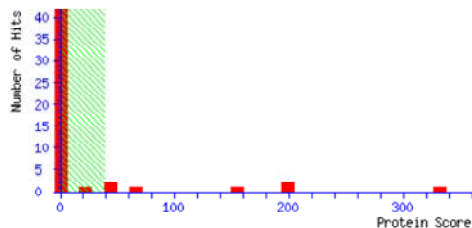


MASCOT SCIENCE Mascot Search Results

User : JPROS  
Email : pro@jbios.co.jp  
Search title : D:\JPROS\L015\4micro.wiff (sample number 1)  
MS data file : mas883.tmp  
Database : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)  
Taxonomy : Homo sapiens (human) (327411 sequences)  
Timestamp : 12 Feb 2019 at 11:40:46 GMT  
Protein hits : [EAL23816.1](#) arsenate resistance protein ARS2 [Homo sapiens]  
[NP\\_006112.3](#) keratin, type II cytoskeletal 1 [Homo sapiens]  
[AFA52006.1](#) keratin 1 [Homo sapiens]  
[AAG24951.1](#) hypothetical protein, partial [Homo sapiens]  
[NP\\_005546.2](#) keratin, type II cytoskeletal 6B [Homo sapiens]  
[NP\\_000412.3](#) keratin, type I cytoskeletal 10 [Homo sapiens]  
[AAC41769.1](#) keratin type II [Homo sapiens]  
[EAW81347.1](#) hCG2040808, 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 > 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. [EAL23816.1](#) Mass: 90194 Score: 332 Matches: 23(11) Sequences: 19(10) emPAI: 0.54  
arsenate resistance protein ARS2 [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"/> <a href="#">193</a>	438.7199	875.4252	875.4786	-0.0534	0	53	0.0037	1	U	K. <a href="#">MLDAAVIK</a> .M + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">207</a>	442.7292	883.4438	883.4875	-0.0437	0	20	6.8	1	U	R.NIAPNISR.A
<input checked="" type="checkbox"/> <a href="#">215</a>	449.7670	897.5194	897.5647	-0.0453	0	32	0.43	1	U	K.LTPLLSVR.E
<input checked="" type="checkbox"/> <a href="#">229</a>	467.2271	932.4396	932.5001	-0.0605	0	(15)	21	1	U	R.AEIIISLCK.R + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">230</a>	467.2344	932.4542	932.5001	-0.0459	0	44	0.032	1	U	R.AEIIISLCK.R + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">282</a>	563.2571	1124.4997	1124.5826	-0.0828	0	(40)	0.069	1	U	R.VALSEPQPER.R
<input checked="" type="checkbox"/> <a href="#">283</a>	563.2621	1124.5096	1124.5826	-0.0730	0	45	0.02	1	U	R.VALSEPQPER.R
<input checked="" type="checkbox"/> <a href="#">290</a>	580.7433	1159.4721	1159.5292	-0.0571	0	19	9.5	2	U	R.ECELSPGVNR.D + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">309</a>	612.2798	1222.5451	1222.6194	-0.0743	0	52	0.0039	1	U	K.FVTSNTQELGK.D
<input checked="" type="checkbox"/> <a href="#">310</a>	612.2919	1222.5693	1222.6194	-0.0500	0	(1)	5.4e+02	1	U	K.FVTSNTQELGK.D
<input checked="" type="checkbox"/> <a href="#">336</a>	634.7363	1267.4581	1267.5245	-0.0664	0	14	18	1	U	R.DLDAPDVDVFF.-
<input checked="" type="checkbox"/> <a href="#">341</a>	427.9006	1280.6799	1280.6837	-0.0038	1	24	2.2	1	U	R.VALSEPQPERR.F
<input checked="" type="checkbox"/> <a href="#">361</a>	442.5431	1324.6076	1324.6775	-0.0699	0	13	31	1	U	R.ISHGEVLEWQK.T
<input checked="" type="checkbox"/> <a href="#">369</a>	673.2981	1344.5817	1344.6608	-0.0791	0	48	0.011	1	U	K.EICWNLQNI.R + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">377</a>	477.2144	1428.6213	1428.7143	-0.0930	1	32	0.32	1	U	R.LRECELSPGVNR.D + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">382</a>	489.5541	1465.6405	1465.7413	-0.1008	1	40	0.049	1	U	K.FVTSNTQELGKDK.W
<input checked="" type="checkbox"/> <a href="#">386</a>	758.3333	1514.6521	1514.7405	-0.0885	0	56	0.0013	1	U	K.EVAFFNNFLTDK.R
<input checked="" type="checkbox"/> <a href="#">418</a>	868.4369	1734.8592	1734.9590	-0.0998	0	(66)	0.00015	1		R.LGSAIEIDLGVPPVPMK.T
<input checked="" type="checkbox"/> <a href="#">419</a>	876.4309	1750.8472	1750.9539	-0.1067	0	70	5.7e-05	1		R.LGSAIEIDLGVPPVPMK.T + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">458</a>	689.3106	2064.9098	2065.0215	-0.1117	1	72	2.4e-05	1	U	K.EFLLSLDSDVDETRVKK.Y
<input checked="" type="checkbox"/> <a href="#">462</a>	709.6216	2125.8429	2126.0015	-0.1585	0	49	0.0036	1	U	R.ILEQEEEEQAGKGPESK.K
<input checked="" type="checkbox"/> <a href="#">471</a>	564.5071	2253.9994	2254.0964	-0.0971	1	21	2.9	1	U	R.ILEQEEEEQAGKGPESK.K
<input checked="" type="checkbox"/> <a href="#">485</a>	891.4247	2671.2524	2671.4221	-0.1697	0	28	0.53	1	U	R.TQLWASEPGTPPLTSLPSQNPIK.N

Proteins matching the same set of peptides:  
[AAH69249.1](#) Mass: 92136 Score: 332 Matches: 23(11) Sequences: 19(10)  
SRRT protein, partial [Homo sapiens]  
[XP\\_016867779.1](#) Mass: 89933 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform X6 [Homo sapiens]  
[XP\\_016867780.1](#) Mass: 89804 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform X7 [Homo sapiens]  
[BAG64018.1](#) Mass: 96183 Score: 332 Matches: 23(11) Sequences: 19(10)

unnamed protein product [Homo sapiens]

[AAM00189.1](#) Mass: 89131 Score: 332 Matches: 23(11) Sequences: 19(10)  
arsenite-resistant protein ASR2 [Homo sapiens]  
[NP\\_056992.4](#) Mass: 100604 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform a [Homo sapiens]  
[EAW76466.1](#) Mass: 101504 Score: 332 Matches: 23(11) Sequences: 19(10)  
ARS2 protein, isoform CRA\_b [Homo sapiens]  
[NP\\_001122324.1](#) Mass: 100475 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform c [Homo sapiens]  
[NP\\_001122325.1](#) Mass: 100214 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform d [Homo sapiens]  
[NP\\_001122326.1](#) Mass: 100085 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform e [Homo sapiens]  
[XP\\_005250462.1](#) Mass: 101333 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform X2 [Homo sapiens]  
[XP\\_005250463.1](#) Mass: 101204 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform X3 [Homo sapiens]  
[XP\\_005250464.1](#) Mass: 100942 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform X4 [Homo sapiens]  
[XP\\_005250465.1](#) Mass: 100813 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform X5 [Homo sapiens]  
[XP\\_024302561.1](#) Mass: 104027 Score: 332 Matches: 23(11) Sequences: 19(10)  
serrate RNA effector molecule homolog isoform X1 [Homo sapiens]

2. [NP\\_006112.3](#) Mass: 65999 Score: 196 Matches: 9(6) Sequences: 9(6) emPAI: 0.38  
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"/> <a href="#">244</a>	487.2494	972.4842	972.5240	-0.0398	0	47	0.014	1		K.IEISELNR.V
<input checked="" type="checkbox"/> <a href="#">272</a>	533.2394	1064.4642	1064.5138	-0.0496	0	35	0.21	1		K.AQYEDIAQK.S
<input checked="" type="checkbox"/> <a href="#">292</a>	590.2770	1178.5394	1178.5931	-0.0537	0	53	0.0036	1		K.YEELQITAGR.H
<input checked="" type="checkbox"/> <a href="#">334</a>	633.2892	1264.5639	1264.6299	-0.0660	0	39	0.071	1		R.TNAENEFVTIK.K
<input checked="" type="checkbox"/> <a href="#">352</a>	651.8171	1301.6197	1301.7078	-0.0881	0	61	0.00051	1	U	R.SLDLDSIIAEVK.A
<input checked="" type="checkbox"/> <a href="#">370</a>	679.2872	1356.5599	1356.6885	-0.1286	0	42	0.036	1		K.LNDLEDALQQAK.E
<input checked="" type="checkbox"/> <a href="#">372</a>	692.3156	1382.6166	1382.6830	-0.0664	0	69	7.5e-05	1		K.SLNNQFASFIDK.V
<input checked="" type="checkbox"/> <a href="#">376</a>	465.2235	1392.6488	1392.7249	-0.0761	1	20	7.2	1		R.TNAENEFVTIKK.D
<input checked="" type="checkbox"/> <a href="#">383</a>	738.3452	1474.6759	1474.7780	-0.1021	0	67	0.00013	1		R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:

[AAG41947.1](#) Mass: 66027 Score: 196 Matches: 9(6) Sequences: 9(6)  
keratin 1 [Homo sapiens]  
[AFA52002.1](#) Mass: 66013 Score: 196 Matches: 9(6) Sequences: 9(6)  
keratin 1 [Homo sapiens]  
[AFA52003.1](#) Mass: 66029 Score: 196 Matches: 9(6) Sequences: 9(6)  
keratin 1 [Homo sapiens]  
[AFA52004.1](#) Mass: 65930 Score: 196 Matches: 9(6) Sequences: 9(6)  
keratin 1 [Homo sapiens]  
[AFA52005.1](#) Mass: 66086 Score: 196 Matches: 9(6) Sequences: 9(6)  
keratin 1 [Homo sapiens]  
[AFA52007.1](#) Mass: 66071 Score: 196 Matches: 9(6) Sequences: 9(6)  
keratin 1 [Homo sapiens]

3. [AFA52006.1](#) Mass: 66026 Score: 188 Matches: 9(6) Sequences: 9(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
<a href="#">244</a>	487.2494	972.4842	972.5240	-0.0398	0	47	0.014	1		K.IEISELNR.V
<a href="#">272</a>	533.2394	1064.4642	1064.5138	-0.0496	0	35	0.21	1		K.AQYEDIAQK.S
<a href="#">292</a>	590.2770	1178.5394	1178.5931	-0.0537	0	53	0.0036	1		K.YEELQITAGR.H
<a href="#">334</a>	633.2892	1264.5639	1264.6299	-0.0660	0	39	0.071	1		R.TNAENEFVTIK.K
<input checked="" type="checkbox"/> <a href="#">362</a>	665.3103	1328.6060	1328.7187	-0.1127	0	42	0.038	1		R.NLDLDSIIAEVK.A
<a href="#">370</a>	679.2872	1356.5599	1356.6885	-0.1286	0	42	0.036	1		K.LNDLEDALQQAK.E
<a href="#">372</a>	692.3156	1382.6166	1382.6830	-0.0664	0	69	7.5e-05	1		K.SLNNQFASFIDK.V
<a href="#">376</a>	465.2235	1392.6488	1392.7249	-0.0761	1	20	7.2	1		R.TNAENEFVTIKK.D
<a href="#">383</a>	738.3452	1474.6759	1474.7780	-0.1021	0	67	0.00013	1		R.FLEQQNQVLQTK.W

4. [AAG24951.1](#) Mass: 12493 Score: 153 Matches: 3(3) Sequences: 2(2) emPAI: 1.24  
hypothetical protein, 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
<a href="#">418</a>	868.4369	1734.8592	1734.9590	-0.0998	0	(66)	0.00015	1		R.LGSIAEIDLGVPPVPMK.T
<a href="#">419</a>	876.4309	1750.8472	1750.9539	-0.1067	0	70	5.7e-05	1		R.LGSIAEIDLGVPPVPMK.T + Oxidation (M)
<a href="#">458</a>	689.3106	2064.9098	2065.0215	-0.1117	1	72	2.4e-05	1	U	K.EFLISLDDSVDETEAVKR.Y

5. [NP\\_005546.2](#) Mass: 60030 Score: 68 Matches: 3(2) Sequences: 3(2) emPAI: 0.13  
keratin, type II cytoskeletal 6B [Homo sapiens]

☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">292</a>	590.2770	1178.5394	1178.5931	-0.0537	0	53	0.0036	1		K.YEELQITAGR.H
<input checked="" type="checkbox"/> <a href="#">304</a>	408.2798	1221.8177	1221.6241	0.1936	0	1	2.4e+02	1		R.TAENEFVTLK.K

[362](#) 665.3103 1328.6060 1328.7187 -0.1127 0 42 0.038 1 R.NL~~D~~LDLSIIAEVK.A

## Proteins matching the same set of peptides:

[EAW96626.1](#) Mass: 59874 Score: 68 Matches: 3(2) Sequences: 3(2)

keratin 6B, isoform CRA\_a [Homo sapiens]

[EAW96627.1](#) Mass: 60003 Score: 68 Matches: 3(2) Sequences: 3(2)

keratin 6B, isoform CRA\_b [Homo sapiens]

6. [NP\\_000412.3](#) Mass: 58766 Score: 52 Matches: 4(1) Sequences: 4(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"/> <a href="#">100</a>	405.1893	808.3640	808.4330	-0.0691	0	24	1.6	1		R.LASYLDK.V
<input checked="" type="checkbox"/> <a href="#">261</a>	516.2738	1030.5331	1030.5910	-0.0579	0	31	0.57	1	U	R.VLDELTLTK.A
<input checked="" type="checkbox"/> <a href="#">279</a>	555.2150	1108.4154	1108.4825	-0.0672	0	20	4.8	1	U	K.DAEAWFNEK.S
<input checked="" type="checkbox"/> <a href="#">371</a>	691.2891	1380.5636	1380.6408	-0.0773	0	52	0.0033	1	U	R.ALEESNYELEGK.I

## Proteins matching the same set of peptides:

[P13645.6](#) Mass: 58792 Score: 52 Matches: 4(1) Sequences: 4(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: 52 Matches: 4(1) Sequences: 4(1)

unnamed protein product [Homo sapiens]

[AAH34697.1](#) Mass: 58792 Score: 52 Matches: 4(1) Sequences: 4(1)

Keratin 10 [Homo sapiens]

[EAW60681.1](#) Mass: 63308 Score: 52 Matches: 4(1) Sequences: 4(1)

keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA\_b [Homo sapiens]

[XP\\_005257400.1](#) Mass: 63308 Score: 52 Matches: 4(1) Sequences: 4(1)

keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]

7. [AAC41769.1](#) Mass: 60163 Score: 42 Matches: 3(1) Sequences: 3(1) emPAI: 0.06

keratin type II [Homo sapiens]

☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">304</a>	408.2798	1221.8177	1221.6241	0.1936	0	1	2.4e+02	1		R.TAAENEVFTLK.K
<a href="#">362</a>	665.3103	1328.6060	1328.7187	-0.1127	0	42	0.038	1		R.NL <del>D</del> LDLSIIAEVK.A
<a href="#">431</a>	609.3041	1824.8906	1824.8901	0.0005	1	1	4.5e+02	9	U	R.ISIGGGS <del>C</del> AISGGYGSRAR.A + Carbamidomethyl (C)

## Proteins matching the same set of peptides:

[AAC41770.1](#) Mass: 60186 Score: 42 Matches: 3(1) Sequences: 3(1)

keratin type II [Homo sapiens]

8. [EAW81347.1](#) Mass: 9756 Score: 18 Matches: 1(0) Sequences: 1(0)

hCG2040808, 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"/> <a href="#">394</a>	522.2629	1563.7669	1563.7464	0.0205	0	18	7.2	1	U	K.SLQGH <del>C</del> HSGLGPTLT.- + Carbamidomethyl (C)

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"/> <a href="#">146</a>	421.7460	841.4774	841.5022	-0.0248	0	27	1	1		GITLSVRP
<input checked="" type="checkbox"/> <a href="#">271</a>	530.7543	1059.4941	1059.5560	-0.0619	0	24	2.7	1		TLLDIDNTR
<input checked="" type="checkbox"/> <a href="#">290</a>	580.7433	1159.4721	1159.6601	-0.1880	0	20	8.2	1		LSFALSGPALGK
<input checked="" type="checkbox"/> <a href="#">145</a>	421.7419	841.4693	841.5022	-0.0328	0	19	6.8	1		GITLSVRP
<input checked="" type="checkbox"/> <a href="#">247</a>	493.2748	984.5350	984.4586	0.0764	0	18	9.8	1		MVPSDPPDK
<input checked="" type="checkbox"/> <a href="#">266</a>	523.2493	1044.4841	1044.6583	-0.1742	0	16	16	1		LLTTFLEPIK
<input checked="" type="checkbox"/> <a href="#">149</a>	423.1886	844.3626	844.5018	-0.1392	1	16	21	1		TALGEVKK
<input checked="" type="checkbox"/> <a href="#">267</a>	523.2525	1044.4905	1044.5564	-0.0658	0	16	16	1		LSSDGLQVAR
<input checked="" type="checkbox"/> <a href="#">172</a>	428.7461	855.4777	855.5429	-0.0652	0	16	14	1		LVLSSLEPK
<input checked="" type="checkbox"/> <a href="#">249</a>	495.2465	988.4785	988.5566	-0.0781	1	14	26	1		RNGAPHLPK
<input checked="" type="checkbox"/> <a href="#">269</a>	523.2615	1044.5084	1044.5564	-0.0480	0	14	29	1		LSSDGLQVAR
<input checked="" type="checkbox"/> <a href="#">263</a>	517.2431	1032.4717	1032.5703	-0.0985	0	13	33	1		LTLEELSTK
<input checked="" type="checkbox"/> <a href="#">208</a>	445.1000	888.1854	888.3760	-0.1905	0	13	1.8	1		DGAPGAMDR
<input checked="" type="checkbox"/> <a href="#">155</a>	425.1461	848.2777	848.4313	-0.1536	0	12	35	1		EMIEALK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">268</a>	523.2553	1044.4961	1044.5564	-0.0603	0	12	43	1		LSSDGLQVAR
<input checked="" type="checkbox"/> <a href="#">470</a>	747.0026	2237.9860	2238.0328	-0.0468	0	12	27	1		GLEYSVGISSDGGSTFYADSVK
<input checked="" type="checkbox"/> <a href="#">119</a>	412.7301	823.4457	823.4487	-0.0030	1	12	28	1		VPRCPFR
<input checked="" type="checkbox"/> <a href="#">328</a>	419.3000	1254.8782	1254.7044	0.1738	1	12	13	1		GAQTAAATAPRIK
<input checked="" type="checkbox"/> <a href="#">130</a>	416.2039	830.3933	830.4610	-0.0677	1	12	48	1		AQSIERK
<input checked="" type="checkbox"/> <a href="#">284</a>	564.7599	1127.5052	1127.5683	-0.0631	1	11	49	1		EAGERRPGEK
<input checked="" type="checkbox"/> <a href="#">188</a>	435.7521	869.4897	869.4971	-0.0074	0	11	39	1		VVDVSVPR
<input checked="" type="checkbox"/> <a href="#">163</a>	427.1737	852.3328	852.4271	-0.0943	0	11	37	1		LAIMMK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">219</a>	450.2544	898.4943	898.5236	-0.0293	0	11	50	1		AGSPPLVSLR
<input checked="" type="checkbox"/> <a href="#">134</a>	419.2806	836.5466	836.3884	0.1581	0	10	38	1		DMLMGVR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">307</a>	408.2913	1221.8521	1221.7193	0.1327	1	10	15	1		LNPKTINPGLR
<input checked="" type="checkbox"/> <a href="#">218</a>	450.2391	898.4636	898.5236	-0.0600	0	10	59	1		AGSPPLVSLR
<input checked="" type="checkbox"/> <a href="#">254</a>	502.7810	1003.5474	1003.5233	0.0241	1	10	80	1		CQLQKATR + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">306</a>	408.2855	1221.8347	1221.7193	0.1154	1	10	23	1		LNPKTINPGLR
<input checked="" type="checkbox"/> <a href="#">195</a>	439.2211	876.4277	876.4626	-0.0349	0	10	76	1		DIMLELK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">150</a>	423.2116	844.4087	844.4403	-0.0316	1	10	94	1		EEARGGVK

<input checked="" type="checkbox"/>	<a href="#">170</a>	428.7396	855.4646	855.4199	0.0448	0	10	60	1	ISQEHSR
<input checked="" type="checkbox"/>	<a href="#">238</a>	480.7710	959.5274	959.4495	0.0779	0	9	92	1	CTDGLAPQR
<input checked="" type="checkbox"/>	<a href="#">190</a>	437.2000	872.3854	872.4868	-0.1014	0	9	1.1e+02	1	GLGNPFLLR
<input checked="" type="checkbox"/>	<a href="#">165</a>	427.2247	852.4348	852.3721	0.0627	0	9	62	1	IEADMMK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">253</a>	500.3288	998.6431	998.4781	0.1650	0	9	76	1	EPAGASSPAGR
<input checked="" type="checkbox"/>	<a href="#">427</a>	897.8497	1793.6849	1793.8028	-0.1179	0	9	38	1	TGTTGQSGAESGTTEPSAR
<input checked="" type="checkbox"/>	<a href="#">175</a>	429.2212	856.4278	856.5746	-0.1467	1	9	1e+02	1	SKAVVILK
<input checked="" type="checkbox"/>	<a href="#">234</a>	474.1797	946.3448	946.4720	-0.1272	0	9	94	1	GSANSSPSLK
<input checked="" type="checkbox"/>	<a href="#">403</a>	550.2955	1647.8647	1647.7241	0.1406	0	9	75	1	MMNCTLQVICSSFR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">171</a>	428.7419	855.4692	855.4199	0.0494	0	9	75	1	ISQEHSR
<input checked="" type="checkbox"/>	<a href="#">113</a>	411.1292	820.2439	820.4416	-0.1977	1	8	51	1	QPARHGR
<input checked="" type="checkbox"/>	<a href="#">199</a>	441.2603	880.5061	880.4290	0.0771	0	8	86	1	ESPGAPLPN
<input checked="" type="checkbox"/>	<a href="#">144</a>	421.2144	840.4143	840.5797	-0.1654	1	8	67	1	AAKVILK
<input checked="" type="checkbox"/>	<a href="#">104</a>	406.2290	810.4435	810.4123	0.0312	0	8	49	1	TYSIAEK
<input checked="" type="checkbox"/>	<a href="#">174</a>	429.1625	856.3105	856.4766	-0.1662	0	8	72	1	NELAALAR
<input checked="" type="checkbox"/>	<a href="#">276</a>	546.8167	1091.6188	1091.5144	0.1044	1	8	1.1e+02	1	CTYCSKLFK
<input checked="" type="checkbox"/>	<a href="#">167</a>	427.2653	852.5160	852.3470	0.1691	0	8	78	1	MLDMGDR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">159</a>	425.3156	848.6167	848.4174	0.1993	1	8	72	1	CRGDLTK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">107</a>	408.2856	814.5566	814.4912	0.0653	1	8	85	1	ATVTKAPK
<input checked="" type="checkbox"/>	<a href="#">278</a>	555.2000	1108.3854	1108.5513	-0.1659	0	8	77	1	EPVVGASVHGAS
<input checked="" type="checkbox"/>	<a href="#">108</a>	408.2871	814.5596	814.4912	0.0684	1	7	88	1	ATVTKAPK
<input checked="" type="checkbox"/>	<a href="#">380</a>	483.2459	1446.7158	1446.6885	0.0272	1	7	1.1e+02	1	VRVGMDTHSSSTNK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">94</a>	401.3000	800.5854	800.4432	0.1422	0	7	84	1	LAEPFPK
<input checked="" type="checkbox"/>	<a href="#">296</a>	400.5620	1198.6643	1198.6458	0.0185	1	7	1.4e+02	1	KLTGGANWQPK
<input checked="" type="checkbox"/>	<a href="#">158</a>	425.3077	848.6009	848.4174	0.1835	1	7	1e+02	1	CRGDLTK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">109</a>	408.2951	814.5757	814.4912	0.0844	1	7	98	1	ATVTKAPK
<input checked="" type="checkbox"/>	<a href="#">124</a>	415.1220	828.2294	828.4051	-0.1757	0	7	29	1	MPLSTSK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">421</a>	883.8395	1765.6645	1765.8379	-0.1734	1	7	58	1	SLSVFRSMMYSGELK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">358</a>	440.9261	1319.7564	1319.6512	0.1052	1	7	1.4e+02	1	MAMEMRLPVAR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">329</a>	419.3027	1254.8863	1254.7044	0.1819	1	7	36	1	GAQTAAATAPRIK
<input checked="" type="checkbox"/>	<a href="#">138</a>	419.2916	836.5687	836.5120	0.0567	0	6	90	1	APLQPLAK
<input checked="" type="checkbox"/>	<a href="#">169</a>	428.2105	854.4065	854.4320	-0.0255	0	6	1.2e+02	1	IMSVYSR
<input checked="" type="checkbox"/>	<a href="#">204</a>	442.2629	882.5113	882.5763	-0.0650	1	6	1.8e+02	1	ILLVGRRR
<input checked="" type="checkbox"/>	<a href="#">114</a>	411.1480	820.2815	820.4304	-0.1489	1	6	1.2e+02	1	ARQGSFR
<input checked="" type="checkbox"/>	<a href="#">222</a>	458.7632	915.5118	915.5463	-0.0345	1	6	2.1e+02	1	KMLLTTPPL
<input checked="" type="checkbox"/>	<a href="#">250</a>	498.3173	994.6201	994.4760	0.1442	0	6	1.7e+02	1	EPQAVFYAA
<input checked="" type="checkbox"/>	<a href="#">398</a>	401.1443	1600.5481	1600.6392	-0.0911	1	6	47	1	SGQEDCVMMRGSGR + Carbamidomethyl (C); 2 Oxidation
<input checked="" type="checkbox"/>	<a href="#">164</a>	427.2087	852.4029	852.4011	0.0018	0	6	1.3e+02	1	ITMTTDR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">154</a>	425.1353	848.2561	848.3811	-0.1250	0	6	1.3e+02	1	CGQDTIR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">123</a>	414.7390	827.4635	827.4250	0.0385	0	5	1.6e+02	1	ASGVTHTR
<input checked="" type="checkbox"/>	<a href="#">221</a>	451.2561	900.4976	900.4851	0.0125	0	5	2.1e+02	1	GPGAIMLSR
<input checked="" type="checkbox"/>	<a href="#">305</a>	408.2835	1221.8287	1221.6387	0.1900	1	5	72	1	TALSEKLMGTR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">473</a>	756.0074	2265.0005	2265.1438	-0.1433	1	5	1e+02	1	LADQMRMLNFPQWFDLLK
<input checked="" type="checkbox"/>	<a href="#">367</a>	445.2000	1332.5782	1332.6422	-0.0640	1	5	1.9e+02	1	SGESEGLWKQR
<input checked="" type="checkbox"/>	<a href="#">191</a>	437.2312	872.4479	872.4967	-0.0488	1	5	2.6e+02	1	KELEGGLK
<input checked="" type="checkbox"/>	<a href="#">192</a>	437.2326	872.4507	872.4716	-0.0208	1	5	2.6e+02	1	EPTRTAAK
<input checked="" type="checkbox"/>	<a href="#">85</a>	631.2000	630.1927	630.3701	-0.1773	0	5	7.5	1	AAALGTK
<input checked="" type="checkbox"/>	<a href="#">180</a>	432.2476	862.4806	862.4153	0.0653	1	5	2.1e+02	1	MGQCPVRK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">224</a>	459.2559	916.4972	916.4766	0.0206	1	5	2.4e+02	1	EDWKAIR
<input checked="" type="checkbox"/>	<a href="#">461</a>	529.2424	2112.9404	2113.1064	-0.1660	0	5	1.5e+02	1	CTHLTNFAILMQVVPLEK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">209</a>	445.1000	888.1854	888.3760	-0.1905	0	5	11	1	DGAPGAMDR
<input checked="" type="checkbox"/>	<a href="#">285</a>	568.2708	1134.5270	1134.4256	0.1014	0	5	2.7e+02	1	ECNDMAHK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">233</a>	472.2711	942.5276	942.5433	-0.0157	1	5	2.2e+02	1	RGLTMLPR
<input checked="" type="checkbox"/>	<a href="#">211</a>	445.2000	888.3854	888.4413	-0.0559	1	5	3e+02	1	TQRAEER
<input checked="" type="checkbox"/>	<a href="#">166</a>	427.2397	852.4649	852.3470	0.1179	0	4	1.7e+02	1	MLDMGDR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">337</a>	425.2077	1272.6013	1272.6899	-0.0886	1	4	2.6e+02	1	SGGGVVQTGRSLR
<input checked="" type="checkbox"/>	<a href="#">429</a>	451.2249	1800.8705	1800.8261	0.0445	0	4	2e+02	1	HVHTGERPHACGVCGK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">177</a>	431.1000	860.1854	860.3851	-0.1996	0	4	14	1	NMWPEGK
<input checked="" type="checkbox"/>	<a href="#">431</a>	609.3041	1824.8906	1824.7077	0.1829	0	4	2e+02	1	EQPVQCDEMDCSTQR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">187</a>	435.7502	869.4858	869.5487	-0.0629	1	4	2e+02	1	VVKFLHK
<input checked="" type="checkbox"/>	<a href="#">326</a>	419.2862	1254.8367	1254.6820	0.1547	0	4	1.2e+02	1	SLVLGPAALDGK
<input checked="" type="checkbox"/>	<a href="#">212</a>	449.2231	896.4317	896.4828	-0.0511	1	4	2.2e+02	1	QQPPSGKR
<input checked="" type="checkbox"/>	<a href="#">476</a>	767.0351	2298.0834	2298.0807	0.0027	0	4	1.5e+02	1	MDLLGMVVVDELHMLGDSHR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">426</a>	448.0293	1788.0882	1787.9855	0.1026	0	4	91	1	MYPATAVPQINITILK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">140</a>	419.2973	836.5801	836.4868	0.0933	0	4	1.3e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	<a href="#">132</a>	419.1440	836.2734	836.3884	-0.1150	0	4	1.4e+02	1	DMLMGVR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">176</a>	431.1000	860.1854	860.3343	-0.1489	0	4	15	1	CCPPPCCK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">139</a>	419.2931	836.5716	836.4868	0.0847	0	4	1.4e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	<a href="#">137</a>	419.2896	836.5646	836.4868	0.0778	0	4	1.5e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	<a href="#">161</a>	425.7532	849.4918	849.4014	0.0904	0	4	2.8e+02	1	TQMAEVR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">301</a>	405.3000	1212.8782	1212.7012	0.1769	0	4	46	1	KPALISAVMQR
<input checked="" type="checkbox"/>	<a href="#">223</a>	459.2452	916.4758	916.4549	0.0210	1	4	3.3e+02	1	KSAACGQPR
<input checked="" type="checkbox"/>	<a href="#">245</a>	487.3336	972.6527	972.4885	0.1642	1	4	2.6e+02	1	MGMKHLPK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">486</a>	927.1553	2778.4440	2778.5407	-0.0967	1	4	1.2e+02	1	ELPAVNLLKVVLLGHWLLTTQFWR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">335</a>	423.1000	1266.2782	1266.4558	-0.1776	0	4	2.9	1	MEPDDSDSEDK
<input checked="" type="checkbox"/>	<a href="#">412</a>	419.9900	1675.9308	1675.9365	-0.0057	0	4	2.5e+02	1	VLALIGSAVTLLVMSMR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">422</a>	443.2006	1768.7735	1768.8955	-0.1220	0	3	2.3e+02	1	SEEVPRNIAIEDIR
<input checked="" type="checkbox"/>	<a href="#">231</a>	471.2845	940.5544	940.3596	0.1948	0	3	2.6e+02	1	ENDEFCK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">210</a>	445.1000	888.1854	888.2598	-0.0744	0	3	16	1	MCDNCCK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">327</a>	419.3000	1254.8782	1254.7044	0.1738	1	3	87	1	GAQTAAATAPRIK
<input checked="" type="checkbox"/>	<a href="#">136</a>	419.2876	836.5606	836.4868	0.0738	0	3	1.8e+02	1	APQPVVAR
<input checked="" type="checkbox"/>	<a href="#">469</a>	742.3438	2224.0095	2224.1384	-0.1289	0	3	2e+02	1	NMITSQDVLHSAWPTLGLK
<input checked="" type="checkbox"/>	<a href="#">194</a>	439.1855	876.3565	876.4553	-0.0988	0	3	3.5e+02	1	TTATATPSK
<input checked="" type="checkbox"/>	<a href="#">186</a>	435.7428	869.4710	869.4607	0.0104	0	3	2.5e+02	1	VHLSSEAK
<input checked="" type="checkbox"/>	<a href="#">302</a>	608.2000	1214.3854	1214.5682	-0.1827	1	3	1e+02	1	TYICYVYKL
<input checked="" type="checkbox"/>	<a href="#">117</a>	412.3000	822.5854	822.4236	0.1619	0	3	1.5e+02	1	FSIDSVR

397	401.1364	1600.5164	1600.5916	-0.0752	1	3	55	1	MDEARNACNDMGK + 2 Oxidation (M)
295	400.2988	1197.8746	1197.7346	0.1400	1	3	51	1	QVLFLEPVARR
452	495.2104	1976.8125	1976.9075	-0.0950	0	3	1.9e+02	1	VPSPPDEHQEAENAVSSGK
148	423.1000	844.1854	844.3208	-0.1353	0	3	24	1	CFDSMSR
448	483.2725	1929.0611	1928.9785	0.0826	0	3	2.2e+02	1	SPFPLSGSLPPTHFWVGG
93	401.3000	800.5854	800.4188	0.1667	1	3	2.5e+02	1	RPGRGCR
141	419.2974	836.5802	836.4868	0.0934	0	3	1.8e+02	1	APQPVVAR
298	401.3000	1200.8782	1200.7064	0.1718	1	3	42	1	RPGRVRPHAR
128	415.3000	828.5854	828.4817	0.1037	1	3	3e+02	1	EGKQLVR
281	561.2455	1120.4764	1120.5877	-0.1113	0	2	4.4e+02	1	EAGTPPPIPSR
106	408.2785	814.5424	814.4912	0.0512	1	2	2.9e+02	1	ATVTKAPK
214	449.2308	896.4471	896.3988	0.0483	1	2	3.3e+02	1	RQGSTYEG
122	413.2430	824.4715	824.4505	0.0210	0	2	2.3e+02	1	HVDISVR
408	555.2000	1662.5782	1662.6913	-0.1131	0	2	1e+02	1	THSGEKP_MVCGECGR + Carbamidomethyl (C); Oxidation
88	657.5000	656.4927	656.3064	0.1863	0	2	17	1	CAGPPGR
289	577.3000	1152.5854	1152.5557	0.0297	1	2	4.5e+02	1	SASETTRVMR + Oxidation (M)
308	408.2915	1221.8527	1221.6904	0.1624	1	2	86	1	MGRTAFLTVVK
353	437.2000	1308.5782	1308.6496	-0.0714	1	2	3.7e+02	1	GLMGQSWTKSAK + Oxidation (M)
246	489.2774	976.5403	976.4695	0.0709	1	2	4.8e+02	1	ACGLCARAR + Carbamidomethyl (C)
156	425.1906	848.3667	848.3811	-0.0144	0	2	3.9e+02	1	QQGDTIR + Carbamidomethyl (C)
125	415.1220	828.2295	828.4090	-0.1795	0	2	87	1	QDGPGLSR
227	463.1171	924.2196	924.3979	-0.1783	1	2	83	1	APRMGCMK + 2 Oxidation (M)
189	435.7620	869.5094	869.4171	0.0924	0	2	3.4e+02	1	YEGIEFI
320	415.3000	1242.8782	1242.6972	0.1810	0	2	1.3e+02	1	VHTILLPQPPE
102	405.3000	808.5854	808.3967	0.1888	1	2	1.6e+02	1	KEAVTFD
451	657.7000	1970.0782	1970.0407	0.0374	1	2	2.7e+02	1	AMAIADALGKNPQTVLWR + Oxidation (M)
475	761.6951	2282.0636	2282.0736	-0.0100	1	2	3.4e+02	1	QEAIYEMSRGEQDLIEDLK + Oxidation (M)
121	413.2245	824.4344	824.3534	0.0811	0	2	2.6e+02	1	CGLHHC
349	429.1831	1284.5274	1284.6133	-0.0858	0	2	3.9e+02	1	CSITYCGVTGTR
359	440.9327	1319.7764	1319.5969	0.1795	0	2	4.2e+02	1	TFSSYAMGWVR + Oxidation (M)
466	737.6742	2210.0008	2210.1228	-0.1220	0	2	3e+02	1	MMITSQDVLHSWAVPTPGLK
135	419.2822	836.5499	836.3884	0.1615	0	2	2.8e+02	1	CABLVMR + Oxidation (M)
360	441.5000	1321.4782	1321.6449	-0.1667	0	2	2.8e+02	1	CGYAVADAQVIR + Carbamidomethyl (C)
444	481.2447	1920.9498	1920.8287	0.1211	0	2	3.4e+02	1	MLESSFTFQCANWWR + Oxidation (M)
101	405.1925	808.3704	808.3394	0.0310	0	2	2.7e+02	1	AMGMMPR + Oxidation (M)
312	409.3000	1224.8782	1224.6801	0.1981	1	1	68	1	FILRFAICSR
413	427.1961	1704.7553	1704.8352	-0.0799	1	1	4.1e+02	1	NGDSQKICLSLSPLSS + Carbamidomethyl (C)
297	401.3000	1200.8782	1200.7064	0.1718	1	1	55	1	RPGRVRPHAR
441	631.2000	1890.5782	1890.7295	-0.1513	1	1	16	1	CPPGRTGEDCEADCEPR
472	566.7239	2262.8665	2263.0262	-0.1598	1	1	1.2e+02	1	CPHCYDAGTQSGSLKYHLQR
459	517.2706	2065.0532	2065.0965	-0.0433	1	1	3.3e+02	1	KPPSHWITMRVALL_CEK + Carbamidomethyl (C)
442	477.2276	1904.8811	1904.9592	-0.0781	1	1	3.9e+02	1	KDDNGIGTAIDFVLSNAR
103	405.3000	808.5854	808.4443	0.1412	1	1	1.9e+02	1	KNYASVK
151	846.3863	845.3790	845.4494	-0.0704	1	1	6.7e+02	1	AELEEKK
374	463.1166	1386.3278	1386.4890	-0.1612	0	1	5.8	1	C_QWMGDELMG + Carbamidomethyl (C); 2 Oxidation (M)
202	441.3178	880.6210	880.4654	0.1555	1	1	2.9e+02	1	NVTKEYK
417	577.3000	1728.8782	1728.8440	0.0342	1	1	4.2e+02	1	NAPGFTALMKAAMQGR + Oxidation (M)
379	481.2445	1440.7117	1440.7395	-0.0278	1	1	4.7e+02	1	HCIKEIQSEINK
275	538.2987	1074.5828	1074.4400	0.1428	0	1	6.1e+02	1	C_SHQVEASGT + Carbamidomethyl (C)
316	412.3000	1233.8782	1233.7597	0.1184	1	1	76	1	IFLPPPPGIRK
205	442.2635	882.5125	882.4013	0.1112	0	1	5.8e+02	1	MMVMDLK + Oxidation (M)
173	429.1000	856.1854	856.3787	-0.1933	0	1	38	1	NETNHSR
407	554.1629	1659.4669	1659.6617	-0.1948	0	1	10	1	MGNAGSMDSQQTDFR + Oxidation (M)
232	472.2685	942.5225	942.4671	0.0554	0	1	5.2e+02	1	GFHNNNIK
446	483.2264	1928.8764	1929.0472	-0.1708	1	1	3.9e+02	1	LAPGKGLQWVAVISYDGR
265	520.2967	1038.5788	1038.4297	0.1492	0	1	5.4e+02	1	C_PAVCT_CTK + 2 Carbamidomethyl (C)
368	445.2000	1332.5782	1332.6786	-0.1004	1	1	5.3e+02	1	APDGYNVSR_LNK
356	657.7000	1313.3854	1313.5228	-0.1373	0	1	69	1	GDTCCSGVDSAMK + Oxidation (M)
240	483.2291	964.4436	964.5454	-0.1018	1	1	8.8e+02	1	RALEHLN
258	509.4000	1016.7854	1016.5940	0.1915	0	1	74	1	AVTILEMIK
457	506.0176	2020.0412	2019.8641	0.1771	0	1	3.8e+02	1	CMYPPGGQDYAGFPGCCLLR + Oxidation (M)
366	445.1128	1332.3165	1332.4567	-0.1402	0	1	17	1	C_MVCGGDSGCSK + 2 Carbamidomethyl (C); Oxidation
481	610.1385	2436.5250	2436.3675	0.1575	1	1	22	1	ITVVPNRNAILAIAFGLATAHK + Oxidation (M)
273	535.2546	1068.4946	1068.5862	-0.0917	1	1	5.2e+02	1	ARDVHC_TV_K + Carbamidomethyl (C)
201	441.2938	880.5731	880.3927	0.1805	0	1	4.6e+02	1	DDATAFNK
262	516.2900	1030.5655	1030.4688	0.0967	0	1	6.1e+02	1	MGALLCDHR + Oxidation (M)
157	425.2754	848.5363	848.4174	0.1188	1	0	5.7e+02	1	ECSVQKR
184	435.3079	868.6013	868.4113	0.1900	0	0	3.3e+02	1	SCVFAGGTK
143	419.3000	836.5854	836.3997	0.1858	1	0	3e+02	1	MAGVKCR + Carbamidomethyl (C); Oxidation (M)
315	411.8978	1232.6717	1232.6659	0.0057	1	0	7.9e+02	1	LVLSACSAGRTAR
474	760.4437	2278.3093	2278.1953	0.1141	1	0	1.8e+02	1	LDFKSLAVPEPS_MLLENVK + Oxidation (M)
110	409.3000	816.5854	816.4276	0.1579	0	0	5.5e+02	1	C_KPAVSR + Carbamidomethyl (C)
120	412.7346	823.4546	823.4664	-0.0118	1	0	4.1e+02	1	VADHRVK
255	503.2651	1004.5156	1004.4749	0.0406	0	0	6.7e+02	1	YCPAVHTSK
455	499.2612	1993.0157	1993.0130	0.0028	1	0	4.6e+02	1	APAPEQRHGPAAGLPEDPV
179	432.2428	862.4710	862.4232	0.0478	0	0	6.5e+02	1	TLPHCHR
396	528.2263	1581.6572	1581.7974	-0.1402	1	0	4.6e+02	1	TYVMTWVRQT_PGK + Oxidation (M)
463	535.2586	2137.0053	2137.1055	-0.1002	1	0	4.4e+02	1	YLGFPQSEGQVLKEATYINK
357	660.8000	1319.5854	1319.4911	0.0944	0	0	7.7e+02	1	CGYFDEEMNR + Carbamidomethyl (C)
409	555.2740	1662.8001	1662.9093	-0.1093	1	0	5.5e+02	1	YGLPIQVRDAGLSFK
487	817.1250	3264.4708	3264.6523	-0.1815	1	0	2.2e+02	1	GDIPTSGPAFSTVIRGTPCPSVGLSFLTCTVGK
259	511.2000	1020.3854	1020.5828	-0.1974	1	0	6.2e+02	1	APSPQIPRR
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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 :  $\pm 0.2$  Da  
Fragment Mass Tolerance :  $\pm 0.2$  Da  
Max Missed Cleavages : 1  
Instrument type : Default  
Number of queries : 488

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