

MASCOT SEARCH RESULTS

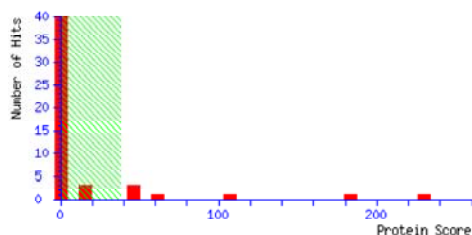
User : JPROS
Email : pro@jbios.co.jp
Search title : D:\JPROS\L015\d_4micro.wiff (sample number 1)
MS data file : mas88B.tmp
Database : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Taxonomy : Homo sapiens (human) (327411 sequences)
Timestamp : 12 Feb 2019 at 11:53:05 GMT
Protein hits : [NP_006112.3](#) keratin, type II cytoskeletal 1 [Homo sapiens]
[Q5VTE0.1](#) PUTATIVE PSEUDOGENE: RecName: Full=Putative elongation factor 1-alpha-like 3; Short=EF-1-alpha-like 3; A:
[BAB14489.1](#) unnamed protein product [Homo sapiens]
[NP_000412.3](#) keratin, type I cytoskeletal 10 [Homo sapiens]
[NP_002085.2](#) eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 1 [Homo sapiens]
[NP_001530.1](#) dnaJ homolog subfamily A member 1 isoform 1 [Homo sapiens]
[NP_000217.2](#) keratin, type I cytoskeletal 9 [Homo sapiens]
[NP_002991.2](#) succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor [Homo sapiens]
[CCQ43188.1](#) alternative protein PSAP [Homo sapiens]
[EAW66317.1](#) hCG2039691, partial [Homo sapiens]

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.

Individual ions scores > 38 indicate identity or extensive homology ($p < 0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

**Peptide Summary Report**

Format As	Peptide Summary	Help
Significance threshold p<	0.05	Max. number of hits
Standard scoring	<input type="radio"/> MudPIT scoring	<input checked="" type="radio"/> Display non-significant matches
Show pop-ups	<input checked="" type="radio"/> Suppress pop-ups	Sort unassigned
Preferred taxonomy	All entries	Require bold red

1. [NP_006112.3](#) Mass: 65999 Score: 230 Matches: 7(3) Sequences: 7(3) emPAI: 0.17
keratin, type II cytoskeletal 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
<input checked="" type="checkbox"/> 271	487.2401	972.4657	972.5240	-0.0582	0	19	9.9	1	U	K.IEISELNR.V
<input checked="" type="checkbox"/> 302	533.2037	1064.3929	1064.5138	-0.1209	0	14	23	1	U	K.AQYEDIAQK.S
<input checked="" type="checkbox"/> 315	590.2698	1178.5250	1178.5931	-0.0681	0	38	0.1	1	U	K.YEELQITAGR.H
<input checked="" type="checkbox"/> 378	651.8142	1301.6138	1301.7078	-0.0940	0	78	9.5e-06	1	U	R.SLDLDSIIAEVK.A
<input checked="" type="checkbox"/> 393	679.2977	1356.5809	1356.6885	-0.1076	0	37	0.13	1	U	K.LNDLEDALQQAK.E
<input checked="" type="checkbox"/> 396	692.3050	1382.5955	1382.6830	-0.0875	0	115	1.9e-09	1	U	K.SLNNQFASFIDK.V
<input checked="" type="checkbox"/> 406	738.3637	1474.7128	1474.7780	-0.0652	0	97	1.3e-07	1	U	R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:

AAG41947.1	Mass: 66027	Score: 230	Matches: 7(3)	Sequences: 7(3)
keratin 1 [Homo sapiens]				
AFA52002.1	Mass: 66013	Score: 230	Matches: 7(3)	Sequences: 7(3)
keratin 1 [Homo sapiens]				
AFA52003.1	Mass: 66029	Score: 230	Matches: 7(3)	Sequences: 7(3)
keratin 1 [Homo sapiens]				
AFA52004.1	Mass: 65930	Score: 230	Matches: 7(3)	Sequences: 7(3)
keratin 1 [Homo sapiens]				
AFA52005.1	Mass: 66086	Score: 230	Matches: 7(3)	Sequences: 7(3)
keratin 1 [Homo sapiens]				
AFA52007.1	Mass: 66071	Score: 230	Matches: 7(3)	Sequences: 7(3)
keratin 1 [Homo sapiens]				

2. [Q5VTE0.1](#) Mass: 50153 Score: 177 Matches: 9(6) Sequences: 5(3) emPAI: 0.32
PUTATIVE PSEUDOGENE: RecName: Full=Putative elongation factor 1-alpha-like 3; Short=EF-1-alpha-like 3; AltName: Full=Eukaryotic
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 252	457.7685	913.5225	913.5597	-0.0372	0	40	0.068	1	U	R.QTVAVGVVIK.A
<input checked="" type="checkbox"/> 272	488.2580	974.5014	974.5437	-0.0423	0	36	0.17	2	U	R.LPLQDVYK.I
<input checked="" type="checkbox"/> 273	488.2674	974.5203	974.5437	-0.0233	0	(14)	31	1	U	R.LPLQDVYK.I
<input checked="" type="checkbox"/> 284	513.2684	1024.5222	1024.6030	-0.0808	0	(64)	0.00024	1	U	K.IGGIGTVPVGR.V

<input checked="" type="checkbox"/>	285	513.2698	1024.5251	1024.6030	-0.0779	0	(45)	0.019	1	U	K.IGGIGTVFPVGR.V
<input checked="" type="checkbox"/>	286	513.2800	1024.5455	1024.6030	-0.0574	0	69	8.5e-05	1	U	K.IGGIGTVFPVGR.V
<input checked="" type="checkbox"/>	400	468.8879	1403.6419	1403.7197	-0.0778	0	43	0.038	1	U	K.YYVTIIDAPGHR.D
<input checked="" type="checkbox"/>	500	839.0897	2514.2473	2514.3768	-0.1295	0	45	0.012	1	U	R.VETGVLKPGMVVTFAPVNVTEVK.S
<input checked="" type="checkbox"/>	501	844.4167	2530.2282	2530.3717	-0.1435	0	(44)	0.017	1	U	R.VETGVLKPGMVVTFAPVNVTEVK.S + Oxidation (M)

Proteins matching the same set of peptides:

[CAA34756.1](#) Mass: 50095 Score: 177 Matches: 9(6) Sequences: 5(3)
unnamed protein product [Homo sapiens]
[AAF36537.1](#) Mass: 46240 Score: 177 Matches: 9(6) Sequences: 5(3)
glucocorticoid receptor AF-1 specific elongation factor, partial [Homo sapiens]
[BAG60202.1](#) Mass: 42569 Score: 177 Matches: 9(6) Sequences: 5(3)
unnamed protein product [Homo sapiens]
[AAH71619.1](#) Mass: 47839 Score: 177 Matches: 9(6) Sequences: 5(3)
EEF1A1 protein [Homo sapiens]
[AAH71727.1](#) Mass: 50153 Score: 177 Matches: 9(6) Sequences: 5(3)
Eukaryotic translation elongation factor 1 alpha 1 [Homo sapiens]
[AAH71841.1](#) Mass: 50091 Score: 177 Matches: 9(6) Sequences: 5(3)
Eukaryotic translation elongation factor 1 alpha 1 [Homo sapiens]
[BAF85328.1](#) Mass: 50169 Score: 177 Matches: 9(6) Sequences: 5(3)
unnamed protein product [Homo sapiens]
[AAK93966.1](#) Mass: 42997 Score: 177 Matches: 9(6) Sequences: 5(3)
translation elongation factor 1 alpha 1-like 14 [Homo sapiens]
[BAD96235.1](#) Mass: 50093 Score: 177 Matches: 9(6) Sequences: 5(3)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
[BAD96243.1](#) Mass: 50167 Score: 177 Matches: 9(6) Sequences: 5(3)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
[BAD96271.1](#) Mass: 50110 Score: 177 Matches: 9(6) Sequences: 5(3)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
[BAD96702.1](#) Mass: 50079 Score: 177 Matches: 9(6) Sequences: 5(3)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
[BAD96766.1](#) Mass: 50081 Score: 177 Matches: 9(6) Sequences: 5(3)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
[WP_094948604.1](#) Mass: 50109 Score: 177 Matches: 9(6) Sequences: 5(3)
MULTISPECIES: translation elongation factor EF-1 subunit alpha [Enterobacteriaceae]

3. [BAB14489.1](#) Mass: 44345 Score: 106 Matches: 6(1) Sequences: 6(1) emPAI: 0.08
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
<input checked="" type="checkbox"/> 260	468.7198	935.4250	935.4712	-0.0463	0	40	0.067	1	U	K.VADEISFR.L
<input checked="" type="checkbox"/> 313	579.8095	1157.6045	1157.6808	-0.0763	0	66	0.00019	1	U	R.TPGGVFLNLLK.N
<input checked="" type="checkbox"/> 345	623.2916	1244.5686	1244.6248	-0.0562	0	27	1.4	1	U	K.NTPSISEEQIK.D
<input checked="" type="checkbox"/> 384	665.2972	1328.5798	1328.6612	-0.0814	0	35	0.19	1	U	R.QSETYNYLLAK.K
<input checked="" type="checkbox"/> 447	598.5864	1792.7373	1792.8315	-0.0942	0	33	0.24	1	U	R.AFQNTATACAPVSHYR.A + Carbamidomethyl (C)
<input checked="" type="checkbox"/> 506	707.3064	2825.1965	2825.3959	-0.1995	0	22	1.6	1	U	K.CFNPPPKPEPFQFGSSQKPPVAGGK.K + Carbamidomethyl

Proteins matching the same set of peptides:

[EAW48850.1](#) Mass: 46023 Score: 106 Matches: 6(1) Sequences: 6(1)
RNA U, small nuclear RNA export adaptor (phosphorylation regulated), partial [Homo sapiens]
[NP_115553.2](#) Mass: 44375 Score: 106 Matches: 6(1) Sequences: 6(1)
phosphorylated adapter RNA export protein [Homo sapiens]

4. [NP_000412.3](#) Mass: 58766 Score: 59 Matches: 1(1) Sequences: 1(1) emPAI: 0.06
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
<input checked="" type="checkbox"/> 395	691.2719	1380.5292	1380.6408	-0.1116	0	59	0.00067	1	U	R.ALEESNYELEGK.I

Proteins matching the same set of peptides:

[P13645.6](#) Mass: 58792 Score: 59 Matches: 1(1) Sequences: 1(1)
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: 59 Matches: 1(1) Sequences: 1(1)
unnamed protein product [Homo sapiens]
[AAH34697.1](#) Mass: 58792 Score: 59 Matches: 1(1) Sequences: 1(1)
Keratin 10 [Homo sapiens]
[AAA59468.1](#) Mass: 46359 Score: 59 Matches: 1(1) Sequences: 1(1)
keratin-10 [Homo sapiens]
[AAA60544.1](#) Mass: 57213 Score: 59 Matches: 1(1) Sequences: 1(1)
keratin 10 [Homo sapiens]
[EAW60681.1](#) Mass: 63308 Score: 59 Matches: 1(1) Sequences: 1(1)
keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA_b [Homo sapiens]
[XP_005257400.1](#) Mass: 63308 Score: 59 Matches: 1(1) Sequences: 1(1)
keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]

5. [NP_002085.2](#) Mass: 68628 Score: 53 Matches: 2(1) Sequences: 1(1) emPAI: 0.05
eukaryotic peptide chain release factor GTP-binding subunit ERF3A 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
<input checked="" type="checkbox"/> 272	488.2580	974.5014	974.5800	-0.0786	1	53	0.0042	1	U	R.LPIVDKYK.D
273	488.2674	974.5203	974.5800	-0.0597	1	(7)	1.4e+02	4	U	R.LPIVDKYK.D

Proteins matching the same set of peptides:

[AAH09503.2](#) Mass: 68404 Score: 53 Matches: 2(1) Sequences: 1(1)
 GSPT1 protein [Homo sapiens]
[AAP35368.1](#) Mass: 55621 Score: 53 Matches: 2(1) Sequences: 1(1)
 G1 to S phase transition 1 [Homo sapiens]
[AAH36077.1](#) Mass: 68915 Score: 53 Matches: 2(1) Sequences: 1(1)
 G1 to S phase transition 2 [Homo sapiens]
[NP_060564.2](#) Mass: 68840 Score: 53 Matches: 2(1) Sequences: 1(1)
 eukaryotic peptide chain release factor GTP-binding subunit ERF3B [Homo sapiens]
[BAG60988.1](#) Mass: 60380 Score: 53 Matches: 2(1) Sequences: 1(1)
 unnamed protein product [Homo sapiens]
[BAF83071.1](#) Mass: 55706 Score: 53 Matches: 2(1) Sequences: 1(1)
 unnamed protein product [Homo sapiens]
[BAA91612.1](#) Mass: 68808 Score: 53 Matches: 2(1) Sequences: 1(1)
 unnamed protein product [Homo sapiens]
[NP_001123478.1](#) Mass: 68529 Score: 53 Matches: 2(1) Sequences: 1(1)
 eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 2 [Homo sapiens]
[NP_001123479.1](#) Mass: 55720 Score: 53 Matches: 2(1) Sequences: 1(1)
 eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 3 [Homo sapiens]

6. [NP_001530.1](#) Mass: 44839 Score: 47 Matches: 2(1) Sequences: 2(1) emPAI: 0.08
 dnaJ homolog subfamily A member 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
<input checked="" type="checkbox"/> 399	464.9308	1391.7705	1391.8137	-0.0432	0	15	19	1	U	R.TIVITSHPGQIVK.H
<input checked="" type="checkbox"/> 404	726.3225	1450.6304	1450.7303	-0.1000	0	47	0.012	1	U	K.QISQAYEVLSDAK.K

Proteins matching the same set of peptides:

[BAA02656.1](#) Mass: 44848 Score: 47 Matches: 2(1) Sequences: 2(1)
 DnaJ protein homolog [Homo sapiens]
[AAO31694.1](#) Mass: 37021 Score: 47 Matches: 2(1) Sequences: 2(1)
 DnaJA2 [Homo sapiens]
[EAW58527.1](#) Mass: 42122 Score: 47 Matches: 2(1) Sequences: 2(1)
 DnaJ (Hsp40) homolog, subfamily A, member 1, isoform CRA_d [Homo sapiens]

7. [NP_000217.2](#) Mass: 62027 Score: 43 Matches: 2(1) Sequences: 2(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
<input checked="" type="checkbox"/> 301	530.7489	1059.4832	1059.5560	-0.0728	0	24	2.9	1	U	K.TLLDIDNTR.M
<input checked="" type="checkbox"/> 309	561.2795	1120.5444	1120.5764	-0.0320	0	43	0.041	1	U	R.QEYEQLIAK.N

Proteins matching the same set of peptides:

[BAA19418.1](#) Mass: 25913 Score: 43 Matches: 2(1) Sequences: 2(1)
 mutant keratin 9, partial [Homo sapiens]
[AAI21171.1](#) Mass: 48057 Score: 43 Matches: 2(1) Sequences: 2(1)
 KRT9 protein, partial [Homo sapiens]
[CAA52924.1](#) Mass: 61950 Score: 43 Matches: 2(1) Sequences: 2(1)
 keratin 9 [Homo sapiens]
[EAW60744.1](#) Mass: 57526 Score: 43 Matches: 2(1) Sequences: 2(1)
 keratin 9 (epidermolytic palmoplantar keratoderma) [Homo sapiens]
[CAA82315.1](#) Mass: 62092 Score: 43 Matches: 2(1) Sequences: 2(1)
 cytokeratin 9 [Homo sapiens]

8. [NP_002991.2](#) Mass: 31609 Score: 22 Matches: 2(0) Sequences: 1(0)
 succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial 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
<input checked="" type="checkbox"/> 349	419.2875	1254.8406	1254.7044	0.1362	1	(3) 1.5e+02	1	1	U	R.GAQTAATAPRIK.K
<input checked="" type="checkbox"/> 351	419.3000	1254.8782	1254.7044	0.1738	1	22	1.1	1	U	R.GAQTAATAPRIK.K

Proteins matching the same set of peptides:

[AAA35708.1](#) Mass: 29946 Score: 22 Matches: 2(0) Sequences: 1(0)
 succinate-ubiquinone oxidoreductase Ip subunit precursor, partial [Homo sapiens]
[ABD77140.1](#) Mass: 28887 Score: 22 Matches: 2(0) Sequences: 1(0)
 succinate dehydrogenase complex subunit B, partial [Homo sapiens]
[AAA80581.1](#) Mass: 31751 Score: 22 Matches: 2(0) Sequences: 1(0)
 succinate dehydrogenase iron-protein subunit B [Homo sapiens]
[AAA81167.1](#) Mass: 31608 Score: 22 Matches: 2(0) Sequences: 1(0)
 succinate dehydrogenase iron-protein subunit [Homo sapiens]

9. [CCQ43188.1](#) Mass: 5053 Score: 16 Matches: 1(0) Sequences: 1(0)
 alternative protein PSAP [Homo sapiens]

☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 366	640.7683	1279.5221	1279.6013	-0.0791	0	16	13	1	U	M.LSSIANAMCGTR.R + Carbamidomethyl (C)

10. [EAW66317.1](#) Mass: 1934 Score: 14 Matches: 1(0) Sequences: 1(0)

hCG2039691, partial [Homo sapiens]

☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 167	422.2274	842.4402	842.3995	0.0407	1	14	29	1	U	K.GNTHRGTT.-

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
<input checked="" type="checkbox"/> 162	421.7335	841.4525	841.5022	-0.0497	0	24	2.3	1		GITLSVRP
<input checked="" type="checkbox"/> 191	428.7428	855.4711	855.5290	-0.0579	1	21	4.7	1		IAEVLRR
<input checked="" type="checkbox"/> 165	421.7381	841.4616	841.5022	-0.0405	0	20	5.8	1		GITLSVRP
<input checked="" type="checkbox"/> 213	435.7528	869.4911	869.4971	-0.0059	0	19	6.4	1		VVDVSVPR
<input checked="" type="checkbox"/> 163	421.7347	841.4548	841.5022	-0.0473	0	18	7.5	1		GITLSVRP
<input checked="" type="checkbox"/> 164	421.7368	841.4590	841.5022	-0.0431	0	18	7.6	1		GITLSVRP
<input checked="" type="checkbox"/> 290	523.2549	1044.4953	1044.5564	-0.0611	0	18	11	1		LSSDGLQVAR
<input checked="" type="checkbox"/> 215	435.7566	869.4986	869.5335	-0.0349	0	17	11	1		VTVLVSPR
<input checked="" type="checkbox"/> 292	523.2621	1044.5096	1044.5716	-0.0620	0	16	16	1		LSSAHVYLR
<input checked="" type="checkbox"/> 296	523.2805	1044.5465	1044.5564	-0.0099	0	16	16	1		LSSDGLQVAR
<input checked="" type="checkbox"/> 289	523.2408	1044.4671	1044.6583	-0.1912	0	16	17	1		LLTTFLEPIK
<input checked="" type="checkbox"/> 340	413.8929	1238.6570	1238.5206	0.1364	0	16	16	1		CMSALSMNNR + Oxidation (M)
<input checked="" type="checkbox"/> 294	523.2659	1044.5173	1044.5564	-0.0391	0	15	20	1		LSSDGLQVAR
<input checked="" type="checkbox"/> 295	523.2660	1044.5174	1044.5564	-0.0390	0	15	21	1		LSSDGLQVAR
<input checked="" type="checkbox"/> 291	523.2550	1044.4955	1044.6179	-0.1223	0	15	23	1		ILAINSSSLK
<input checked="" type="checkbox"/> 169	423.1955	844.3765	844.5018	-0.1253	1	14	36	1		TALGEVKK
<input checked="" type="checkbox"/> 143	416.2136	830.4127	830.3770	0.0357	0	13	37	1		LSDDPR
<input checked="" type="checkbox"/> 275	493.2628	984.5111	984.5063	0.0049	0	12	36	1		SVCVPLPR
<input checked="" type="checkbox"/> 168	423.1789	844.3433	844.5018	-0.1585	1	12	58	1		TALGEVKK
<input checked="" type="checkbox"/> 235	445.1000	888.1854	888.3180	-0.1325	0	11	2.4	1		SCWTVM + 2 Oxidation (M)
<input checked="" type="checkbox"/> 131	412.7237	823.4328	823.3746	0.0582	0	11	33	1		GSVMVDTK + Oxidation (M)
<input checked="" type="checkbox"/> 147	419.2839	836.5533	836.3884	0.1649	0	11	30	1		DMLMGVR + Oxidation (M)
<input checked="" type="checkbox"/> 190	428.7354	855.4563	855.5429	-0.0867	0	11	43	1		LVLSSLPK
<input checked="" type="checkbox"/> 145	419.2750	836.5355	836.3884	0.1471	0	11	32	1		DMLMGVR + Oxidation (M)
<input checked="" type="checkbox"/> 211	435.7497	869.4847	869.4607	0.0241	0	11	42	1		VAEAVPER
<input checked="" type="checkbox"/> 220	437.2146	872.4147	872.4603	-0.0456	1	11	68	1		EPDQKAVK
<input checked="" type="checkbox"/> 234	445.1000	888.1854	888.3760	-0.1905	0	11	2.7	1		DGAPGAMDR
<input checked="" type="checkbox"/> 446	896.3523	1790.6900	1790.8662	-0.1762	0	11	26	1		MHVLDLGGFFPGTEGAK + Oxidation (M)
<input checked="" type="checkbox"/> 193	428.7491	855.4837	855.4199	0.0639	0	11	46	1		ISQEHRS
<input checked="" type="checkbox"/> 488	767.0194	2298.0363	2298.0863	-0.0500	1	11	31	1		GASSSTNDASPTTKFETLIK
<input checked="" type="checkbox"/> 132	412.7277	823.4409	823.4262	0.0147	0	11	38	1		VMLGNFK + Oxidation (M)
<input checked="" type="checkbox"/> 149	419.2926	836.5706	836.3884	0.1822	0	10	32	1		DMLMGVR + Oxidation (M)
<input checked="" type="checkbox"/> 194	428.7497	855.4848	855.5290	-0.0442	1	10	53	1		IALKQQR
<input checked="" type="checkbox"/> 152	419.2934	836.5722	836.3884	0.1838	0	10	34	1		DMLMGVR + Oxidation (M)
<input checked="" type="checkbox"/> 326	407.3000	1218.8782	1218.7560	0.1221	1	9	7.1	1		LIVIHLENNR
<input checked="" type="checkbox"/> 509	835.1497	3336.5696	3336.4533	0.1163	1	9	29	1		CLGRSEAMSWHTSGMGGCPGLASSSPASSWPAP + Oxidation (M)
<input checked="" type="checkbox"/> 192	428.7491	855.4836	855.5178	-0.0342	0	9	69	1		LSIIPASR
<input checked="" type="checkbox"/> 219	437.2132	872.4118	872.4174	-0.0056	0	9	1.1e+02	1		EPQQLAR + Carbamidomethyl (C)
<input checked="" type="checkbox"/> 280	499.2775	996.5405	996.5968	-0.0563	0	9	82	1		TPQGIGLLAK
<input checked="" type="checkbox"/> 483	747.0077	2238.0014	2238.1864	-0.1851	1	9	57	1		QKEQSPHHVQVISLIMGK
<input checked="" type="checkbox"/> 334	411.3000	1230.8782	1230.6972	0.1810	0	9	12	1		LGIINYNPSLK
<input checked="" type="checkbox"/> 264	476.2475	950.4804	950.3876	0.0928	1	9	94	1		CEESDRR + Carbamidomethyl (C)
<input checked="" type="checkbox"/> 434	428.7430	1710.9430	1710.8619	0.0811	1	8	70	1		IALCASVCYLRLI + 3 Carbamidomethyl (C)
<input checked="" type="checkbox"/> 288	516.2716	1030.5287	1030.4212	0.1075	0	8	1e+02	1		YECGLMSR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/> 444	887.9157	1773.8168	1773.9777	-0.1609	1	8	80	1		INNLAVDSKLYFHIK
<input checked="" type="checkbox"/> 507	713.3380	2849.3230	2849.2645	0.0585	1	8	44	1		SGAGPESSTQDLPCMWPKECCCHK
<input checked="" type="checkbox"/> 238	445.2000	888.3854	888.4553	-0.0698	0	8	1.3e+02	1		DGGVIDSVK
<input checked="" type="checkbox"/> 392	674.2630	1346.5115	1346.6619	-0.1504	0	8	81	1		VSEDGWISLWR
<input checked="" type="checkbox"/> 394	687.3147	1372.6148	1372.6557	-0.0409	1	8	1.1e+02	1		NYSFSLACNAKR
<input checked="" type="checkbox"/> 175	424.2838	846.5530	846.4447	0.1083	0	8	1.2e+02	1		ESIVNASK
<input checked="" type="checkbox"/> 170	423.1976	844.3807	844.4151	-0.0344	1	8	1.5e+02	1		EAEAGRR
<input checked="" type="checkbox"/> 178	425.1905	848.3665	848.4174	-0.0509	1	8	1.1e+02	1		CRGDLTK + Carbamidomethyl (C)
<input checked="" type="checkbox"/> 202	429.2514	856.4883	856.4039	0.0844	0	8	1.4e+02	1		LNSDSGHK
<input checked="" type="checkbox"/> 282	503.2671	1004.5196	1004.5325	-0.0128	1	7	1.3e+02	1		CTKAVGELK + Carbamidomethyl (C)
<input checked="" type="checkbox"/> 277	495.2518	988.4891	988.5124	-0.0233	1	7	1.3e+02	1		RQNEIMAK
<input checked="" type="checkbox"/> 247	450.2603	898.5061	898.4232	0.0829	0	7	1.1e+02	1		HFMVGHRR + Oxidation (M)
<input checked="" type="checkbox"/> 102	402.1880	802.3614	802.4661	-0.1047	1	7	1.1e+02	1		TAGTAKVR
<input checked="" type="checkbox"/> 187	427.2391	852.4637	852.4271	0.0366	0	7	96	1		LAIMMMK + Oxidation (M)
<input checked="" type="checkbox"/> 207	433.2000	864.3854	864.3622	0.0232	0	7	1.3e+02	1		VECCHFK
<input checked="" type="checkbox"/> 253	459.2429	916.4712	916.3960	0.0751	0	7	1.6e+02	1		TGGTYSTCK
<input checked="" type="checkbox"/> 115	406.2320	810.4494	810.4963	-0.0469	0	7	68	1		ILGPGLNK
<input checked="" type="checkbox"/> 261	469.2694	936.5243	936.4586	0.0657	0	7	1.5e+02	1		VAISMADSK + Oxidation (M)
<input checked="" type="checkbox"/> 129	412.1875	822.3605	822.4236	-0.0630	0	6	91	1		TSLSLPR
<input checked="" type="checkbox"/> 209	433.3205	864.6265	864.4375	0.1890	1	6	77	1		ENMVTKK + Oxidation (M)
<input checked="" type="checkbox"/> 130	412.7226	823.4306	823.3494	0.0812	0	6	1e+02	1		AMSQTD + Oxidation (M)
<input checked="" type="checkbox"/> 484	756.0121	2265.0143	2265.1438	-0.1295	1	6	88	1		LADQMRMLNFPQWFDLLK
<input checked="" type="checkbox"/> 144	417.2258	832.4370	832.3563	0.0808	0	6	1.5e+02	1		QGEEGEGK
<input checked="" type="checkbox"/> 254	459.2544	916.4943	916.4978	-0.0035	1	6	2e+02	1		SGVNLGKK
<input checked="" type="checkbox"/> 117	407.1883	812.3621	812.4756	-0.1135	0	6	96	1		DIVPTLR
<input checked="" type="checkbox"/> 505	898.3587	2692.0544	2692.2357	-0.1814	0	6	36	1		LSCPCFSHAALHMLCFHFCR + Carbamidomethyl (C); O:
<input checked="" type="checkbox"/> 482	1117.4111	2332.8077	2332.9627	-0.1550	0	6	27	1		LPQDHADSCMVSSDDELLSR + Oxidation (M)
<input checked="" type="checkbox"/> 111	405.1792	808.3438	808.3498	-0.0059	0	6	1e+02	1		MGSGAGGTR + Oxidation (M)
<input checked="" type="checkbox"/> 401	472.2621	1413.7645	1413.7762	-0.0117	1	6	1.6e+02	1		AMGEQAVALARAVK
<input checked="" type="checkbox"/> 160	420.2245	838.4345	838.3677	0.0668	0	6	1.2e+02	1		MGLSMER + Oxidation (M)
<input checked="" type="checkbox"/> 374	429.1782	1284.5128	1284.6674	-0.1546	0	5	1.6e+02	1		NEVSKPAEVQCK

<input checked="" type="checkbox"/>	263	472.2456	942.4766	942.4923	-0.0157	0	5	1.8e+02	1	TWSVVVSHK
<input checked="" type="checkbox"/>	180	425.2421	848.4697	848.4287	0.0410	1	5	1.9e+02	1	GSMLGRGR + Oxidation (M)
<input checked="" type="checkbox"/>	135	413.1000	824.1854	824.3738	-0.1884	0	5	33	1	YTPCVDK
<input checked="" type="checkbox"/>	457	463.9983	1851.9640	1851.8785	0.0855	1	5	1.5e+02	1	AGFNQTSVEGQCKATPGTK
<input checked="" type="checkbox"/>	329	408.2902	1221.8489	1221.7193	0.1296	1	5	48	1	LNPKTINPGLR
<input checked="" type="checkbox"/>	433	421.2339	1680.9064	1680.8869	0.0195	1	5	1.6e+02	1	VGMKVAPHLKETLNK + Oxidation (M)
<input checked="" type="checkbox"/>	443	883.8428	1765.6710	1765.8094	-0.1383	0	5	95	1	LEWMGWINTSNGNTK + Oxidation (M)
<input checked="" type="checkbox"/>	237	445.1071	888.1996	888.3825	-0.1829	0	5	17	1	QETGDDPK
<input checked="" type="checkbox"/>	354	423.3055	1266.8947	1266.7547	0.1400	1	5	27	1	ALPAPIEKTISK
<input checked="" type="checkbox"/>	262	472.2260	942.4374	942.5498	-0.1124	1	5	2.1e+02	1	LEGLKDLR
<input checked="" type="checkbox"/>	376	649.2102	1296.4059	1296.5802	-0.1743	0	5	55	1	LESGMQNMSIR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	431	419.9828	1675.9022	1675.7584	0.1438	1	5	1.9e+02	1	LGAEAAARAVDDGGCSR
<input checked="" type="checkbox"/>	493	581.3003	2321.1720	2321.1508	0.0213	0	4	1.6e+02	1	AASPLGSPELCP ⁺ SALHGLSQAMK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	206	433.1562	864.2979	864.4341	-0.1362	1	4	2.1e+02	1	REETIFA
<input checked="" type="checkbox"/>	189	428.2264	854.4383	854.4208	0.0175	1	4	1.8e+02	1	KDTLYIC
<input checked="" type="checkbox"/>	122	409.1908	816.3671	816.4065	-0.0394	0	4	2.4e+02	1	LMGFGHR
<input checked="" type="checkbox"/>	150	419.2930	836.5715	836.3923	0.1793	1	4	1.3e+02	1	MGRSSQR + Oxidation (M)
<input checked="" type="checkbox"/>	158	419.3008	836.5871	836.4868	0.1003	0	4	1.2e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	245	450.2405	898.4664	898.4807	-0.0142	1	4	2.2e+02	1	MKALHQR + Oxidation (M)
<input checked="" type="checkbox"/>	228	441.3243	880.6340	880.5243	0.1097	1	4	1.1e+02	1	VPSGLPRR
<input checked="" type="checkbox"/>	486	761.6906	2282.0501	2282.1278	-0.0777	1	4	2e+02	1	GASSSTNDASVPTTK ⁺ EFETLIK
<input checked="" type="checkbox"/>	155	419.2977	836.5808	836.3923	0.1885	1	4	1.3e+02	1	MGRSSQR + Oxidation (M)
<input checked="" type="checkbox"/>	259	468.2511	934.4876	934.5600	-0.0724	1	4	3.1e+02	1	AVIFTTKR
<input checked="" type="checkbox"/>	218	436.2566	870.4986	870.4092	0.0894	1	4	2.5e+02	1	VFCSGCKK
<input checked="" type="checkbox"/>	153	419.2961	836.5776	836.4868	0.0907	0	4	1.4e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	407	743.2654	1484.5162	1484.6024	-0.0862	0	4	86	1	MGSSSSHMT ⁺ EFPR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	184	425.7614	849.5083	849.4313	0.0770	1	4	2.9e+02	1	VMAAMRR + Oxidation (M)
<input checked="" type="checkbox"/>	133	412.7418	823.4691	823.4300	0.0390	0	4	1.8e+02	1	ENGIVHR
<input checked="" type="checkbox"/>	125	411.1805	820.3465	820.4265	-0.0800	0	4	2e+02	1	LTPGMFR
<input checked="" type="checkbox"/>	306	543.1902	1084.3658	1084.5513	-0.1855	1	4	1.3e+02	1	PATPGTKKEER
<input checked="" type="checkbox"/>	335	617.3000	1232.5854	1232.6700	-0.0845	1	4	3.6e+02	1	RSGWILLQMGK + Oxidation (M)
<input checked="" type="checkbox"/>	236	445.1017	888.1889	888.3825	-0.1936	0	4	16	1	GDQEPEK
<input checked="" type="checkbox"/>	251	457.2130	912.4115	912.4301	-0.0186	0	4	2.5e+02	1	QSENPPNK
<input checked="" type="checkbox"/>	103	402.3000	802.5854	802.4119	0.1735	0	4	2e+02	1	KPGTCAAR
<input checked="" type="checkbox"/>	230	442.2927	882.5709	882.3761	0.1948	0	4	2.8e+02	1	ELCICMR + Oxidation (M)
<input checked="" type="checkbox"/>	118	407.3000	812.5854	812.4756	0.1098	0	4	1.3e+02	1	VVIPTER
<input checked="" type="checkbox"/>	148	419.2905	836.5664	836.4868	0.0796	0	4	1.6e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	151	419.2933	836.5721	836.4868	0.0853	0	4	1.5e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	112	405.1912	808.3678	808.4517	-0.0839	0	4	1.6e+02	1	IAALFMK + Oxidation (M)
<input checked="" type="checkbox"/>	159	419.3046	836.5947	836.4868	0.1079	0	4	1.3e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	389	445.1130	1332.3171	1332.4567	-0.1396	0	4	8.5	1	CMVCGDGGSGCSK + 2 Carbamidomethyl (C); Oxidation
<input checked="" type="checkbox"/>	480	737.6729	2209.9969	2210.0862	-0.0893	1	3	2e+02	1	AGADTHGRLLQGNICND ⁺ AVTK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	216	435.7591	869.5037	869.4984	0.0053	1	3	2.3e+02	1	VVGRHFR
<input checked="" type="checkbox"/>	154	419.2961	836.5777	836.3923	0.1854	1	3	1.6e+02	1	MGRSSQR + Oxidation (M)
<input checked="" type="checkbox"/>	475	515.2545	2056.9890	2056.9801	0.0090	0	3	1.9e+02	1	GTLSDSEIETNSATSTIFGK
<input checked="" type="checkbox"/>	307	547.2992	1092.5839	1092.5056	0.0784	1	3	2.9e+02	1	CRSMAPVEK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	223	441.2000	880.3854	880.4225	-0.0371	0	3	2.7e+02	1	CQYVVGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	491	581.2846	2321.1095	2321.2276	-0.1181	1	3	2.1e+02	1	LGMPPQLSPEAQSLRLMLFK + Oxidation (M)
<input checked="" type="checkbox"/>	390	445.2000	1332.5782	1332.6633	-0.0852	1	3	3e+02	1	BGETLSRDIASR
<input checked="" type="checkbox"/>	448	897.8497	1793.6849	1793.7704	-0.0855	1	3	1.4e+02	1	SEDDDDQSVRVSEDK
<input checked="" type="checkbox"/>	201	429.2004	856.3863	856.4766	-0.0903	1	3	3.8e+02	1	SQKAAPOK
<input checked="" type="checkbox"/>	161	420.2759	838.5372	838.4119	0.1253	0	3	2.1e+02	1	APQHQM
<input checked="" type="checkbox"/>	481	742.3282	2223.9626	2224.0529	-0.0903	1	3	1.9e+02	1	DSLCLVSGETLAAGTSSPKTEGK
<input checked="" type="checkbox"/>	176	424.2841	846.5536	846.3719	0.1817	0	3	3.4e+02	1	EAEDVER
<input checked="" type="checkbox"/>	242	449.1000	896.1854	896.3593	-0.1738	1	3	29	1	SERCCSR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	403	483.2334	1446.6785	1446.5326	0.1459	0	3	3.1e+02	1	CHGCDPCVEAGDK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	375	429.2000	1284.5782	1284.7037	-0.1256	1	3	3.4e+02	1	SPLPSSTAKEIR
<input checked="" type="checkbox"/>	243	449.2333	896.4521	896.4100	0.0420	1	3	3e+02	1	EPGGSRAHS
<input checked="" type="checkbox"/>	270	485.2000	968.3854	968.5039	-0.1185	0	3	2.7e+02	1	ELLQHSSR
<input checked="" type="checkbox"/>	204	430.3535	858.6925	858.4997	0.1928	0	3	1.1e+02	1	MIVDLLR
<input checked="" type="checkbox"/>	197	429.1000	856.1854	856.3823	-0.1968	0	3	25	1	MDPLGMK + Oxidation (M)
<input checked="" type="checkbox"/>	199	429.1984	856.3823	856.3935	-0.0113	1	3	4.2e+02	1	MCGKAFK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	357	639.3237	1276.6329	1276.6631	-0.0302	1	3	4.3e+02	1	KPISKLCMDSR
<input checked="" type="checkbox"/>	120	408.2857	814.5568	814.4046	0.1522	1	3	2.7e+02	1	GDPGRGTR
<input checked="" type="checkbox"/>	353	630.2000	1258.3854	1258.5257	-0.1402	1	2	73	1	ECFLCSGCRK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	248	450.2666	898.5187	898.5348	-0.0161	1	2	3.3e+02	1	SASIRIPR
<input checked="" type="checkbox"/>	503	664.0543	2652.1879	2652.1340	0.0540	0	2	3e+02	1	QANVCNELLHCQNGGTCHNNVR + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	231	445.0780	888.1415	888.3290	-0.1875	0	2	2.4	1	DGYADYW
<input checked="" type="checkbox"/>	305	538.2732	1074.5318	1074.5934	-0.0616	1	2	4.3e+02	1	FGNQKAAAIR
<input checked="" type="checkbox"/>	146	419.2758	836.5370	836.3884	0.1486	0	2	2.4e+02	1	CAELMVR + Oxidation (M)
<input checked="" type="checkbox"/>	200	429.2000	856.3854	856.4151	-0.0297	0	2	4.6e+02	1	NAGANASPR
<input checked="" type="checkbox"/>	328	408.2845	1221.8317	1221.6387	0.1930	1	2	1.3e+02	1	TALSEKLMGTR + Oxidation (M)
<input checked="" type="checkbox"/>	331	408.2942	1221.8606	1221.7193	0.1413	1	2	67	1	LNPKTINPGLR
<input checked="" type="checkbox"/>	356	425.7725	1274.2958	1274.4907	-0.1949	1	2	5.9	1	EKQYDCSDCGK
<input checked="" type="checkbox"/>	141	415.1303	828.2460	828.4454	-0.1993	0	2	1.4e+02	1	QSPTLQR
<input checked="" type="checkbox"/>	166	421.7424	841.4702	841.4657	0.0044	0	2	3.1e+02	1	VAEPLSR
<input checked="" type="checkbox"/>	458	465.0285	1856.0850	1855.9284	0.1566	0	2	1.9e+02	1	MPAAILTMNLLEQHSR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	221	437.2186	872.4227	872.4715	-0.0489	0	2	5.1e+02	1	ELAALNSR
<input checked="" type="checkbox"/>	346	419.1448	1254.4126	1254.5049	-0.0923	0	2	1.3e+02	1	YTMEMDFFR + Oxidation (M)
<input checked="" type="checkbox"/>	128	411.3000	820.5854	820.4079	0.1776	0	2	2.2e+02	1	SAANPSFK
<input checked="" type="checkbox"/>	355	425.1987	1272.5743	1272.5955	-0.0212	1	2	4.2e+02	1	CKISSLSYCR + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	116	407.1000	812.1854	812.3777	-0.1922	0	2	39	1	EHLGDSR
<input checked="" type="checkbox"/>	239	445.2518	888.4890	888.4665	0.0225	1	2	5.2e+02	1	ATEVKGER
<input checked="" type="checkbox"/>	441	585.3103	1752.9090	1752.9444	-0.0354	0	2	3.2e+02	1	MQIEHIIENIVAVTK + Oxidation (M)
<input checked="" type="checkbox"/>	468	481.2404	1920.9327	1920.8611	0.0716	1	2	3e+02	1	IHNQCRYPGFDVMDLN
<input checked="" type="checkbox"/>	504	893.0485	2676.1238	2676.2408	-0.1171	0	2	1.7e+02	1	LSCP ⁺ CSHAALAHLMILCFHFRCR + Carbamidomethyl (C)

442	440.9208	1759.6541	1759.6456	0.0085	0	2	1.5e+02	1	MCDQCQCVCQDLVDR + 2 Carbamidomethyl (C); Oxidation (M)
497	815.1469	2442.4187	2442.2837	0.1351	0	2	1e+02	1	ALGIMTAVGIALIACMGVAAADPWK
100	401.3000	800.5854	800.4253	0.1602	1	2	3e+02	1	TPGQSR
233	445.0964	888.1782	888.3760	-0.1978	0	2	18	1	DGAPGAMDR
450	609.3010	1824.8813	1824.9655	-0.0842	1	2	3.6e+02	1	EPKDGSPVQPSLLSLMK
494	776.1000	2325.2782	2325.1754	0.1028	1	2	2.6e+02	1	DSSGYRWVFGGGTTLTVLGQPK
138	414.5939	827.1733	827.3306	-0.1573	1	2	27	1	CEACGKAF
276	493.3463	984.6781	984.5466	0.1315	1	2	2.9e+02	1	KCFIFLSK
332	408.3052	1221.8937	1221.7193	0.1744	1	2	31	1	LNPKTINPGLR
224	441.2207	880.4269	880.4178	0.0091	0	2	3.9e+02	1	TIDEFEK
246	450.2549	898.4953	898.5097	-0.0144	1	2	4e+02	1	VERRPSR
181	425.2614	848.5082	848.3876	0.1206	1	2	4.5e+02	1	QDESDDK
383	441.2000	1320.5782	1320.6319	-0.0537	0	2	4.4e+02	1	HNLSLNMCFVK + Oxidation (M)
203	430.3533	858.6920	858.4923	0.1997	1	2	1.9e+02	1	ASGQAIGKK
172	423.3055	844.5965	844.5018	0.0947	1	2	5.8e+02	1	KQISELK
293	523.2634	1044.5122	1044.5386	-0.0265	1	2	4.8e+02	1	MGPKGVAVDR + Oxidation (M)
256	463.2378	924.4610	924.4409	0.0201	0	1	4.3e+02	1	MGLTCTISK + Carbamidomethyl (C); Oxidation (M)
232	445.0905	888.1665	888.3544	-0.1879	0	1	11	1	CFICMEK + Oxidation (M)
174	424.2658	846.5171	846.3719	0.1452	0	1	5e+02	1	EADVER
412	769.2597	1536.5049	1536.6540	-0.1491	0	1	78	1	SISADDDDLQESSR
398	463.9811	1388.9215	1388.7929	0.1286	1	1	1.6e+02	1	LGFTGVNKGVVAR
496	610.1402	2436.5316	2436.3675	0.1641	1	1	16	1	ITVVPNRRNMLAIAFGLATAHK + Oxidation (M)
210	434.1740	866.3335	866.3990	-0.0655	0	1	3.8e+02	1	DMAMLV + 2 Oxidation (M)
157	419.3000	836.5854	836.3923	0.1932	1	1	2.4e+02	1	RNTGMSR + Oxidation (M)
361	639.7625	1277.5104	1277.6476	-0.1373	1	1	4.4e+02	1	QLEQSAVRGAR
186	427.2007	852.3869	852.4858	-0.0989	0	1	3.6e+02	1	ILNLFFH
456	617.3000	1848.8782	1848.9015	-0.0233	0	1	4.2e+02	1	GMAPNGLPDHIMAPVWK + Oxidation (M)
269	483.6314	965.2483	965.3913	-0.1431	0	1	1.3e+02	1	GMDVWGQGT + Oxidation (M)
308	554.1400	1106.2654	1106.4233	-0.1579	0	1	41	1	CHTCNTTDR + Carbamidomethyl (C)
113	405.3000	808.5854	808.4919	0.0935	1	1	1.9e+02	1	GHNLLK
119	408.2839	814.5533	814.4912	0.0620	1	1	4e+02	1	ATVTKAPK
377	433.2000	1296.5782	1296.7037	-0.1256	0	1	5.2e+02	1	LSEHLTESILR
268	483.2356	964.4567	964.5494	-0.0928	0	1	8.5e+02	1	GFVFNILR
440	437.2004	1744.7725	1744.8124	-0.0399	1	1	4.7e+02	1	MIGENSGLVSYMREK + 2 Oxidation (M)
330	408.2923	1221.8550	1221.7193	0.1357	1	1	1.1e+02	1	LNPKTINPGLR
445	446.9682	1783.8435	1783.7908	0.0528	1	1	4.5e+02	1	MANPSGGPGGSPSERDR + Oxidation (M)
110	405.1785	808.3424	808.3901	-0.0477	0	1	3.3e+02	1	EFAACIR
214	435.7559	869.4973	869.4252	0.0722	1	1	4.6e+02	1	TFCLCKR
470	481.2451	1920.9511	1920.9226	0.0285	0	0	4.3e+02	1	NIITQDCMWSGFPAAK

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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 : 509

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