	0	8.7e+02	1	MGHAGCQFK + Carbamidomethyl (C); Oxidation (M)
☑	353	639.4000	1276.7854	1276.6710	0.1144	1	0	5.2e+02	1	TYRSLMTHLR
☑	156	424.2720	846.5294	846.3905	0.1388	0	0	6.9e+02	1	CEPETLR
☑	1	400.2000	399.1927							
☑	2	401.1472	400.1400							
☑	3	401.3000	400.2927							
☑	4	402.3000	401.2927							
☑	5	403.0000	401.9927							
☑	6	404.3000	403.2927							
☑	7	405.2038	404.1965							
☑	8	405.2045	404.1973							
☑	9	405.2054	404.1982							
☑	10	405.2057	404.1984							
☑	11	405.2086	404.2014							
☑	12	405.2097	404.2025							
☑	13	405.2099	404.2027							
☑	14	407.3000	406.2927							
☑	15	409.1000	408.0927							
☑	16	409.2144	408.2071							
☑	17	409.2152	408.2079							
☑	18	409.2172	408.2099							
☑	19	411.3000	410.2927							
☑	20	413.4000	412.3927							
☑	21	416.2048	415.1976							
☑	22	416.2053	415.1980							
☑	23	416.2054	415.1981							
☑	24	416.2073	415.2001							
☑	25	416.2103	415.2030							
☑	26	416.3606	415.3533							
☑	27	419.2000	418.1927							
☑	28	419.2902	418.2830							
☑	29	419.3000	418.2927							
☑	30	419.3000	418.2927							
☑	31	420.2919	419.2846							
☑	32	420.2945	419.2872							
☑	33	423.3040	422.2967							
☑	34	424.2265	423.2192							
☑	35	425.2525	424.2453							
☑	36	426.4000	425.3927							
☑	37	427.1000	426.0927							
☑	38	427.2011	426.1938							
☑	39	427.2044	426.1971							
☑	40	429.1000	428.0927							
☑	41	429.1000	428.0927							
☑	42	430.2167	429.2094							
☑	43	430.2220	429.2147							
☑	44	431.1000	430.0927							
☑	45	432.2157	431.2084							
☑	46	432.4000	431.3927							
☑	47	433.2195	432.2122							
☑	48	440.3718	439.3646							
☑	49	441.3394	440.3321							
☑	50	441.3447	440.3374							
☑	51	442.2722	441.2649							
☑	52	445.1000	444.0927							
☑	53	445.1000	444.0927							
☑	54	445.2000	444.1927							
☑	55	445.2310	444.2238							
☑	56	447.2000	446.1927							
☑	57	451.2000	450.1927							
☑	58	456.3579	455.3506							
☑	59	463.2000	462.1927							
☑	60	469.2000	468.1927							
☑	61	487.2000	486.1927							
☑	62	495.3969	494.3897							
☑	63	509.2648	508.2575							
☑	64	511.2000	510.1927							
☑	65	527.4000	526.3927							
	66	529.3904	528.3831							

☑			
☑	67	531.3000	530.2927
☑	68	537.1207	536.1135
☑	69	555.3427	554.3354
☑	70	555.3770	554.3698
☑	71	599.3575	598.3503
☑	72	599.3600	598.3528
☑	73	599.3651	598.3578
☑	74	613.2000	612.1927
☑	75	613.2000	612.1927
☑	76	626.3576	625.3503
☑	77	628.3000	627.2927
☑	78	639.4000	638.3927
☑	79	639.4000	638.3927
☑	80	639.5915	638.5842
☑	81	639.7000	638.6927
☑	82	639.7846	638.7773
☑	83	640.5947	639.5874
☑	84	657.7000	656.6927
☑	85	704.3000	703.2927
☑	90	401.3000	800.5854
☑	91	402.1813	802.3481
☑	92	402.3000	802.5854
☑	93	403.0000	803.9854
☑	94	404.0015	805.9885
☑	98	405.2045	808.3945
☑	103	407.2097	812.4049
☑	113	409.3757	816.7368
☑	114	410.3512	818.6879
☑	117	411.2039	820.3932
☑	119	412.3299	822.6453
☑	120	412.3454	822.6763
☑	125	413.3648	824.7151
☑	126	413.4000	824.7854
☑	129	415.3631	828.7117
☑	132	419.1448	836.2751
☑	133	419.1500	836.2854
☑	141	419.3000	836.5854
☑	142	419.3000	836.5854
☑	159	424.2831	846.5516
☑	160	424.2853	846.5560
☑	162	425.2682	848.5218
☑	166	426.2819	850.5493
☑	167	426.4000	850.7854
☑	168	852.1000	851.0927
☑	172	427.3561	852.6977
☑	177	429.1000	856.1854
☑	178	429.1000	856.1854
☑	180	429.2246	856.4346
☑	182	431.1000	860.1854
☑	184	432.4000	862.7854
☑	185	433.1578	864.3011
☑	187	433.3266	864.6387
☑	188	435.3347	868.6549
☑	197	437.3543	872.6940
☑	198	437.3587	872.7028
☑	199	439.1806	876.3466
☑	201	439.3645	876.7144
☑	202	440.3209	878.6272
☑	203	441.2120	880.4095
☑	205	441.2815	880.5485
☑	206	441.3187	880.6228
☑	207	441.3191	880.6236
☑	209	442.2550	882.4955
☑	211	443.2358	884.4570
☑	213	445.0887	888.1629
☑	216	445.2000	888.3854
☑	218	445.3633	888.7121
☑	220	447.1349	892.2553
☑	229	451.2000	900.3854
☑	231	459.7890	917.5634
☑	232	460.7905	919.5664
☑	233	462.4260	922.8374
☑	235	465.3796	928.7446
☑	236	465.3897	928.7648
☑	245	472.2639	942.5133
☑	246	475.5902	949.1659
☑	247	477.7959	953.5772
☑	248	477.7988	953.5831
☑	249	477.8090	953.6034
☑	250	479.3949	956.7753
☑	253	484.3581	966.7016
☑	257	503.0901	1004.1657
☑	258	504.2461	1006.4777
☑	259	505.2965	1008.5784
	262	515.4036	1028.7927

☑			
☑	266	519.0926	1036.1707
☑	269	521.1094	1040.2043
☑	277	527.4000	1052.7854
☑	278	527.5888	1053.1630
☑	288	538.3012	1074.5879
☑	290	540.2607	1078.5069
☑	300	571.5312	1141.0478
☑	311	401.1475	1200.4207
☑	312	401.3000	1200.8782
☑	313	402.3000	1203.8782
☑	314	403.0000	1205.9782
☑	315	404.3000	1209.8782
☑	317	406.1420	1215.4041
☑	318	407.3000	1218.8782
☑	320	408.2872	1221.8399
☑	322	612.1550	1222.2954
☑	323	409.1000	1224.2782
☑	325	613.2000	1224.3854
☑	326	409.3716	1225.0929
☑	331	412.3429	1234.0068
☑	332	412.3458	1234.0155
☑	333	412.7436	1235.2088
☑	334	413.4000	1237.1782
☑	335	415.0450	1242.1133
☑	340	419.1455	1254.4146
☑	348	425.7531	1274.2375
☑	349	425.7587	1274.2542
☑	350	426.3590	1276.0551
☑	351	426.4000	1276.1782
☑	354	639.4000	1276.7854
☑	355	639.7000	1277.3854
☑	356	427.1000	1278.2782
☑	358	640.7000	1279.3854
☑	359	640.7000	1279.3854
☑	362	428.7435	1283.2085
☑	363	428.7445	1283.2116
☑	364	428.7469	1283.2189
☑	365	428.7477	1283.2214
☑	366	429.0651	1284.1735
☑	367	429.1000	1284.2782
☑	368	429.1000	1284.2782
☑	369	429.1000	1284.2782
☑	370	430.3539	1288.0399
☑	371	430.3584	1288.0534
☑	372	431.1000	1290.2782
☑	373	432.4000	1294.1782
☑	376	435.3356	1302.9849
☑	377	435.3433	1303.0081
☑	380	657.7000	1313.3854
☑	381	440.9309	1319.7710
☑	382	441.3486	1321.0241
☑	384	667.1393	1332.2641
☑	386	445.1000	1332.2782
☑	387	445.1004	1332.2793
☑	388	445.1195	1332.3367
☑	389	445.2000	1332.5782
☑	390	446.9732	1337.8976
☑	391	447.2000	1338.5782
☑	393	451.2000	1350.5782
☑	402	702.0382	1402.0618
☑	408	470.3741	1408.1005
☑	409	480.7636	1439.2689
☑	416	511.2000	1530.5782
☑	420	519.1000	1554.2782
☑	421	519.1117	1554.3134
☑	422	519.1133	1554.3180
☑	423	521.0996	1560.2770
☑	424	522.4640	1564.3702
☑	426	527.4000	1579.1782
☑	427	527.5907	1579.7503
☑	429	531.3000	1590.8782
☑	431	537.1220	1608.3443
☑	432	537.1417	1608.4033
☑	433	537.1440	1608.4103
☑	435	538.1282	1611.3627
☑	436	404.9645	1615.8288
☑	437	411.8999	1643.5704
☑	439	415.3605	1657.4128
☑	440	554.1502	1659.4289
☑	441	835.2000	1668.3854
☑	442	419.1380	1672.5229
☑	443	419.1480	1672.5627
☑	444	419.9939	1675.9466
☑	445	421.1352	1680.5116
	446	852.1000	1702.1854

☑			
☑	447	*571.5165*	*1711.5277*
☑	448	*429.0722*	*1712.2599*
☑	449	*429.6055*	*1714.3930*
☑	450	*430.3686*	*1717.4453*
☑	452	*577.2898*	*1728.8477*
☑	453	*440.9250*	*1759.6710*
☑	454	*440.9283*	*1759.6842*
☑	455	*441.1355*	*1760.5127*
☑	458	*445.0971*	*1776.3594*
☑	459	*445.1024*	*1776.3805*
☑	460	*445.1109*	*1776.4146*
☑	461	*447.0832*	*1784.3037*
☑	464	*599.3540*	*1795.0401*
☑	465	*599.3796*	*1795.1171*
☑	467	*612.1225*	*1833.3458*
☑	468	*613.2000*	*1836.5782*
☑	469	*613.2000*	*1836.5782*
☑	471	*463.1073*	*1848.4001*
☑	472	*463.1205*	*1848.4530*
☑	474	*465.0323*	*1856.1000*
☑	476	*628.1641*	*1881.4705*
☑	479	*477.2353*	*1904.9123*
☑	480	*477.2423*	*1904.9401*
☑	483	*639.4000*	*1915.1782*
☑	485	*480.1304*	*1916.4924*
☑	487	*481.2525*	*1920.9811*
☑	489	*657.7000*	*1970.0782*
☑	498	*517.2407*	*2064.9336*
☑	499	*519.1197*	*2072.4498*
☑	501	*520.1268*	*2076.4780*
☑	502	*701.0548*	*2100.1424*
☑	505	*528.7000*	*2110.7709*
☑	506	*532.2765*	*2125.0770*
☑	507	*536.1412*	*2140.5359*
☑	510	*554.1458*	*2212.5541*
☑	511	*554.1527*	*2212.5816*
☑	517	*767.0229*	*2298.0468*
☑	518	*577.3000*	*2305.1707*
☑	519	*581.2875*	*2321.1210*
☑	521	*896.0395*	*2685.0967*
☑	524	*687.1519*	*2744.5787*
☑	527	*817.1501*	*3264.5712*
☑	528	*817.1517*	*3264.5777*

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      : 528
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Mascot: http://www.matrixscience.com/