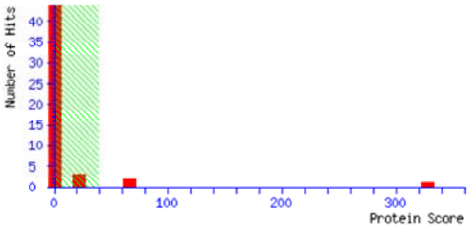
MATRIX SCIENCE Mascot Search Results

```
User          : JPROS
Email         : pro@jbios.co.jp
Search title  : D:\JPROS\L046\1_4micro-2.wiff (sample number 1)
MS data file  : mas125.tmp
Database      : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Taxonomy      : Homo sapiens (human) (327411 sequences)
Timestamp     : 23 Apr 2019 at 09:57:26 GMT
Protein hits  : NP_005338.1 endoplasmic reticulum chaperone BiP precursor [Homo sapiens]
                BAG36698.1  unnamed protein product [Homo sapiens]
                NP_002146.2 heat shock 70 kDa protein 6 [Homo sapiens]
                Q5VTE0.1    PUTATIVE PSEUDOGENE: RecName: Full=Putative elongation factor 1-alpha-like 3; Short=EF-1-alpha-like 3; A
                EAW63420.1  hCG1993117, partial [Homo sapiens]
                BAB40929.2  alpha 1,6-fucosyltransferase [Homo sapiens]
```

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 39 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05 | Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● | Display non-significant matches ☑ | Show sub-sets 0

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

Preferred taxonomy All entries

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

1. NP_005338.1 **Mass:** 72288 **Score:** 328 **Matches:** 18(9) **Sequences:** 17(9) **emPAI:** 0.57
endoplasmic reticulum chaperone BiP 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
☑	217	459.7824	917.5502	917.4706	0.0797	0	21	5.5	1	U	K.VLEDSDLK.K
☑	242	493.8028	985.5910	985.5080	0.0830	0	19	8.6	1	U	R.LTPEEIER.M
☑	289	404.2499	1209.7279	1209.5778	0.1500	1	0	5.5e+02	1	U	K.EFFNGKEPSR.G
☑	295	609.3797	1216.7448	1216.6234	0.1214	0	17	13	1	U	K.DAGTIAGLNVMR.I
☑	296	614.8856	1227.7567	1227.6207	0.1359	0	59	0.00074	1	U	R.VEIIANDQGNR.I
☑	299	617.3705	1232.7265	1232.6183	0.1082	0	(5)	2.6e+02	1	U	K.DAGTIAGLNVMR.I + Oxidation (M)
☑	340	658.8930	1315.7715	1315.6295	0.1420	0	62	0.00043	1	U	R.NELESYAYSLK.N
☑	356	715.9343	1429.8541	1429.6838	0.1703	0	20	5	1	U	R.TWNDPSVQQDIK.F
☑	365	768.9838	1535.9530	1535.7905	0.1625	0	58	0.0005	1	U	K.TFAPEEISAMVLTK.M
☑	367	783.9749	1565.9352	1565.7726	0.1626	0	43	0.022	1	U	R.ITPSYVAFTPEGER.L
☑	371	530.3349	1587.9830	1587.8468	0.1362	1	24	1.1	1	U	K.KSDIDEIVLVGGSTR.I
☑	384	535.6853	1604.0341	1603.8570	0.1771	0	20	1.5	1	U	K.TKPYIQVDIGGGQTK.T
☑	394	839.4860	1676.9575	1676.8006	0.1569	0	25	1.8	1	U	K.NQLTSNPENTVFDAK.R
☑	405	606.0636	1815.1690	1814.9890	0.1800	1	78	1.2e-06	1	U	R.IINEPTAAAIAYGLDKR.E
☑	407	612.0353	1833.0841	1832.9017	0.1825	1	47	0.0064	1	U	K.NQLTSNPENTVFDAKR.L
☑	408	919.0547	1836.0949	1835.9265	0.1684	0	39	0.044	1	U	K.SQIFSTASDNQPTVTIK.V
☑	415	630.0501	1887.1284	1886.9639	0.1645	0	63	0.00014	1	U	K.VTHAVVTVPAYFNDAQR.Q
☑	418	645.4053	1933.1940	1933.0058	0.1882	0	42	0.0097	1	U	K.DNHLLGTFDLTGIPPAPR.G

Proteins matching the same set of peptides:
AAF13605.1 **Mass:** 70888 **Score:** 328 **Matches:** 18(9) **Sequences:** 17(9)
BiP protein, partial [Homo sapiens]
NP_071705.3 **Mass:** 72377 **Score:** 328 **Matches:** 18(9) **Sequences:** 17(9)
endoplasmic reticulum chaperone BiP precursor [Mus musculus]

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2. BAG36698.1 **Mass:** 65980 **Score:** 74 **Matches:** 5(1) **Sequences:** 5(1) **emPAI:** 0.06
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
	273	533.2885	1064.5625	1064.5138	0.0487	0	15	21	3	U	K.AQYEDIAQK.S
☑	284	590.3560	1178.6974	1178.5931	0.1043	0	39	0.07	1	U	K.YEELQITAGR.H
☑	336	651.9289	1301.8432	1301.7078	0.1354	0	47	0.0066	1	U	R.SLDLDSIIAEVK.A
☑	351	465.2790	1392.8151	1392.7249	0.0902	1	31	0.51	1	U	R.TNAENEFVTIKK.D

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   ☑  360  738.4686  1474.9227  1474.7780  0.1447   0    35    0.13   1     U    R.FLEQQNQVLQTK.W


      Proteins matching the same set of peptides:
      NP_006112.3    Mass: 65999    Score: 74     Matches: 5(1)  Sequences: 5(1)
      keratin, type II cytoskeletal 1 [Homo sapiens]
      AAG41947.1    Mass: 66027    Score: 74     Matches: 5(1)  Sequences: 5(1)
      keratin 1 [Homo sapiens]
      AFA52002.1    Mass: 66013    Score: 74     Matches: 5(1)  Sequences: 5(1)
      keratin 1 [Homo sapiens]
      AFA52003.1    Mass: 66029    Score: 74     Matches: 5(1)  Sequences: 5(1)
      keratin 1 [Homo sapiens]
      AFA52004.1    Mass: 65930    Score: 74     Matches: 5(1)  Sequences: 5(1)
      keratin 1 [Homo sapiens]
      AFA52005.1    Mass: 66086    Score: 74     Matches: 5(1)  Sequences: 5(1)
      keratin 1 [Homo sapiens]
      AFA52007.1    Mass: 66071    Score: 74     Matches: 5(1)  Sequences: 5(1)
      keratin 1 [Homo sapiens]
```

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3.    NP_002146.2    Mass: 70984    Score: 59     Matches: 1(1)  Sequences: 1(1)  emPAI: 0.05
      heat shock 70 kDa protein 6 [Homo sapiens]
   ☐  Check to include this hit in error tolerant search

     Query  Observed    Mr(expt)    Mr(calc)    Delta Miss Score  Expect Rank Unique  Peptide
       296  614.8856  1227.7567  1227.6207  0.1359   0    59  0.00074   1     U    R.VEILANDQGNR.T


      Proteins matching the same set of peptides:
      BAG35622.1    Mass: 70914    Score: 59     Matches: 1(1)  Sequences: 1(1)
      unnamed protein product [Homo sapiens]
      CAA36061.1    Mass: 70810    Score: 59     Matches: 1(1)  Sequences: 1(1)
      unnamed protein product [Homo sapiens]
      P48741.2    Mass: 40220    Score: 59     Matches: 1(1)  Sequences: 1(1)
      PUTATIVE PSEUDOGENE: RecName: Full=Putative heat shock 70 kDa protein 7; AltName: Full=Heat shock 70 kDa protein B
      EAW50343.1    Mass: 13346    Score: 59     Matches: 1(1)  Sequences: 1(1)
      hCG2043448, partial [Homo sapiens]
      AAA52696.1    Mass: 26890    Score: 59     Matches: 1(1)  Sequences: 1(1)
      70 kDa heat shock protein, partial [Homo sapiens]
      BAG52788.1    Mass: 70928    Score: 59     Matches: 1(1)  Sequences: 1(1)
      unnamed protein product [Homo sapiens]
      BAD97082.1    Mass: 70960    Score: 59     Matches: 1(1)  Sequences: 1(1)
      heat shock 70kDa protein 6 (HSP70B') variant, partial [Homo sapiens]
```

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4.    Q5VTE0.1    Mass: 50153    Score: 21     Matches: 8(0)  Sequences: 2(0)
      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
       240  488.3083   974.6021   974.5437  0.0584   0     4  3.3e+02   8     U    R.LPLQDVYK.I
   ☑   251  513.3278  1024.6410  1024.6030  0.0380   0  (16)      15   1     U    K.IGGIGTVPVGR.V
   ☑   252  513.3416  1024.6687  1024.6030  0.0658   0  (15)      15   1     U    K.IGGIGTVPVGR.V
   ☑   253  513.3424  1024.6702  1024.6030  0.0673   0  (10)      55   1     U    K.IGGIGTVPVGR.V
       254  513.3446  1024.6746  1024.6030  0.0716   0   (7)   1e+02   2     U    K.IGGIGTVPVGR.V
   ☑   256  513.3507  1024.6869  1024.6030  0.0840   0  (19)     5.3   1     U    K.IGGIGTVPVGR.V
   ☑   257  513.3520  1024.6895  1024.6030  0.0865   0  (21)     3.2   1     U    K.IGGIGTVPVGR.V
   ☑   258  513.3525  1024.6905  1024.6030  0.0875   0    22     2.5   1     U    K.IGGIGTVPVGR.V


      Proteins matching the same set of peptides:
      NP_001949.1    Mass: 50438    Score: 21     Matches: 8(0)  Sequences: 2(0)
      elongation factor 1-alpha 2 [Homo sapiens]
      AAN09722.1    Mass: 38644    Score: 21     Matches: 8(0)  Sequences: 2(0)
      CTCL tumor antigen HD-CL-08 [Homo sapiens]
      AAH14377.1    Mass: 30681    Score: 21     Matches: 8(0)  Sequences: 2(0)
      Unknown (protein for IMAGE:4041545), partial [Homo sapiens]
      AAH14892.1    Mass: 26300    Score: 21     Matches: 8(0)  Sequences: 2(0)
      Unknown (protein for IMAGE:3909122), partial [Homo sapiens]
      AAH22412.1    Mass: 26471    Score: 21     Matches: 8(0)  Sequences: 2(0)
      Unknown (protein for IMAGE:4134193), partial [Homo sapiens]
      CAA34756.1    Mass: 50095    Score: 21     Matches: 8(0)  Sequences: 2(0)
      unnamed protein product [Homo sapiens]
      AAF36537.1    Mass: 46240    Score: 21     Matches: 8(0)  Sequences: 2(0)
      glucocorticoid receptor AF-1 specific elongation factor, partial [Homo sapiens]
      AAA52367.1    Mass: 35205    Score: 21     Matches: 8(0)  Sequences: 2(0)
      elongation factor 1-alpha, partial [Homo sapiens]
      BAG60202.1    Mass: 42569    Score: 21     Matches: 8(0)  Sequences: 2(0)
      unnamed protein product [Homo sapiens]
      AAH63511.1    Mass: 31040    Score: 21     Matches: 8(0)  Sequences: 2(0)
      EEF1A1 protein, partial [Homo sapiens]
      BAG65087.1    Mass: 33168    Score: 21     Matches: 8(0)  Sequences: 2(0)
      unnamed protein product [Homo sapiens]
      AAH65761.1    Mass: 26600    Score: 21     Matches: 8(0)  Sequences: 2(0)
      EEF1A1 protein, partial [Homo sapiens]
      AAH71619.1    Mass: 47839    Score: 21     Matches: 8(0)  Sequences: 2(0)
      EEF1A1 protein [Homo sapiens]
      AAH71727.1    Mass: 50153    Score: 21     Matches: 8(0)  Sequences: 2(0)
      Eukaryotic translation elongation factor 1 alpha 1 [Homo sapiens]
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AAH71841.1 **Mass:** 50091 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
Eukaryotic translation elongation factor 1 alpha 1 [Homo sapiens]
BAF85328.1 **Mass:** 50169 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
unnamed protein product [Homo sapiens]
AAA91835.1 **Mass:** 47426 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
elongation factor-1 alpha, partial [Homo sapiens]
BAD92301.1 **Mass:** 36888 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
eukaryotic translation elongation factor 1 alpha 2 variant, partial [Homo sapiens]
AAK93966.1 **Mass:** 42997 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
translation elongation factor 1 alpha 1-like 14 [Homo sapiens]
AAH94687.1 **Mass:** 33221 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
EEF1A1 protein [Homo sapiens]
BAD96235.1 **Mass:** 50093 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
BAD96239.1 **Mass:** 39231 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
BAD96243.1 **Mass:** 50167 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
BAD96271.1 **Mass:** 50110 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
BAD96702.1 **Mass:** 50079 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
BAD96750.1 **Mass:** 50079 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
BAD96766.1 **Mass:** 50081 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
eukaryotic translation elongation factor 1 alpha 1 variant, partial [Homo sapiens]
WP_094948604.1 **Mass:** 50109 **Score:** 21 **Matches:** 8(0) **Sequences:** 2(0)
MULTISPECIES: translation elongation factor EF-1 subunit alpha [Enterobacteriaceae]

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5. EAW63420.1 **Mass:** 26635 **Score:** 21 **Matches:** 1(0) **Sequences:** 1(0)
hCG1993117, 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
☑	93	409.2814	816.5483	816.3800	0.1684	0	21	5.2	1	U	K.IHMGSEK.I + Oxidation (M)

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6. BAB40929.2 **Mass:** 35772 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
alpha 1,6-fucosyltransferase [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	355	710.4525	1418.8905	1418.7518	0.1388	0	20	3.5	1	U	R.IPEGPIDQGPAIGR.V

Proteins matching the same set of peptides:
AAI42959.1 **Mass:** 35798 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
FUT8 protein [Homo sapiens]
EAW80914.1 **Mass:** 51782 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
fucosyltransferase 8 (alpha (1,6) fucosyltransferase), isoform CRA_d [Homo sapiens]
BAF85102.1 **Mass:** 66474 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
unnamed protein product [Homo sapiens]
BAA92858.1 **Mass:** 32161 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
alpha1,6 fucosyltransferase, partial [Homo sapiens]
NP_835368.1 **Mass:** 66474 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
alpha-(1,6)-fucosyltransferase isoform a [Homo sapiens]
XP_016876625.1 **Mass:** 70347 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
alpha-(1,6)-fucosyltransferase isoform X1 [Homo sapiens]
XP_016876629.1 **Mass:** 62866 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
alpha-(1,6)-fucosyltransferase isoform X2 [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
☑	134	421.7978	841.5811	841.5022	0.0789	0	22	2.8	1		GITLSVRP
☑	404	897.9997	1793.9848	1793.9321	0.0527	0	19	5.8	1		CLGHLFLSLGMVYLR + Carbamidomethyl (C); Oxidation
☑	133	421.7880	841.5614	841.5022	0.0593	0	19	6.3	1		GITLSVRP
☑	331	644.8827	1287.7508	1287.6241	0.1267	0	18	9.3	1		SPVSQLDCLNR + Carbamidomethyl (C)
☑	273	533.2885	1064.5625	1064.5358	0.0267	1	17	13	1		GMMKELQTK
☑	265	523.3209	1044.6272	1044.6583	-0.0311	0	16	17	1		LLTTFLPIK
☑	266	523.3241	1044.6336	1044.6583	-0.0247	0	15	22	1		LLTTFLPIK
☑	196	445.1590	888.3034	888.4553	-0.1519	0	15	24	1		DGGVIDSVK
☑	137	423.2648	844.5150	844.4515	0.0636	1	15	31	1		TAAEAARR
☑	153	428.2784	854.5423	854.4610	0.0813	0	15	16	1		QSLPASPR
☑	267	523.3352	1044.6558	1044.6179	0.0380	0	14	25	1		ILAINSSSLK
☑	172	435.8162	869.6178	869.5447	0.0732	1	13	21	1		VVVERLR
☑	100	412.7839	823.5533	823.4487	0.1046	1	12	23	1		VPRCPPR
☑	156	428.8000	855.5854	855.5290	0.0564	1	12	29	1		LALDRLR
☑	173	436.2556	870.4966	870.5650	-0.0684	1	12	41	1		KASLALIR
☑	349	695.4141	1388.8137	1388.6718	0.1419	0	12	38	1		CQALEENNLSLR
☑	409	616.6405	1846.8997	1847.0517	-0.1519	1	12	31	1		LVFLGEQSVGKTSLITR
☑	238	488.2869	974.5592	974.5372	0.0221	0	12	51	1		LPFQCLVR
☑	185	439.2706	876.5266	876.4124	0.1142	0	12	50	1		CGGELSVR + Carbamidomethyl (C)
☑	200	446.2708	890.5270	890.4862	0.0408	0	12	54	1		TASPPPPPK
☑	218	460.3124	918.6102	918.4957	0.1146	1	11	49	1		VGLARMEK + Oxidation (M)
☑	195	445.1548	888.2950	888.3825	-0.0875	0	11	51	1		DDQSPAEK
☑	171	435.8090	869.6034	869.4971	0.1063	0	11	33	1		VVDVSVPR

☑	240	488.3083	974.6021	974.5372	0.0649	0	11	58	1	LPFQCLVR
☑	121	418.2713	834.5281	834.4422	0.0859	0	11	44	1	APMTFLR
☑	112	416.2534	830.4923	830.4134	0.0789	0	11	56	1	GGPTTPSSK
☑	344	668.4060	1334.7974	1334.6639	0.1335	0	11	41	1	LLSEVMEELEK + Oxidation (M)
☑	194	443.2855	884.5565	884.4212	0.1353	1	11	46	1	RSNSEHR
☑	132	420.2799	838.5452	838.4436	0.1015	0	10	39	1	GTLVTVYS
☑	352	698.9023	1395.7901	1395.6114	0.1788	0	10	59	1	EGSTGTSESSVEAR
☑	186	439.3376	876.6606	876.5433	0.1174	0	10	25	1	ILITVYR
☑	109	415.1844	828.3542	828.4705	-0.1163	0	10	61	1	DQVVGLAK
☑	245	498.3791	994.7437	994.5447	0.1990	1	9	14	1	KSYTEVIR
☑	216	459.3178	916.6210	916.4403	0.1807	0	9	87	1	TNFEGPPR
☑	192	442.3306	882.6467	882.5399	0.1068	1	9	39	1	RAGPLITR
☑	182	439.2351	876.4556	876.4930	-0.0374	1	9	94	1	LGRNVYR
☑	155	428.7980	855.5814	855.5178	0.0636	0	9	63	1	LSIIPASR
☑	157	428.8042	855.5938	855.5178	0.0761	0	9	63	1	LSIIPASR
☑	239	488.3052	974.5959	974.5219	0.0740	0	9	1e+02	1	LSAMGLVER
☑	68	400.6353	799.2560	799.4011	-0.1451	0	9	37	1	QPGMPVR + Oxidation (M)
☑	136	423.2635	844.5125	844.5018	0.0107	1	8	1.3e+02	1	TALGEVKK
☑	395	565.3325	1692.9756	1692.8505	0.1251	1	8	64	1	DLGGRDDLLYNVICK
☑	161	430.2450	858.4754	858.4559	0.0195	1	8	1.3e+02	1	NEALKER
☑	176	437.2526	872.4906	872.4716	0.0190	0	8	1.4e+02	1	VTSGGPLSR
☑	420	998.0425	1994.0705	1993.8907	0.1797	1	8	71	1	VSMTRDMSTDTAYMTLR + Oxidation (M)
☑	99	411.2914	820.5683	820.4555	0.1128	1	7	77	1	EPGHRLL
☑	259	514.2564	1026.4983	1026.6186	-0.1202	1	7	1.1e+02	1	LNVDVIRAK
☑	158	429.1273	856.2400	856.3974	-0.1573	1	7	32	1	DAHCQRK
☑	254	513.3446	1024.6746	1024.5777	0.0968	1	7	96	1	LLEQNPRR
☑	147	427.2362	852.4578	852.4527	0.0050	1	7	1e+02	1	LFGCKASK
☑	97	411.2469	820.4793	820.3749	0.1045	0	7	1.1e+02	1	AEMEIGR + Oxidation (M)
☑	406	913.9795	1825.9444	1825.8008	0.1436	1	6	1.1e+02	1	AKSCENDLEMGMLNSK + Carbamidomethyl (C)
☑	263	521.3568	1040.6990	1040.5978	0.1012	1	6	93	1	LEPTLKNAR
☑	199	445.2891	888.5637	888.4553	0.1084	0	6	1.9e+02	1	DGGVIDSVK
☑	381	401.1904	1600.7326	1600.6133	0.1192	0	6	1.3e+02	1	DMAGFEAECAEAER + Carbamidomethyl (C); Oxidation (
☑	342	445.1590	1332.4551	1332.5551	-0.0999	0	6	64	1	GNAALCSSCHADK + Carbamidomethyl (C)
☑	202	448.3156	894.6167	894.4671	0.1496	0	6	1.1e+02	1	GINVHEAR
☑	70	402.2000	802.3854	802.3756	0.0099	1	6	1.4e+02	1	RGAAGPMAG + Oxidation (M)
☑	319	425.5000	1273.4782	1273.6455	-0.1673	1	6	1.3e+02	1	FPKENHEVFK
☑	91	409.2494	816.4843	816.4566	0.0277	1	6	1.6e+02	1	TASGRGLR
☑	255	513.3475	1024.6804	1024.5705	0.1098	1	6	1.2e+02	1	IQAAFKGYK
☑	108	414.8003	827.5861	827.4250	0.1611	0	6	1.3e+02	1	ASGVTHTR
☑	390	414.2130	1652.8228	1652.8609	-0.0381	1	6	1.4e+02	1	MVLAGLAYGFRNWR
☑	387	544.3355	1629.9848	1629.8322	0.1526	0	6	90	1	TLQEVTQLSQEAQR
☑	230	481.3188	960.6231	960.5426	0.0805	1	6	2e+02	1	VVCTKINK + Carbamidomethyl (C)
☑	286	400.2000	1197.5782	1197.5673	0.0109	1	6	1.6e+02	1	GGSCPSGPQPRR
☑	278	568.3458	1134.6770	1134.4984	0.1786	1	6	2.1e+02	1	THLCDMCGKK
☑	301	414.7956	1241.3649	1241.5538	-0.1888	0	5	69	1	GTGAESHQGGWR
☑	149	427.2806	852.5466	852.4818	0.0648	0	5	1.3e+02	1	LVTDHLR
☑	124	419.3473	836.6801	836.4980	0.1820	1	5	12	1	APAPVARR
☑	145	425.8182	849.6218	849.4344	0.1874	0	5	1.2e+02	1	NDGIIYR
☑	326	428.7947	1283.3623	1283.5539	-0.1916	0	5	17	1	LSCPECWPHR + Carbamidomethyl (C)
☑	227	476.2932	950.5719	950.4127	0.1592	1	5	2e+02	1	DKMETGDR
☑	277	561.3471	1120.6797	1120.5005	0.1792	0	5	2.4e+02	1	EQPSLCTMR + Carbamidomethyl (C)
☑	154	428.2901	854.5657	854.5086	0.0571	1	5	1.4e+02	1	LRVGAPSR
☑	229	481.3185	960.6225	960.5426	0.0799	1	5	2.6e+02	1	VVCTKINK + Carbamidomethyl (C)
☑	403	896.5447	1791.0748	1790.9051	0.1697	0	5	91	1	VSLGPVSYVLVDSEDGR
☑	334	430.5000	1288.4782	1288.6744	-0.1962	1	5	1.7e+02	1	MLGENLRMLGR
☑	152	427.2988	852.5830	852.4011	0.1819	0	5	1.4e+02	1	ITMTTDR + Oxidation (M)
☑	72	403.2004	804.3862	804.4202	-0.0339	1	4	1.9e+02	1	SSRASAAR
☑	401	445.2000	1776.7709	1776.8941	-0.1232	1	4	2e+02	1	ARIAPDVIGPACTDHGK + Carbamidomethyl (C)
☑	126	419.3553	836.6960	836.4980	0.1979	1	4	8.5	1	APAPVARR
☑	160	429.1370	856.2594	856.4290	-0.1696	0	4	94	1	ITTLHGES
☑	347	462.2569	1383.7490	1383.6453	0.1037	1	4	2.1e+02	1	NRYTVMSGTPDK + Oxidation (M)
☑	241	490.3147	978.6148	978.4150	0.1998	0	4	2.6e+02	1	SEKPAPTMC + Oxidation (M)
☑	244	497.2999	992.5852	992.5291	0.0561	0	4	3.1e+02	1	YNIVTLDR
☑	249	504.3316	1006.6486	1006.5447	0.1039	0	4	2.7e+02	1	GLFISISDR
☑	231	483.2897	964.5649	964.4648	0.1001	0	4	4.1e+02	1	VIDGATMSR + Oxidation (M)
☑	228	477.3056	952.5966	952.5342	0.0625	0	4	2.3e+02	1	SPPLTVSPR
☑	385	537.2019	1608.5838	1608.7025	-0.1187	0	4	1.1e+02	1	SHTGVKPYGCSECGK + Carbamidomethyl (C)
☑	96	411.2011	820.3877	820.3715	0.0162	0	4	2e+02	1	AEDPAYR
☑	175	437.2489	872.4832	872.4352	0.0480	0	4	3.6e+02	1	ENGGDLLR
☑	328	428.7990	1283.3752	1283.5539	-0.1788	0	4	38	1	LSCPECWPHR + Carbamidomethyl (C)
☑	345	446.1679	1335.4820	1335.5223	-0.0403	0	4	1.8e+02	1	AEDAAMYYCAR + Carbamidomethyl (C); Oxidation (M)
☑	174	436.3833	870.7521	870.5650	0.1870	1	3	24	1	KASLALIR
☑	327	428.7978	1283.3717	1283.5539	-0.1823	0	3	37	1	LSCPECWPHR + Carbamidomethyl (C)
☑	233	483.3699	964.7252	964.5679	0.1573	1	3	62	1	NRIPRPGR
☑	67	400.6297	799.2448	799.4188	-0.1740	0	3	90	1	GGDSLVPR
☑	225	475.6533	949.2920	949.4473	-0.1553	0	3	2.3e+02	1	CAAALMASR + Carbamidomethyl (C)
☑	180	437.2726	872.5307	872.4174	0.1133	0	3	4e+02	1	EAPALCGR + Carbamidomethyl (C)
☑	110	415.2061	828.3976	828.4705	-0.0729	0	3	2.8e+02	1	DQVVGLAK
☑	329	428.8028	1283.3866	1283.5784	-0.1918	1	3	52	1	MRNNCTASLMK + Oxidation (M)
☑	223	474.2525	946.4904	946.5270	-0.0366	1	3	3.7e+02	1	CQVVVSKK + Carbamidomethyl (C)
☑	348	463.1716	1386.4931	1386.6568	-0.1637	1	3	1.4e+02	1	GSNKGFEATYWK
☑	330	428.8070	1283.3990	1283.5539	-0.1549	0	3	67	1	LSCPECWPHR + Carbamidomethyl (C)
☑	335	431.8610	1292.5611	1292.7023	-0.1412	0	3	3e+02	1	CQGPALPGKPLR + Carbamidomethyl (C)
☑	84	407.2496	812.4846	812.5120	-0.0273	0	3	1.9e+02	1	VVILDVR
☑	77	405.2555	808.4965	808.4079	0.0886	0	3	2e+02	1	NSGGFLSK
	382	401.1938	1600.7460	1600.7958	-0.0498	0	3	3e+02	1	TVTGAVNFGHQISDR

☑										
☑	71	402.2448	802.4751	802.4297	0.0454	1	3	3e+02	1	KTGNQQK
☑	63	400.2000	798.3854	798.4170	-0.0316	1	3	2e+02	1	KACVHGGK
☑	209	450.3048	898.5951	898.4807	0.1144	1	2	3e+02	1	MKALHQR + Oxidation (M)
☑	177	437.2666	872.5187	872.5079	0.0107	1	2	4.9e+02	1	ELRQLSK
☑	141	425.3269	848.6392	848.4643	0.1749	0	2	1.5e+02	1	EEIAFLK
☑	261	517.3307	1032.6469	1032.5240	0.1229	1	2	4.2e+02	1	KGDPGPTFSK
☑	399	883.9878	1765.9610	1765.9098	0.0512	1	2	4.1e+02	1	FTNLLTSILDSAETKN
☑	221	469.3000	936.5854	936.4521	0.1333	1	2	4.2e+02	1	TTMPGMKR + Oxidation (M)
☑	208	450.3014	898.5882	898.4041	0.1841	0	2	3.3e+02	1	MGFQCLK + Carbamidomethyl (C); Oxidation (M)
☑	272	531.3000	1060.5854	1060.5526	0.0328	0	2	4.3e+02	1	HAAGATHALGR
☑	83	406.2722	810.5299	810.4058	0.1241	0	2	2e+02	1	MGIVYGR + Oxidation (M)
☑	123	419.3400	836.6654	836.4868	0.1785	0	2	45	1	APQPVVAR
☑	317	425.2647	1272.7722	1272.5777	0.1945	0	2	4.2e+02	1	CVPNMVCLHK + 2 Carbamidomethyl (C); Oxidation (M)
☑	275	538.3672	1074.7199	1074.5934	0.1265	1	2	3.6e+02	1	FGNQKAAAIR
☑	150	427.2813	852.5481	852.3544	0.1937	0	2	3.1e+02	1	LPDMCMK + Oxidation (M)
☑	429	737.7882	2210.3428	2210.2171	0.1257	1	2	77	1	LAALRQGPEGLVGADKPISYR
☑	90	409.2394	816.4642	816.3734	0.0908	0	2	4.5e+02	1	LMASCHR
☑	98	411.2753	820.5360	820.3497	0.1863	0	1	3.4e+02	1	AAGQGDMR + Oxidation (M)
☑	220	466.7414	931.4682	931.5240	-0.0557	0	1	5.2e+02	1	GFQTVKPR
☑	211	453.2525	904.4905	904.4324	0.0581	0	1	5.4e+02	1	IIMEDER
☑	236	485.3542	968.6938	968.5403	0.1535	1	1	2e+02	1	EILRADPR
☑	279	568.3504	1134.6863	1134.5604	0.1259	1	1	5.7e+02	1	GFRCTSSLHK
☑	343	445.2000	1332.5782	1332.7476	-0.1694	0	1	4.6e+02	1	LAVGCVVELVFK + Carbamidomethyl (C)
☑	215	458.6528	915.2911	915.4232	-0.1321	0	1	3.4e+02	1	CKPGDPSR + Carbamidomethyl (C)
☑	198	445.2000	888.3854	888.4553	-0.0698	0	1	6.4e+02	1	DGGVIDSVK
☑	178	437.2693	872.5240	872.5266	-0.0026	1	1	6.4e+02	1	KLGCLLAR
☑	389	410.2823	1637.1002	1637.0127	0.0874	1	1	37	1	LLVILATEQPLTAKK
☑	165	432.6000	863.1854	863.3708	-0.1854	0	1	75	1	GYHGMQR + Oxidation (M)
☑	104	413.2732	824.5319	824.4141	0.1179	0	1	2.9e+02	1	DIVDHAR
☑	120	418.2652	834.5159	834.4824	0.0335	1	1	4.3e+02	1	APRAAPPR
☑	151	427.2980	852.5815	852.4051	0.1763	0	1	3.2e+02	1	MDPYALK + Oxidation (M)
☑	400	445.2000	1776.7709	1776.8319	-0.0610	1	1	4.3e+02	1	SGWGELSASTEWKDPK
☑	282	572.7000	1143.3854	1143.5573	-0.1719	0	1	3.1e+02	1	NNAAWNWIR
☑	248	503.3172	1004.6198	1004.4644	0.1554	1	1	5.7e+02	1	CPLRSGCR + 2 Carbamidomethyl (C)
☑	85	407.2592	812.5038	812.3857	0.1181	0	1	3.1e+02	1	LSGFFWG
☑	183	439.2476	876.4806	876.3912	0.0893	0	1	6.2e+02	1	MPQGSWR + Oxidation (M)
☑	322	639.8628	1277.7110	1277.5848	0.1263	1	1	5.5e+02	1	AGKGGAASGSDSADK
☑	107	414.2531	826.4917	826.4198	0.0719	1	1	3.8e+02	1	KGHGWSR
☑	431	742.4524	2224.3353	2224.1748	0.1605	0	1	1e+02	1	LVFALVTAVCCLADGALIYR + 2 Carbamidomethyl (C)
☑	321	426.3131	1275.9174	1275.7438	0.1736	1	1	58	1	LLAEAKEYVIK
☑	397	572.6906	1715.0500	1714.8508	0.1992	1	1	2.3e+02	1	GQIRHFCNQQCLLR
☑	92	409.2648	816.5151	816.4640	0.0511	1	1	5.6e+02	1	LRCALNK
☑	280	569.4336	1136.8527	1136.6553	0.1973	1	0	43	1	LVKTHDLSPK
☑	246	500.4123	998.8100	998.6236	0.1864	1	0	48	1	KTAAQVLIR
☑	159	429.1352	856.2558	856.4039	-0.1481	0	0	2.2e+02	1	LNSDSGHK
☑	101	413.2580	824.5015	824.3334	0.1681	0	0	3.6e+02	1	ETSMDSR
☑	243	494.3360	986.6575	986.4781	0.1794	1	0	5.7e+02	1	RTVAAPSGDN
☑	197	445.2000	888.3854	888.4341	-0.0487	0	0	7.9e+02	1	GILGYTEH
☑	268	525.2988	1048.5830	1048.5414	0.0416	1	0	6.6e+02	1	GGFEGSLRAR
☑	260	516.3405	1030.6665	1030.5382	0.1283	1	0	5.9e+02	1	CVHGVGFKK + Carbamidomethyl (C)
☑	148	427.2427	852.4708	852.3726	0.0983	0	0	4.6e+02	1	EEDAPHR
☑	388	545.6000	1633.7782	1633.7678	0.0104	1	0	5.2e+02	1	VHAGARPHACRDCGK + Carbamidomethyl (C)
☑	354	704.4000	1406.7854	1406.7306	0.0548	1	0	5.1e+02	1	AEFPEHATHLKK
☑	436	736.6403	2942.5319	2942.4960	0.0359	0	0	2.6e+02	1	GLYQLQTDHGVIEAETLVLACGLWTR + Carbamidomethyl (C)
☑	201	448.2757	894.5368	894.6266	-0.0897	1	0	6.2e+02	1	IIPLKALK
☑	76	405.2443	808.4740	808.4919	-0.0179	0	0	3.8e+02	1	HVITALR
☑	1	*400.2000*	*399.1927*							
☑	2	*402.2045*	*401.1972*							
☑	3	*403.2068*	*402.1995*							
☑	4	*403.2073*	*402.2000*							
☑	5	*403.2090*	*402.2017*							
☑	6	*403.4000*	*402.3927*							
☑	7	*404.2432*	*403.2360*							
☑	8	*405.4000*	*404.3927*							
☑	9	*405.4000*	*404.3927*							
☑	10	*405.4000*	*404.3927*							
☑	11	*405.4000*	*404.3927*							
☑	12	*405.4000*	*404.3927*							
☑	13	*407.2999*	*406.2926*							
☑	14	*410.4000*	*409.3927*							
☑	15	*413.4000*	*412.3927*							
☑	16	*414.3052*	*413.2979*							
☑	17	*415.4000*	*414.3927*							
☑	18	*416.4000*	*415.3927*							
☑	19	*416.4000*	*415.3927*							
☑	20	*416.4000*	*415.3927*							
☑	21	*416.4000*	*415.3927*							
☑	22	*416.4000*	*415.3927*							
☑	23	*417.1000*	*416.0927*							
☑	24	*417.2508*	*416.2435*							
☑	25	*417.2543*	*416.2471*							
☑	26	*419.2055*	*418.1982*							
☑	27	*420.3510*	*419.3437*							
☑	28	*425.2000*	*424.1927*							
	29	*425.2096*	*424.2024*							

☑			
☑	30	425.5000	424.4927
☑	31	427.2855	426.2782
☑	32	430.4000	429.3927
☑	33	430.4000	429.3927
☑	34	430.4000	429.3927
☑	35	430.5000	429.4927
☑	36	432.3107	431.3034
☑	37	441.1919	440.1846
☑	38	441.3992	440.3919
☑	39	442.3387	441.3314
☑	40	445.1590	444.1517
☑	41	445.2000	444.1927
☑	42	445.2760	444.2688
☑	43	445.3653	444.3580
☑	44	449.3975	448.3903
☑	45	451.4000	450.3927
☑	46	459.3079	458.3007
☑	47	462.3013	461.2940
☑	48	469.3000	468.2927
☑	49	483.3000	482.2927
☑	50	484.6991	483.6918
☑	51	485.4000	484.3927
☑	52	488.3105	487.3033
☑	53	511.3000	510.2927
☑	54	514.2564	513.2492
☑	55	529.4523	528.4450
☑	56	545.6000	544.5927
☑	57	572.7000	571.6927
☑	58	599.4688	598.4615
☑	59	628.3776	627.3703
☑	60	639.6809	638.6736
☑	61	657.6956	656.6883
☑	62	704.4000	703.3927
☑	64	400.3861	798.7577
☑	65	400.3914	798.7683
☑	66	400.3958	798.7770
☑	69	401.3569	800.6992
☑	73	403.3395	804.6645
☑	74	403.4000	804.7854
☑	75	404.0739	806.1332
☑	78	405.4000	808.7854
☑	79	405.4000	808.7854
☑	80	405.4000	808.7854
☑	81	405.4000	808.7854
☑	82	405.4000	808.7854
☑	86	407.3432	812.6718
☑	87	407.3579	812.7013
☑	88	409.2154	816.4162
☑	89	409.2286	816.4426
☑	94	409.4000	816.7854
☑	95	410.4000	818.7854
☑	102	413.2594	824.5042
☑	103	413.2700	824.5255
☑	105	413.2894	824.5643
☑	106	413.4000	824.7854
☑	111	415.4000	828.7854
☑	113	416.4000	830.7854
☑	114	416.4000	830.7854
☑	115	416.4000	830.7854
☑	116	416.4000	830.7854
☑	117	416.4000	830.7854
☑	118	417.1000	832.1854
☑	119	834.5741	833.5668
☑	122	418.6126	835.2107
☑	125	419.3487	836.6829
☑	127	419.3567	836.6989
☑	128	419.3580	836.7014
☑	129	419.3600	836.7055
☑	130	419.3602	836.7058
☑	131	419.3609	836.7072
☑	135	422.4000	842.7854
☑	138	425.2000	848.3854
☑	139	425.2574	848.5002
☑	140	425.2603	848.5061
☑	142	425.3380	848.6615
☑	143	425.3605	848.7064
☑	144	425.5000	848.9854
☑	146	426.2953	850.5760
☑	162	430.4000	858.7854
☑	163	430.4000	858.7854
☑	164	430.5000	858.9854
☑	166	433.3566	864.6987
☑	167	433.3771	864.7397
☑	168	433.3779	864.7412
	169	435.3792	868.7438

☑			
☑	170	435.4040	868.7935
☑	179	437.2713	872.5280
☑	181	438.2282	874.4418
☑	184	439.2479	876.4813
☑	187	440.4207	878.8269
☑	188	441.3044	880.5943
☑	189	441.3549	880.6952
☑	190	441.3560	880.6974
☑	191	441.3570	880.6994
☑	193	442.3574	882.7003
☑	203	449.2487	896.4829
☑	204	449.4064	896.7983
☑	205	449.4110	896.8074
☑	206	449.4166	896.8186
☑	207	450.2698	898.5250
☑	210	451.4000	900.7854
☑	212	453.2908	904.5671
☑	213	453.3843	904.7540
☑	214	455.2648	908.5151
☑	219	465.2634	928.5123
☑	222	472.3297	942.6448
☑	224	474.3292	946.6438
☑	226	476.2861	950.5577
☑	232	483.3000	964.5854
☑	234	483.3914	964.7682
☑	235	483.7259	965.4372
☑	237	485.4000	968.7854
☑	247	502.8584	1003.7023
☑	250	511.3000	1020.5854
☑	262	520.5000	1038.9854
☑	264	522.3585	1042.7024
☑	269	525.5124	1049.0103
☑	270	528.3000	1054.5854
☑	271	529.4469	1056.8793
☑	274	537.5450	1073.0755
☑	276	545.6000	1089.1854
☑	281	571.6271	1141.2397
☑	283	578.3803	1154.7461
☑	285	400.0800	1197.2183
☑	287	400.3953	1198.1640
☑	288	403.4000	1207.1782
☑	290	405.4000	1213.1782
☑	291	405.4000	1213.1782
☑	292	405.4000	1213.1782
☑	293	405.4000	1213.1782
☑	294	405.4000	1213.1782
☑	297	410.4000	1228.1782
☑	298	616.7769	1231.5392
☑	300	413.4000	1237.1782
☑	302	415.4000	1243.1782
☑	303	415.6855	1244.0346
☑	304	416.4000	1246.1782
☑	305	416.4000	1246.1782
☑	306	416.4000	1246.1782
☑	307	416.4000	1246.1782
☑	308	416.4000	1246.1782
☑	309	417.1000	1248.2782
☑	310	418.7726	1253.2960
☑	311	419.3417	1255.0033
☑	312	419.3484	1255.0233
☑	313	419.3540	1255.0400
☑	314	419.3798	1255.1177
☑	315	423.2727	1266.7963
☑	316	425.2000	1272.5782
☑	318	425.3585	1273.0536
☑	320	425.8113	1274.4122
☑	323	639.8633	1277.7120
☑	324	639.8636	1277.7126
☑	325	640.8000	1279.5854
☑	332	430.4000	1288.1782
☑	333	430.4000	1288.1782
☑	337	435.3946	1303.1619
☑	338	435.4037	1303.1893
☑	339	656.3886	1310.7627
☑	341	441.2041	1320.5904
☑	346	451.4000	1351.1782
☑	350	465.0981	1392.2726
☑	353	469.3000	1404.8782
☑	357	481.3123	1440.9152
☑	358	483.3000	1446.8782
☑	359	485.4000	1453.1782
☑	361	499.3383	1494.9929
☑	362	500.1240	1497.3502
☑	363	509.3399	1524.9979
	364	511.3000	1530.8782

☑			
☑	366	*514.2564*	*1539.7475*
☑	368	*528.4461*	*1582.3165*
☑	369	*528.4543*	*1582.3412*
☑	370	*528.4616*	*1582.3630*
☑	372	*530.3721*	*1588.0944*
☑	373	*530.3864*	*1588.1372*
☑	374	*530.6654*	*1588.9745*
☑	375	*530.6681*	*1588.9825*
☑	376	*532.6000*	*1594.7782*
☑	377	*400.0806*	*1596.2931*
☑	378	*400.0832*	*1596.3035*
☑	379	*400.0863*	*1596.3161*
☑	380	*400.6290*	*1598.4868*
☑	383	*401.3642*	*1601.4279*
☑	386	*404.3555*	*1613.3928*
☑	391	*552.0590*	*1653.1551*
☑	392	*420.0415*	*1676.1369*
☑	393	*420.2000*	*1676.7709*
☑	396	*571.6422*	*1711.9047*
☑	398	*572.7000*	*1715.0782*
☑	402	*447.1561*	*1784.5955*
☑	410	*463.1593*	*1848.6080*
☑	411	*463.1714*	*1848.6565*
☑	412	*628.2386*	*1881.6940*
☑	413	*628.2401*	*1881.6984*
☑	414	*628.2498*	*1881.7274*
☑	416	*639.5237*	*1915.5492*
☑	417	*481.3158*	*1921.2341*
☑	419	*499.3295*	*1993.2890*
☑	421	*500.1220*	*1996.4590*
☑	422	*509.3402*	*2033.3315*
☑	423	*519.3218*	*2073.2583*
☑	424	*526.3669*	*2101.4387*
☑	425	*704.4000*	*2110.1782*
☑	426	*530.3785*	*2117.4849*
☑	427	*530.3835*	*2117.5051*
☑	428	*530.3911*	*2117.5353*
☑	430	*554.2344*	*2212.9086*
☑	432	*761.8097*	*2282.4072*
☑	433	*767.1595*	*2298.4567*
☑	434	*581.3663*	*2321.4359*
☑	435	*581.3733*	*2321.4640*

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      : 436
```

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