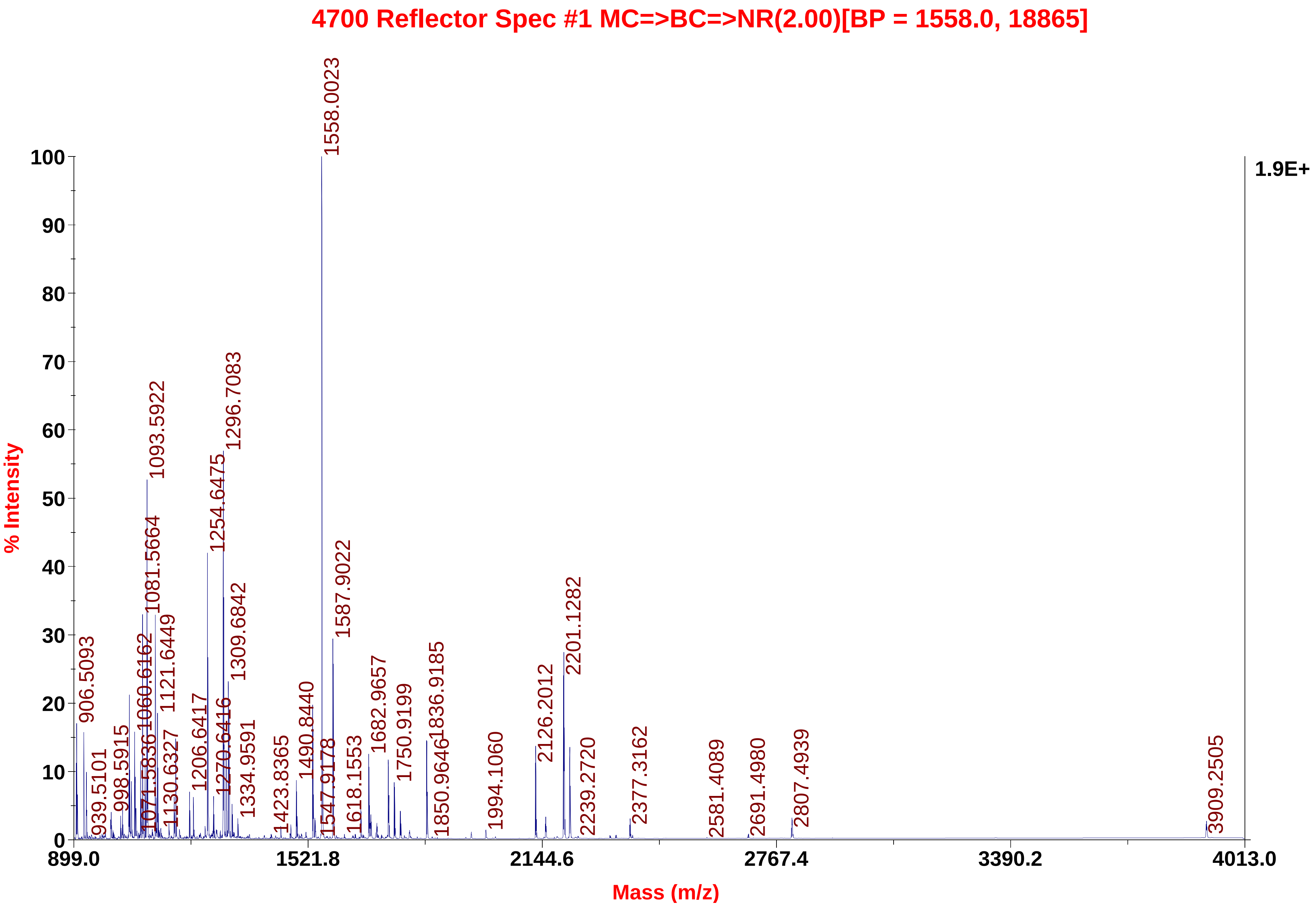
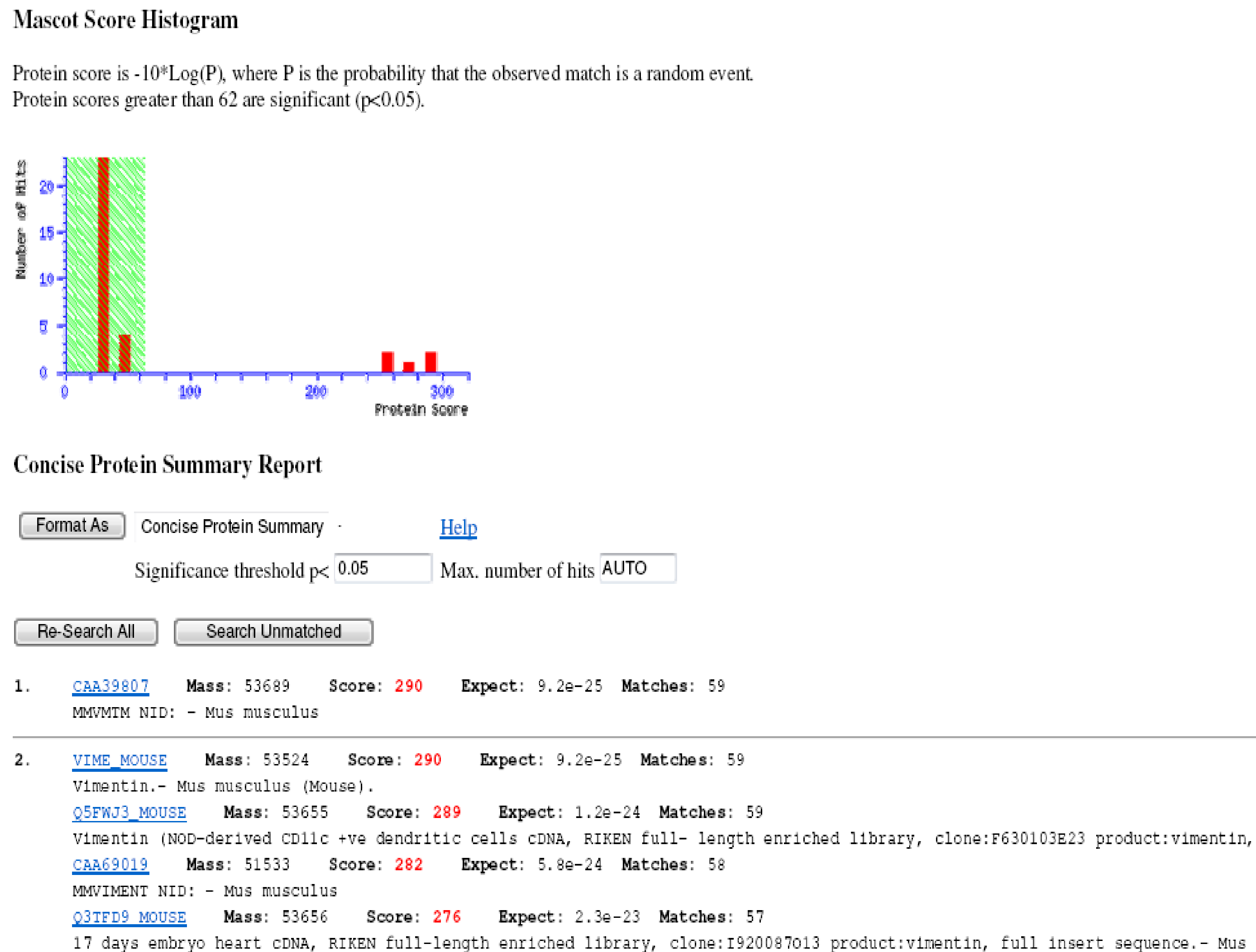
Sample M1


4700 Reflector Spec #1 MC=>BC=>NR(2.00)[BP = 1558.0, 18865]
% Intensity
100
90
80
70
60
50
40
30
20
10
0
1.9E+
906.5093
939.5101
998.5915
1060.6162
1071.5836
1081.5664
1093.5922
1121.6449
1130.6327
1206.6417
1254.6475
1270.6416
1296.7083
1309.6842
1334.9591
1423.8365
1490.8440
1547.9178
1558.0023
1587.9022
1618.1553
1682.9657
1750.9199
1836.9185
1850.9646
1994.1060
2126.2012
2201.1282
2239.2720
2377.3162
2581.4089
2691.4980
2807.4939
3909.2505
899.0
1521.8
2144.6
2767.4
3390.2
4013.0
Mass (m/z)



Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 62 are significant (p<0.05).

Concise Protein Summary Report

Format As: Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

1. **CAA39807** **Mass**: 53689 **Score**: 290 **Expect**: 9.2e-25 **Matches**: 59
MMVMTM NID: - Mus musculus

---

2. **VIME_MOUSE** **Mass**: 53524 **Score**: 290 **Expect**: 9.2e-25 **Matches**: 59
Vimentin.- Mus musculus (Mouse).
Q5FWJ3_MOUSE **Mass**: 53655 **Score**: 289 **Expect**: 1.2e-24 **Matches**: 59
Vimentin (NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full- length enriched library, clone:F630103E23 product:vimentin,
CAA69019 **Mass**: 51533 **Score**: 282 **Expect**: 5.8e-24 **Matches**: 58
MMVIMENT NID: - Mus musculus
Q3TFD9_MOUSE **Mass**: 53656 **Score**: 276 **Expect**: 2.3e-23 **Matches**: 57
17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920087013 product:vimentin, full insert sequence.- Mus

Protein View

Match to: **CAA39807** Score: **290** Expect: **9.2e-25**
MMVMTM NID: - Mus musculus
Found in search of pmf_A2_129990848800.txt

Nominal mass (M_r): **53689**; Calculated pI value: **5.06**
NCBI BLAST search of CAA39807 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **132**
Number of mass values matched: **59**
Sequence Coverage: **77%**

Matched peptides shown in **Bold Red**

1 M**STRSVSSSS YRR**MFGGSGT SSRPSSNRSY VTTSTRTYSL GSALRPSTSR
51 SLYSSSPGGA YVTRSSAVRL RSSVPGVR**LL QDSVDFSLAD AINTEFK**NTR
101 **TNEKVELQEL NDRFANYIDK VRFLEQQNKI LLAELEQLKG QGK**SR**LGDLY**
151 **EEEMRELR**RQ **VDQFTNDKAR VEVERDNLAE DIMR**LR**EKLQ EEMLQREEAE**
201 **STLQSFRQDV DNASLARLDL ER**K**VESLQEE IAFLKKLHDE EIQELQAQIQ**
251 **EQHVQIDVDV SKPDLTAALR** DVR**QQYESVA AK**NLQEAEEW YK**SKFADLSE**
301 **AANRNNDALR** QAK**QESNEYR RQVQSLTCEV DALKGTNESL ER**QMR**EMEEN**
351 **FALEAANYQD TIGRLQDEIQ NMKEEMAR**HL R**EYQDLLNVK MALDIEIATY**
401 **RKLLEGEESR ISLPLPTFSS LNLRETNLES LPLVDTHSKR** TLLIKTVETR
451 **DGQVINETSQ HHDDLE**

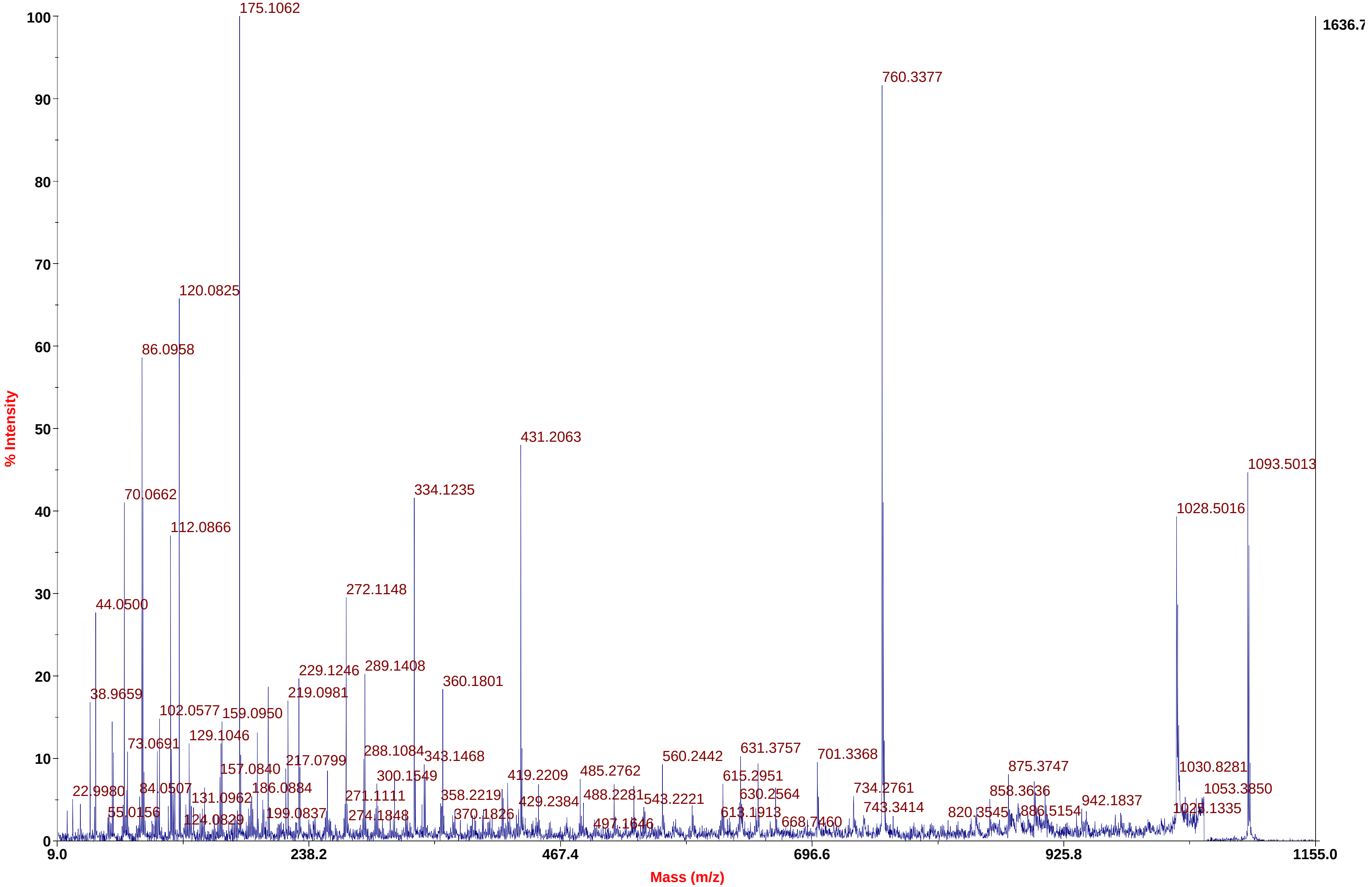
Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
     2 - 12     1216.7050  1215.6977  1215.5844       93      1   M.STRSVSSSSYR.R
     5 - 13     1028.5620  1027.5547  1027.5047       49      1   R.SVSSSSYRR.M
    79 - 97     2126.1985  2125.1912  2125.0579       63      0   R.LLQDSVDFSLADAINTEFK.N
   101 - 113    1587.9003  1586.8930  1586.7900       65      1   R.TNEKVELQELNDR.F
   105 - 113    1115.6379  1114.6306  1114.5618       62      0   K.VELQELNDR.F
   114 - 122    1125.6663  1124.6590  1124.5978       54      1   R.FANYIDKVR.F
   123 - 129     906.5092   905.5019   905.4607       46      0   R.FLEQQNK.I
   123 - 129     908.4391   907.4318   907.4287        3      0   R.FLEQQNK.I  2 Deamidated (NQ)
   130 - 139    1169.7773  1168.7700  1168.7067       54      0   K.ILLAELEQLK.G
   130 - 143    1540.0043  1538.9970  1538.9032       61      1   K.ILLAELEQLKGQGK.S
   146 - 155    1254.6475  1253.6402  1253.5598       64      0   R.LGDLYEEEMR.E
   146 - 155    1270.6410  1269.6337  1269.5547       62      0   R.LGDLYEEEMR.E  Oxidation (M)
   146 - 158    1668.8984  1667.8911  1667.7824       65      1   R.LGDLYEEEMRELR.R  Oxidation (M)
   160 - 170    1323.7225  1322.7152  1322.6102       79      1   R.QVDQFTNDKAR.V  2 Deamidated (NQ)
   171 - 184    1688.9368  1687.9295  1687.8199       65      1   R.VEVERDNLAEDIMR.L
   171 - 184    1704.9309  1703.9236  1703.8148       64      1   R.VEVERDNLAEDIMR.L  Oxidation (M)
```

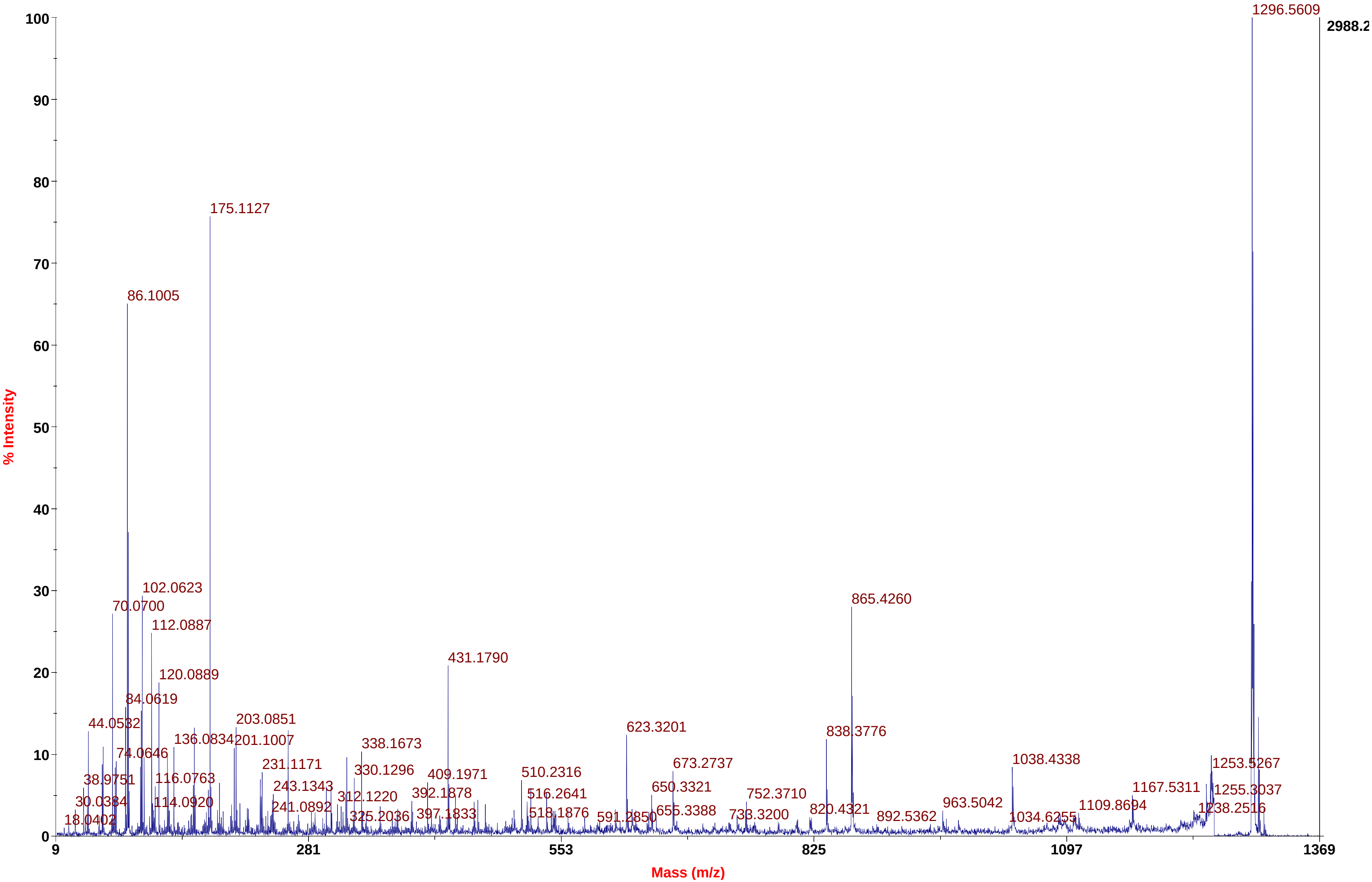
M1

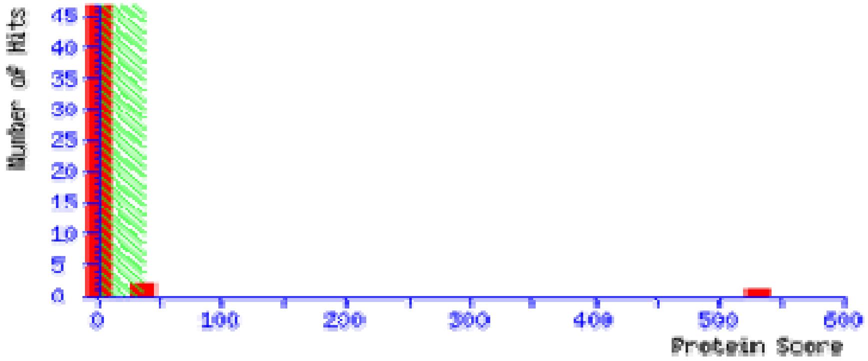
4700 MS/MS Precursor 1093.59 Spec #1 MC[BP = 175.1, 1637]

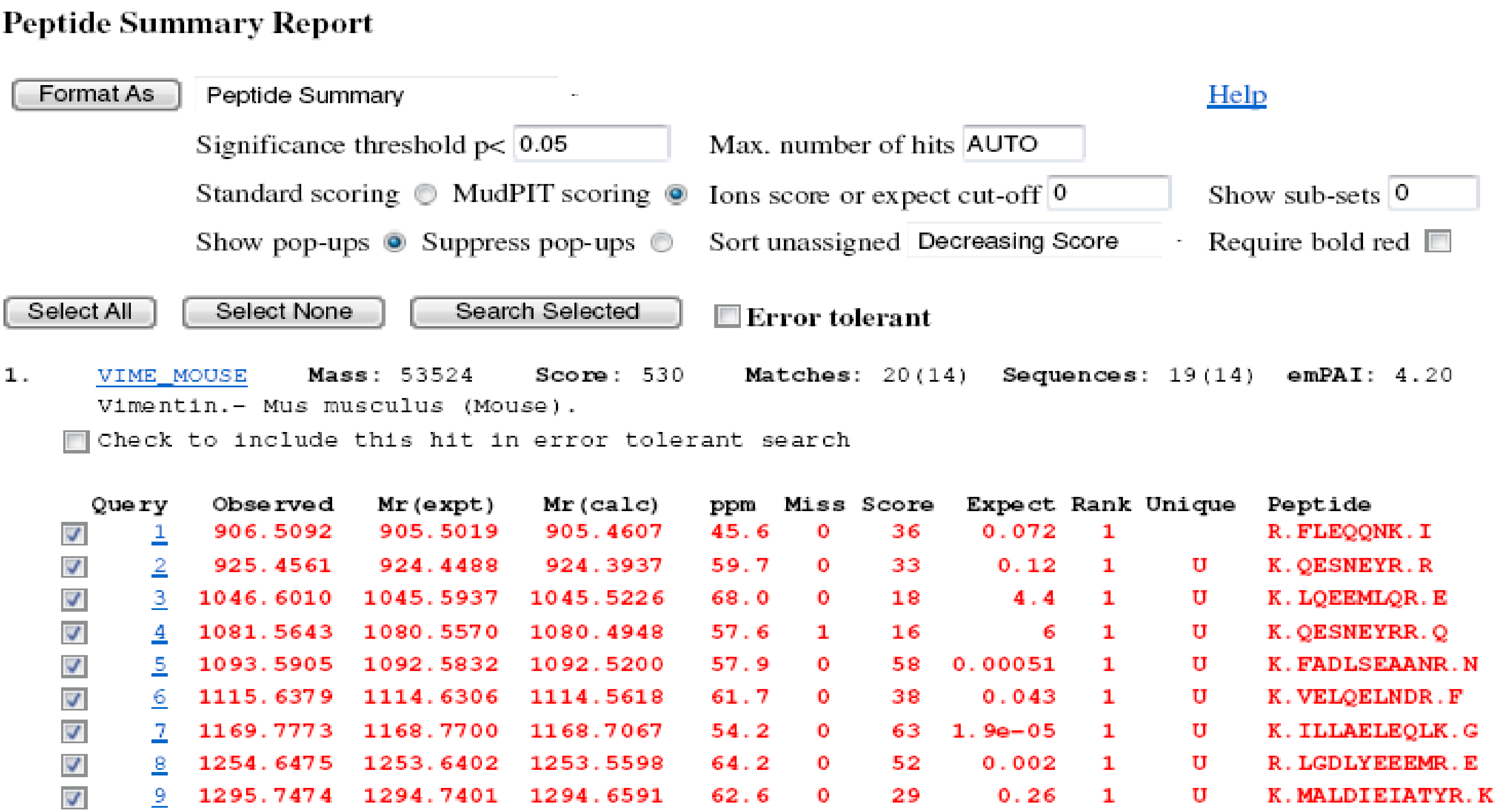


M1

4700 MS/MS Precursor 1295.75 Spec #1 MC[BP = 1296.6, 2988]







Peptide Summary Report

Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

☐ **Error tolerant**

```
1.    VIME_MOUSE     Mass: 53524     Score: 530     Matches: 20(14)   Sequences: 19(14)   emPAI: 4.20
      Vimentin.- Mus musculus (Mouse).
    ☐ Check to include this hit in error tolerant search

      Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss  Score   Expect  Rank  Unique   Peptide
  ☑     1     906.5092   905.5019   905.4607   45.6    0     36    0.072    1            R.FLEQQNK.I
  ☑     2     925.4561   924.4488   924.3937   59.7    0     33     0.12    1       U    K.QESNEYR.R
  ☑     3    1046.6010  1045.5937  1045.5226   68.0    0     18      4.4    1       U    K.LQEEMLQR.E
  ☑     4    1081.5643  1080.5570  1080.4948   57.6    1     16        6    1       U    K.QESNEYRR.Q
  ☑     5    1093.5905  1092.5832  1092.5200   57.9    0     58  0.00051    1       U    K.FADLSEAANR.N
  ☑     6    1115.6379  1114.6306  1114.5618   61.7    0     38    0.043    1       U    K.VELQELNDR.F
  ☑     7    1169.7773  1168.7700  1168.7067   54.2    0     63  1.9e-05    1       U    K.ILLAELEQLK.G
  ☑     8    1254.6475  1253.6402  1253.5598   64.2    0     52    0.002    1       U    R.LGDLYEEEMR.E
  ☑     9    1295.7474  1294.7401  1294.6591   62.6    0     29     0.26    1       U    K.MALDIEIATYR.K
```

Protein View

```
Match to: VIME_MOUSE Score: 530
Vimentin.- Mus musculus (Mouse).
Found in search of ppw_A2_129990854000.txt

Nominal mass (Mr): 53524; Calculated pI value: 5.06
NCBI BLAST search of VIME_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 45%

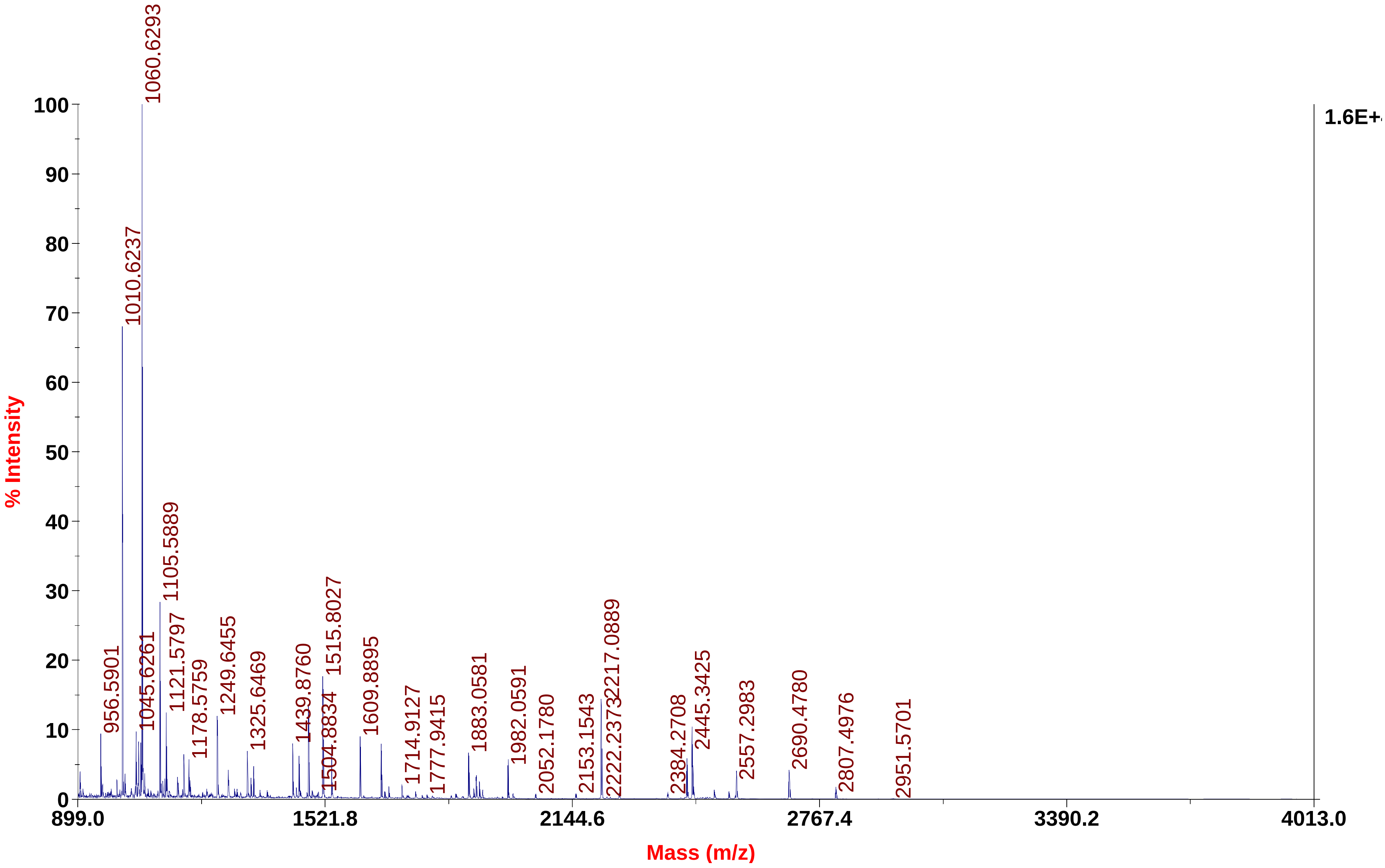
Matched peptides shown in Bold Red

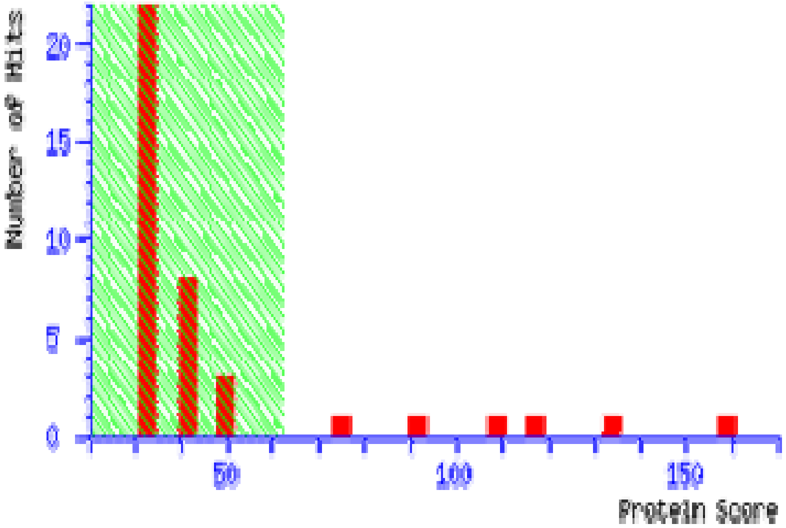
    1 STRSVSSSSY RRMFGGSGTS SRPSSNRSYV TTSTRTYSLG SALRPSTSRS
   51 LYSSSPGGAY VTRSSAVRLR SSVPGVRLLQ DSVDFSLADA INTEFKNTRT
  101 NEKVELQELN DRFANYIDKV RFLEQQNKIL LAELEQLKGQ GKSRLGDLYE
  151 EEMRELRRQV DQLTNDKARV EVERDNLAED IMRLREKLQE EMLQREEAES
  201 TLQSFRQDVD NASLARLDLE RKVESLQEEI AFLKKLHDEE IQELQAQIQE
  251 QHVQIDVDVS KPDLTAALRD VRQQYESVAA KNLQEAEEWY KSKFADLSEA
  301 ANRNNDALRQ AKQESNEYRR QVQSLTCEVD ALKGTNESLE RQMREMEENF
  351 ALEAANYQDT IGRLQDEIQN MKEEMARHLR EYQDLLNVKM ALDIEIATYR
  401 KLLEGEESRI SLPLPTFSSL NLRETNLESL PLVDTHSKRT LLIKTVETRD
  451 GQVINETSQH HDDLE
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
   78 - 96      2126.1985  2125.1912  2125.0579      63     0  R.LLQDSVDFSLADAINTEFK.N  (Ions score 109)
  100 - 112     1587.9003  1586.8930  1586.7900      65     1  R.TNEKVELQELNDR.F  (Ions score 58)
  104 - 112     1115.6379  1114.6306  1114.5618      62     0  K.VELQELNDR.F  (Ions score 38)
  122 - 128      906.5092   905.5019   905.4607      46     0  R.FLEQQNK.I  (Ions score 36)
  129 - 138     1169.7773  1168.7700  1168.7067      54     0  K.ILLAELEQLK.G  (Ions score 63)
  145 - 154     1254.6475  1253.6402  1253.5598      64     0  R.LGDLYEEEMR.E  (Ions score 52)
  188 - 195     1046.6010  1045.5937  1045.5226      68     0  K.LQEEMLQR.E  (Ions score 18)
  222 - 234     1533.9469  1532.9396  1532.8450      62     1  R.KVESLQEEIAFLK.K  (Ions score 78)
  282 - 291     1309.6841  1308.6768  1308.5986      60     0  K.NLQEAEEWYK.S  (Ions score 46)
```

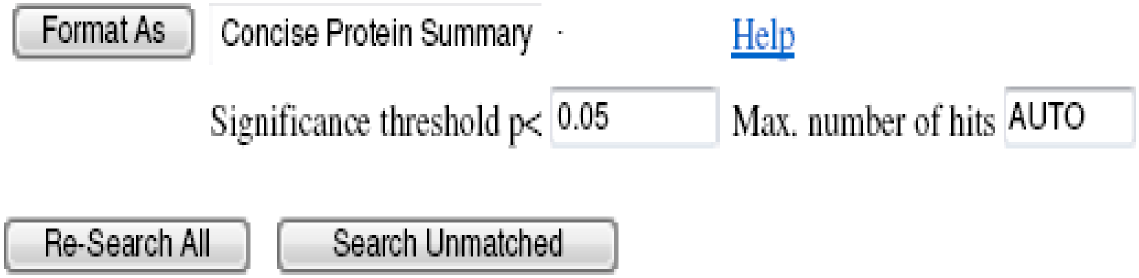
Sample M2

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1060.6, 16121]





Concise Protein Summary Report



Format As: Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

1. **Mixture 1** **Total score:** 159 **Expect:** 1.2e-11 **Matches:** 60

Components (only one family member shown for each component):

Q8C7C7_MOUSE **Mass:** 64961 **Score:** 132 **Expect:** 5.8e-09 **Matches:** 36

2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920028B14 product:albumin 1,

Q6S9I1_MOUSE **Mass:** 53172 **Score:** 86 **Expect:** 0.00021 **Matches:** 31

HMW kininogen-I variant (High molecular weight kininogen I isoform DeltaD5).- Mus musculus (Mouse).

Protein View

```
Match to: Q8C7C7_MOUSE Score: 132 Expect: 5.8e-09
2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone
Found in search of pmf_B2_129990848801.txt

Nominal mass (Mr): 64961; Calculated pI value: 5.49
NCBI BLAST search of Q8C7C7_MOUSE against nr
Unformatted sequence string for pasting into other applications

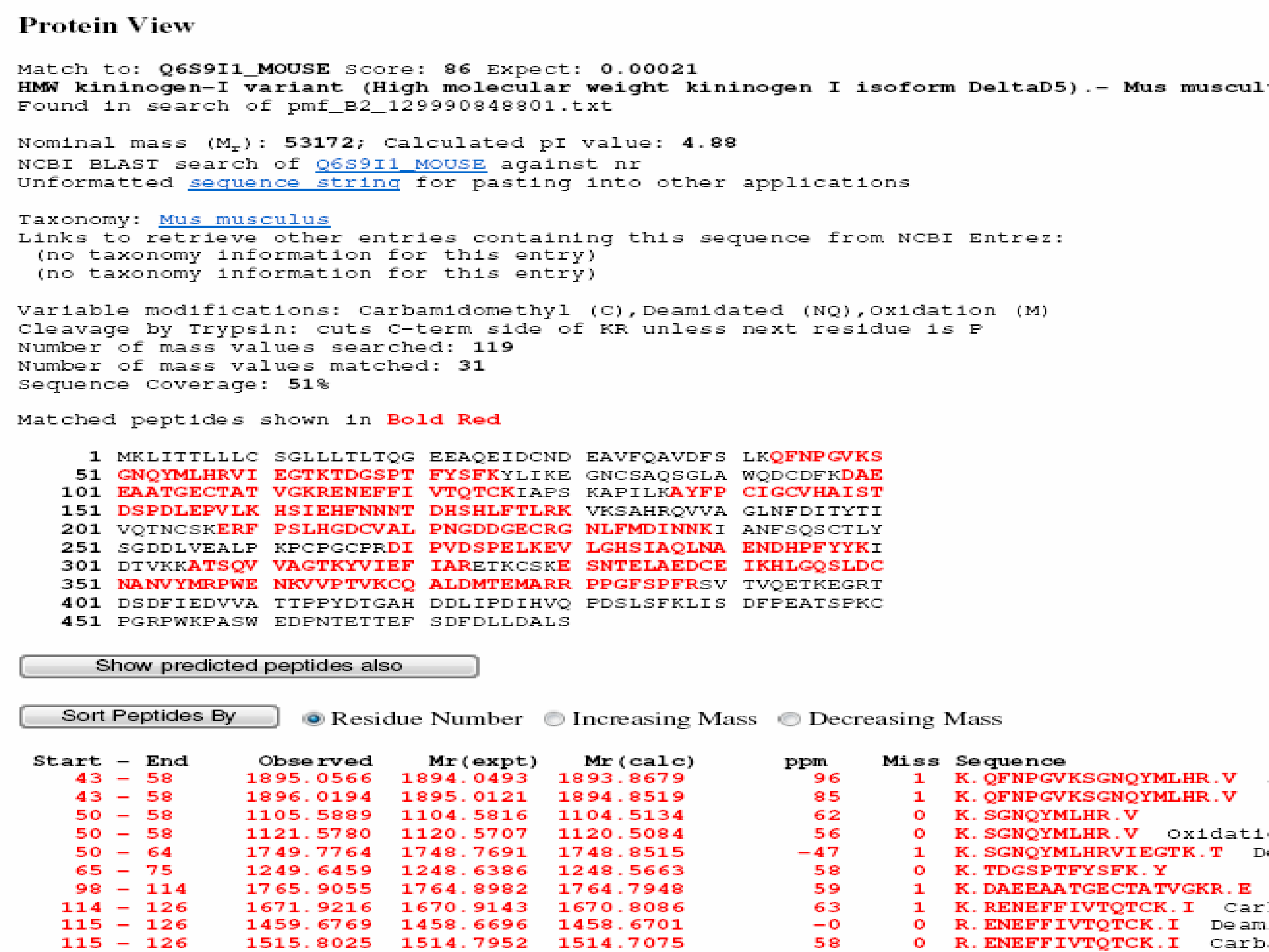
Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 119
Number of mass values matched: 36
Sequence Coverage: 59%

Matched peptides shown in Bold Red

    1 NRYNDLGEQH FKGLVLIAFS QYLQKCSYDE HAKLVQEVTD FAKTCVADES
   51 AANCDKSLHT LFGDKLCAIP NLRENYGELA DCCTKQEPER NECFLQHKDD
  101 NPSLPPFERP EAEAMCTSFK ENPTTFMGHY LHEVARRHPY FYAPELLYYA
  151 EQYNEILTQC CAEADKESCL TPKLDGVKEK ALVSSVRQRM KCSSMQKFGE
  201 RAFKAWAVAR LSQTFPNADF AEITKLATDL TKVNKECCHG DLLECADDRA
  251 ELAKYMCENQ ATISSKLQTC CDKPLLKKAH CLSEVEHDTM PADLPAIAAD
  301 FVEDQEVCKN YAEAKDVFLG TFLYEYSRRH PDYSVSLLLR LAKKYEATLE
  351 KCCAEANPPA CYGTVLAEFQ PLVEEPKNLV KTNCDLYEKL GEYGFQNAIL
  401 VRYTQKAPQV STPTLVEAAR NLGRVGTKCC TLPEDQRLPC VEDYLSAILN
  451 RVCLLHEKTP VSEHVTKCCS GSLVERRPCF SALTVDETYV PKEFKAETFT
  501 FHSDICTLPE KEKQIKKQTA LAELVKHKPK ATAEQLKTVM DDFAQFLDTC
  551 CKAADKDTCF STEGPNLVTR CKDALA
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)       ppm    Miss  Sequence
    13 - 25     1479.8933  1478.8860  1478.8497        25      0   K.GLVLIAFSQYLQK.
    13 - 33     2472.3254  2471.3181  2471.2042        46      1   K.GLVLIAFSQYLQKC
    34 - 43     1149.6647  1148.6574  1148.6077        43      0   K.LVQEVTDFAK.T
    57 - 65     1017.5847  1016.5774  1016.5291        48      0   K.SLHTLFGDK.L
    66 - 73      956.5888   955.5815   955.5273        57      0   K.LCAIPNLR.E   Ca
    74 - 85     1459.6769  1458.6696  1458.5755        65      0   R.ENYGELADCCTK.Q
```



Protein View

```
Match to: Q6S9I1_MOUSE Score: 86 Expect: 0.00021
HMW kininogen-I variant (High molecular weight kininogen I isoform DeltaD5).- Mus muscul
Found in search of pmf_B2_129990848801.txt

Nominal mass (Mr): 53172; Calculated pI value: 4.88
NCBI BLAST search of Q6S9I1_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 119
Number of mass values matched: 31
Sequence Coverage: 51%

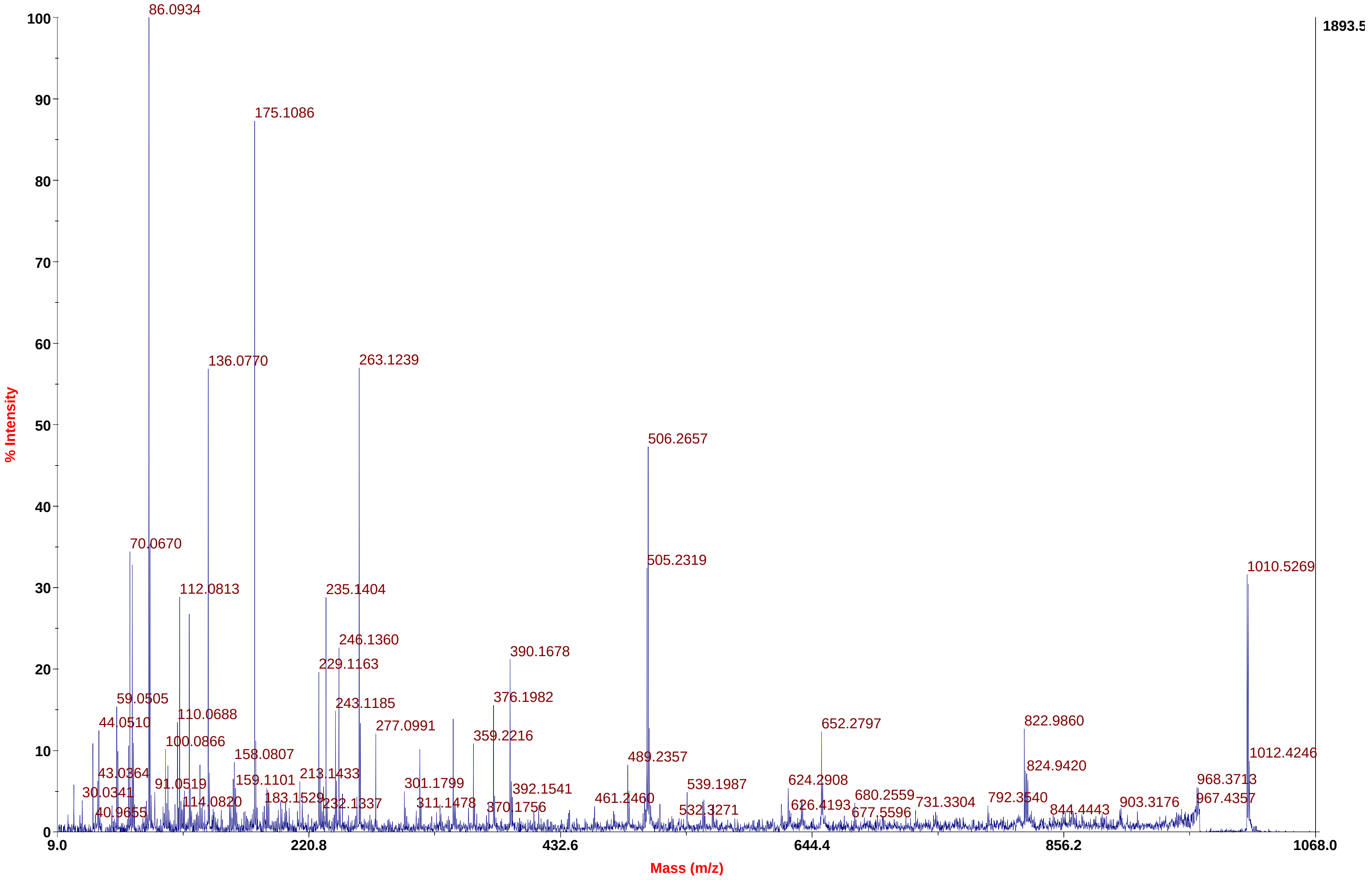
Matched peptides shown in Bold Red

    1 MKLITTLLLC SGLLLTLTQG EEAQEIDCND EAVFQAVDFS LKQFNPGVKS
   51 GNQYMLHRVI EGTKTDGSPT FYSFKYLIKE GNCSAQSGLA WQDCDFKDAE
  101 EAATGECTAT VGKRENEFFI VTQTCKIAPS KAPILKAYFP CIGCVHAIST
  151 DSPDLEPVLK HSIEHFNNNT DHSHLFTLRK VKSAHRQVVA GLNFDITYTI
  201 VQTNCSKERF PSLHGDCVAL PNGDDGECRG NLFMDINNKI ANFSQSCTLY
  251 SGDDLVEALP KPCPGCPRDI PVDSPELKEV LGHSIAQLNA ENDHPFYYKI
  301 DTVKKATSQV VAGTKYVIEF IARETKCSKE SNTELAEDCE IKHLGQSLDC
  351 NANVYMRPWE NKVVPTVKCQ ALDMTEMARR PPGFSPFRSV TVQETKEGRT
  401 DSDFIEDVVA TTPPYDTGAH DDLIPDIHVQ PDSLSFKLIS DFPEATSPKC
  451 PGRPWKPASW EDPNTETTEF SDFDLLDALS
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss  Sequence
   43 - 58     1895.0566  1894.0493  1893.8679       96     1   K.QFNPGVKSGNQYMLHR.V
   43 - 58     1896.0194  1895.0121  1894.8519       85     1   K.QFNPGVKSGNQYMLHR.V
   50 - 58     1105.5889  1104.5816  1104.5134       62     0   K.SGNQYMLHR.V
   50 - 58     1121.5780  1120.5707  1120.5084       56     0   K.SGNQYMLHR.V  Oxidati
   50 - 64     1749.7764  1748.7691  1748.8515      -47     1   K.SGNQYMLHRVIEGTK.T  De
   65 - 75     1249.6459  1248.6386  1248.5663       58     0   K.TDGSPTFYSFK.Y
   98 - 114    1765.9055  1764.8982  1764.7948       59     1   K.DAEEAATGECTATVGKR.E
  114 - 126    1671.9216  1670.9143  1670.8086       63     1   K.RENEFFIVTQTCK.I  Car
  115 - 126    1459.6769  1458.6696  1458.6701       -0     0   R.ENEFFIVTQTCK.I  Deam
  115 - 126    1515.8025  1514.7952  1514.7075       58     0   R.ENEFFIVTQTCK.I  Carb
```

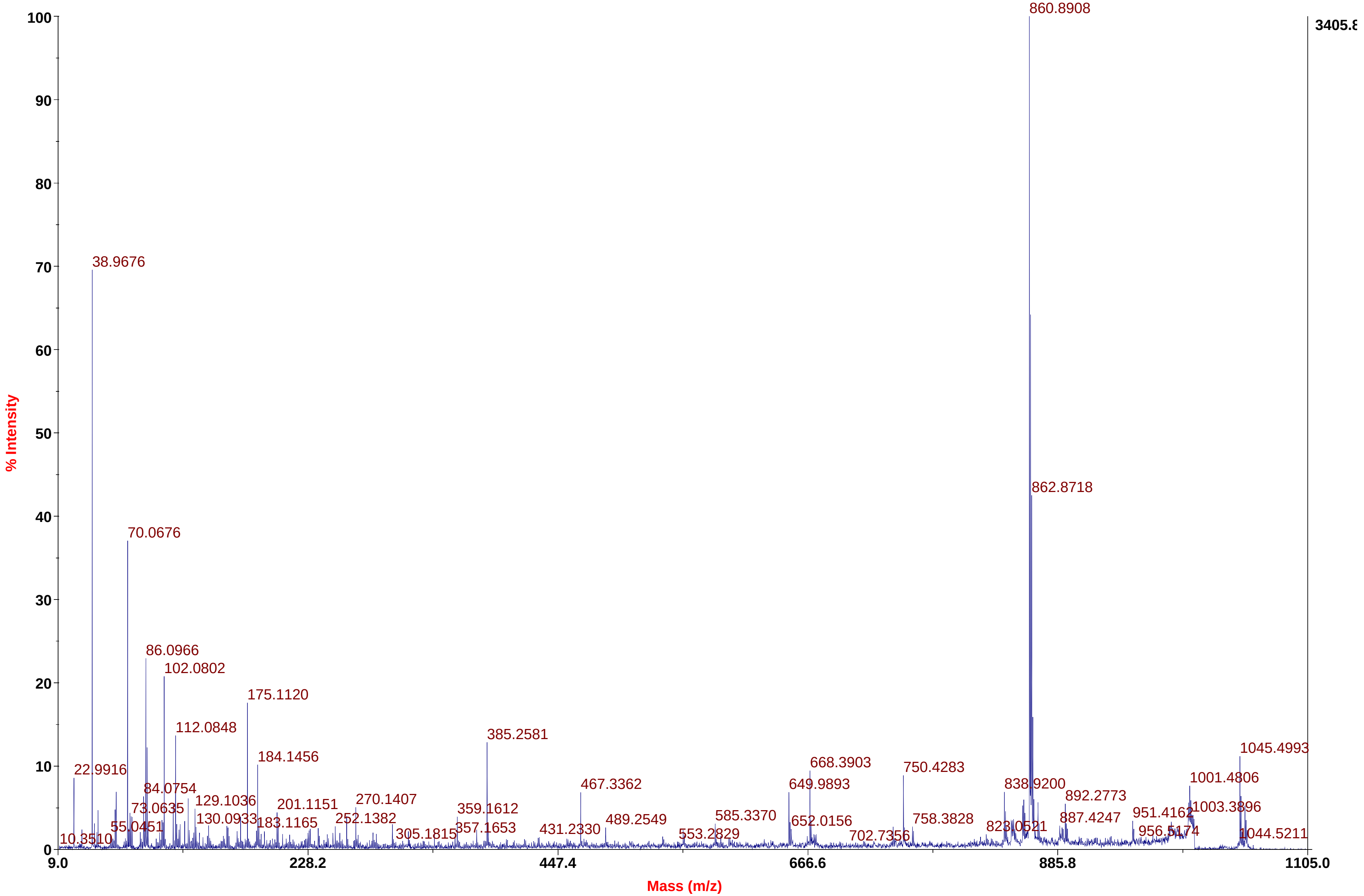
M2

4700 MS/MS Precursor 1010.62 Spec #1 MC[BP = 86.1, 1894]



M2

4700 MS/MS Precursor 1045.63 Spec #1 MC[BP = 860.9, 3406]



Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05 Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 Show sub-sets 0

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

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

1. Q6S9I1_MOUSE **Mass:** 53172 **Score:** 77 **Matches:** 8(1) **Sequences:** 8(1) **emPAI:** 0.58

HMW kininogen-I variant (High molecular weight kininogen I isoform DeltaD5).- Mus musculus (Mouse).

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	2	1010.6234	1009.6161	1009.5596	55.9	0	29	0.1	1	U	K.YVIEFIAR.E
☑	6	1105.5889	1104.5816	1104.5134	61.7	0	12	21	1	U	K.SGNQYMLHR.V
☑	8	1249.6459	1248.6386	1248.5663	57.9	0	32	0.2	1	U	K.TDGSPTFYSFK.Y
☑	9	1325.6459	1324.6386	1324.5574	61.4	0	26	0.94	1	U	K.CQALDMTEMAR.R + Carbamidomethyl (C)
☑	13	1515.8025	1514.7952	1514.7075	57.9	0	32	0.2	1	U	R.ENEFFIVTQTCK.I + Carbamidomethyl (C)
	25	1982.0591	1981.0518	1980.9319	60.6	1	2	1.7e+02	9	U	K.VVPTVKCQALDMTEMAR.R + Carbamidomethyl (C); Deamid
☑	45	2216.0903	2215.0830	2214.9423	63.5	0	61	0.00026	1	U	R.FPSLHGDCVALPNGDDGECR.G + 2 Carbamidomethyl (C)
☑	60	2432.2815	2431.2742	2431.1161	65.0	0	8	51	1		K.HLGQSLDCNANVYMRPWENK.V + Carbamidomethyl (C)

Protein View

Match to: Q6S9I1_MOUSE Score: 77
HMW kininogen-I variant (High molecular weight kininogen I isoform DeltaD5).- Mus musculus (Mouse).
Found in search of ppw_B2_12990854101.txt

Nominal mass (M_r): **53172**; Calculated pI value: **4.88**
NCBI BLAST search of Q6S9I1_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 20%

Matched peptides shown in **Bold Red**

```
  1 MKLITTLLLC SGLLLTLTQG EEAQEIDCND EAVFQAVDFS LKQFNPGVKS
 51 GNQYMLHRVI EGTKTDGSPT FYSFKYLIKE GNCSAQSGLA WQDCDFKDAE
101 EAATGECTAT VGKRENEFFI VTQTCKIAPS KAPILKAYFP CIGCVHAIST
151 DSPDLEPVLK HSIEHFNNNT DHSHLFTLRK VKSAHRQVVA GLNFDITYTI
201 VQTNCSKERF PSLHGDCVAL PNGDDGECRG NLFMDINNKI ANFSQSCTLY
251 SGDDLVEALP KPCPGCPRDI PVDSPELKEV LGHSIAQLNA ENDHPFYYKI
301 DTVKKATSQV VAGTKYVIEF IARETKCSKE SNTELAEDCE IKHLGQSLDC
351 NANVYMRPWE NKVVPTVKCQ ALDMTEMARR PPGFSPFRSV TVQETKEGRT
401 DSDFIEDVVA TTPPYDTGAH DDLIPDIHVQ PDSLSFKLIS DFPEATSPKC
451 PGRPWKPASW EDPNTETTEF SDFDLLDALS
```

Show predicted peptides also

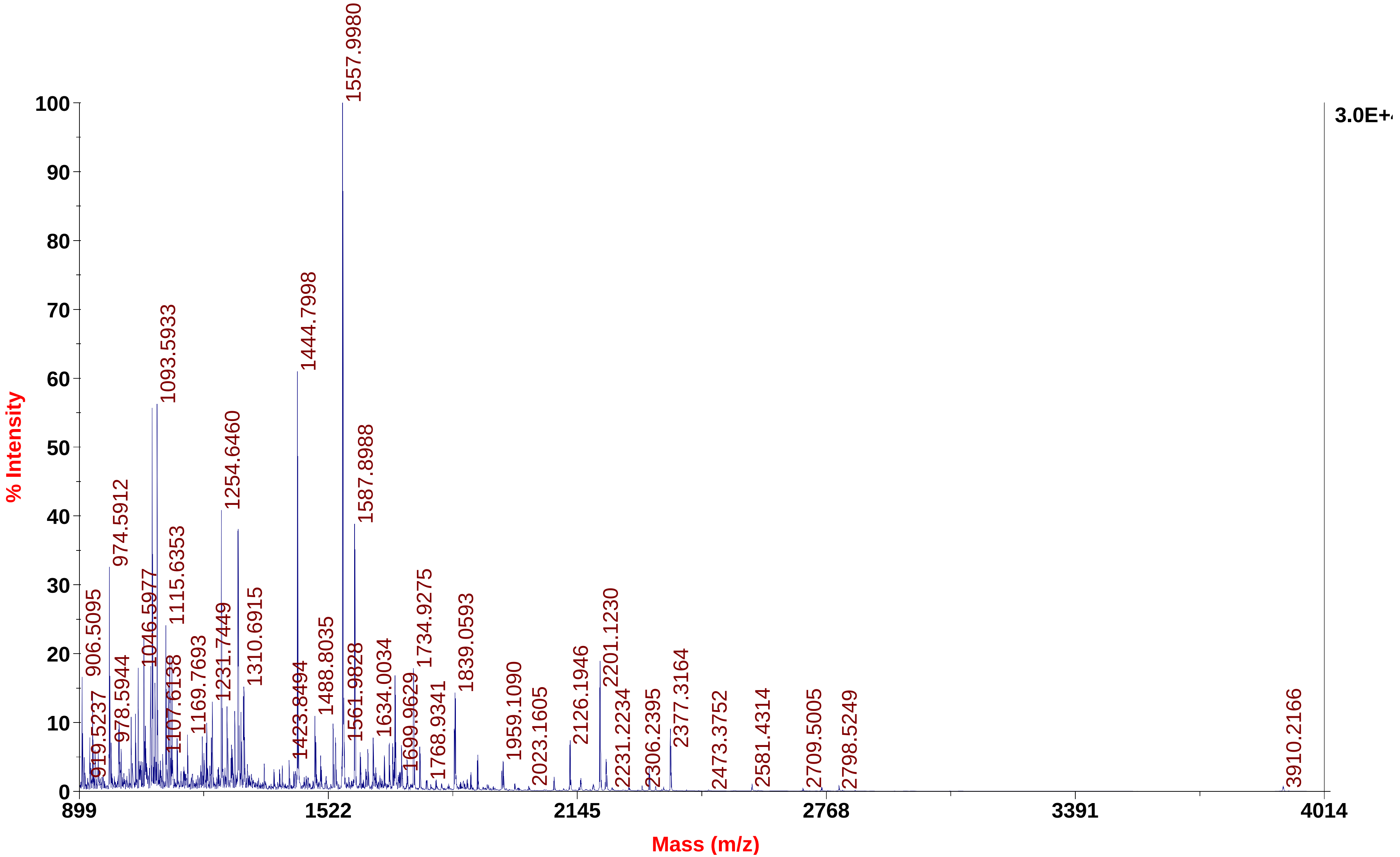
Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

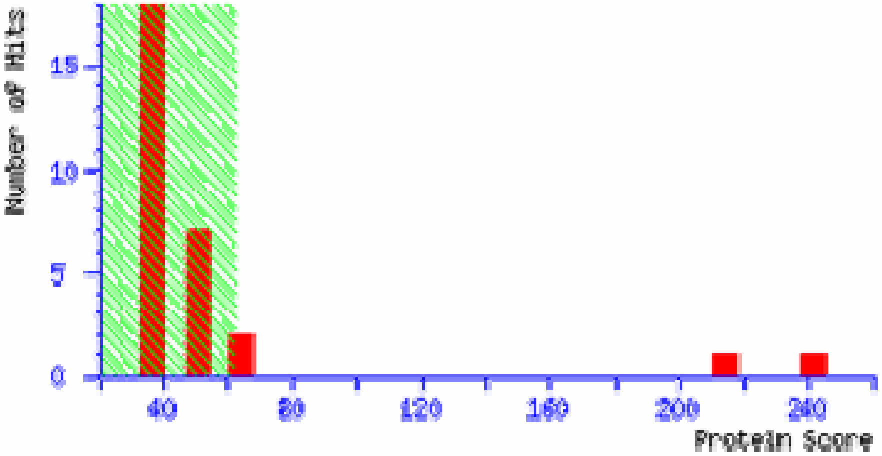
```
Start - End    Observed   Mr(expt)   Mr(calc)    ppm  Miss Sequence
   50 - 58    1105.5889  1104.5816  1104.5134    62    0  K.SGNQYMLHR.V   (Ions score 12)
   65 - 75    1249.6459  1248.6386  1248.5663    58    0  K.TDGSPTFYSFK.Y   (Ions score 32)
  115 - 126   1515.8025  1514.7952  1514.7075    58    0  R.ENEFFIVTQTCK.I  Carbamidomethyl
  210 - 229   2216.0903  2215.0830  2214.9423    64    0  R.FPSLHGDCVALPNGDDGECR.G  2 Carbam
  316 - 323   1010.6234  1009.6161  1009.5596    56    0  K.YVIEFIAR.E   (Ions score 29)
  343 - 362   2432.2815  2431.2742  2431.1161    65    0  K.HLGQSLDCNANVYMRPWENK.V  Carbamid
  363 - 379   1982.0591  1981.0518  1980.9319    61    1  K.VVPTVKCQALDMTEMAR.R  Carbamidome
  369 - 379   1325.6459  1324.6386  1324.5574    61    0  K.CQALDMTEMAR.R  Carbamidomethyl (
```

RMS error 60 ppm

Sample M3

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1558.0, 30001]





Concise Protein Summary Report

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.     VIME_MOUSE     Mass: 53524     Score: 241     Expect: 7.3e-20   Matches: 61
       Vimentin.- Mus musculus (Mouse).
       Q5FWJ3_MOUSE     Mass: 53655     Score: 241     Expect: 7.3e-20   Matches: 61
       Vimentin (NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full- length enriched library, clone:F
       CAA39807     Mass: 53689     Score: 233     Expect: 4.6e-19   Matches: 58
       MMVMTM NID: - Mus musculus
       Q3U6S1_MOUSE     Mass: 53641     Score: 232     Expect: 5.8e-19   Matches: 59
       Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830119C09 product:vimenti
       Q3TFD9_MOUSE     Mass: 53656     Score: 230     Expect: 9.2e-19   Matches: 59
       17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920087O13 product:vimentin,
       AAA40555     Mass: 53641     Score: 229     Expect: 1.2e-18   Matches: 58
```

Protein View

Match to: **VIME_MOUSE** Score: **241** Expect: **7.3e-20**
Vimentin.- Mus musculus (Mouse).
Found in search of pmf_C2_129990848802.txt

Nominal mass (M_r): **53524**; Calculated pI value: **5.06**
NCBI BLAST search of VIME_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **176**
Number of mass values matched: **61**
Sequence Coverage: **85%**

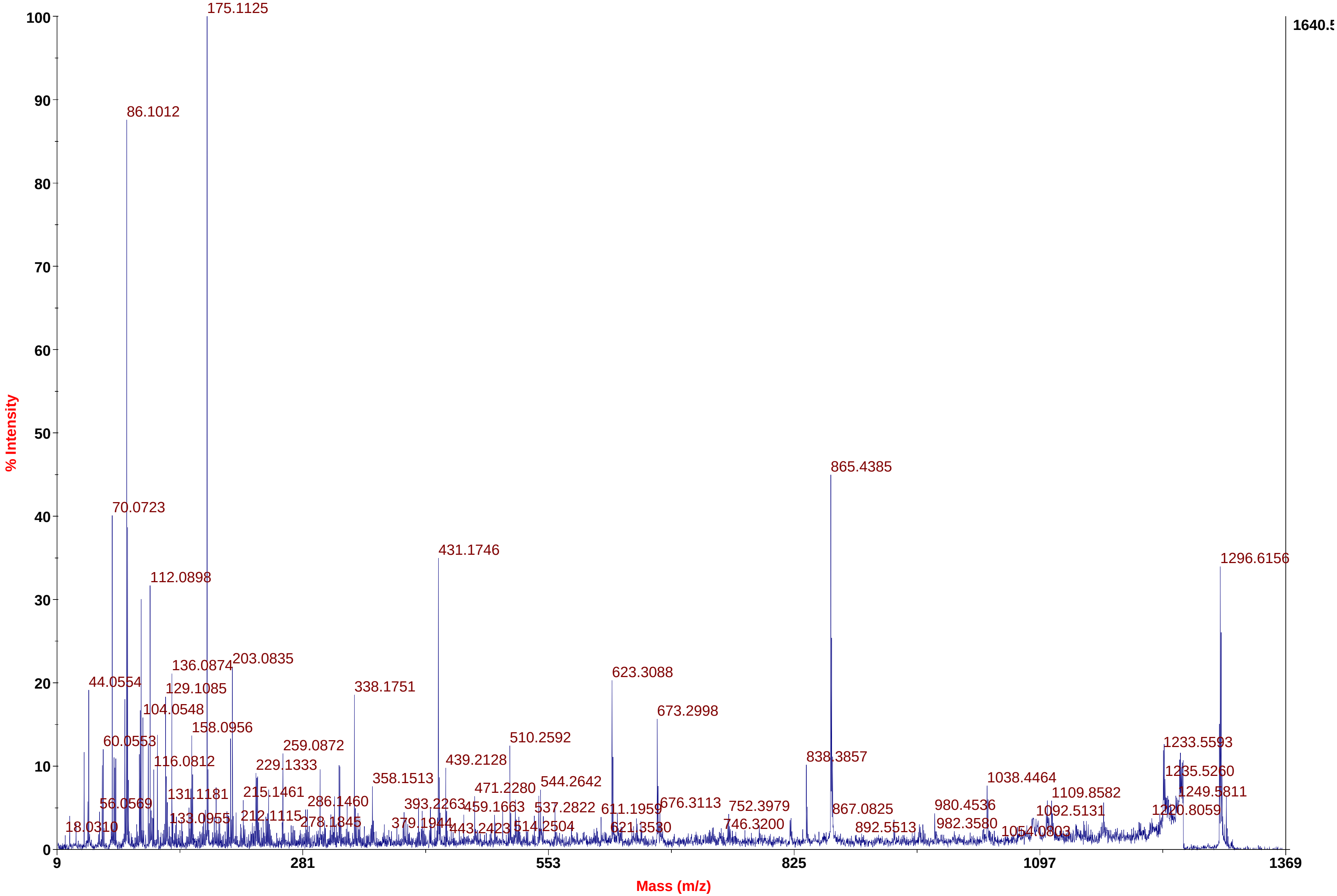
Matched peptides shown in **Bold Red**

```
  1 STRSVSSSSY RRMFGGSGTS SRPSSNRSYV TTSTRTYSLG SALRPSTSRS
 51 LYSSSPGGAY VTRSSAVRLR SSVPGVRLLQ DSVDFSLADA INTEFKNTRT
101 NEKVELQELN DRFANYIDKV RFLEQQNKIL LAELEQLKGQ GKSRLGDLYE
151 EEMRELRRQV DQLTNDKARV EVERDNLAED IMRLREKLQE EMLQREEAES
201 TLQSFRQDVD NASLARLDLE RKVESLQEEI AFLKKLHDEE IQELQAQIQE
251 QHVQIDVDVS KPDLTAALRD VRQQYESVAA KNLQEAEEWY KSKFADLSEA
301 ANRNNDALRQ AKQESNEYRR QVQSLTCEVD ALKGTNESLE RQMREMEENF
351 ALEAANYQDT IGRLQDEIQN MKEEMARHLR EYQDLLNVKM ALDIEIATYR
401 KLLEGEESRI SLPLPTFSSL NLRETNLESL PLVDTHSKRT LLIKTVETRD
451 GQVINETSQH HDDLE
```

```
 Start - End      Observed    Mr(expt)   Mr(calc)       ppm    Miss  Sequence
    4 - 12       1028.5881   1027.5808  1027.5047        74      1   R.SVSSSSYRR.M
   12 - 27       1699.9598   1698.9525  1698.7856        98      1   R.RMFGGSGTSSRPSSNR.S  Oxida
   28 - 49       2391.3157   2390.3084  2390.2190        37      1   R.SYVTTSTRTYSLGSALRPSTSR.S
   50 - 63       1444.7992   1443.7919  1443.6994        64      0   R.SLYSSSPGGAYVTR.S
   78 - 96       2126.1914   2125.1841  2125.0579        59      0   R.LLQDSVDFSLADAINTEFK.N
  100 - 112      1587.8977   1586.8904  1586.7900        63      1   R.TNEKVELQELNDR.F
  104 - 112      1115.6348   1114.6275  1114.5618        59      0   K.VELQELNDR.F
  113 - 121      1125.6698   1124.6625  1124.5978        58      1   R.FANYIDKVR.F
  122 - 128       906.5101    905.5028   905.4607        47      0   R.FLEQQNK.I
  129 - 138      1169.7720   1168.7647  1168.7067        50      0   K.ILLAELEQLK.G
  129 - 142      1540.0029   1538.9956  1538.9032        60      1   K.ILLAELEQLKGQGK.S
```

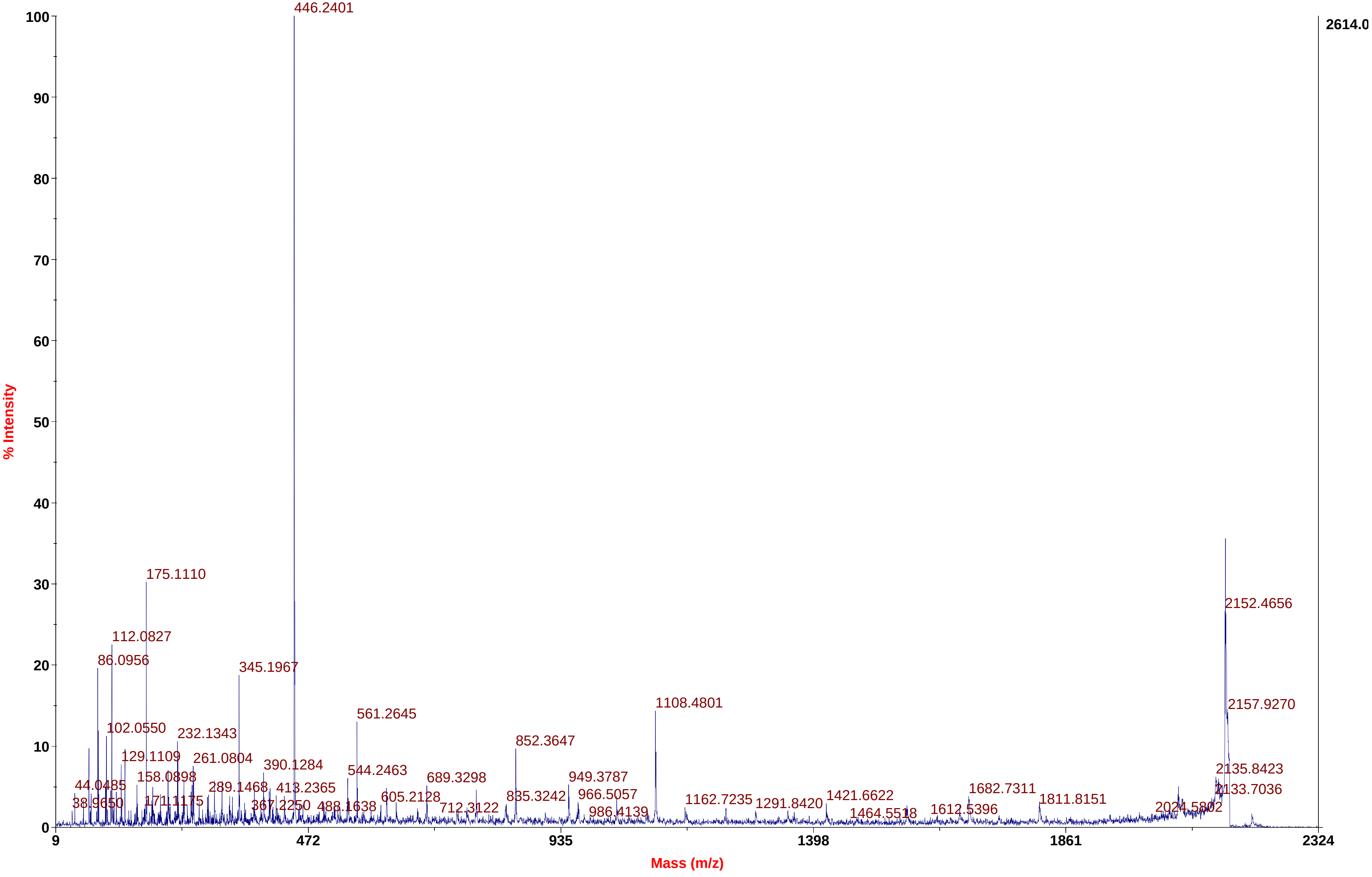
M3

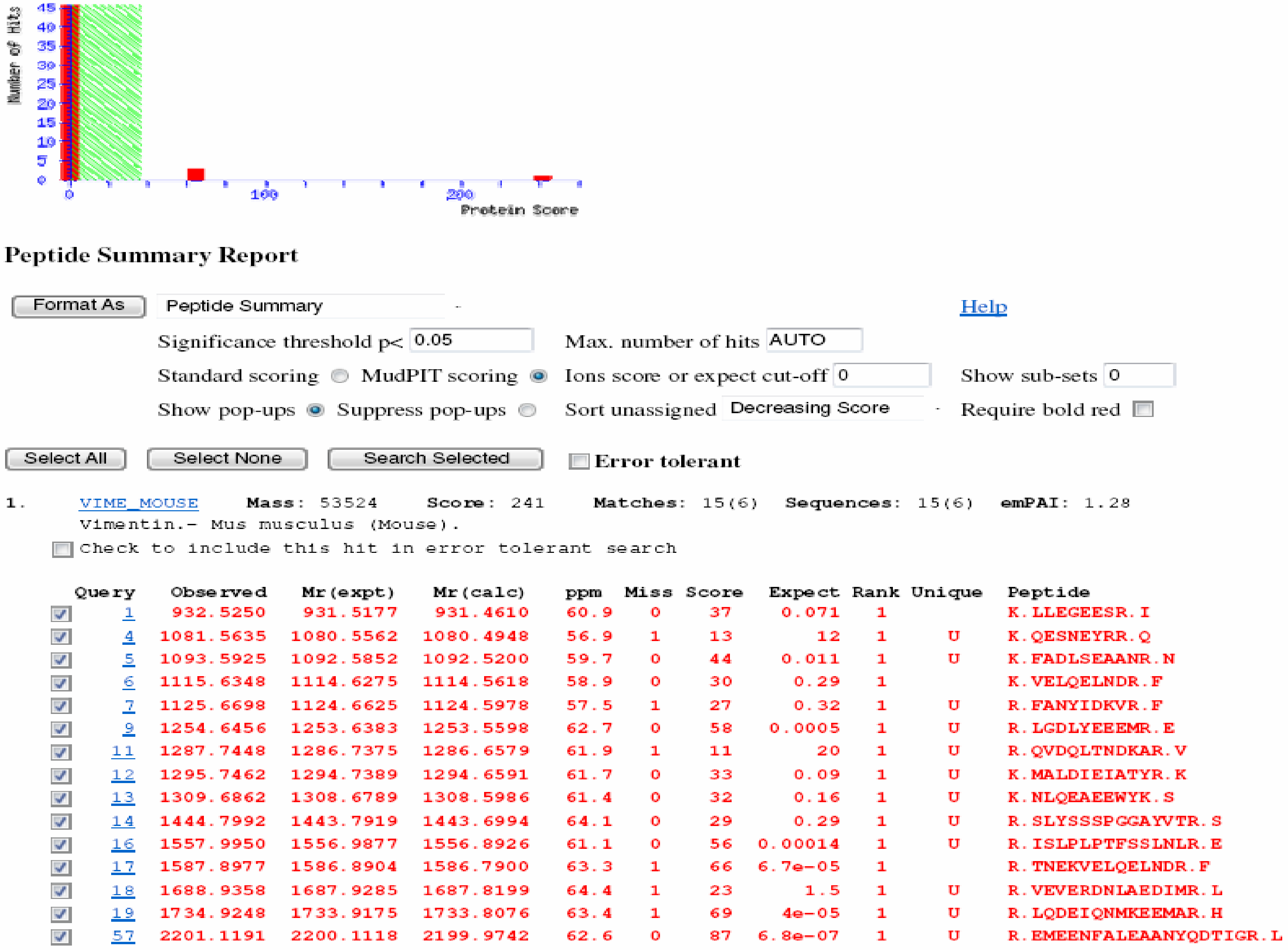
4700 MS/MS Precursor 1295.75 Spec #1 MC[BP = 175.1, 1640]



M3

4700 MS/MS Precursor 2201.12 Spec #1 MC[BP = 446.2, 2614]





Peptide Summary Report

Format As: Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

☐ Error tolerant

1. VIME_MOUSE **Mass:** 53524 **Score:** 241 **Matches:** 15(6) **Sequences:** 15(6) **emPAI:** 1.28

Vimentin.- Mus musculus (Mouse).

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	932.5250	931.5177	931.4610	60.9	0	37	0.071	1		K.LLEGEESR.I
☑	4	1081.5635	1080.5562	1080.4948	56.9	1	13	12	1	U	K.QESNEYRR.Q
☑	5	1093.5925	1092.5852	1092.5200	59.7	0	44	0.011	1	U	K.FADLSEAANR.N
☑	6	1115.6348	1114.6275	1114.5618	58.9	0	30	0.29	1		K.VELQELNDR.F
☑	7	1125.6698	1124.6625	1124.5978	57.5	1	27	0.32	1	U	R.FANYIDKVR.F
☑	9	1254.6456	1253.6383	1253.5598	62.7	0	58	0.0005	1	U	R.LGDLYEEEMR.E
☑	11	1287.7448	1286.7375	1286.6579	61.9	1	11	20	1	U	R.QVDQLTNDKAR.V
☑	12	1295.7462	1294.7389	1294.6591	61.7	0	33	0.09	1	U	K.MALDIEIATYR.K
☑	13	1309.6862	1308.6789	1308.5986	61.4	0	32	0.16	1	U	K.NLQEAEEWYK.S
☑	14	1444.7992	1443.7919	1443.6994	64.1	0	29	0.29	1	U	R.SLYSSSPGGAYVTR.S
☑	16	1557.9950	1556.9877	1556.8926	61.1	0	56	0.00014	1	U	R.ISLPLPTFSSLNLR.E
☑	17	1587.8977	1586.8904	1586.7900	63.3	1	66	6.7e-05	1		R.TNEKVELQELNDR.F
☑	18	1688.9358	1687.9285	1687.8199	64.4	1	23	1.5	1	U	R.VEVERDNLAEDIMR.L
☑	19	1734.9248	1733.9175	1733.8076	63.4	1	69	4e-05	1	U	R.LQDEIQNMKEEMAR.H
☑	57	2201.1191	2200.1118	2199.9742	62.6	0	87	6.8e-07	1	U	R.EMEENFALEAANYQDTIGR.L

Protein View

Match to: **VIME_MOUSE** Score: **241**
Vimentin.- Mus musculus (Mouse).
Found in search of ppw_C2_129990854302.txt

Nominal mass (M_r): **53524**; Calculated pI value: **5.06**
NCBI BLAST search of VIME_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **35%**

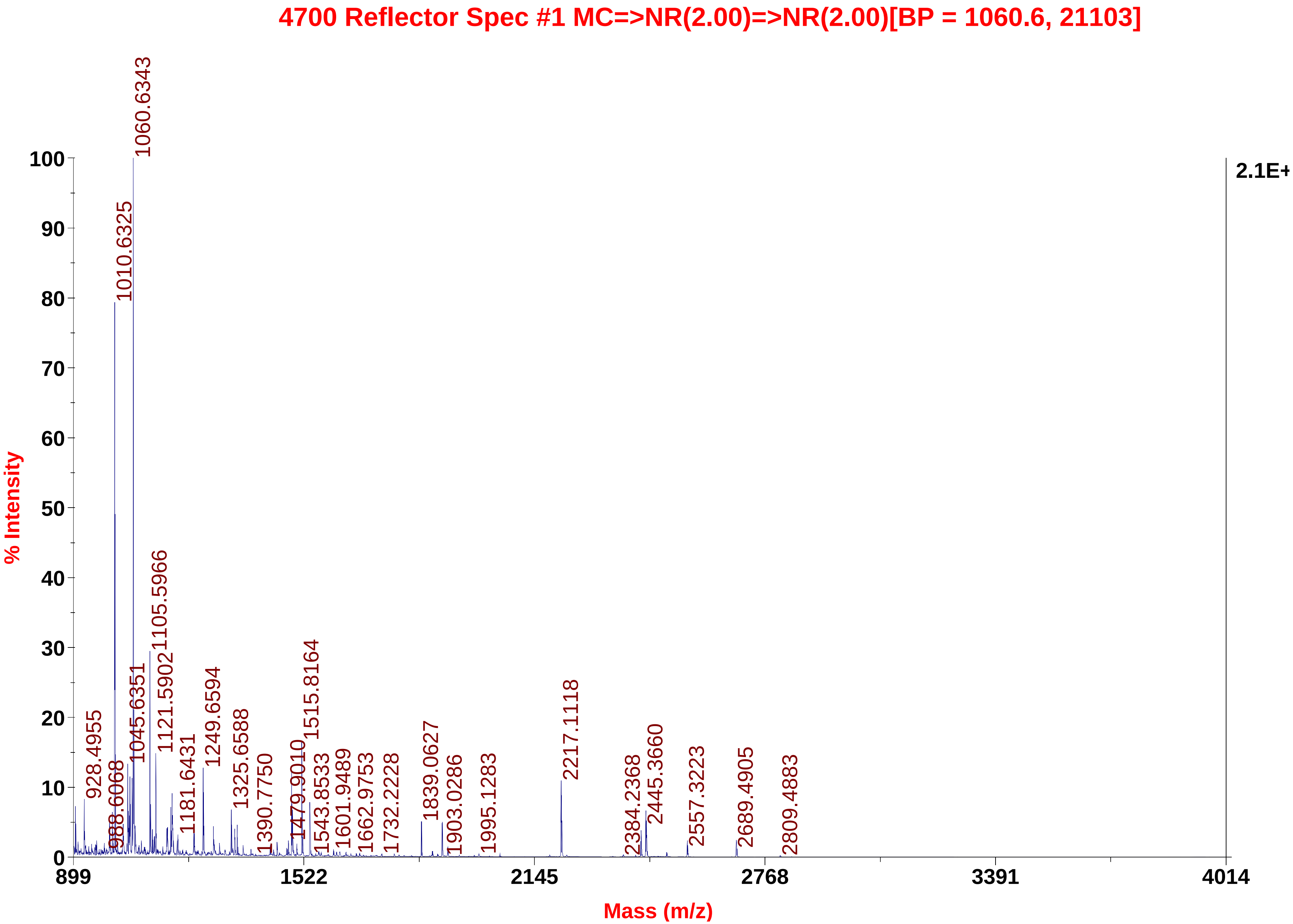
Matched peptides shown in **Bold Red**

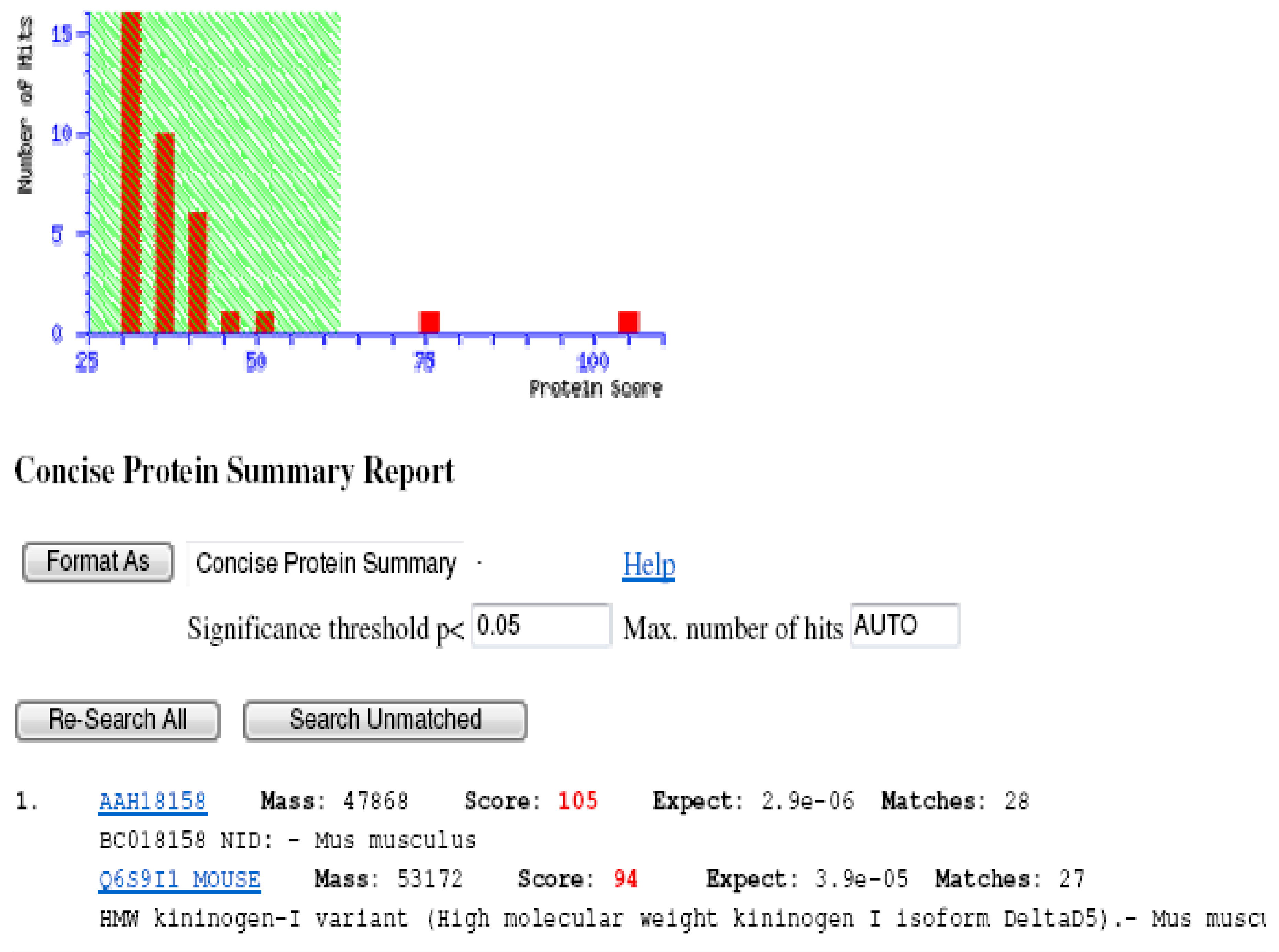
```
  1 STRSVSSSSY RRMFGGSGTS SRPSSNRSYV TTSTRTYSLG SALRPSTSRS
 51 LYSSSPGGAY VTRSSAVRLR SSVPGVRLLQ DSVDFSLADA INTEFKNTRT
101 NEKVELQELN DRFANYIDKV RFLEQQNKIL LAELEQLKGQ GKSRLGDLYE
151 EEMRELRRQV DQLTNDKARV EVERDNLAED IMRLREKLQE EMLQREEAES
201 TLQSFRQDVD NASLARLDLE RKVESLQEEI AFLKKLHDEE IQELQAQIQE
251 QHVQIDVDVS KPDLTAALRD VRQQYESVAA KNLQEAEEWY KSKFADLSEA
301 ANRNNDALRQ AKQESNEYRR QVQSLTCEVD ALKGTNESLE RQMREMEENF
351 ALEAANYQDT IGRLQDEIQN MKEEMARHLR EYQDLLNVKM ALDIEIATYR
401 KLLEGEESRI SLPLPTFSSL NLRETNLESL PLVDTHSKRT LLIKTVETRD
451 GQVINETSQH HDDLE
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
  50 - 63      1444.7992  1443.7919  1443.6994      64      0    R.SLYSSSPGGAYVTR.S  (Ions score 29)
 100 - 112     1587.8977  1586.8904  1586.7900      63      1    R.TNEKVELQELNDR.F  (Ions score 66)
 104 - 112     1115.6348  1114.6275  1114.5618      59      0    K.VELQELNDR.F  (Ions score 30)
 113 - 121     1125.6698  1124.6625  1124.5978      58      1    R.FANYIDKVR.F  (Ions score 27)
 145 - 154     1254.6456  1253.6383  1253.5598      63      0    R.LGDLYEEEMR.E  (Ions score 58)
 159 - 169     1287.7448  1286.7375  1286.6579      62      1    R.QVDQLTNDKAR.V  (Ions score 11)
 170 - 183     1688.9358  1687.9285  1687.8199      64      1    R.VEVERDNLAEDIMR.L  (Ions score 23)
 282 - 291     1309.6862  1308.6789  1308.5986      61      0    K.NLQEAEEWYK.S  (Ions score 32)
 294 - 303     1093.5925  1092.5852  1092.5200      60      0    K.FADLSEAANR.N  (Ions score 44)
 313 - 320     1081.5635  1080.5562  1080.4948      57      1    K.QESNEYRR.Q  (Ions score 13)
 345 - 363     2201.1191  2200.1118  2199.9742      63      0    R.EMEENFALEAANYQDTIGR.L  (Ions scor
 364 - 377     1734.9248  1733.9175  1733.8076      63      1    R.LQDEIQNMKEEMAR.H  (Ions score 69)
 390 - 400     1295.7462  1294.7389  1294.6591      62      0    K.MALDIEIATYR.K  (Ions score 33)
 402 - 409      932.5250   931.5177   931.4610      61      0    K.LLEGEESR.I  (Ions score 37)
 410 - 423     1557.9950  1556.9877  1556.8926      61      0    R.ISLPLPTFSSLNLR.E  (Ions score 56)
```

Sample M4


4700 Reflector Spec #1 MC=>NR(2.00)=>NR(2.00)[BP = 1060.6, 21103]
% Intensity
Mass (m/z)
2.1E+
100
90
80
70
60
50
40
30
20
10
0
899
1522
2145
2768
3391
4014
1060.6343
1010.6325
1105.5966
1121.5902
1045.6351
928.4955
988.6068
1181.6431
1249.6594
1325.6588
1390.7750
1479.9010
1515.8164
1543.8533
1601.9489
1662.9753
1732.2228
1839.0627
1903.0286
1995.1283
2217.1118
2384.2368
2445.3660
2557.3223
2689.4905
2809.4883



Concise Protein Summary Report

Format As: Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

1. **AAH18158** **Mass:** 47868 **Score:** 105 **Expect:** 2.9e-06 **Matches:** 28
   BC018158 NID: - Mus musculus
   Q6S9I1_MOUSE **Mass:** 53172 **Score:** 94 **Expect:** 3.9e-05 **Matches:** 27
   HMW kininogen-I variant (High molecular weight kininogen I isoform DeltaD5).- Mus muscu

Protein View

Match to: **AAH18158** Score: **105** Expect: **2.9e-06**
BC018158 NID: – Mus musculus
Found in search of pmf_D2_129990848803.txt

Nominal mass (M_r): **47868**; Calculated pI value: **5.74**
NCBI BLAST search of AAH18158 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **147**
Number of mass values matched: **28**
Sequence Coverage: **56%**

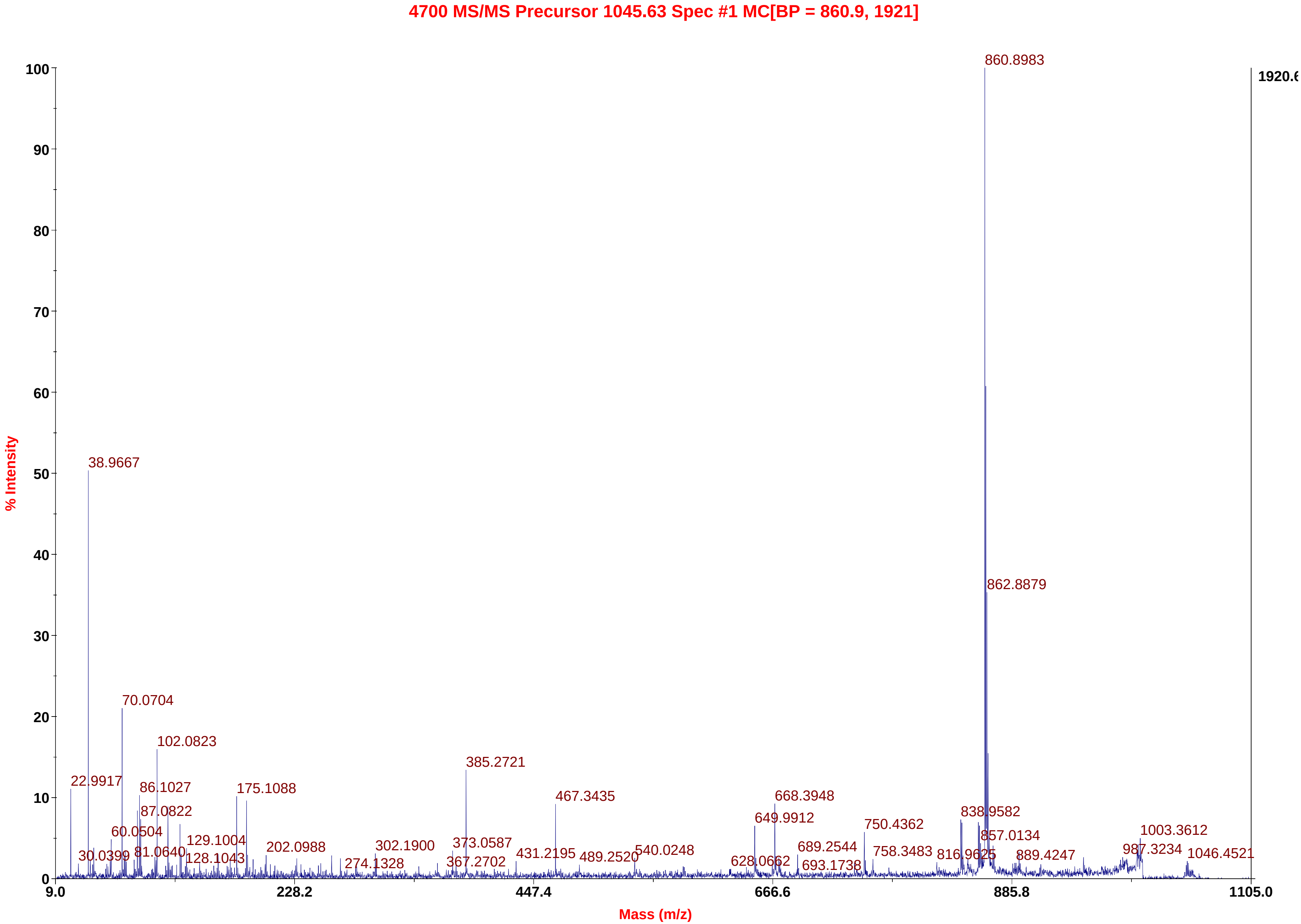
Matched peptides shown in **Bold Red**

```
  1 MKLITTLLLC SGLLLTLTQG EEAQEIDCND EAVFQAVDFS LKQFNPGVKS
 51 GNQYMLHRVI EGTKTDGSPT FYSFKYLIKE GNCSAQSGLA WQDCDFKDAE
101 EAATGECTAT VGKRENEFFI VTQTCKIAPS KAPILKAYFP CIGCVHAIST
151 DSPDLEPVLK HSIEHFNNNT DHSHLFTLRK VKSAHRQVVA GLNFDITYTI
201 VQTNCSKERF PSLHGDCVAL PNGDDGECRG NLFMDINNKI ANFSQSCTLY
251 SGDDLVEALP KPCPGCPRDI PVDSPELKEV LGHSIAQLNA ENDHPFYYKI
301 DTVKKATSQV VAGTKYVIEF IARETKCSKE SNTELAEDCE IKHLGQSLDC
351 NANVYMRPWE NKVVPTVKCQ ALDMTEMARR PPGFSPFRSV TVQETKEGRT
401 RLLRACEYKG RLSKAGAEPA PERQAESSQV KQ
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

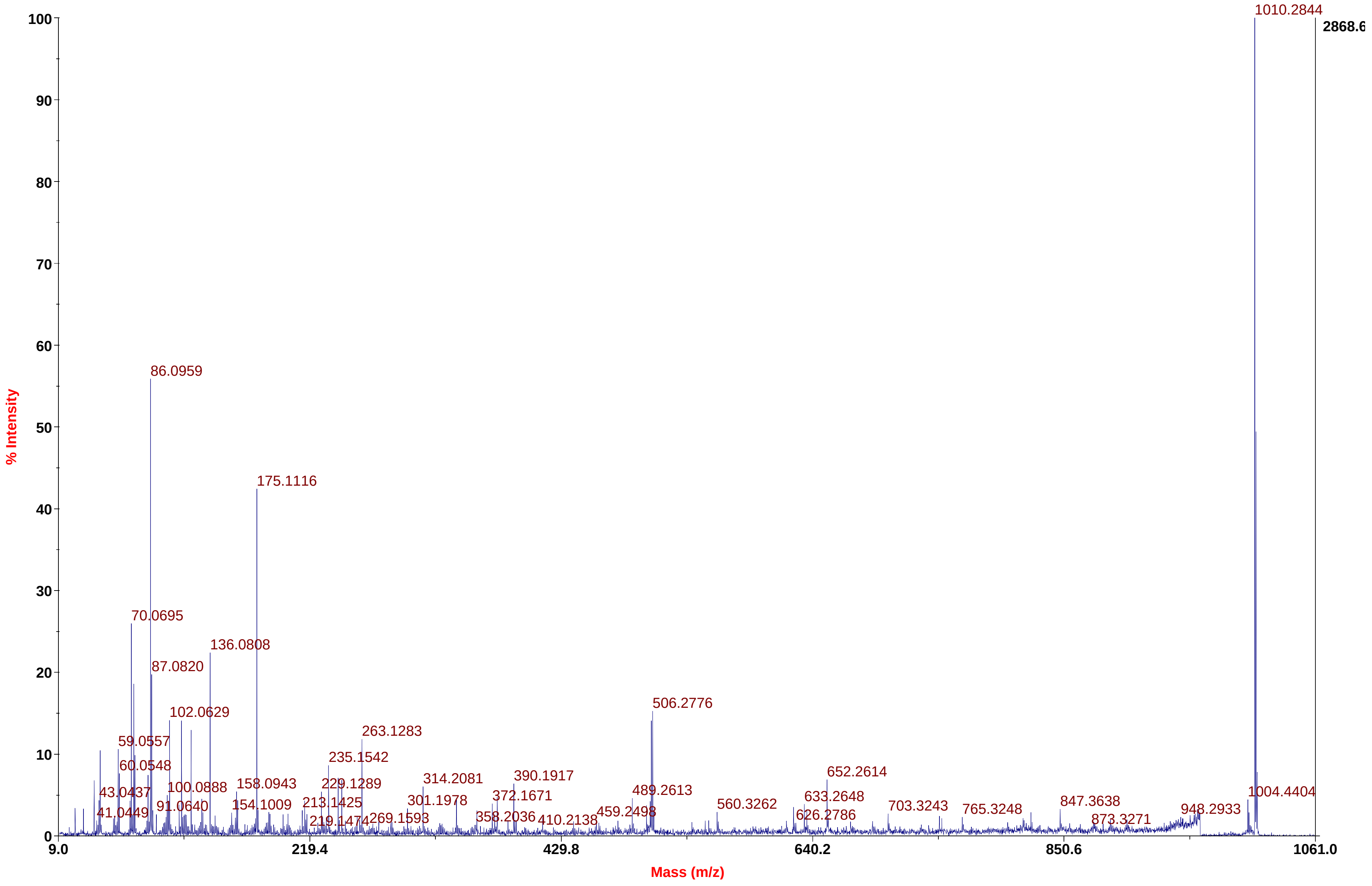
```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   50 - 58     1105.5961  1104.5888  1104.5134       68      0  K.SGNQYMLHR.V
   50 - 58     1121.5890  1120.5817  1120.5084       65      0  K.SGNQYMLHR.V  Oxidation (M
   65 - 75     1249.6566  1248.6493  1248.5663       67      0  K.TDGSPTFYSFK.Y
   98 - 114    1765.9282  1764.9209  1764.7948       71      1  K.DAEEAATGECTATVGKR.E  Carba
  114 - 126    1671.9396  1670.9323  1670.8086       74      1  K.RENEFFIVTQTCK.I  Carbamid
  115 - 126    1515.8158  1514.8085  1514.7075       67      0  R.ENEFFIVTQTCK.I  Carbamido
  137 - 160    2689.4998  2688.4925  2688.2928       74      0  K.AYFPCIGCVHAISTDSPDLEPVLK.
  161 - 180    2449.3303  2448.3230  2448.1570       68      1  K.HSIEHFNNNTDHSHLFTLRK.V  2
  208 - 229    2501.2832  2500.2759  2500.0860       76      1  K.ERFPSLHGDCVALPNGDDGECR.G
  208 - 229    2502.2778  2501.2705  2501.0700       80      1  K.ERFPSLHGDCVALPNGDDGECR.G
  210 - 229    2216.1101  2215.1028  2214.9423       72      0  R.FPSLHGDCVALPNGDDGECR.G  2
```

M4


4700 MS/MS Precursor 1045.63 Spec #1 MC[BP = 860.9, 1921]
% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
9.0
228.2
447.4
666.6
885.8
1105.0
1920.6
860.8983
862.8879
38.9667
70.0704
102.0823
22.9917
86.1027
87.0822
60.0504
30.0399
81.0640
129.1004
128.1043
175.1088
202.0988
274.1328
302.1900
385.2721
373.0587
367.2702
431.2195
467.3435
489.2520
540.0248
628.0662
649.9912
668.3948
689.2544
693.1738
750.4362
758.3483
816.9625
838.9582
857.0134
889.4247
987.3234
1003.3612
1046.4521

M4

4700 MS/MS Precursor 1004.56 Spec #1 MC[BP = 1010.3, 2869]



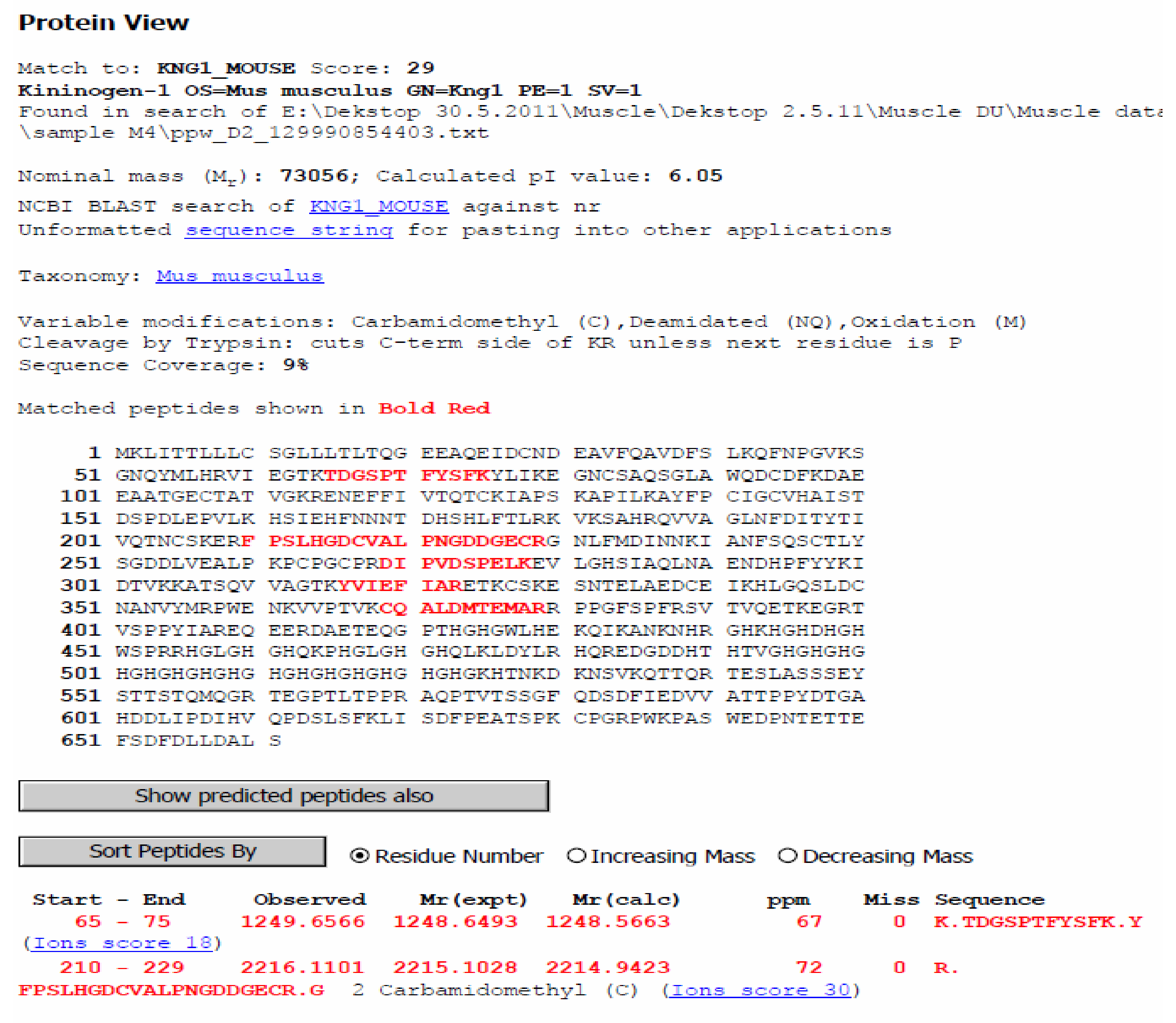
Peptide Summary Report

KNG1_MOUSE **Mass:** 73056 **Score:** 29 **Matches:** 5 (0) **Sequences:** 5(0) **emPAI:** 0.18

Kininogen-1 OS=Mus musculus GN=Kng1 PE=1 SV=1

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	4	1010.6306	1009.6233	1009.5596	63.1	0	18	0.33	1	U	K.YVIEFIAR.E
☑	9	1112.6533	1111.6460	1111.5761	62.9	0	11	3.5	1	U	R.DIPVDSPELK.E
☑	12	1249.6566	1248.6493	1248.5663	66.5	0	18	1.4	1	U	K.TDGSPTFYSFK.Y
☑	13	1325.6593	1324.6520	1324.5574	71.5	0	17	1.4	1	U	K.CQALDMTEMAR.R + Carbamidomethyl (C)
☑	47	2216.1101	2215.1028	2214.9423	72.5	0	30	0.088	1	U	R.FPSLHGDCVALPNGDDGECR.G + 2 Carbamidomethyl (C)



Protein View

Match to: **KNG1_MOUSE** Score: **29**
Kininogen-1 OS=Mus musculus GN=Kng1 PE=1 SV=1
Found in search of E:\Dekstop 30.5.2011\Muscle\Dekstop 2.5.11\Muscle DU\Muscle dat
\sample M4\ppw_D2_129990854403.txt

Nominal mass (M_r): **73056**; Calculated pI value: **6.05**

NCBI BLAST search of KNG1_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

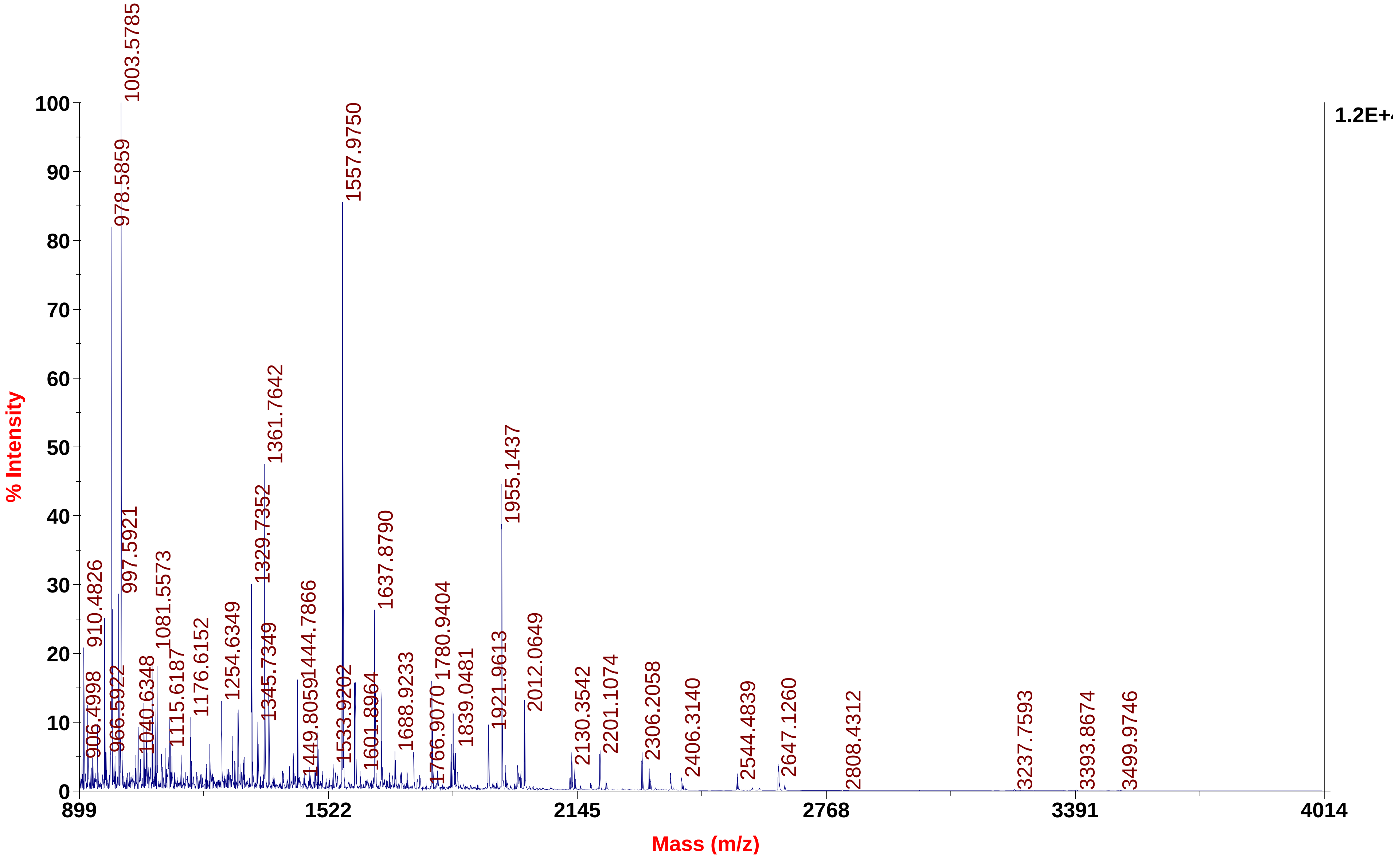
```
  1 MKLITTLLLC SGLLLTLTQG EEAQEIDCND EAVFQAVDFS LKQFNPGVKS
 51 GNQYMLHRVI EGTKTDGSPT FYSFKYLIKE GNCSAQSGLA WQDCDFKDAE
101 EAATGECTAT VGKRENEFFI VTQTCKIAPS KAPILKAYFP CIGCVHAIST
151 DSPDLEPVLK HSIEHFNNNT DHSHLFTLRK VKSAHRQVVA GLNFDITYTI
201 VQTNCSKERF PSLHGDCVAL PNGDDGECRG NLFMDINNKI ANFSQSCTLY
251 SGDDLVEALP KPCPGCPRDI PVDSPELKEV LGHSIAQLNA ENDHPFYYKI
301 DTVKKATSQV VAGTKYVIEF IARETKCSKE SNTELAEDCE IKHLGQSLDC
351 NANVYMRPWE NKVVPTVKCQ ALDMTEMARR PPGFSPFRSV TVQETKEGRT
401 VSPPYIAREQ EERDAETEQG PTHGHGWLHE KQIKANKNHR GHKHGHDHGH
451 WSPRRHGLGH GHQKPHGLGH GHQLKLDYLR HQREDGDDHT HTVGHGHGHG
501 HGHGHGHGHG HGHGHGHGHG HGHGKHTNKD KNSVKQTTQR TESLASSSEY
551 STTSTQMQGR TEGPTLTPPR AQPTVTSSGF QDSDFIEDVV ATTPPYDTGA
601 HDDLIPDIHV QPDSLSFKLI SDFPEATSPK CPGRPWKPAS WEDPNTETTE
651 FSDFDLLDAL S
```

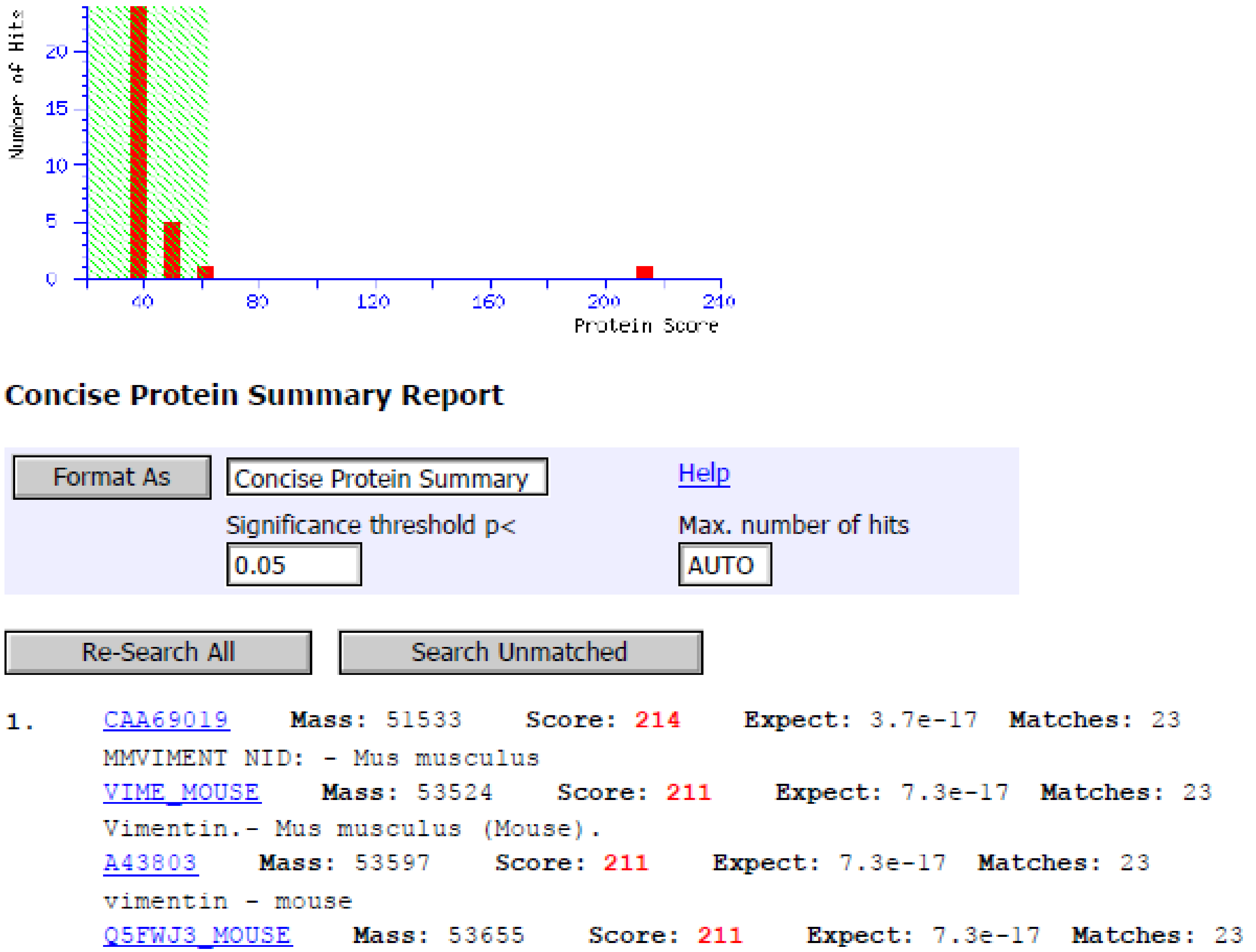
● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   65 - 75      1249.6566  1248.6493  1248.5663       67      0  K.TDGSPTFYSFK.Y
(Ions score 18)
  210 - 229     2216.1101  2215.1028  2214.9423       72      0  R.
FPSLHGDCVALPNGDDGECR.G  2 Carbamidomethyl (C)  (Ions score 30)
```

Sample M5

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1003.6, 11606]



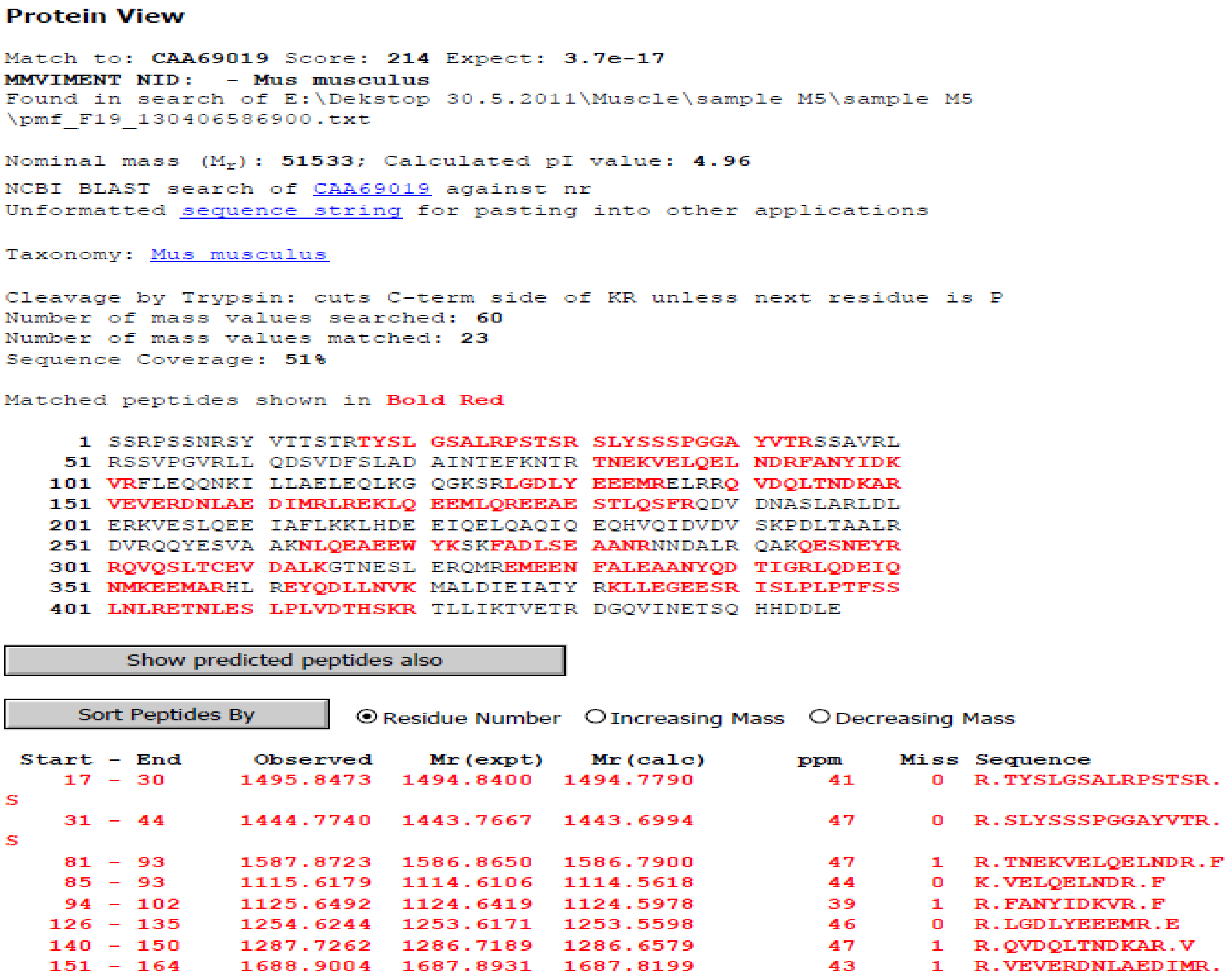


Concise Protein Summary Report

Significance threshold p< 0.05

Max. number of hits AUTO

```
1.    CAA69019     Mass: 51533     Score: 214     Expect: 3.7e-17   Matches: 23
      MMVIMENT NID: - Mus musculus
      VIME_MOUSE     Mass: 53524     Score: 211     Expect: 7.3e-17   Matches: 23
      Vimentin.- Mus musculus (Mouse).
      A43803     Mass: 53597     Score: 211     Expect: 7.3e-17   Matches: 23
      vimentin - mouse
      Q5FWJ3_MOUSE     Mass: 53655     Score: 211     Expect: 7.3e-17   Matches: 23
```



Protein View

Match to: **CAA69019** **Score:** **214** **Expect:** **3.7e-17**
MMVIMENT NID: – Mus musculus
Found in search of E:\Dekstop 30.5.2011\Muscle\sample M5\sample M5 \pmf_F19_13040658690O.txt

Nominal mass (M_r): **51533**; Calculated pI value: **4.96**

NCBI BLAST search of CAA69019 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **60**
Number of mass values matched: **23**
Sequence Coverage: **51%**

Matched peptides shown in **Bold Red**

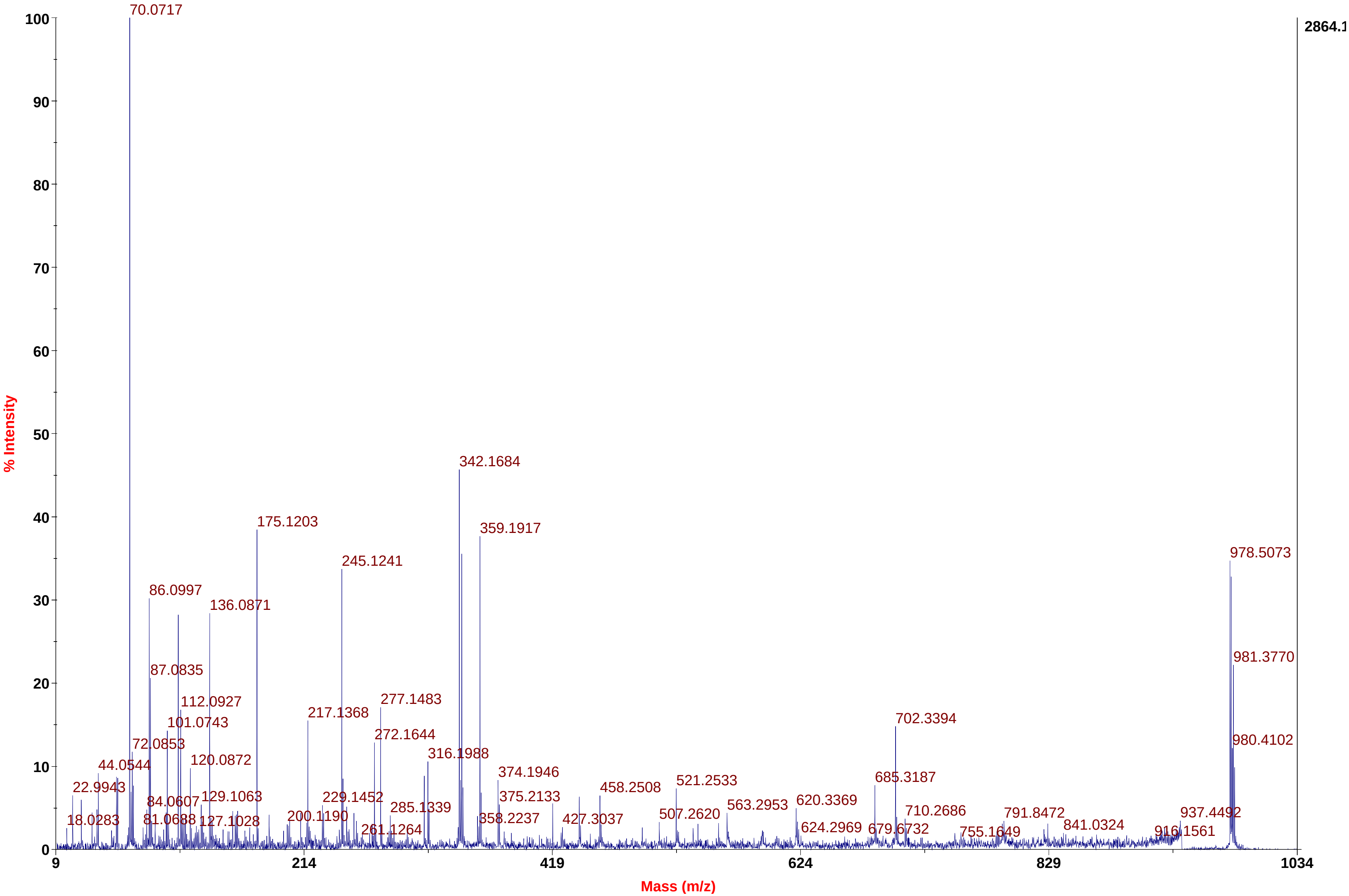
```
    1 SSRPSSNRSY VTTSTRTYSL GSALRPSTSR SLYSSSPGGA YVTRSSAVRL
   51 RSSVPGVRLL QDSVDFSLAD AINTEFKNTR TNEKVELQEL NDRFANYIDK
  101 VRFLEQQNKI LLAELEQLKG QGKSRLGDLY EEEMRELRRQ VDQLTNDKAR
  151 VEVERDNLAE DIMRLREKLQ EEMLQREEAE STLQSFRQDV DNASLARLDL
  201 ERKVESLQEE IAFLKKLHDE EIQELQAQIQ EQHVQIDVDV SKPDLTAALR
  251 DVRQQYESVA AKNLQEAEEW YKSKFADLSE AANRNNDALR QAKQESNEYR
  301 RQVQSLTCEV DALKGTNESL ERQMREMEEN FALEAANYQD TIGRLQDEIQ
  351 NMKEEMARHL REYQDLLNVK MALDIEIATY RKLLEGEESR ISLPLPTFSS
  401 LNLRETNLES LPLVDTHSKR TLLIKTVETR DGQVINETSQ HHDDLE
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
    17 - 30     1495.8473  1494.8400  1494.7790      41     0  R.TYSLGSALRPSTSR.
S
    31 - 44     1444.7740  1443.7667  1443.6994      47     0  R.SLYSSSPGGAYVTR.
S
    81 - 93     1587.8723  1586.8650  1586.7900      47     1  R.TNEKVELQELNDR.F
    85 - 93     1115.6179  1114.6106  1114.5618      44     0  K.VELQELNDR.F
    94 - 102    1125.6492  1124.6419  1124.5978      39     1  R.FANYIDKVR.F
   126 - 135    1254.6244  1253.6171  1253.5598      46     0  R.LGDLYEEEMR.E
   140 - 150    1287.7262  1286.7189  1286.6579      47     1  R.QVDQLTNDKAR.V
   151 - 164    1688.9004  1687.8931  1687.8199      43     1  R.VEVERDNLAEDIMR.
```

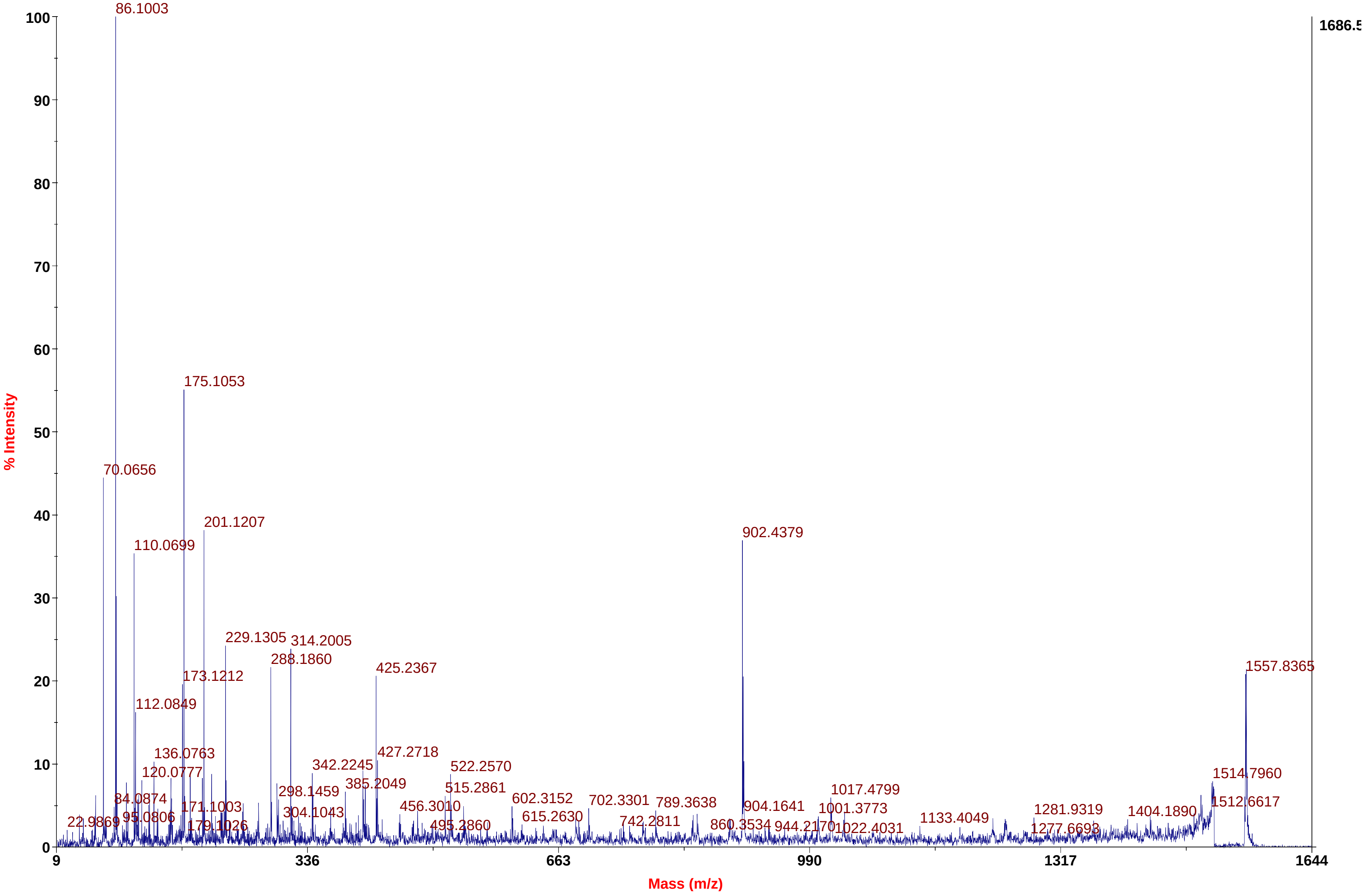
M5

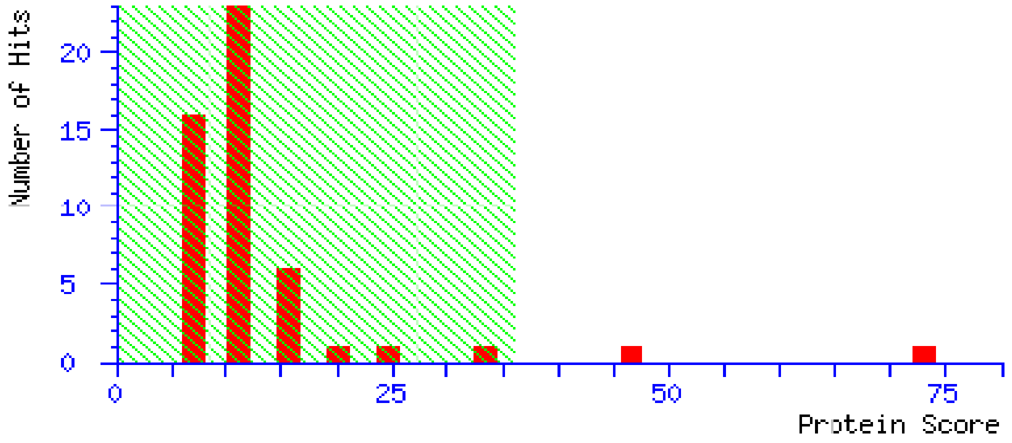
4700 MS/MS Precursor 978.586 Spec #1 MC[BP = 70.1, 2864]

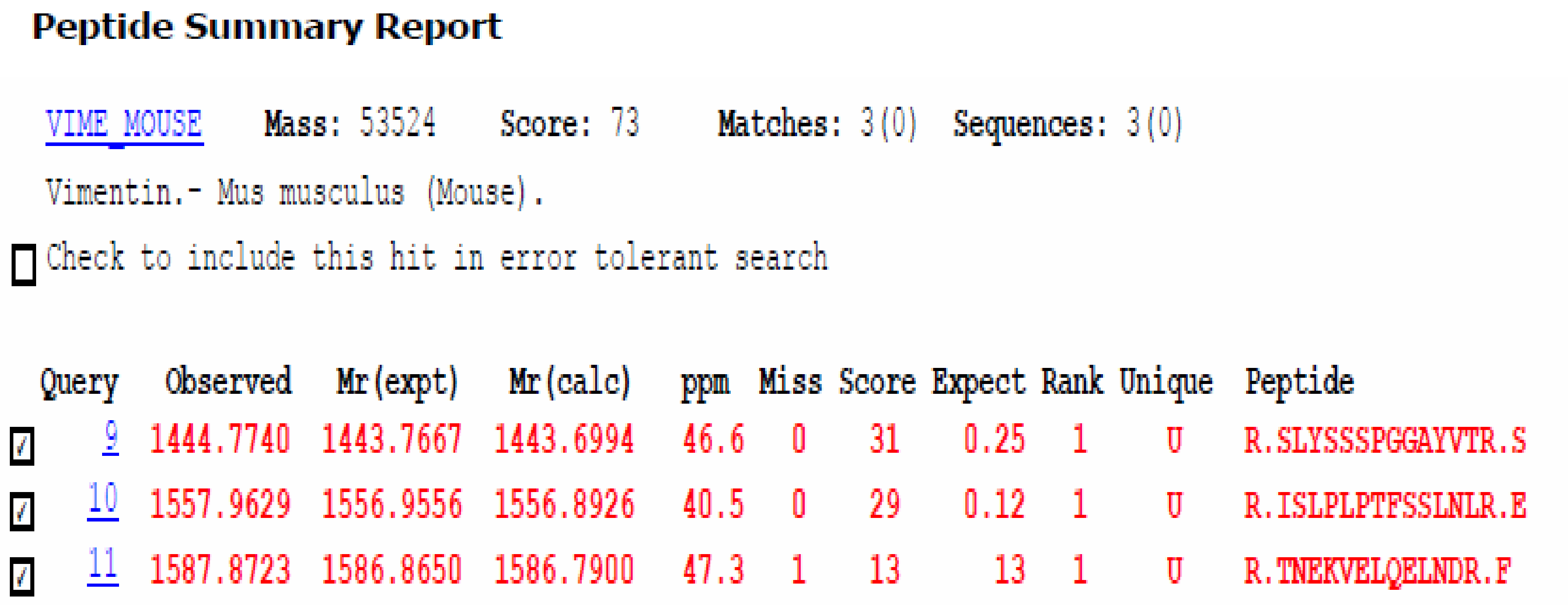


M5

4700 MS/MS Precursor 1556.96 Spec #1 MC[BP = 86.1, 1687]







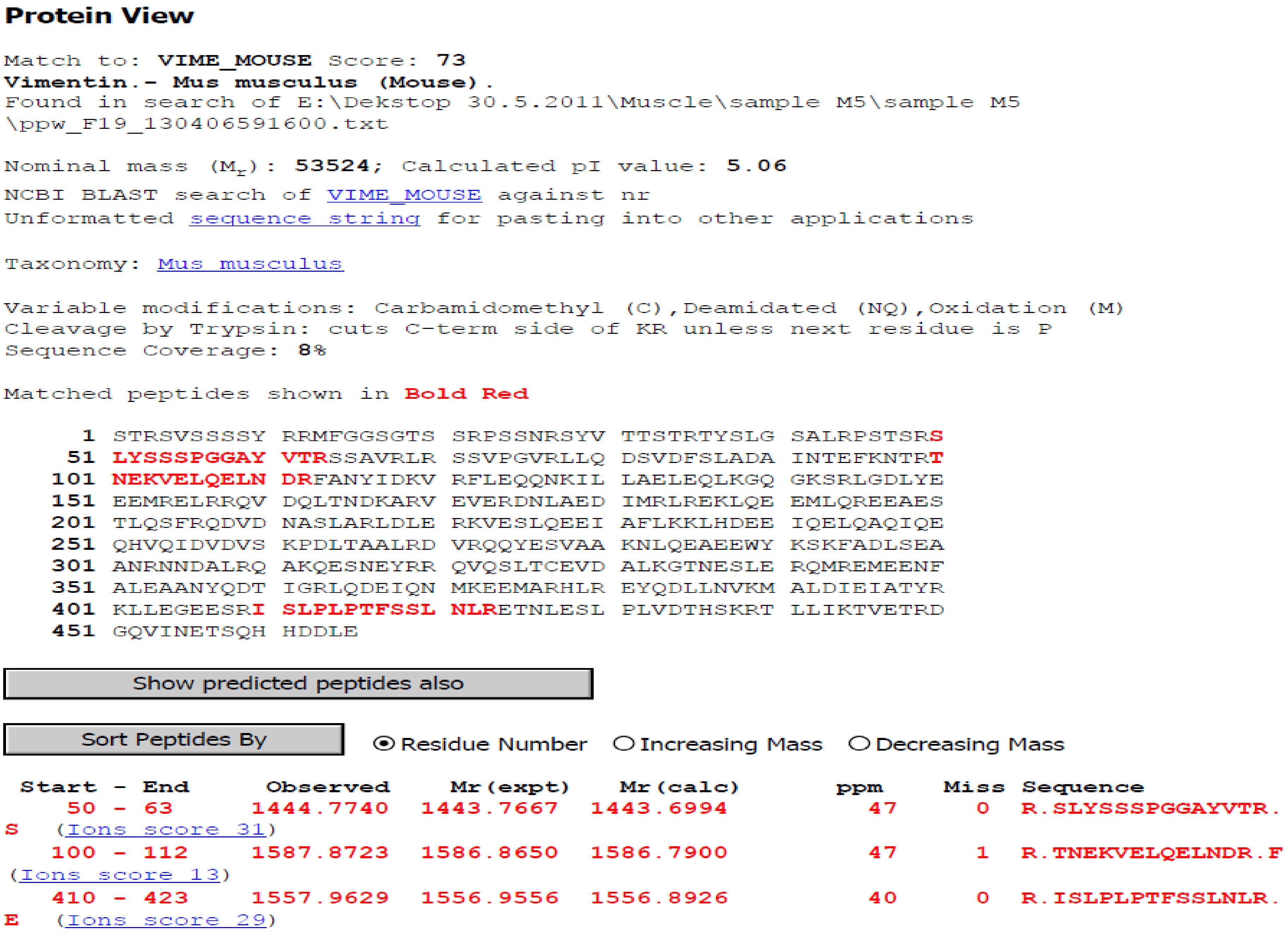
Peptide Summary Report

VIME_MOUSE **Mass:** 53524 **Score:** 73 **Matches:** 3(0) **Sequences:** 3(0)

Vimentin.- Mus musculus (Mouse).

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	9	1444.7740	1443.7667	1443.6994	46.6	0	31	0.25	1	U	R.SLYSSSPGGAYVTR.S
☑	10	1557.9629	1556.9556	1556.8926	40.5	0	29	0.12	1	U	R.ISLPLPTFSSLNLR.E
☑	11	1587.8723	1586.8650	1586.7900	47.3	1	13	13	1	U	R.TNEKVELQELNDR.F



Protein View

Match to: **VIME_MOUSE** Score: **73**
Vimentin.- Mus musculus (Mouse).
Found in search of E:\Dekstop 30.5.2011\Muscle\sample M5\sample M5
\ppw_F19_130406591600.txt

Nominal mass (M_r): **53524**; Calculated pI value: **5.06**
NCBI BLAST search of VIME_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

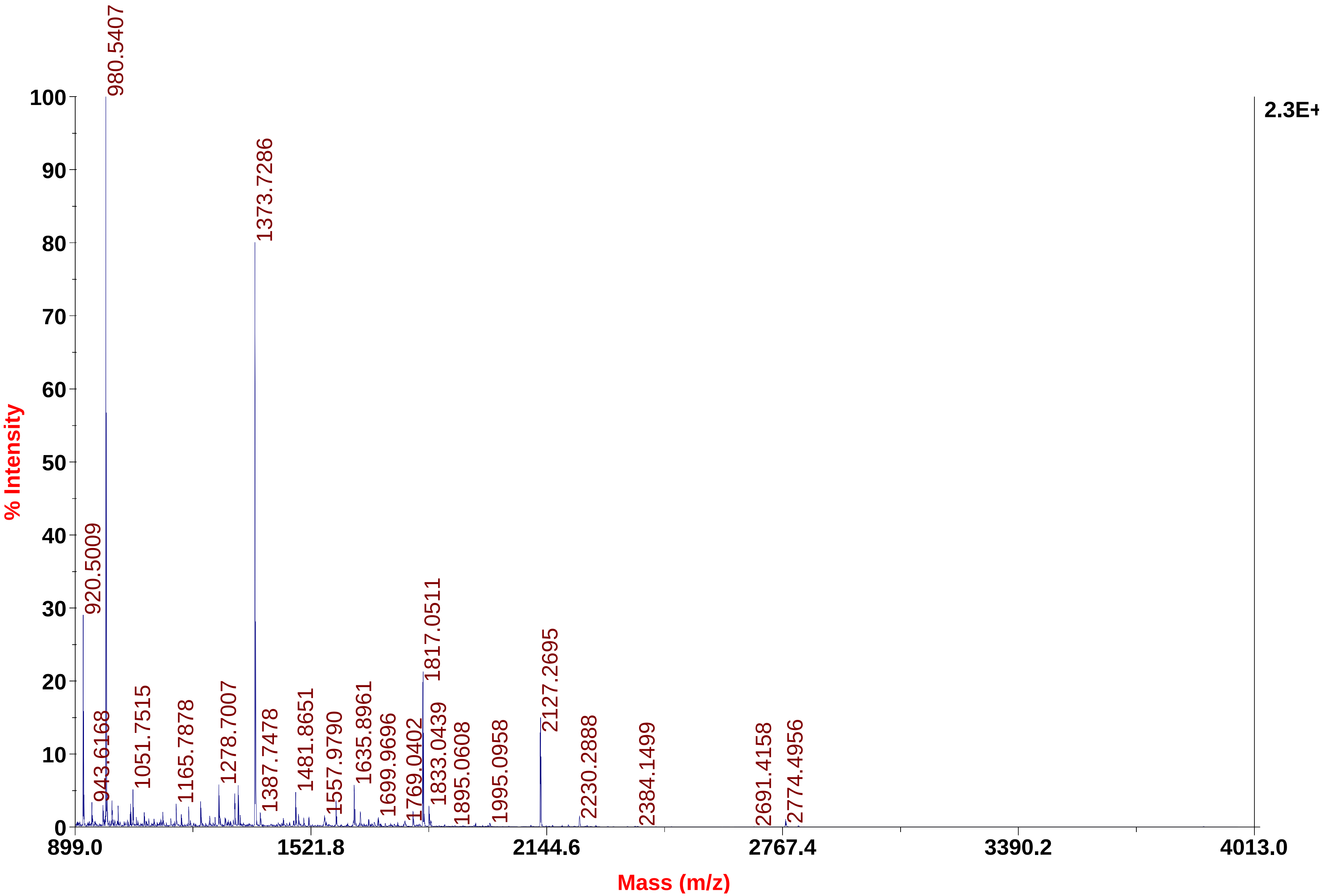
Matched peptides shown in **Bold Red**

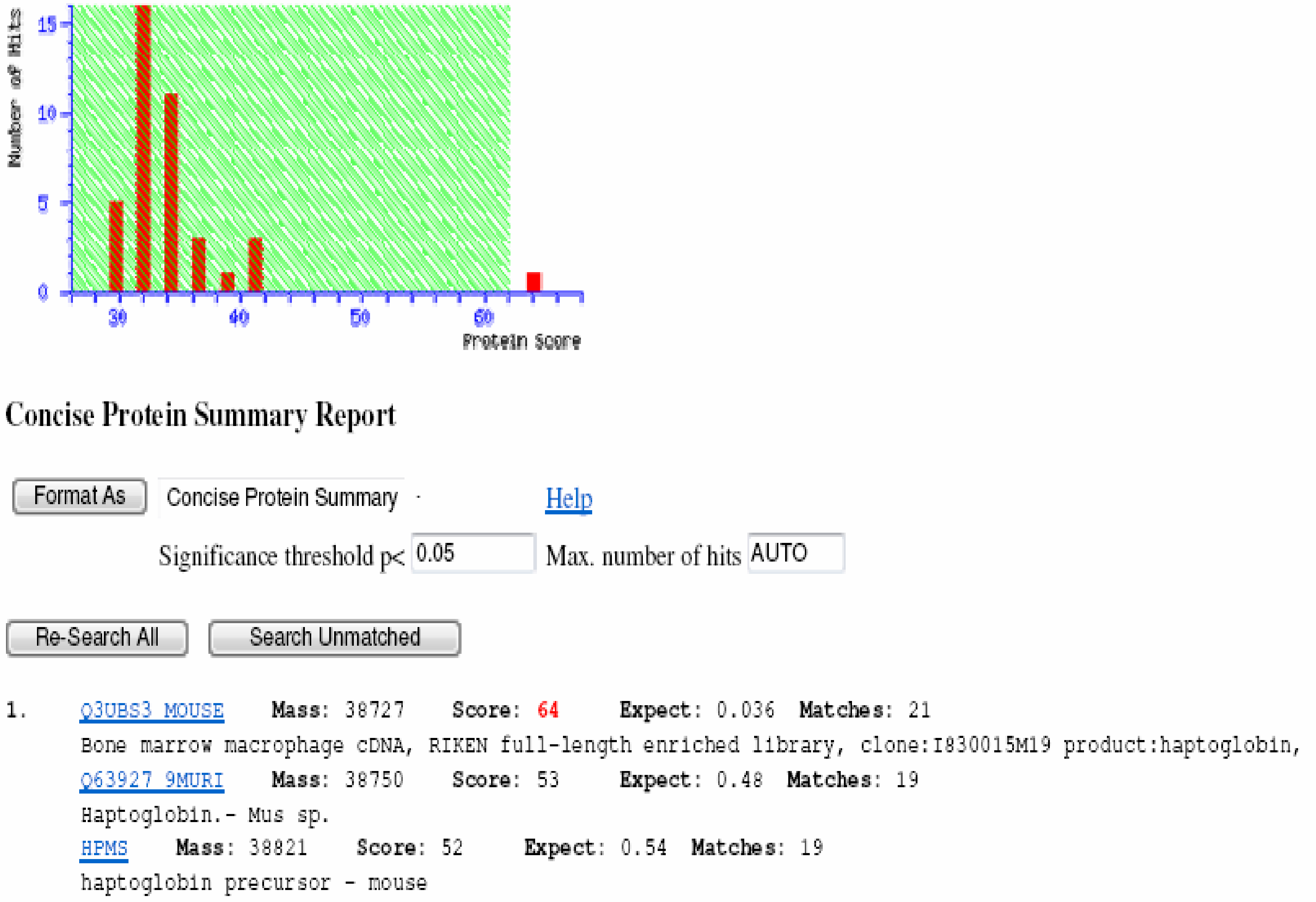
```
  1 STRSVSSSSY RRMFGGSGTS SRPSSNRSYV TTSTRTYSLG SALRPSTSRS
 51 LYSSSPGGAY VTRSSAVRLR SSVPGVRLLQ DSVDFSLADA INTEFKNTRT
101 NEKVELQELN DRFANYIDKV RFLEQQNKIL LAELEQLKGQ GKSRLGDLYE
151 EEMRELRRQV DQLTNDKARV EVERDNLAED IMRLREKLQE EMLQREEAES
201 TLQSFRQDVD NASLARLDLE RKVESLQEEI AFLKKLHDEE IQELQAQIQE
251 QHVQIDVDVS KPDLTAALRD VRQQYESVAA KNLQEAEEWY KSKFADLSEA
301 ANRNNDALRQ AKQESNEYRR QVQSLTCEVD ALKGTNESLE RQMREMEENF
351 ALEAANYQDT IGRLQDEIQN MKEEMARHLR EYQDLLNVKM ALDIEIATYR
401 KLLEGEESRI SLPLPTFSSL NLRETNLESL PLVDTHSKRT LLIKTVETRD
451 GQVINETSQH HDDLE
```

```
 Start - End     Observed    Mr(expt)    Mr(calc)      ppm    Miss  Sequence
    50 - 63     1444.7740   1443.7667   1443.6994       47      0   R.SLYSSSPGGAYVTR.
S   (Ions score 31)
   100 - 112    1587.8723   1586.8650   1586.7900       47      1   R.TNEKVELQELNDR.F
(Ions score 13)
   410 - 423    1557.9629   1556.9556   1556.8926       40      0   R.ISLPLPTFSSLNLR.
E   (Ions score 29)
```

Sample M6

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 980.5, 23361]



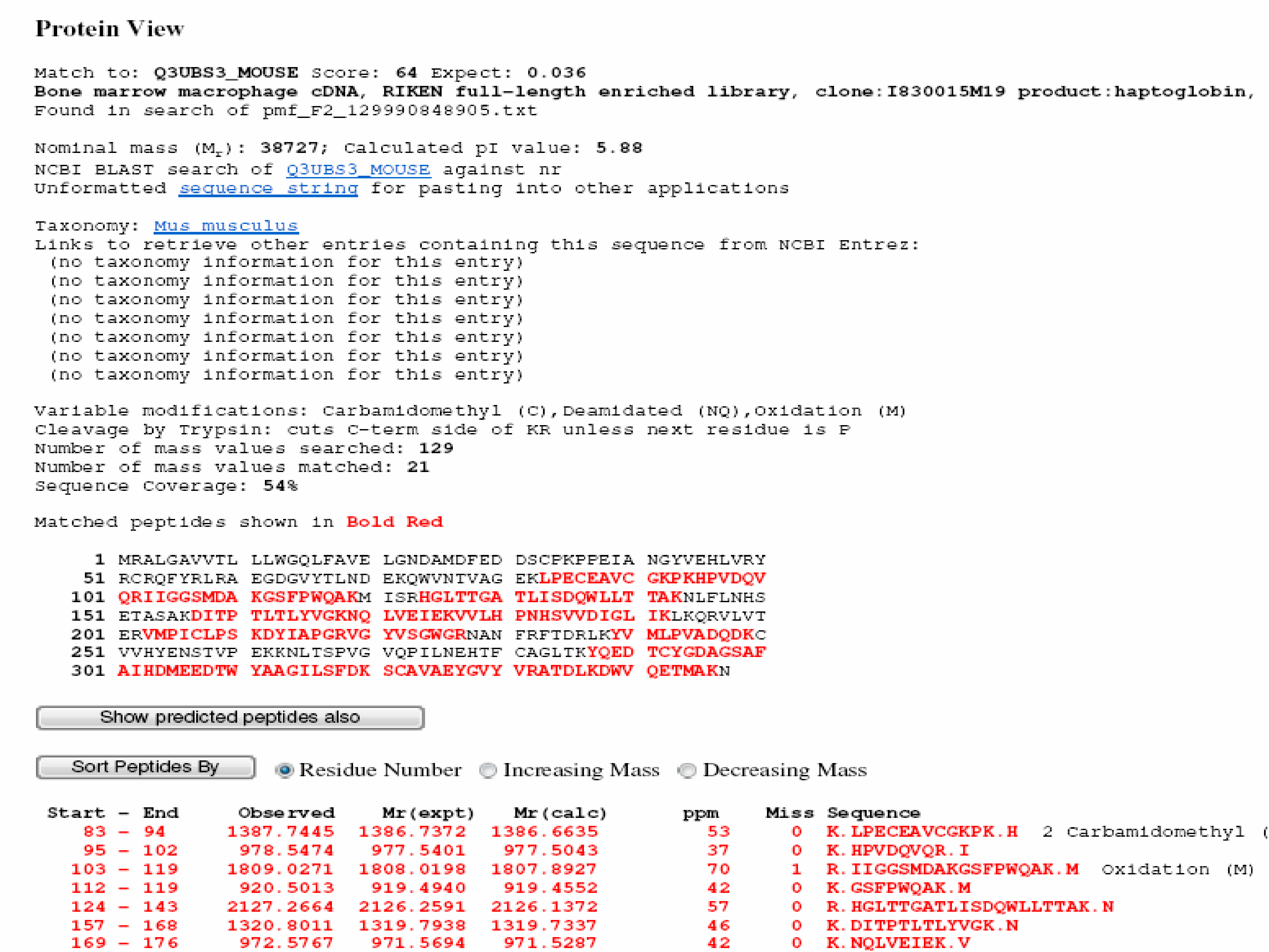


Concise Protein Summary Report

Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

1. Q3UBS3_MOUSE **Mass:** 38727 **Score:** 64 **Expect:** 0.036 **Matches:** 21
Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830015M19 product:haptoglobin,
Q63927_9MURI **Mass:** 38750 **Score:** 53 **Expect:** 0.48 **Matches:** 19
Haptoglobin.- Mus sp.
HPMS **Mass:** 38821 **Score:** 52 **Expect:** 0.54 **Matches:** 19
haptoglobin precursor - mouse



Protein View

Match to: **Q3UBS3_MOUSE** Score: **64** Expect: **0.036**
Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830015M19 product:haptoglobin,
Found in search of pmf_F2_129990848905.txt

Nominal mass (M_r): **38727**; Calculated pI value: **5.88**
NCBI BLAST search of Q3UBS3_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **129**
Number of mass values matched: **21**
Sequence Coverage: **54%**

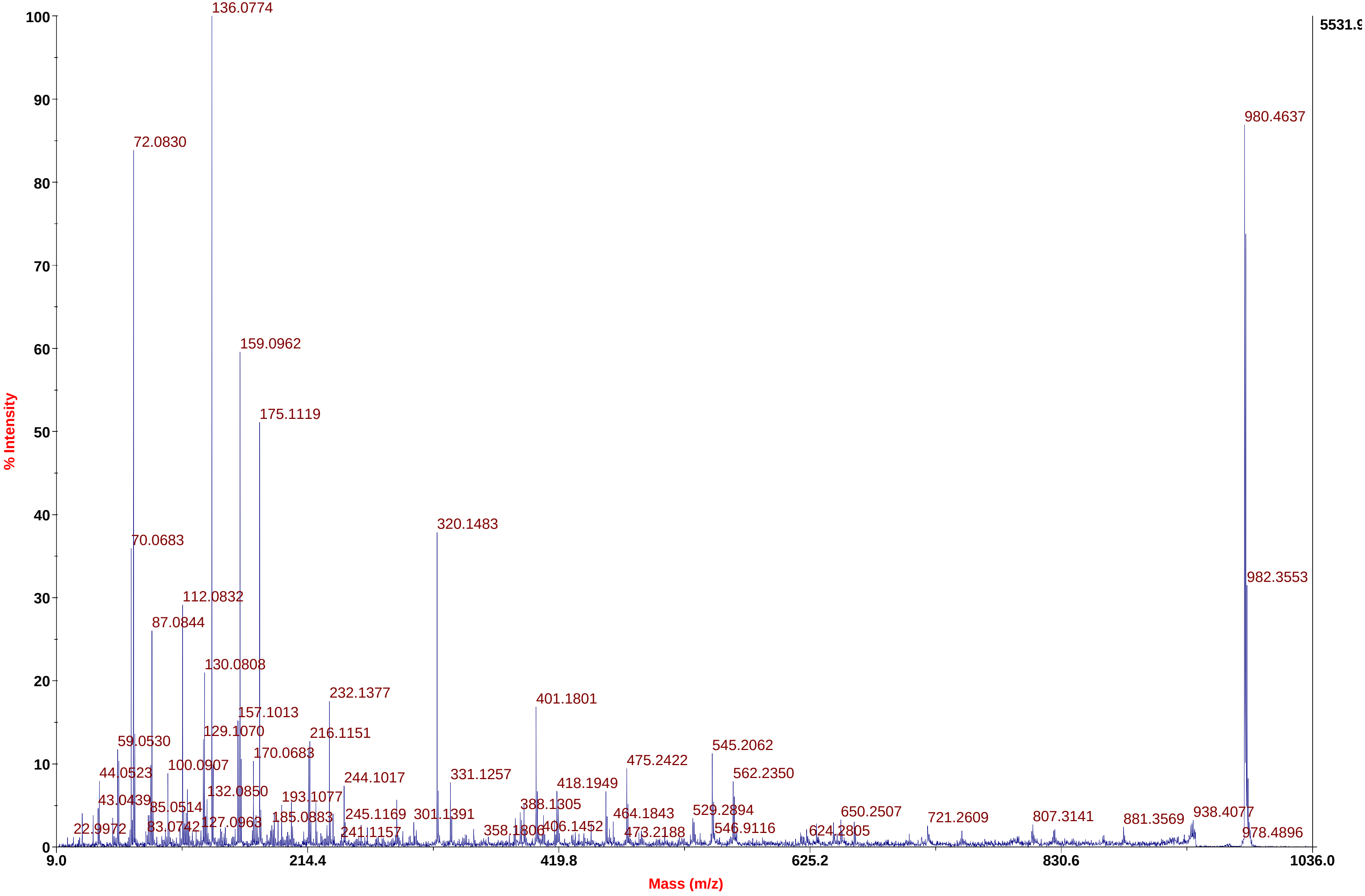
Matched peptides shown in **Bold Red**

```
  1 MRALGAVVTL LLWGQLFAVE LGNDAMDFED DSCPKPPEIA NGYVEHLVRY
 51 RCRQFYRLRA EGDGVYTLND EKQWVNTVAG EKLPECEAVC GKPKHPVDQV
101 QRIIGGSMDA KGSFPWQAKM ISRHGLTTGA TLISDQWLLT TAKNLFLNHS
151 ETASAKDITP TLTLYVGKNQ LVEIEKVVLH PNHSVVDIGL IKLKQRVLVT
201 ERVMPICLPS KDYIAPGRVG YVSGWGRNAN FRFTDRLKYV MLPVADQDKC
251 VVHYENSTVP EKKNLTSPVG VQPILNEHTF CAGLTKYQED TCYGDAGSAF
301 AIHDMEEDTW YAAGILSFDK SCAVAEYGVY VRATDLKDWV QETMAKN
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss  Sequence
   83 - 94      1387.7445  1386.7372  1386.6635       53     0   K.LPECEAVCGKPK.H  2 Carbamidomethyl (
   95 - 102      978.5474   977.5401   977.5043       37     0   K.HPVDQVQR.I
  103 - 119     1809.0271  1808.0198  1807.8927       70     1   R.IIGGSMDAKGSFPWQAK.M  Oxidation (M)
  112 - 119      920.5013   919.4940   919.4552       42     0   K.GSFPWQAK.M
  124 - 143     2127.2664  2126.2591  2126.1372       57     0   R.HGLTTGATLISDQWLLTTAK.N
  157 - 168     1320.8011  1319.7938  1319.7337       46     0   K.DITPTLTLYVGK.N
  169 - 176      972.5767   971.5694   971.5287       42     0   K.NQLVEIEK.V
```

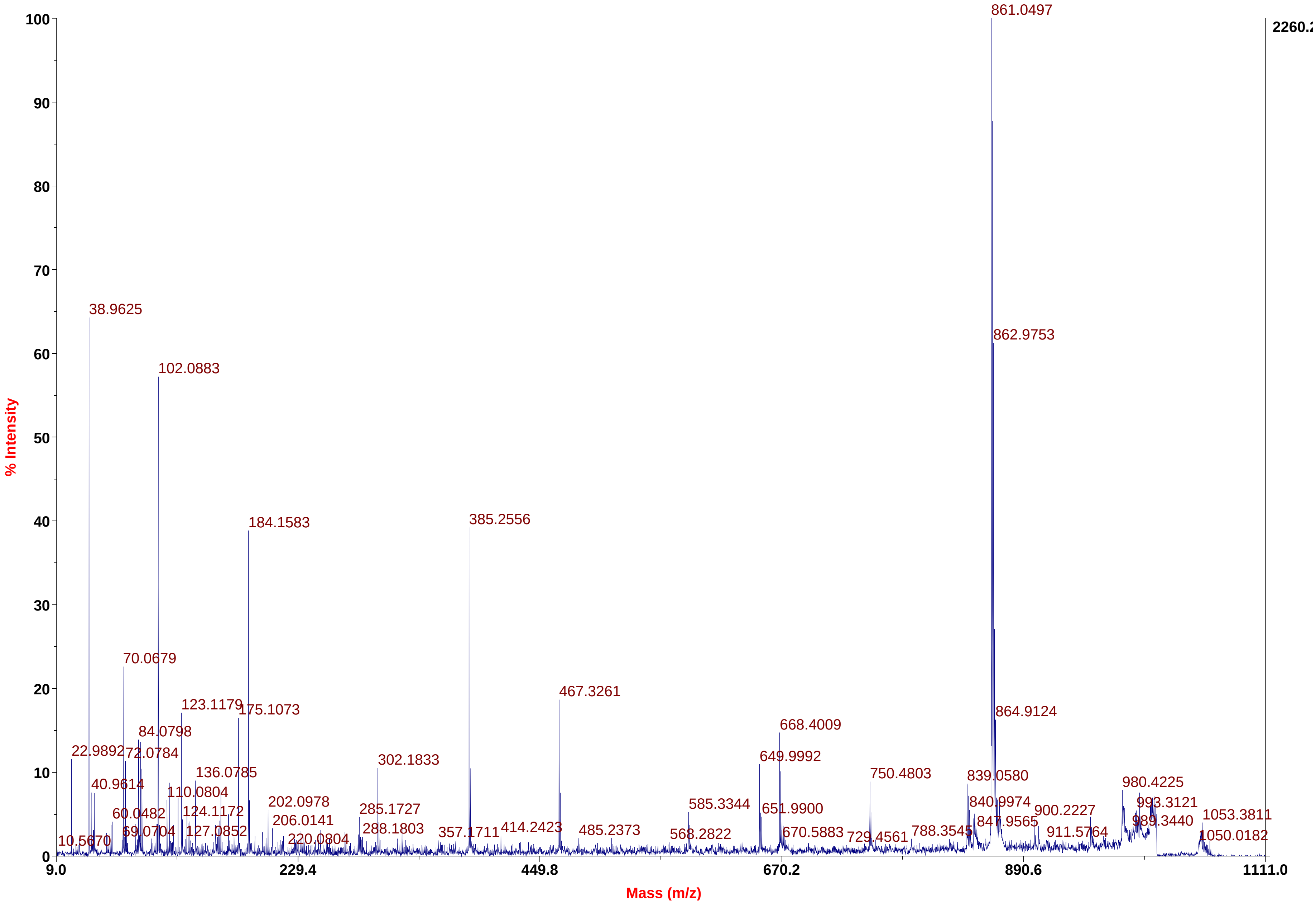
M6

4700 MS/MS Precursor 980.541 Spec #1 MC[BP = 136.1, 5532]



M6

4700 MS/MS Precursor 1051.75 Spec #1 MC[BP = 861.0, 2260]



Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05 Max. number of hits AUTO

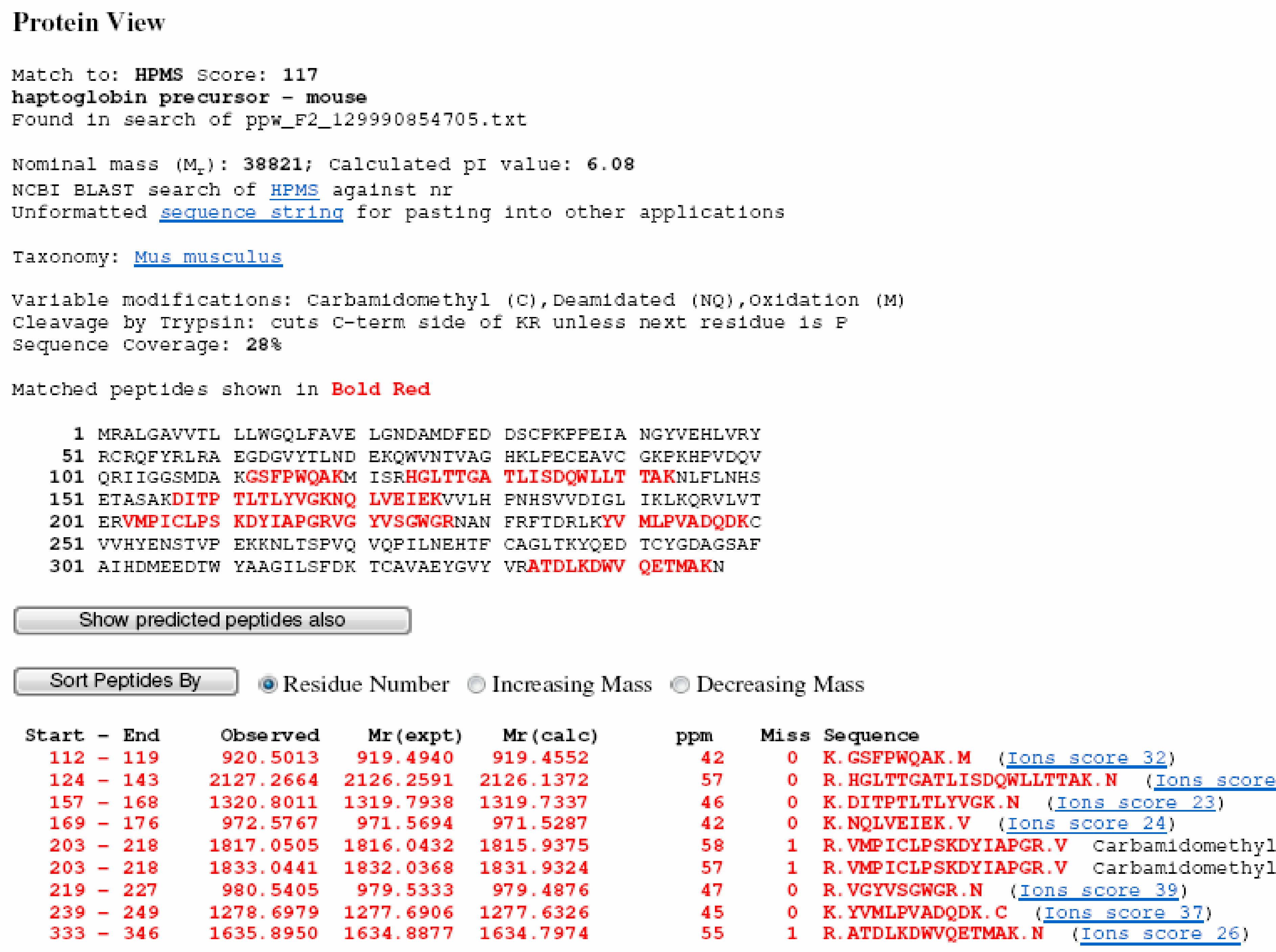
Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 Show sub-sets 0

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

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

1. HPMS **Mass**: 38821 **Score**: 117 **Matches**: 9(3) **Sequences**: 8(3) **emPAI**: 1.03
haptoglobin precursor - mouse
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	920.5013	919.4940	919.4552	42.2	0	32	0.17	1	U	K.GSFPWQAK.M
☑	3	972.5767	971.5694	971.5287	41.8	0	24	0.94	1	U	K.NQLVEIEK.V
☑	4	980.5405	979.5333	979.4876	46.6	0	39	0.03	1	U	R.VGYVSGWGR.N
☑	10	1278.6979	1277.6906	1277.6326	45.4	0	37	0.058	1	U	K.YVMLPVADQDK.C
☑	11	1320.8011	1319.7938	1319.7337	45.6	0	23	0.66	1	U	K.DITPTLTLYVGK.N
☑	16	1635.8950	1634.8877	1634.7974	55.3	1	26	0.76	1	U	R.ATDLKDWVQETMAK.N
☑	18	1817.0505	1816.0432	1815.9375	58.2	1	52	0.0013	1	U	R.VMPICLPSKDYIAPGR.V + Car
☑	19	1833.0441	1832.0368	1831.9324	57.0	1	(22)	1.3	1	U	R.VMPICLPSKDYIAPGR.V + Car
☑	38	2127.2664	2126.2591	2126.1372	57.4	0	57	0.00022	1	U	R.HGLTTGATLISDQWLLTTAK.N



Protein View

```
Match to: HPMS Score: 117
haptoglobin precursor - mouse
Found in search of ppw_F2_129990854705.txt

Nominal mass (Mr): 38821; Calculated pI value: 6.08
NCBI BLAST search of HPMS against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

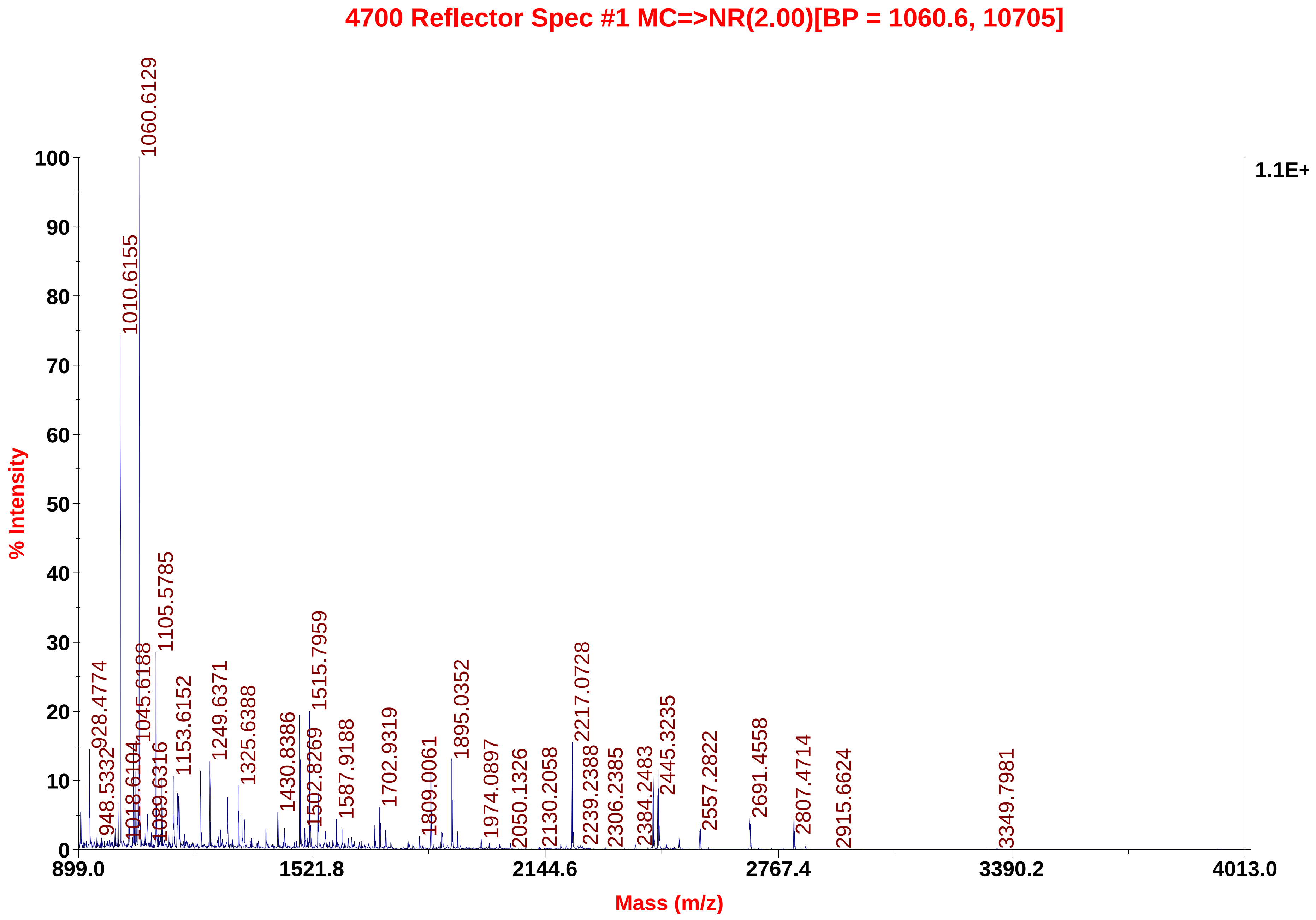
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 28%

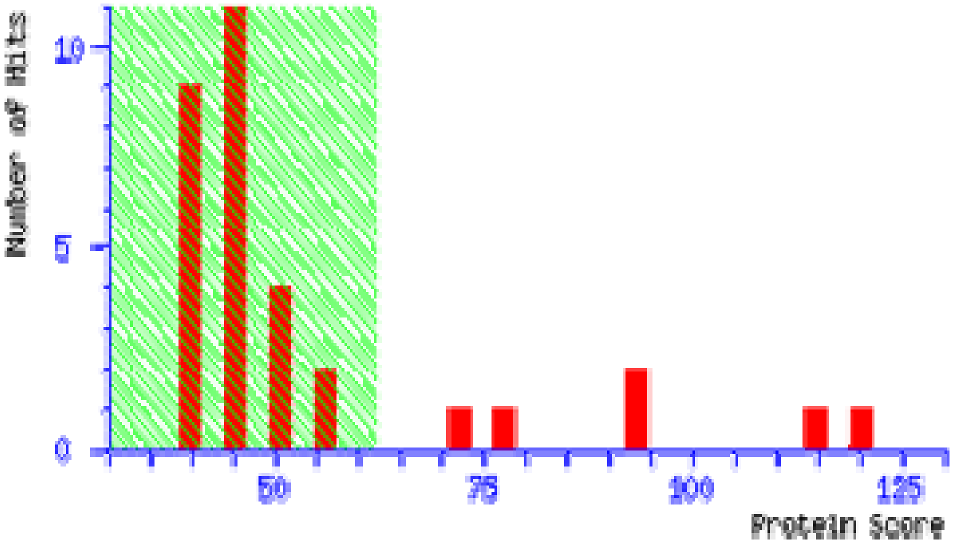
Matched peptides shown in Bold Red

      1 MRALGAVVTL LLWGQLFAVE LGNDAMDFED DSCPKPPEIA NGYVEHLVRY
     51 RCRQFYRLRA EGDGVYTLND EKQWVNTVAG HKLPECEAVC GKPKHPVDQV
    101 QRIIGGSMDA KGSFPWQAKM ISRHGLTTGA TLISDQWLLT TAKNLFLNHS
    151 ETASAKDITP TLTLYVGKNQ LVEIEKVVLH PNHSVVDIGL IKLKQRVLVT
    201 ERVMPICLPS KDYIAPGRVG YVSGWGRNAN FRFTDRLKYV MLPVADQDKC
    251 VVHYENSTVP EKKNLTSPVQ VQPILNEHTF CAGLTKYQED TCYGDAGSAF
    301 AIHDMEEDTW YAAGILSFDK TCAVAEYGVY VRATDLKDWV QETMAKN
```

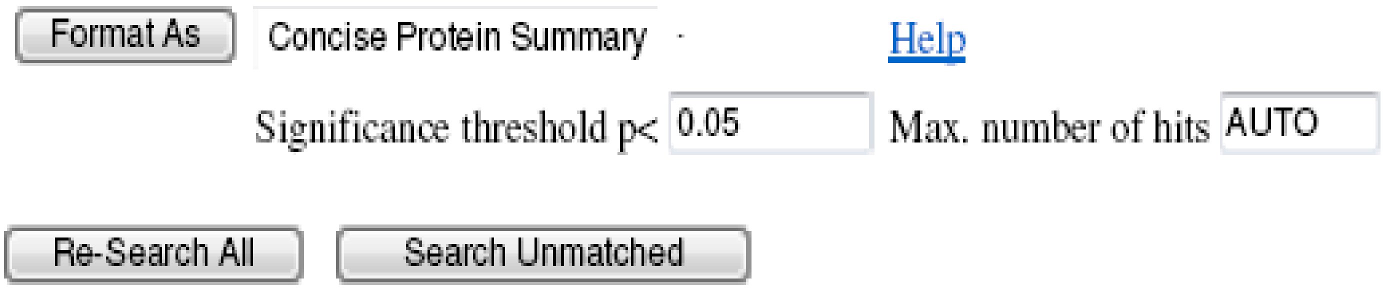
```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
   112 - 119     920.5013   919.4940   919.4552      42     0  K.GSFPWQAK.M   (Ions score 32)
   124 - 143    2127.2664  2126.2591  2126.1372      57     0  R.HGLTTGATLISDQWLLTTAK.N   (Ions score
   157 - 168    1320.8011  1319.7938  1319.7337      46     0  K.DITPTLTLYVGK.N   (Ions score 23)
   169 - 176     972.5767   971.5694   971.5287      42     0  K.NQLVEIEK.V   (Ions score 24)
   203 - 218    1817.0505  1816.0432  1815.9375      58     1  R.VMPICLPSKDYIAPGR.V   Carbamidomethyl
   203 - 218    1833.0441  1832.0368  1831.9324      57     1  R.VMPICLPSKDYIAPGR.V   Carbamidomethyl
   219 - 227     980.5405   979.5333   979.4876      47     0  R.VGYVSGWGR.N   (Ions score 39)
   239 - 249    1278.6979  1277.6906  1277.6326      45     0  K.YVMLPVADQDK.C   (Ions score 37)
   333 - 346    1635.8950  1634.8877  1634.7974      55     1  R.ATDLKDWVQETMAK.N   (Ions score 26)
```

Sample M7


4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1060.6, 10705]
% Intensity
Mass (m/z)
1.1E+
100
90
80
70
60
50
40
30
20
10
0
899.0
1521.8
2144.6
2767.4
3390.2
4013.0
928.4774
948.5332
1010.6155
1018.6104
1045.6188
1060.6129
1089.6316
1105.5785
1153.6152
1249.6371
1325.6388
1430.8386
1502.8269
1515.7959
1587.9188
1702.9319
1809.0061
1895.0352
1974.0897
2050.1326
2130.2058
2217.0728
2239.2388
2306.2385
2384.2483
2445.3235
2557.2822
2691.4558
2807.4714
2915.6624
3349.7981



Concise Protein Summary Report



Concise Protein Summary

Significance threshold p< 0.05

Max. number of hits AUTO

1. Q32P18_MOUSE **Mass:** 223203 **Score:** 120 **Expect:** 9.2e-08 **Matches:** 95
   Myosin, heavy polypeptide 1, skeletal muscle, adult.- Mus musculus (Mouse).
   Q9ESW6_MOUSE **Mass:** 54545 **Score:** 40 **Expect:** 9.2 **Matches:** 31
   Myosin heavy chain IIX (Fragment).- Mus musculus (Mouse).

Protein View

```
Match to: Q32P18_MOUSE Score: 120 Expect: 9.2e-08
Myosin, heavy polypeptide 1, skeletal muscle, adult.- Mus musculus (Mous
Found in search of pmf_G2_12990848906.txt

Nominal mass (Mr): 223203; Calculated pI value: 5.60
NCBI BLAST search of Q32P18_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entre
  (no taxonomy information for this entry)
  (no taxonomy information for this entry)
  (no taxonomy information for this entry)

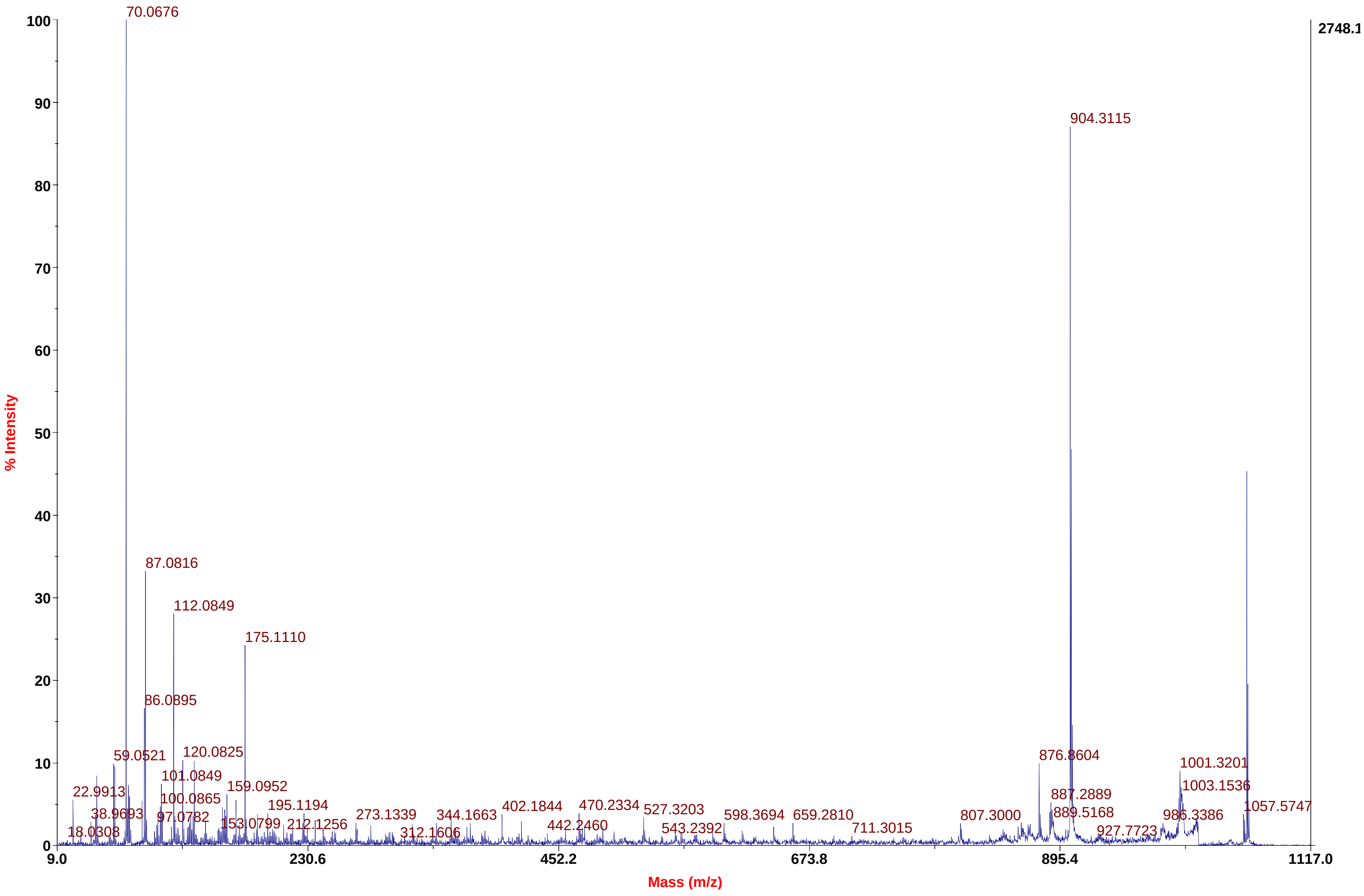
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 167
Number of mass values matched: 95
Sequence Coverage: 48%

Matched peptides shown in Bold Red

     1 MSSDAEMAVF GEAAPYLRKS EKERIEAQNK PFDAKSSVFV VDAKESFVKA
    51 TVQSREGGKV TAKTEGGTTV TVKDDQVYPM NPPKYDKIED MAMMTHLHEP
   101 AVLYNLKERY AAWMIYTYSG LFCVTVNPYK WLPVYNAEVV AAYRGKKRQE
   151 APPHIFSISD NAYQFMLTDR ENQSILITGE SGAGKTVNTK RVIQYFATIA
   201 VTGEKKKEEA TSGKMQGTLE DQIISANPLL EAFGNAKTVR NDNSSRFGKF
   251 IRIHFGTTGK LASADIETYL LEKSRVTFQL KAERSYHIFY QIMSNKKPDL
   301 IEMLLITTNP YDYAFVSQGE ITVPSIDDQE ELMATDSAID ILGFTSDERV
   351 SIYKLTGAVM HYGNMKFKQK QREEQAEPDG TEVADKAAYL QNLNSADLLK
   401 ALCYPRVKVG NEYVTKGQTV QQVYNSVGAL AKAVYEKMFL WMVTRINQQL
   451 DTKQPRQYFI GVLDIAGFEI FDFNSLEQLC INFTNEKLQQ FFNHHMFVLE
   501 QEEYKKEGIE WEFIDFGMDL AACIELIEKP MGIFSILEEE CMFPKATDTS
   551 FKNKLYEQHL GKSNNFQKPK PAKGKVEAHF SLVHYAGTVD YNIAGWLDKN
   601 KDPLNETVVG LYQKSSMKTL AYLFSGAAAA AEAESGGGGG KKGAKKKGSS
   651 FQTVSALFRE NLNKLMTNLR STHPHFVRCI IPNETKTPGA MEHELVLHQL
   701 RCNGVLEGIR ICRKGFPSRI LYADFKQRYK VLNASAIPEG QFIDSKKASE
   751 KLLGSIDIDH TQYKFGHTKV FFKAGLLGLL EEMRDDKLAQ LITRTQAMCR
   801 GYLARVEYQK MVERRESIFC IQYNVRAFMN VKHWPWMKLY FKIKPLLKSA
   851 ETEKEMANMK EEFEKAKENL AKAEAKRKEL EEKMVALMQE KNDLQLQVQS
   901 EADSLADAEE RCDQLIKTKI QLEAKIKEVT ERAEDEEEIN AELTAKKRKL
   951 EDECSELKKD IDDLELTLAK VEKEKHATEN KVKNLTEEMA GLDETIAKLT
  1001 KEKKALQEAH QQTLDDLQAE EDKVNTLTKA KIKLEQQVDD LEGSLEQEKK
  1051 IRMDLERAKR KLEGDLKLAQ ESTMDVENDK QQLDEKLKKK EFEMSNLQSK
  1101 IEDEQALGMQ LQKKIKELQA RIEELEEEIE AERASRAKAE KQRSDLSREL
  1151 EEISERLEEA GGATSAQIEM NKKREAEFQK MRRDLEEATL QHEATAATLR
  1201 KKHADSVAEL GEQIDNLQRV KQKLEKEKSE MKMEIDDLAS NMEVISKSKG
  1251 NLEKMCRTLE DQVSELKTKE EEQQRLINEL TAQRGRLQTE SGEYSRQLDE
  1301 KDSLVSQLSR GKQAFTQQIE ELKRQLEEEI KAKSALAHAL QSSRHDCDLL
  1351 REQYEEEQEA KAELQRAMSK ANSEVAQWRT KYETDAIQRT EELEEAKKKL
  1401 AQRLQDAEEH VEAVNAKCAS LEKTKQRLQN EVEDLMIDVE RTNAACAALD
  1451 KKQRNFDKIL AEWKQKYEET HAELEASQKE SRSLSTELFK IKNAYEESLD
  1501 HLETLKRENK NLQQEISDLT EQIAEGGKRI HELEKIKKQI EQEKSELQAA
  1551 LEEAEASLEH EEGKILRIQL ELNQVKSEID RKIAEKDEEI DQLKRNHIRV
  1601 VESMQSTLDA EIRSRNDAIR LKKKMEGDLN EMEIQLNHSN RMAAEALRNY
  1651 RNTQGILKDT QLHLDDALRG QEDLKEQLAM VERRANLLQA EIEELRATLE
  1701 QTERSRKIAE QELLDASERV QLLHTQNTSL INTKKKLETD ISQIQGEMED
  1751 IVQEARNAEE KAKKAITDAA MMAEELKKEQ DTSAHLERMK KNLEQTVKDL
  1801 QHRLDEAEQL ALKGGKKQIQ KLEARVRELE GEVENEQKRN VEAIKGLRKH
  1851 ERRVKELTYQ TEEDRKNVLR LQDLVDKLQS KVKAYKRQAE EAEEQSNVNL
  1901 AKFRKIQHEL EEAEERADIA ESQVNKLRVK SREVHTKIIS EE
```

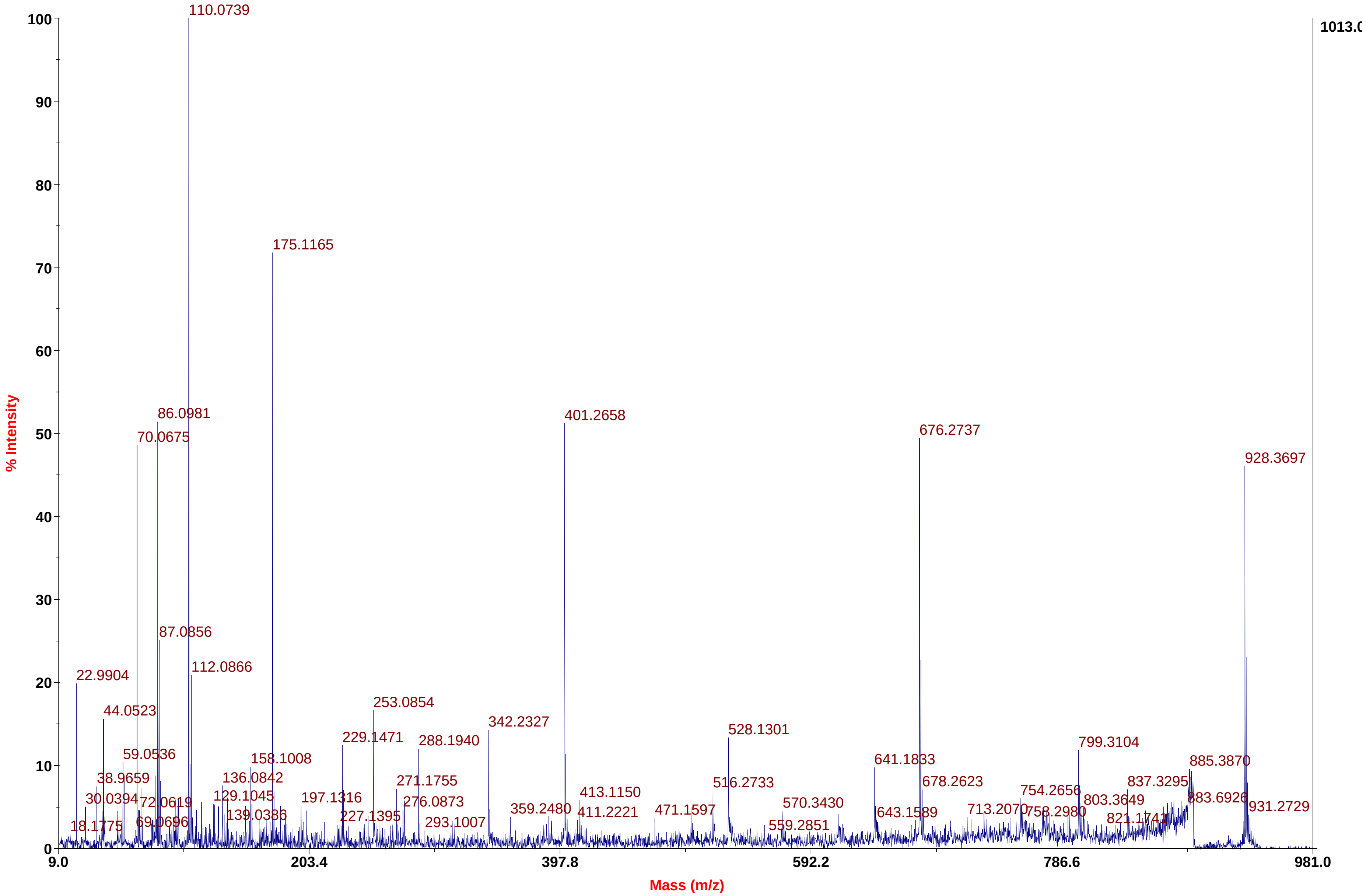
M7

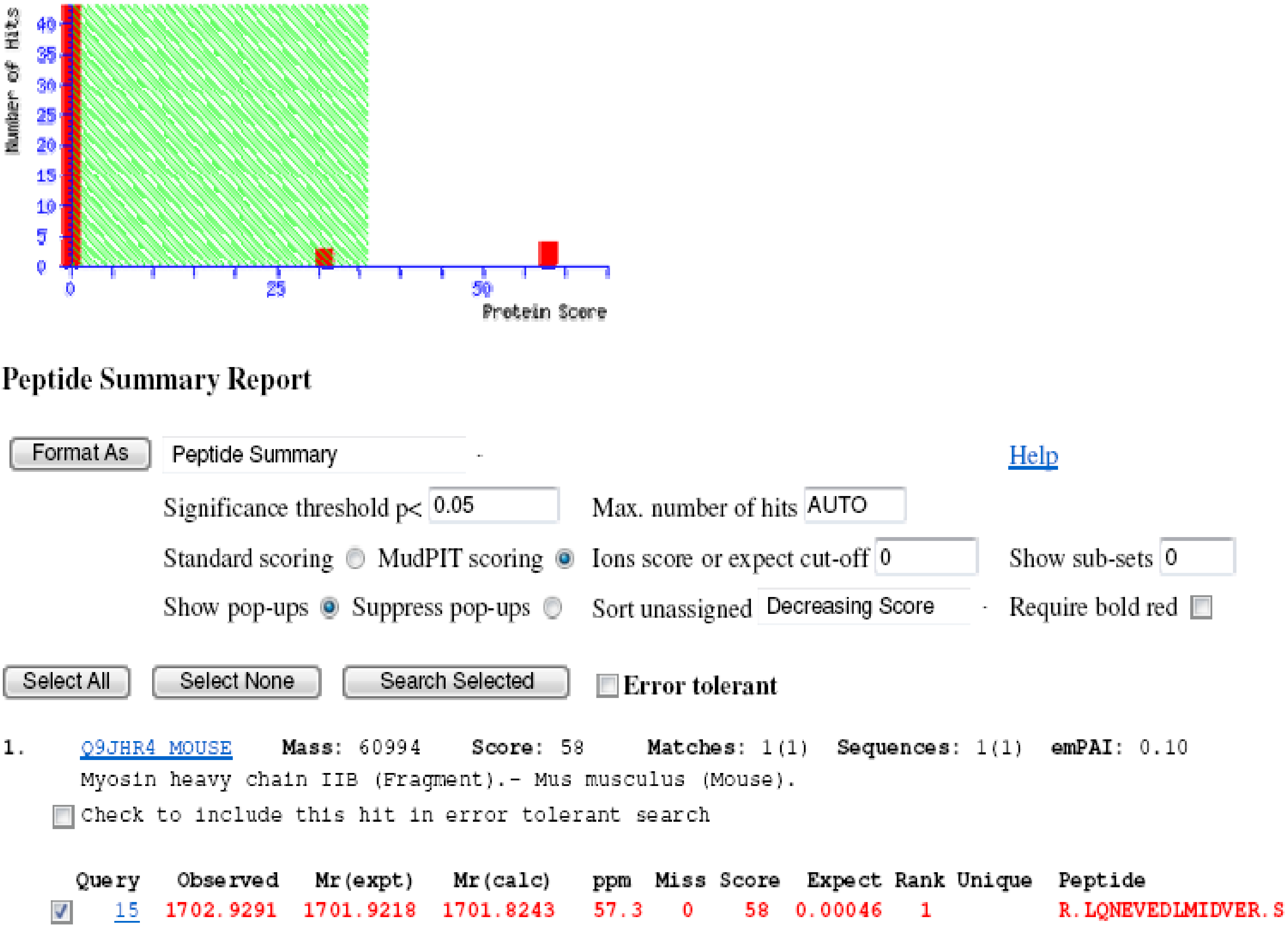
4700 MS/MS Precursor 1057.65 Spec #1 MC[BP = 70.1, 2748]



M7

4700 MS/MS Precursor 928.478 Spec #1 MC[BP = 110.1, 1013]





Peptide Summary Report

Peptide Summary

Significance threshold p< 0.05 Max. number of hits AUTO

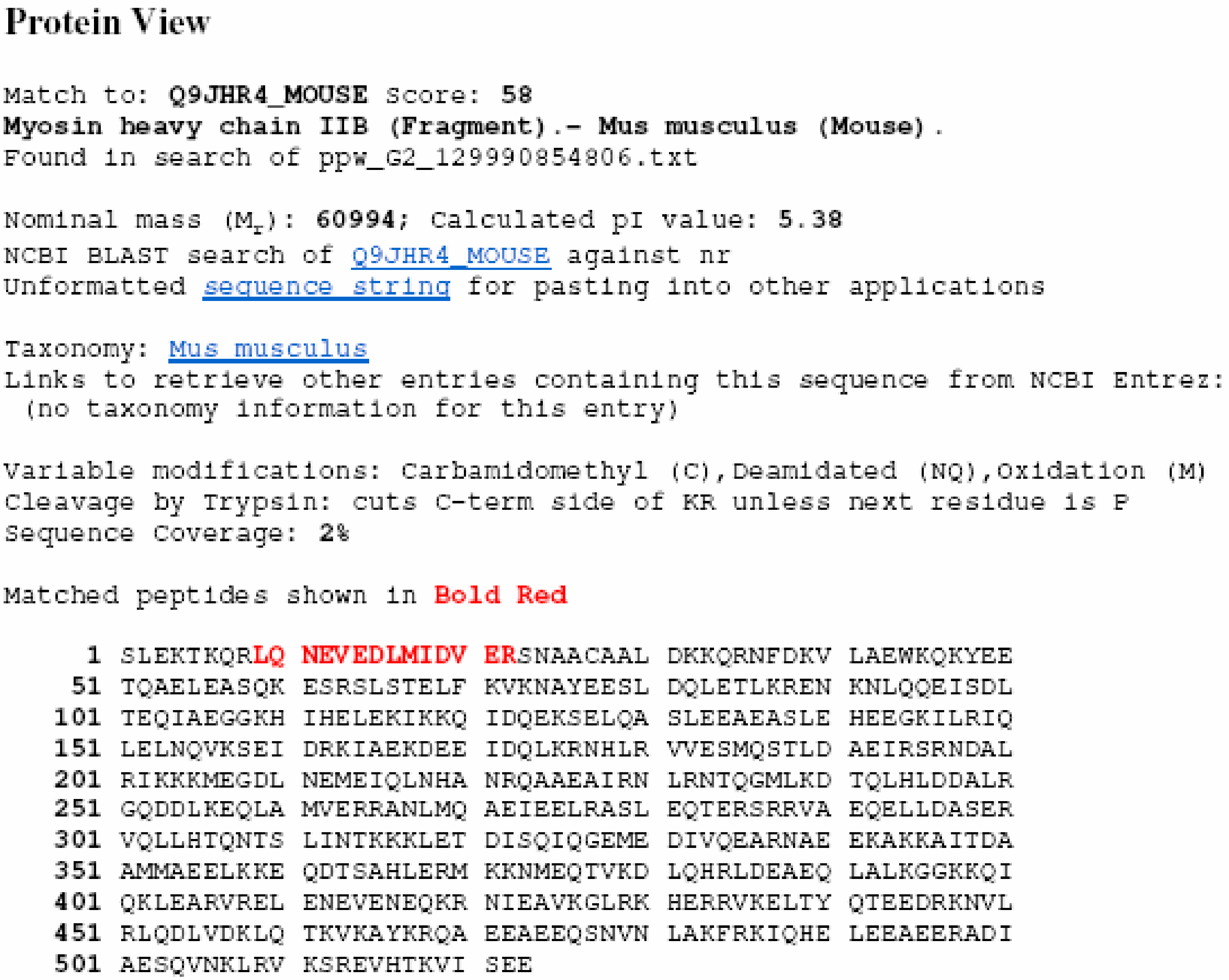
Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 Show sub-sets 0

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

☐ Error tolerant

```
1.     Q9JHR4_MOUSE     Mass: 60994     Score: 58     Matches: 1(1)  Sequences: 1(1)  emPAI: 0.10
       Myosin heavy chain IIB (Fragment).- Mus musculus (Mouse).
     ☐ Check to include this hit in error tolerant search

      Query    Observed     Mr(expt)     Mr(calc)     ppm   Miss  Score   Expect  Rank  Unique   Peptide
    ☑   15    1702.9291    1701.9218    1701.8243    57.3    0     58   0.00046    1            R.LQNEVEDLMIDVER.S
```



Protein View

Match to: **Q9JHR4_MOUSE** Score: **58**
Myosin heavy chain IIB (Fragment).- Mus musculus (Mouse).
Found in search of ppw_G2_129990854806.txt

Nominal mass (M_r): **60994**; Calculated pI value: **5.38**
NCBI BLAST search of Q9JHR4_MOUSE against nr
Unformatted sequence string for pasting into other applications

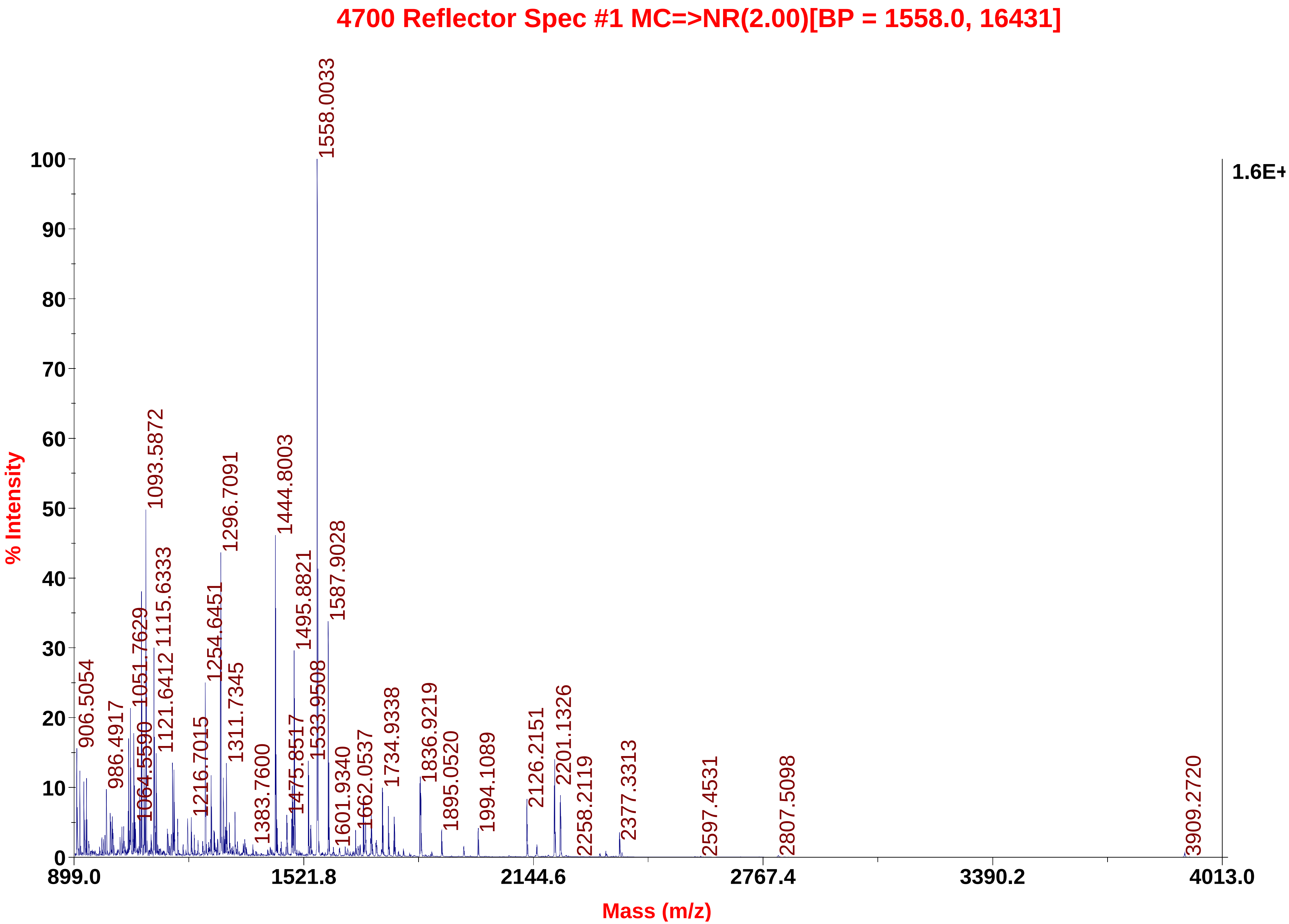
Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)

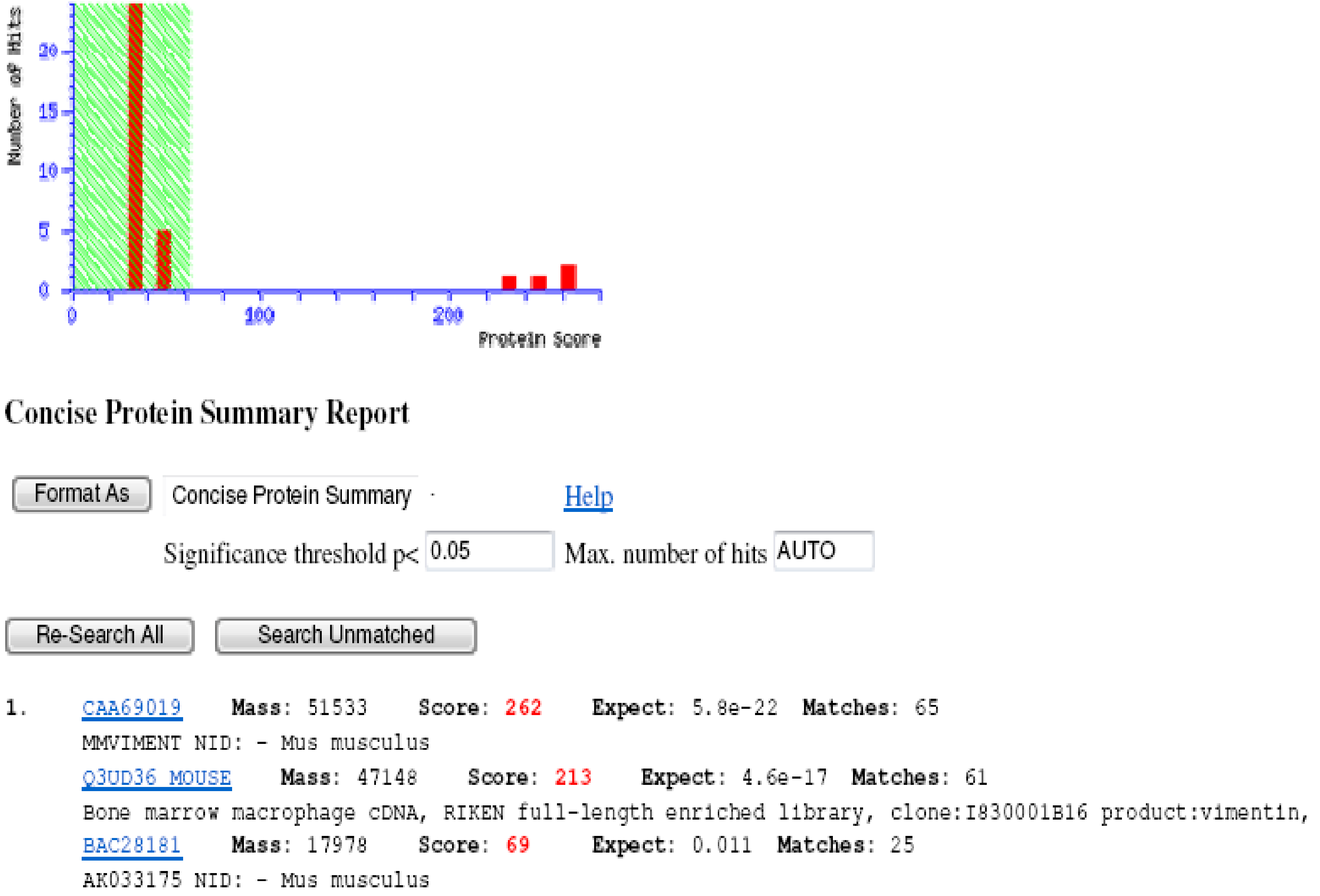
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **2%**

Matched peptides shown in **Bold Red**

```
  1 SLEKTKQRLQ NEVEDLMIDV ERSNAACAAL DKKQRNFDKV LAEWKQKYEE
 51 TQAELEASQK ESRSLSTELF KVKNAYEESL DQLETLKREN KNLQQEISDL
101 TEQIAEGGKH IHELEKIKKQ IDQEKSELQA SLEEAEASLE HEEGKILRIQ
151 LELNQVKSEI DRKIAEKDEE IDQLKRNHLR VVESMQSTLD AEIRSRNDAL
201 RIKKKMEGDL NEMEIQLNHA NRQAAEAIRN LRNTQGMLKD TQLHLDDALR
251 GQDDLKEQLA MVERRANLMQ AEIEELRASL EQTERSRRVA EQELLDASER
301 VQLLHTQNTS LINTKKKLET DISQIQGEME DIVQEARNAE EKAKKAITDA
351 AMMAEELKKE QDTSAHLERM KKNMEQTVKD LQHRLDEAEQ LALKGGKKQI
401 QKLEARVREL ENEVENEQKR NIEAVKGLRK HERRVKELTY QTEEDRKNVL
451 RLQDLVDKLQ TKVKAYKRQA EEAEEQSNVN LAKFRKIQHE LEEAEERADI
501 AESQVNKLRV KSREVHTKVI SEE
```

Sample M8


4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1558.0, 16431]
% Intensity
100
90
80
70
60
50
40
30
20
10
0
1.6E+
Mass (m/z)
899.0
1521.8
2144.6
2767.4
3390.2
4013.0
906.5054
986.4917
1051.7629
1064.5590
1093.5872
1115.6333
1121.6412
1216.7015
1254.6451
1296.7091
1311.7345
1383.7600
1444.8003
1475.8517
1495.8821
1533.9508
1558.0033
1587.9028
1601.9340
1662.0537
1734.9338
1836.9219
1895.0520
1994.1089
2126.2151
2201.1326
2258.2119
2377.3313
2597.4531
2807.5098
3909.2720



Concise Protein Summary Report

Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.     CAA69019     Mass: 51533     Score: 262     Expect: 5.8e-22  Matches: 65
       MMVIMENT NID: - Mus musculus
       Q3UD36_MOUSE     Mass: 47148     Score: 213     Expect: 4.6e-17  Matches: 61
       Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830001B16 product:vimentin,
       BAC28181     Mass: 17978     Score: 69     Expect: 0.011  Matches: 25
       AK033175 NID: - Mus musculus
```

Protein View

```
Match to: CAA69019 Score: 262 Expect: 5.8e-22
MMVIMENT NID:  – Mus musculus
Found in search of pmf_H2_129990848907.txt

Nominal mass (Mr): 51533; Calculated pI value: 4.96
NCBI BLAST search of CAA69019 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 162
Number of mass values matched: 65
Sequence Coverage: 89%

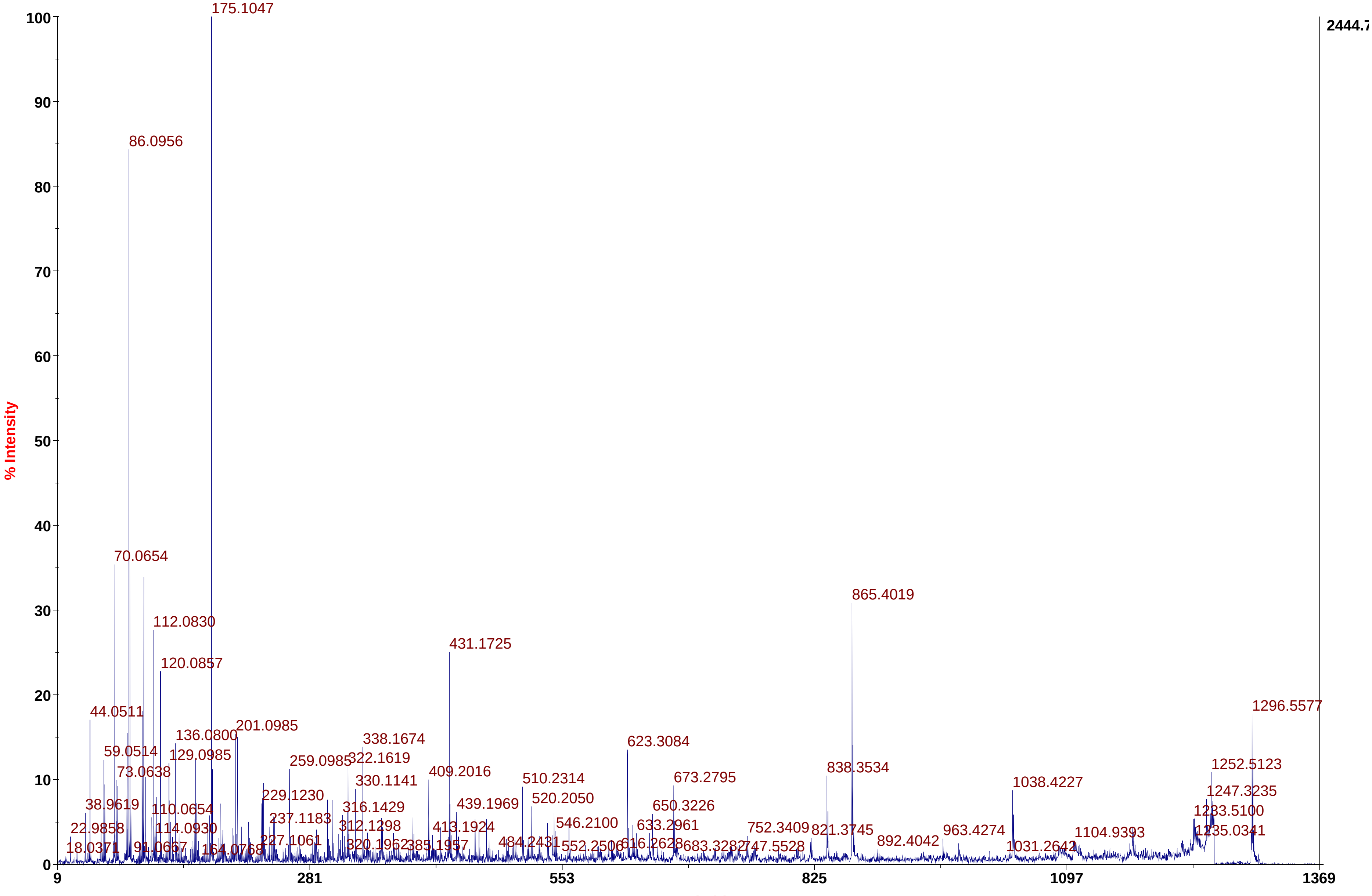
Matched peptides shown in Bold Red

     1 SSRPSSNRSY VTTSTRTYSL GSALRPSTSR SLYSSSPGGA YVTRSSAVRL
    51 RSSVPGVRLL QDSVDFSLAD AINTEFKNTR TNEKVELQEL NDRFANYIDK
   101 VRFLEQQNKI LLAELEQLKG QGKSRLGDLY EEEMRELRRQ VDQLTNDKAR
   151 VEVERDNLAE DIMRLREKLQ EEMLQREEAE STLQSFRQDV DNASLARLDL
   201 ERKVESLQEE IAFLKKLHDE EIQELQAQIQ EQHVQIDVDV SKPDLTAALR
   251 DVRQQYESVA AKNLQEAEEW YKSKFADLSE AANRNNDALR QAKQESNEYR
   301 RQVQSLTCEV DALKGTNESL ERQMREMEEN FALEAANYQD TIGRLQDEIQ
   351 NMKEEMARHL REYQDLLNVK MALDIEIATY RKLLEGEESR ISLPLPTFSS
   401 LNLRETNLES LPLVDTHSKR TLLIKTVETR DGQVINETSQ HHDDLE
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
     9 - 16      914.5060   913.4988   913.4505      53     0  R.SYVTTSTR.T
    17 - 30     1495.8798  1494.8725  1494.7790      63     0  R.TYSLGSALRPSTSR.S
    31 - 44     1444.7979  1443.7906  1443.6994      63     0  R.SLYSSSPGGAYVTR.S
    59 - 77     2126.2109  2125.2036  2125.0579      69     0  R.LLQDSVDFSLADAINTEFK.N
    81 - 93     1587.9003  1586.8930  1586.7900      65     1  R.TNEKVELQELNDR.F
    85 - 93     1115.6313  1114.6240  1114.5618      56     0  K.VELQELNDR.F
    94 - 102    1125.6686  1124.6613  1124.5978      56     1  R.FANYIDKVR.F
   101 - 109    1162.6250  1161.6177  1161.6142       3     1  K.VRFLEQQNK.I   Deamidated (NQ)
   103 - 109     906.5054   905.4981   905.4607      41     0  R.FLEQQNK.I
   103 - 109     908.4515   907.4443   907.4287      17     0  R.FLEQQNK.I  2 Deamidated (NQ)
   110 - 119    1169.7764  1168.7691  1168.7067      53     0  K.ILLAELEQLK.G
   110 - 123    1540.0065  1538.9992  1538.9032      62     1  K.ILLAELEQLKGQGK.S
```

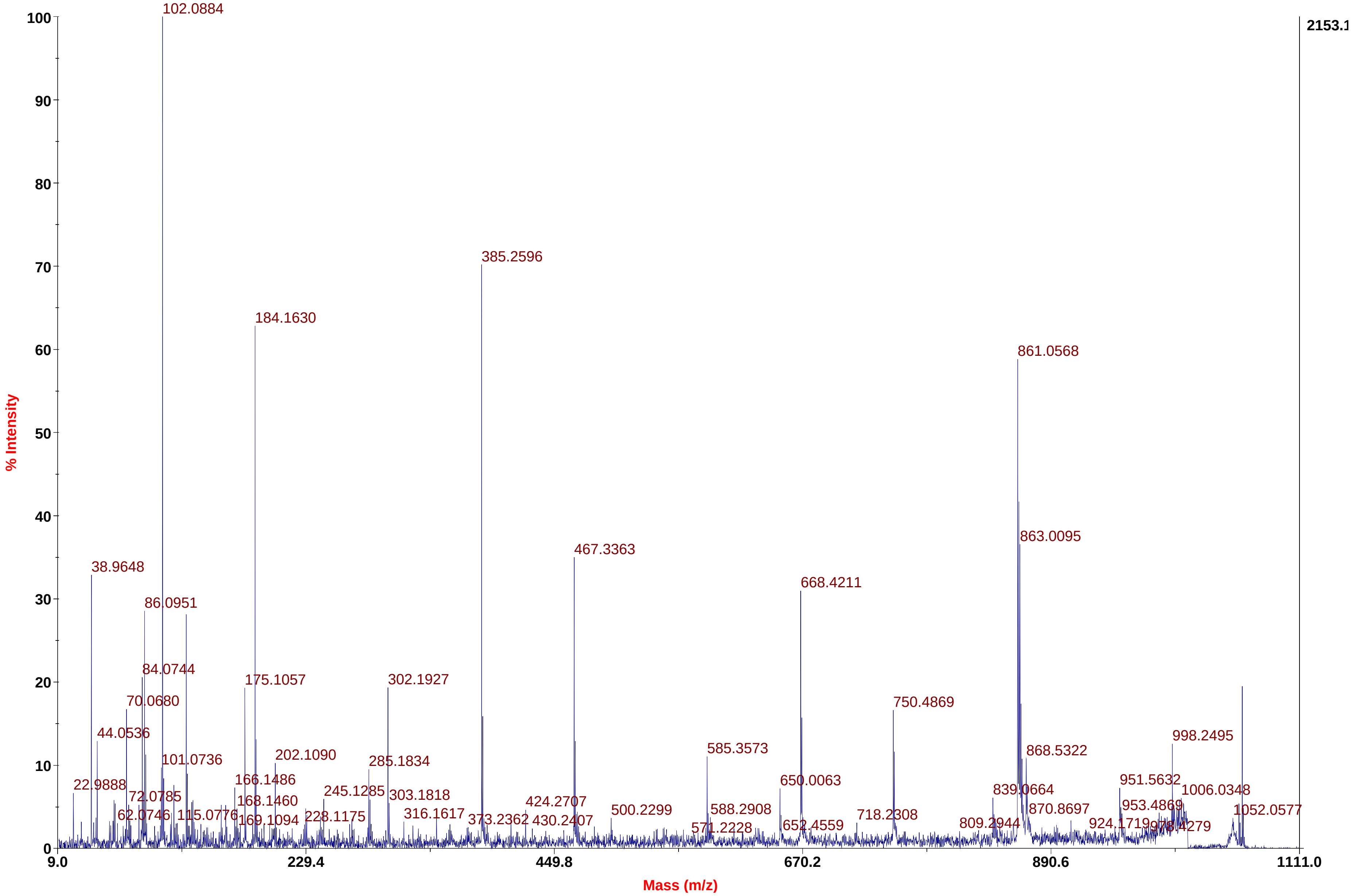
M8

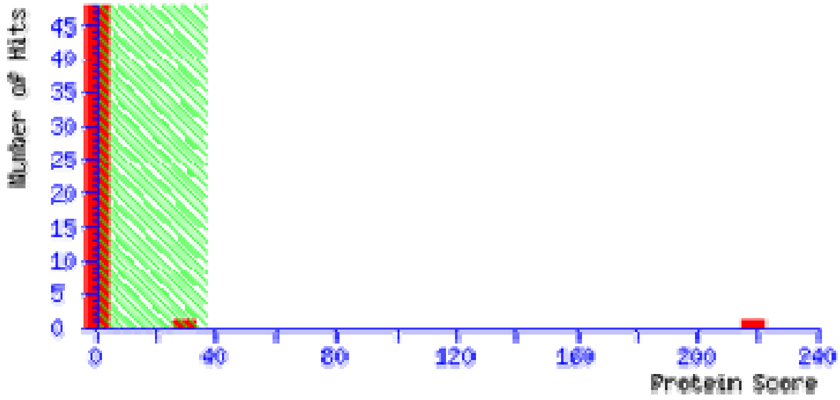
4700 MS/MS Precursor 1295.74 Spec #1 MC[BP = 175.1, 2445]



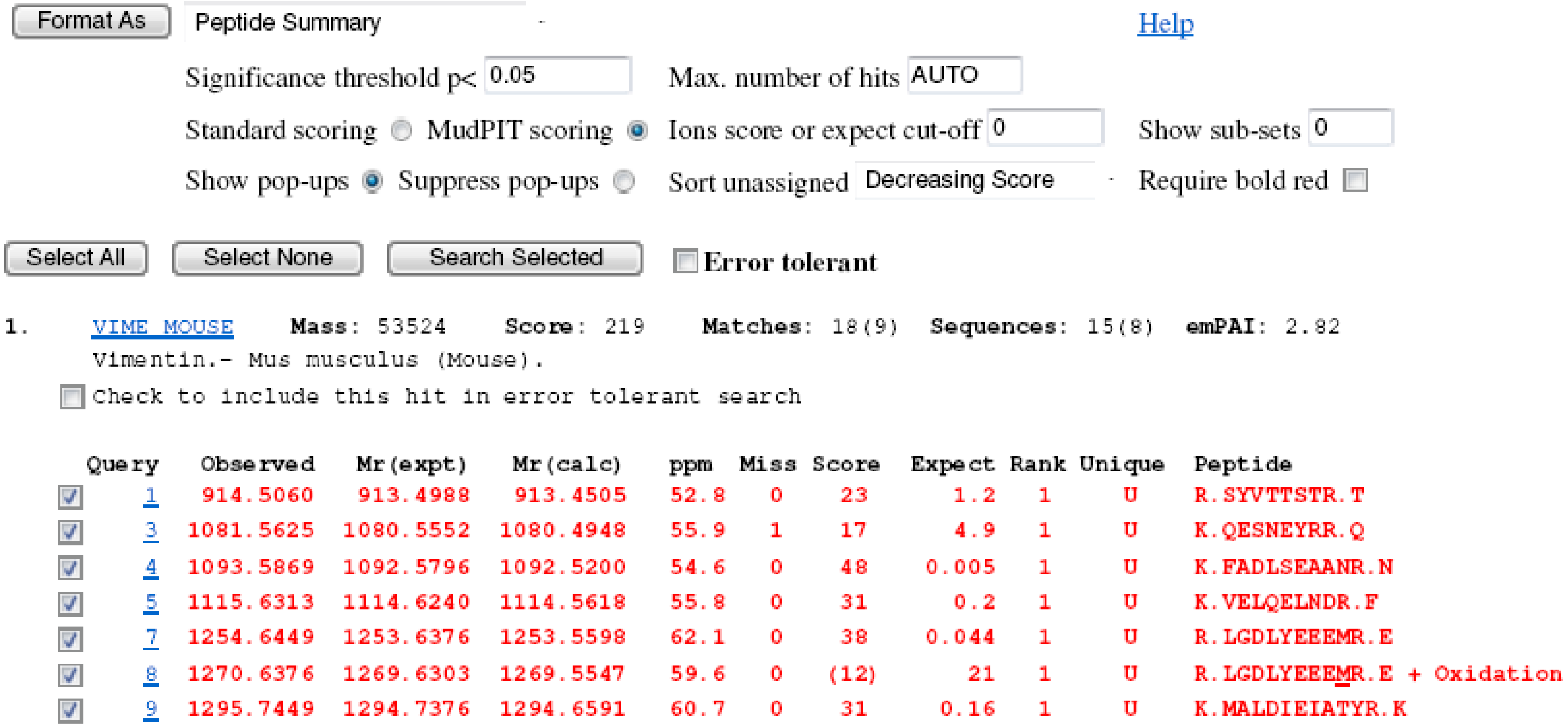
M8

4700 MS/MS Precursor 1051.76 Spec #1 MC[BP = 102.1, 2153]





Peptide Summary Report



Peptide Summary

Significance threshold p< 0.05 Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 Show sub-sets 0

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

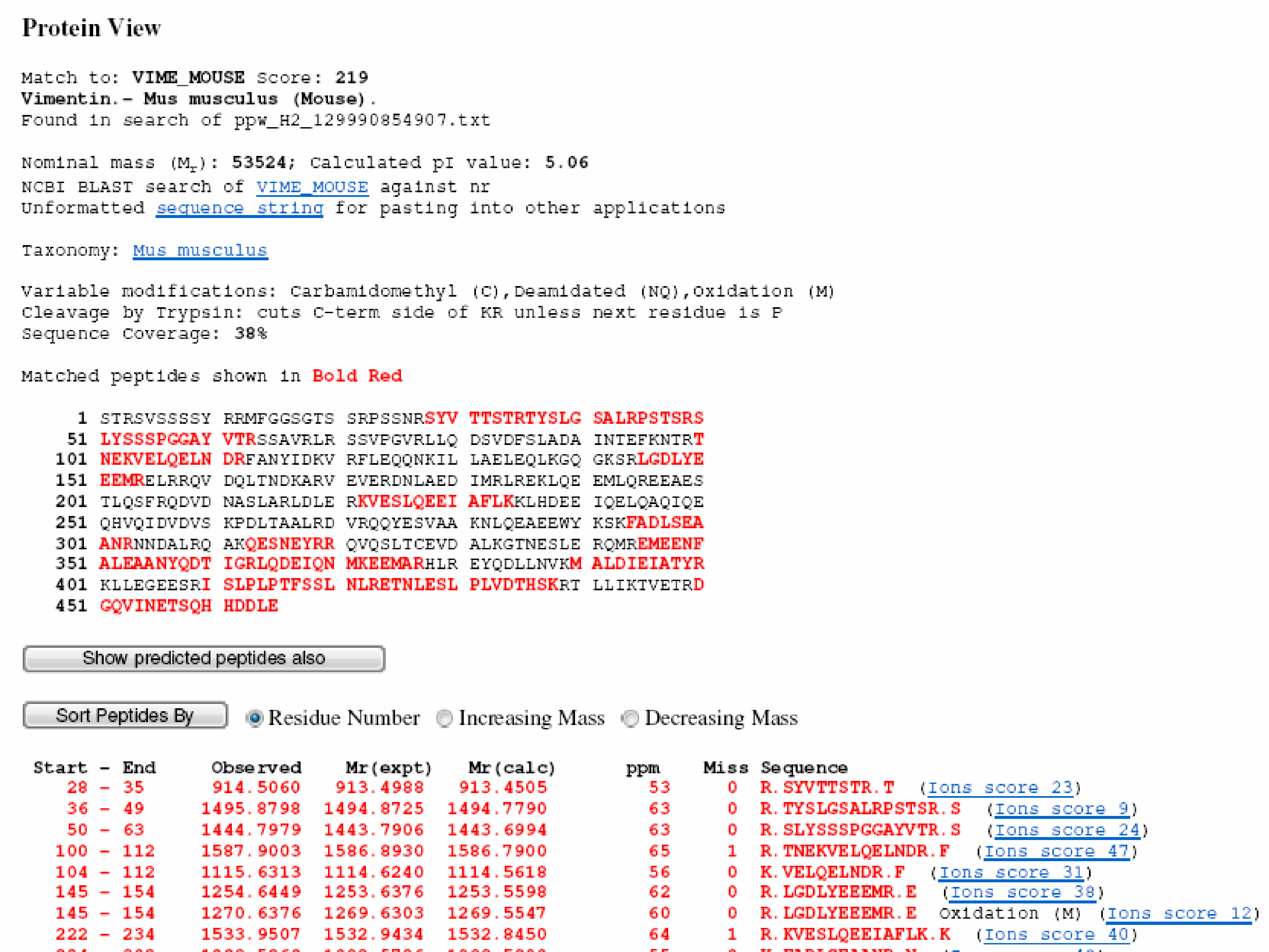
☐ **Error tolerant**

1. VIME_MOUSE **Mass:** 53524 **Score:** 219 **Matches:** 18(9) **Sequences:** 15(8) **emPAI:** 2.82

Vimentin.- Mus musculus (Mouse).

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	914.5060	913.4988	913.4505	52.8	0	23	1.2	1	U	R.SYVTTSTR.T
☑	3	1081.5625	1080.5552	1080.4948	55.9	1	17	4.9	1	U	K.QESNEYRR.Q
☑	4	1093.5869	1092.5796	1092.5200	54.6	0	48	0.005	1	U	K.FADLSEAANR.N
☑	5	1115.6313	1114.6240	1114.5618	55.8	0	31	0.2	1	U	K.VELQELNDR.F
☑	7	1254.6449	1253.6376	1253.5598	62.1	0	38	0.044	1	U	R.LGDLYEEEMR.E
☑	8	1270.6376	1269.6303	1269.5547	59.6	0	(12)	21	1	U	R.LGDLYEEEMR.E + Oxidation
☑	9	1295.7449	1294.7376	1294.6591	60.7	0	31	0.16	1	U	K.MALDIEIATYR.K



Protein View

Match to: **VIME_MOUSE** Score: **219**
Vimentin.- Mus musculus (Mouse).
Found in search of ppw_H2_129990854907.txt

Nominal mass (M_r): **53524**; Calculated pI value: **5.06**
NCBI BLAST search of VIME_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 38%

Matched peptides shown in **Bold Red**

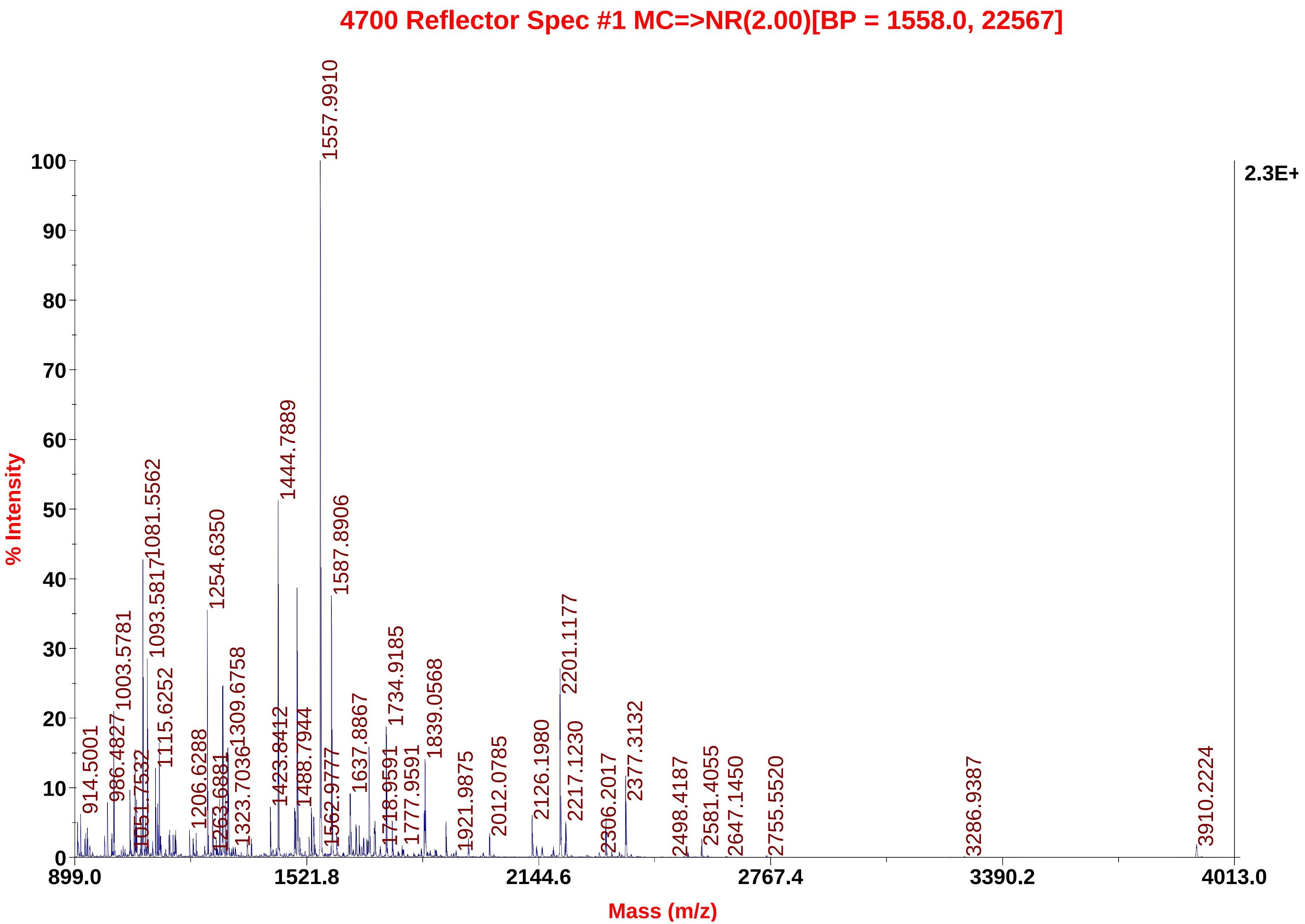
1 STRSVSSSSY RRMFGGSGTS SRPSSNR**SYV TTSTRTYSLG SALRPSTSRS**
51 **LYSSSPGGAY VTR**SSAVRLR SSVPGVRLLQ DSVDFSLADA INTEFKNTR**T**
101 **NEKVELQELN DR**FANYIDKV RFLEQQNKIL LAELEQLKGQ GKSR**LGDLYE**
151 **EEMR**ELRRQV DQLTNDKARV EVERDNLAED IMRLREKLQE EMLQREEAES
201 TLQSFRQDVD NASLARLDLE R**KVESLQEEI AFLK**KLHDEE IQELQAQIQE
251 QHVQIDVDVS KPDLTAALRD VRQQYESVAA KNLQEAEEWY KSK**FADLSEA**
301 **ANR**NNDALRQ AK**QESNEYRR** QVQSLTCEVD ALKGTNESLE RQMR**EMEENF**
351 **ALEAANYQDT IGRLQDEIQN MKEEMAR**HLR EYQDLLNVK**M ALDIEIATYR**
401 KLLEGEESR**I SLPLPTFSSL NLRETNLESL PLVDTHSK**RT LLIKTVETR**D**
451 **GQVINETSQH HDDLE**

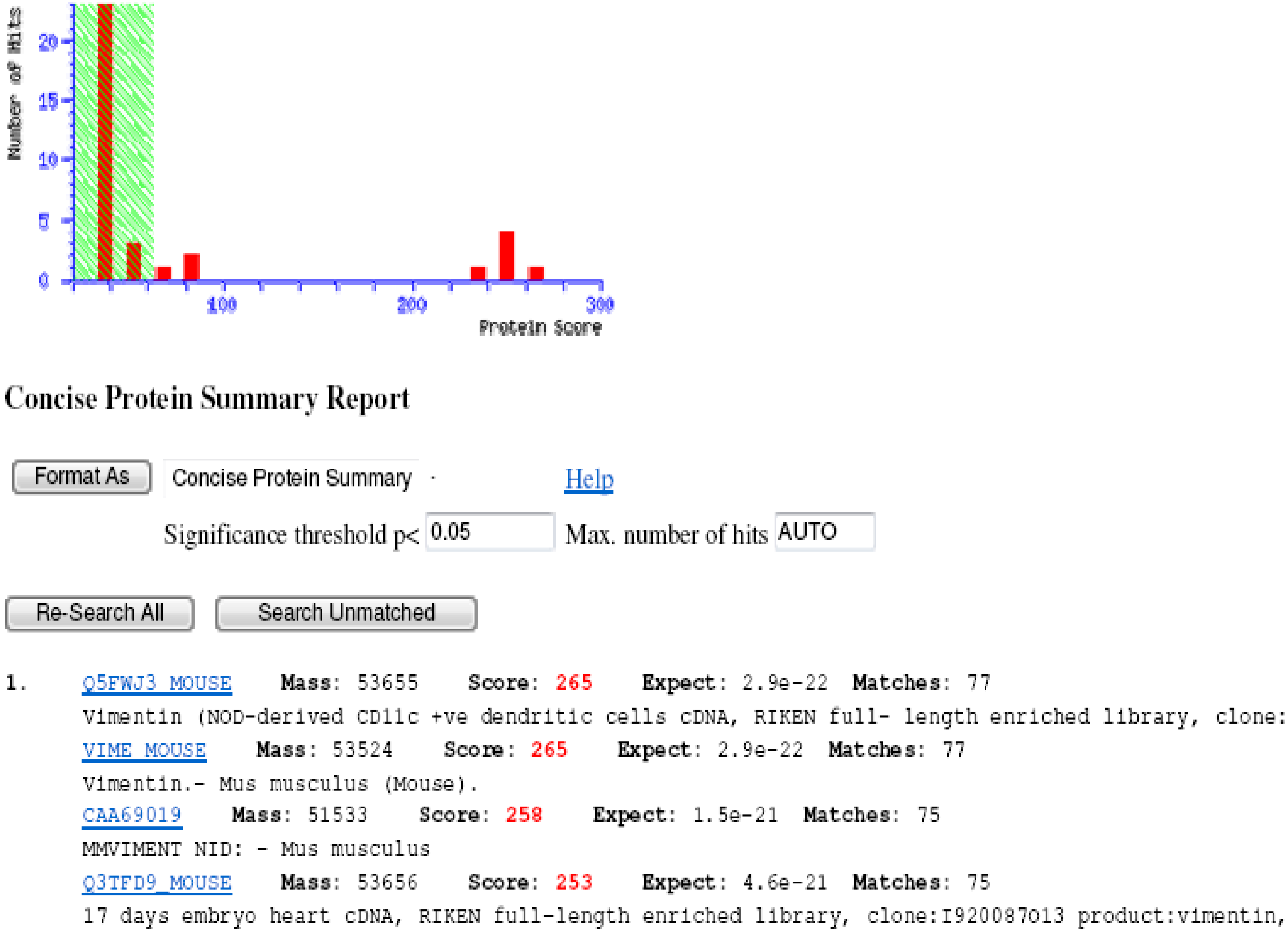
Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
28 - 35	914.5060	913.4988	913.4505	53	0	R.SYVTTSTR.T (Ions score 23)
36 - 49	1495.8798	1494.8725	1494.7790	63	0	R.TYSLGSALRPSTSR.S (Ions score 9)
50 - 63	1444.7979	1443.7906	1443.6994	63	0	R.SLYSSSPGGAYVTR.S (Ions score 24)
100 - 112	1587.9003	1586.8930	1586.7900	65	1	R.TNEKVELQELNDR.F (Ions score 47)
104 - 112	1115.6313	1114.6240	1114.5618	56	0	K.VELQELNDR.F (Ions score 31)
145 - 154	1254.6449	1253.6376	1253.5598	62	0	R.LGDLYEEEMR.E (Ions score 38)
145 - 154	1270.6376	1269.6303	1269.5547	60	0	R.LGDLYEEEMR.E Oxidation (M) (Ions score 12)
222 - 234	1533.9507	1532.9434	1532.8450	64	1	R.KVESLQEEIAFLK.K (Ions score 40)

Sample M9


4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1558.0, 22567]
2.3E+
% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
899.0
1521.8
2144.6
2767.4
3390.2
4013.0
914.5001
986.4827
1003.5781
1051.7532
1081.5562
1093.5817
1115.6252
1206.6288
1254.6350
1263.6881
1309.6758
1323.7036
1423.8412
1444.7889
1488.7944
1557.9910
1562.9777
1587.8906
1637.8867
1718.9591
1734.9185
1777.9591
1839.0568
1921.9875
2012.0785
2126.1980
2201.1177
2217.1230
2306.2017
2377.3132
2498.4187
2581.4055
2647.1450
2755.5520
3286.9387
3910.2224



Concise Protein Summary Report

Significance threshold p< 0.05 Max. number of hits AUTO

1. Q5FWJ3_MOUSE **Mass**: 53655 **Score**: 265 **Expect**: 2.9e-22 **Matches**: 77

Vimentin (NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full- length enriched library, clone:

VIME_MOUSE **Mass**: 53524 **Score**: 265 **Expect**: 2.9e-22 **Matches**: 77

Vimentin.- Mus musculus (Mouse).

CAA69019 **Mass**: 51533 **Score**: 258 **Expect**: 1.5e-21 **Matches**: 75

MMVIMENT NID: - Mus musculus

Q3TFD9_MOUSE **Mass**: 53656 **Score**: 253 **Expect**: 4.6e-21 **Matches**: 75

17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920087O13 product:vimentin,

Protein View

```
Match to: Q5FWJ3_MOUSE Score: 265 Expect: 2.9e-22
Vimentin (NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full- length enriched library,
Found in search of pmf_I2_12990848908.txt

Nominal mass (Mr): 53655; Calculated pI value: 5.06
NCBI BLAST search of Q5FWJ3_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 181
Number of mass values matched: 77
Sequence Coverage: 89%

Matched peptides shown in Bold Red

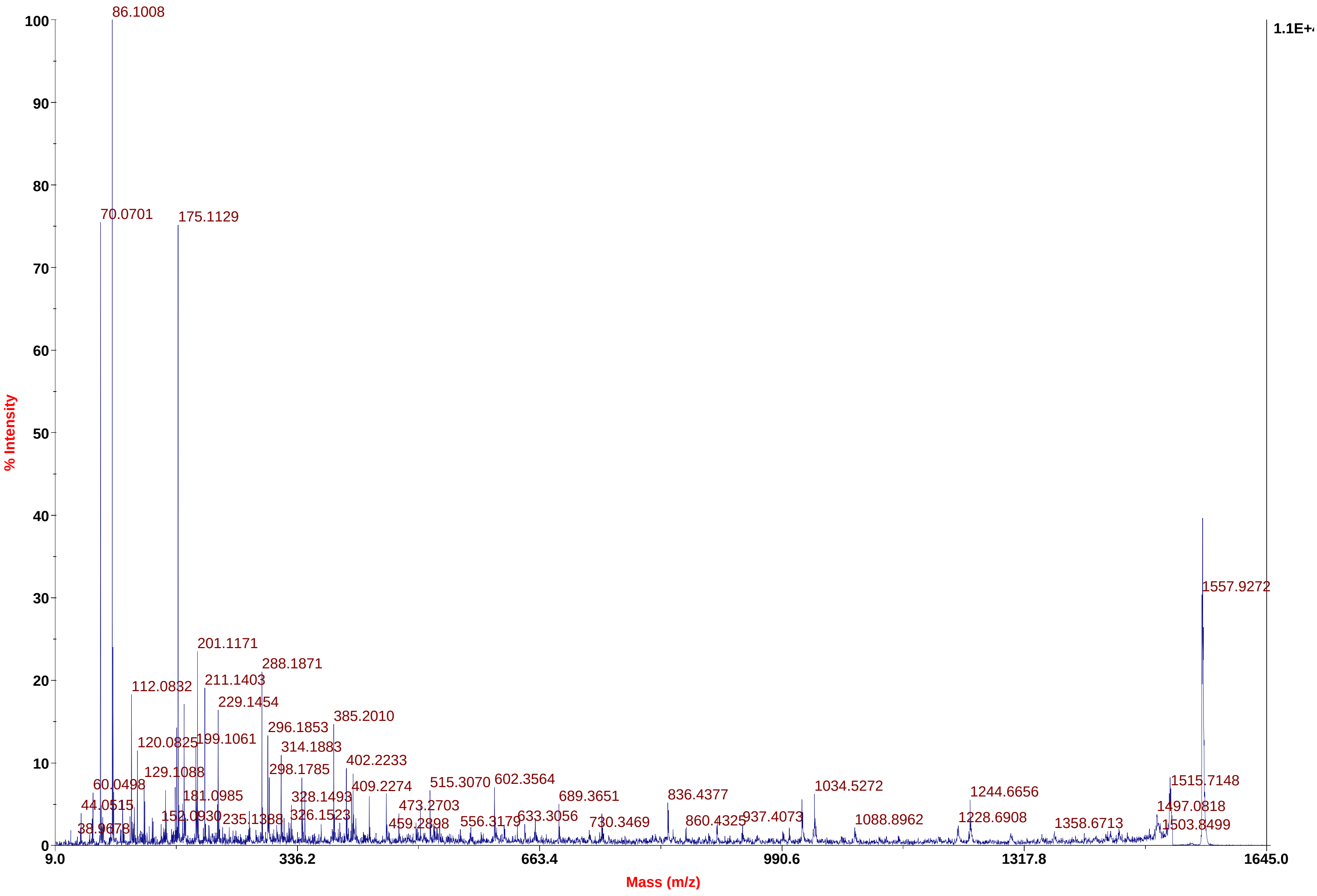
     1 MSTRSVSSSS YRRMFGGSGT SSRPSSNRSY VTTSTRTYSL GSALRPSTSR
    51 SLYSSSPGGA YVTRSSAVRL RSSVPGVRLL QDSVDFSLAD AINTEFKNTR
   101 TNEKVELQEL NDRFANYIDK VRFLEQQNKI LLAELEQLKG QGKSRLGDLY
   151 EEEMRELRRQ VDQLTNDKAR VEVERDNLAE DIMRLREKLQ EEMLQREEAE
   201 STLQSFRQDV DNASLARLDL ERKVESLQEE IAFLKKLHDE EIQELQAQIQ
   251 EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEEW YKSKFADLSE
   301 AANRNNDALR QAKQESNEYR RQVQSLTCEV DALKGTNESL ERQMREMEEN
   351 FALEAANYQD TIGRLQDEIQ NMKEEMARHL REYQDLLNVK MALDIEIATY
   401 RKLLEGEESR ISLPLPTFSS LNLRETNLES LPLVDTHSKR TLLIKTVETR
   451 DGQVINETSQ HHDDLE
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End      Observed    Mr(expt)    Mr(calc)      ppm    Miss  Sequence
     5 - 13      1028.5667   1027.5594   1027.5047       53      1   R.SVSSSSYRR.M
    14 - 28      1543.7866   1542.7793   1542.6845       61      0   R.MFGGSGTSSRPSSNR.S  Oxi
    29 - 36       914.5001    913.4928    913.4505       46      0   R.SYVTTSTR.T
    29 - 50      2391.3230   2390.3157   2390.2190       40      1   R.SYVTTSTRTYSLGSALRPSTSR
    37 - 50      1495.8713   1494.8640   1494.7790       57      0   R.TYSLGSALRPSTSR.S
    51 - 64      1444.7861   1443.7788   1443.6994       55      0   R.SLYSSSPGGAYVTR.S
    79 - 97      2126.1934   2125.1861   2125.0579       60      0   R.LLQDSVDFSLADAINTEFK.N
    79 - 100     2498.3972   2497.3899   2497.2336       63      1   R.LLQDSVDFSLADAINTEFKNTR
   101 - 113     1587.8877   1586.8804   1586.7900       57      1   R.TNEKVELQELNDR.F
   105 - 113     1115.6230   1114.6157   1114.5618       48      0   K.VELQELNDR.F
   114 - 122     1125.6603   1124.6530   1124.5978       49      1   R.FANYIDKVR.F
   121 - 129     1162.6176   1161.6103   1161.6142       -3      1   K.VRFLEQQNK.I  Deamidate
```

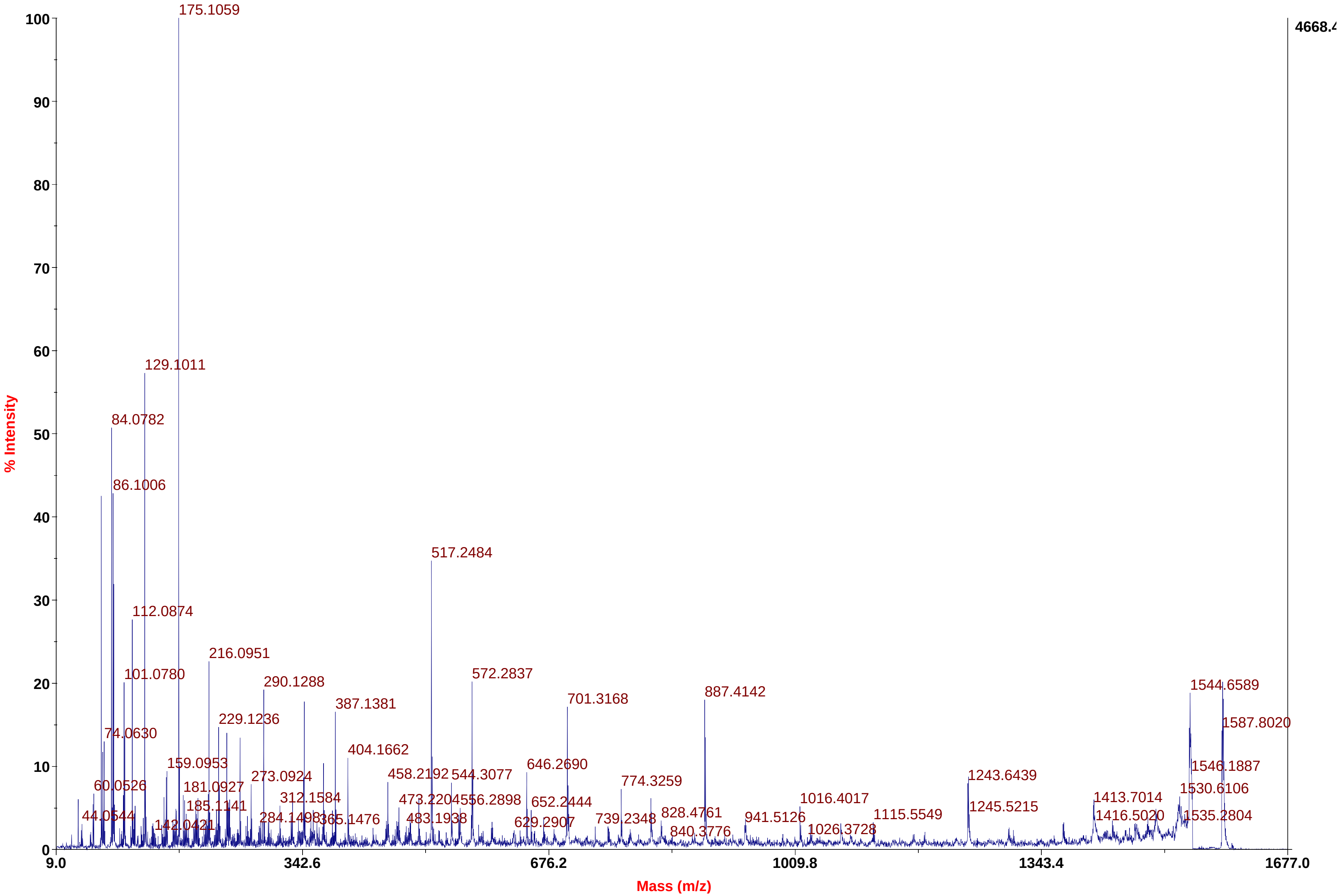
M9

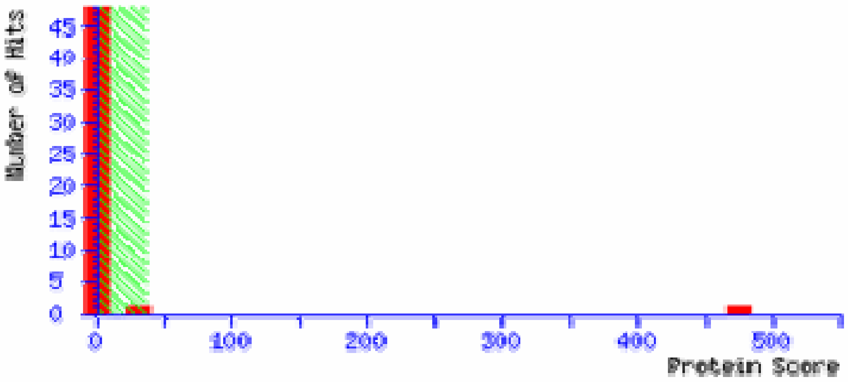
4700 MS/MS Precursor 1557.99 Spec #1 MC[BP = 86.1, 11204]

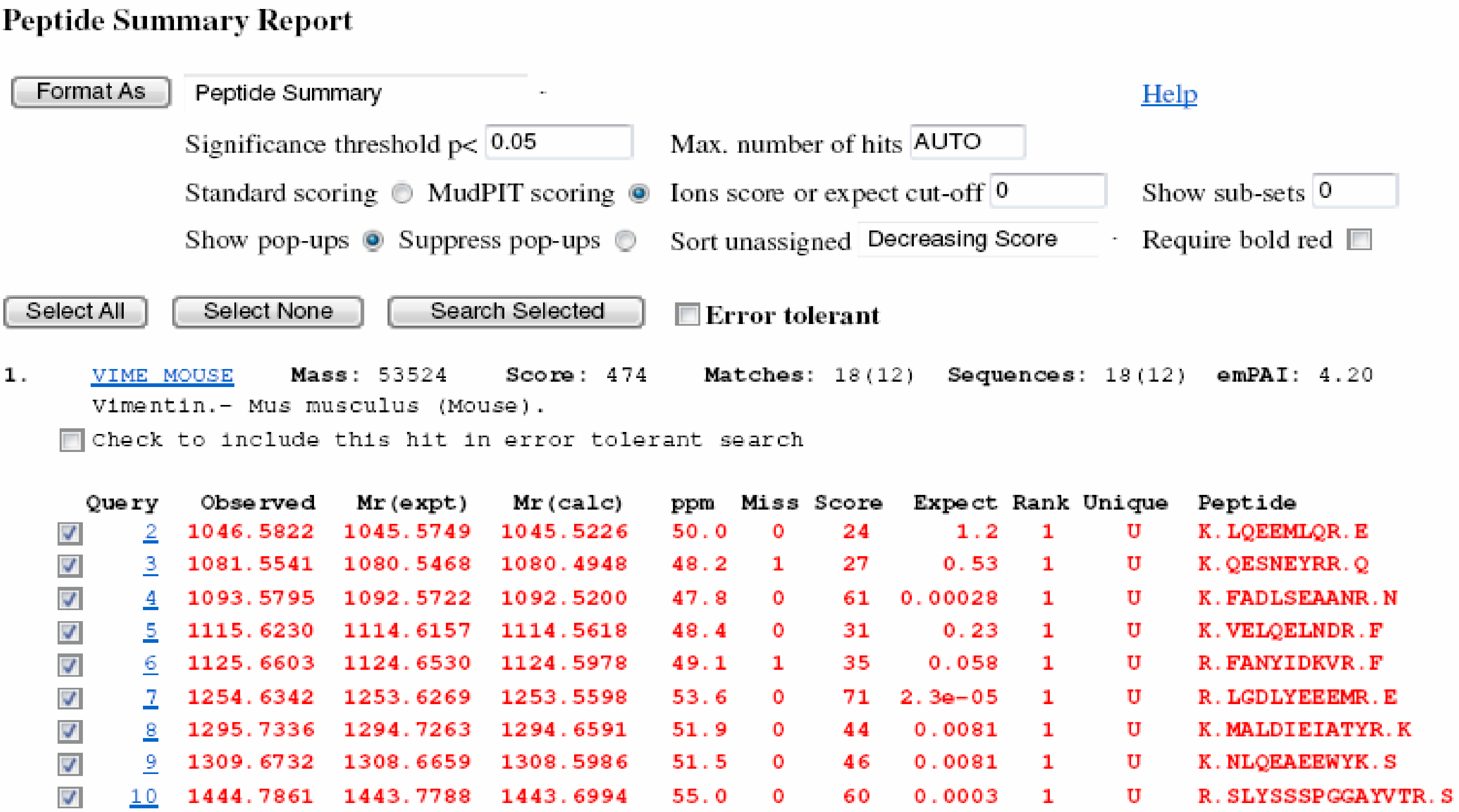


M9

4700 MS/MS Precursor 1587.89 Spec #1 MC[BP = 175.1, 4668]







Peptide Summary Report

Format As: Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

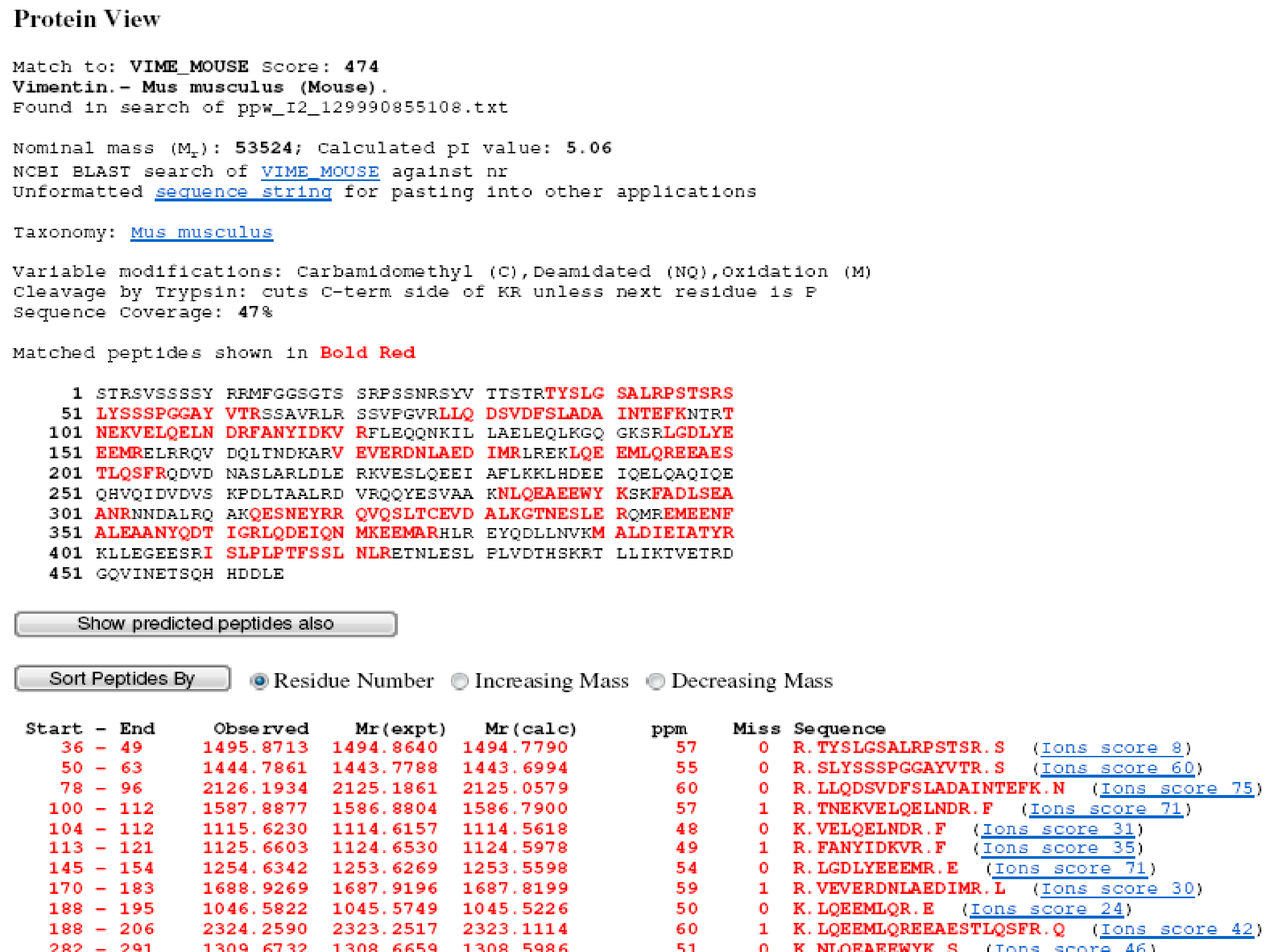
☐ **Error tolerant**

1. VIME_MOUSE **Mass:** 53524 **Score:** 474 **Matches:** 18(12) **Sequences:** 18(12) **emPAI:** 4.20

Vimentin.- Mus musculus (Mouse).

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	2	1046.5822	1045.5749	1045.5226	50.0	0	24	1.2	1	U	K.LQEEMLQR.E
☑	3	1081.5541	1080.5468	1080.4948	48.2	1	27	0.53	1	U	K.QESNEYRR.Q
☑	4	1093.5795	1092.5722	1092.5200	47.8	0	61	0.00028	1	U	K.FADLSEAANR.N
☑	5	1115.6230	1114.6157	1114.5618	48.4	0	31	0.23	1	U	K.VELQELNDR.F
☑	6	1125.6603	1124.6530	1124.5978	49.1	1	35	0.058	1	U	R.FANYIDKVR.F
☑	7	1254.6342	1253.6269	1253.5598	53.6	0	71	2.3e-05	1	U	R.LGDLYEEEMR.E
☑	8	1295.7336	1294.7263	1294.6591	51.9	0	44	0.0081	1	U	K.MALDIEIATYR.K
☑	9	1309.6732	1308.6659	1308.5986	51.5	0	46	0.0081	1	U	K.NLQEAEEWYK.S
☑	10	1444.7861	1443.7788	1443.6994	55.0	0	60	0.0003	1	U	R.SLYSSSPGGAYVTR.S



Protein View

```
Match to: VIME_MOUSE Score: 474
Vimentin.- Mus musculus (Mouse).
Found in search of ppw_I2_129990855108.txt

Nominal mass (Mr): 53524; Calculated pI value: 5.06
NCBI BLAST search of VIME_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 47%

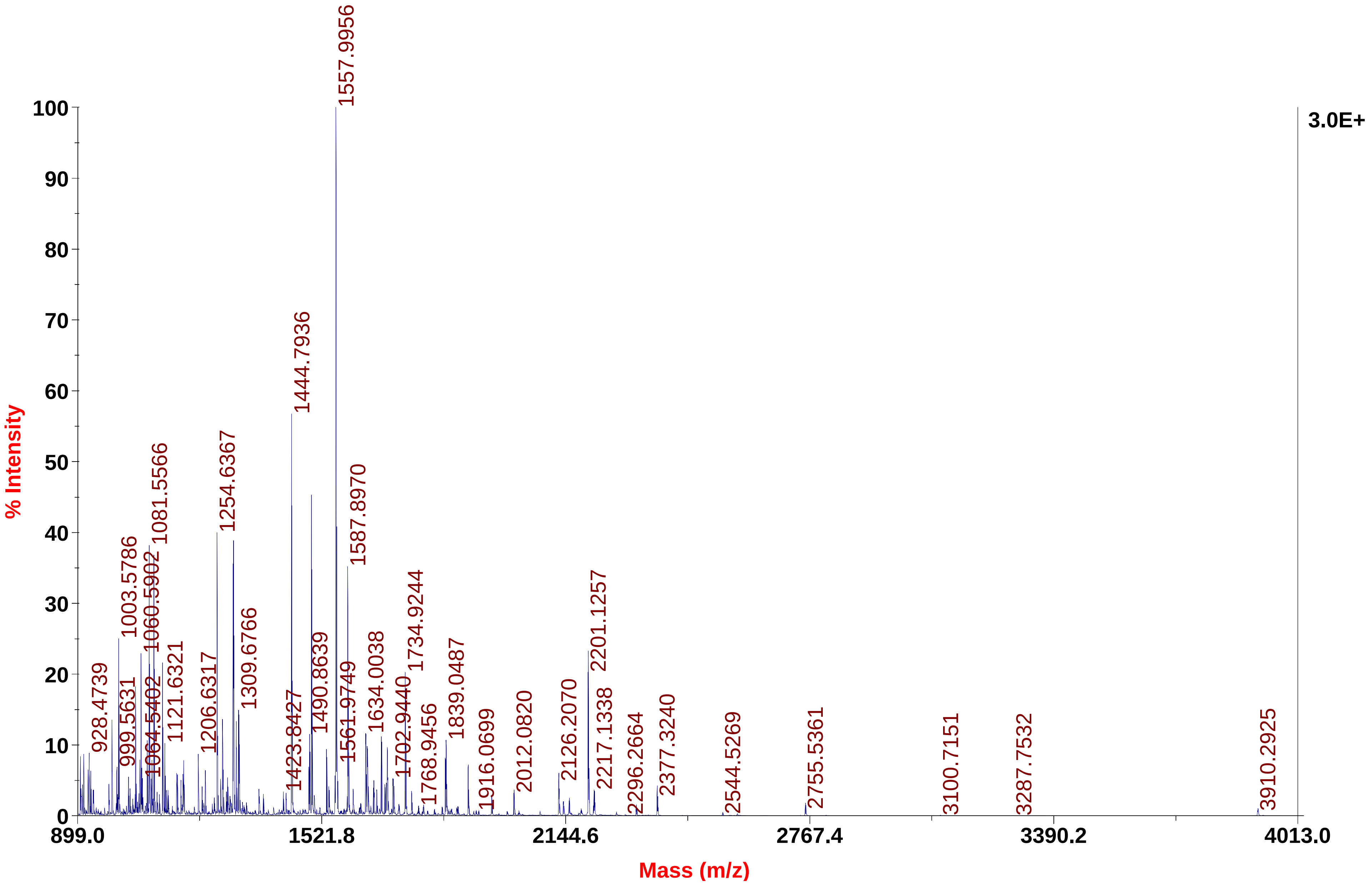
Matched peptides shown in Bold Red

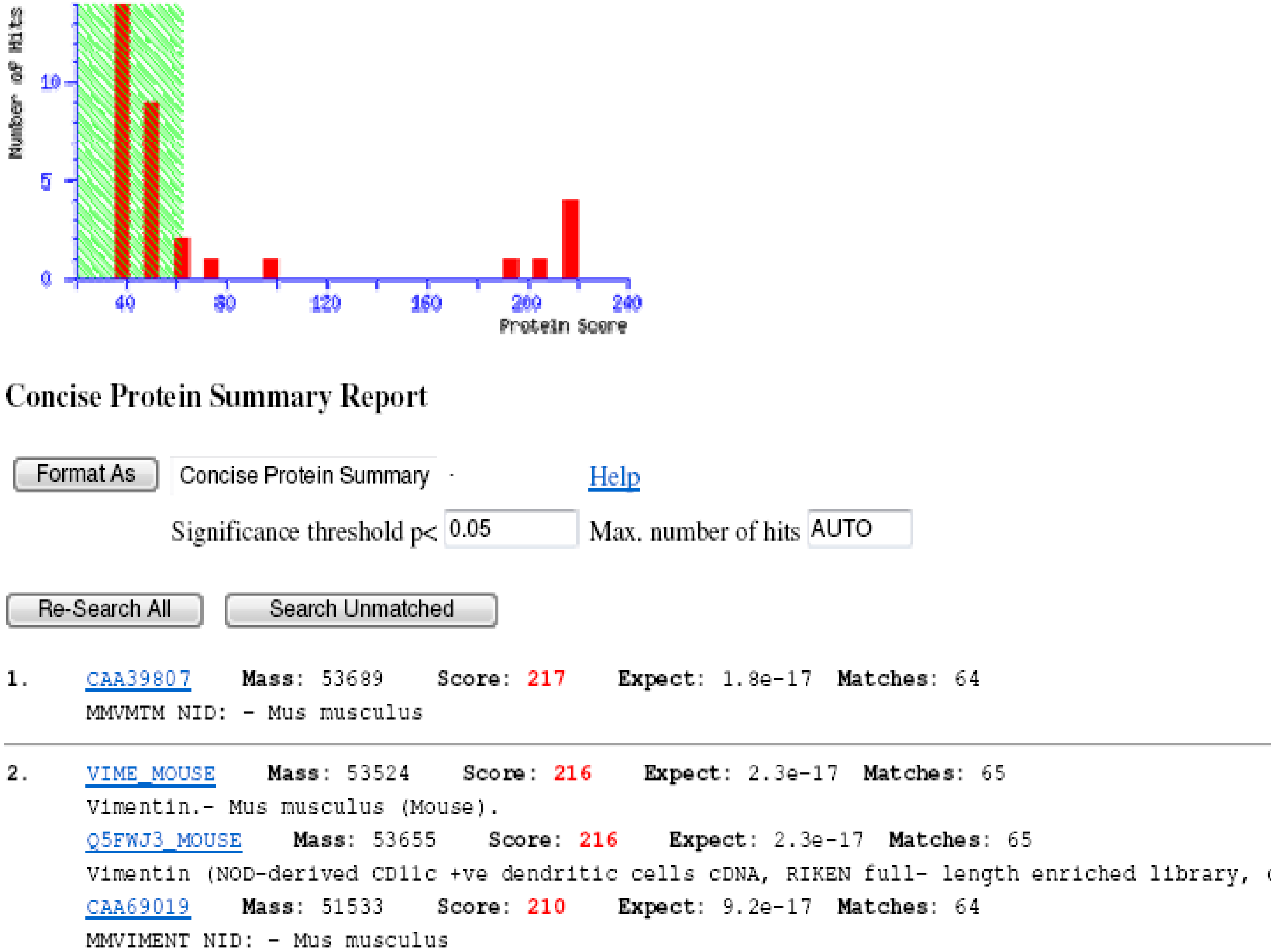
    1 STRSVSSSSY RRMFGGSGTS SRPSSNRSYV TTSTRTYSLG SALRPSTSRS
   51 LYSSSPGGAY VTRSSAVRLR SSVPGVRLLQ DSVDFSLADA INTEFKNTRT
  101 NEKVELQELN DRFANYIDKV RFLEQQNKIL LAELEQLKGQ GKSRLGDLYE
  151 EEMRELRRQV DQLTNDKARV EVERDNLAED IMRLREKLQE EMLQREEAES
  201 TLQSFRQDVD NASLARLDLE RKVESLQEEI AFLKKLHDEE IQELQAQIQE
  251 QHVQIDVDVS KPDLTAALRD VRQQYESVAA KNLQEAEEWY KSKFADLSEA
  301 ANRNNDALRQ AKQESNEYRR QVQSLTCEVD ALKGTNESLE RQMREMEENF
  351 ALEAANYQDT IGRLQDEIQN MKEEMARHLR EYQDLLNVKM ALDIEIATYR
  401 KLLEGEESRI SLPLPTFSSL NLRETNLESL PLVDTHSKRT LLIKTVETRD
  451 GQVINETSQH HDDLE
```

```
  Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss  Sequence
    36 - 49      1495.8713  1494.8640  1494.7790       57     0  R.TYSLGSALRPSTSR.S  (Ions score 8)
    50 - 63      1444.7861  1443.7788  1443.6994       55     0  R.SLYSSSPGGAYVTR.S  (Ions score 60)
    78 - 96      2126.1934  2125.1861  2125.0579       60     0  R.LLQDSVDFSLADAINTEFK.N  (Ions score 75)
   100 - 112     1587.8877  1586.8804  1586.7900       57     1  R.TNEKVELQELNDR.F  (Ions score 71)
   104 - 112     1115.6230  1114.6157  1114.5618       48     0  K.VELQELNDR.F  (Ions score 31)
   113 - 121     1125.6603  1124.6530  1124.5978       49     1  R.FANYIDKVR.F  (Ions score 35)
   145 - 154     1254.6342  1253.6269  1253.5598       54     0  R.LGDLYEEEMR.E  (Ions score 71)
   170 - 183     1688.9269  1687.9196  1687.8199       59     1  R.VEVERDNLAEDIMR.L  (Ions score 30)
   188 - 195     1046.5822  1045.5749  1045.5226       50     0  K.LQEEMLQR.E  (Ions score 24)
   188 - 206     2324.2590  2323.2517  2323.1114       60     1  K.LQEEMLQREEAESTLQSFR.Q  (Ions score 42)
   282 - 291     1309.6732  1308.6659  1308.5986       51     0  K.NLQEAEEWYK.S  (Ions score 46)
```

Sample M10

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1558.0, 29698]





Concise Protein Summary Report

Format As: Concise Protein Summary

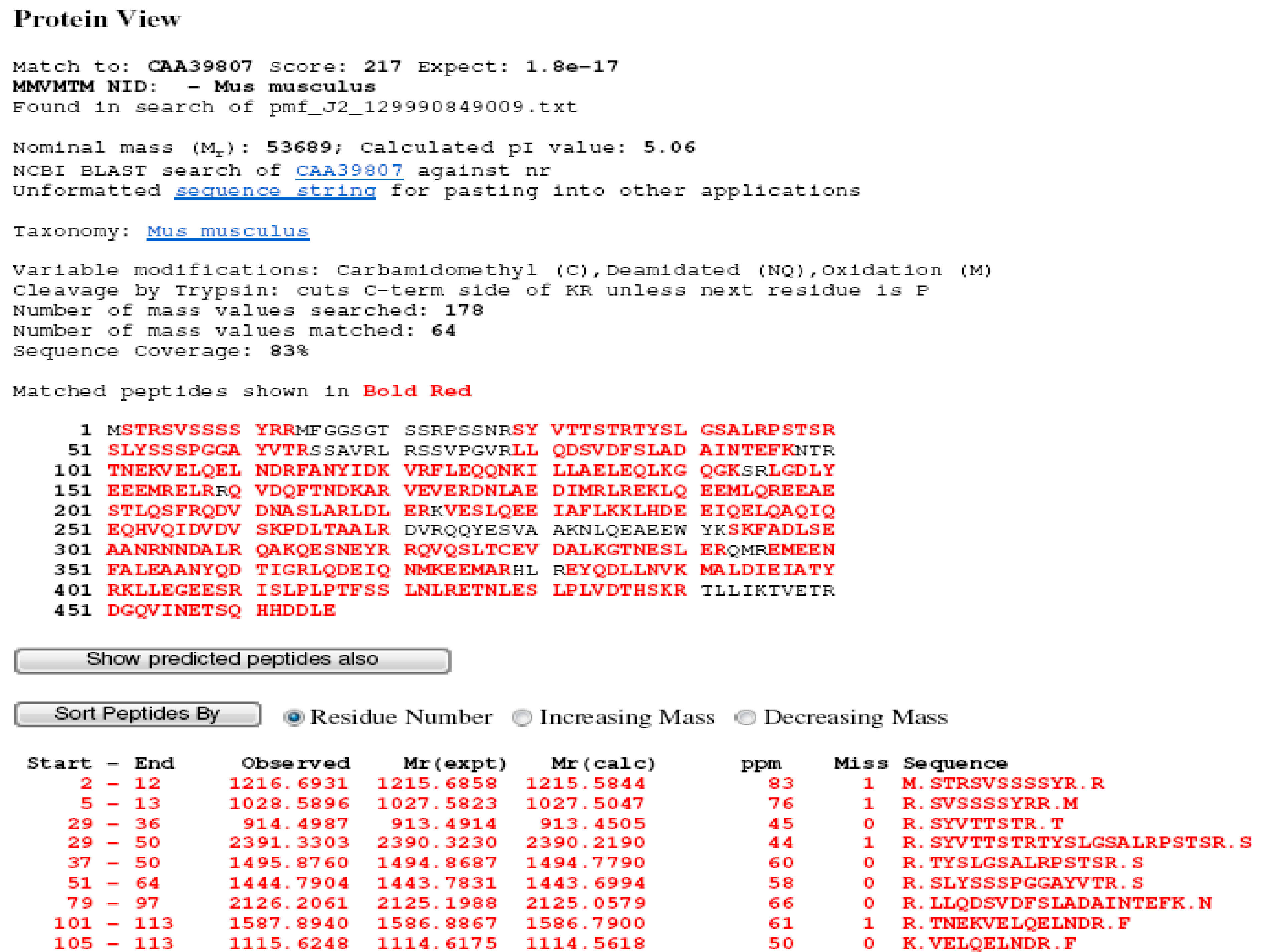
Help

Significance threshold p< 0.05

Max. number of hits AUTO

```
1.     CAA39807     Mass: 53689     Score: 217     Expect: 1.8e-17  Matches: 64
       MMVMTM NID: - Mus musculus

2.     VIME_MOUSE     Mass: 53524     Score: 216     Expect: 2.3e-17  Matches: 65
       Vimentin.- Mus musculus (Mouse).
       Q5FWJ3_MOUSE     Mass: 53655     Score: 216     Expect: 2.3e-17  Matches: 65
       Vimentin (NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full- length enriched library,
       CAA69019     Mass: 51533     Score: 210     Expect: 9.2e-17  Matches: 64
       MMVIMENT NID: - Mus musculus
```



Protein View

Match to: **CAA39807** Score: **217** Expect: **1.8e-17**
MMVMTM NID: - Mus musculus
Found in search of pmf_J2_129990849009.txt

Nominal mass (M_r): **53689**; Calculated pI value: **5.06**
NCBI BLAST search of CAA39807 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **178**
Number of mass values matched: **64**
Sequence Coverage: **83%**

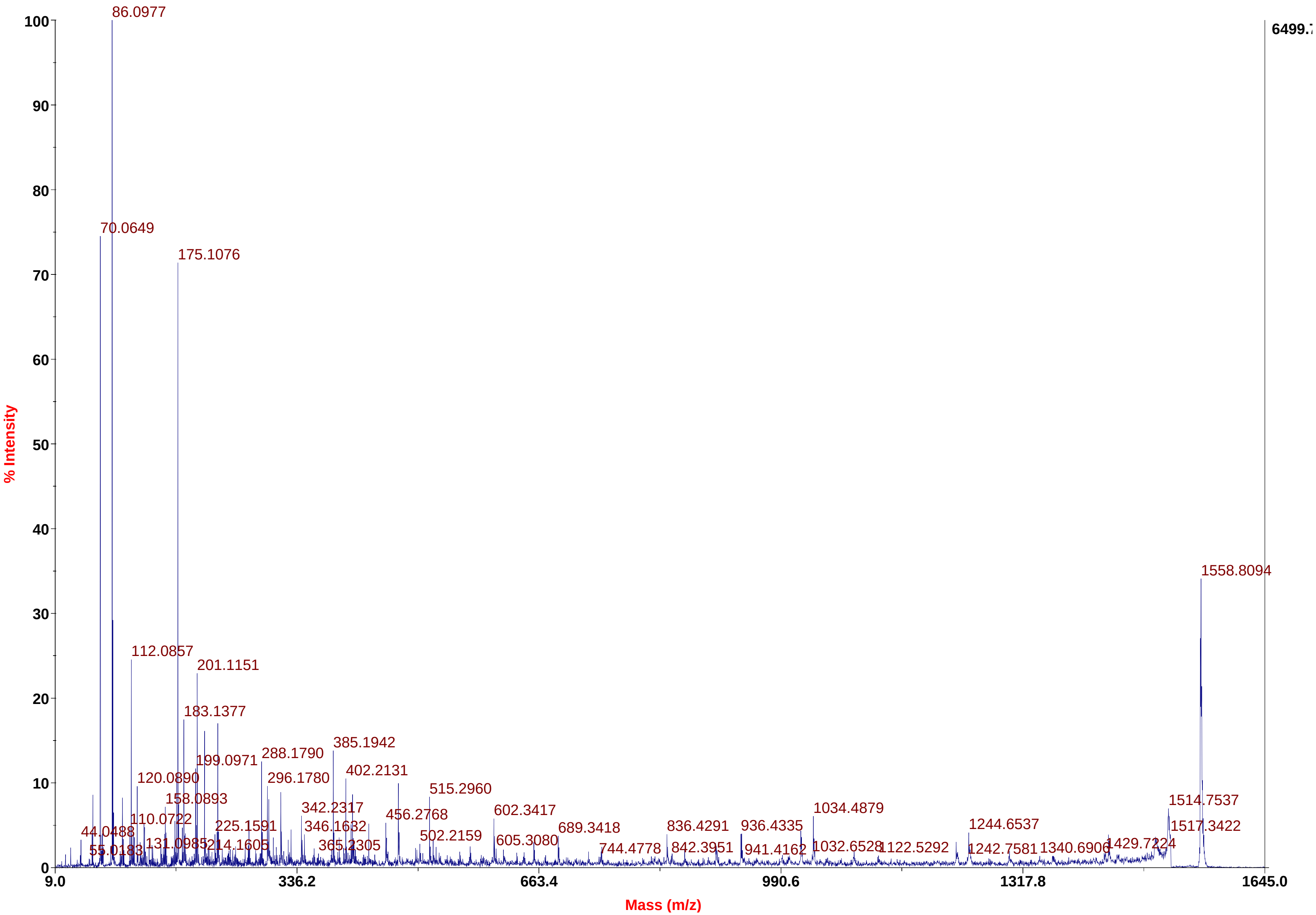
Matched peptides shown in **Bold Red**

```
    1 MSTRSVSSSS YRRMFGGSGT SSRPSSNRSY VTTSTRTYSL GSALRPSTSR
   51 SLYSSSPGGA YVTRSSAVRL RSSVPGVRLL QDSVDFSLAD AINTEFKNTR
  101 TNEKVELQEL NDRFANYIDK VRFLEQQNKI LLAELEQLKG QGKSRLGDLY
  151 EEEMRELRRQ VDQFTNDKAR VEVERDNLAE DIMRLREKLQ EEMLQREEAE
  201 STLQSFRQDV DNASLARLDL ERKVESLQEE IAFLKKLHDE EIQELQAQIQ
  251 EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEEW YKSKFADLSE
  301 AANRNNDALR QAKQESNEYR RQVQSLTCEV DALKGTNESL ERQMREMEEN
  351 FALEAANYQD TIGRLQDEIQ NMKEEMARHL REYQDLLNVK MALDIEIATY
  401 RKLLEGEESR ISLPLPTFSS LNLRETNLES LPLVDTHSKR TLLIKTVETR
  451 DGQVINETSQ HHDDLE
```

```
 Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss  Sequence
     2 - 12      1216.6931   1215.6858   1215.5844        83      1   M.STRSVSSSSYR.R
     5 - 13      1028.5896   1027.5823   1027.5047        76      1   R.SVSSSSYRR.M
    29 - 36       914.4987    913.4914    913.4505        45      0   R.SYVTTSTR.T
    29 - 50      2391.3303   2390.3230   2390.2190        44      1   R.SYVTTSTRTYSLGSALRPSTSR.S
    37 - 50      1495.8760   1494.8687   1494.7790        60      0   R.TYSLGSALRPSTSR.S
    51 - 64      1444.7904   1443.7831   1443.6994        58      0   R.SLYSSSPGGAYVTR.S
    79 - 97      2126.2061   2125.1988   2125.0579        66      0   R.LLQDSVDFSLADAINTEFK.N
   101 - 113     1587.8940   1586.8867   1586.7900        61      1   R.TNEKVELQELNDR.F
   105 - 113     1115.6248   1114.6175   1114.5618        50      0   K.VELQELNDR.F
```

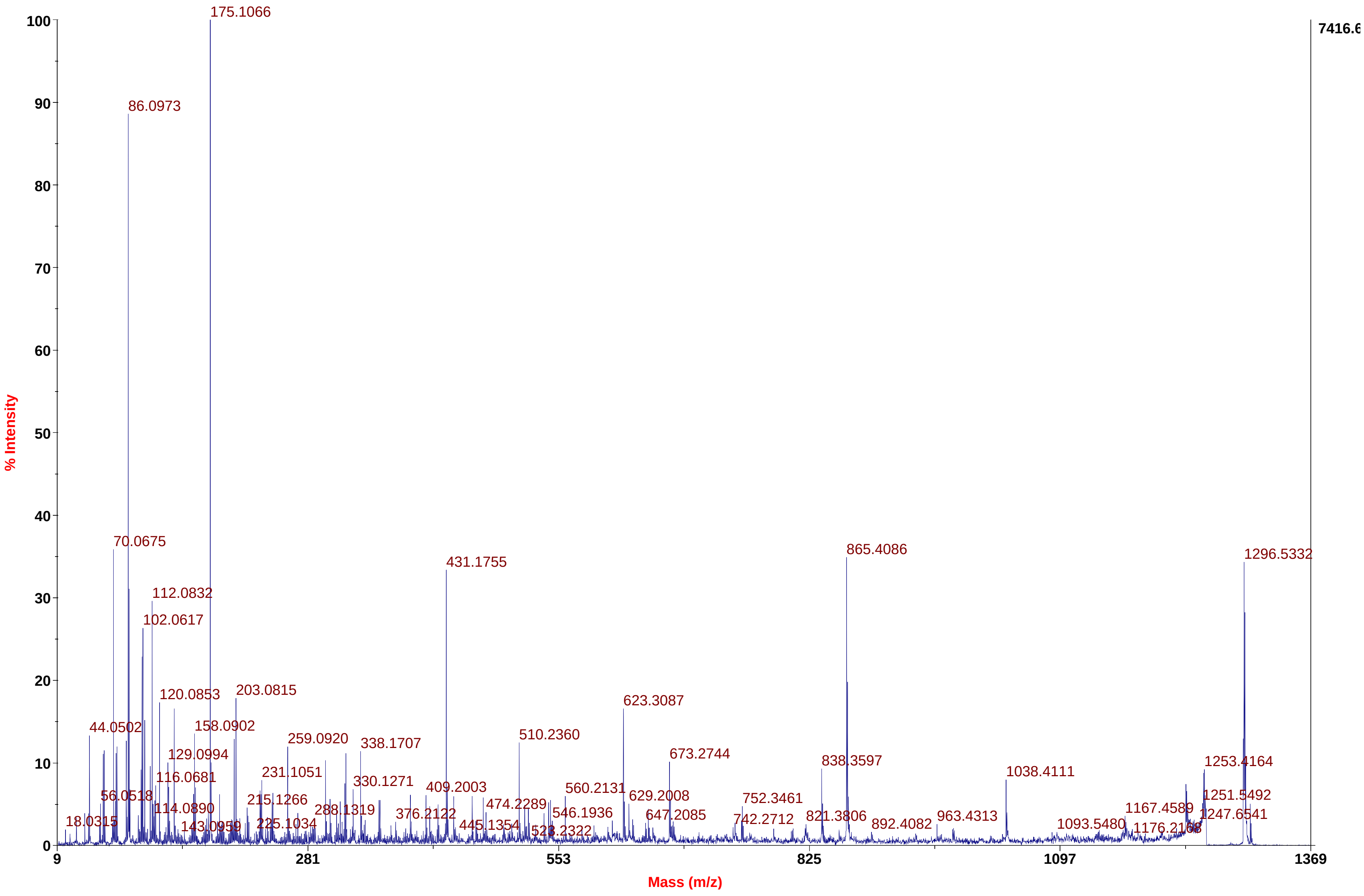
M10

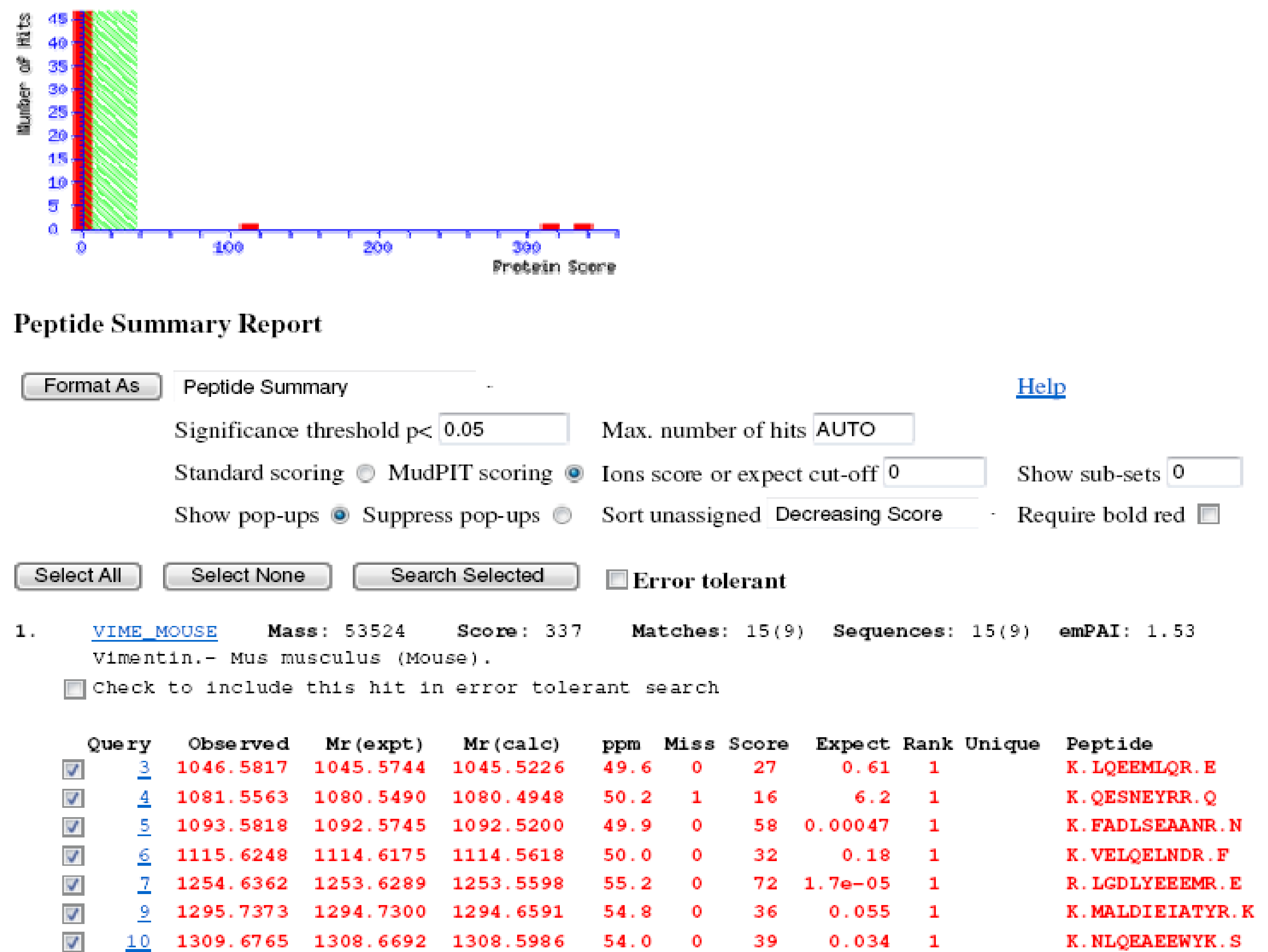
4700 MS/MS Precursor 1557.99 Spec #1 MC[BP = 86.1, 6500]



M10

4700 MS/MS Precursor 1295.74 Spec #1 MC[BP = 175.1, 7417]





Peptide Summary Report

Format As: Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

☐ **Error tolerant**

1. VIME_MOUSE **Mass:** 53524 **Score:** 337 **Matches:** 15(9) **Sequences:** 15(9) **emPAI:** 1.53

Vimentin.- Mus musculus (Mouse).

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	3	1046.5817	1045.5744	1045.5226	49.6	0	27	0.61	1		K.LQEEMLQR.E
☑	4	1081.5563	1080.5490	1080.4948	50.2	1	16	6.2	1		K.QESNEYRR.Q
☑	5	1093.5818	1092.5745	1092.5200	49.9	0	58	0.00047	1		K.FADLSEAANR.N
☑	6	1115.6248	1114.6175	1114.5618	50.0	0	32	0.18	1		K.VELQELNDR.F
☑	7	1254.6362	1253.6289	1253.5598	55.2	0	72	1.7e-05	1		R.LGDLYEEEMR.E
☑	9	1295.7373	1294.7300	1294.6591	54.8	0	36	0.055	1		K.MALDIEIATYR.K
☑	10	1309.6765	1308.6692	1308.5986	54.0	0	39	0.034	1		K.NLQEAEEWYK.S

Protein View

```
Match to: VIME_MOUSE Score: 337
Vimentin.- Mus musculus (Mouse).
Found in search of ppw_J2_129990855309.txt

Nominal mass (Mr): 53524; Calculated pI value: 5.06
NCBI BLAST search of VIME_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

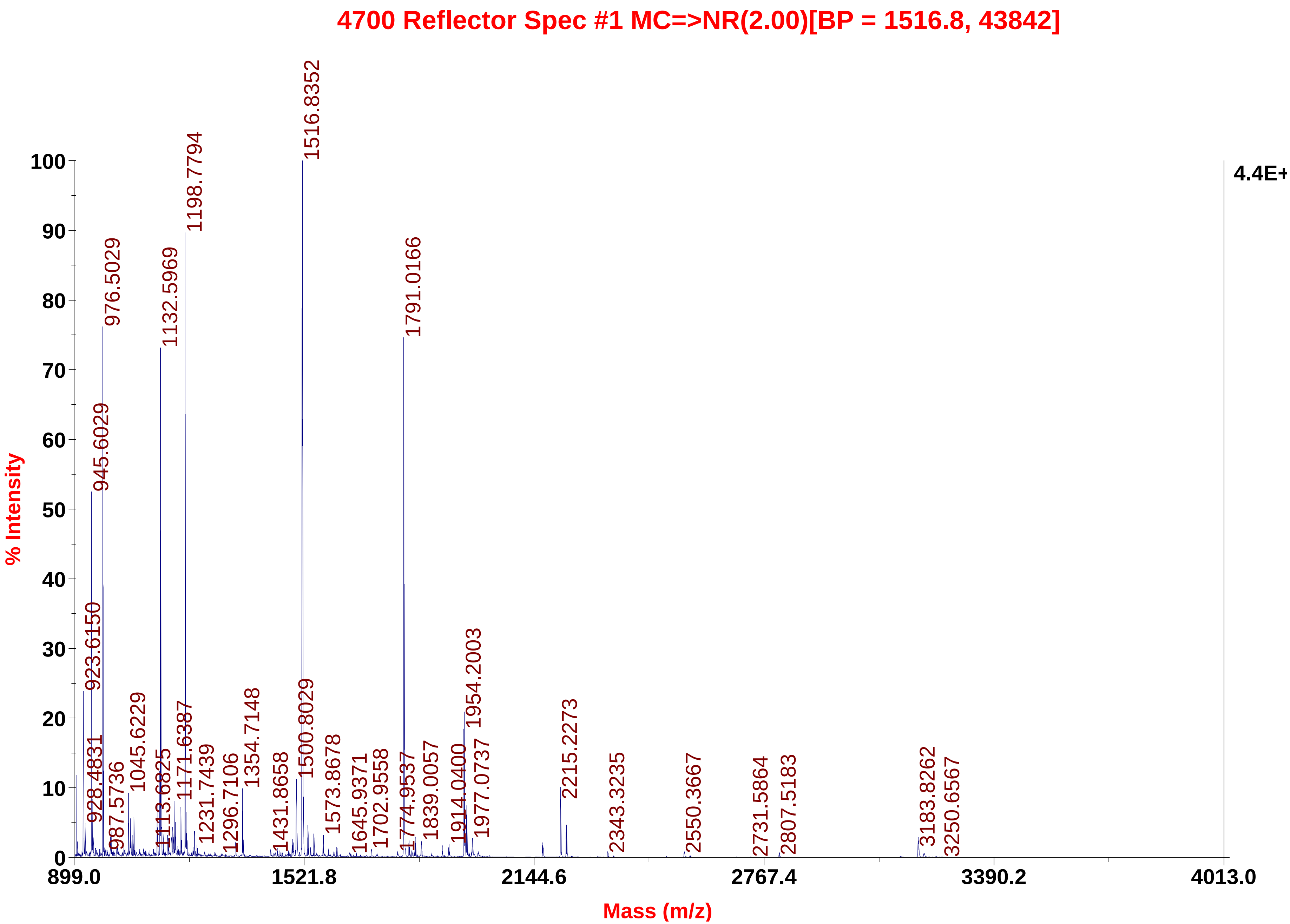
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 36%

Matched peptides shown in Bold Red

  1 STRSVSSSSY RRMFGGSGTS SRPSSNRSYV TTSTRTYSLG SALRPSTSRS
 51 LYSSSPGGAY VTRSSAVRLR SSVPGVRLLQ DSVDFSLADA INTEFKNTRT
101 NEKVELQELN DRFANYIDKV RFLEQQNKIL LAELEQLKGQ GKSRLGDLYE
151 EEMRELRRQV DQLTNDKARV EVERDNLAED IMRLREKLQE EMLQREEAES
201 TLQSFRQDVD NASLARLDLE RKVESLQEEI AFLKKLHDEE IQELQAQIQE
251 QHVQIDVDVS KPDLTAALRD VRQQYESVAA KNLQEAEEWY KSKFADLSEA
301 ANRNNDALRQ AKQESNEYRR QVQSLTCEVD ALKGTNESLE RQMREMEENF
351 ALEAANYQDT IGRLQDEIQN MKEEMARHLR EYQDLLNVKM ALDIEIATYR
401 KLLEGEESRI SLPLPTFSSL NLRETNLESL PLVDTHSKRT LLIKTVETRD
451 GQVINETSQH HDDLE
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     ppm    Miss  Sequence
   36 - 49     1495.8760  1494.8687  1494.7790      60     0   R.TYSLGSALRPSTSR.S  (Ions score 7)
   50 - 63     1444.7904  1443.7831  1443.6994      58     0   R.SLYSSSPGGAYVTR.S  (Ions score 39)
  100 - 112    1587.8940  1586.8867  1586.7900      61     1   R.TNEKVELQELNDR.F  (Ions score 66)
  104 - 112    1115.6248  1114.6175  1114.5618      50     0   K.VELQELNDR.F  (Ions score 32)
  145 - 154    1254.6362  1253.6289  1253.5598      55     0   R.LGDLYEEEMR.E  (Ions score 72)
  170 - 183    1688.9337  1687.9264  1687.8199      63     1   R.VEVERDNLAEDIMR.L  (Ions score 14)
  188 - 195    1046.5817  1045.5744  1045.5226      50     0   K.LQEEMLQR.E  (Ions score 27)
  222 - 234    1533.9412  1532.9339  1532.8450      58     1   R.KVESLQEEIAFLK.K  (Ions score 44)
  282 - 291    1309.6765  1308.6692  1308.5986      54     0   K.NLQEAEEWYK.S  (Ions score 39)
  294 - 303    1093.5818  1092.5745  1092.5200      50     0   K.FADLSEAANR.N  (Ions score 58)
  313 - 320    1081.5563  1080.5490  1080.4948      50     1   K.QESNEYRR.Q  (Ions score 16)
  345 - 363    2201.1218  2200.1145  2199.9742      64     0   R.EMEENFALEAANYQDTIGR.L  (Ions score 122)
  364 - 377    1734.9233  1733.9160  1733.8076      63     1   R.LQDEIQNMKEEMAR.H  (Ions score 95)
  390 - 400    1295.7373  1294.7300  1294.6591      55     0   K.MALDIEIATYR.K  (Ions score 36)
  410 - 423    1557.9924  1556.9851  1556.8926      59     0   R.ISLPLPTFSSLNLR.E  (Ions score 51)
```

Sample M11


4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1516.8, 43842]
% Intensity
Mass (m/z)
4.4E+
100
90
80
70
60
50
40
30
20
10
0
899.0
1521.8
2144.6
2767.4
3390.2
4013.0
923.6150
928.4831
945.6029
976.5029
987.5736
1045.6229
1113.6825
1132.5969
1171.6387
1198.7794
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1296.7106
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1431.8658
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1516.8352
1573.8678
1645.9371
1702.9558
1774.9537
1791.0166
1839.0057
1914.0400
1954.2003
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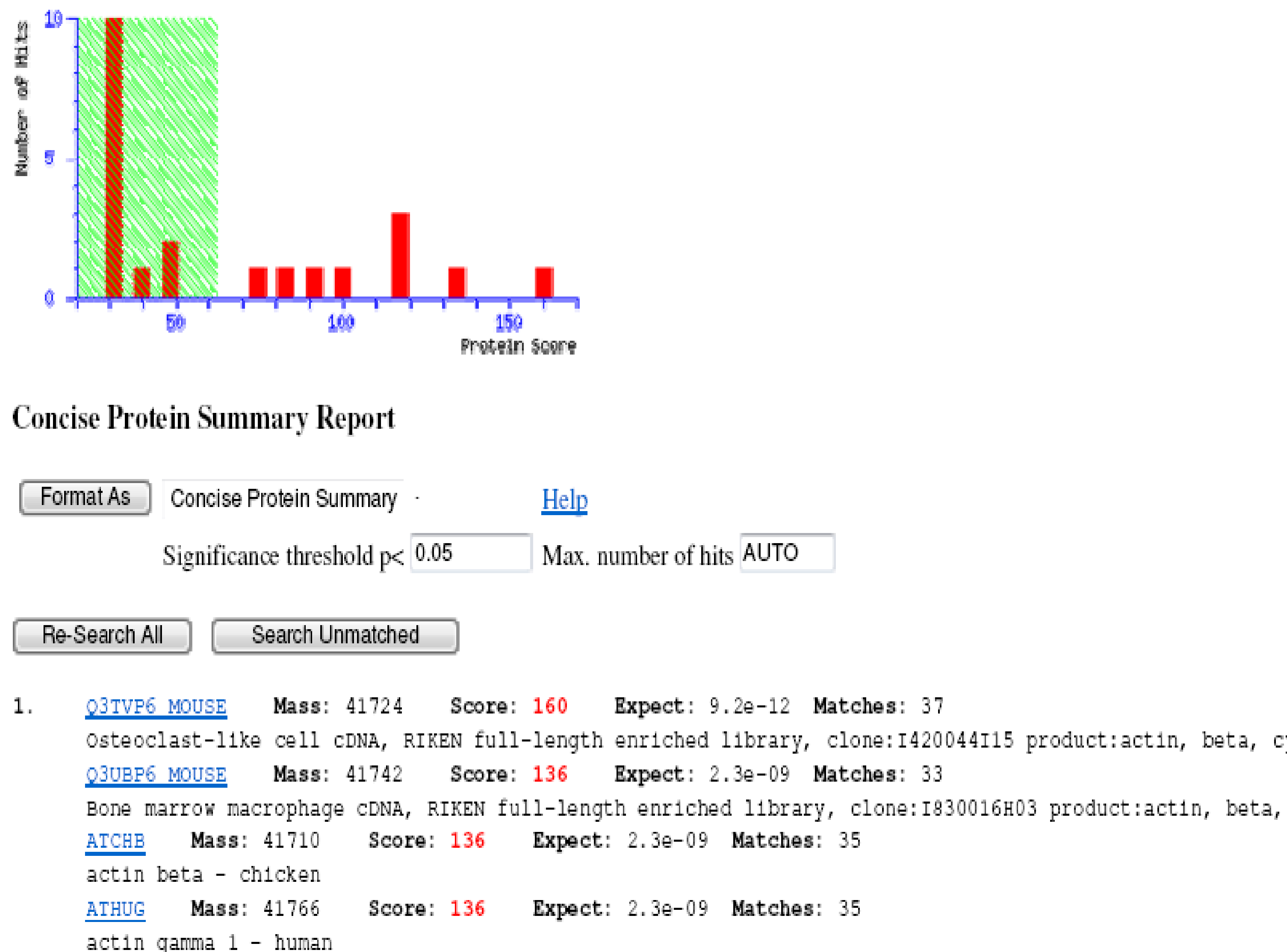
2807.5183
3183.8262
3250.6567



Concise Protein Summary Report

Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.     Q3TVP6_MOUSE     Mass: 41724     Score: 160     Expect: 9.2e-12   Matches: 37
       Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420044I15 product:actin, beta, c
       Q3UBP6_MOUSE     Mass: 41742     Score: 136     Expect: 2.3e-09   Matches: 33
       Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830016H03 product:actin, beta,
       ATCHB     Mass: 41710     Score: 136     Expect: 2.3e-09   Matches: 35
       actin beta - chicken
       ATHUG     Mass: 41766     Score: 136     Expect: 2.3e-09   Matches: 35
       actin gamma 1 - human
```

Protein View

```
Match to: Q3TVP6_MOUSE Score: 160 Expect: 9.2e-12
Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420044I15 product:acti
Found in search of pmf_K2_129990849010.txt

Nominal mass (Mr): 41724; Calculated pI value: 5.30
NCBI BLAST search of Q3TVP6_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 125
Number of mass values matched: 37
Sequence Coverage: 82%

Matched peptides shown in Bold Red

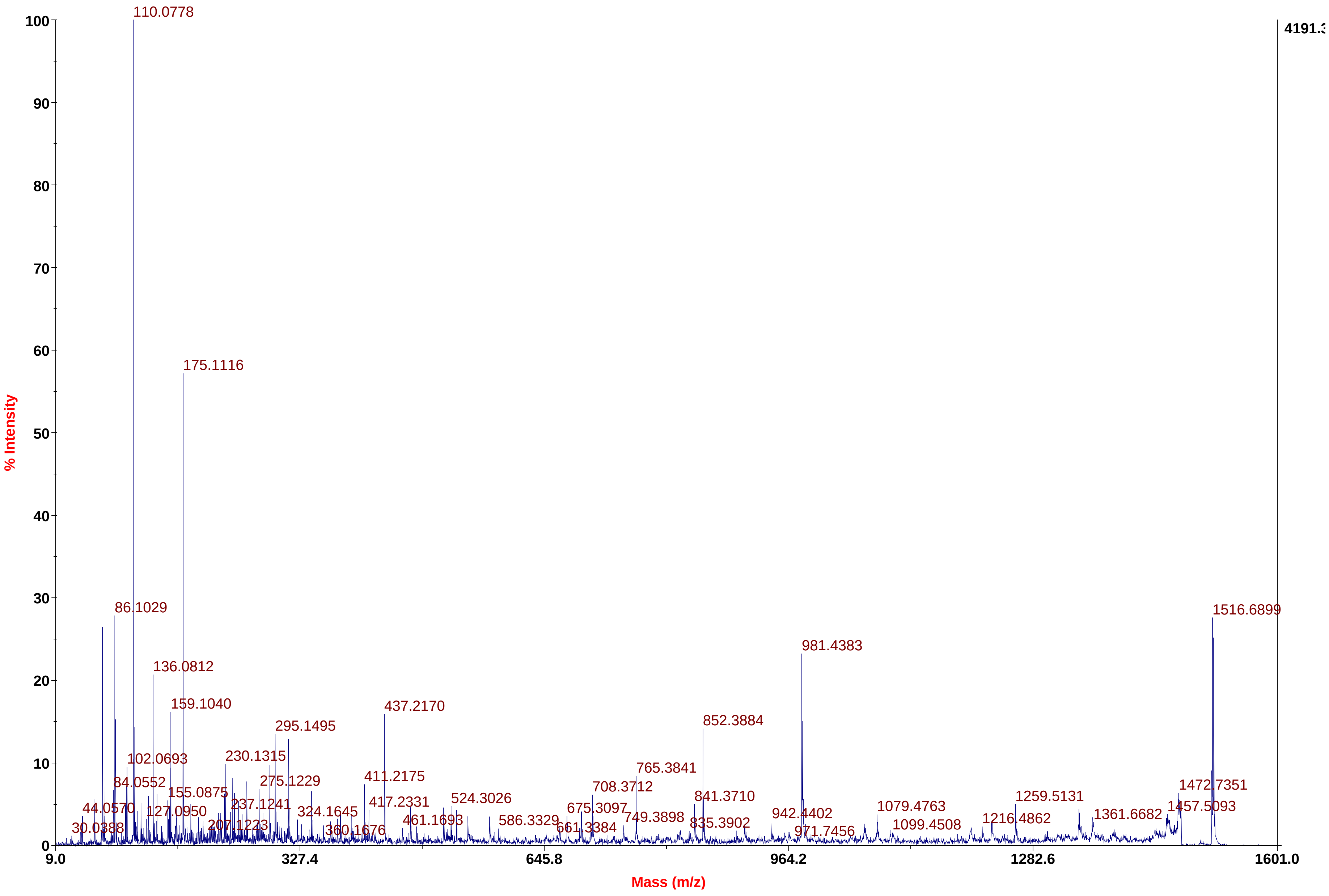
     1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK
    51 DSYVGDEAQS KRGILTLKYP IEHGIVTNWE DMEKIWHHTF YNELRVAPEE
   101 HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG
   151 IVMDSGDGVT HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF
   201 TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY ELPDGQVITI
   251 GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS
   301 GGTTMYPGIA DRMQKEITAL APSTMKIKII APPERKYSVW IGGSILASLS
   351 TFQQMWISKQ EYDESGPSIV HRKCF
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
  Start - End      Observed    Mr(expt)   Mr(calc)      ppm    Miss  Sequence
    19 - 28       976.5027    975.4955   975.4410        56      0   K.AGFAGDDAPR.A
    29 - 39      1198.7769   1197.7696  1197.6982        60      0   R.AVFPSIVGRPR.H
    40 - 50      1171.6378   1170.6305  1170.5638        57      0   R.HQGVMVGMGQK.D
    40 - 50      1173.6477   1172.6404  1172.5318        93      0   R.HQGVMVGMGQK.D  2 Deamidat
    40 - 50      1187.6346   1186.6273  1186.5587        58      0   R.HQGVMVGMGQK.D  Oxidation
    40 - 50      1203.6329   1202.6256  1202.5536        60      0   R.HQGVMVGMGQK.D  2 Oxidati
    51 - 62      1354.7119   1353.7046  1353.6161        65      1   K.DSYVGDEAQSKR.G
    69 - 84      1961.0471   1960.0398  1959.9036        69      0   K.YPIEHGIVTNWEDMEK.I
    69 - 84      1977.0839   1976.0766  1975.8986        90      0   K.YPIEHGIVTNWEDMEK.I  Oxida
    85 - 95      1515.8496   1514.8423  1514.7419        66      0   K.IWHHTFYNELR.V
    85 - 95      1516.8330   1515.8257  1515.7259        66      0   K.IWHHTFYNELR.V  Deamidate
    96 - 113     1954.1995   1953.1922  1953.0571        69      0   R.VAPEEHPVLLTEAPLNPK.A
    96 - 116     2295.3442   2294.3369  2294.2382        43      1   R.VAPEEHPVLLTEAPLNPKANR.E
```

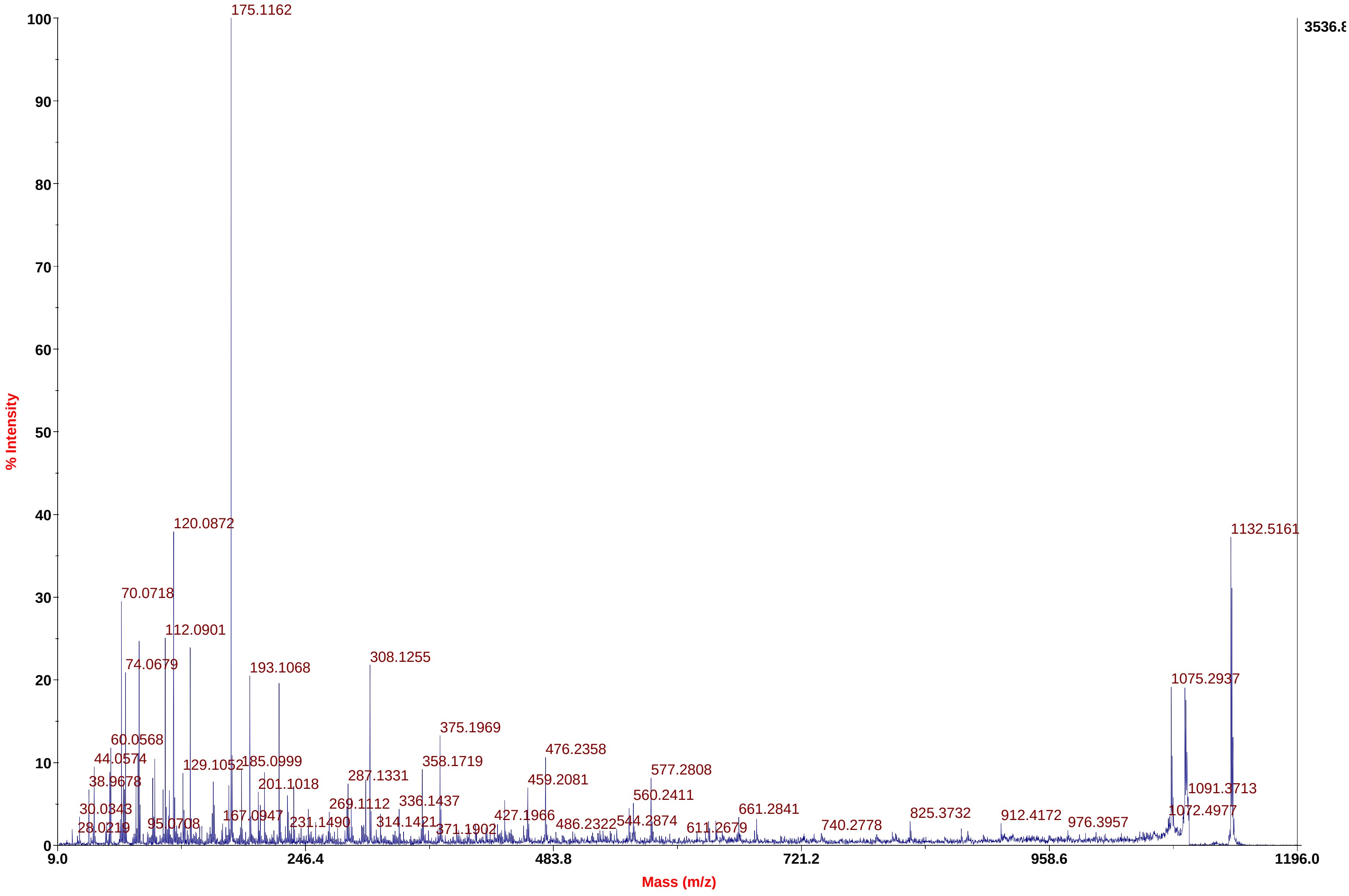
M11

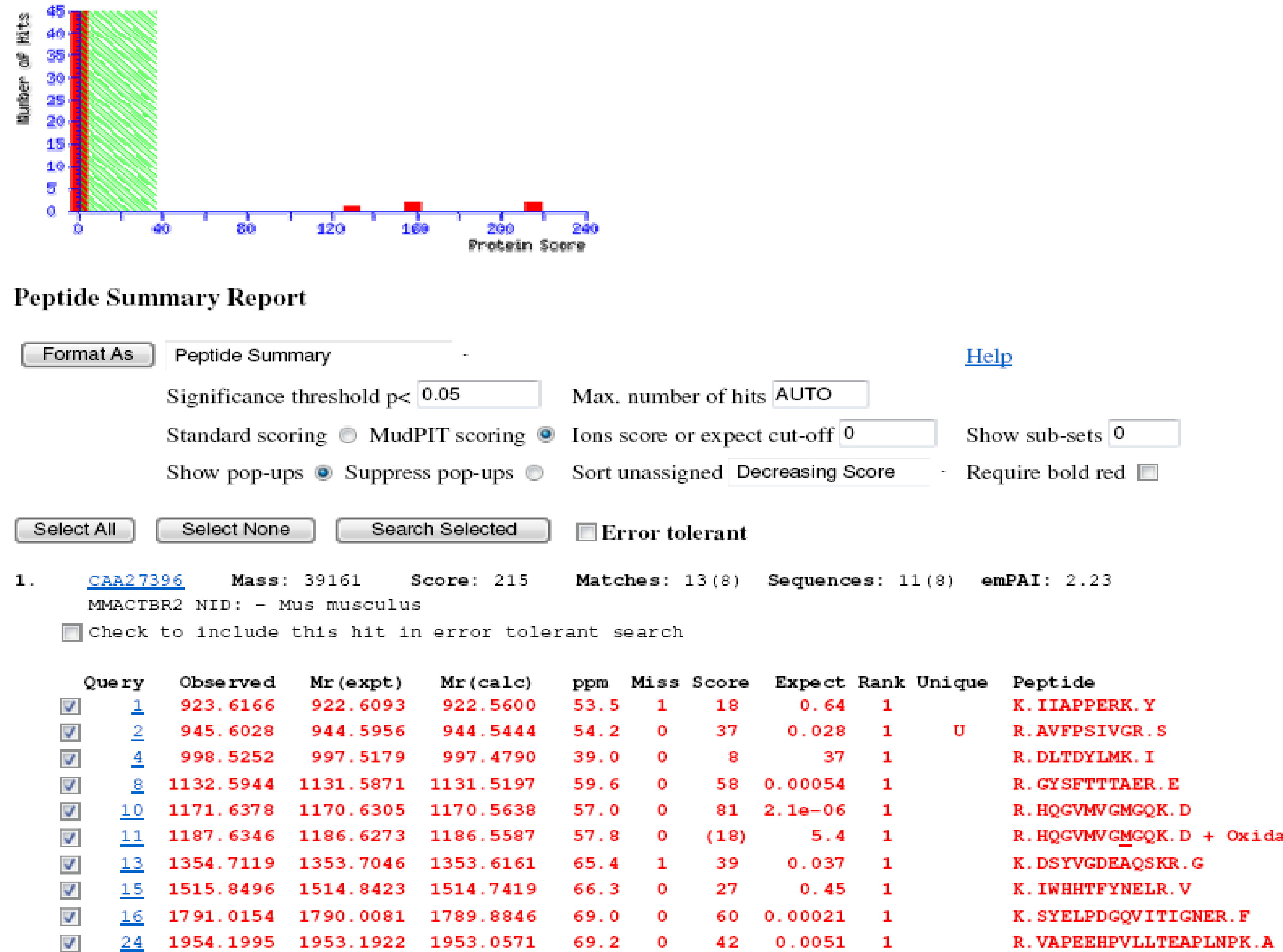
4700 MS/MS Precursor 1515.85 Spec #1 MC[BP = 110.1, 4191]



M11

4700 MS/MS Precursor 1132.59 Spec #1 MC[BP = 175.1, 3537]





Peptide Summary Report

Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

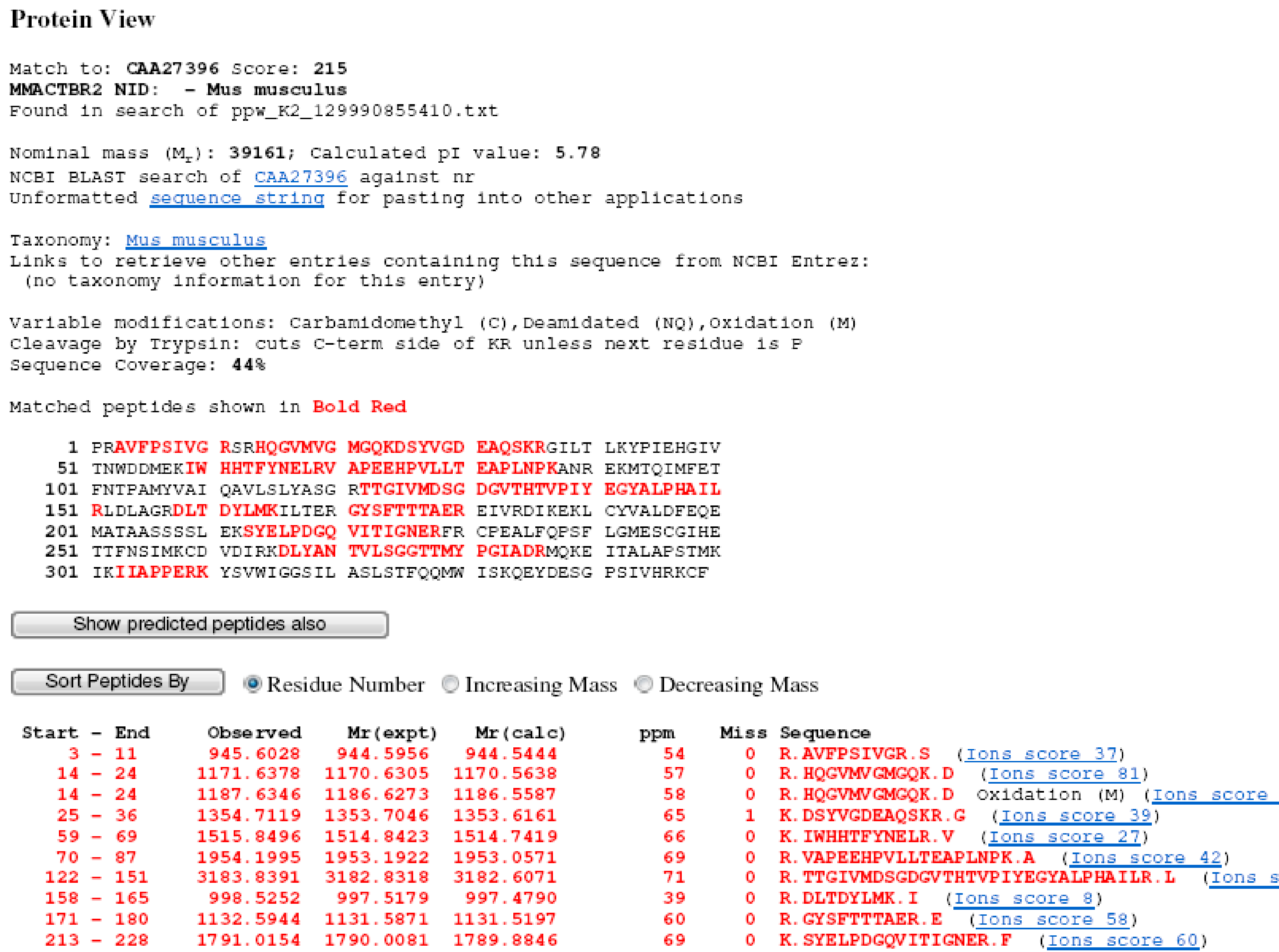
Sort unassigned Decreasing Score

Require bold red ☐

☐ **Error tolerant**

1. CAA27396 **Mass:** 39161 **Score:** 215 **Matches:** 13(8) **Sequences:** 11(8) **emPAI:** 2.23
MMACTBR2 NID: - Mus musculus
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	923.6166	922.6093	922.5600	53.5	1	18	0.64	1		K.IIAPPERK.Y
☑	2	945.6028	944.5956	944.5444	54.2	0	37	0.028	1	U	R.AVFPSIVGR.S
☑	4	998.5252	997.5179	997.4790	39.0	0	8	37	1		R.DLTDYLMK.I
☑	8	1132.5944	1131.5871	1131.5197	59.6	0	58	0.00054	1		R.GYSFTTTAER.E
☑	10	1171.6378	1170.6305	1170.5638	57.0	0	81	2.1e-06	1		R.HQGVMVGMGQK.D
☑	11	1187.6346	1186.6273	1186.5587	57.8	0	(18)	5.4	1		R.HQGVMVGMGQK.D + Oxida
☑	13	1354.7119	1353.7046	1353.6161	65.4	1	39	0.037	1		K.DSYVGDEAQSKR.G
☑	15	1515.8496	1514.8423	1514.7419	66.3	0	27	0.45	1		K.IWHHTFYNELR.V
☑	16	1791.0154	1790.0081	1789.8846	69.0	0	60	0.00021	1		K.SYELPDGQVITIGNER.F
☑	24	1954.1995	1953.1922	1953.0571	69.2	0	42	0.0051	1		R.VAPEEHPVLLTEAPLNPK.A



Protein View

```
Match to: CAA27396 Score: 215
MMACTBR2 NID:  - Mus musculus
Found in search of ppw_K2_129990855410.txt

Nominal mass (Mr): 39161; Calculated pI value: 5.78
NCBI BLAST search of CAA27396 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 44%

Matched peptides shown in Bold Red

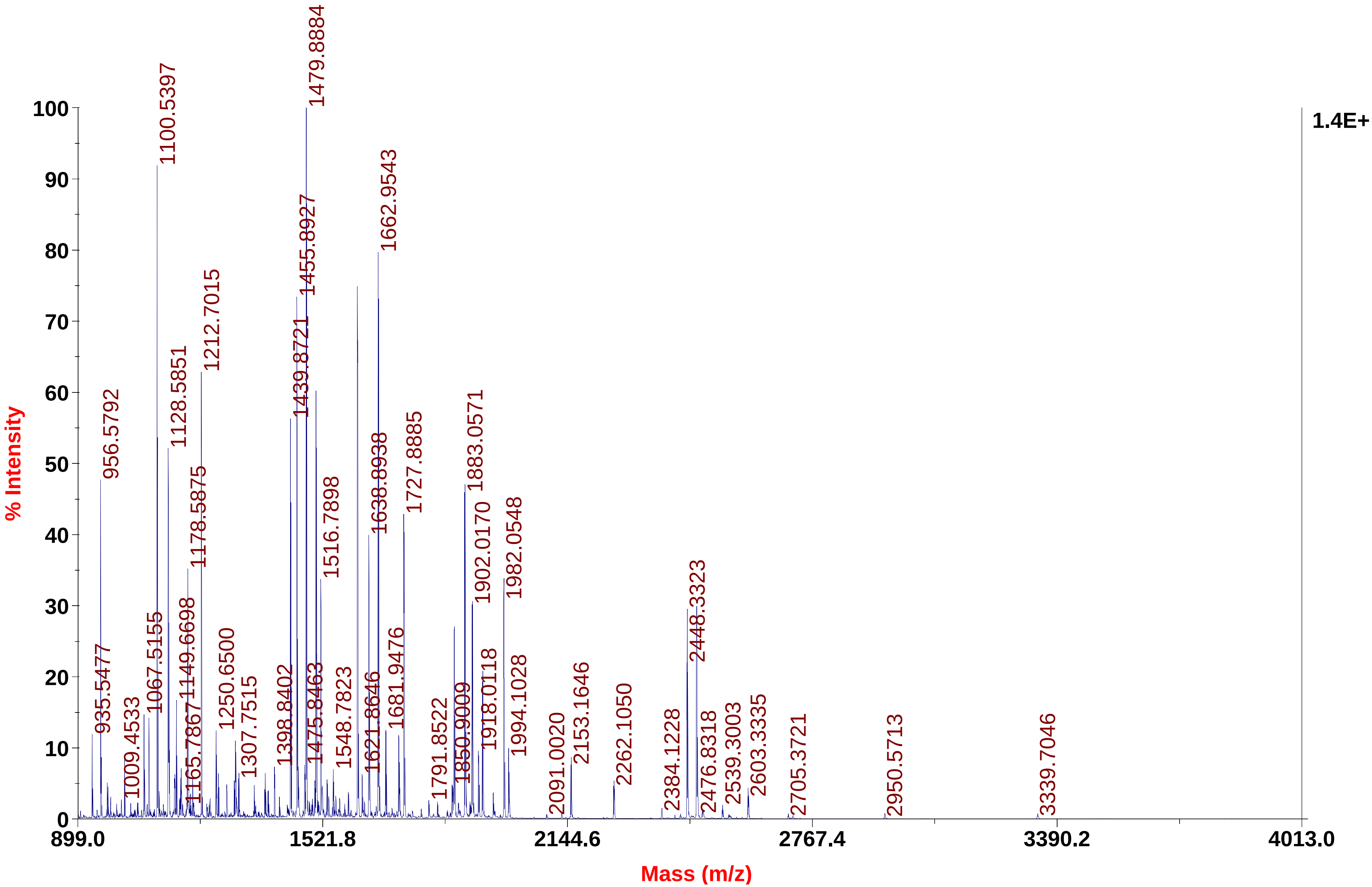
     1 PRAVFPSIVG RSRHQGVMVG MGQKDSYVGD EAQSKRGILT LKYPIEHGIV
    51 TNWDDMEKIW HHTFYNELRV APEEHPVLLT EAPLNPKANR EKMTQIMFET
   101 FNTPAMYVAI QAVLSLYASG RTTGIVMDSG DGVTHTVPIY EGYALPHAIL
   151 RLDLAGRDLT DYLMKILTER GYSFTTTAER EIVRDIKEKL CYVALDFEQE
   201 MATAASSSSL EKSYELPDGQ VITIGNERFR CPEALFQPSF LGMESCGIHE
   251 TTFNSIMKCD VDIRKDLYAN TVLSGGTTMY PGIADRMQKE ITALAPSTMK
   301 IKIIAPPERK YSVWIGGSIL ASLSTFQQMW ISKQEYDESG PSIVHRKCF
```

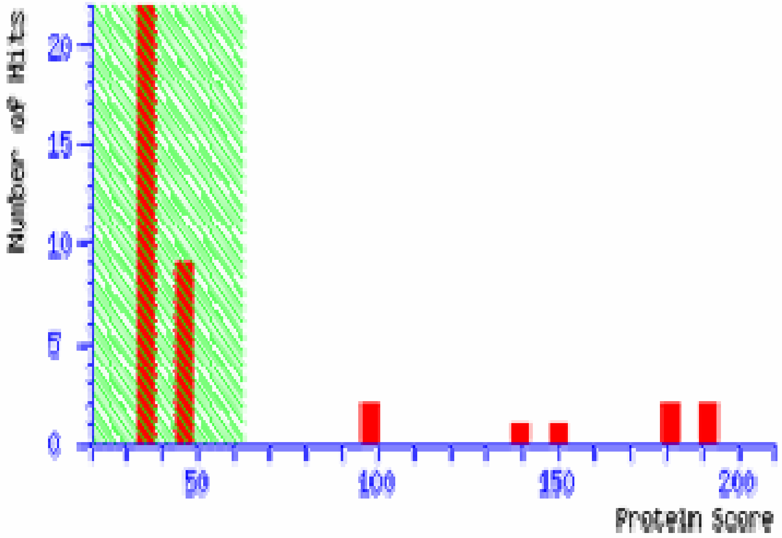
● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    3 - 11       945.6028   944.5956   944.5444       54     0   R.AVFPSIVGR.S  (Ions score 37)
   14 - 24      1171.6378  1170.6305  1170.5638       57     0   R.HQGVMVGMGQK.D  (Ions score 81)
   14 - 24      1187.6346  1186.6273  1186.5587       58     0   R.HQGVMVGMGQK.D  Oxidation (M)  (Ions score
   25 - 36      1354.7119  1353.7046  1353.6161       65     1   K.DSYVGDEAQSKR.G  (Ions score 39)
   59 - 69      1515.8496  1514.8423  1514.7419       66     0   K.IWHHTFYNELR.V  (Ions score 27)
   70 - 87      1954.1995  1953.1922  1953.0571       69     0   R.VAPEEHPVLLTEAPLNPK.A  (Ions score 42)
  122 - 151     3183.8391  3182.8318  3182.6071       71     0   R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  (Ions s
  158 - 165      998.5252   997.5179   997.4790       39     0   R.DLTDYLMK.I  (Ions score 8)
  171 - 180     1132.5944  1131.5871  1131.5197       60     0   R.GYSFTTTAER.E  (Ions score 58)
  213 - 228     1791.0154  1790.0081  1789.8846       69     0   K.SYELPDGQVITIGNER.F  (Ions score 60)
```

Sample M12

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1479.9, 14361]





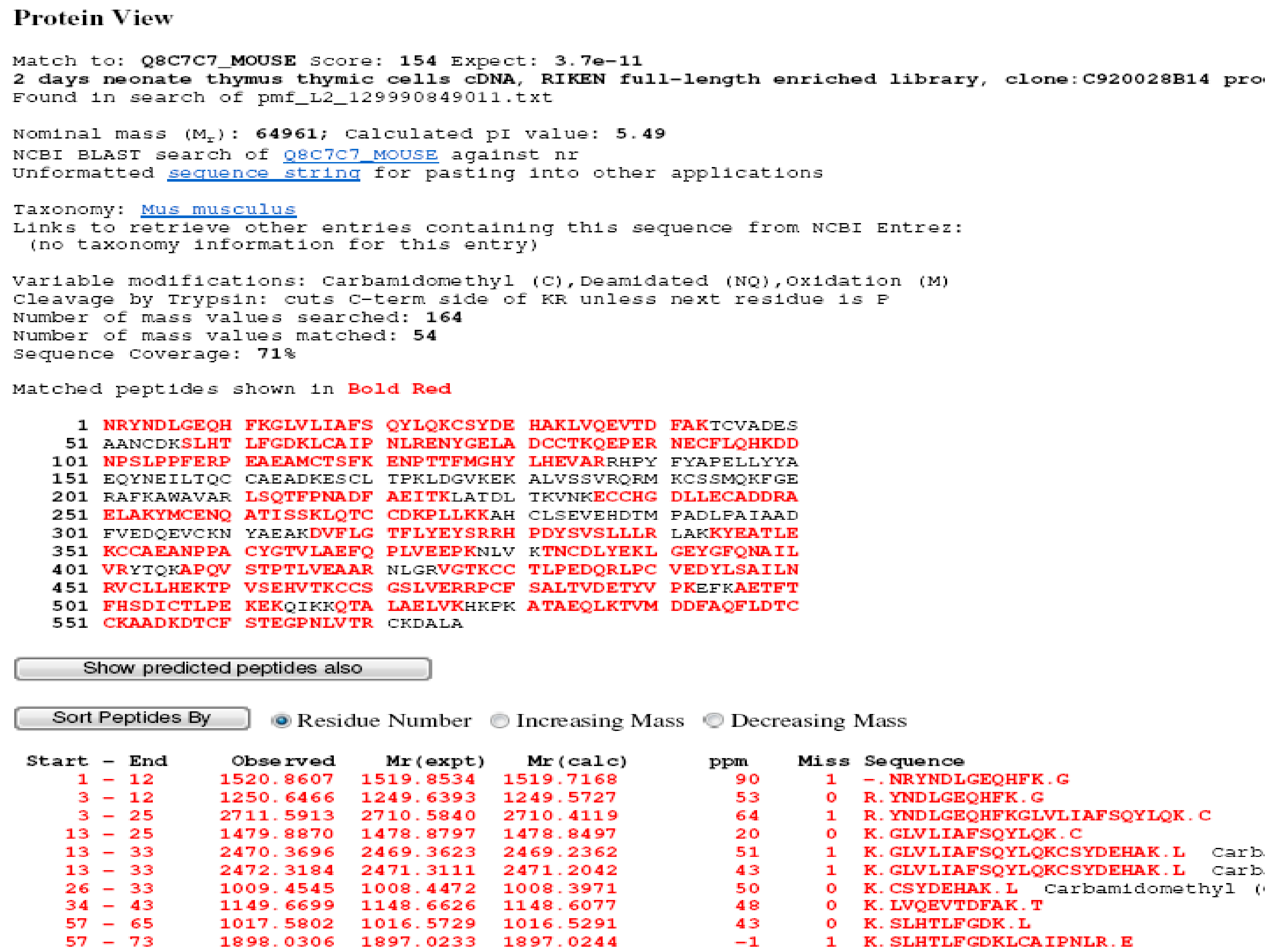
Concise Protein Summary Report

[Format As] Concise Protein Summary [Help](#)

Significance threshold p< 0.05 Max. number of hits AUTO

[Re-Search All] [Search Unmatched]

```
1.     Mixture 1     Total score: 192     Expect: 5.8e-15  Matches: 76
       Components (only one family member shown for each component):
       Q8C7C7_MOUSE     Mass: 64961     Score: 154     Expect: 3.7e-11  Matches: 54
       2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920028B14 product:albumin 1,
       AAB49490     Mass: 50514     Score: 98     Expect: 1.4e-05  Matches: 27
       MMU89889 NID: - Mus musculus
```



Protein View

```
Match to: Q8C7C7_MOUSE Score: 154 Expect: 3.7e-11
2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920028B14 pro
Found in search of pmf_L2_129990849011.txt

Nominal mass (Mr): 64961; Calculated pI value: 5.49
NCBI BLAST search of Q8C7C7_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 164
Number of mass values matched: 54
Sequence Coverage: 71%

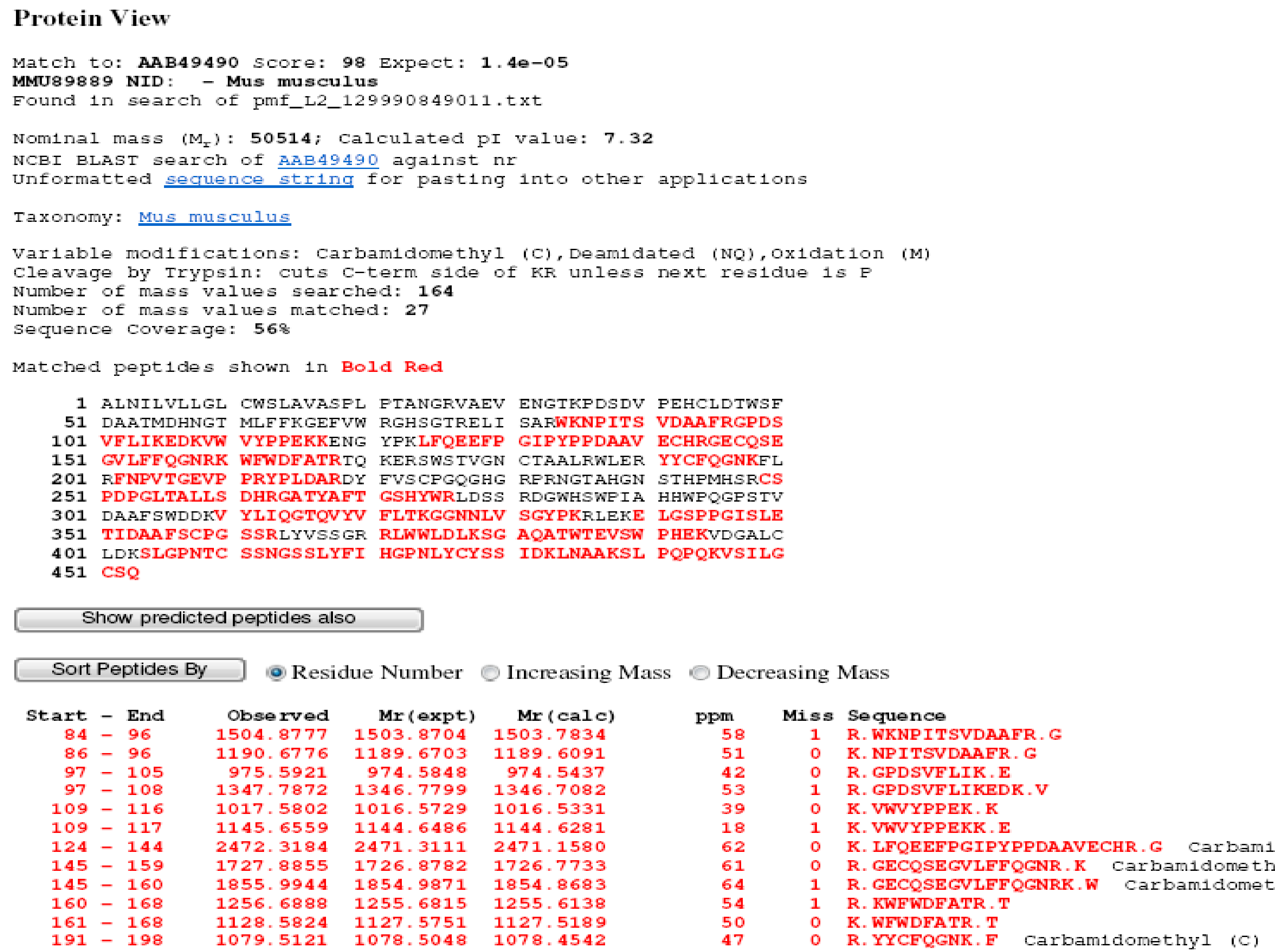
Matched peptides shown in Bold Red

     1 NRYNDLGEQH FKGLVLIAFS QYLQKCSYDE HAKLVQEVTD FAKTCVADES
    51 AANCDKSLHT LFGDKLCAIP NLRENYGELA DCCTKQEPER NECFLQHKDD
   101 NPSLPPFERP EAEAMCTSFK ENPTTFMGHY LHEVARRHPY FYAPELLYYA
   151 EQYNEILTQC CAEADKESCL TPKLDGVKEK ALVSSVRQRM KCSSMQKFGE
   201 RAFKAWAVAR LSQTFPNADF AEITKLATDL TKVNKECCHG DLLECADDRA
   251 ELAKYMCENQ ATISSKLQTC CDKPLLKKAH CLSEVEHDTM PADLPAIAAD
   301 FVEDQEVCKN YAEAKDVFLG TFLYEYSRRH PDYSVSLLLR LAKKYEATLE
   351 KCCAEANPPA CYGTVLAEFQ PLVEEPKNLV KTNCDLYEKL GEYGFQNAIL
   401 VRYTQKAPQV STPTLVEAAR NLGRVGTKCC TLPEDQRLPC VEDYLSAILN
   451 RVCLLHEKTP VSEHVTKCCS GSLVERRPCF SALTVDETYV PKEFKAETFT
   501 FHSDICTLPE KEKQIKKQTA LAELVKHKPK ATAEQLKTVM DDFAQFLDTC
   551 CKAADKDTCF STEGPNLVTR CKDALA
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss  Sequence
     1 - 12    1520.8607  1519.8534  1519.7168      90     1   -.NRYNDLGEQHFK.G
     3 - 12    1250.6466  1249.6393  1249.5727      53     0   R.YNDLGEQHFK.G
     3 - 25    2711.5913  2710.5840  2710.4119      64     1   R.YNDLGEQHFKGLVLIAFSQYLQK.C
    13 - 25    1479.8870  1478.8797  1478.8497      20     0   K.GLVLIAFSQYLQK.C
    13 - 33    2470.3696  2469.3623  2469.2362      51     1   K.GLVLIAFSQYLQKCSYDEHAK.L  Carb
    13 - 33    2472.3184  2471.3111  2471.2042      43     1   K.GLVLIAFSQYLQKCSYDEHAK.L  Carb
    26 - 33    1009.4545  1008.4472  1008.3971      50     0   K.CSYDEHAK.L  Carbamidomethyl (
    34 - 43    1149.6699  1148.6626  1148.6077      48     0   K.LVQEVTDFAK.T
    57 - 65    1017.5802  1016.5729  1016.5291      43     0   K.SLHTLFGDK.L
    57 - 73    1898.0306  1897.0233  1897.0244      -1     1   K.SLHTLFGDKLCAIPNLR.E
```



Protein View

```
Match to: AAB49490 Score: 98 Expect: 1.4e-05
MMU89889 NID:  - Mus musculus
Found in search of pmf_L2_129990849011.txt

Nominal mass (Mr): 50514; Calculated pI value: 7.32
NCBI BLAST search of AAB49490 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

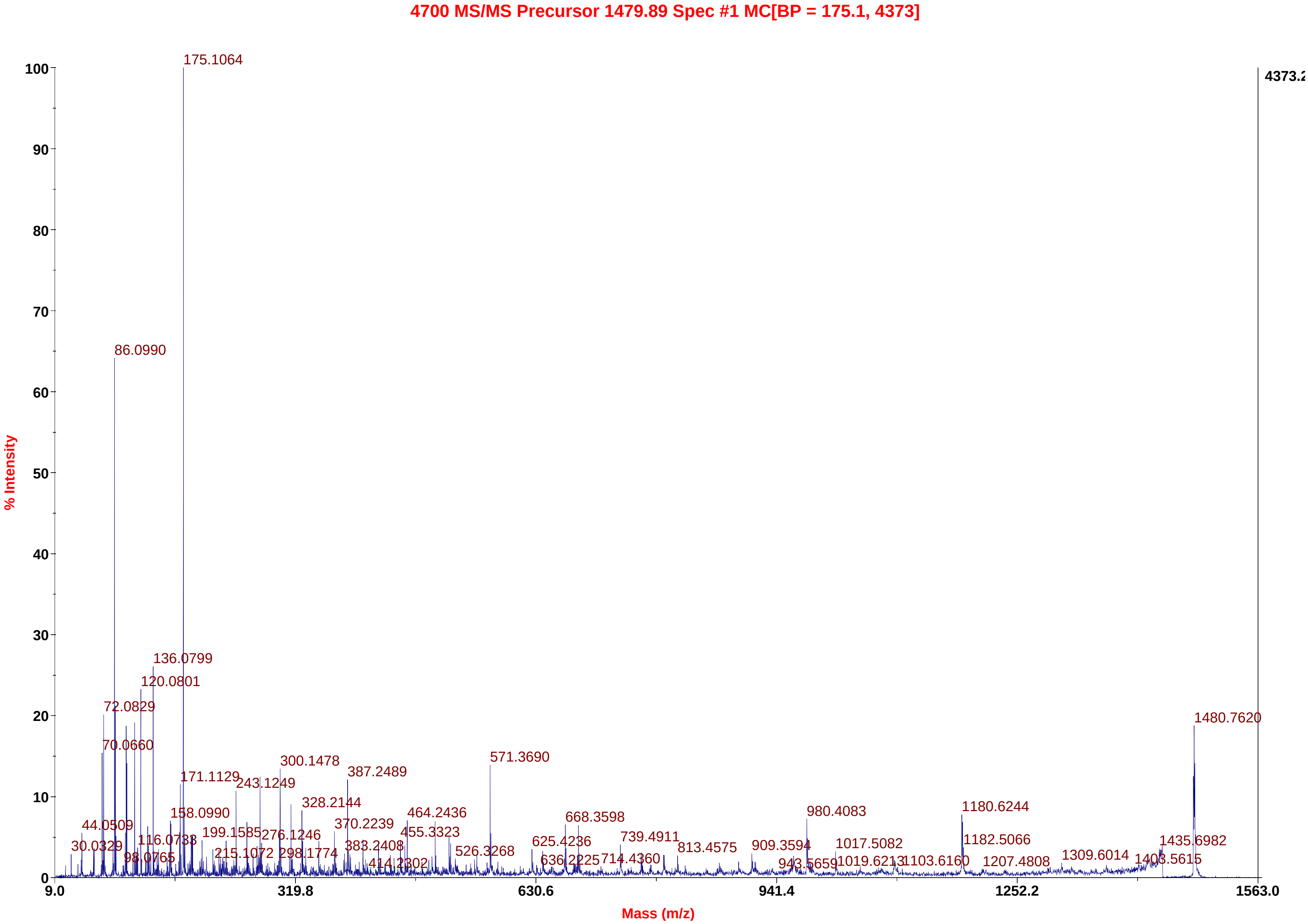
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 164
Number of mass values matched: 27
Sequence Coverage: 56%

Matched peptides shown in Bold Red

     1 ALNILVLLGL CWSLAVASPL PTANGRVAEV ENGTKPDSDV PEHCLDTWSF
    51 DAATMDHNGT MLFFKGEFVW RGHSGTRELI SARWKNPITS VDAAFRGPDS
   101 VFLIKEDKVW VYPPEKKENG YPKLFQEEFP GIPYPPDAAV ECHRGECQSE
   151 GVLFFQGNRK WFWDFATRTQ KERSWSTVGN CTAALRWLER YYCFQGNKFL
   201 RFNPVTGEVP PRYPLDARDY FVSCPGQGHG RPRNGTAHGN STHPMHSRCS
   251 PDPGLTALLS DHRGATYAFT GSHYWRLDSS RDGWHSWPIA HHWPQGPSTV
   301 DAAFSWDDKV YLIQGTQVYV FLTKGGNNLV SGYPKRLEKE LGSPPGISLE
   351 TIDAAFSCPG SSRLYVSSGR RLWWLDLKSG AQATWTEVSW PHEKVDGALC
   401 LDKSLGPNTC SSNGSSLYFI HGPNLYCYSS IDKLNAAKSL PQPQKVSILG
   451 CSQ
```

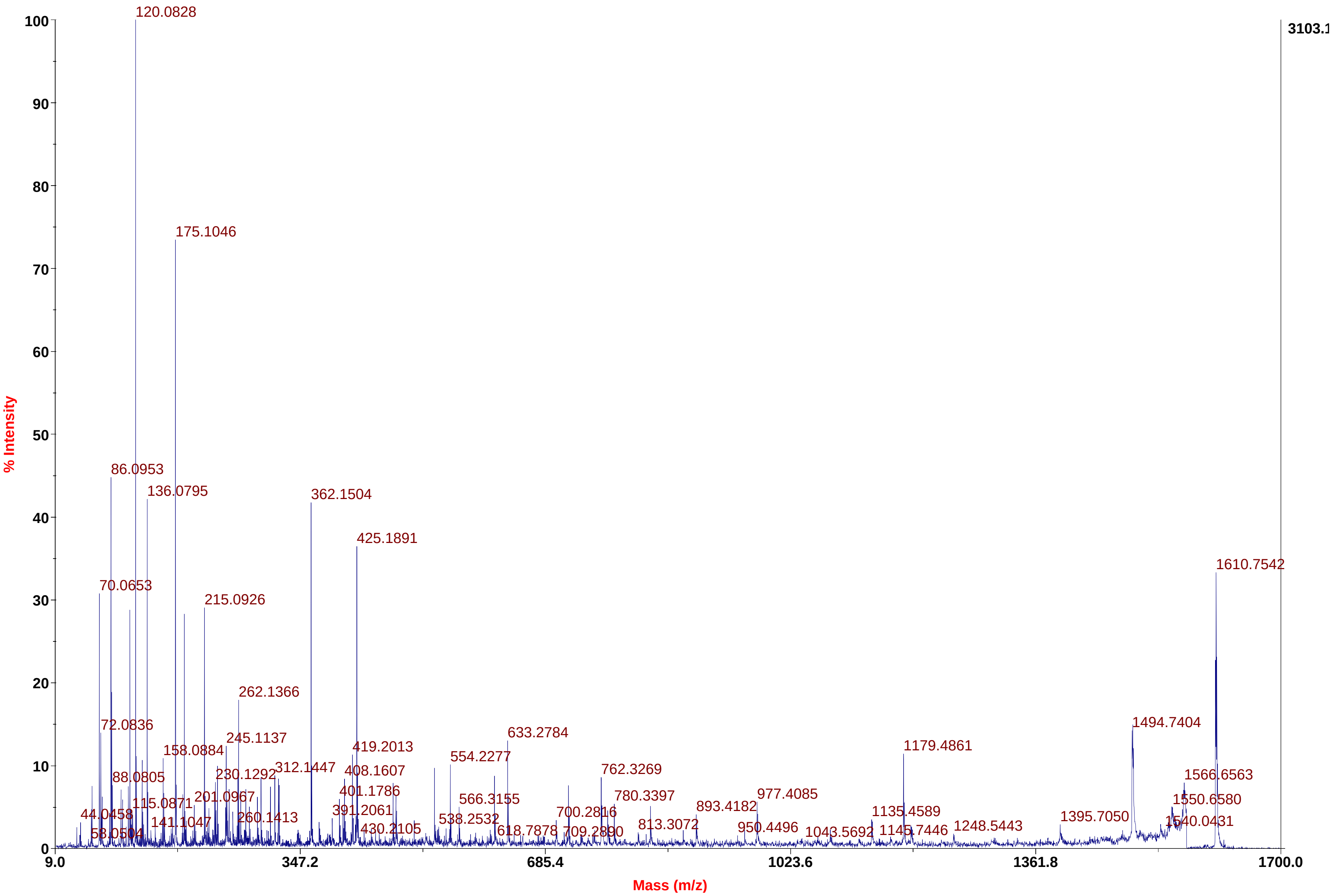
```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   84 - 96      1504.8777  1503.8704  1503.7834       58      1  R.WKNPITSVDAAFR.G
   86 - 96      1190.6776  1189.6703  1189.6091       51      0  K.NPITSVDAAFR.G
   97 - 105     975.5921   974.5848   974.5437        42      0  R.GPDSVFLIK.E
   97 - 108     1347.7872  1346.7799  1346.7082       53      1  R.GPDSVFLIKEDK.V
  109 - 116     1017.5802  1016.5729  1016.5331       39      0  K.VWVYPPEK.K
  109 - 117     1145.6559  1144.6486  1144.6281       18      1  K.VWVYPPEKK.E
  124 - 144     2472.3184  2471.3111  2471.1580       62      0  K.LFQEEFPGIPYPPDAAVECHR.G  Carbami
  145 - 159     1727.8855  1726.8782  1726.7733       61      0  R.GECQSEGVLFFQGNR.K  Carbamidometh
  145 - 160     1855.9944  1854.9871  1854.8683       64      1  R.GECQSEGVLFFQGNRK.W  Carbamidomet
  160 - 168     1256.6888  1255.6815  1255.6138       54      1  R.KWFWDFATR.T
  161 - 168     1128.5824  1127.5751  1127.5189       50      0  K.WFWDFATR.T
  191 - 198     1079.5121  1078.5048  1078.4542       47      0  R.YYCFQGNK.F  Carbamidomethyl (C)
```

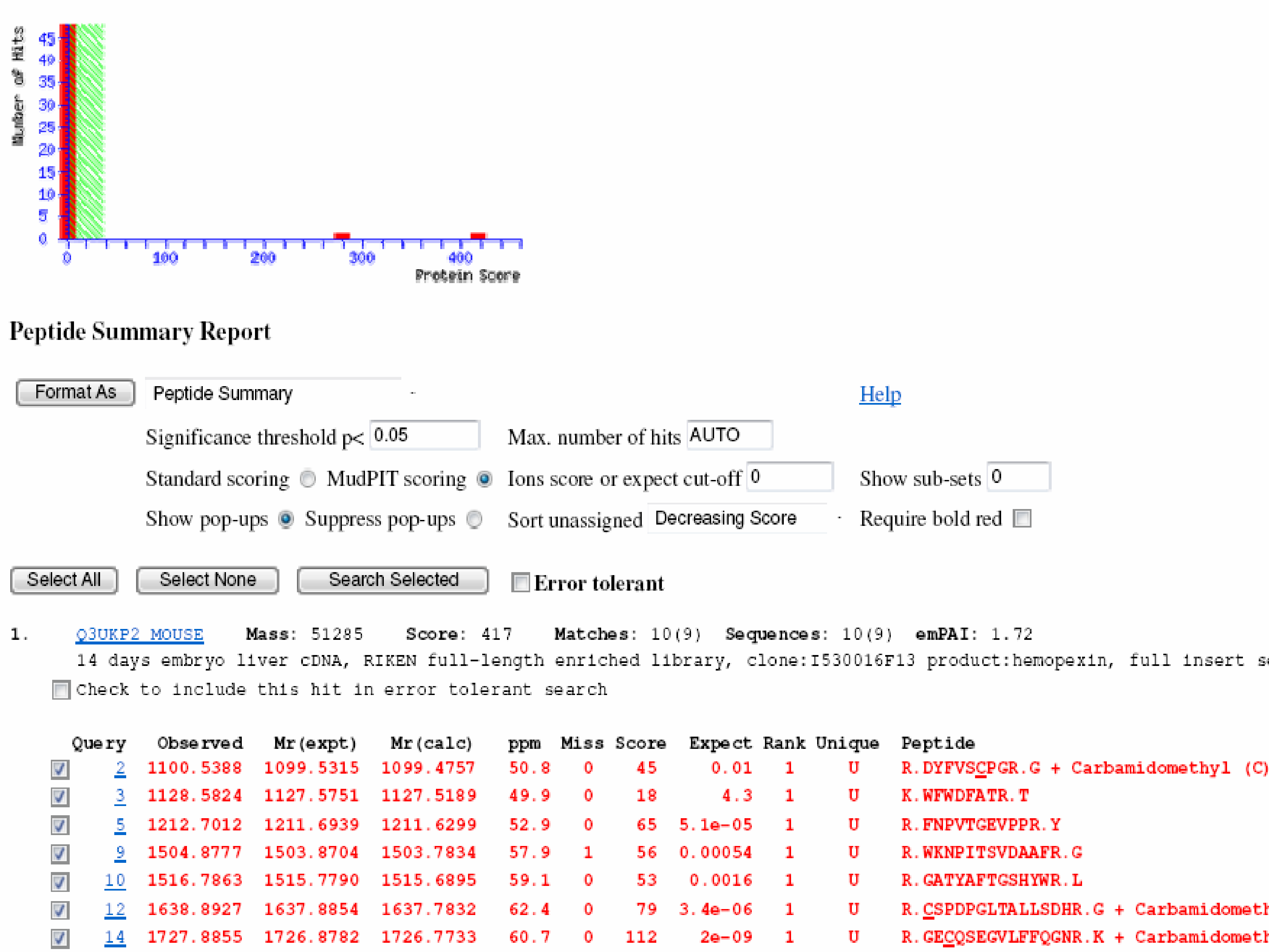
M12


4700 MS/MS Precursor 1479.89 Spec #1 MC[BP = 175.1, 4373]
% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
4373.2
9.0
319.8
630.6
941.4
1252.2
1563.0
175.1064
86.0990
136.0799
120.0801
72.0829
70.0660
44.0509
30.0329
116.0733
98.0765
171.1129
158.0990
199.1585
215.1072
243.1249
276.1246
298.1774
300.1478
328.2144
370.2239
383.2408
387.2489
414.2302
455.3323
464.2436
526.3268
571.3690
625.4236
636.2225
668.3598
714.4360
739.4911
813.4575
909.3594
943.5659
980.4083
1017.5082
1019.6213
1103.6160
1180.6244
1182.5066
1207.4808
1309.6014
1403.5615
1435.6982
1480.7620

M12

4700 MS/MS Precursor 1609.88 Spec #1 MC[BP = 120.1, 3103]





Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05   Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●   Ions score or expect cut-off 0   Show sub-sets 0

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

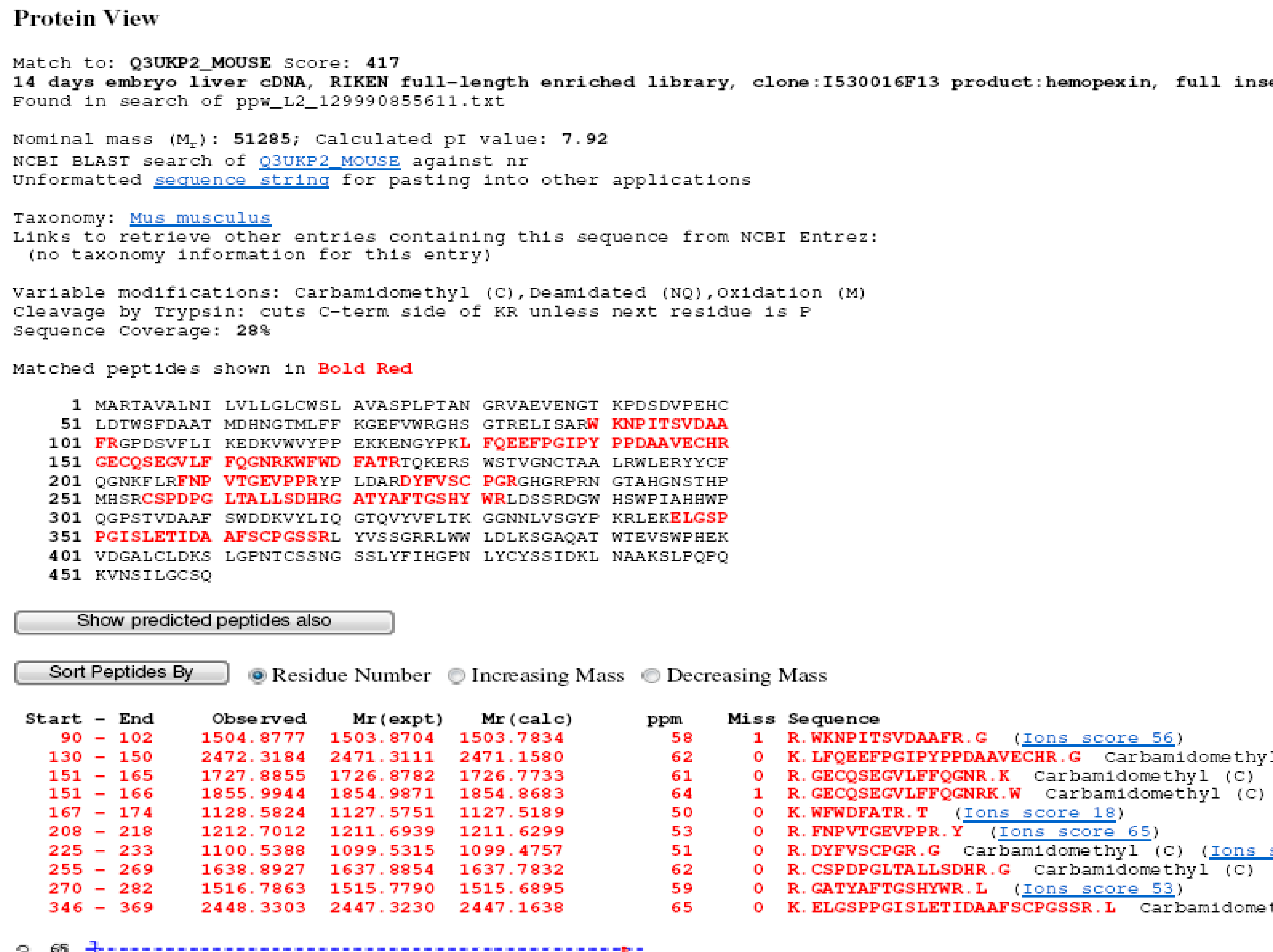
Select All | Select None | Search Selected | ☐ **Error tolerant**

1. Q3UKP2_MOUSE **Mass:** 51285 **Score:** 417 **Matches:** 10(9) **Sequences:** 10(9) **emPAI:** 1.72

14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full insert s

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	2	1100.5388	1099.5315	1099.4757	50.8	0	45	0.01	1	U	R.DYFVSCPGR.G + Carbamidomethyl (C
☑	3	1128.5824	1127.5751	1127.5189	49.9	0	18	4.3	1	U	K.WFWDFATR.T
☑	5	1212.7012	1211.6939	1211.6299	52.9	0	65	5.1e-05	1	U	R.FNPVTGEVPPR.Y
☑	9	1504.8777	1503.8704	1503.7834	57.9	1	56	0.00054	1	U	R.WKNPITSVDAAFR.G
☑	10	1516.7863	1515.7790	1515.6895	59.1	0	53	0.0016	1	U	R.GATYAFTGSHYWR.L
☑	12	1638.8927	1637.8854	1637.7832	62.4	0	79	3.4e-06	1	U	R.CSPDPGLTALLSDHR.G + Carbamidometh
☑	14	1727.8855	1726.8782	1726.7733	60.7	0	112	2e-09	1	U	R.GECQSEGVLFFQGNR.K + Carbamidometh



Protein View

```
Match to: Q3UKP2_MOUSE Score: 417
14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full inse
Found in search of ppw_L2_129990855611.txt

Nominal mass (Mr): 51285; Calculated pI value: 7.92
NCBI BLAST search of Q3UKP2_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 28%

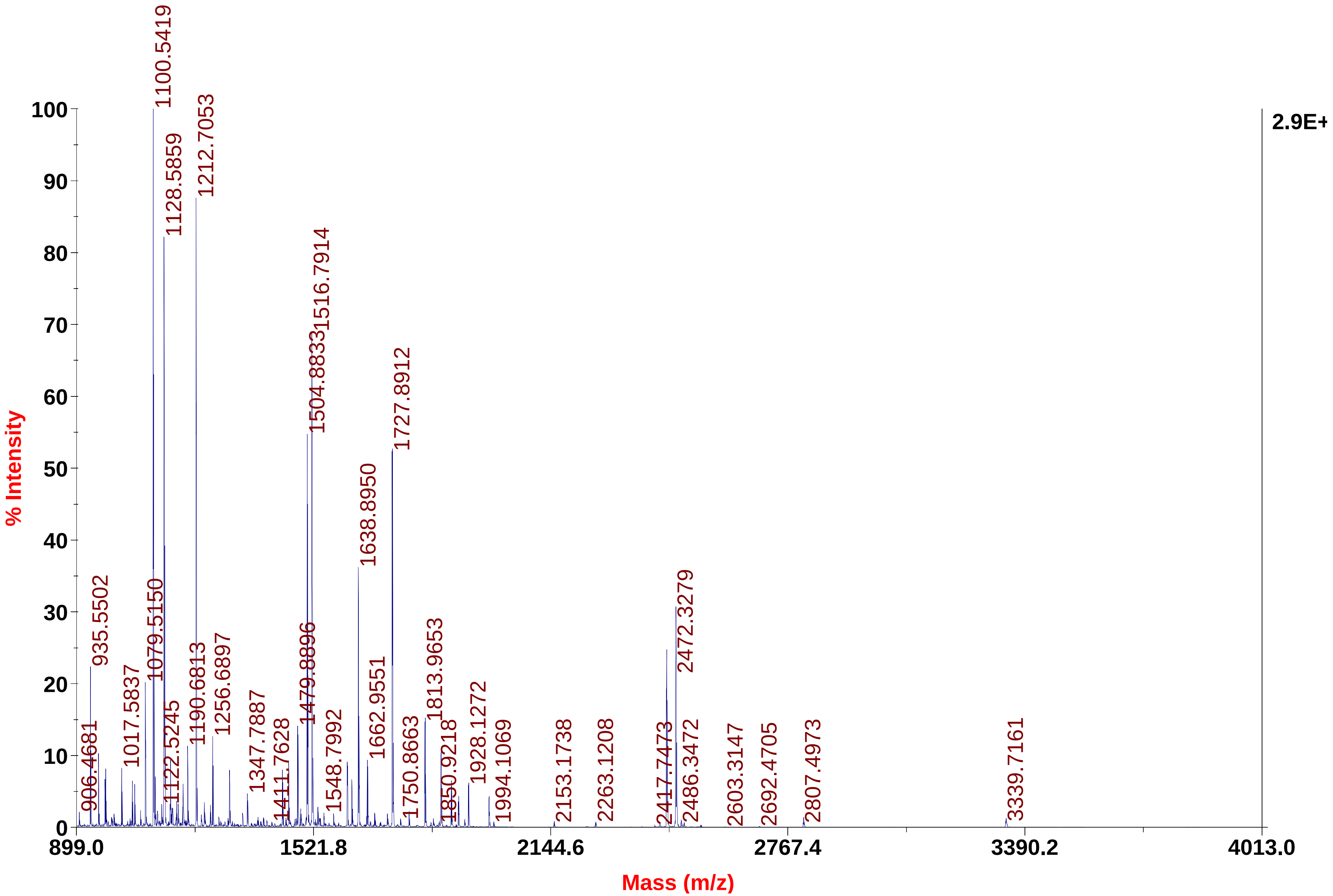
Matched peptides shown in Bold Red

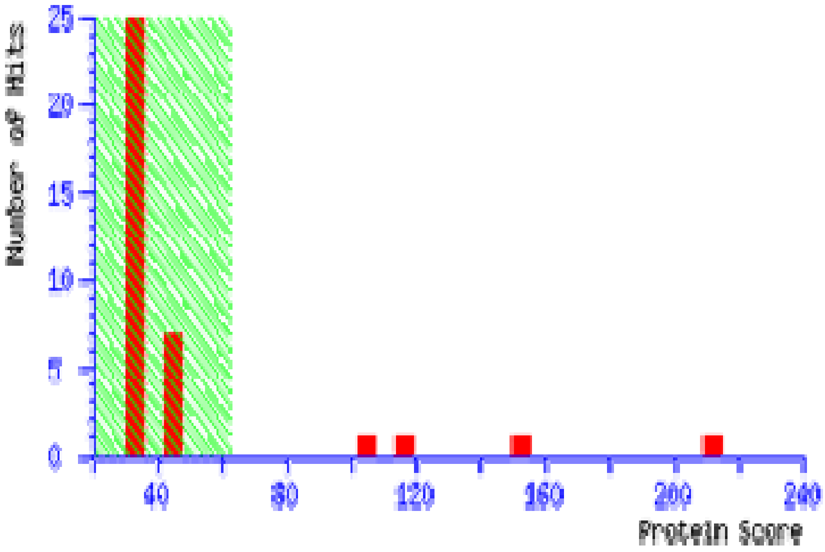
      1 MARTAVALNI LVLLGLCWSL AVASPLPTAN GRVAEVENGT KPDSDVPEHC
     51 LDTWSFDAAT MDHNGTMLFF KGEFVWRGHS GTRELISARW KNPITSVDAA
    101 FRGPDSVFLI KEDKVWVYPP EKKENGYPKL FQEEFPGIPY PPDAAVECHR
    151 GECQSEGVLF FQGNRKWFWD FATRTQKERS WSTVGNCTAA LRWLERYYCF
    201 QGNKFLRFNP VTGEVPPRYP LDARDYFVSC PGRGHGRPRN GTAHGNSTHP
    251 MHSRCSPDPG LTALLSDHRG ATYAFTGSHY WRLDSSRDGW HSWPIAHHWP
    301 QGPSTVDAAF SWDDKVYLIQ GTQVYVFLTK GGNNLVSGYP KRLEKELGSP
    351 PGISLETIDA AFSCPGSSRL YVSSGRRLWW LDLKSGAQAT WTEVSWPHEK
    401 VDGALCLDKS LGPNTCSSNG SSLYFIHGPN LYCYSSIDKL NAAKSLPQPQ
    451 KVNSILGCSQ
```

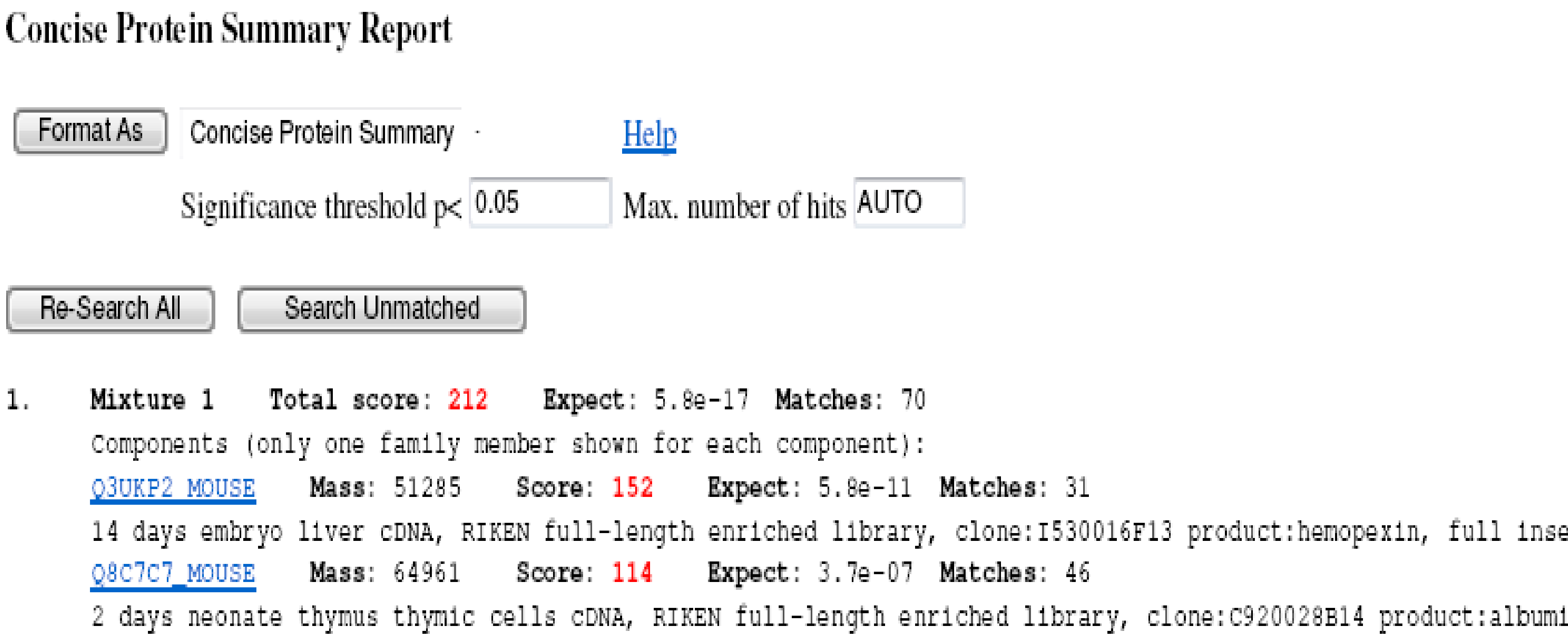
```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm  Miss Sequence
   90 - 102    1504.8777  1503.8704  1503.7834      58    1  R.WKNPITSVDAAFR.G  (Ions score 56)
  130 - 150    2472.3184  2471.3111  2471.1580      62    0  K.LFQEEFPGIPYPPDAAVECHR.G  Carbamidomethy
  151 - 165    1727.8855  1726.8782  1726.7733      61    0  R.GECQSEGVLFFQGNR.K  Carbamidomethyl (C)
  151 - 166    1855.9944  1854.9871  1854.8683      64    1  R.GECQSEGVLFFQGNRK.W  Carbamidomethyl (C)
  167 - 174    1128.5824  1127.5751  1127.5189      50    0  K.WFWDFATR.T  (Ions score 18)
  208 - 218    1212.7012  1211.6939  1211.6299      53    0  R.FNPVTGEVPPR.Y  (Ions score 65)
  225 - 233    1100.5388  1099.5315  1099.4757      51    0  R.DYFVSCPGR.G  Carbamidomethyl (C) (Ions
  255 - 269    1638.8927  1637.8854  1637.7832      62    0  R.CSPDPGLTALLSDHR.G  Carbamidomethyl (C)
  270 - 282    1516.7863  1515.7790  1515.6895      59    0  R.GATYAFTGSHYWR.L  (Ions score 53)
  346 - 369    2448.3303  2447.3230  2447.1638      65    0  K.ELGSPPGISLETIDAAFSCPGSSR.L  Carbamidome
```

Sample M13

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1100.5, 28668]



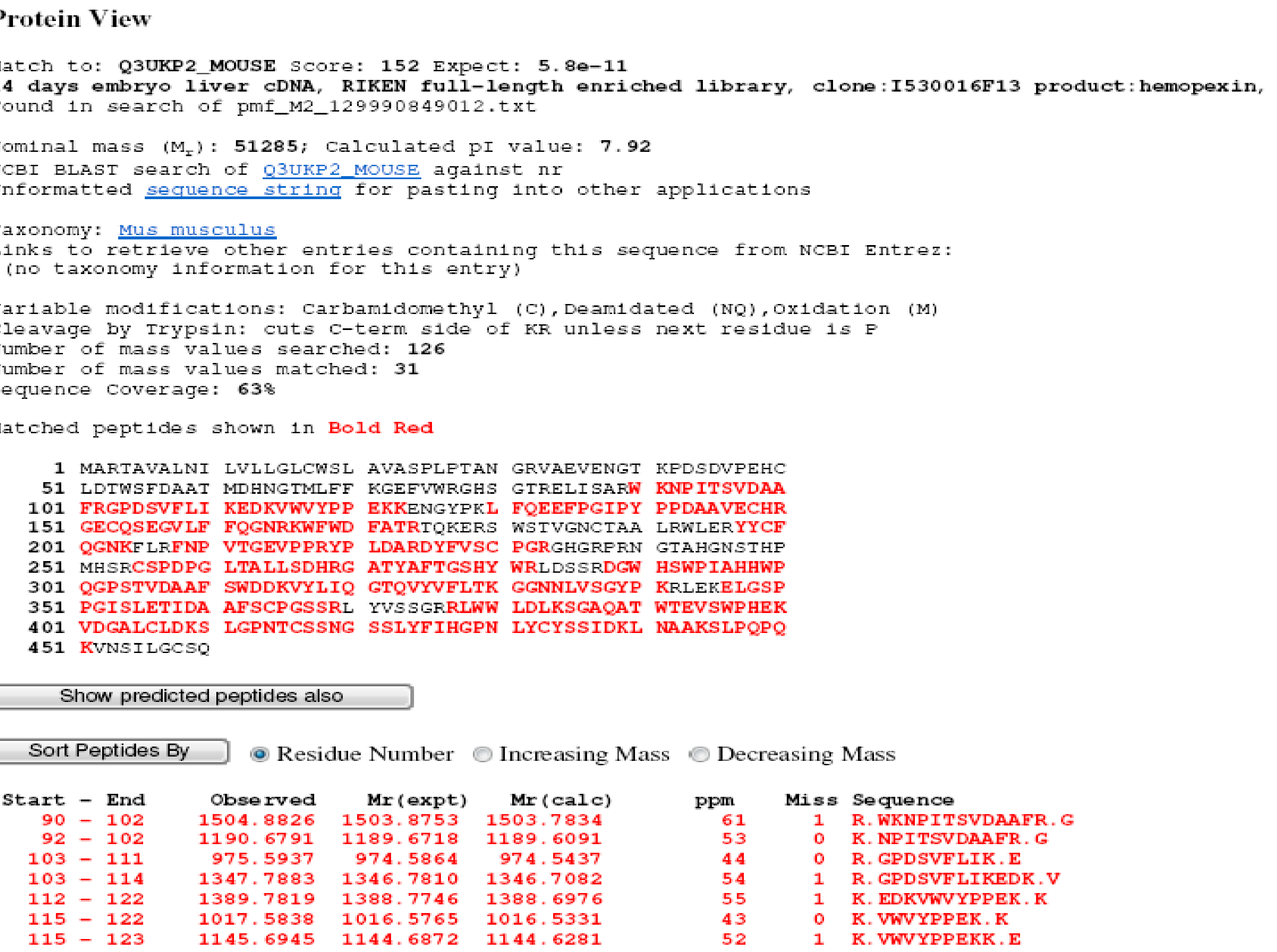




Concise Protein Summary Report

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.     Mixture 1    Total score: 212    Expect: 5.8e-17  Matches: 70
       Components (only one family member shown for each component):
       Q3UKP2_MOUSE    Mass: 51285    Score: 152    Expect: 5.8e-11  Matches: 31
       14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full inse
       Q8C7C7_MOUSE    Mass: 64961    Score: 114    Expect: 3.7e-07  Matches: 46
       2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920028B14 product:albumi
```



rotein View

```
atch to: Q3UKP2_MOUSE Score: 152 Expect: 5.8e-11
4 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin,
ound in search of pmf_M2_129990849012.txt

ominal mass (Mr): 51285; Calculated pI value: 7.92
CBI BLAST search of Q3UKP2_MOUSE against nr
nformatted sequence string for pasting into other applications

axonomy: Mus musculus
inks to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

ariable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
leavage by Trypsin: cuts C-term side of KR unless next residue is P
umber of mass values searched: 126
umber of mass values matched: 31
equence Coverage: 63%

atched peptides shown in Bold Red

   1 MARTAVALNI LVLLGLCWSL AVASPLPTAN GRVAEVENGT KPDSDVPEHC
  51 LDTWSFDAAT MDHNGTMLFF KGEFVWRGHS GTRELISARW KNPITSVDAA
 101 FRGPDSVFLI KEDKVWVYPP EKKENGYPKL FQEEFPGIPY PPDAAVECHR
 151 GECQSEGVLF FQGNRKWFWD FATRTQKERS WSTVGNCTAA LRWLERYYCF
 201 QGNKFLRFNP VTGEVPPRYP LDARDYFVSC PGRGHGRPRN GTAHGNSTHP
 251 MHSRCSPDPG LTALLSDHRG ATYAFTGSHY WRLDSSRDGW HSWPIAHHWP
 301 QGPSTVDAAF SWDDKVYLIQ GTQVYVFLTK GGNNLVSGYP KRLEKELGSP
 351 PGISLETIDA AFSCPGSSRL YVSSGRRLWW LDLKSGAQAT WTEVSWPHEK
 401 VDGALCLDKS LGPNTCSSNG SSLYFIHGPN LYCYSSIDKL NAAKSLPQPQ
 451 KVNSILGCSQ
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   90 - 102    1504.8826  1503.8753  1503.7834       61      1  R.WKNPITSVDAAFR.G
   92 - 102    1190.6791  1189.6718  1189.6091       53      0  K.NPITSVDAAFR.G
  103 - 111     975.5937   974.5864   974.5437       44      0  R.GPDSVFLIK.E
  103 - 114    1347.7883  1346.7810  1346.7082       54      1  R.GPDSVFLIKEDK.V
  112 - 122    1389.7819  1388.7746  1388.6976       55      1  K.EDKVWVYPPEK.K
  115 - 122    1017.5838  1016.5765  1016.5331       43      0  K.VWVYPPEK.K
  115 - 123    1145.6945  1144.6872  1144.6281       52      1  K.VWVYPPEKK.E
```

Protein View

```
Match to: Q8C7C7_MOUSE Score: 114 Expect: 3.7e-07
2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C92002
Found in search of pmf_M2_129990849012.txt

Nominal mass (Mr): 64961; Calculated pI value: 5.49
NCBI BLAST search of Q8C7C7_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 126
Number of mass values matched: 46
Sequence Coverage: 69%

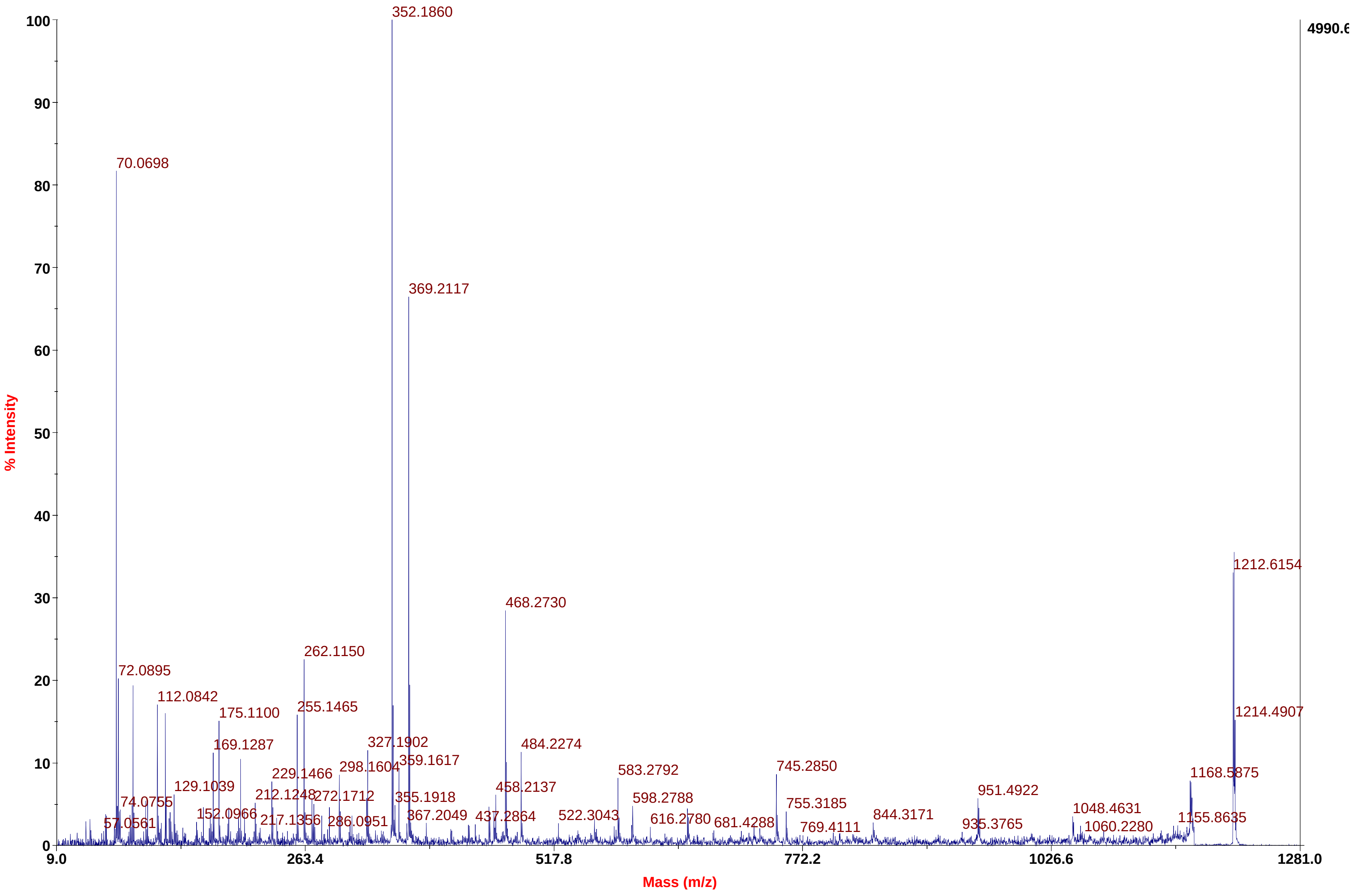
Matched peptides shown in Bold Red

     1 NRYNDLGEQH FKGLVLIAFS QYLQKCSYDE HAKLVQEVTD FAKTCVADES
    51 AANCDKSLHT LFGDKLCAIP NLRENYGELA DCCTKQEPER NECFLQHKDD
   101 NPSLPPFERP EAEAMCTSFK ENPTTFMGHY LHEVARRHPY FYAPELLYYA
   151 EQYNEILTQC CAEADKESCL TPKLDGVKEK ALVSSVRQRM KCSSMQKFGE
   201 RAFKAWAVAR LSQTFPNADF AEITKLATDL TKVNKECCHG DLLECADDRA
   251 ELAKYMCENQ ATISSKLQTC CDKPLLKKAH CLSEVEHDTM PADLPAIAAD
   301 FVEDQEVCKN YAEAKDVFLG TFLYEYSRRH PDYSVSLLLR LAKKYEATLE
   351 KCCAEANPPA CYGTVLAEFQ PLVEEPKNLV KTNCDLYEKL GEYGFQNAIL
   401 VRYTQKAPQV STPTLVEAAR NLGRVGTKCC TLPEDQRLPC VEDYLSAILN
   451 RVCLLHEKTP VSEHVTKCCS GSLVERRPCF SALTVDETYV PKEFKAETFT
   501 FHSDICTLPE KEKQIKKQTA LAELVKHKPK ATAEQLKTVM DDFAQFLDTC
   551 CKAADKDTCF STEGPNLVTR CKDALA
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss  Sequence
    1 - 12     1520.8362  1519.8289  1519.7168       74     1   -.NRYNDLGEQHFK.G
   13 - 25     1479.8887  1478.8814  1478.8497       21     0   K.GLVLIAFSQYLQK.C
   13 - 33     2415.3196  2414.3123  2414.1828       54     1   K.GLVLIAFSQYLQKCSYDEHAK
   13 - 33     2470.3232  2469.3159  2469.2362       32     1   K.GLVLIAFSQYLQKCSYDEHAK
   13 - 33     2472.3269  2471.3196  2471.2042       47     1   K.GLVLIAFSQYLQKCSYDEHAK
   34 - 43     1149.6681  1148.6608  1148.6077       46     0   K.LVQEVTDFAK.T
   34 - 56     2457.3489  2456.3416  2456.1199       90     1   K.LVQEVTDFAKTCVADESAANC
   57 - 65     1017.5838  1016.5765  1016.5291       47     0   K.SLHTLFGDK.L
```

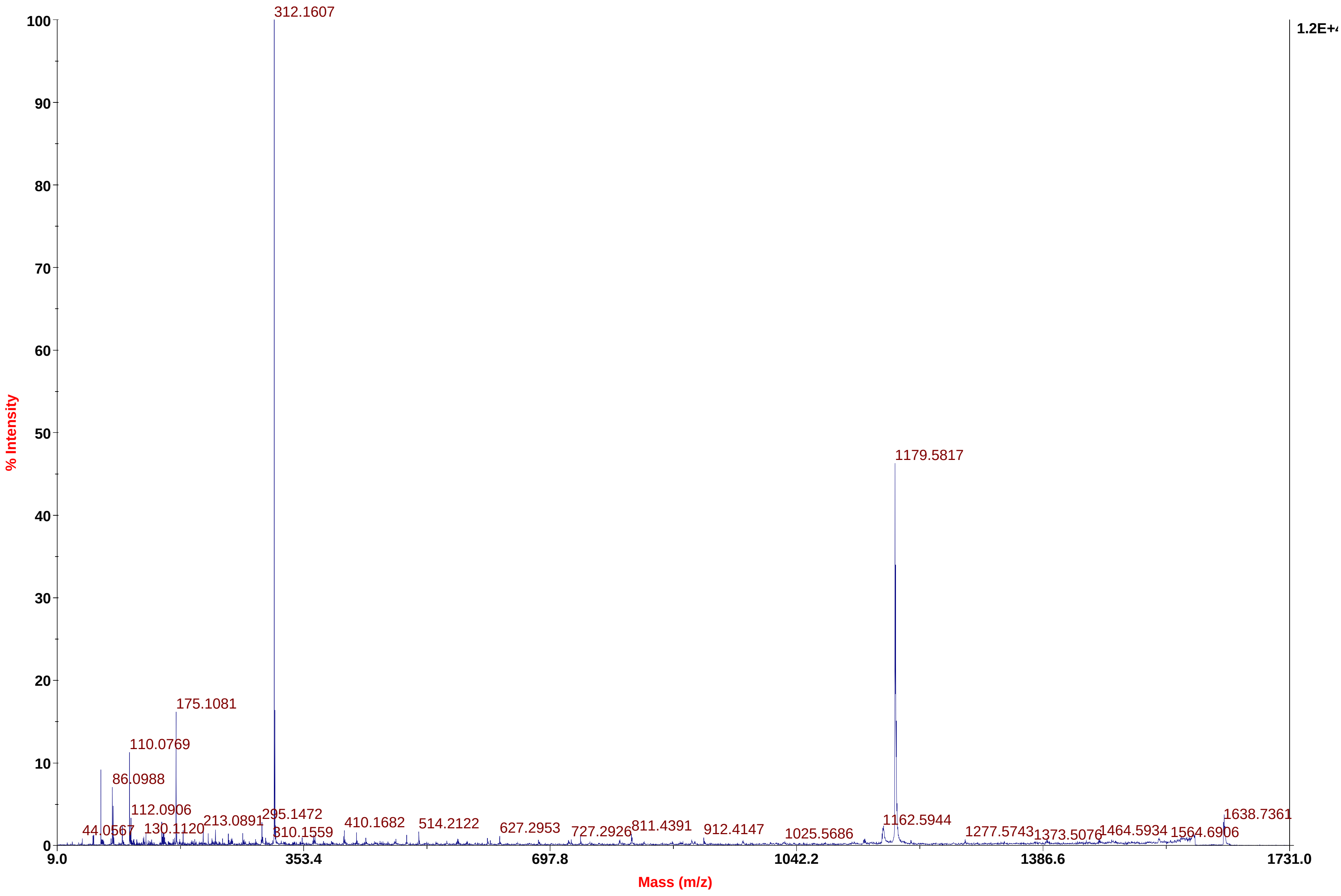
M13

4700 MS/MS Precursor 1212.7 Spec #1 MC[BP = 352.2, 4991]



M13

4700 MS/MS Precursor 1638.89 Spec #1 MC[BP = 312.2, 11579]



Peptide Summary Report

Format As: Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

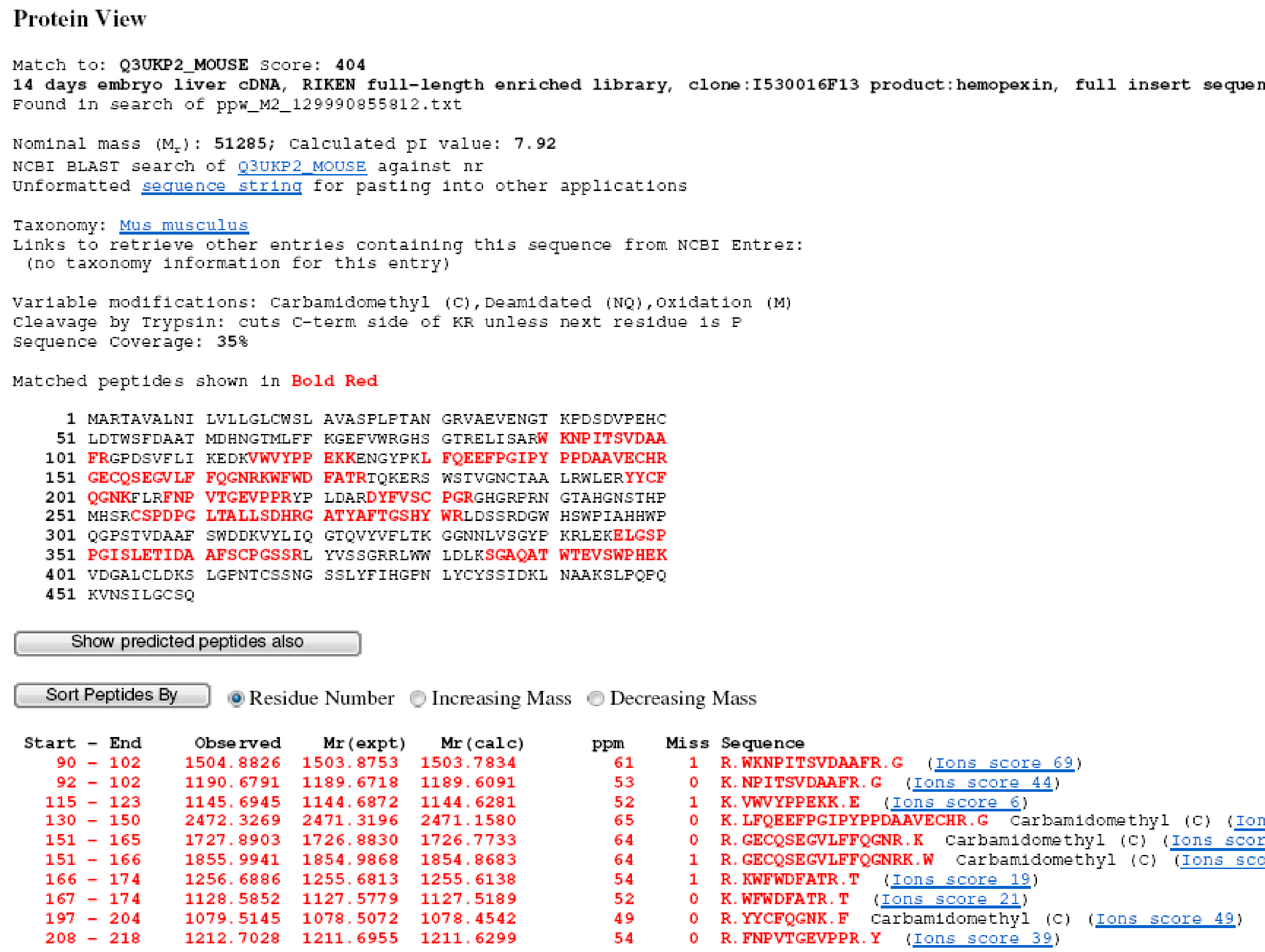
☐ **Error tolerant**

1. Q3UKP2_MOUSE **Mass:** 51285 **Score:** 404 **Matches:** 15(9) **Sequences:** 15(9) **emPAI:** 2.80

14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full insert se

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	2	1079.5145	1078.5072	1078.4542	49.2	0	49	0.0041	1	U	R.YYCFQGNK.F + Carbamidomethyl (C)
☑	3	1100.5393	1099.5320	1099.4757	51.2	0	36	0.067	1	U	R.DYFVSCPGR.G + Carbamidomethyl (C)
☑	4	1128.5852	1127.5779	1127.5189	52.4	0	21	2.5	1	U	K.WFWDFATR.T



Protein View

```
Match to: Q3UKP2_MOUSE Score: 404
14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full insert sequen
Found in search of ppw_M2_129990855812.txt

Nominal mass (Mr): 51285; Calculated pI value: 7.92
NCBI BLAST search of Q3UKP2_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 35%

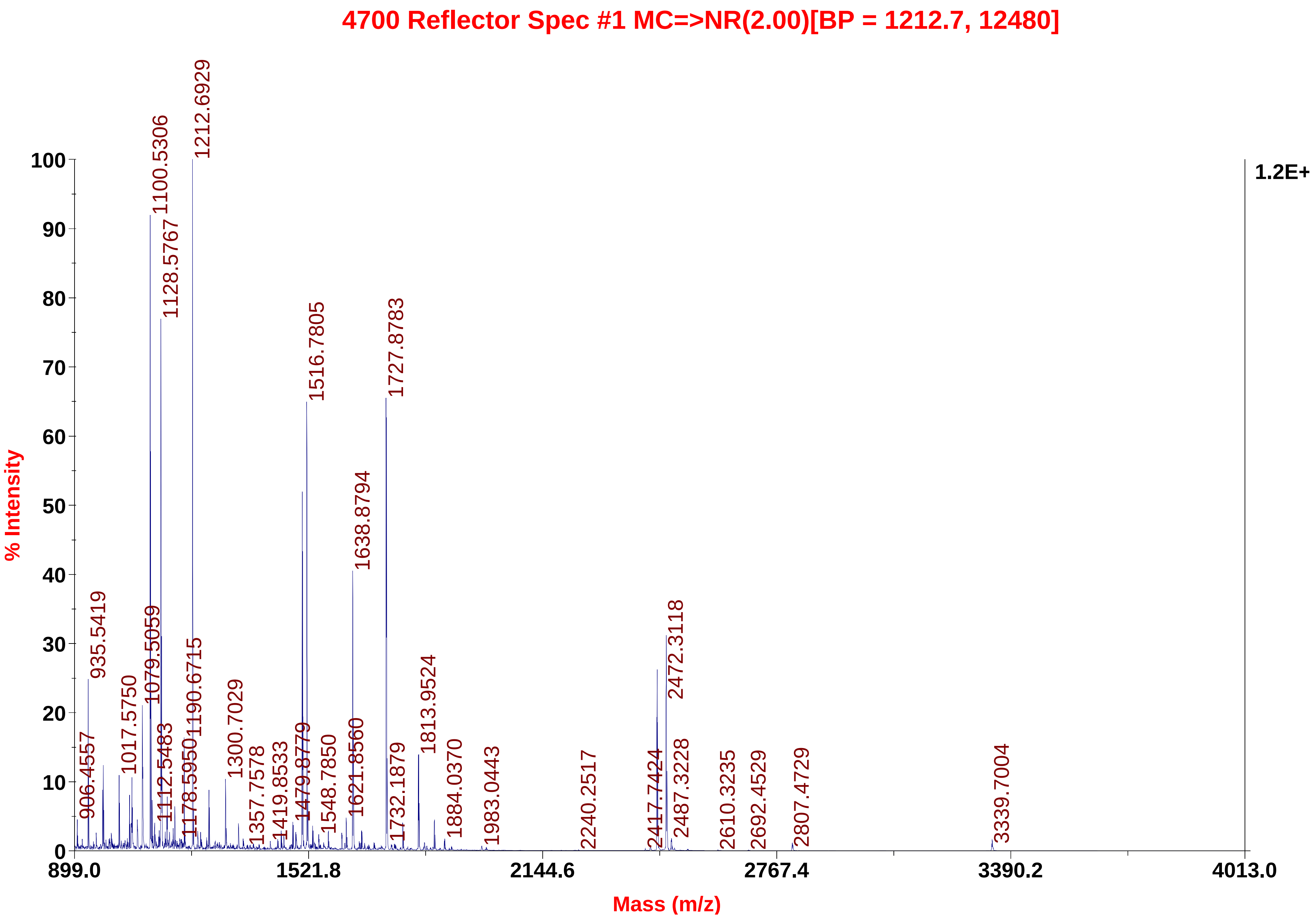
Matched peptides shown in Bold Red

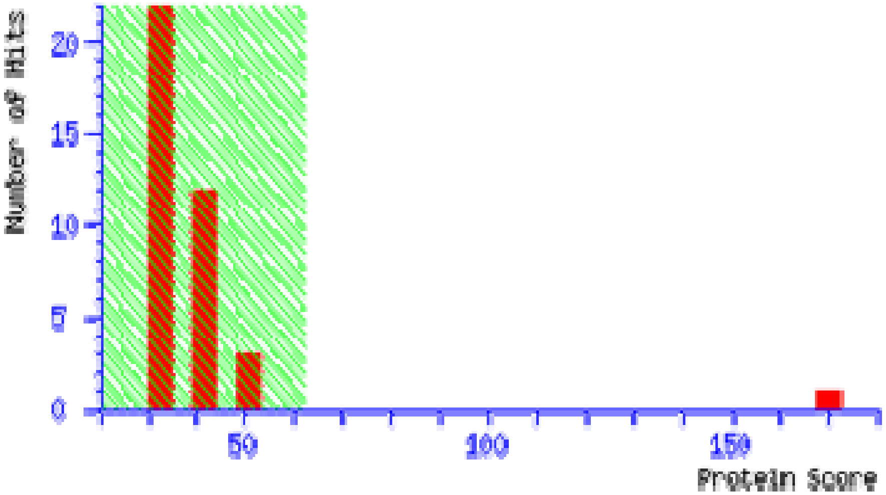
      1 MARTAVALNI LVLLGLCWSL AVASPLPTAN GRVAEVENGT KPDSDVPEHC
     51 LDTWSFDAAT MDHNGTMLFF KGEFVWRGHS GTRELISARW KNPITSVDAA
    101 FRGPDSVFLI KEDKVWVYPP EKKENGYPKL FQEEFPGIPY PPDAAVECHR
    151 GECQSEGVLF FQGNRKWFWD FATRTQKERS WSTVGNCTAA LRWLERYYCF
    201 QGNKFLRFNP VTGEVPPRYP LDARDYFVSC PGRGHGRPRN GTAHGNSTHP
    251 MHSRCSPDPG LTALLSDHRG ATYAFTGSHY WRLDSSRDGW HSWPIAHHWP
    301 QGPSTVDAAF SWDDKVYLIQ GTQVYVFLTK GGNNLVSGYP KRLEKELGSP
    351 PGISLETIDA AFSCPGSSRL YVSSGRRLWW LDLKSGAQAT WTEVSWPHEK
    401 VDGALCLDKS LGPNTCSSNG SSLYFIHGPN LYCYSSIDKL NAAKSLPQPQ
    451 KVNSILGCSQ
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

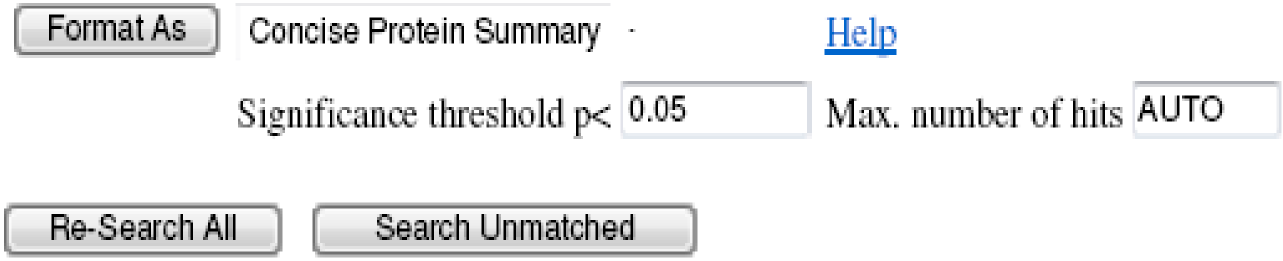
```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm    Miss Sequence
   90 - 102    1504.8826  1503.8753  1503.7834      61      1  R.WKNPITSVDAAFR.G  (Ions score 69)
   92 - 102    1190.6791  1189.6718  1189.6091      53      0  K.NPITSVDAAFR.G  (Ions score 44)
  115 - 123    1145.6945  1144.6872  1144.6281      52      1  K.VWVYPPEKK.E  (Ions score 6)
  130 - 150    2472.3269  2471.3196  2471.1580      65      0  K.LFQEEFPGIPYPPDAAVECHR.G  Carbamidomethyl (C) (Ion
  151 - 165    1727.8903  1726.8830  1726.7733      64      0  R.GECQSEGVLFFQGNR.K  Carbamidomethyl (C) (Ions scor
  151 - 166    1855.9941  1854.9868  1854.8683      64      1  R.GECQSEGVLFFQGNRK.W  Carbamidomethyl (C) (Ions sco
  166 - 174    1256.6886  1255.6813  1255.6138      54      1  R.KWFWDFATR.T  (Ions score 19)
  167 - 174    1128.5852  1127.5779  1127.5189      52      0  K.WFWDFATR.T  (Ions score 21)
  197 - 204    1079.5145  1078.5072  1078.4542      49      0  R.YYCFQGNK.F  Carbamidomethyl (C) (Ions score 49)
  208 - 218    1212.7028  1211.6955  1211.6299      54      0  R.FNPVTGEVPPR.Y  (Ions score 39)
```

Sample M14


4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1212.7, 12480]
% Intensity
Mass (m/z)
1.2E+
100
90
80
70
60
50
40
30
20
10
0
899.0
1521.8
2144.6
2767.4
3390.2
4013.0
906.4557
935.5419
1017.5750
1079.5059
1100.5306
1112.5483
1128.5767
1178.5950
1190.6715
1212.6929
1300.7029
1357.7578
1419.8533
1479.8779
1516.7805
1548.7850
1621.8560
1638.8794
1727.8783
1732.1879
1813.9524
1884.0370
1983.0443
2240.2517
2417.7424
2472.3118
2487.3228
2610.3235
2692.4529
2807.4729
3339.7004



Concise Protein Summary Report



Significance threshold p< 0.05 Max. number of hits AUTO

```
1.    Q3UKP2_MOUSE    Mass: 51285    Score: 170    Expect: 9.2e-13  Matches: 25
      14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexi
      AAH11246    Mass: 51308    Score: 170    Expect: 9.2e-13  Matches: 25
      BC011246 NID: - Mus musculus
      AAB49490    Mass: 50514    Score: 157    Expect: 1.8e-11  Matches: 24
      MMU89889 NID: - Mus musculus
      Q8K1U6_MOUSE    Mass: 31027    Score: 110    Expect: 9.2e-07  Matches: 15
      Hemopexin (Fragment).- Mus musculus (Mouse).
```

Protein View

Match to: **Q3UKP2_MOUSE** Score: **170** Expect: **9.2e-13**
14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, f
Found in search of pmf_N2_129990849013.txt

Nominal mass (M_r): **51285**; Calculated pI value: **7.92**
NCBI BLAST search of Q3UKP2_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **108**
Number of mass values matched: **25**
Sequence Coverage: **51%**

Matched peptides shown in **Bold Red**

```
  1 MARTAVALNI LVLLGLCWSL AVASPLPTAN GRVAEVENGT KPDSDVPEHC
 51 LDTWSFDAAT MDHNGTMLFF KGEFVWRGHS GTRELISARW KNPITSVDAA
101 FRGPDSVFLI KEDKVWVYPP EKKENGYPKL FQEEFPGIPY PPDAAVECHR
151 GECQSEGVLF FQGNRKWFWD FATRTQKERS WSTVGNCTAA LRWLERYYCF
201 QGNKFLRFNP VTGEVPPRYP LDARDYFVSC PGRGHGRPRN GTAHGNSTHP
251 MHSRCSPDPG LTALLSDHRG ATYAFTGSHY WRLDSSRDGW HSWPIAHHWP
301 QGPSTVDAAF SWDDKVYLIQ GTQVYVFLTK GGNNLVSGYP KRLEKELGSP
351 PGISLETIDA AFSCPGSSRL YVSSGRRLWW LDLKSGAQAT WTEVSWPHEK
401 VDGALCLDKS LGPNTCSSNG SSLYFIHGPN LYCYSSIDKL NAAKSLPQPQ
451 KVNSILGCSQ
```

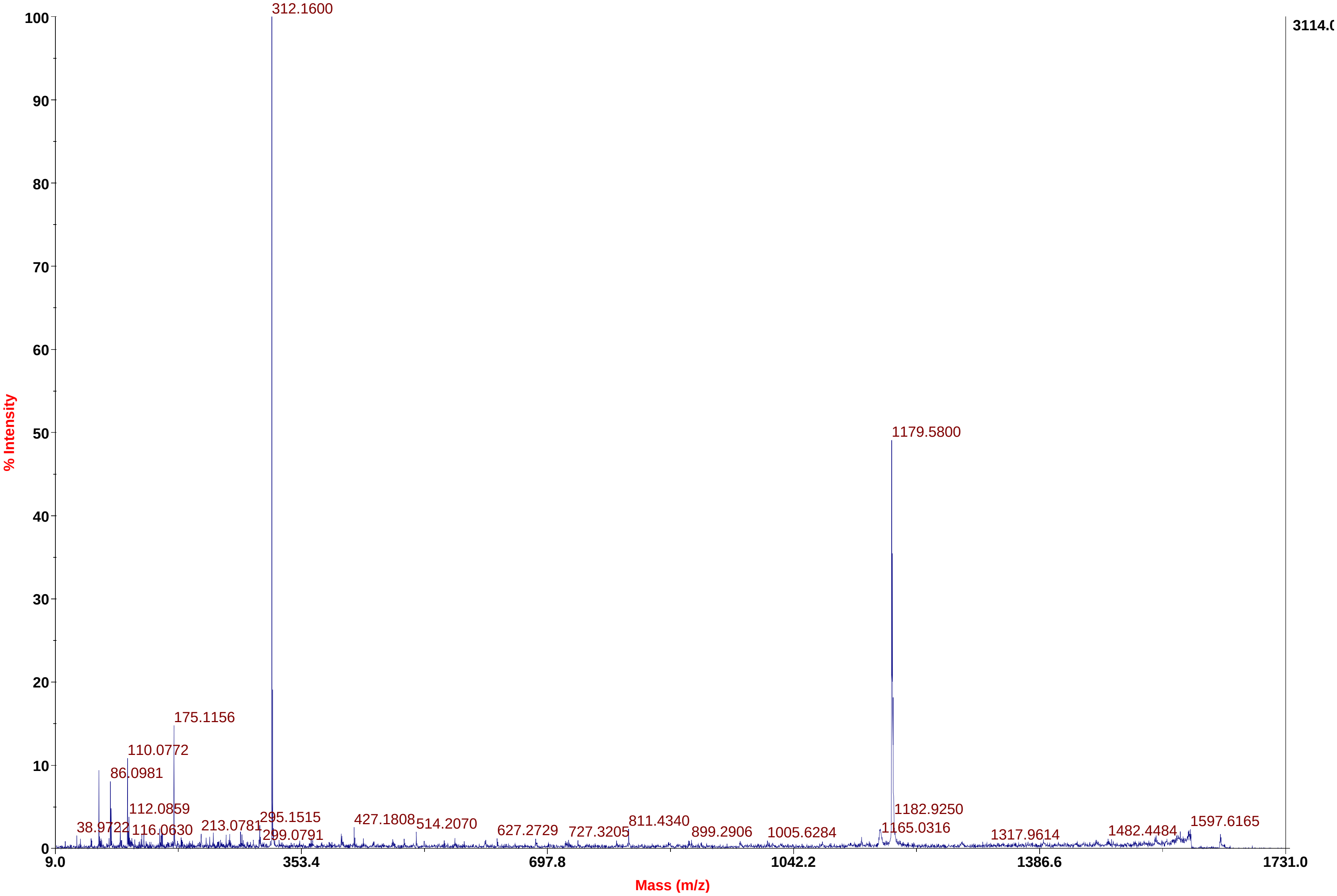
Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss  Sequence
   90 - 102    1504.8705  1503.8632  1503.7834       53     1   R.WKNPITSVDAAFR.G
   92 - 102    1190.6692  1189.6619  1189.6091       44     0   K.NPITSVDAAFR.G
  103 - 111     975.5863   974.5790   974.5437       36     0   R.GPDSVFLIK.E
  103 - 114    1347.7714  1346.7641  1346.7082       42     1   R.GPDSVFLIKEDK.V
  115 - 122    1017.5754  1016.5681  1016.5331       34     0   K.VWVYPPEK.K
  115 - 123    1145.6865  1144.6792  1144.6281       45     1   K.VWVYPPEKK.E
  130 - 150    2472.3081  2471.3008  2471.1580       58     0   K.LFQEEFPGIPYPPDAAVECHR.G  Carbami
  151 - 165    1670.8501  1669.8428  1669.7519       54     0   R.GECQSEGVLFFQGNR.K
  151 - 165    1727.8776  1726.8703  1726.7733       56     0   R.GECQSEGVLFFQGNR.K  Carbamidometh
  151 - 166    1855.9836  1854.9763  1854.8683       58     1   R.GECQSEGVLFFQGNRK.W  Carbamidomet
  166 - 174    1256.6799  1255.6726  1255.6138       47     1   R.KWFWDFATR.T
```

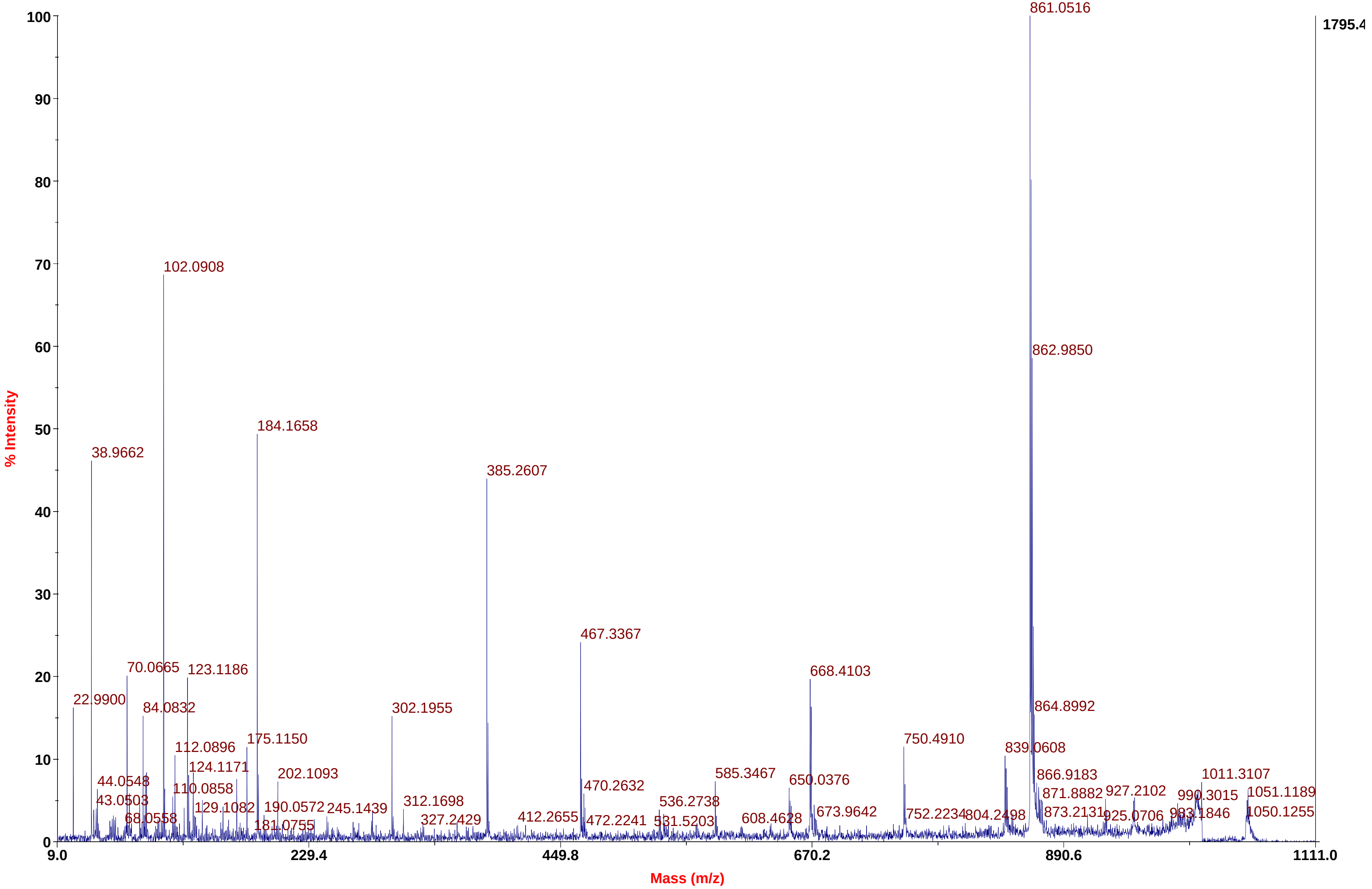
M14

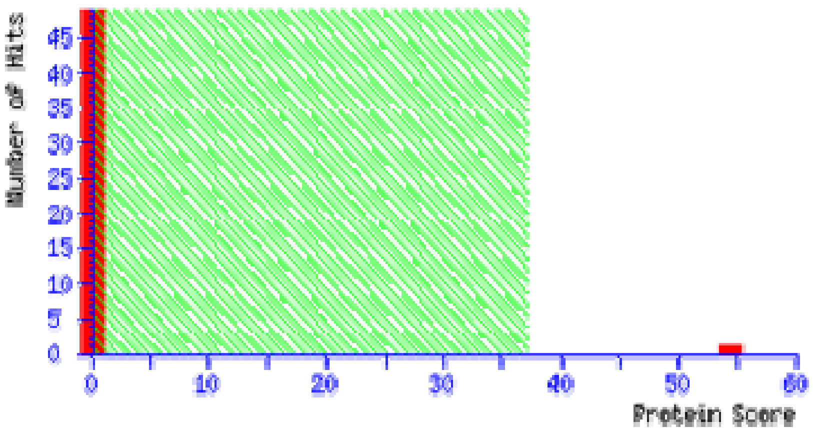
4700 MS/MS Precursor 1638.88 Spec #1 MC[BP = 312.2, 3114]

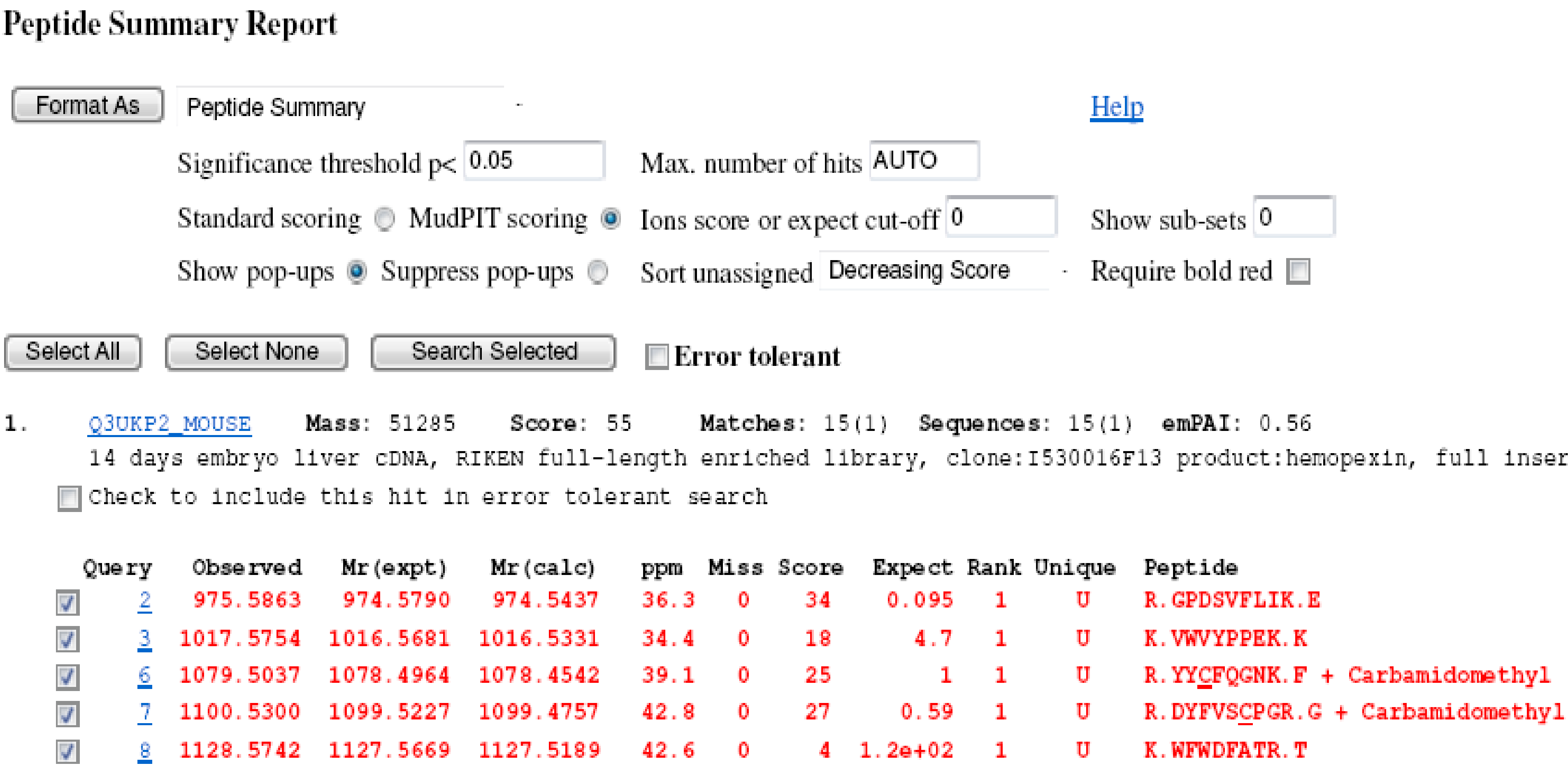


M14

4700 MS/MS Precursor 1051.75 Spec #1 MC[BP = 861.0, 1795]







Peptide Summary Report

Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

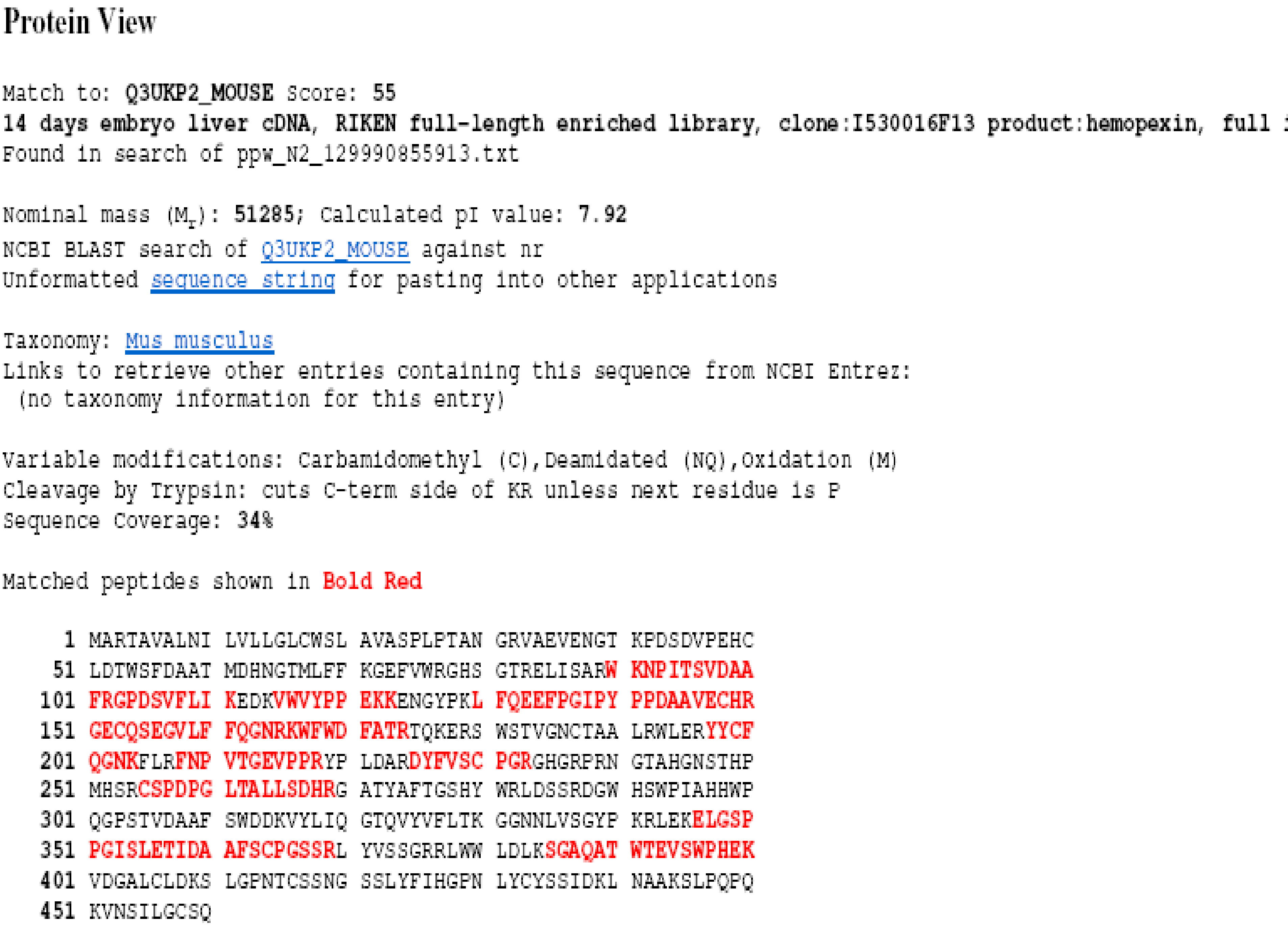
☐ **Error tolerant**

1. Q3UKP2_MOUSE **Mass:** 51285 **Score:** 55 **Matches:** 15(1) **Sequences:** 15(1) **emPAI:** 0.56

14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full inser

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	2	975.5863	974.5790	974.5437	36.3	0	34	0.095	1	U	R.GPDSVFLIK.E
☑	3	1017.5754	1016.5681	1016.5331	34.4	0	18	4.7	1	U	K.VWVYPPEK.K
☑	6	1079.5037	1078.4964	1078.4542	39.1	0	25	1	1	U	R.YYCFQGNK.F + Carbamidomethyl
☑	7	1100.5300	1099.5227	1099.4757	42.8	0	27	0.59	1	U	R.DYFVSCPGR.G + Carbamidomethyl
☑	8	1128.5742	1127.5669	1127.5189	42.6	0	4	1.2e+02	1	U	K.WFWDFATR.T



Protein View

Match to: **Q3UKP2_MOUSE** Score: **55**

14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full

Found in search of ppw_N2_129990855913.txt

Nominal mass (M_r): **51285**; Calculated pI value: **7.92**

NCBI BLAST search of Q3UKP2_MOUSE against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Links to retrieve other entries containing this sequence from NCBI Entrez:

(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

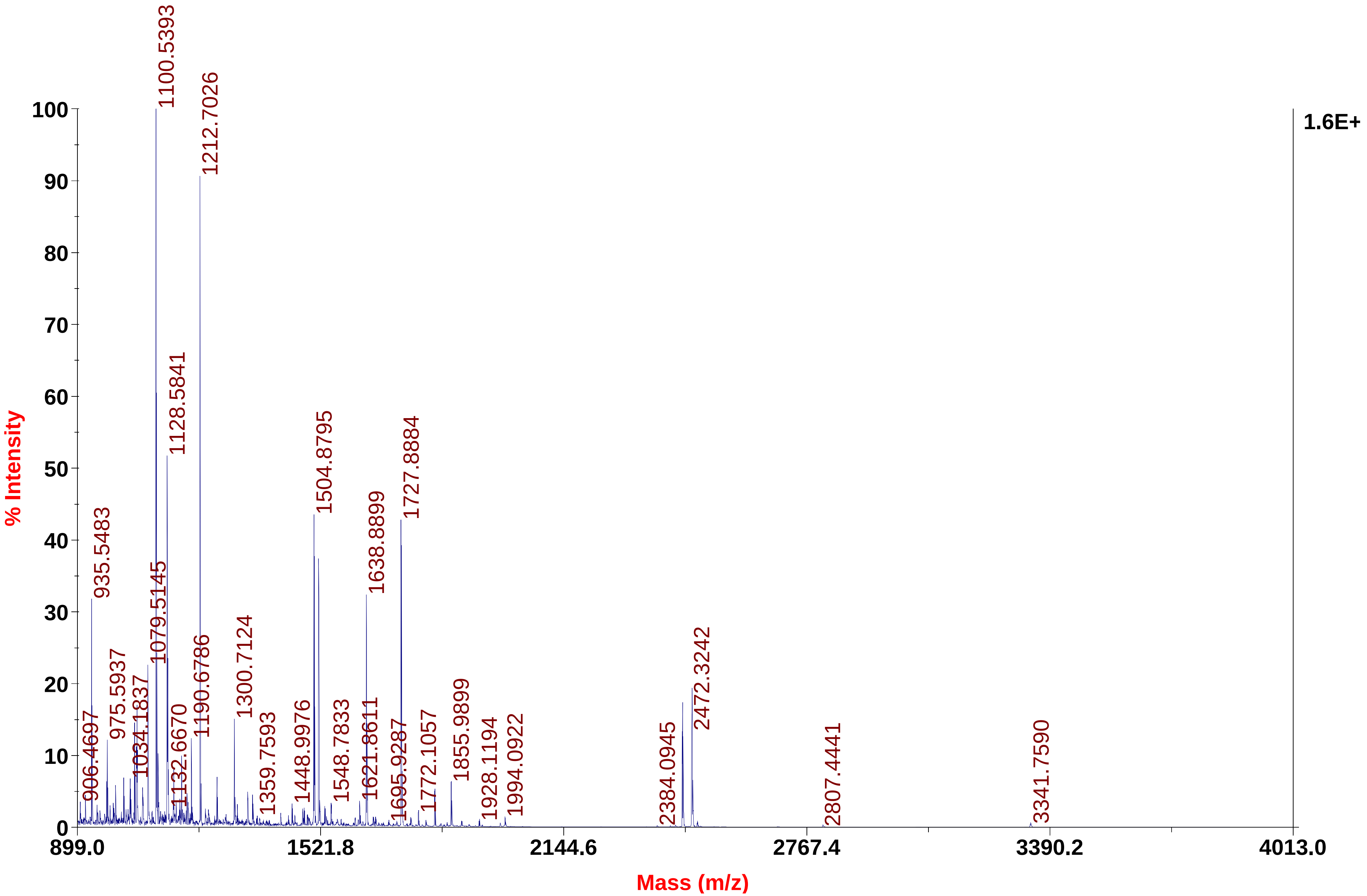
Sequence Coverage: **34%**

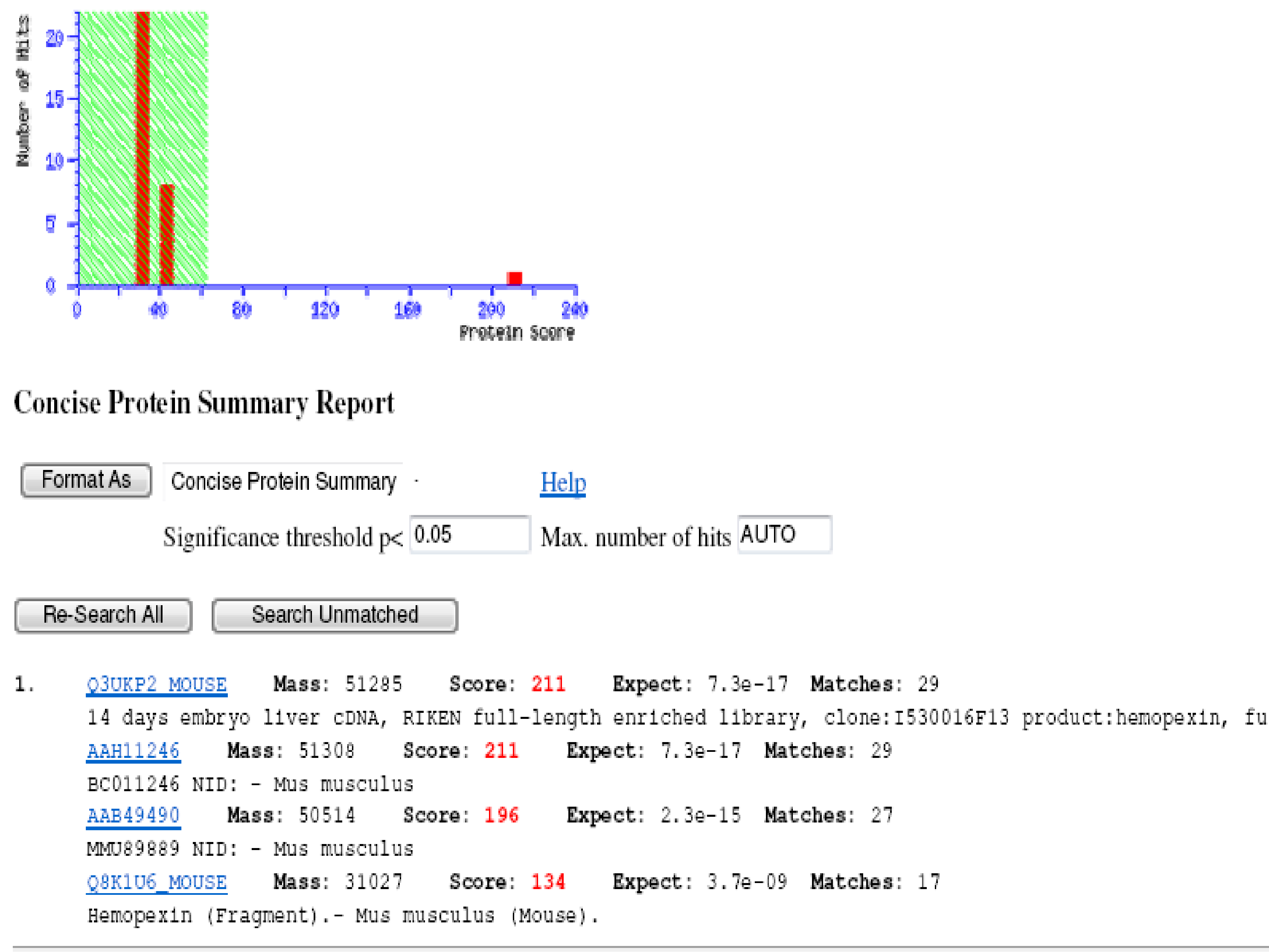
Matched peptides shown in **Bold Red**

1 MARTAVALNI LVLLGLCWSL AVASPLPTAN GRVAEVENGT KPDSDVPEHC
51 LDTWSFDAAT MDHNGTMLFF KGEFVWRGHS GTRELISAR**W KNPITSVDAA**
101 **FRGPDSVFLI K**EDK**VWVYPP EKK**ENGYPK**L FQEEFPGIPY PPDAAVECHR**
151 **GECQSEGVLF FQGNRKWFWD FATR**TQKERS WSTVGNCTAA LRWLER**YYCF**
201 **QGNK**FLR**FNP VTGEVPPR**YP LDAR**DYFVSC PGR**GHGRPRN GTAHGNSTHP
251 MHSR**CSPDPG LTALLSDHR**G ATYAFTGSHY WRLDSSRDGW HSWPIAHHWP
301 QGPSTVDAAF SWDDKVYLIQ GTQVYVFLTK GGNNLVSGYP KRLEK**ELGSP**
351 **PGISLETIDA AFSCPGSSR**L YVSSGRRLWW LDLK**SGAQAT WTEVSWPHEK**
401 VDGALCLDKS LGPNTCSSNG SSLYFIHGPN LYCYSSIDKL NAAKSLPQPQ
451 KVNSILGCSQ

Sample M15

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1100.5, 15842]

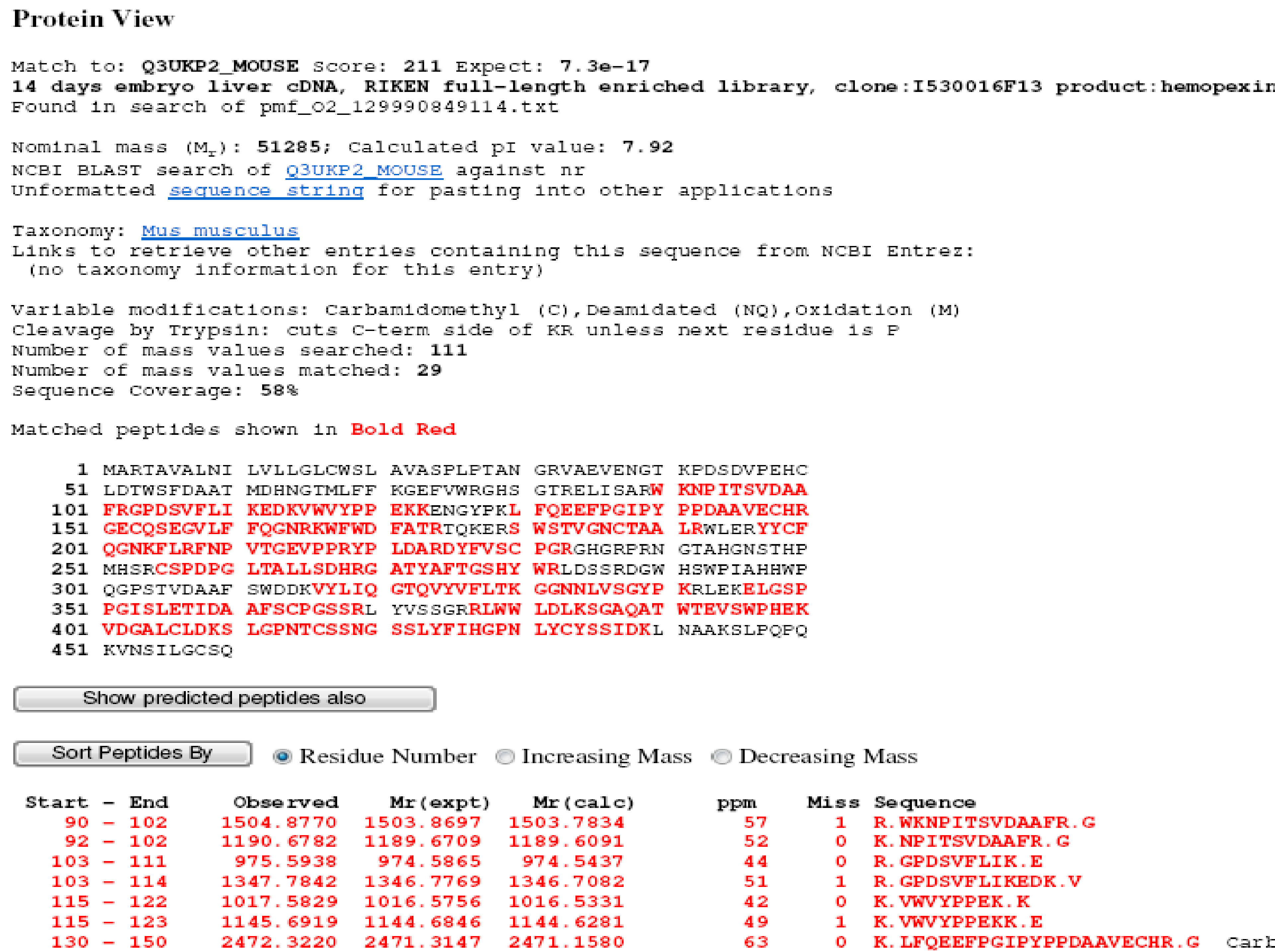




Concise Protein Summary Report

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.     Q3UKP2_MOUSE     Mass: 51285     Score: 211     Expect: 7.3e-17   Matches: 29
       14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, fu
       AAH11246     Mass: 51308     Score: 211     Expect: 7.3e-17   Matches: 29
       BC011246 NID: - Mus musculus
       AAB49490     Mass: 50514     Score: 196     Expect: 2.3e-15   Matches: 27
       MMU89889 NID: - Mus musculus
       Q8K1U6_MOUSE     Mass: 31027     Score: 134     Expect: 3.7e-09   Matches: 17
       Hemopexin (Fragment).- Mus musculus (Mouse).
```



Protein View

Match to: **Q3UKP2_MOUSE** Score: **211** Expect: **7.3e-17**
14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin
Found in search of pmf_02_129990849114.txt

Nominal mass (M_r): **51285**; Calculated pI value: **7.92**
NCBI BLAST search of Q3UKP2_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **111**
Number of mass values matched: **29**
Sequence Coverage: **58%**

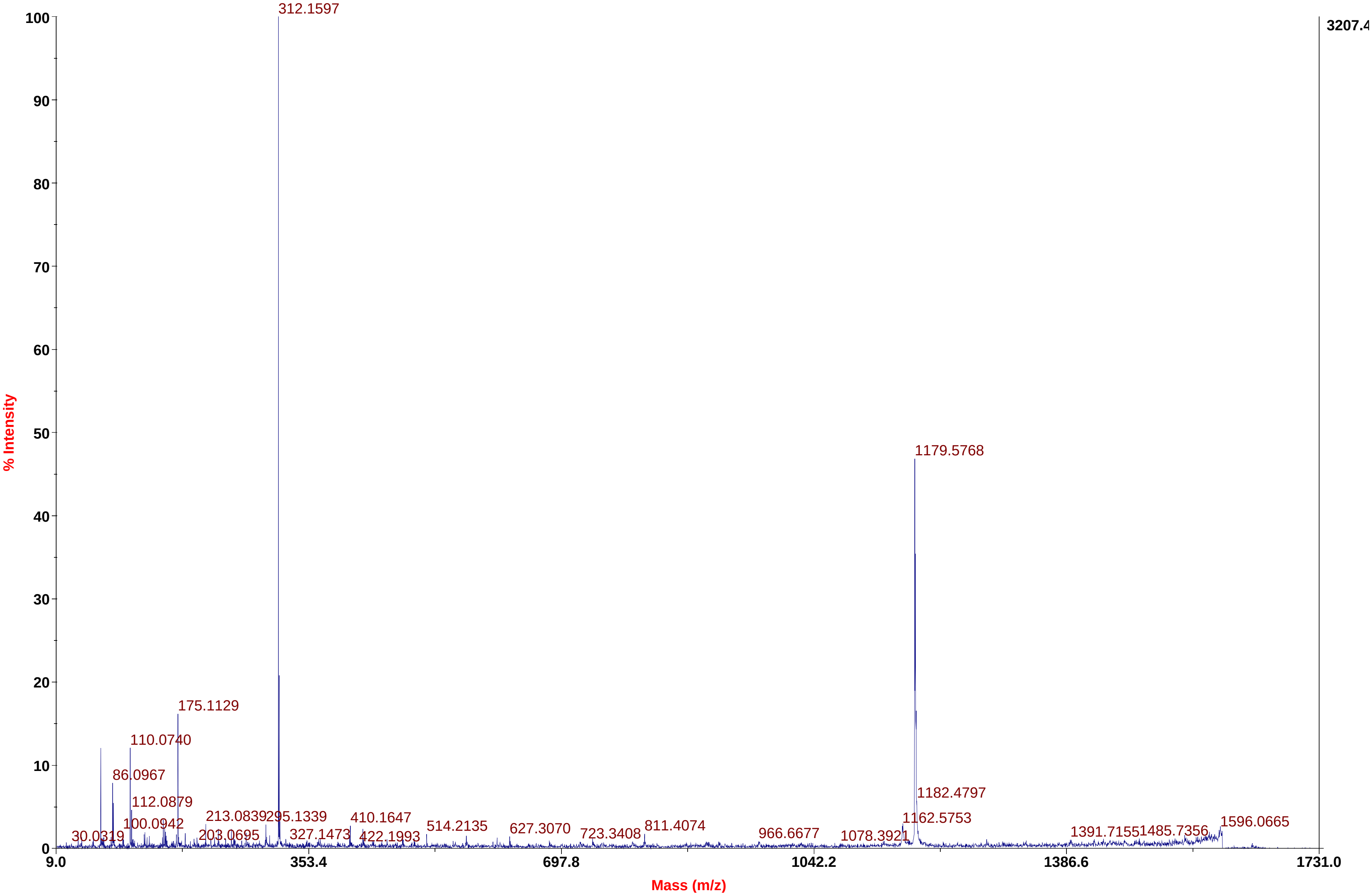
Matched peptides shown in **Bold Red**

```
    1 MARTAVALNI LVLLGLCWSL AVASPLPTAN GRVAEVENGT KPDSDVPEHC
   51 LDTWSFDAAT MDHNGTMLFF KGEFVWRGHS GTRELISARW KNPITSVDAA
  101 FRGPDSVFLI KEDKVWVYPP EKKENGYPKL FQEEFPGIPY PPDAAVECHR
  151 GECQSEGVLF FQGNRKWFWD FATRTQKERS WSTVGNCTAA LRWLERYYCF
  201 QGNKFLRFNP VTGEVPPRYP LDARDYFVSC PGRGHGRPRN GTAHGNSTHP
  251 MHSRCSPDPG LTALLSDHRG ATYAFTGSHY WRLDSSRDGW HSWPIAHHWP
  301 QGPSTVDAAF SWDDKVYLIQ GTQVYVFLTK GGNNLVSGYP KRLEKELGSP
  351 PGISLETIDA AFSCPGSSRL YVSSGRRLWW LDLKSGAQAT WTEVSWPHEK
  401 VDGALCLDKS LGPNTCSSNG SSLYFIHGPN LYCYSSIDKL NAAKSLPQPQ
  451 KVNSILGCSQ
```

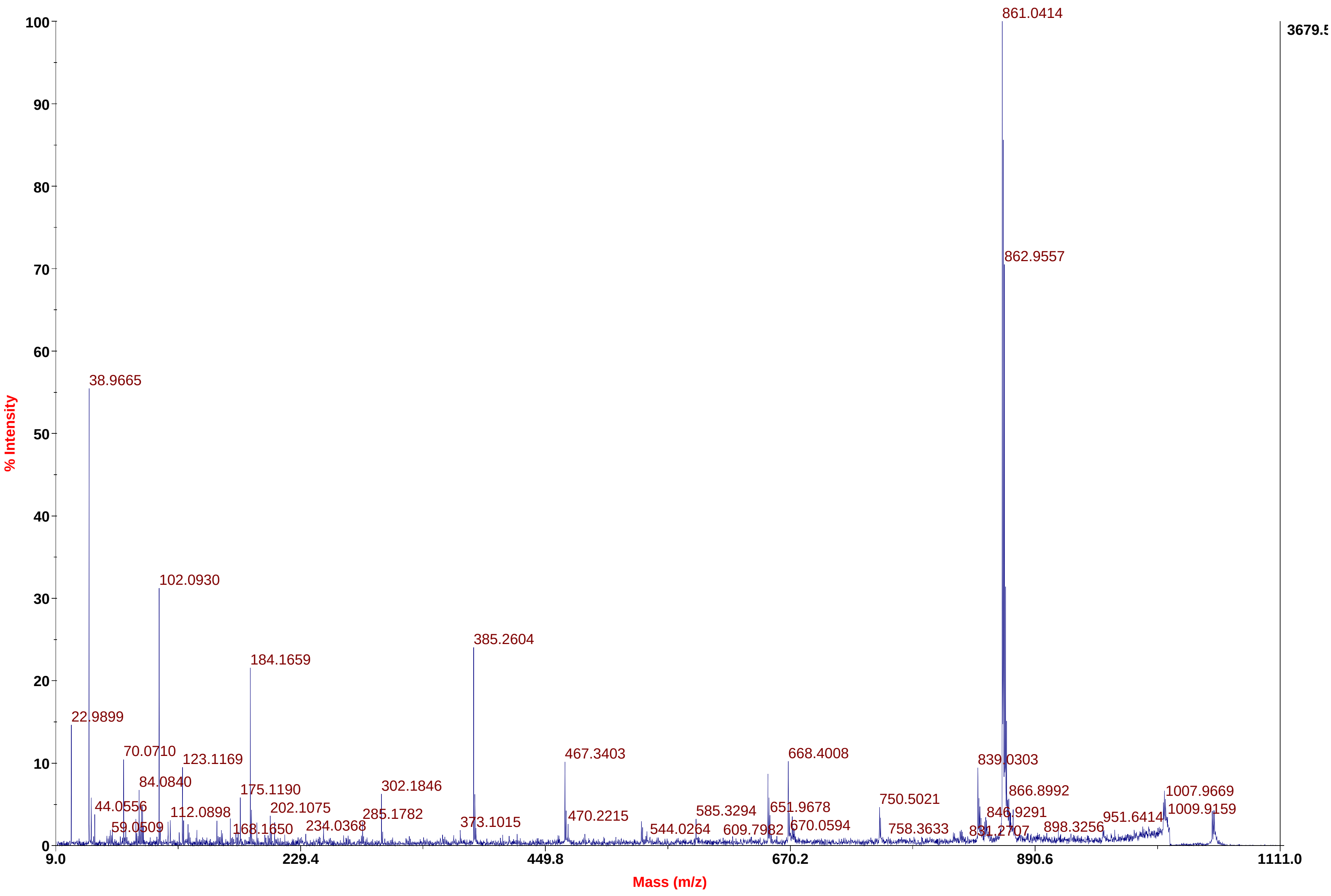
```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   90 - 102    1504.8770  1503.8697  1503.7834       57      1  R.WKNPITSVDAAFR.G
   92 - 102    1190.6782  1189.6709  1189.6091       52      0  K.NPITSVDAAFR.G
  103 - 111     975.5938   974.5865   974.5437       44      0  R.GPDSVFLIK.E
  103 - 114    1347.7842  1346.7769  1346.7082       51      1  R.GPDSVFLIKEDK.V
  115 - 122    1017.5829  1016.5756  1016.5331       42      0  K.VWVYPPEK.K
  115 - 123    1145.6919  1144.6846  1144.6281       49      1  K.VWVYPPEKK.E
  130 - 150    2472.3220  2471.3147  2471.1580       63      0  K.LFQEEFPGIPYPPDAAVECHR.G   Carb
```

M15

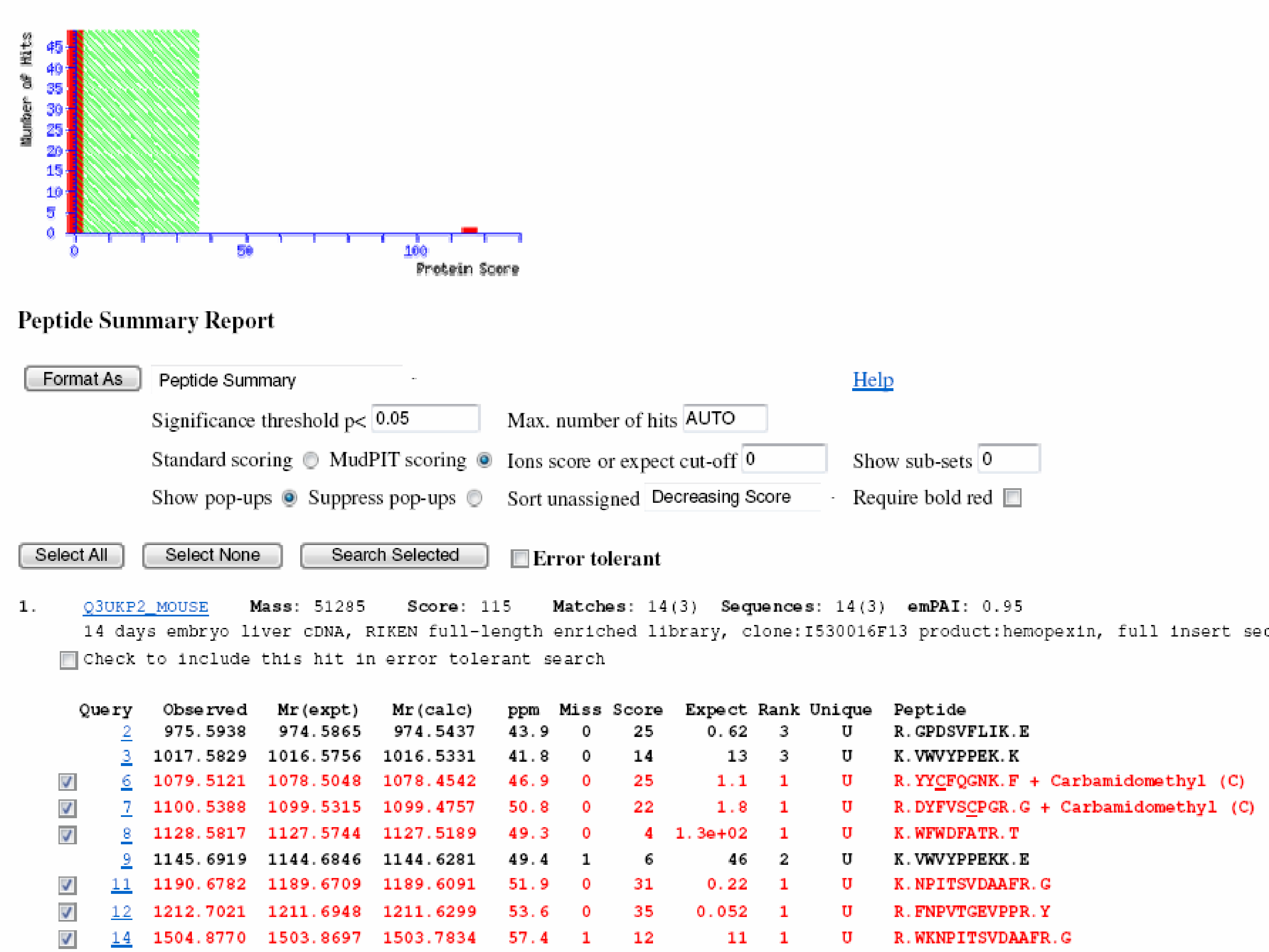
4700 MS/MS Precursor 1638.89 Spec #1 MC[BP = 312.1, 3207]



M15



4700 MS/MS Precursor 1051.75 Spec #1 MC[BP = 861.0, 3680]



Peptide Summary Report

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

☐ **Error tolerant**

1. Q3UKP2_MOUSE **Mass:** 51285 **Score:** 115 **Matches:** 14(3) **Sequences:** 14(3) **emPAI:** 0.95

14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full insert se

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2	975.5938	974.5865	974.5437	43.9	0	25	0.62	3	U	R.GPDSVFLIK.E
	3	1017.5829	1016.5756	1016.5331	41.8	0	14	13	3	U	K.VWVYPPEK.K
☑	6	1079.5121	1078.5048	1078.4542	46.9	0	25	1.1	1	U	R.YYCFQGNK.F + Carbamidomethyl (C)
☑	7	1100.5388	1099.5315	1099.4757	50.8	0	22	1.8	1	U	R.DYFVSCPGR.G + Carbamidomethyl (C)
☑	8	1128.5817	1127.5744	1127.5189	49.3	0	4	1.3e+02	1	U	K.WFWDFATR.T
	9	1145.6919	1144.6846	1144.6281	49.4	1	6	46	2	U	K.VWVYPPEKK.E
☑	11	1190.6782	1189.6709	1189.6091	51.9	0	31	0.22	1	U	K.NPITSVDAAFR.G
☑	12	1212.7021	1211.6948	1211.6299	53.6	0	35	0.052	1	U	R.FNPVTGEVPPR.Y
☑	14	1504.8770	1503.8697	1503.7834	57.4	1	12	11	1	U	R.WKNPITSVDAAFR.G

Protein View

```
Match to: Q3UKP2_MOUSE Score: 115
14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530016F13 product:hemopexin, full
Found in search of ppw_o2_129990856114.txt

Nominal mass (Mr): 51285; Calculated pI value: 7.92
NCBI BLAST search of Q3UKP2_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 33%

Matched peptides shown in Bold Red

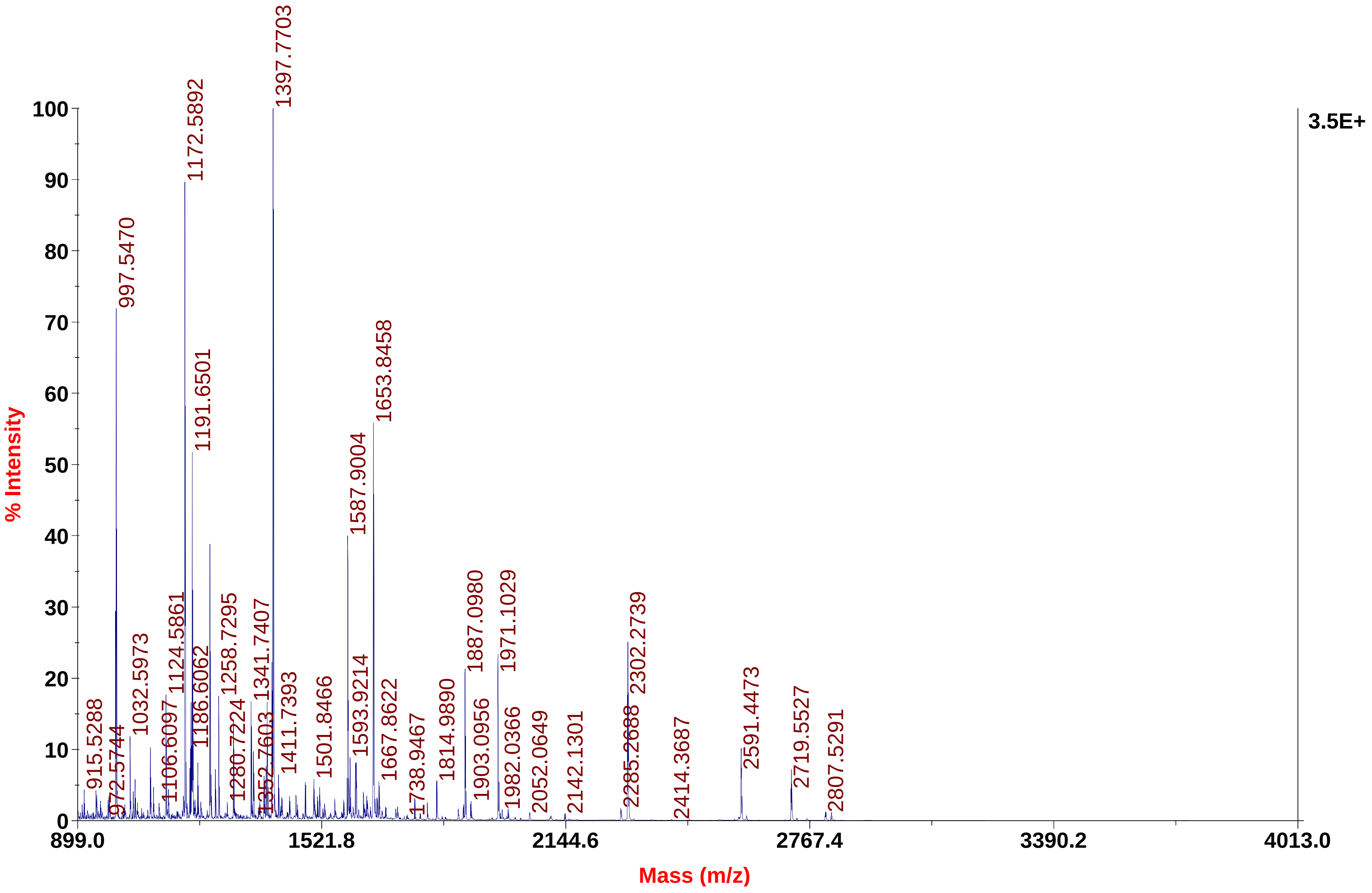
      1 MARTAVALNI LVLLGLCWSL AVASPLPTAN GRVAEVENGT KPDSDVPEHC
     51 LDTWSFDAAT MDHNGTMLFF KGEFVWRGHS GTRELISARW KNPITSVDAA
    101 FRGPDSVFLI KEDKVWVYPP EKKENGYPKL FQEEFPGIPY PPDAAVECHR
    151 GECQSEGVLF FQGNRKWFWD FATRTQKERS WSTVGNCTAA LRWLERYYCF
    201 QGNKFLRFNP VTGEVPPRYP LDARDYFVSC PGRGHGRPRN GTAHGNSTHP
    251 MHSRCSPDPG LTALLSDHRG ATYAFTGSHY WRLDSSRDGW HSWPIAHHWP
    301 QGPSTVDAAF SWDDKVYLIQ GTQVYVFLTK GGNLVSGYP KRLEKELGSP
    351 PGISLETIDA AFSCPGSSRL YVSSGRRLWW LDLKSGAQAT WTEVSWPHEK
    401 VDGALCLDKS LGPNTCSSNG SSLYFIHGPN LYCYSSIDKL NAAKSLPQPQ
    451 KVNSILGCSQ
```

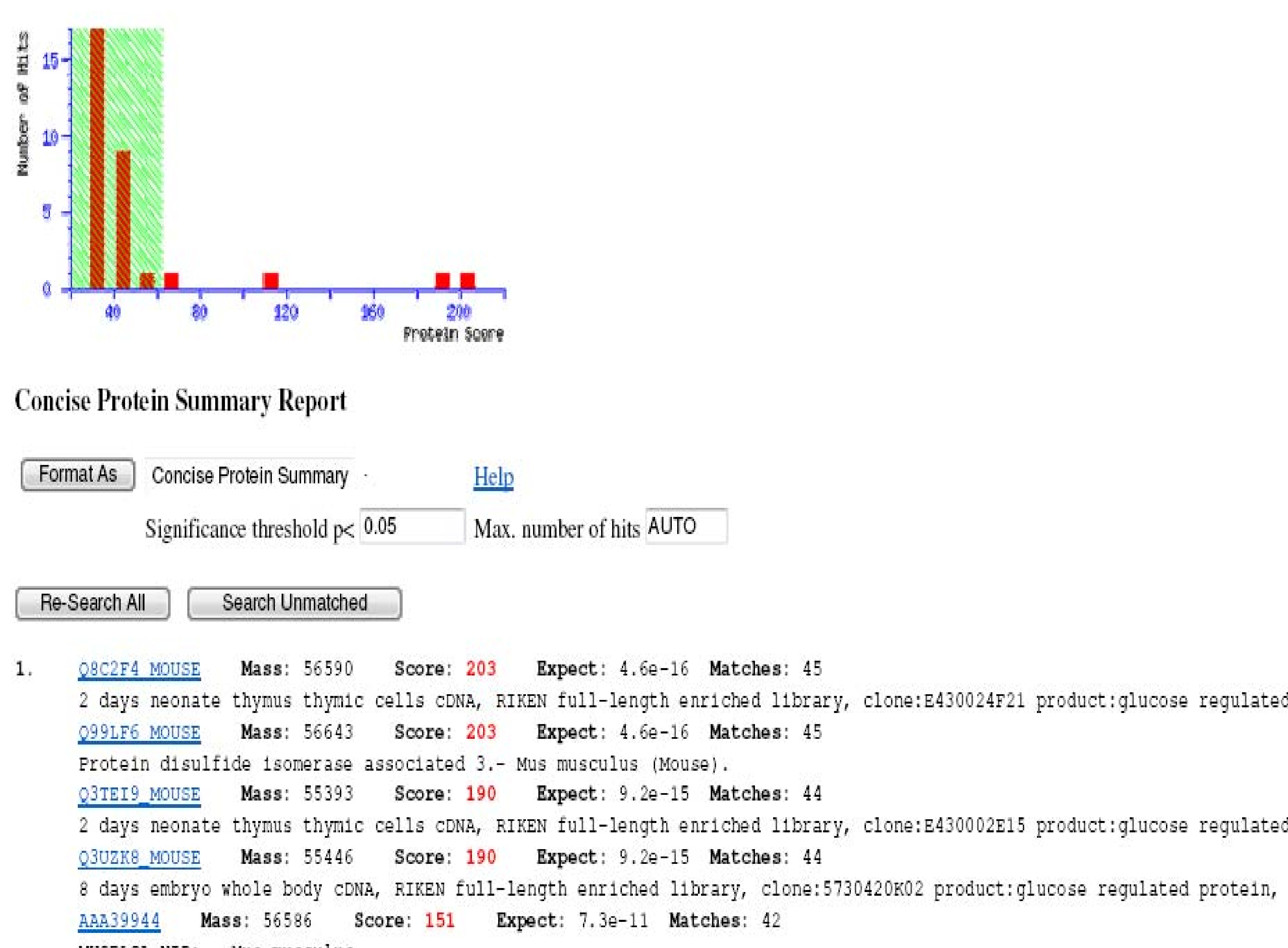
● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss  Sequence
    90 - 102    1504.8770   1503.8697  1503.7834       57       1  R.WKNPITSVDAAFR.G   (Ions score 12)
    92 - 102    1190.6782   1189.6709  1189.6091       52       0  K.NPITSVDAAFR.G   (Ions score 31)
   103 - 111     975.5938    974.5865   974.5437       44       0  R.GPDSVFLIK.E   (Ions score 25)
   115 - 122    1017.5829   1016.5756  1016.5331       42       0  K.VWVYPPEK.K   (Ions score 14)
   115 - 123    1145.6919   1144.6846  1144.6281       49       1  K.VWVYPPEKK.E   (Ions score 6)
   130 - 150    2472.3220   2471.3147  2471.1580       63       0  K.LFQEEFPGIPYPPDAAVECHR.G   Carbamidom
   151 - 165    1727.8873   1726.8800  1726.7733       62       0  R.GECQSEGVLFFQGNR.K   Carbamidomethyl
   167 - 174    1128.5817   1127.5744  1127.5189       49       0  K.WFWDFATR.T   (Ions score 4)
   197 - 204    1079.5121   1078.5048  1078.4542       47       0  R.YYCFQGNK.F   Carbamidomethyl (C) (Io
```

Sample M16

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1397.8, 35164]



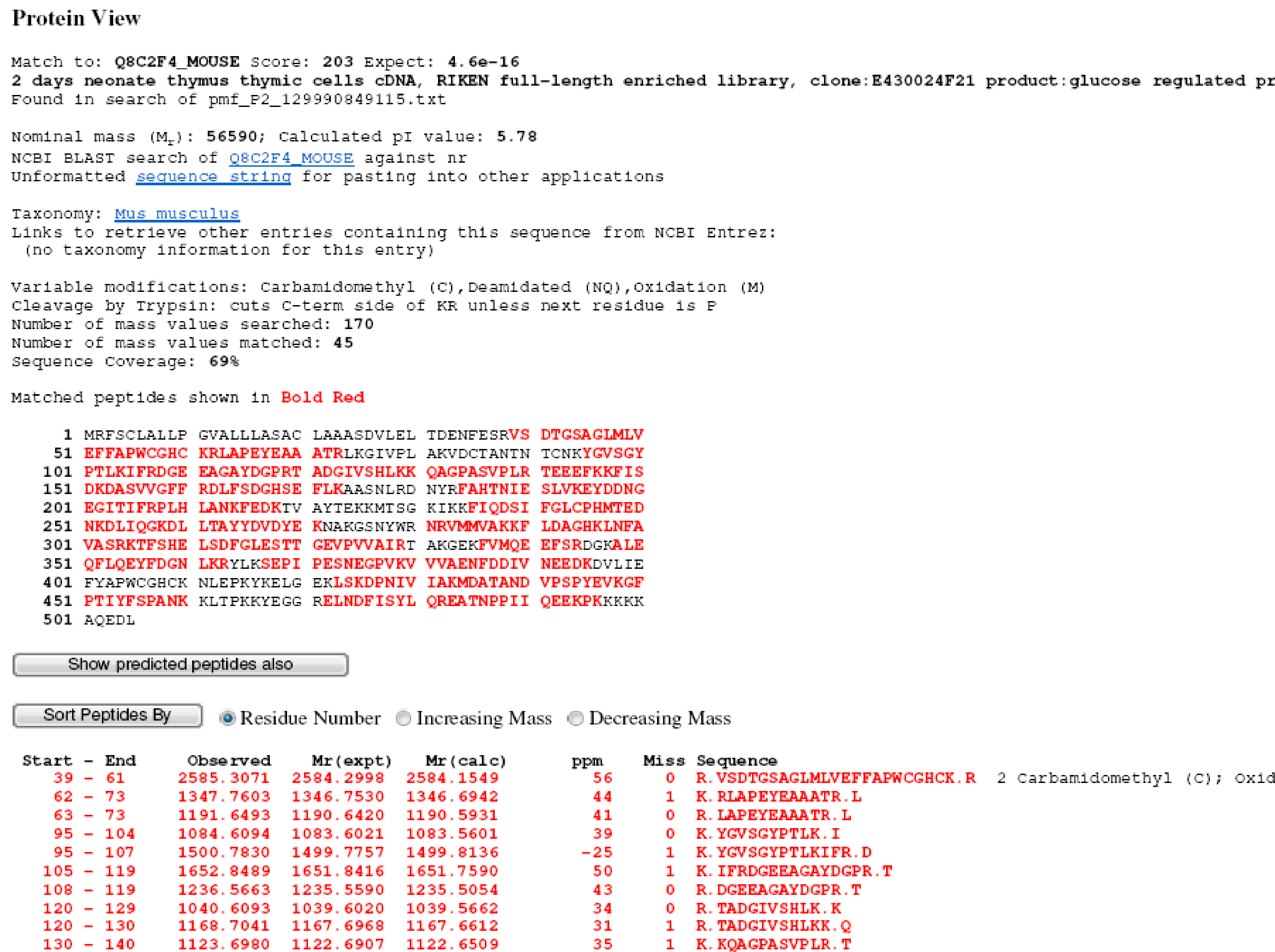


Concise Protein Summary Report

Format As: Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.     Q8C2F4_MOUSE     Mass: 56590     Score: 203     Expect: 4.6e-16  Matches: 45
       2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430024F21 product:glucose regulated
       Q99LF6_MOUSE     Mass: 56643     Score: 203     Expect: 4.6e-16  Matches: 45
       Protein disulfide isomerase associated 3.- Mus musculus (Mouse).
       Q3TEI9_MOUSE     Mass: 55393     Score: 190     Expect: 9.2e-15  Matches: 44
       2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430002E15 product:glucose regulated
       Q3UZK8_MOUSE     Mass: 55446     Score: 190     Expect: 9.2e-15  Matches: 44
       8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730420K02 product:glucose regulated protein,
       AAA39944     Mass: 56586     Score: 151     Expect: 7.3e-11  Matches: 42
```



Protein View

```
Match to: Q8C2F4_MOUSE Score: 203 Expect: 4.6e-16
2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430024F21 product:glucose regulated pr
Found in search of pmf_P2_129990849115.txt

Nominal mass (Mr): 56590; Calculated pI value: 5.78
NCBI BLAST search of Q8C2F4_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 170
Number of mass values matched: 45
Sequence Coverage: 69%

Matched peptides shown in Bold Red

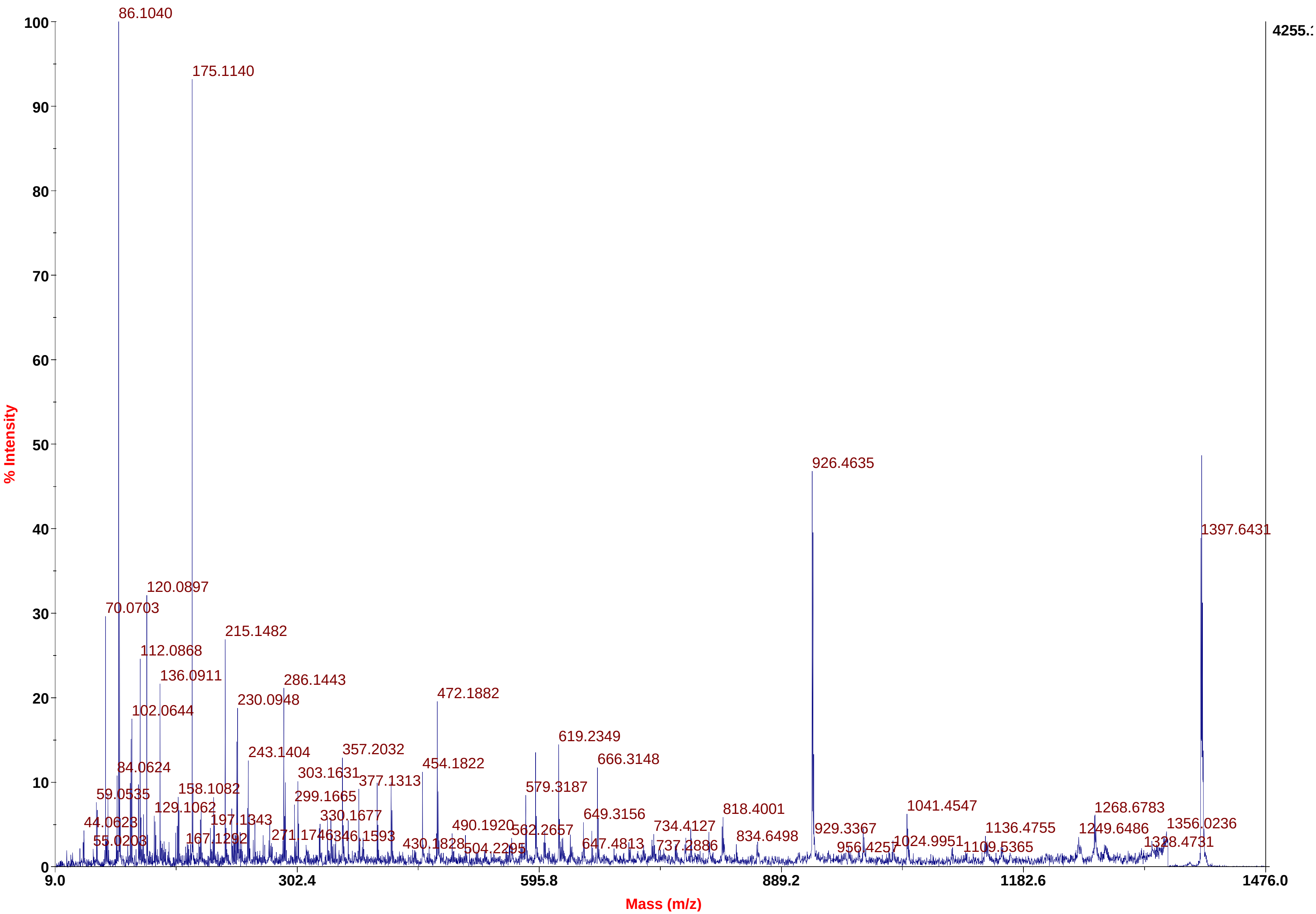
     1 MRFSCLALLP GVALLLASAC LAAASDVLEL TDENFESRVS DTGSAGLMLV
    51 EFFAPWCGHC KRLAPEYEAA ATRLKGIVPL AKVDCTANTN TCNKYGVSGY
   101 PTLKIFRDGE EAGAYDGPRT ADGIVSHLKK QAGPASVPLR TEEEFKKFIS
   151 DKDASVVGFF RDLFSDGHSE FLKAASNLRD NYRFAHTNIE SLVKEYDDNG
   201 EGITIFRPLH LANKFEDKTV AYTEKKMTSG KIKKFIQDSI FGLCPHMTED
   251 NKDLIQGKDL LTAYYDVDYE KNAKGSNYWR NRVMMVAKKF LDAGHKLNFA
   301 VASRKTFSHE LSDFGLESTT GEVPVVAIRT AKGEKFVMQE EFSRDGKALE
   351 QFLQEYFDGN LKRYLKSEPI PESNEGPVKV VVAENFDDIV NEEDKDVLIE
   401 FYAPWCGHCK NLEPKYKELG EKLSKDPNIV IAKMDATAND VPSPYEVKGF
   451 PTIYFSPANK KLTPKKYEGG RELNDFISYL QREATNPPII QEEKPKKKKK
   501 AQEDL
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   39 - 61      2585.3071  2584.2998  2584.1549       56      0  R.VSDTGSAGLMLVEFFAPWCGHCK.R  2 Carbamidomethyl (C); Oxid
   62 - 73      1347.7603  1346.7530  1346.6942       44      1  K.RLAPEYEAAATR.L
   63 - 73      1191.6493  1190.6420  1190.5931       41      0  R.LAPEYEAAATR.L
   95 - 104     1084.6094  1083.6021  1083.5601       39      0  K.YGVSGYPTLK.I
   95 - 107     1500.7830  1499.7757  1499.8136      -25      1  K.YGVSGYPTLKIFR.D
  105 - 119     1652.8489  1651.8416  1651.7590       50      1  K.IFRDGEEAGAYDGPR.T
  108 - 119     1236.5663  1235.5590  1235.5054       43      0  R.DGEEAGAYDGPR.T
  120 - 129     1040.6093  1039.6020  1039.5662       34      0  R.TADGIVSHLK.K
  120 - 130     1168.7041  1167.6968  1167.6612       31      1  R.TADGIVSHLKK.Q
  130 - 140     1123.6980  1122.6907  1122.6509       35      1  K.KQAGPASVPLR.T
```

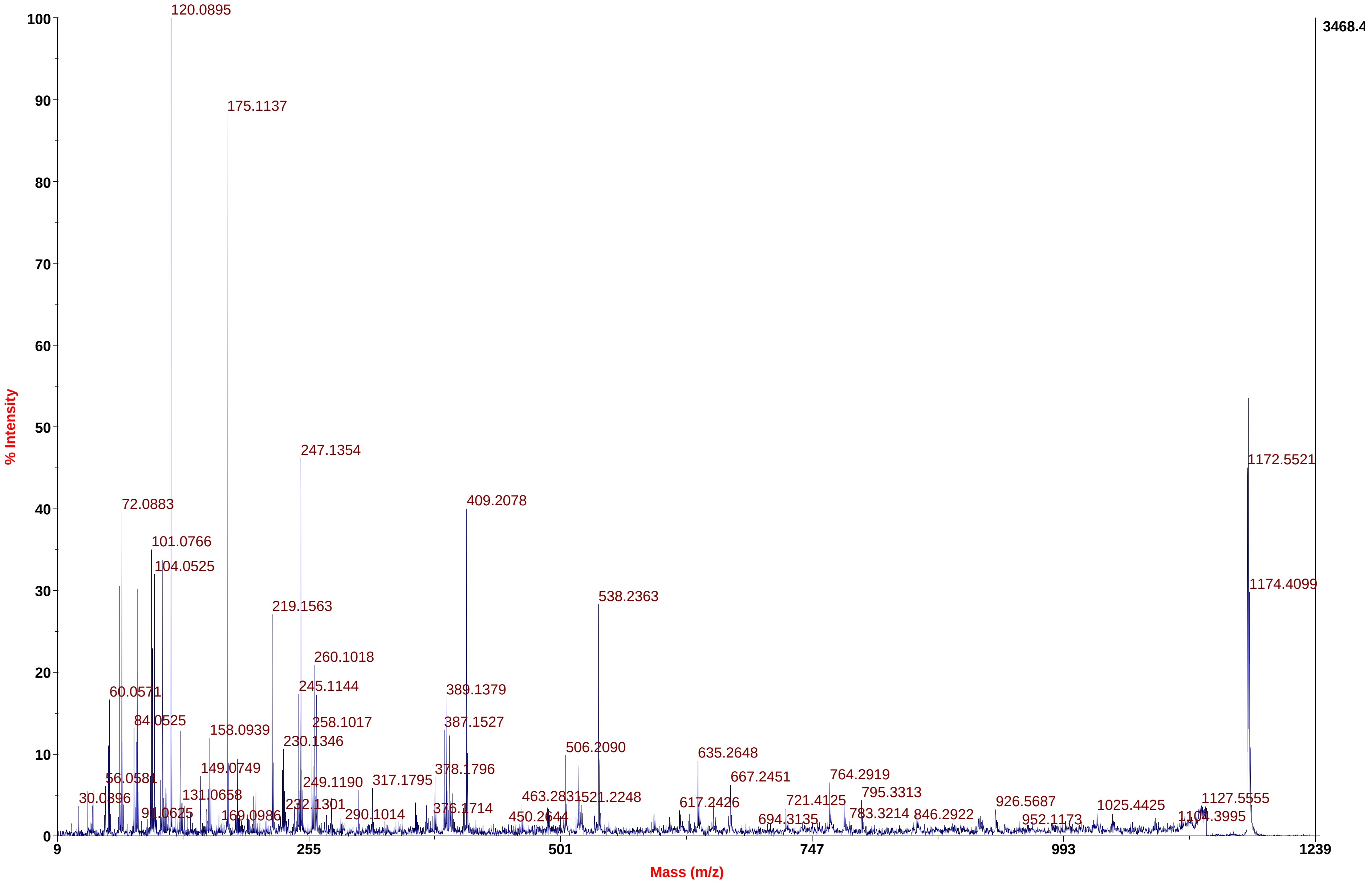
M16

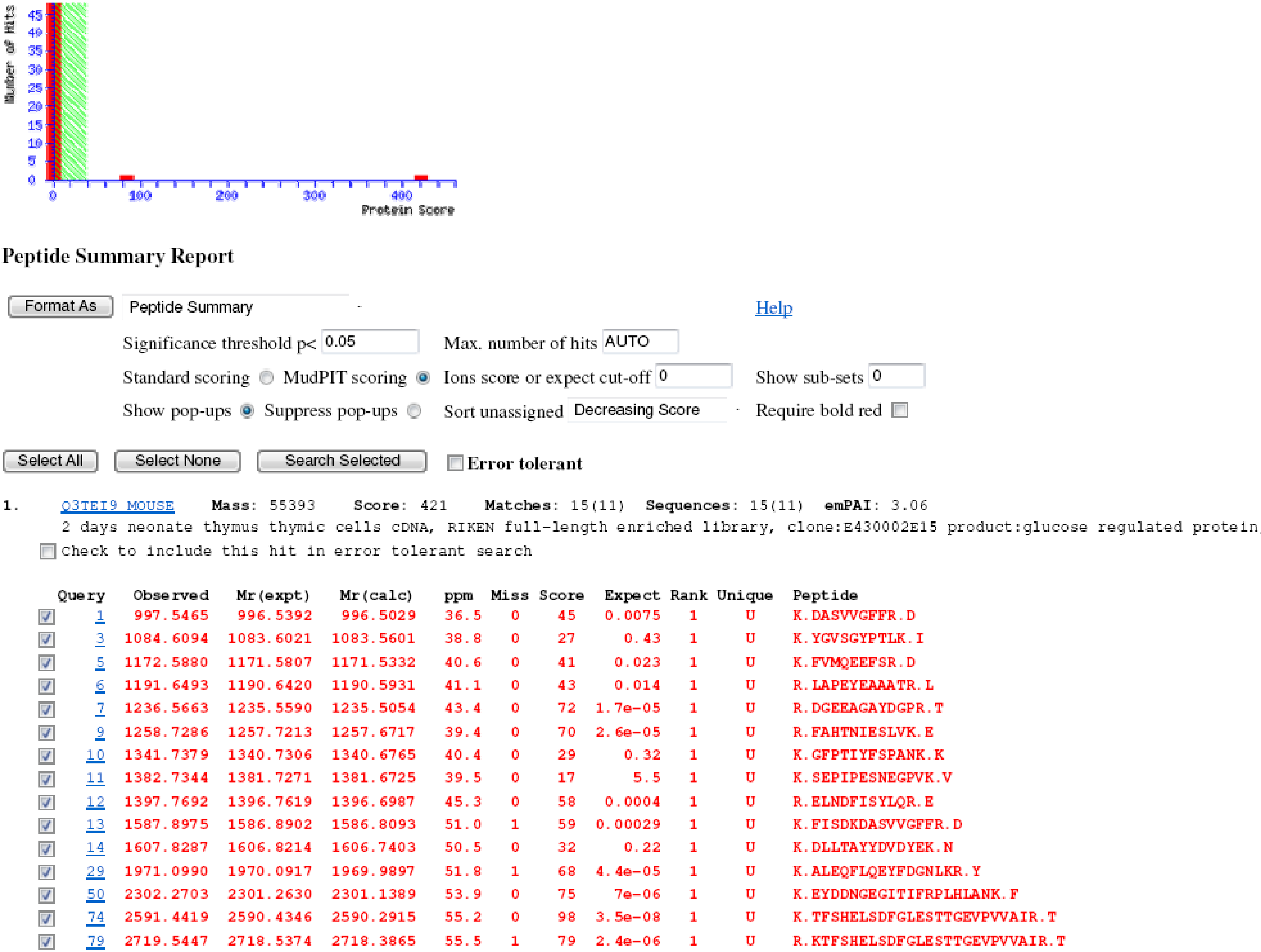
4700 MS/MS Precursor 1397.77 Spec #1 MC[BP = 86.1, 4255]



M16

4700 MS/MS Precursor 1172.59 Spec #1 MC[BP = 120.1, 3468]





Peptide Summary Report

Format As: Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

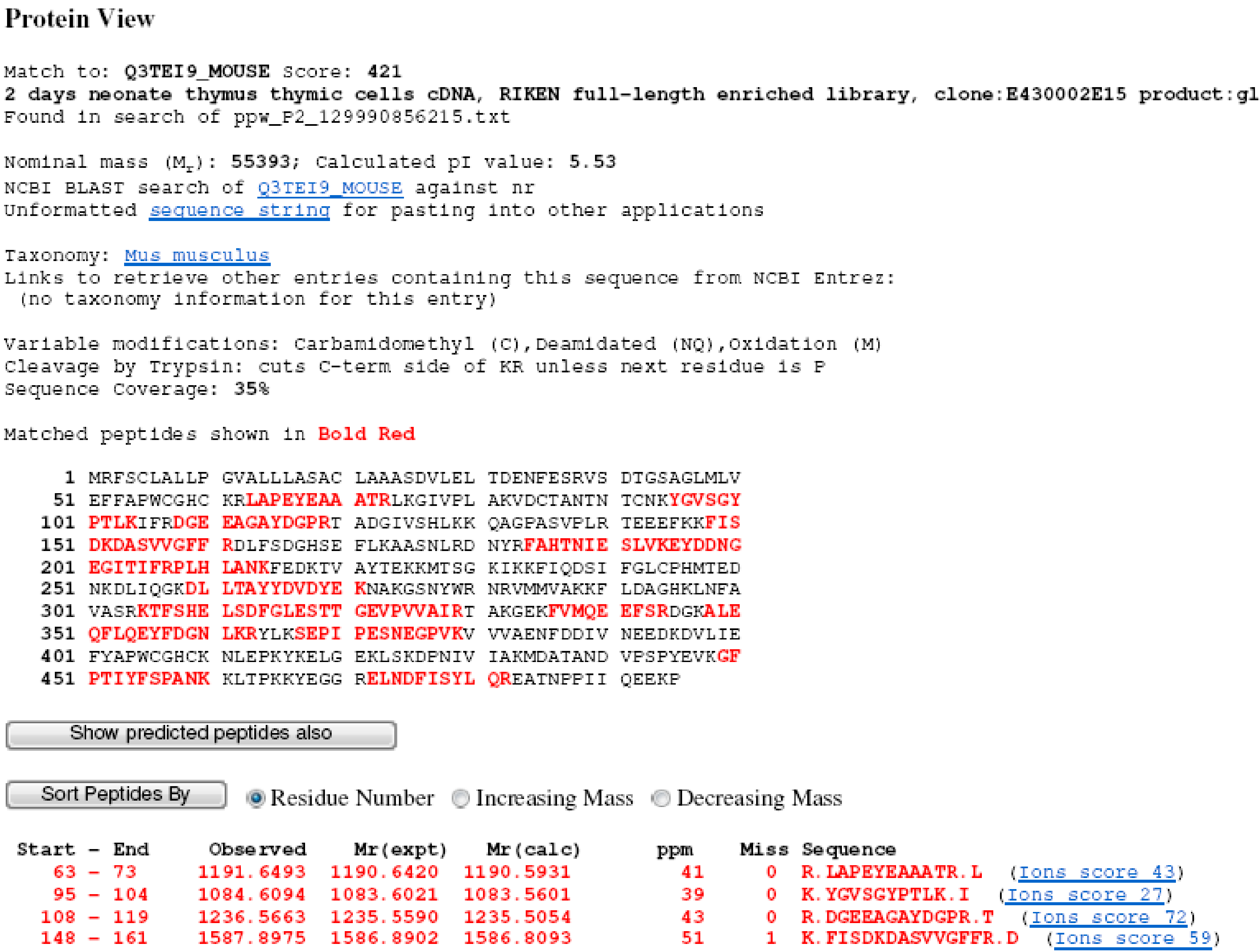
☐ **Error tolerant**

1. Q3TEI9_MOUSE **Mass:** 55393 **Score:** 421 **Matches:** 15(11) **Sequences:** 15(11) **emPAI:** 3.06

2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430002E15 product:glucose regulated protein,

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	997.5465	996.5392	996.5029	36.5	0	45	0.0075	1	U	K.DASVVGFFR.D
☑	3	1084.6094	1083.6021	1083.5601	38.8	0	27	0.43	1	U	K.YGVSGYPTLK.I
☑	5	1172.5880	1171.5807	1171.5332	40.6	0	41	0.023	1	U	K.FVMQEEFSR.D
☑	6	1191.6493	1190.6420	1190.5931	41.1	0	43	0.014	1	U	R.LAPEYEAAATR.L
☑	7	1236.5663	1235.5590	1235.5054	43.4	0	72	1.7e-05	1	U	R.DGEEAGAYDGPR.T
☑	9	1258.7286	1257.7213	1257.6717	39.4	0	70	2.6e-05	1	U	R.FAHTNIESLVK.E
☑	10	1341.7379	1340.7306	1340.6765	40.4	0	29	0.32	1	U	K.GFPTIYFSPANK.K
☑	11	1382.7344	1381.7271	1381.6725	39.5	0	17	5.5	1	U	K.SEPIPESNEGPVK.V
☑	12	1397.7692	1396.7619	1396.6987	45.3	0	58	0.0004	1	U	R.ELNDFISYLQR.E
☑	13	1587.8975	1586.8902	1586.8093	51.0	1	59	0.00029	1	U	K.FISDKDASVVGFFR.D
☑	14	1607.8287	1606.8214	1606.7403	50.5	0	32	0.22	1	U	K.DLLTAYYDVDYEK.N
☑	29	1971.0990	1970.0917	1969.9897	51.8	1	68	4.4e-05	1	U	K.ALEQFLQEYFDGNLKR.Y
☑	50	2302.2703	2301.2630	2301.1389	53.9	0	75	7e-06	1	U	K.EYDDNGEGITIFRPLHLANK.F
☑	74	2591.4419	2590.4346	2590.2915	55.2	0	98	3.5e-08	1	U	K.TFSHELSDFGLESTTGEVPVVAIR.T
☑	79	2719.5447	2718.5374	2718.3865	55.5	1	79	2.4e-06	1	U	R.KTFSHELSDFGLESTTGEVPVVAIR.T



Protein View

Match to: **Q3TEI9_MOUSE** Score: **421**
2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430002E15 product:gl
Found in search of ppw_P2_129990856215.txt

Nominal mass (M_r): **55393**; Calculated pI value: **5.53**
NCBI BLAST search of Q3TEI9_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **35%**

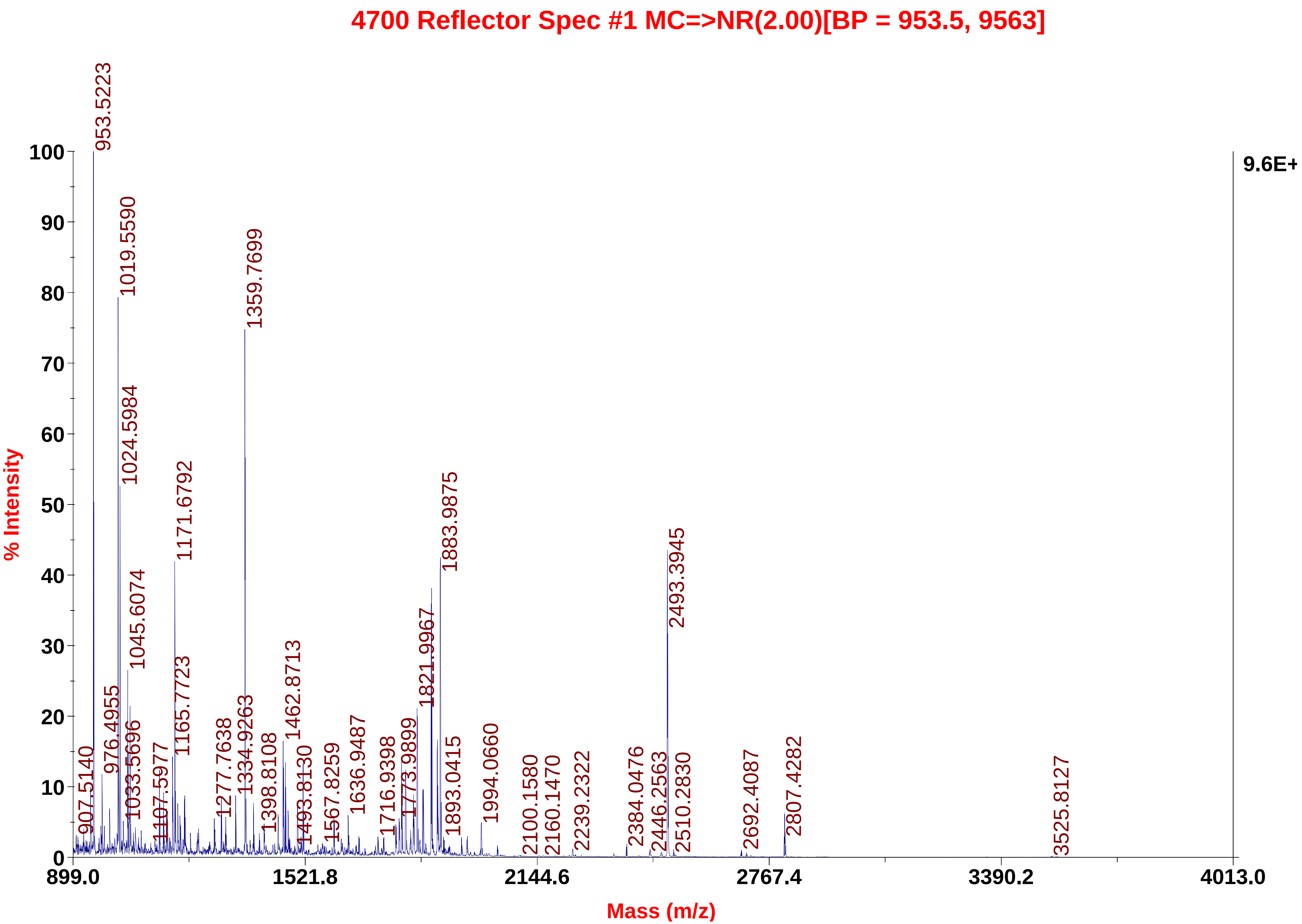
Matched peptides shown in **Bold Red**

```
     1 MRFSCLALLP GVALLLASAC LAAASDVLEL TDENFESRVS DTGSAGLMLV
    51 EFFAPWCGHC KRLAPEYEAA ATRLKGIVPL AKVDCTANTN TCNKYGVSGY
   101 PTLKIFRDGE EAGAYDGPRT ADGIVSHLKK QAGPASVPLR TEEEFKKFIS
   151 DKDASVVGFF RDLFSDGHSE FLKAASNLRD NYRFAHTNIE SLVKEYDDNG
   201 EGITIFRPLH LANKFEDKTV AYTEKKMTSG KIKKFIQDSI FGLCPHMTED
   251 NKDLIQGKDL LTAYYDVDYE KNAKGSNYWR NRVMMVAKKF LDAGHKLNFA
   301 VASRKTFSHE LSDFGLESTT GEVPVVAIRT AKGEKFVMQE EFSRDGKALE
   351 QFLQEYFDGN LKRYLKSEPI PESNEGPVKV VVAENFDDIV NEEDKDVLIE
   401 FYAPWCGHCK NLEPKYKELG EKLSKDPNIV IAKMDATAND VPSPYEVKGF
   451 PTIYFSPANK KLTPKKYEGG RELNDFISYL QREATNPPII QEEKP
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm  Miss Sequence
   63 - 73     1191.6493  1190.6420  1190.5931      41    0  R.LAPEYEAAATR.L  (Ions score 43)
   95 - 104    1084.6094  1083.6021  1083.5601      39    0  K.YGVSGYPTLK.I  (Ions score 27)
  108 - 119    1236.5663  1235.5590  1235.5054      43    0  R.DGEEAGAYDGPR.T  (Ions score 72)
  148 - 161    1587.8975  1586.8902  1586.8093      51    1  K.FISDKDASVVGFFR.D  (Ions score 59)
```

Sample M17


4700 Reflector Spec #1 MC=>NR(2.00)[BP = 953.5, 9563]
% Intensity
Mass (m/z)
9.6E+
100
90
80
70
60
50
40
30
20
10
0
899.0
1521.8
2144.6
2767.4
3390.2
4013.0
907.5140
953.5223
976.4955
1019.5590
1024.5984
1033.5696
1045.6074
1107.5977
1165.7723
1171.6792
1277.7638
1334.9263
1359.7699
1398.8108
1462.8713
1493.8130
1567.8259
1636.9487
1716.9398
1773.9899
1821.9967
1883.9875
1893.0415
1994.0660
2100.1580
2160.1470
2239.2322
2384.0476
2446.2563
2493.3945
2510.2830
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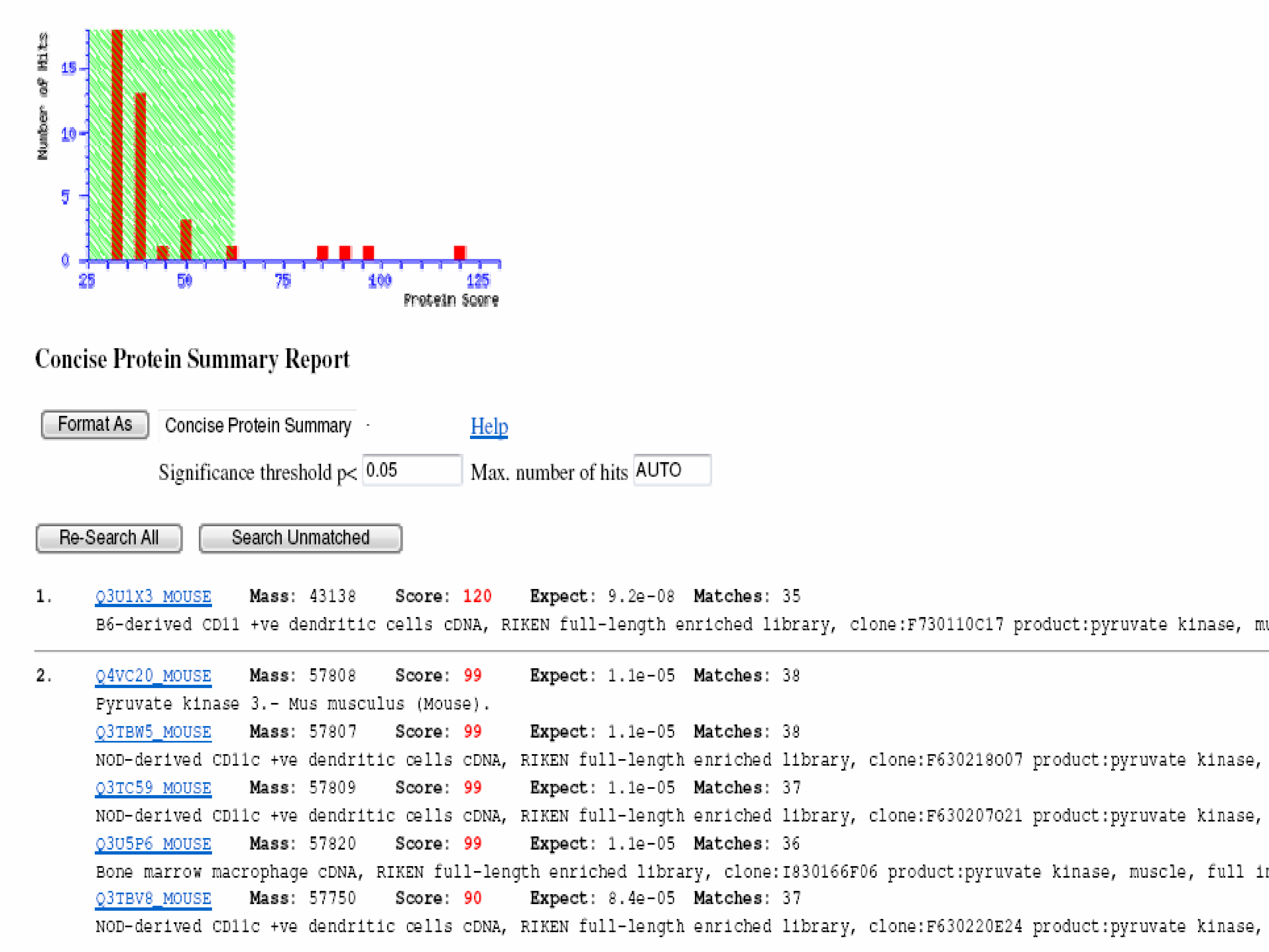
2807.4282
3525.8127



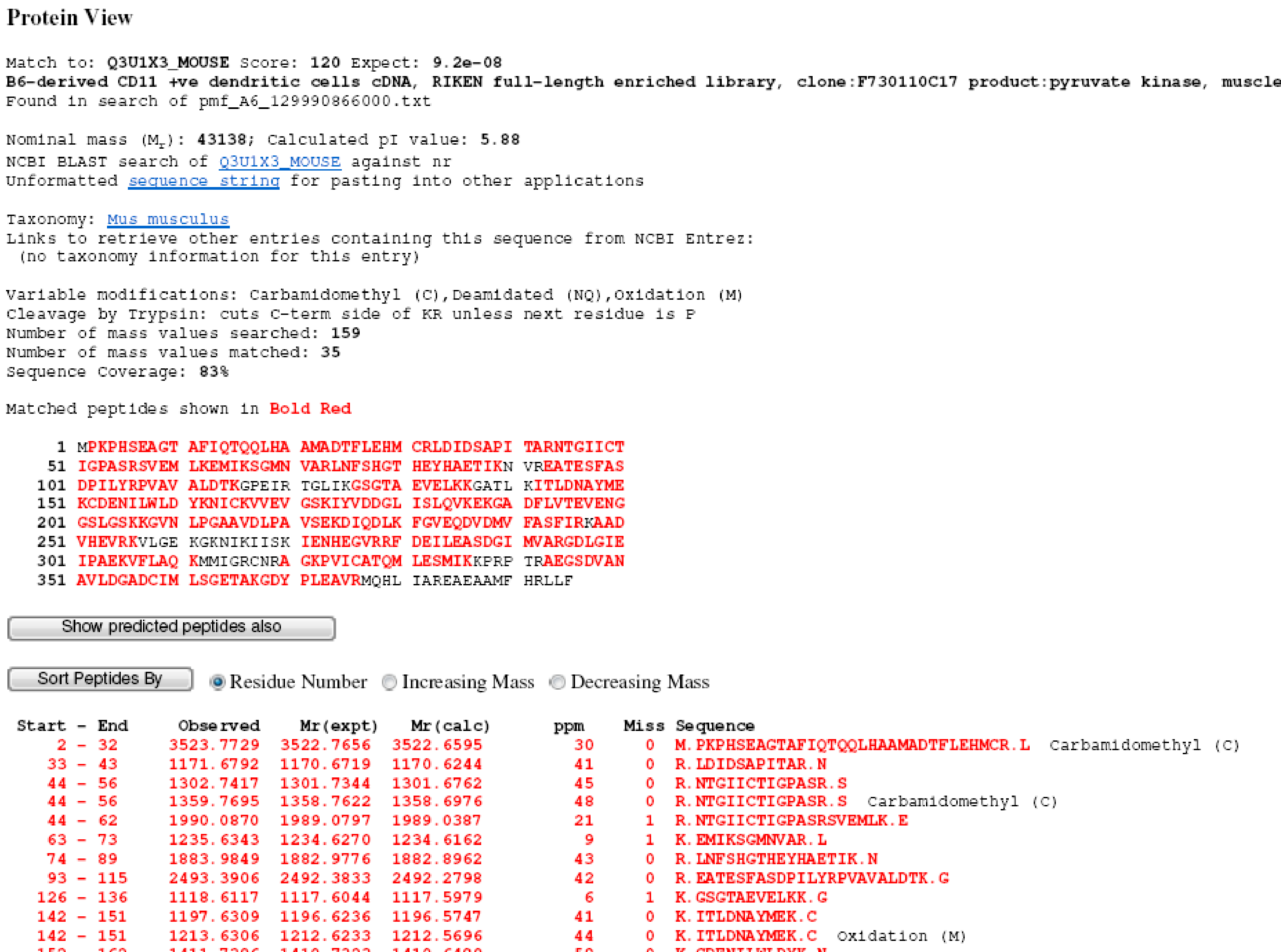
Concise Protein Summary Report

Format As: Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

1. Q3U1X3_MOUSE **Mass:** 43138 **Score:** 120 **Expect:** 9.2e-08 **Matches:** 35
B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730110C17 product:pyruvate kinase, mu

2. Q4VC20_MOUSE **Mass:** 57808 **Score:** 99 **Expect:** 1.1e-05 **Matches:** 38
Pyruvate kinase 3.- Mus musculus (Mouse).
Q3TBW5_MOUSE **Mass:** 57807 **Score:** 99 **Expect:** 1.1e-05 **Matches:** 38
NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630218O07 product:pyruvate kinase,
Q3TC59_MOUSE **Mass:** 57809 **Score:** 99 **Expect:** 1.1e-05 **Matches:** 37
NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630207O21 product:pyruvate kinase,
Q3U5P6_MOUSE **Mass:** 57820 **Score:** 99 **Expect:** 1.1e-05 **Matches:** 36
Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830166F06 product:pyruvate kinase, muscle, full i
Q3TBV8_MOUSE **Mass:** 57750 **Score:** 90 **Expect:** 8.4e-05 **Matches:** 37
NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630220E24 product:pyruvate kinase,



Protein View

```
Match to: Q3U1X3_MOUSE Score: 120 Expect: 9.2e-08
B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730110C17 product:pyruvate kinase, muscle
Found in search of pmf_A6_129990866000.txt

Nominal mass (Mr): 43138; Calculated pI value: 5.88
NCBI BLAST search of Q3U1X3_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 159
Number of mass values matched: 35
Sequence Coverage: 83%

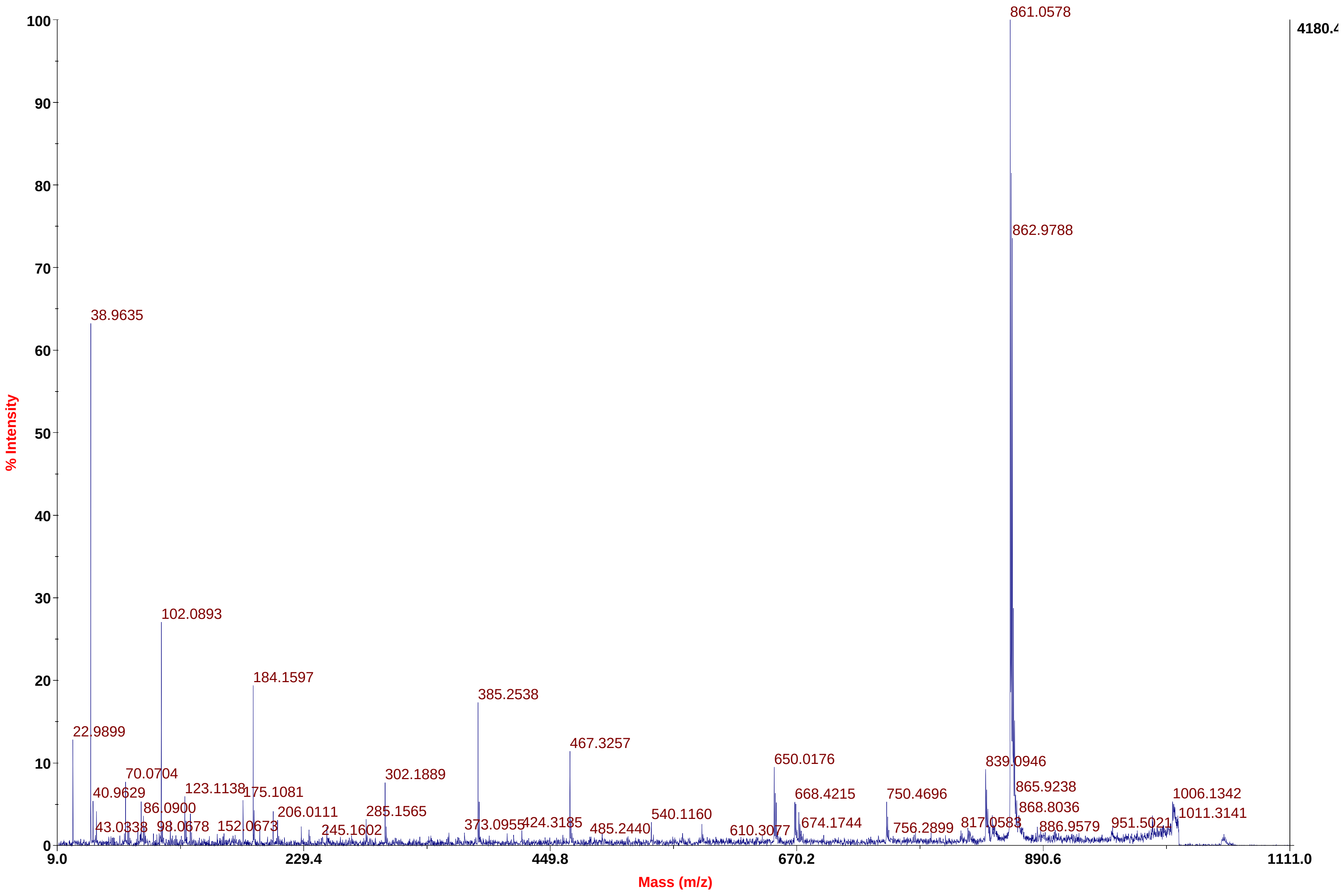
Matched peptides shown in Bold Red

     1 MPKPHSEAGT AFIQTQQLHA AMADTFLEHM CRLDIDSAPI TARNTGIICT
    51 IGPASRSVEM LKEMIKSGMN VARLNFSHGT HEYHAETIKN VREATESFAS
   101 DPILYRPVAV ALDTKGPEIR TGLIKGSGTA EVELKKGATL KITLDNAYME
   151 KCDENILWLD YKNICKVVEV GSKIYVDDGL ISLQVKEKGA DFLVTEVENG
   201 GSLGSKKGVN LPGAAVDLPA VSEKDIQDLK FGVEQDVDMV FASFIRKAAD
   251 VHEVRKVLGE KGKNIKIISK IENHEGVRRF DEILEASDGI MVARGDLGIE
   301 IPAEKVFLAQ KMMIGRCNRA GKPVICATQM LESMIKKPRP TRAEGSDVAN
   351 AVLDGADCIM LSGETAKGDY PLEAVRMQHL IAREAEAAMF HRLLF
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss  Sequence
     2 - 32     3523.7729  3522.7656  3522.6595      30     0  M.PKPHSEAGTAFIQTQQLHAAMADTFLEHMCR.L  Carbamidomethyl (C)
    33 - 43     1171.6792  1170.6719  1170.6244      41     0  R.LDIDSAPITAR.N
    44 - 56     1302.7417  1301.7344  1301.6762      45     0  R.NTGIICTIGPASR.S
    44 - 56     1359.7695  1358.7622  1358.6976      48     0  R.NTGIICTIGPASR.S  Carbamidomethyl (C)
    44 - 62     1990.0870  1989.0797  1989.0387      21     1  R.NTGIICTIGPASRSVEMLK.E
    63 - 73     1235.6343  1234.6270  1234.6162       9     1  K.EMIKSGMNVAR.L
    74 - 89     1883.9849  1882.9776  1882.8962      43     0  R.LNFSHGTHEYHAETIK.N
    93 - 115    2493.3906  2492.3833  2492.2798      42     0  R.EATESFASDPILYRPVAVALDTK.G
   126 - 136    1118.6117  1117.6044  1117.5979       6     1  K.GSGTAEVELKK.G
   142 - 151    1197.6309  1196.6236  1196.5747      41     0  K.ITLDNAYMEK.C
   142 - 151    1213.6306  1212.6233  1212.5696      44     0  K.ITLDNAYMEK.C  Oxidation (M)
```

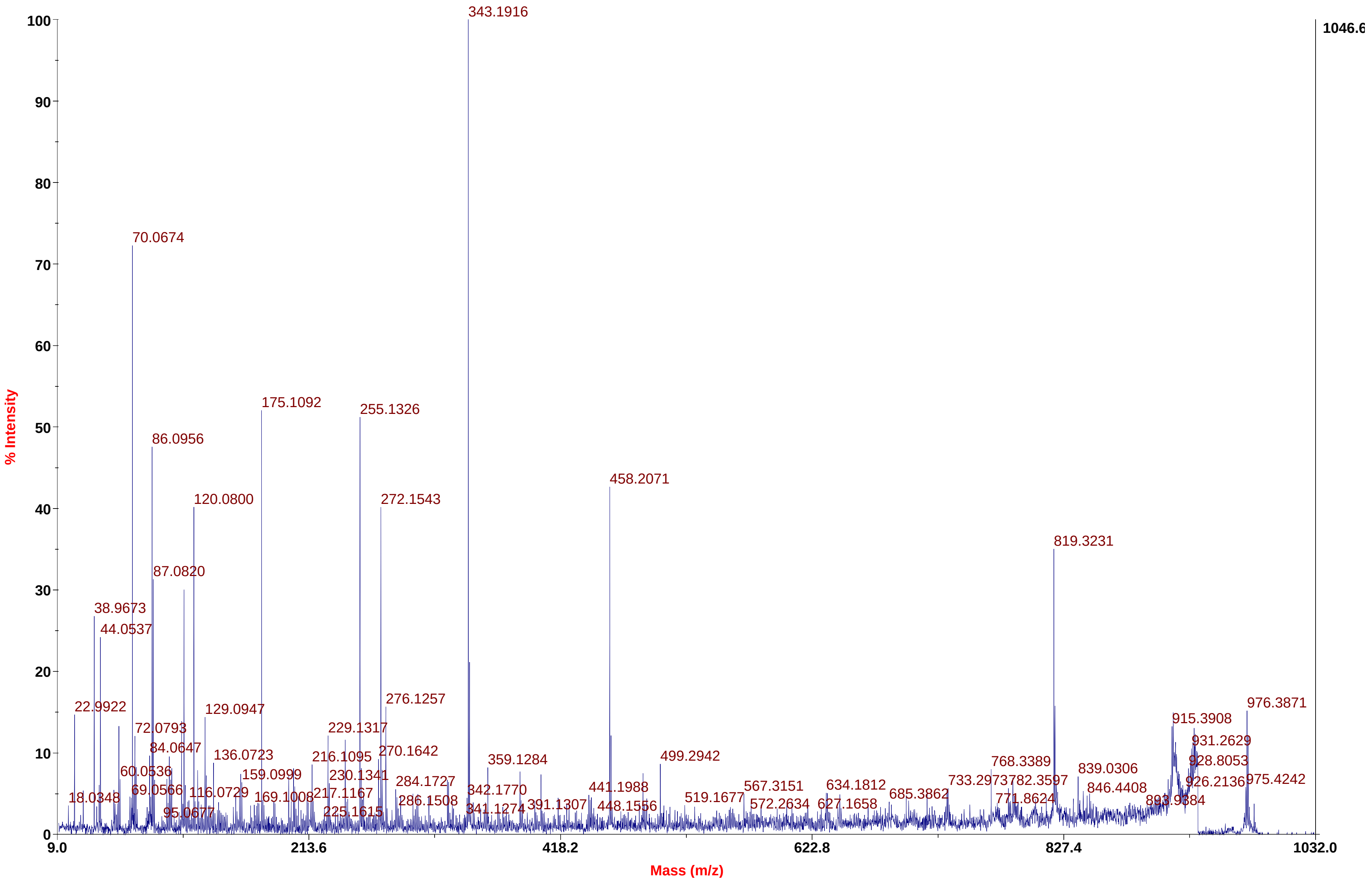
M17

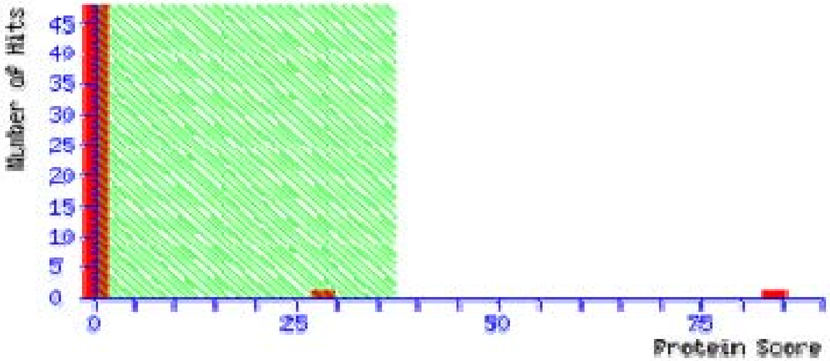
4700 MS/MS Precursor 1051.74 Spec #1 MC[BP = 861.0, 4180]

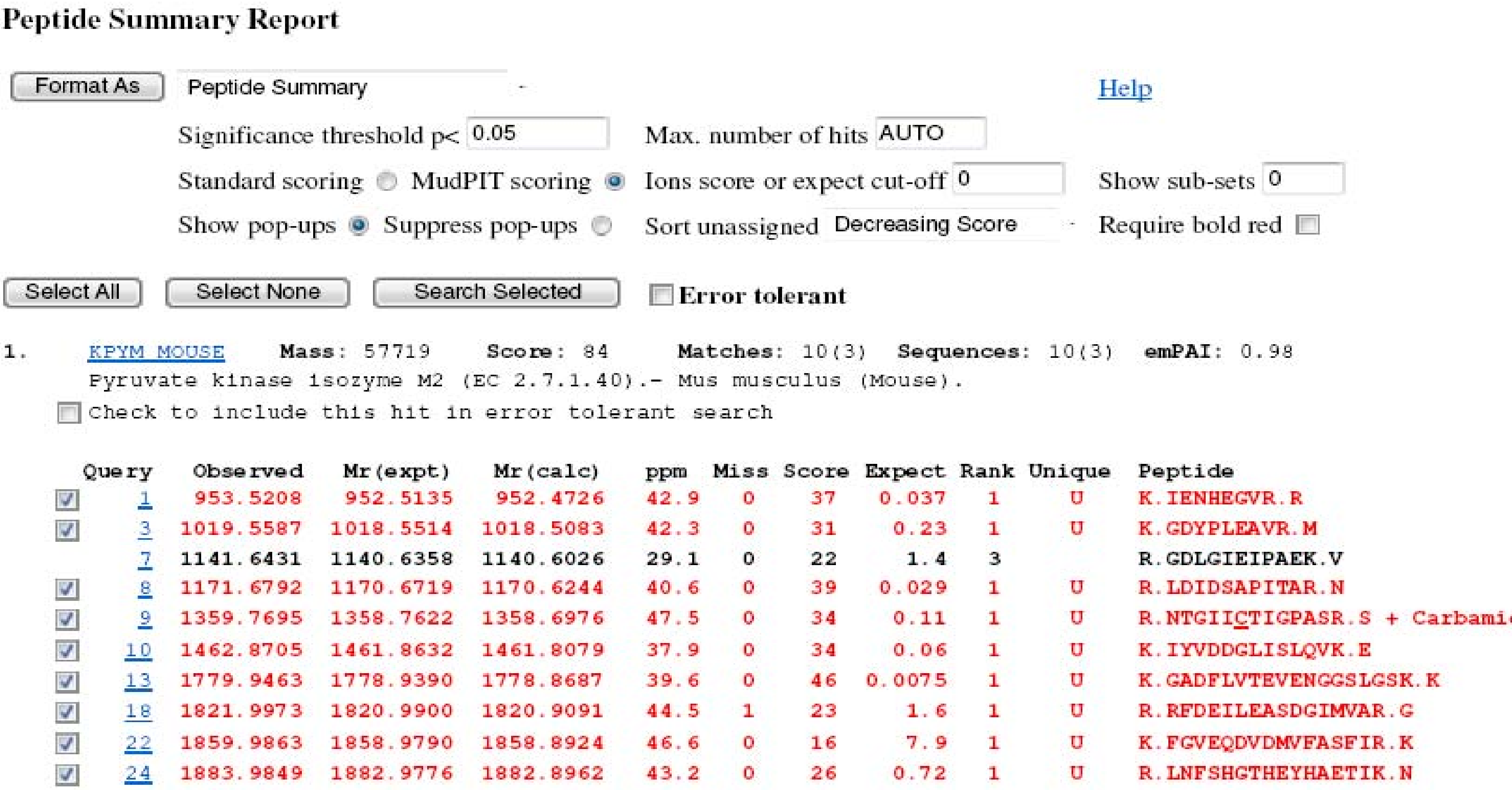


M17

4700 MS/MS Precursor 976.496 Spec #1 MC[BP = 343.2, 1047]







Peptide Summary Report

Format As: Peptide Summary

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

Standard scoring ○ MudPIT scoring ● | Ions score or expect cut-off 0 | Show sub-sets 0

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

☐ **Error tolerant**

1. KPYM_MOUSE **Mass:** 57719 **Score:** 84 **Matches:** 10(3) **Sequences:** 10(3) **emPAI:** 0.98
Pyruvate kinase isozyme M2 (EC 2.7.1.40).- Mus musculus (Mouse).
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	953.5208	952.5135	952.4726	42.9	0	37	0.037	1	U	K.IENHEGVR.R
☑	3	1019.5587	1018.5514	1018.5083	42.3	0	31	0.23	1	U	K.GDYPLEAVR.M
	7	1141.6431	1140.6358	1140.6026	29.1	0	22	1.4	3		R.GDLGIEIPAEK.V
☑	8	1171.6792	1170.6719	1170.6244	40.6	0	39	0.029	1	U	R.LDIDSAPITAR.N
☑	9	1359.7695	1358.7622	1358.6976	47.5	0	34	0.11	1	U	R.NTGIICTIGPASR.S + Carbami
☑	10	1462.8705	1461.8632	1461.8079	37.9	0	34	0.06	1	U	K.IYVDDGLISLQVK.E
☑	13	1779.9463	1778.9390	1778.8687	39.6	0	46	0.0075	1	U	K.GADFLVTEVENGGSLGSK.K
☑	18	1821.9973	1820.9900	1820.9091	44.5	1	23	1.6	1	U	R.RFDEILEASDGIMVAR.G
☑	22	1859.9863	1858.9790	1858.8924	46.6	0	16	7.9	1	U	K.FGVEQDVDMVFASFIR.K
☑	24	1883.9849	1882.9776	1882.8962	43.2	0	26	0.72	1	U	R.LNFSHGTHEYHAETIK.N

Protein View

Match to: **KPYM_MOUSE** Score: **84**
Pyruvate kinase isozyme M2 (EC 2.7.1.40).- Mus musculus (Mouse).
Found in search of ppw_A6_129990871300.txt

Nominal mass (M_r): **57719**; Calculated pI value: **7.42**
NCBI BLAST search of KPYM_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **24%**

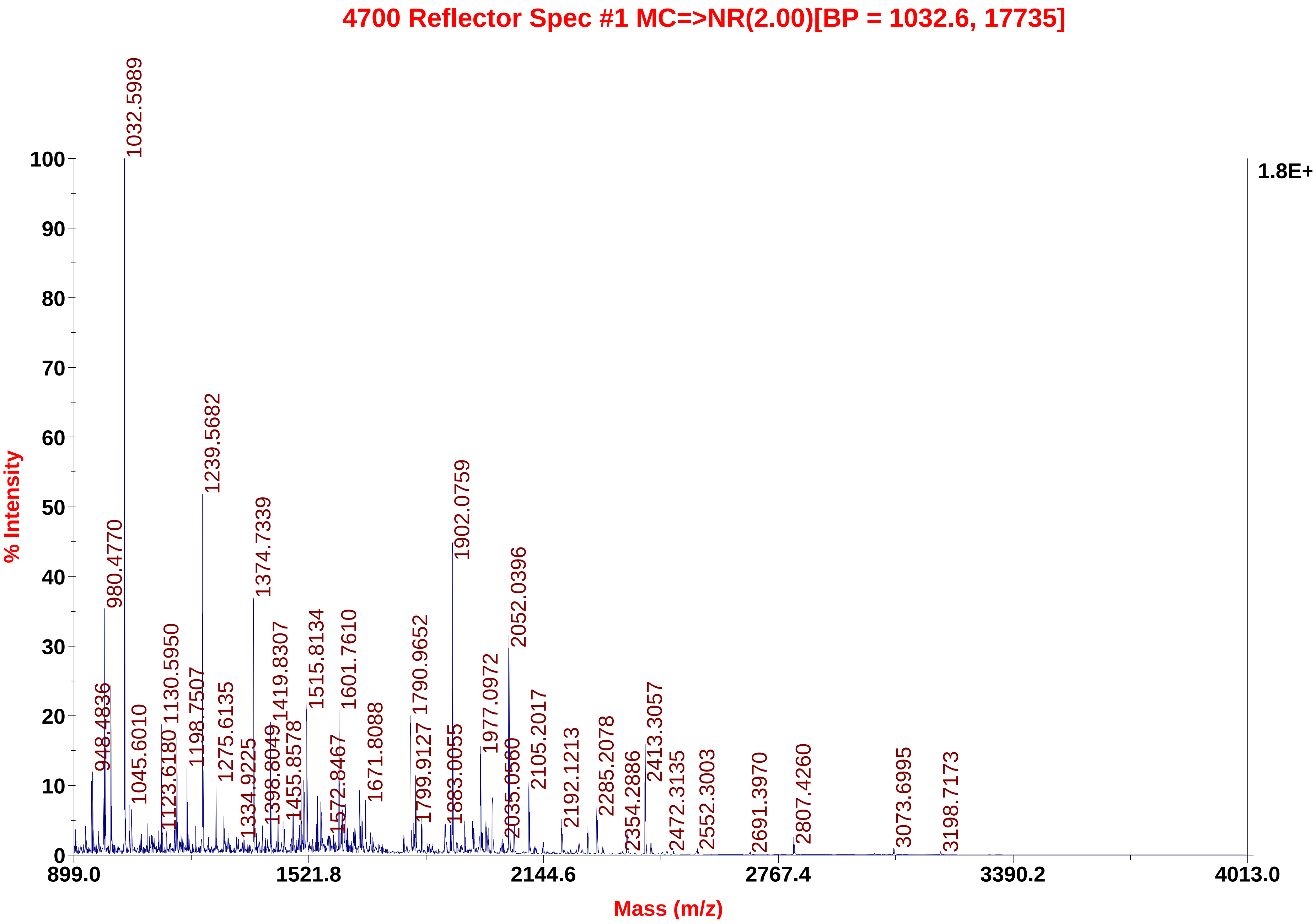
Matched peptides shown in **Bold Red**

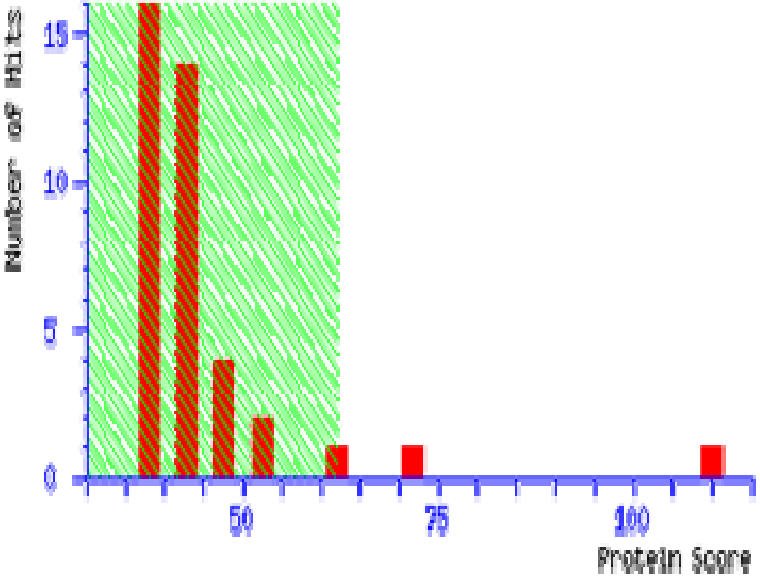
```
  1 PKPHSEAGTA FIQTQQLHAA MADTFLEHMC RLDIDSAPIT ARNTGIICTI
 51 GPASRSVEML KEMIKSGMNV ARLNFSHGTH EYHAETIKNV REATESFASD
101 PILYRPVAVA LDTKGPEIRT GLIKGSGTAE VELKKGATLK ITLDNAYMEK
151 CDENILWLDY KNICKVVEVG SKIYVDDGLI SLQVKEKGAD FLVTEVENGG
201 SLGSKKGVNL PGAAVDLPAV SEKDIQDLKF GVEQDVDMVF ASFIRKAADV
251 HEVRKVLGEK GKNIKIISKI ENHEGVRRFD EILEASDGIM VARGDLGIEI
301 PAEKVFLAQK MMIGRCNRAG KPVICSTQML EIMIKKPRPT RAEGSDVANA
351 VLDGADCIML SGETAKGDYP LEAVRMQHLI AREAEAAIYH LQLFEELRRL
401 APITSDPTEA AAVGAVEASF KCCSGAIIVL TKSGRSAHQV ARYRPRAPII
451 AVTRNPQTAR QAHLYRGIFP VLCKDAVLNA WAEDVDLRVN LAMDVGKARG
501 FFKKGDVVIV LTGWRPGSGF TNTMRVVPVP
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss  Sequence
   32 - 42      1171.6792  1170.6719  1170.6244      41     0   R.LDIDSAPITAR.N  (Ions score 39)
   43 - 55      1359.7695  1358.7622  1358.6976      48     0   R.NTGIICTIGPASR.S  Carbamidomethyl (C)
   73 - 88      1883.9849  1882.9776  1882.8962      43     0   R.LNFSHGTHEYHAETIK.N  (Ions score 26)
  173 - 185     1462.8705  1461.8632  1461.8079      38     0   K.IYVDDGLISLQVK.E  (Ions score 34)
  188 - 205     1779.9463  1778.9390  1778.8687      40     0   K.GADFLVTEVENGGSLGSK.K  (Ions score 46)
  230 - 245     1859.9863  1858.9790  1858.8924      47     0   K.FGVEQDVDMVFASFIR.K  (Ions score 16)
  270 - 277      953.5208   952.5135   952.4726      43     0   K.IENHEGVR.R  (Ions score 37)
  278 - 293     1821.9973  1820.9900  1820.9091      44     1   R.RFDEILEASDGIMVAR.G  (Ions score 23)
  294 - 304     1141.6431  1140.6358  1140.6026      29     0   R.GDLGIEIPAEK.V  (Ions score 22)
  367 - 375     1019.5587  1018.5514  1018.5083      42     0   K.GDYPLEAVR.M  (Ions score 31)
```

Sample M18


4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1032.6, 17735]
% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
1.8E+
899.0
1521.8
2144.6
2767.4
3390.2
4013.0
948.4836
980.4770
1032.5989
1045.6010
1123.6180
1130.5950
1198.7507
1239.5682
1275.6135
1334.9225
1374.7339
1398.8049
1419.8307
1455.8578
1515.8134
1572.8467
1601.7610
1671.8088
1790.9652
1799.9127
1883.0055
1902.0759
1977.0972
2035.0560
2052.0396
2105.2017
2192.1213
2285.2078
2354.2886
2413.3057
2472.3135
2552.3003
2691.3970
2807.4260
3073.6995
3198.7173



Concise Protein Summary Report

Format As | Concise Protein Summary | Help

Significance threshold p< 0.05 Max. number of hits AUTO

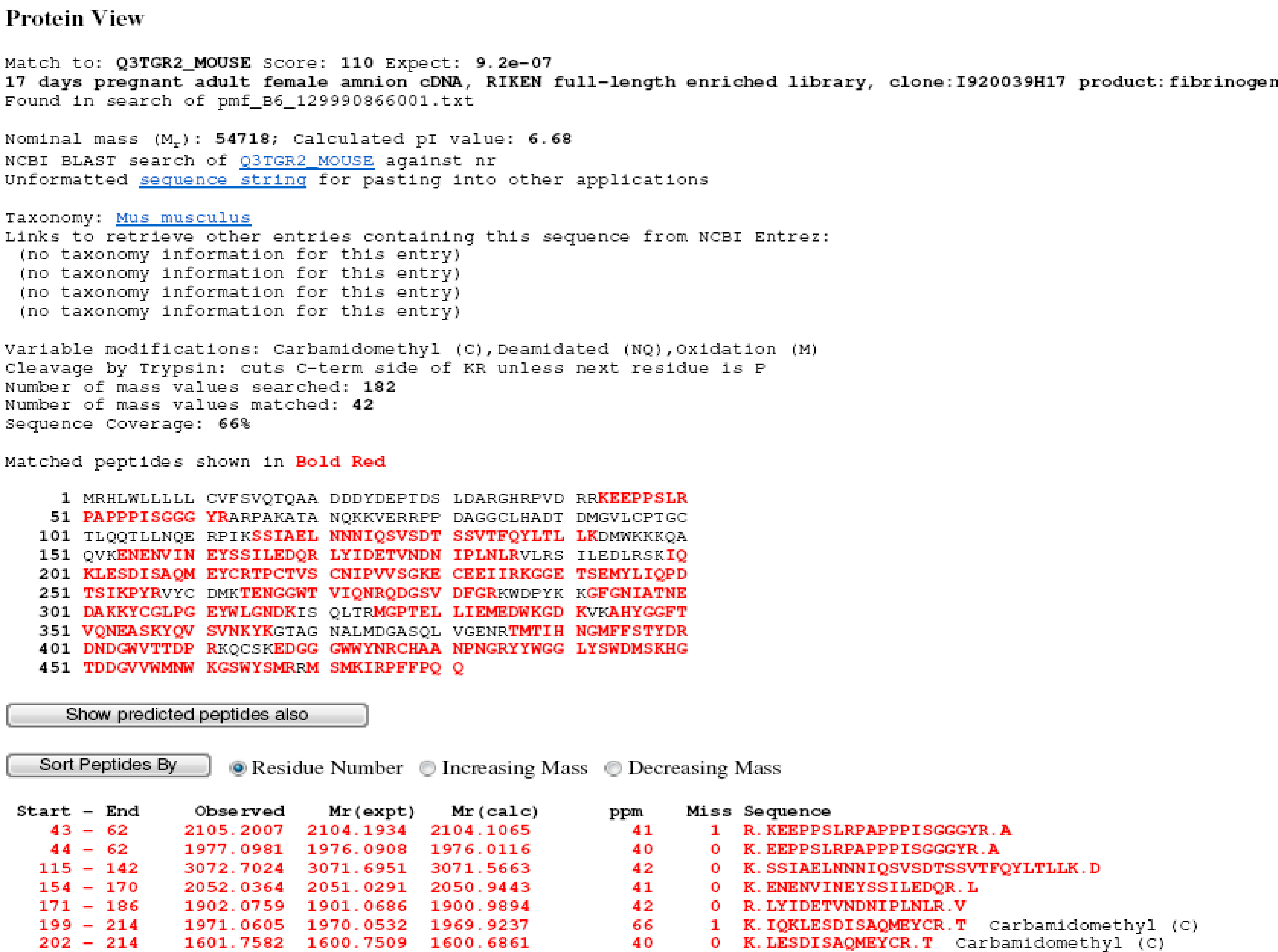
Re-Search All | Search Unmatched

1. Q3TGR2_MOUSE **Mass:** 54718 **Score:** 110 **Expect:** 9.2e-07 **Matches:** 42

17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920039H17 product:fibrinogen,

AAL02225 **Mass:** 27037 **Score:** 71 **Expect:** 0.0072 **Matches:** 26

AF413205 NID: - Mus musculus



Protein View

```
Match to: Q3TGR2_MOUSE Score: 110 Expect: 9.2e-07
17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920039H17 product:fibrinogen
Found in search of pmf_B6_129990866001.txt

Nominal mass (Mr): 54718; Calculated pI value: 6.68
NCBI BLAST search of Q3TGR2_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 182
Number of mass values matched: 42
Sequence Coverage: 66%

Matched peptides shown in Bold Red

     1 MRHLWLLLLL CVFSVQTQAA DDDYDEPTDS LDARGHRPVD RRKEEPPSLR
    51 PAPPPISGGG YRARPAKATA NQKKVERRPP DAGGCLHADT DMGVLCPTGC
   101 TLQQTLLNQE RPIKSSIAEL NNNIQSVSDT SSVTFQYLTL LKDMWKKKQA
   151 QVKENENVIN EYSSILEDQR LYIDETVNDN IPLNLRVLRS ILEDLRSKIQ
   201 KLESDISAQM EYCRTPCTVS CNIPVVSGKE CEEIIRKGGE TSEMYLIQPD
   251 TSIKPYRVYC DMKTENGGWT VIQNRQDGSV DFGRKWDPYK KGFGNIATNE
   301 DAKKYCGLPG EYWLGNDKIS QLTRMGPTEL LIEMEDWKGD KVKAHYGGFT
   351 VQNEASKYQV SVNKYKGTAG NALMDGASQL VGENRTMTIH NGMFFSTYDR
   401 DNDGWVTTDP RKQCSKEDGG GWWYNRCHAA NPNGRYYWGG LYSWDMSKHG
   451 TDDGVVWMNW KGSWYSMRRM SMKIRPFFPQ Q
```

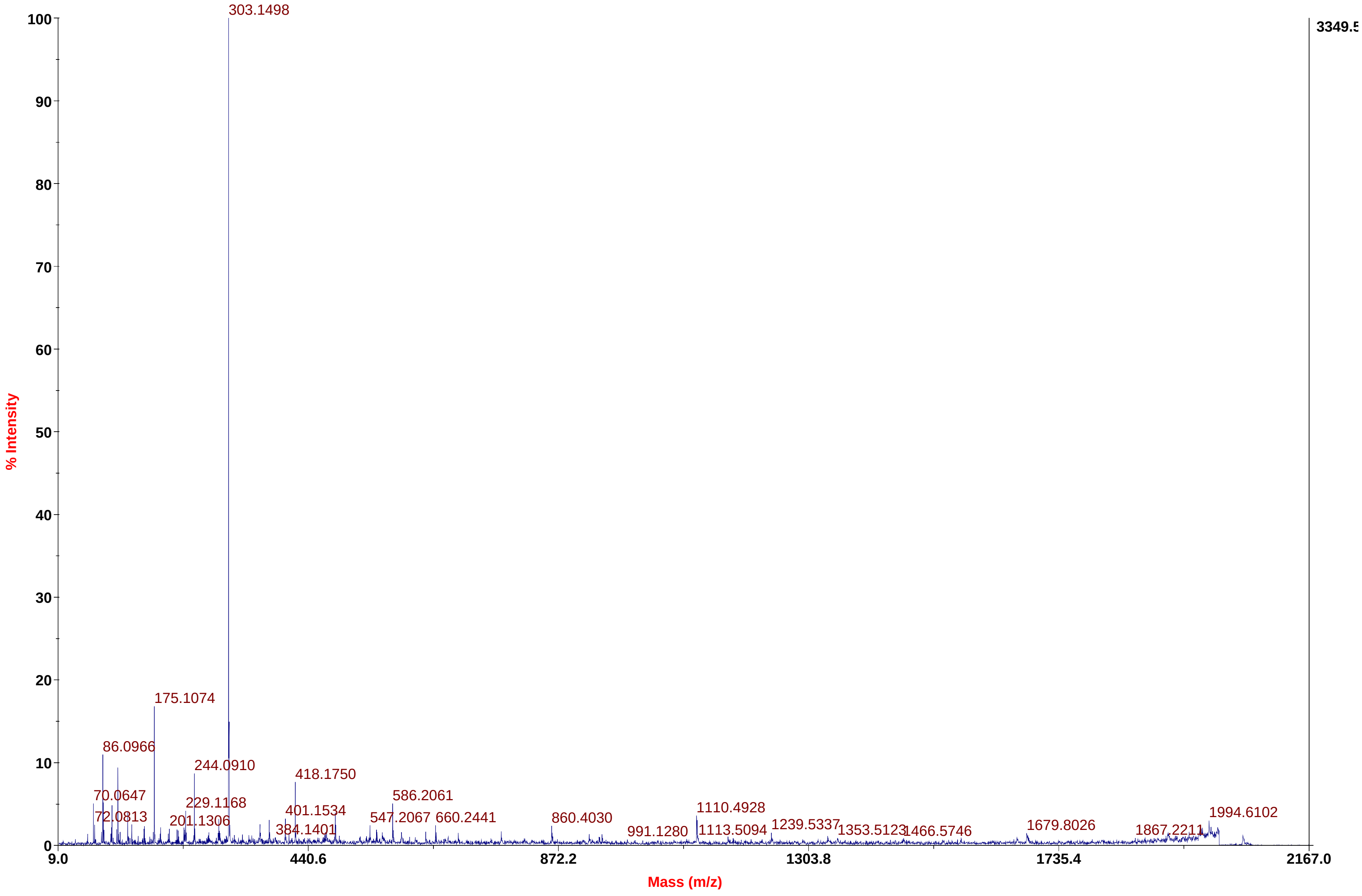
Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
   43 - 62      2105.2007  2104.1934  2104.1065       41      1  R.KEEPPSLRPAPPPISGGGYR.A
   44 - 62      1977.0981  1976.0908  1976.0116       40      0  K.EEPPSLRPAPPPISGGGYR.A
  115 - 142     3072.7024  3071.6951  3071.5663       42      0  K.SSIAELNNNIQSVSDTSSVTFQYLTLLK.D
  154 - 170     2052.0364  2051.0291  2050.9443       41      0  K.ENENVINEYSSILEDQR.L
  171 - 186     1902.0759  1901.0686  1900.9894       42      0  R.LYIDETVNDNIPLNLR.V
  199 - 214     1971.0605  1970.0532  1969.9237       66      1  K.IQKLESDISAQMEYCR.T  Carbamidomethyl (C)
  202 - 214     1601.7582  1600.7509  1600.6861       40      0  K.LESDISAQMEYCR.T  Carbamidomethyl (C)
```

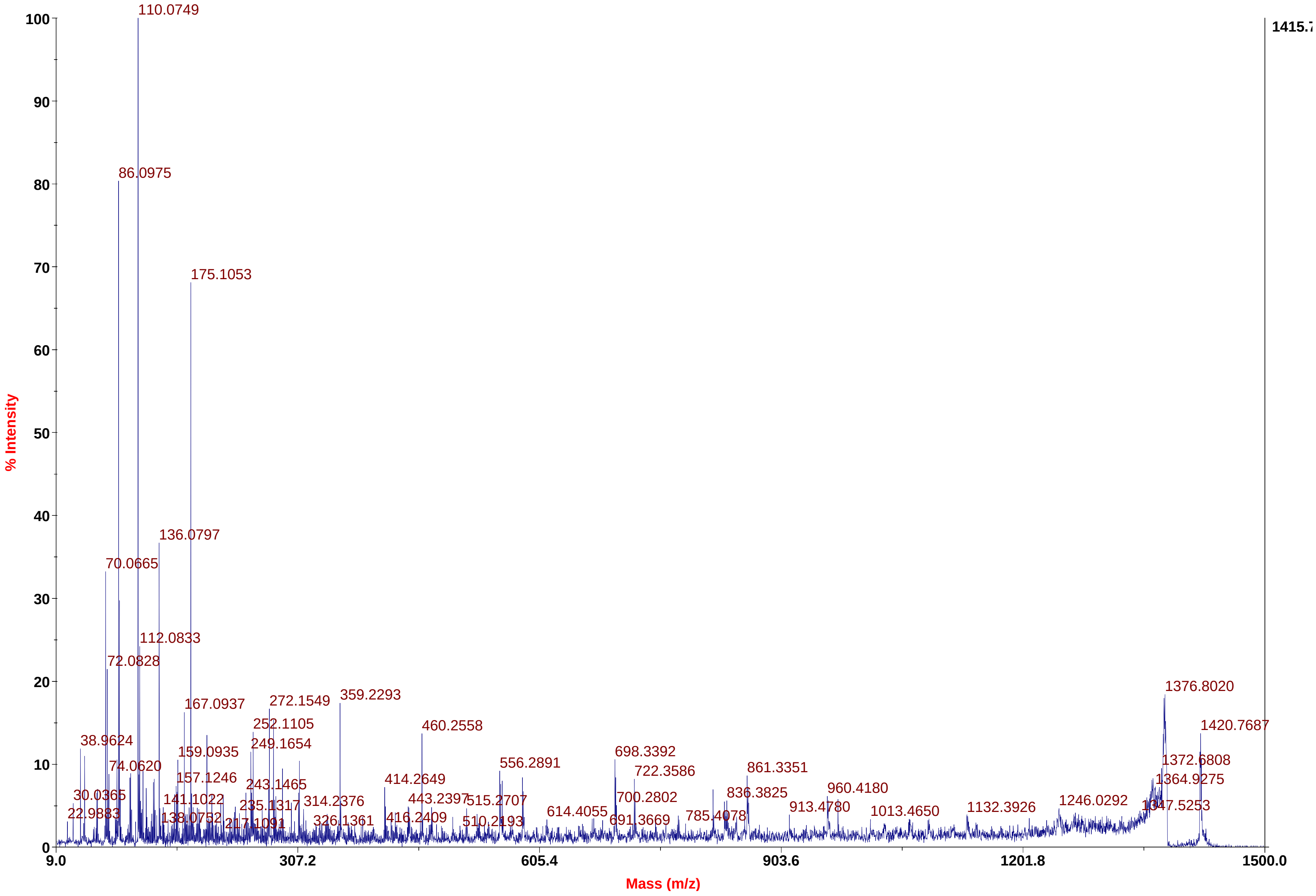
M18

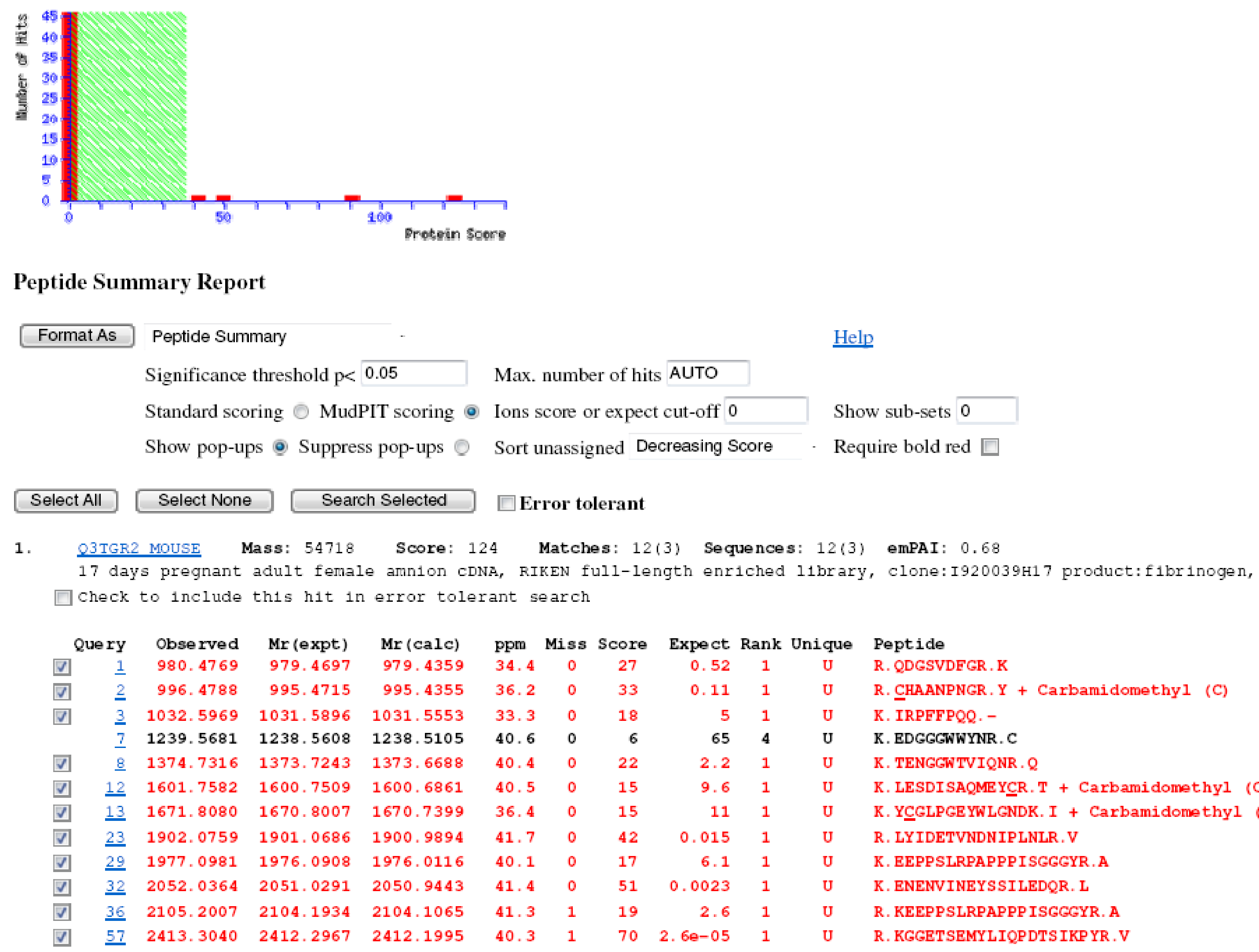
4700 MS/MS Precursor 2052.04 Spec #1 MC[BP = 303.1, 3349]



M18

4700 MS/MS Precursor 1419.83 Spec #1 MC[BP = 110.1, 1416]





Peptide Summary Report

Significance threshold p< 0.05
Max. number of hits AUTO
Standard scoring ○ MudPIT scoring ●
Ions score or expect cut-off 0
Show sub-sets 0
Show pop-ups ● Suppress pop-ups ○
Sort unassigned Decreasing Score
Require bold red ☐

☐ **Error tolerant**

1. Q3TGR2_MOUSE **Mass:** 54718 **Score:** 124 **Matches:** 12(3) **Sequences:** 12(3) **emPAI:** 0.68
17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920039H17 product:fibrinogen,
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	980.4769	979.4697	979.4359	34.4	0	27	0.52	1	U	R.QDGSVDFGR.K
☑	2	996.4788	995.4715	995.4355	36.2	0	33	0.11	1	U	R.CHAANPNGR.Y + Carbamidomethyl (C)
☑	3	1032.5969	1031.5896	1031.5553	33.3	0	18	5	1	U	K.IRPFFPQQ.-
	7	1239.5681	1238.5608	1238.5105	40.6	0	6	65	4	U	K.EDGGGWWYNR.C
☑	8	1374.7316	1373.7243	1373.6688	40.4	0	22	2.2	1	U	K.TENGGWTVIQNR.Q
☑	12	1601.7582	1600.7509	1600.6861	40.5	0	15	9.6	1	U	K.LESDISAQMEYCR.T + Carbamidomethyl (
☑	13	1671.8080	1670.8007	1670.7399	36.4	0	15	11	1	U	K.YCGLPGEYWLGNDK.I + Carbamidomethyl
☑	23	1902.0759	1901.0686	1900.9894	41.7	0	42	0.015	1	U	R.LYIDETVNDNIPLNLR.V
☑	29	1977.0981	1976.0908	1976.0116	40.1	0	17	6.1	1	U	K.EEPPSLRPAPPPISGGGYR.A
☑	32	2052.0364	2051.0291	2050.9443	41.4	0	51	0.0023	1	U	K.ENENVINEYSSILEDQR.L
☑	36	2105.2007	2104.1934	2104.1065	41.3	1	19	2.6	1	U	R.KEEPPSLRPAPPPISGGGYR.A
☑	57	2413.3040	2412.2967	2412.1995	40.3	1	70	2.6e-05	1	U	R.KGGETSEMYLIQPDTSIKPYR.V

Protein View

```
Match to: Q3TGR2_MOUSE Score: 124
17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920039H17 product:fibrinogen, B beta
Found in search of ppw_B6_129990871401.txt

Nominal mass (Mr): 54718; Calculated pI value: 6.68
NCBI BLAST search of Q3TGR2_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 30%

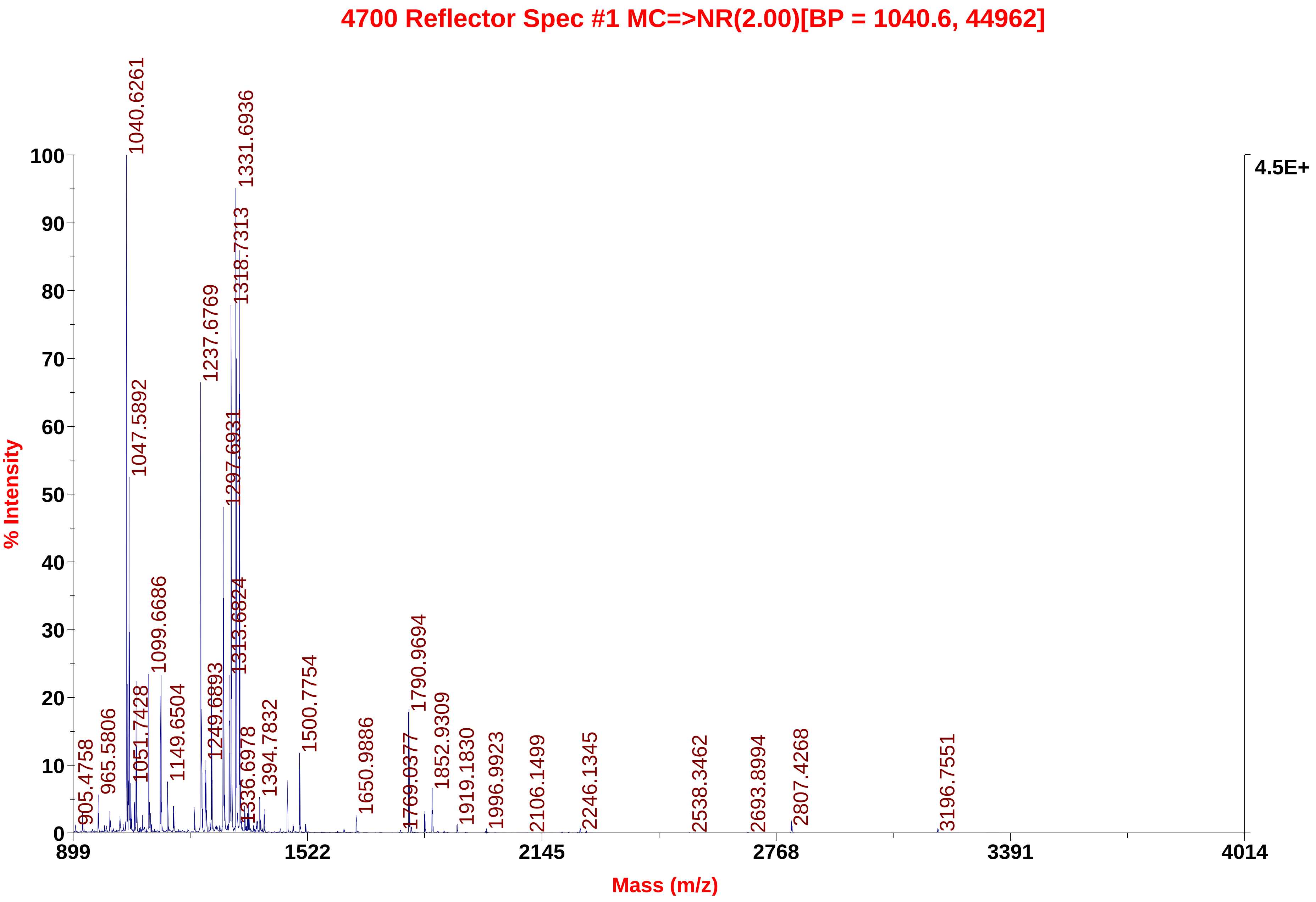
Matched peptides shown in Bold Red

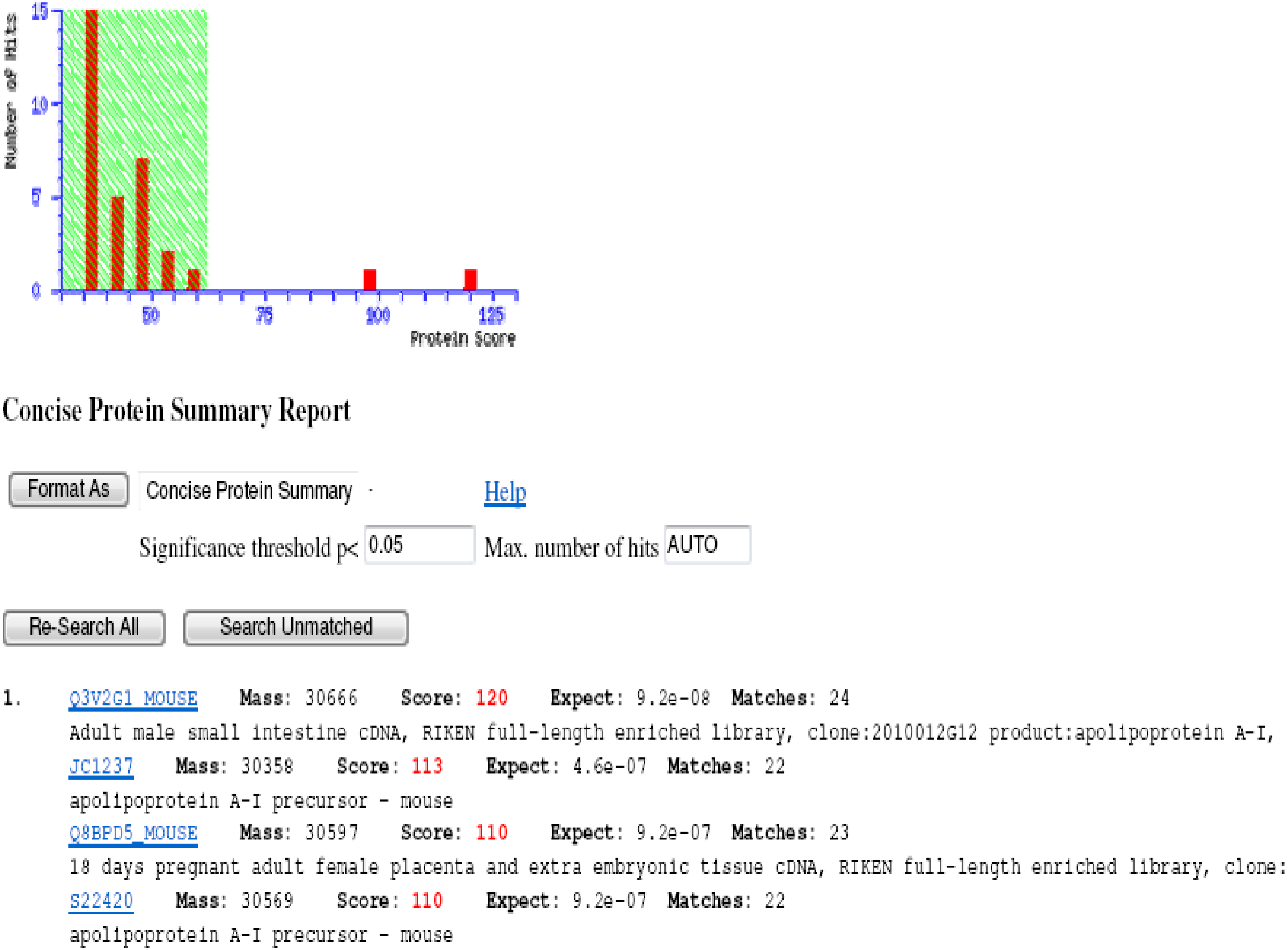
      1 MRHLWLLLLL CVFSVQTQAA DDDYDEPTDS LDARGHRPVD RRKEEPPSLR
     51 PAPPPISGGG YRARPAKATA NQKKVERRPP DAGGCLHADT DMGVLCPTGC
    101 TLQQTLLNQE RPIKSSIAEL NNNIQSVSDT SSVTFQYLTL LKDMWKKKQA
    151 QVKENENVIN EYSSILEDQR LYIDETVNDN IPLNLRVLRS ILEDLRSKIQ
    201 KLESDISAQM EYCRTPCTVS CNIPVVSGKE CEEIIRKGGE TSEMYLIQPD
    251 TSIKPYRVYC DMKTENGGWT VIQNRQDGSV DFGRKWDPYK KGFGNIATNE
    301 DAKKYCGLPG EYWLGNDKIS QLTRMGPTEL LIEMEDWKGD KVKAHYGGFT
    351 VQNEASKYQV SVNKYKGTAG NALMDGASQL VGENRTMTIH NGMFFSTYDR
    401 DNDGWVTTDP RKQCSKEDGG GWWYNRCHAA NPNGRYYWGG LYSWDMSKHG
    451 TDDGVVWMNW KGSWYSMRRM SMKIRPFFPQ Q
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss  Sequence
   43 - 62      2105.2007  2104.1934  2104.1065      41     1   R.KEEPPSLRPAPPPISGGGYR.A  (Ions score 19)
   44 - 62      1977.0981  1976.0908  1976.0116      40     0   K.EEPPSLRPAPPPISGGGYR.A  (Ions score 17)
  154 - 170     2052.0364  2051.0291  2050.9443      41     0   K.ENENVINEYSSILEDQR.L  (Ions score 51)
  171 - 186     1902.0759  1901.0686  1900.9894      42     0   R.LYIDETVNDNIPLNLR.V  (Ions score 42)
  202 - 214     1601.7582  1600.7509  1600.6861      40     0   K.LESDISAQMEYCR.T  Carbamidomethyl (C)  (Ions score 15)
  237 - 257     2413.3040  2412.2967  2412.1995      40     1   R.KGGETSEMYLIQPDTSIKPYR.V  (Ions score 70)
  264 - 275     1374.7316  1373.7243  1373.6688      40     0   K.TENGGWTVIQNR.Q  (Ions score 22)
  276 - 284      980.4769   979.4697   979.4359      34     0   R.QDGSVDFGR.K  (Ions score 27)
  305 - 318     1671.8080  1670.8007  1670.7399      36     0   K.YCGLPGEYWLGNDK.I  Carbamidomethyl (C)  (Ions score 15)
  417 - 426     1239.5681  1238.5608  1238.5105      41     0   K.EDGGGWWYNR.C  (Ions score 6)
  427 - 435      996.4788   995.4715   995.4355      36     0   R.CHAANPNGR.Y  Carbamidomethyl (C)  (Ions score 33)
  474 - 481     1032.5969  1031.5896  1031.5553      33     0   K.IRPFFPQQ.-  (Ions score 18)
```

Sample M19


4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1040.6, 44962]
% Intensity
100
90
80
70
60
50
40
30
20
10
0
4.5E+
905.4758
965.5806
1040.6261
1047.5892
1051.7428
1099.6686
1149.6504
1237.6769
1249.6893
1297.6931
1313.6824
1318.7313
1331.6936
1336.6978
1394.7832
1500.7754
1650.9886
1769.0377
1790.9694
1852.9309
1919.1830
1996.9923
2106.1499
2246.1345
2538.3462
2693.8994
2807.4268
3196.7551
899
1522
2145
2768
3391
4014
Mass (m/z)

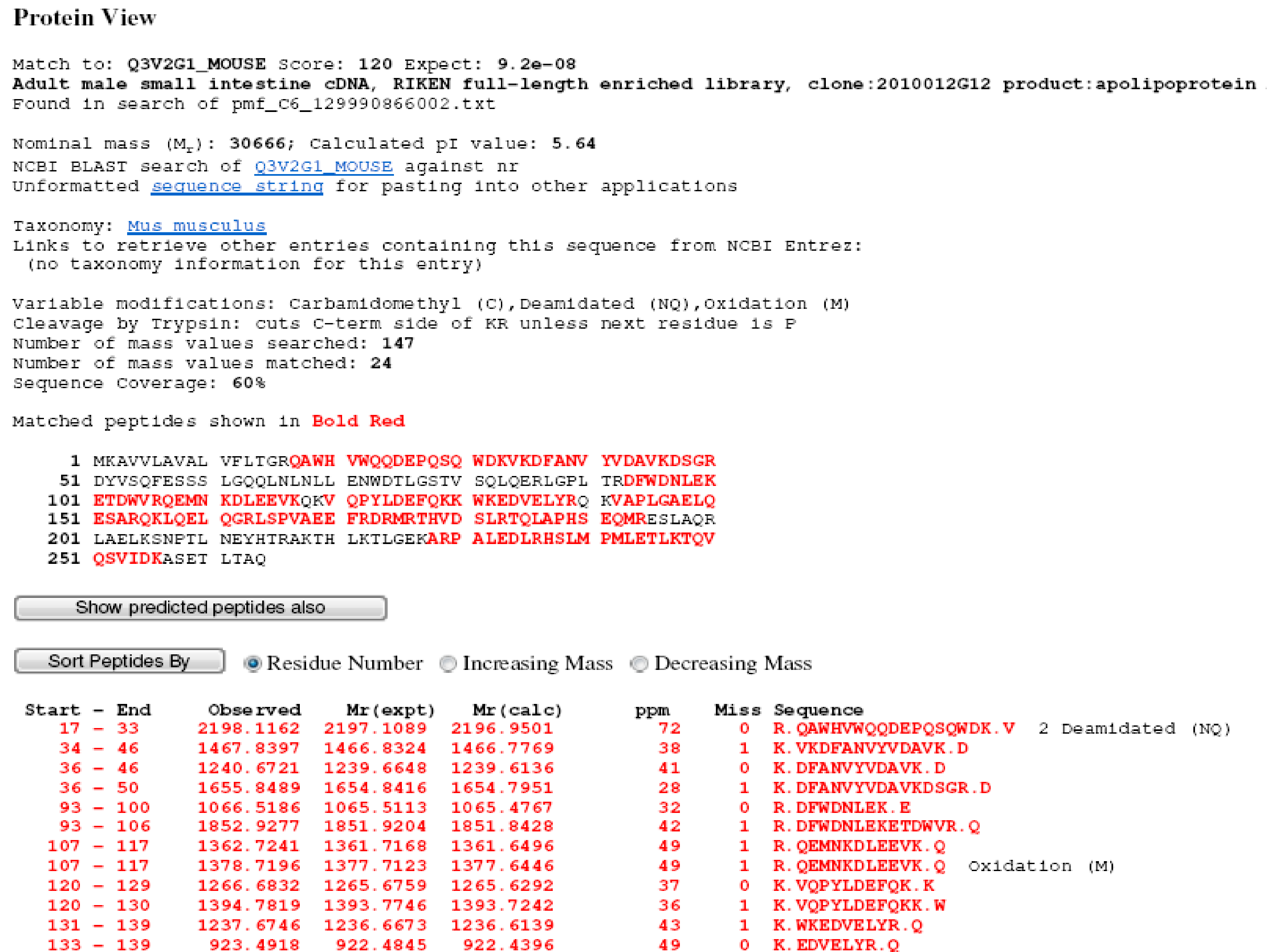


Concise Protein Summary Report

Format As Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.   Q3V2G1_MOUSE    Mass: 30666    Score: 120    Expect: 9.2e-08  Matches: 24
     Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010012G12 product:apolipoprotein A-I,
     JC1237    Mass: 30358    Score: 113    Expect: 4.6e-07  Matches: 22
     apolipoprotein A-I precursor - mouse
     Q8BPD5_MOUSE    Mass: 30597    Score: 110    Expect: 9.2e-07  Matches: 23
     18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:
     S22420    Mass: 30569    Score: 110    Expect: 9.2e-07  Matches: 22
     apolipoprotein A-I precursor - mouse
```



Protein View

Match to: **Q3V2G1_MOUSE** Score: **120** Expect: **9.2e-08**
Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010012G12 product:apolipoprotein
Found in search of pmf_C6_129990866002.txt

Nominal mass (M$_r$): **30666**; Calculated pI value: **5.64**
NCBI BLAST search of Q3V2G1_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **147**
Number of mass values matched: **24**
Sequence Coverage: **60%**

Matched peptides shown in **Bold Red**

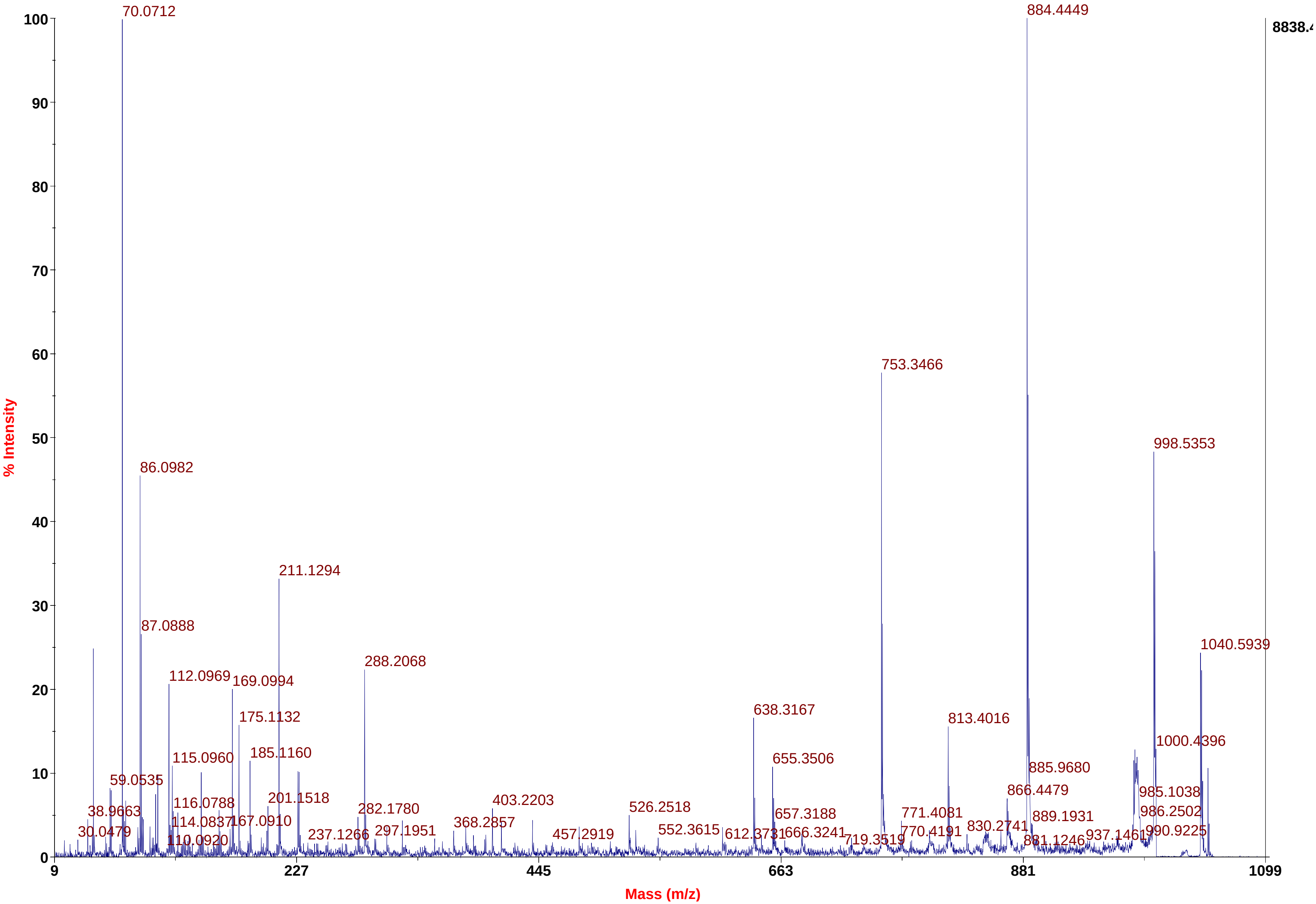
```
  1 MKAVVLAVAL VFLTGRQAWH VWQQDEPQSQ WDKVKDFANV YVDAVKDSGR
 51 DYVSQFESSS LGQQLNLNLL ENWDTLGSTV SQLQERLGPL TRDFWDNLEK
101 ETDWVRQEMN KDLEEVKQKV QPYLDEFQKK WKEDVELYRQ KVAPLGAELQ
151 ESARQKLQEL QGRLSPVAEE FRDRMRTHVD SLRTQLAPHS EQMRESLAQR
201 LAELKSNPTL NEYHTRAKTH LKTLGEKARP ALEDLRHSLM PMLETLKTQV
251 QSVIDKASET LTAQ
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed    Mr(expt)    Mr(calc)      ppm   Miss Sequence
  17 - 33      2198.1162   2197.1089   2196.9501       72     0  R.QAWHVWQQDEPQSQWDK.V  2 Deamidated (NQ)
  34 - 46      1467.8397   1466.8324   1466.7769       38     1  K.VKDFANVYVDAVK.D
  36 - 46      1240.6721   1239.6648   1239.6136       41     0  K.DFANVYVDAVK.D
  36 - 50      1655.8489   1654.8416   1654.7951       28     1  K.DFANVYVDAVKDSGR.D
  93 - 100     1066.5186   1065.5113   1065.4767       32     0  R.DFWDNLEK.E
  93 - 106     1852.9277   1851.9204   1851.8428       42     1  R.DFWDNLEKETDWVR.Q
 107 - 117     1362.7241   1361.7168   1361.6496       49     1  R.QEMNKDLEEVK.Q
 107 - 117     1378.7196   1377.7123   1377.6446       49     1  R.QEMNKDLEEVK.Q  Oxidation (M)
 120 - 129     1266.6832   1265.6759   1265.6292       37     0  K.VQPYLDEFQK.K
 120 - 130     1394.7819   1393.7746   1393.7242       36     1  K.VQPYLDEFQKK.W
 131 - 139     1237.6746   1236.6673   1236.6139       43     1  K.WKEDVELYR.Q
 133 - 139      923.4918    922.4845    922.4396       49     0  K.EDVELYR.Q
```

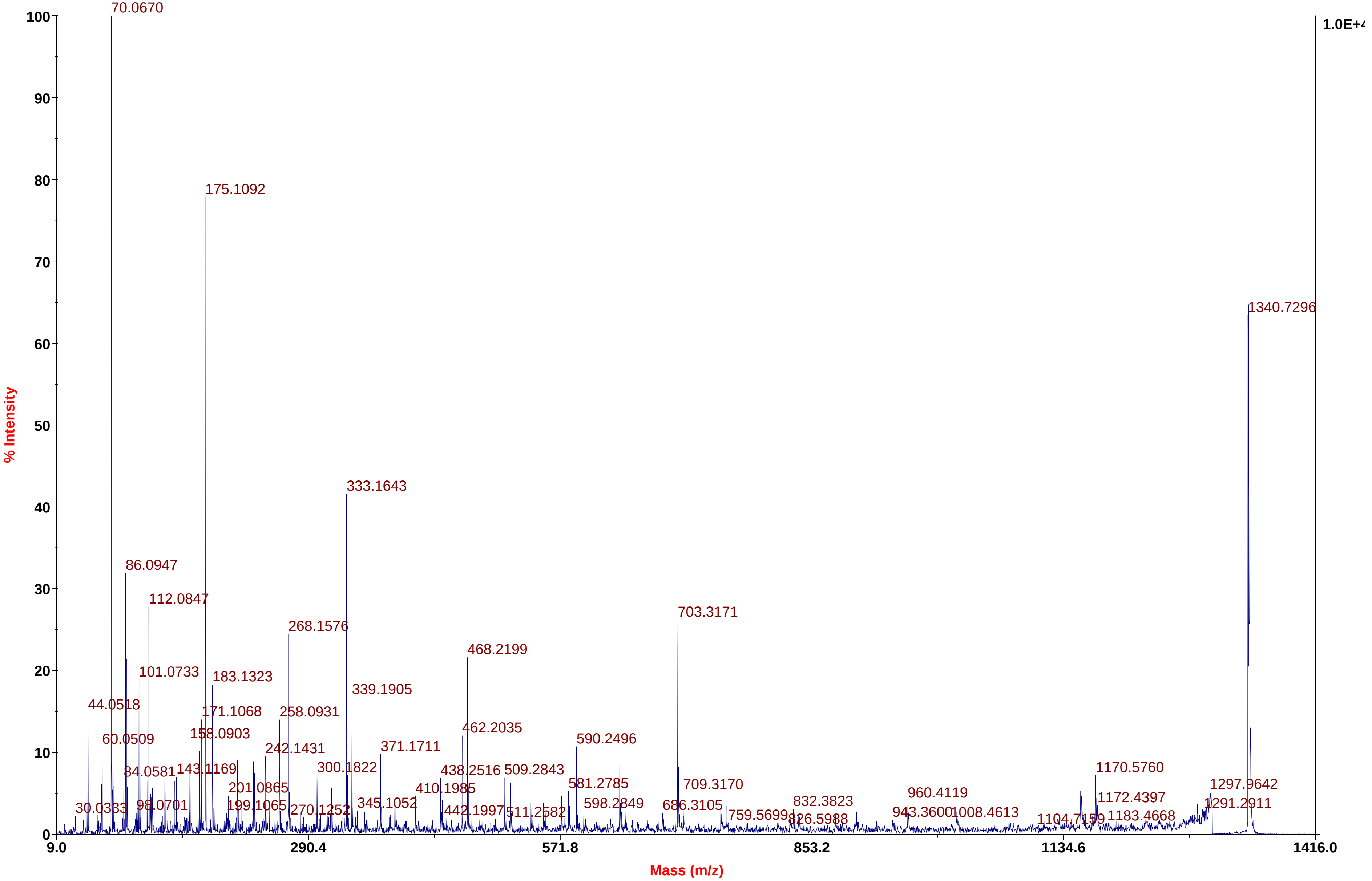
M19

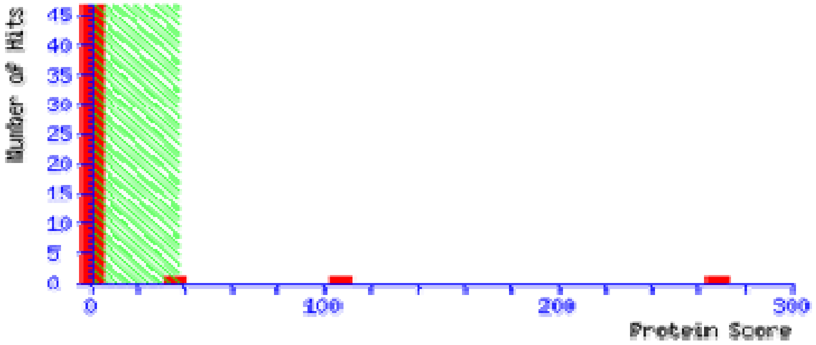
4700 MS/MS Precursor 1040.63 Spec #1 MC[BP = 884.4, 8838]

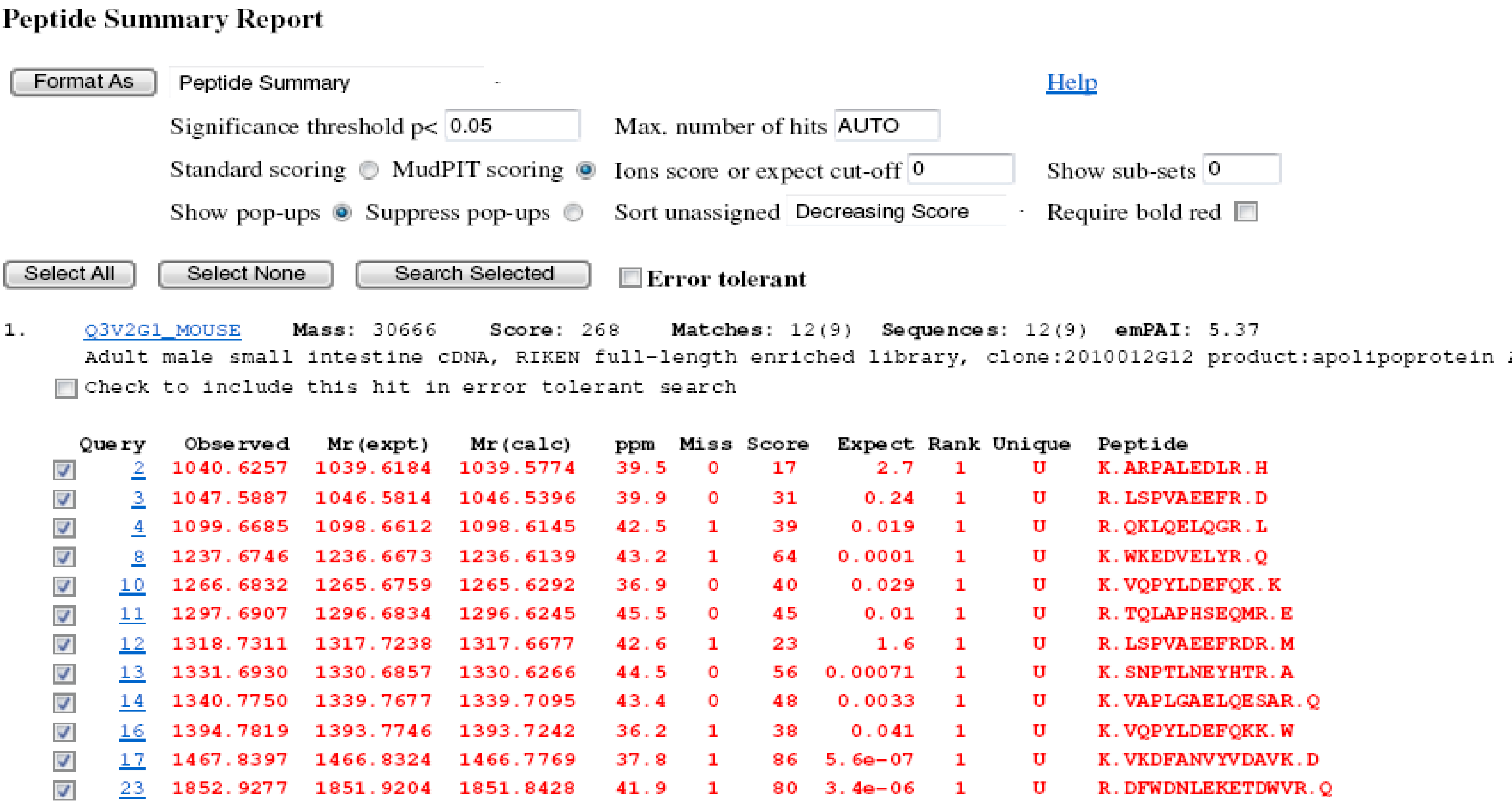


M19

4700 MS/MS Precursor 1340.78 Spec #1 MC[BP = 70.1, 10449]







Peptide Summary Report

Format As | Peptide Summary | Help

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

Standard scoring ○ MudPIT scoring ● | Ions score or expect cut-off 0 | Show sub-sets 0

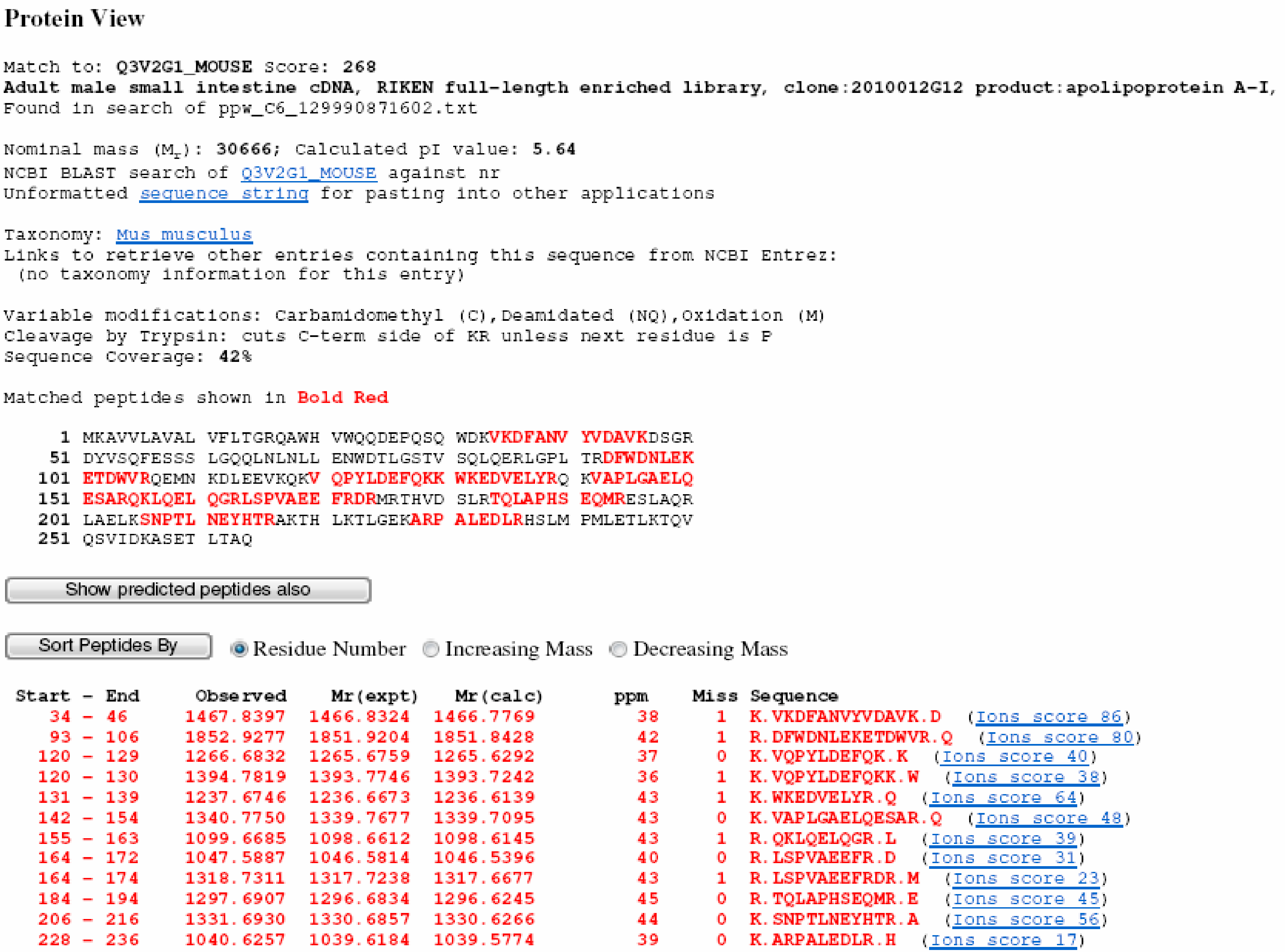
Show pop-ups ● Suppress pop-ups ○ | Sort unassigned Decreasing Score | Require bold red ☐

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

1. Q3V2G1_MOUSE **Mass:** 30666 **Score:** 268 **Matches:** 12(9) **Sequences:** 12(9) **emPAI:** 5.37
Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010012G12 product:apolipoprotein

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	2	1040.6257	1039.6184	1039.5774	39.5	0	17	2.7	1	U	K.ARPALEDLR.H
☑	3	1047.5887	1046.5814	1046.5396	39.9	0	31	0.24	1	U	R.LSPVAEEFR.D
☑	4	1099.6685	1098.6612	1098.6145	42.5	1	39	0.019	1	U	R.QKLQELQGR.L
☑	8	1237.6746	1236.6673	1236.6139	43.2	1	64	0.0001	1	U	K.WKEDVELYR.Q
☑	10	1266.6832	1265.6759	1265.6292	36.9	0	40	0.029	1	U	K.VQPYLDEFQK.K
☑	11	1297.6907	1296.6834	1296.6245	45.5	0	45	0.01	1	U	R.TQLAPHSEQMR.E
☑	12	1318.7311	1317.7238	1317.6677	42.6	1	23	1.6	1	U	R.LSPVAEEFRDR.M
☑	13	1331.6930	1330.6857	1330.6266	44.5	0	56	0.00071	1	U	K.SNPTLNEYHTR.A
☑	14	1340.7750	1339.7677	1339.7095	43.4	0	48	0.0033	1	U	K.VAPLGAELQESAR.Q
☑	16	1394.7819	1393.7746	1393.7242	36.2	1	38	0.041	1	U	K.VQPYLDEFQKK.W
☑	17	1467.8397	1466.8324	1466.7769	37.8	1	86	5.6e-07	1	U	K.VKDFANVYVDAVK.D
☑	23	1852.9277	1851.9204	1851.8428	41.9	1	80	3.4e-06	1	U	R.DFWDNLEKETDWVR.Q



Protein View

```
Match to: Q3V2G1_MOUSE Score: 268
Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010012G12 product:apolipoprotein A-I,
Found in search of ppw_C6_129990871602.txt

Nominal mass (Mr): 30666; Calculated pI value: 5.64
NCBI BLAST search of Q3V2G1_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 42%

Matched peptides shown in Bold Red

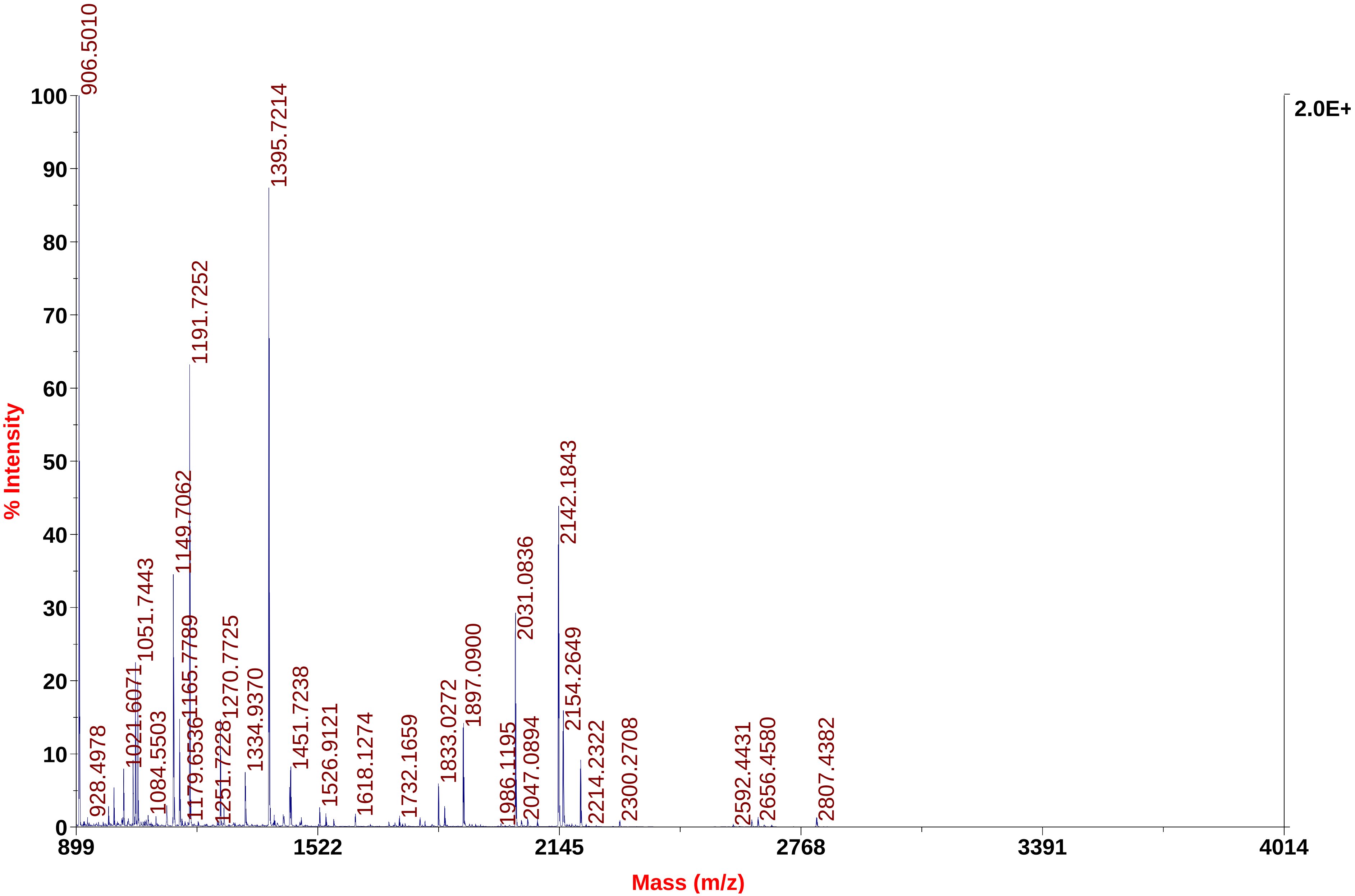
     1 MKAVVLAVAL VFLTGRQAWH VWQQDEPQSQ WDKVKDFANV YVDAVKDSGR
    51 DYVSQFESSS LGQQLNLNLL ENWDTLGSTV SQLQERLGPL TRDFWDNLEK
   101 ETDWVRQEMN KDLEEVKQKV QPYLDEFQKK WKEDVELYRQ KVAPLGAELQ
   151 ESARQKLQEL QGRLSPVAEE FRDRMRTHVD SLRTQLAPHS EQMRESLAQR
   201 LAELKSNPTL NEYHTRAKTH LKTLGEKARP ALEDLRHSLM PMLETLKTQV
   251 QSVIDKASET LTAQ
```

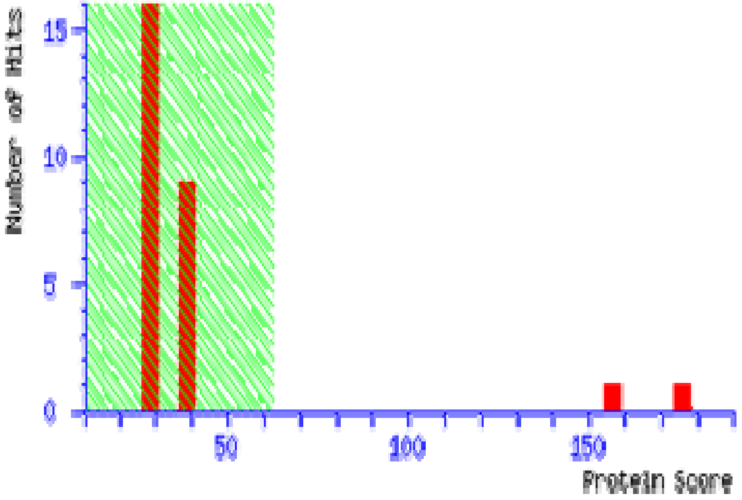
● Residue Number ○ Increasing Mass ○ Decreasing Mass

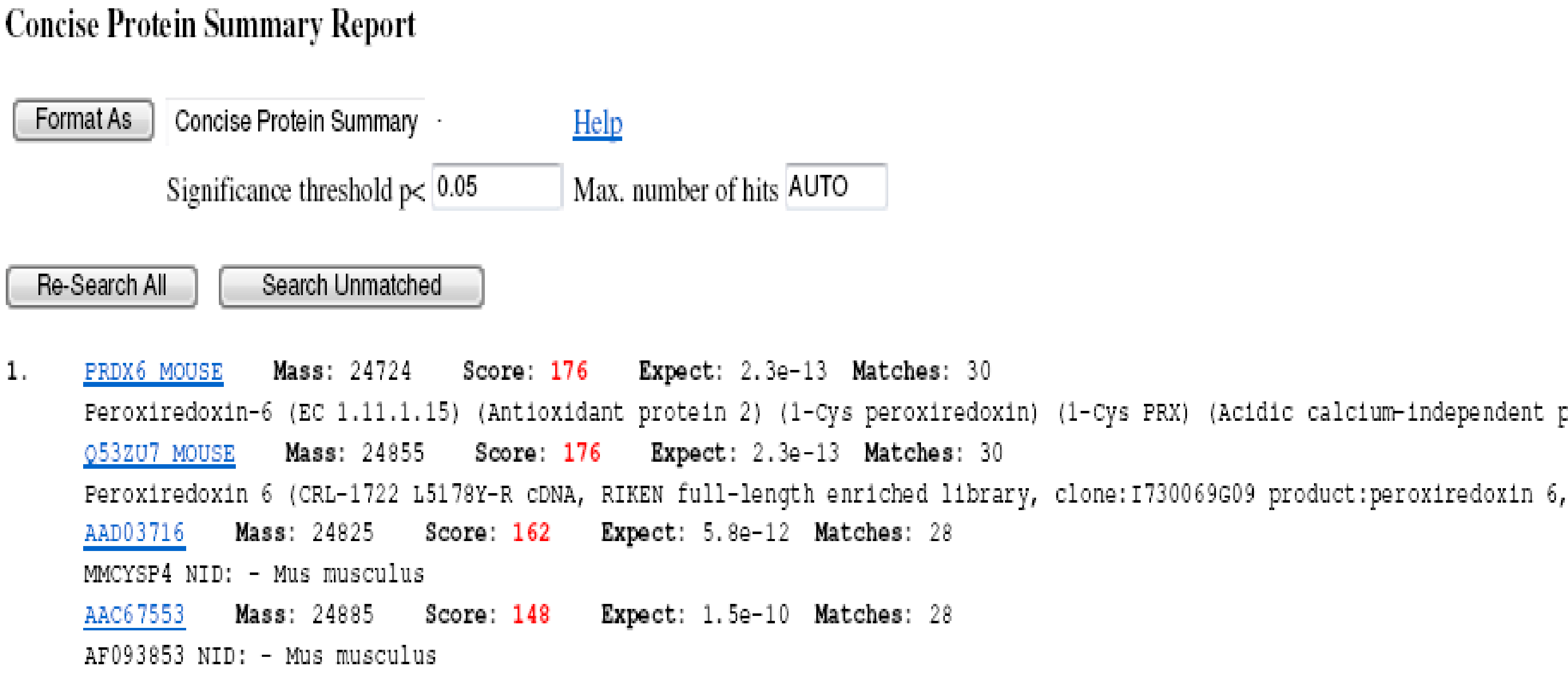
```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   34 - 46     1467.8397  1466.8324  1466.7769       38      1  K.VKDFANVYVDAVK.D  (Ions score 86)
   93 - 106    1852.9277  1851.9204  1851.8428       42      1  R.DFWDNLEKETDWVR.Q  (Ions score 80)
  120 - 129    1266.6832  1265.6759  1265.6292       37      0  K.VQPYLDEFQK.K  (Ions score 40)
  120 - 130    1394.7819  1393.7746  1393.7242       36      1  K.VQPYLDEFQKK.W  (Ions score 38)
  131 - 139    1237.6746  1236.6673  1236.6139       43      1  K.WKEDVELYR.Q  (Ions score 64)
  142 - 154    1340.7750  1339.7677  1339.7095       43      0  K.VAPLGAELQESAR.Q  (Ions score 48)
  155 - 163    1099.6685  1098.6612  1098.6145       43      1  R.QKLQELQGR.L  (Ions score 39)
  164 - 172    1047.5887  1046.5814  1046.5396       40      0  R.LSPVAEEFR.D  (Ions score 31)
  164 - 174    1318.7311  1317.7238  1317.6677       43      1  R.LSPVAEEFRDR.M  (Ions score 23)
  184 - 194    1297.6907  1296.6834  1296.6245       45      0  R.TQLAPHSEQMR.E  (Ions score 45)
  206 - 216    1331.6930  1330.6857  1330.6266       44      0  K.SNPTLNEYHTR.A  (Ions score 56)
  228 - 236    1040.6257  1039.6184  1039.5774       39      0  K.ARPALEDLR.H  (Ions score 17)
```

Sample M20

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 906.5, 19962]



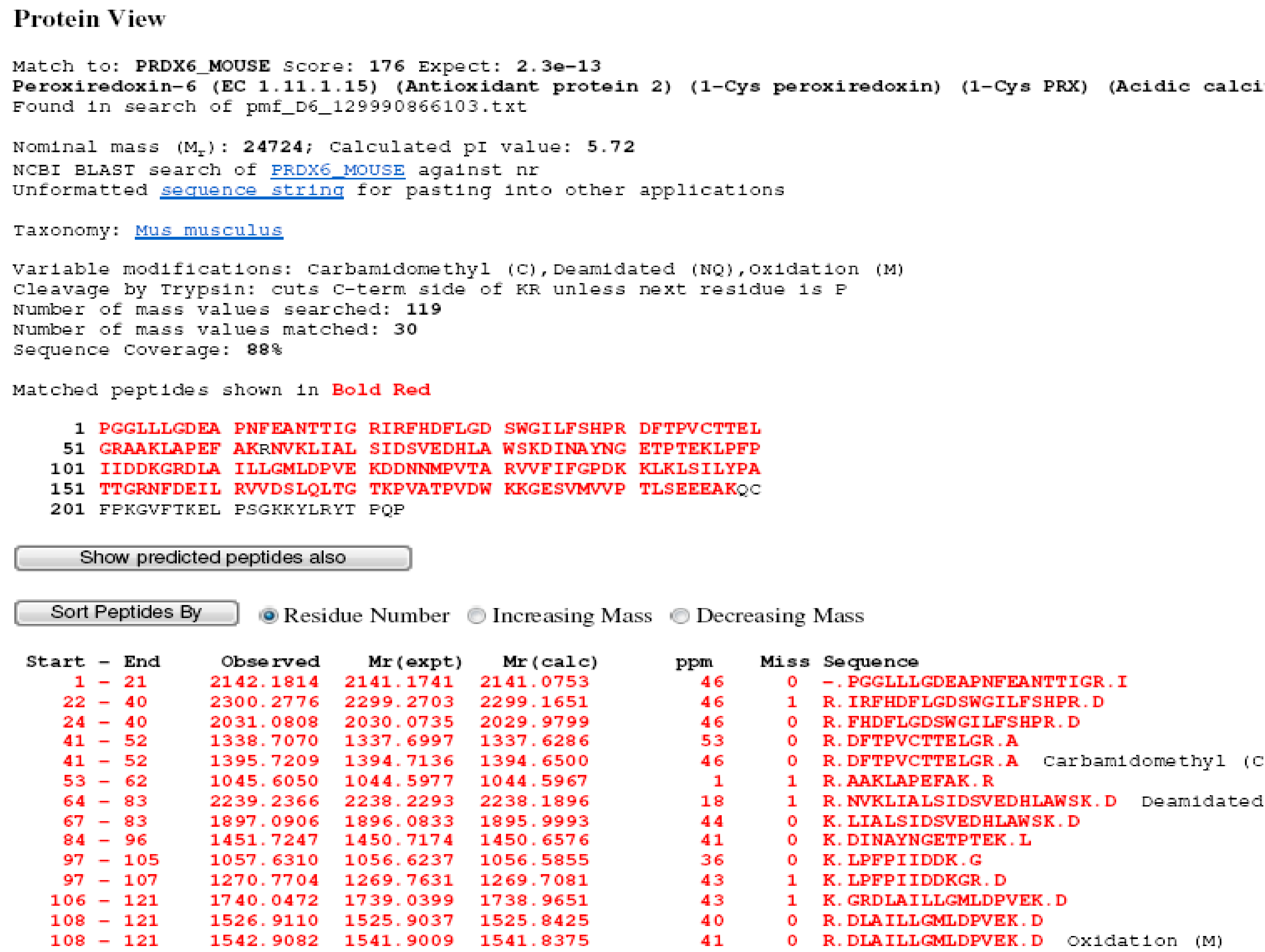




Concise Protein Summary Report

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.   PRDX6_MOUSE    Mass: 24724    Score: 176    Expect: 2.3e-13  Matches: 30
     Peroxiredoxin-6 (EC 1.11.1.15) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent p
     Q53ZU7_MOUSE    Mass: 24855    Score: 176    Expect: 2.3e-13  Matches: 30
     Peroxiredoxin 6 (CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730069G09 product:peroxiredoxin 6,
     AAD03716    Mass: 24825    Score: 162    Expect: 5.8e-12  Matches: 28
     MMCYSP4 NID: - Mus musculus
     AAC67553    Mass: 24885    Score: 148    Expect: 1.5e-10  Matches: 28
     AF093853 NID: - Mus musculus
```



Protein View

```
Match to: PRDX6_MOUSE Score: 176 Expect: 2.3e-13
Peroxiredoxin-6 (EC 1.11.1.15) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calci
Found in search of pmf_D6_129990866103.txt

Nominal mass (Mr): 24724; Calculated pI value: 5.72
NCBI BLAST search of PRDX6_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 119
Number of mass values matched: 30
Sequence Coverage: 88%

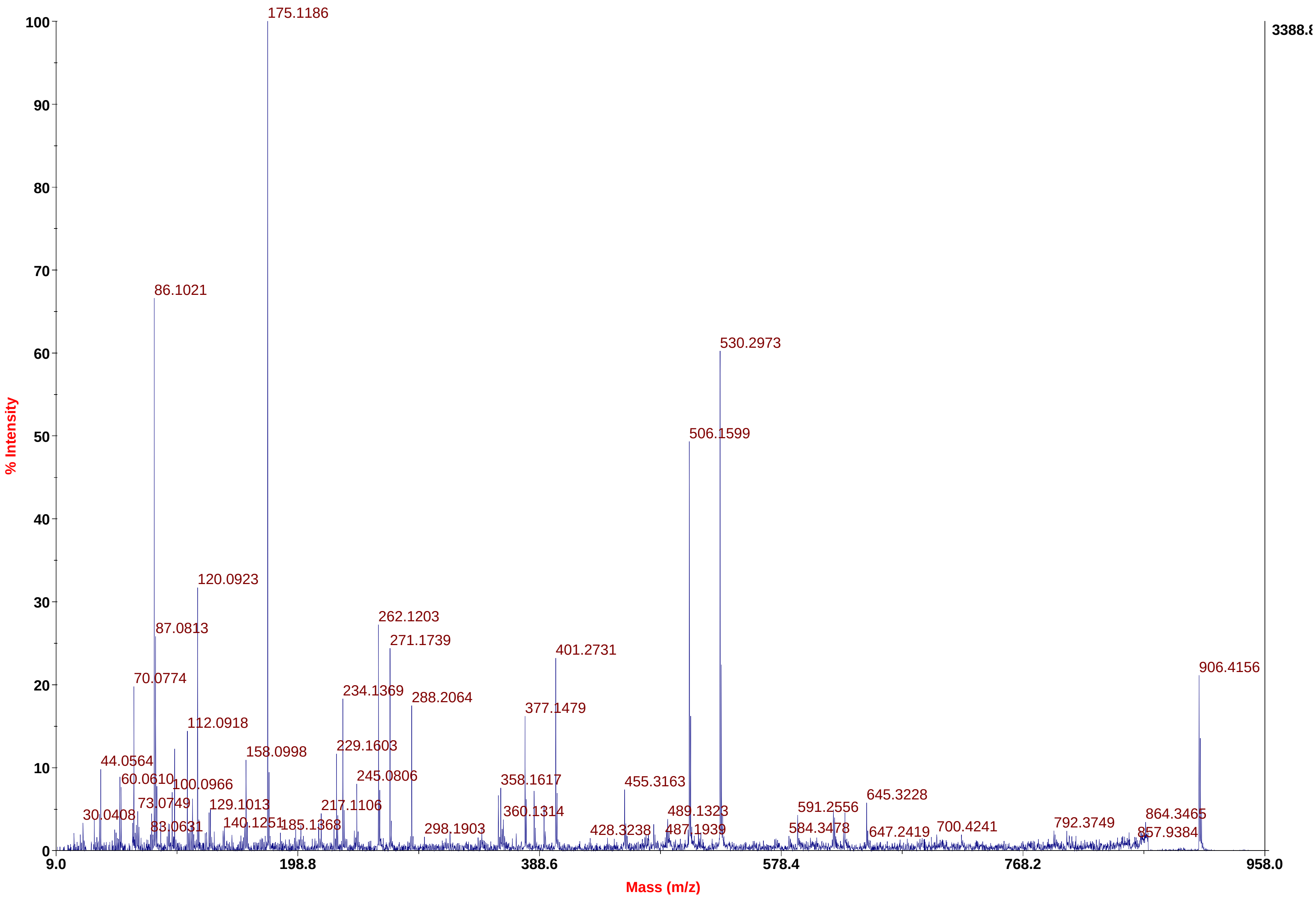
Matched peptides shown in Bold Red

     1 PGGLLLGDEA PNFEANTTIG RIRFHDFLGD SWGILFSHPR DFTPVCTTEL
    51 GRAAKLAPEF AKRNVKLIAL SIDSVEDHLA WSKDINAYNG ETPTEKLPFP
   101 IIDDKGRDLA ILLGMLDPVE KDDNNMPVTA RVVFIFGPDK KLKLSILYPA
   151 TTGRNFDEIL RVVDSLQLTG TKPVATPVDW KKGESVMVVP TLSEEEAKQC
   201 FPKGVFTKEL PSGKKYLRYT PQP
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     ppm    Miss Sequence
    1 - 21      2142.1814  2141.1741  2141.0753      46     0   -.PGGLLLGDEAPNFEANTTIGR.I
   22 - 40      2300.2776  2299.2703  2299.1651      46     1   R.IRFHDFLGDSWGILFSHPR.D
   24 - 40      2031.0808  2030.0735  2029.9799      46     0   R.FHDFLGDSWGILFSHPR.D
   41 - 52      1338.7070  1337.6997  1337.6286      53     0   R.DFTPVCTTELGR.A
   41 - 52      1395.7209  1394.7136  1394.6500      46     0   R.DFTPVCTTELGR.A   Carbamidomethyl (C
   53 - 62      1045.6050  1044.5977  1044.5967       1     1   R.AAKLAPEFAK.R
   64 - 83      2239.2366  2238.2293  2238.1896      18     1   R.NVKLIALSIDSVEDHLAWSK.D  Deamidated
   67 - 83      1897.0906  1896.0833  1895.9993      44     0   K.LIALSIDSVEDHLAWSK.D
   84 - 96      1451.7247  1450.7174  1450.6576      41     0   K.DINAYNGETPTEK.L
   97 - 105     1057.6310  1056.6237  1056.5855      36     0   K.LPFPIIDDK.G
   97 - 107     1270.7704  1269.7631  1269.7081      43     1   K.LPFPIIDDKGR.D
  106 - 121     1740.0472  1739.0399  1738.9651      43     1   K.GRDLAILLGMLDPVEK.D
  108 - 121     1526.9110  1525.9037  1525.8425      40     0   R.DLAILLGMLDPVEK.D
  108 - 121     1542.9082  1541.9009  1541.8375      41     0   R.DLAILLGMLDPVEK.D  Oxidation (M)
```

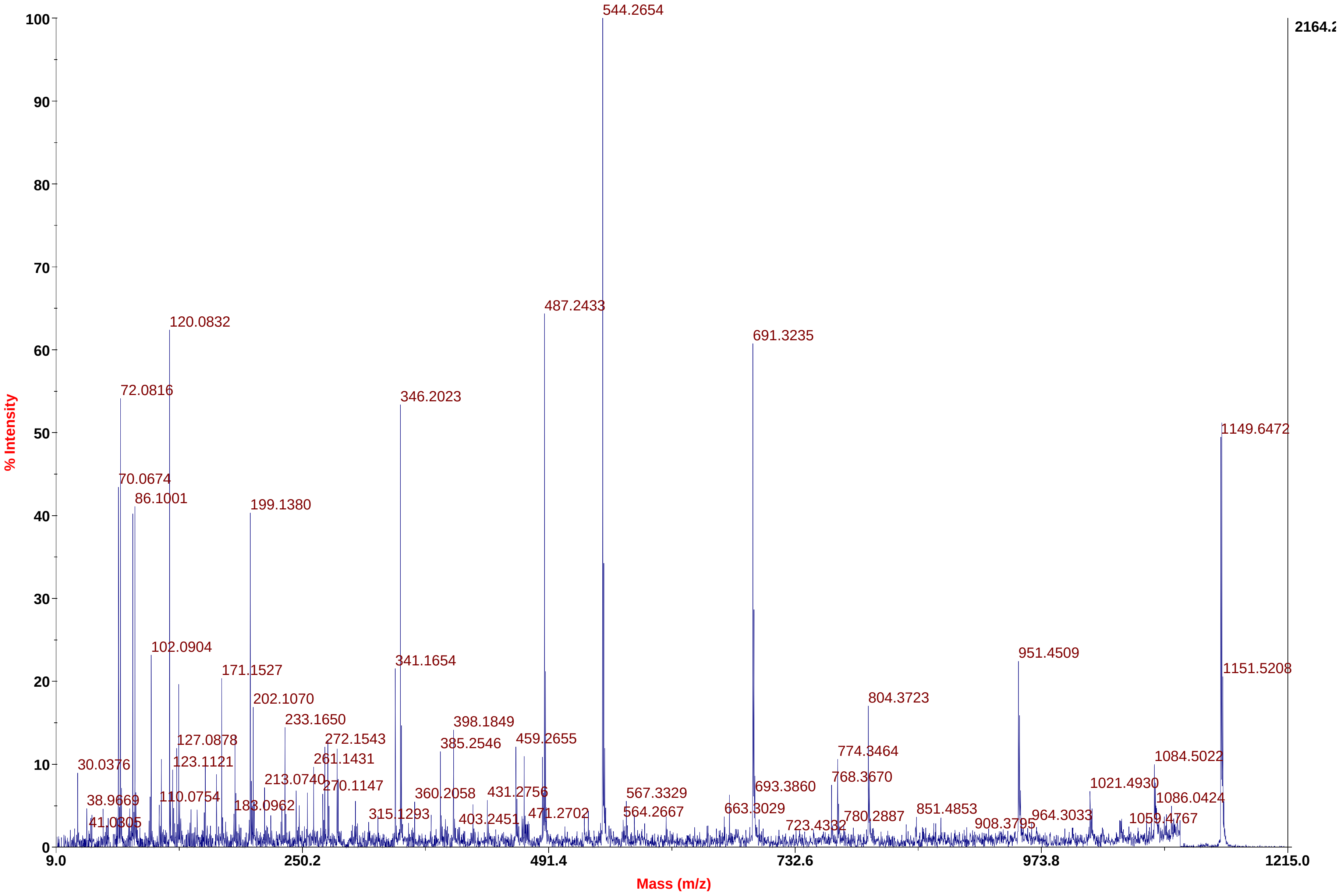
M20

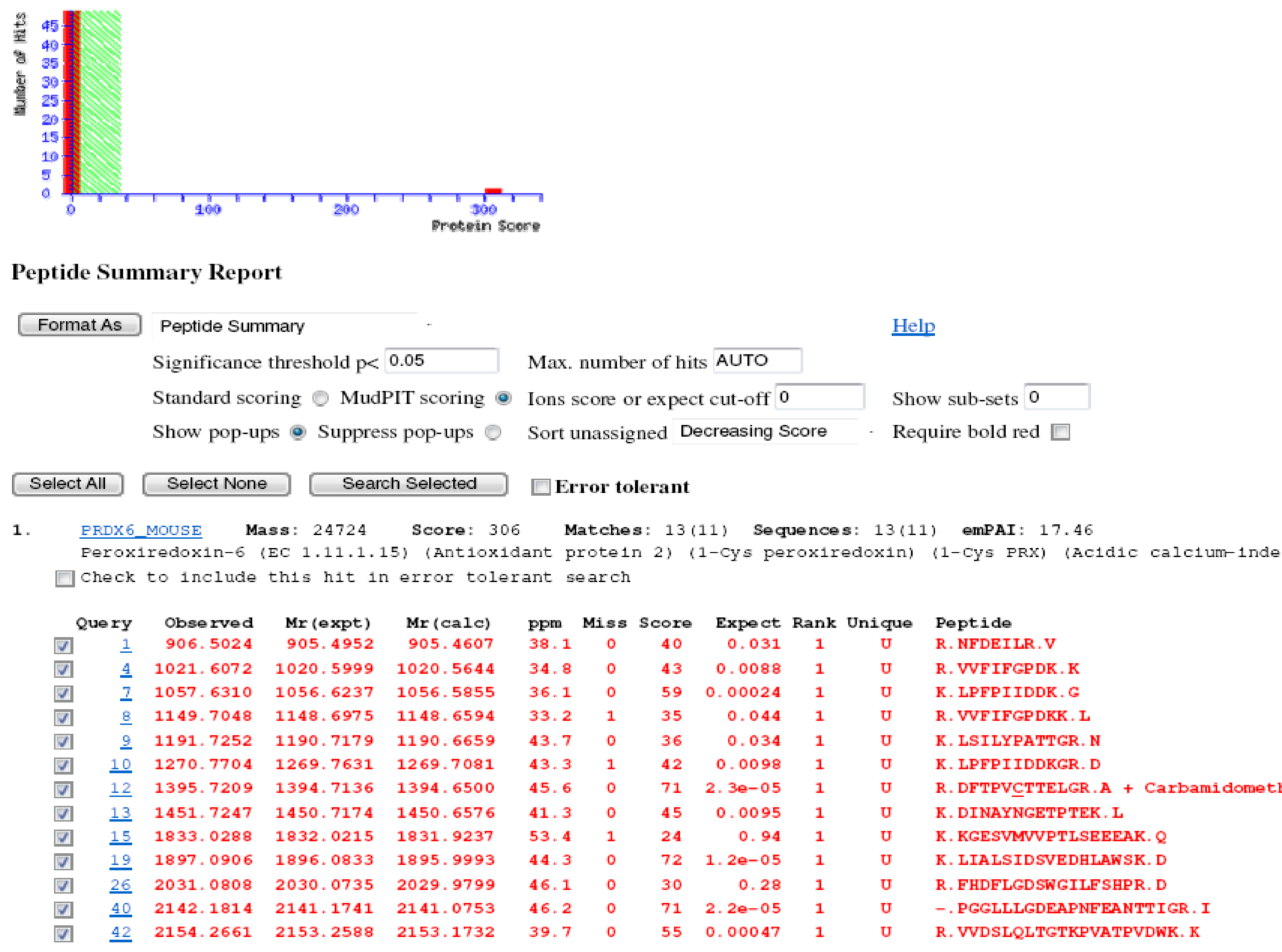
4700 MS/MS Precursor 906.502 Spec #1 MC[BP = 175.1, 3389]



M20

4700 MS/MS Precursor 1149.7 Spec #1 MC[BP = 544.3, 2164]





Peptide Summary Report

Format As: Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

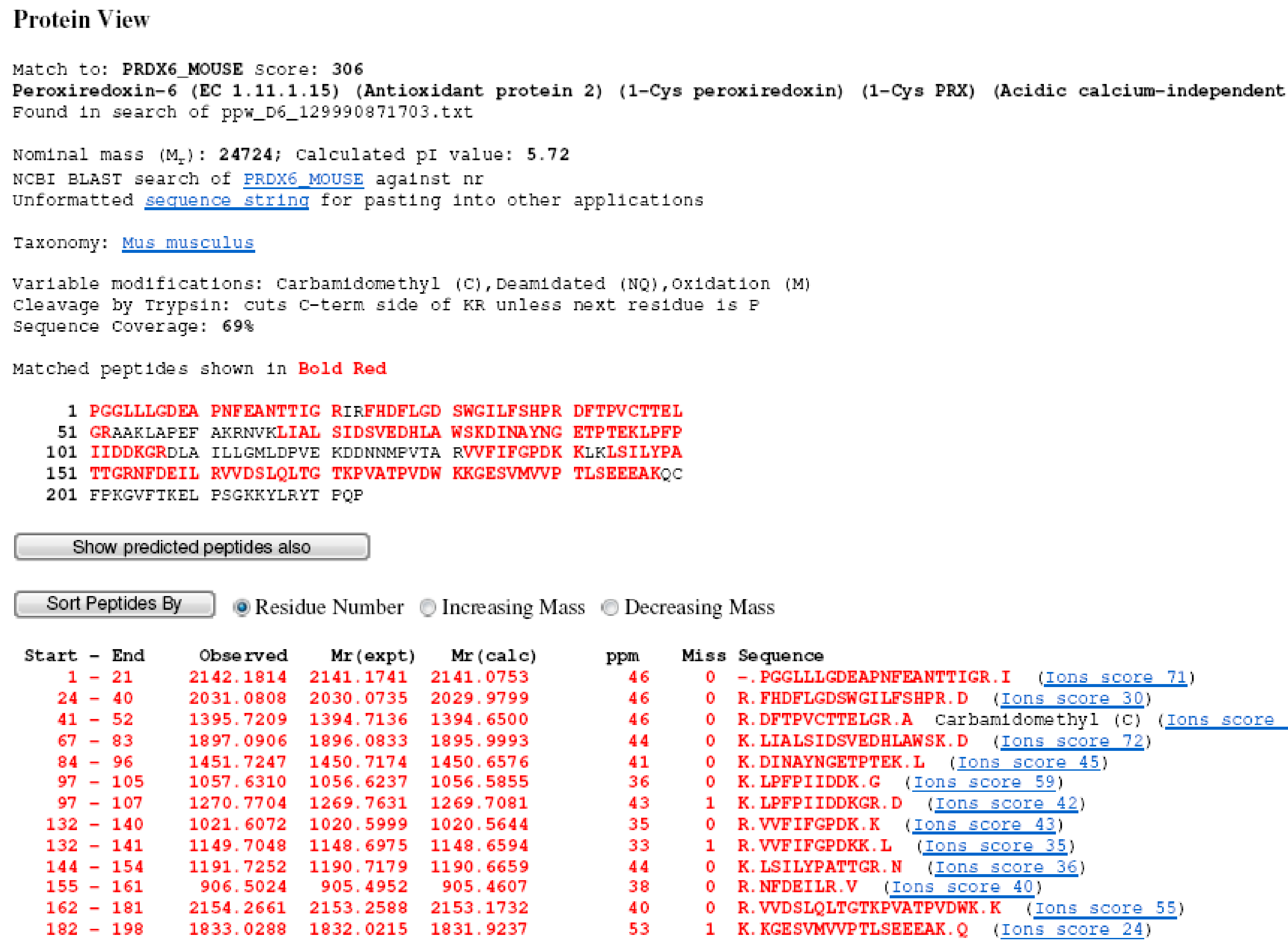
☐ **Error tolerant**

1. PRDX6_MOUSE **Mass:** 24724 **Score:** 306 **Matches:** 13(11) **Sequences:** 13(11) **emPAI:** 17.46

Peroxiredoxin-6 (EC 1.11.1.15) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-inde

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	906.5024	905.4952	905.4607	38.1	0	40	0.031	1	U	R.NFDEILR.V
☑	4	1021.6072	1020.5999	1020.5644	34.8	0	43	0.0088	1	U	R.VVFIFGPDK.K
☑	7	1057.6310	1056.6237	1056.5855	36.1	0	59	0.00024	1	U	K.LPFPIIDDK.G
☑	8	1149.7048	1148.6975	1148.6594	33.2	1	35	0.044	1	U	R.VVFIFGPDKK.L
☑	9	1191.7252	1190.7179	1190.6659	43.7	0	36	0.034	1	U	K.LSILYPATTGR.N
☑	10	1270.7704	1269.7631	1269.7081	43.3	1	42	0.0098	1	U	K.LPFPIIDDKGR.D
☑	12	1395.7209	1394.7136	1394.6500	45.6	0	71	2.3e-05	1	U	R.DFTPVCTTELGR.A + Carbamidometh
☑	13	1451.7247	1450.7174	1450.6576	41.3	0	45	0.0095	1	U	K.DINAYNGETPTEK.L
☑	15	1833.0288	1832.0215	1831.9237	53.4	1	24	0.94	1	U	K.KGESVMVVPTLSEEEAK.Q
☑	19	1897.0906	1896.0833	1895.9993	44.3	0	72	1.2e-05	1	U	K.LIALSIDSVEDHLAWSK.D
☑	26	2031.0808	2030.0735	2029.9799	46.1	0	30	0.28	1	U	R.FHDFLGDSWGILFSHPR.D
☑	40	2142.1814	2141.1741	2141.0753	46.2	0	71	2.2e-05	1	U	-.PGGLLLGDEAPNFEANTTIGR.I
☑	42	2154.2661	2153.2588	2153.1732	39.7	0	55	0.00047	1	U	R.VVDSLQLTGTKPVATPVDWK.K



Protein View

Match to: **PRDX6_MOUSE** Score: **306**
Peroxiredoxin-6 (EC 1.11.1.15) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent
Found in search of ppw_D6_129990871703.txt

Nominal mass (M_r): **24724**; Calculated pI value: **5.72**
NCBI BLAST search of PRDX6_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 69%

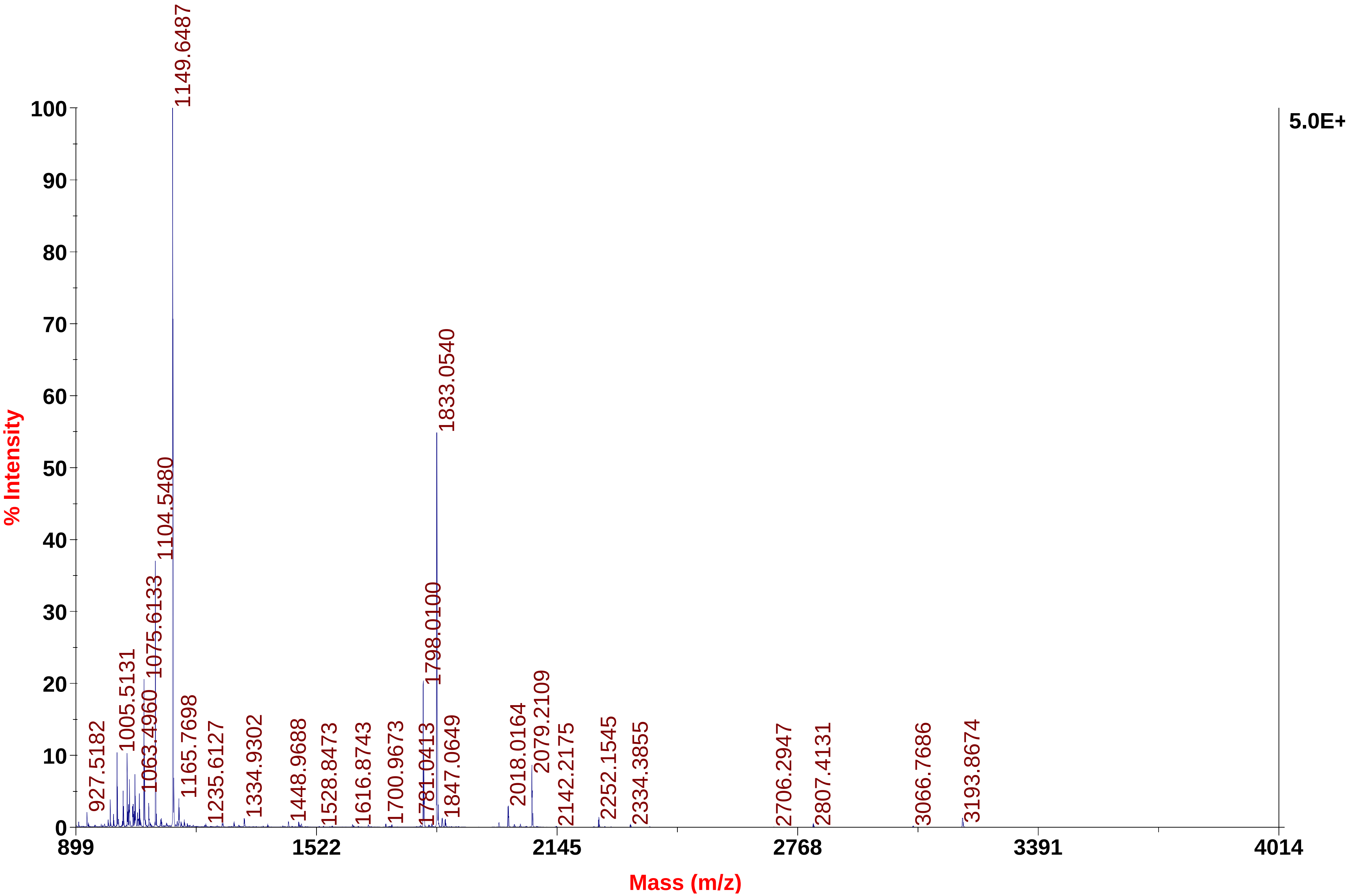
Matched peptides shown in **Bold Red**

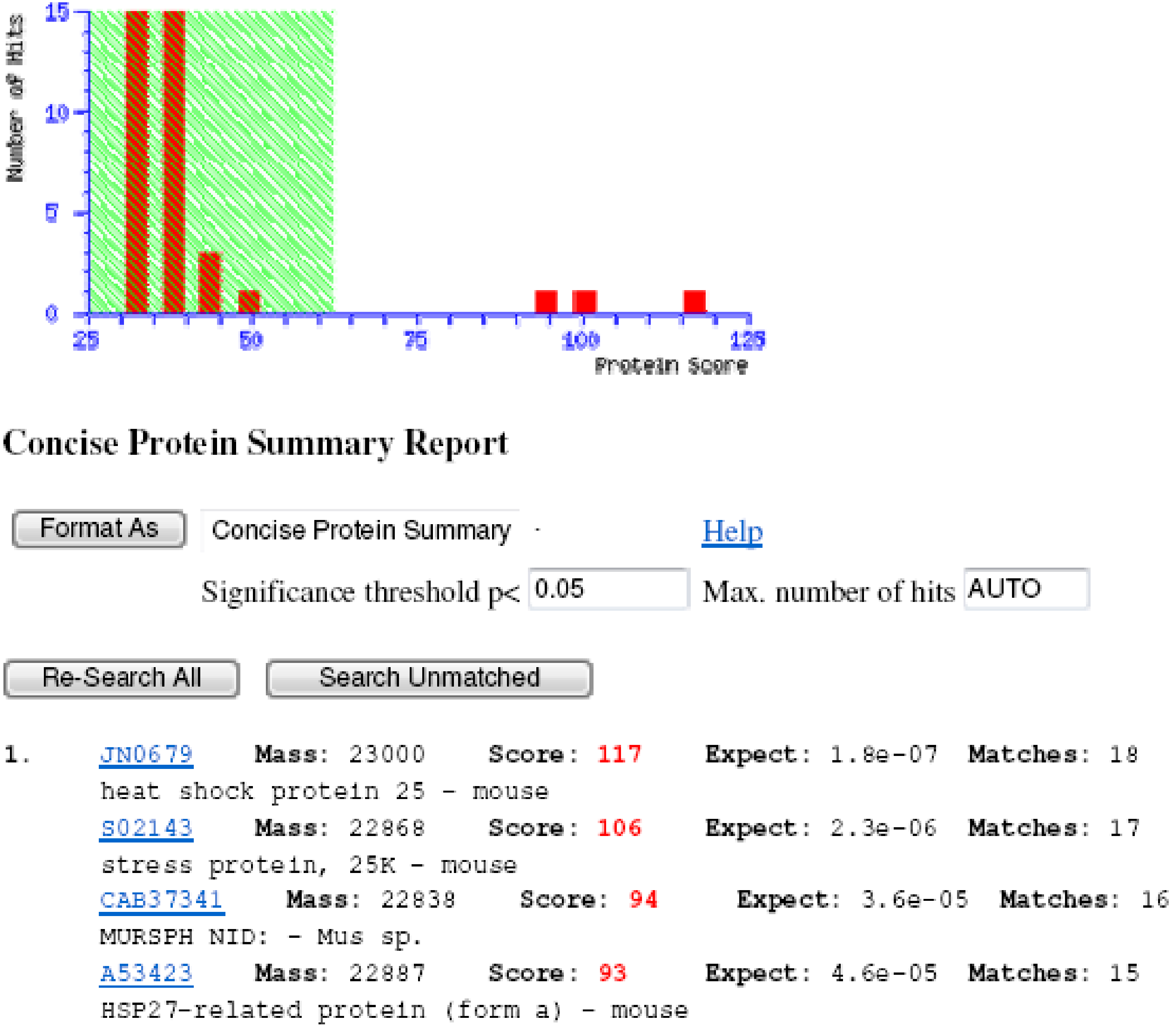
```
  1 PGGLLLGDEA PNFEANTTIG RIRFHDFLGD SWGILFSHPR DFTPVCTTEL
 51 GRAAKLAPEF AKRNVKLIAL SIDSVEDHLA WSKDINAYNG ETPTEKLPFP
101 IIDDKGRDLA ILLGMLDPVE KDDNNMPVTA RVVFIFGPDK KLKLSILYPA
151 TTGRNFDEIL RVVDSLQLTG TKPVATPVDW KKGESVMVVP TLSEEEAKQC
201 FPKGVFTKEL PSGKKYLRYT PQP
```

```
Start - End    Observed   Mr(expt)   Mr(calc)     ppm   Miss  Sequence
   1 - 21     2142.1814  2141.1741  2141.0753     46     0   -.PGGLLLGDEAPNFEANTTIGR.I   (Ions score 71)
  24 - 40     2031.0808  2030.0735  2029.9799     46     0   R.FHDFLGDSWGILFSHPR.D   (Ions score 30)
  41 - 52     1395.7209  1394.7136  1394.6500     46     0   R.DFTPVCTTELGR.A  Carbamidomethyl (C)  (Ions score
  67 - 83     1897.0906  1896.0833  1895.9993     44     0   K.LIALSIDSVEDHLAWSK.D   (Ions score 72)
  84 - 96     1451.7247  1450.7174  1450.6576     41     0   K.DINAYNGETPTEK.L   (Ions score 45)
  97 - 105    1057.6310  1056.6237  1056.5855     36     0   K.LPFPIIDDK.G   (Ions score 59)
  97 - 107    1270.7704  1269.7631  1269.7081     43     1   K.LPFPIIDDKGR.D   (Ions score 42)
 132 - 140    1021.6072  1020.5999  1020.5644     35     0   R.VVFIFGPDK.K   (Ions score 43)
 132 - 141    1149.7048  1148.6975  1148.6594     33     1   R.VVFIFGPDKK.L   (Ions score 35)
 144 - 154    1191.7252  1190.7179  1190.6659     44     0   K.LSILYPATTGR.N   (Ions score 36)
 155 - 161     906.5024   905.4952   905.4607     38     0   R.NFDEILR.V   (Ions score 40)
 162 - 181    2154.2661  2153.2588  2153.1732     40     0   R.VVDSLQLTGTKPVATPVDWK.K   (Ions score 55)
 182 - 198    1833.0288  1832.0215  1831.9237     53     1   K.KGESVMVVPTLSEEEAK.Q   (Ions score 24)
```

Sample M21

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1149.6, 49685]





Concise Protein Summary Report

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.     JN0679    Mass: 23000    Score: 117    Expect: 1.8e-07   Matches: 18
       heat shock protein 25 - mouse
       S02143    Mass: 22868    Score: 106    Expect: 2.3e-06   Matches: 17
       stress protein, 25K - mouse
       CAB37341    Mass: 22838    Score: 94    Expect: 3.6e-05   Matches: 16
       MURSPH NID: - Mus sp.
       A53423    Mass: 22887    Score: 93    Expect: 4.6e-05   Matches: 15
       HSP27-related protein (form a) - mouse
```

Protein View

Match to: **JN0679** Score: **117** Expect: **1.8e-07**
heat shock protein 25 - mouse
Found in search of pmf_E6_129990866104.txt

Nominal mass (M_r): **23000**; Calculated pI value: **6.12**
NCBI BLAST search of JN0679 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)

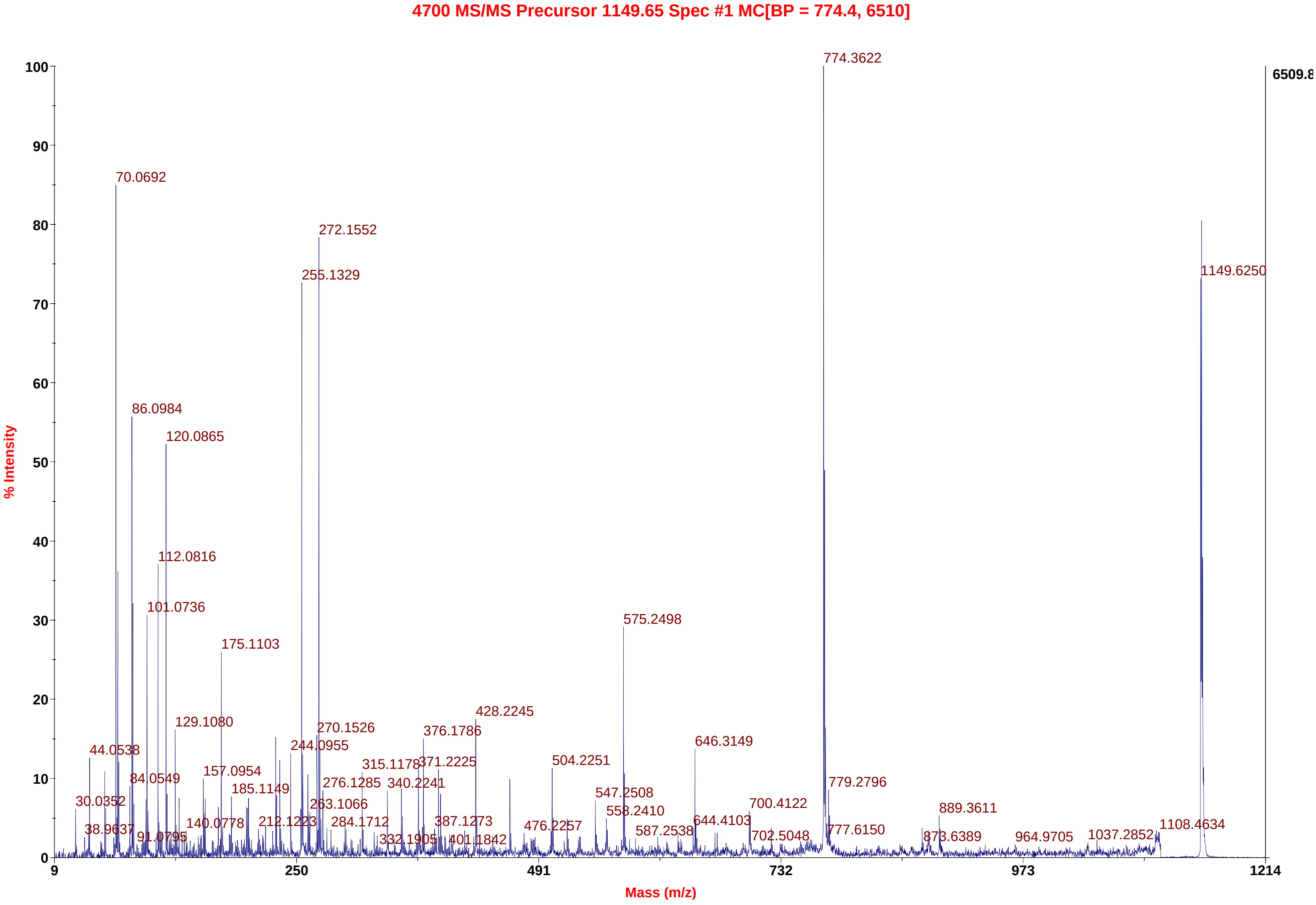
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **110**
Number of mass values matched: **18**
Sequence Coverage: **71%**

Matched peptides shown in **Bold Red**

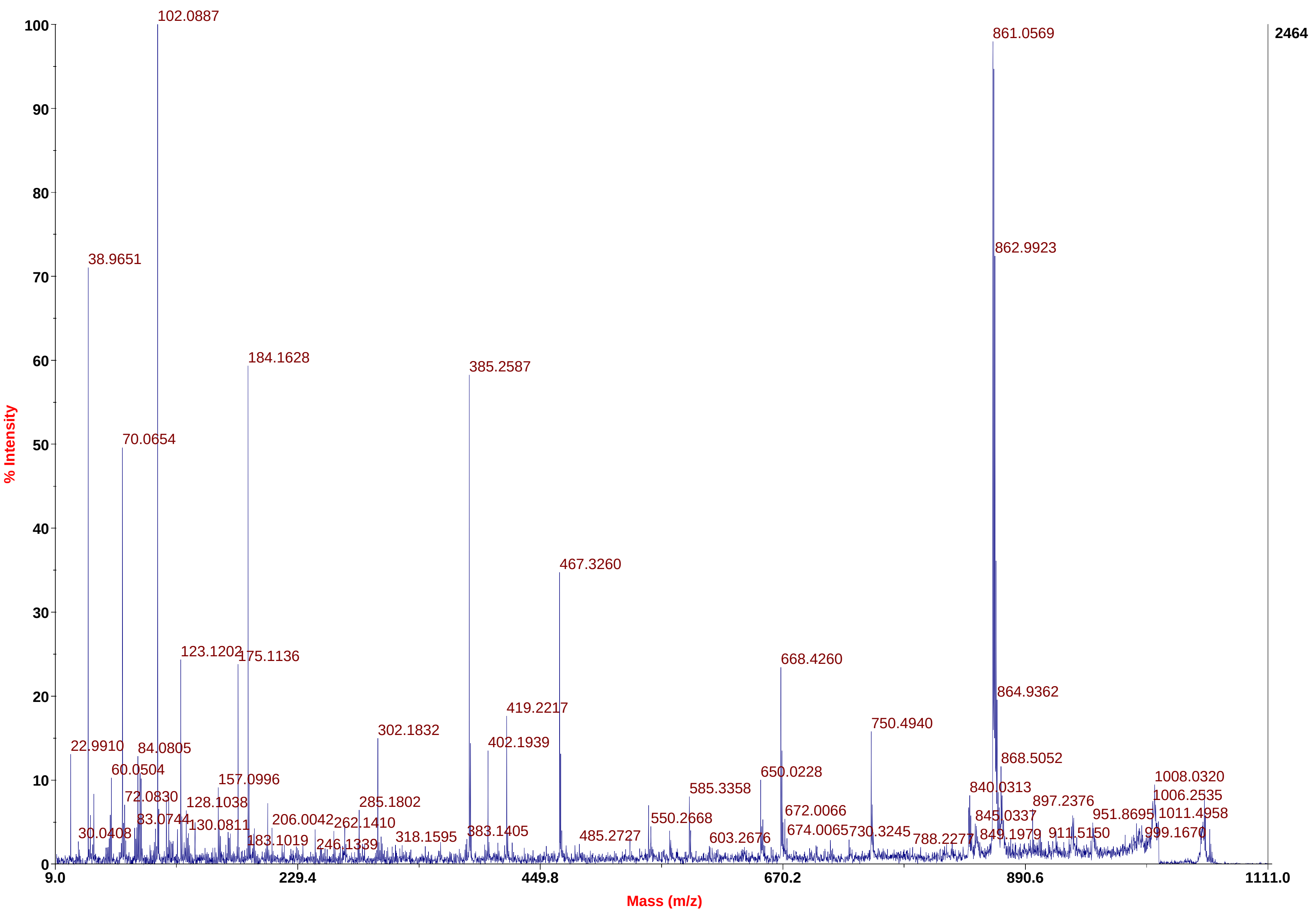
```
      1 MTERRVPFSL LRSPSWEPFR DWYPAHSRLF DQAFGVPRLP DEWSQWFSAA
     51 GWPGYVRPLP AATAEGPAAV TLAAPAFSRA LNRQLSSGVS EIRQTADRWR
    101 VSLDVNHFAP EELTVKTKEG VVEITGKHEE RQDEHGYISR CFTRKYTLPP
    151 GVDPTLVSSS LSPEGTLTVE APLPKAVTQS AEITIPVTFE ARAQIGGPEA
    201 GKSEQSGAK
```

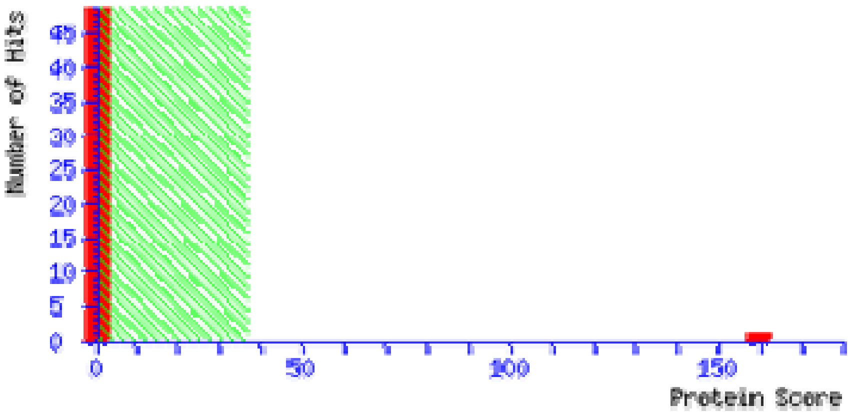
```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss  Sequence
     5 - 12      987.6417   986.6344   986.6025       32     1   R.RVPFSLLR.S
     6 - 20     1818.0321  1817.0248  1816.9624       34     1   R.VPFSLLRSPSWEPFR.D
    13 - 20     1005.5128  1004.5055  1004.4716       34     0   R.SPSWEPFR.D
    13 - 28     2018.0139  2017.0066  2016.9231       41     1   R.SPSWEPFRDWYPAHSR.L
    21 - 28     1031.5046  1030.4973  1030.4621       34     0   R.DWYPAHSR.L
    29 - 38     1149.6465  1148.6392  1148.5979       36     0   R.LFDQAFGVPR.L
    84 - 93     1075.6113  1074.6040  1074.5669       35     0   R.QLSSGVSEIR.Q
   101 - 116    1798.0094  1797.0021  1796.9309       40     0   R.VSLDVNHFAPEELTVK.T
   117 - 127    1160.6812  1159.6739  1159.6449       25     1   K.TKEGVVEITGK.H
   119 - 127     931.5301   930.5228   930.5022       22     0   K.EGVVEITGK.H
```

M21

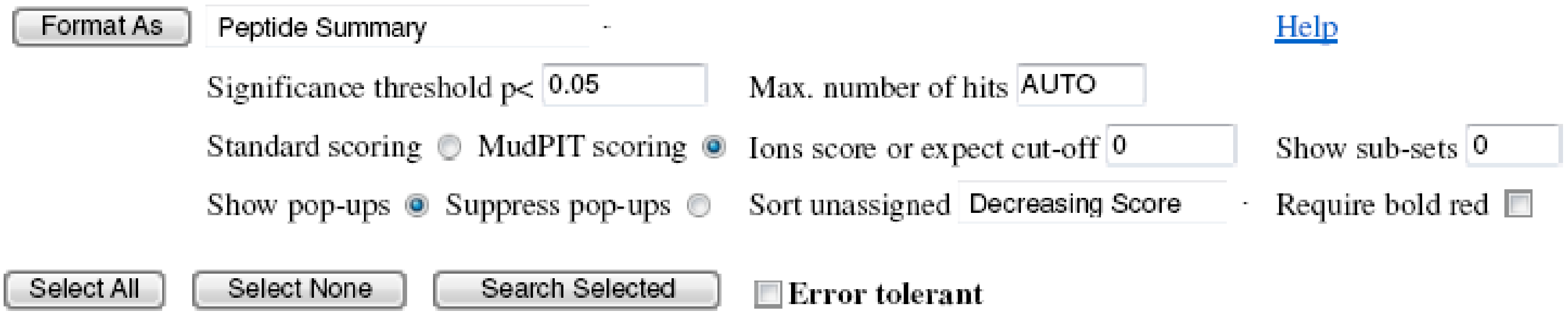

4700 MS/MS Precursor 1149.65 Spec #1 MC[BP = 774.4, 6510]
% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
9
250
491
732
973
1214
6509.8
774.3622
70.0692
272.1552
1149.6250
255.1329
86.0984
120.0865
112.0816
101.0736
575.2498
175.1103
428.2245
129.1080
270.1526
376.1786
646.3149
44.0538
244.0955
315.1178
371.2225
504.2251
157.0954
84.0549
185.1149
276.1285
340.2241
779.2796
547.2508
30.0352
263.1066
700.4122
889.3611
558.2410
140.0778
212.1223
284.1712
387.1273
476.2257
644.4103
1108.4634
38.9637
587.2538
777.6150
91.0795
332.1905
401.1842
702.5048
873.6389
964.9705
1037.2852

M21


4700 MS/MS Precursor 1051.74 Spec #1 MC[BP = 102.1, 2464]



Peptide Summary Report



Peptide Summary

Significance threshold p< 0.05 Max. number of hits AUTO

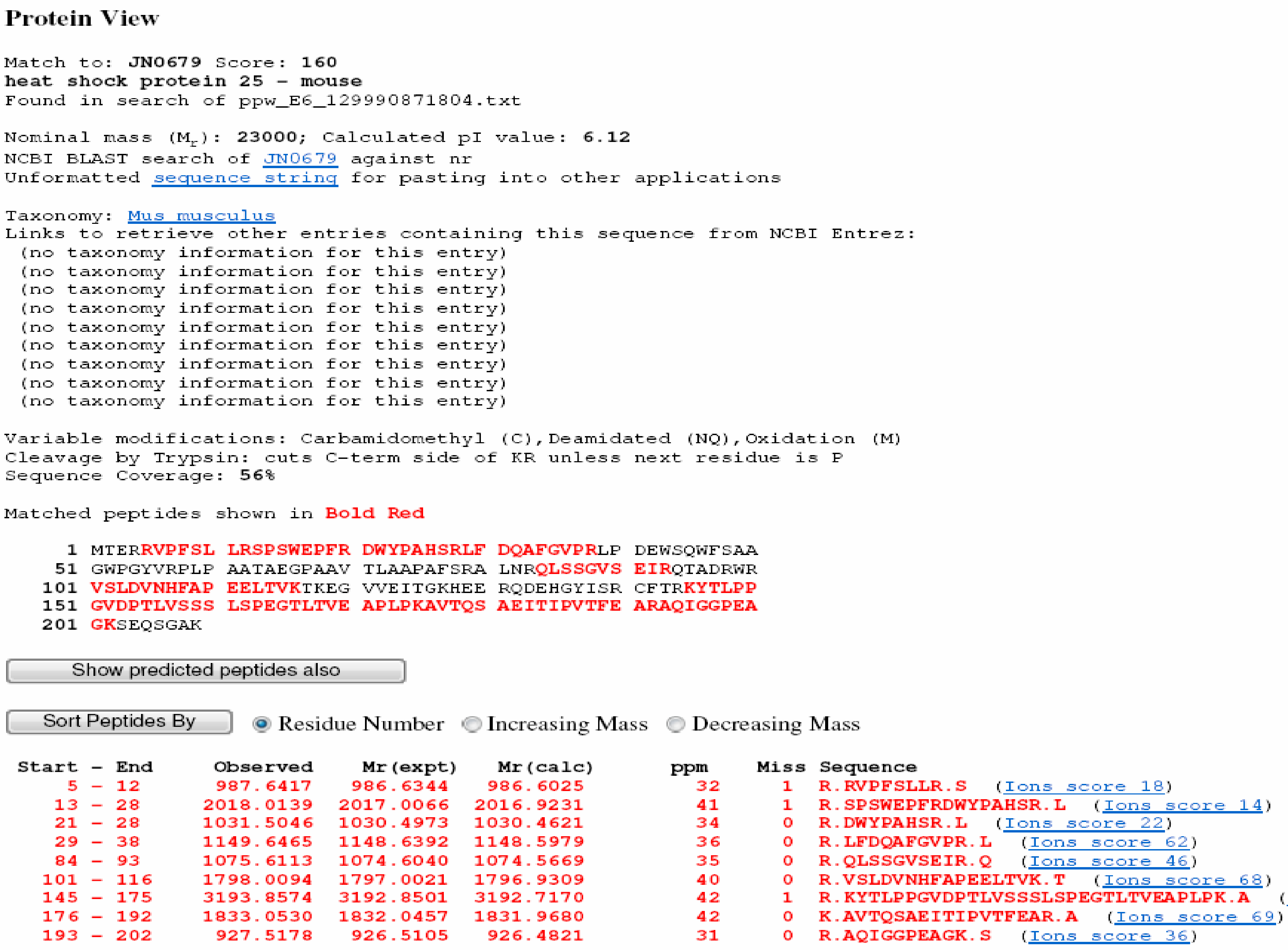
Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 Show sub-sets 0

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

☐ **Error tolerant**

1. JN0679 **Mass:** 23000 **Score:** 160 **Matches:** 9(5) **Sequences:** 9(5) **emPAI:** 2.46
heat shock protein 25 - mouse
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	927.5178	926.5105	926.4821	30.7	0	36	0.051	1	U	R.AQIGGPEAGK.S
☑	2	987.6417	986.6344	986.6025	32.4	1	18	2.1	1	U	R.RVPFSLLR.S
☑	6	1031.5046	1030.4973	1030.4621	34.2	0	22	2.3	1	U	R.DWYPAHSR.L
☑	9	1075.6113	1074.6040	1074.5669	34.5	0	46	0.0067	1	U	R.QLSSGVSEIR.Q
☑	12	1149.6465	1148.6392	1148.5979	36.0	0	62	0.00016	1	U	R.LFDQAFGVPR.L
☑	14	1798.0094	1797.0021	1796.9309	39.7	0	68	3.6e-05	1	U	R.VSLDVNHFAPEELTVK.T



Protein View

```
Match to: JN0679 Score: 160
heat shock protein 25 - mouse
Found in search of ppw_E6_129990871804.txt

Nominal mass (Mr): 23000; Calculated pI value: 6.12
NCBI BLAST search of JN0679 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 56%

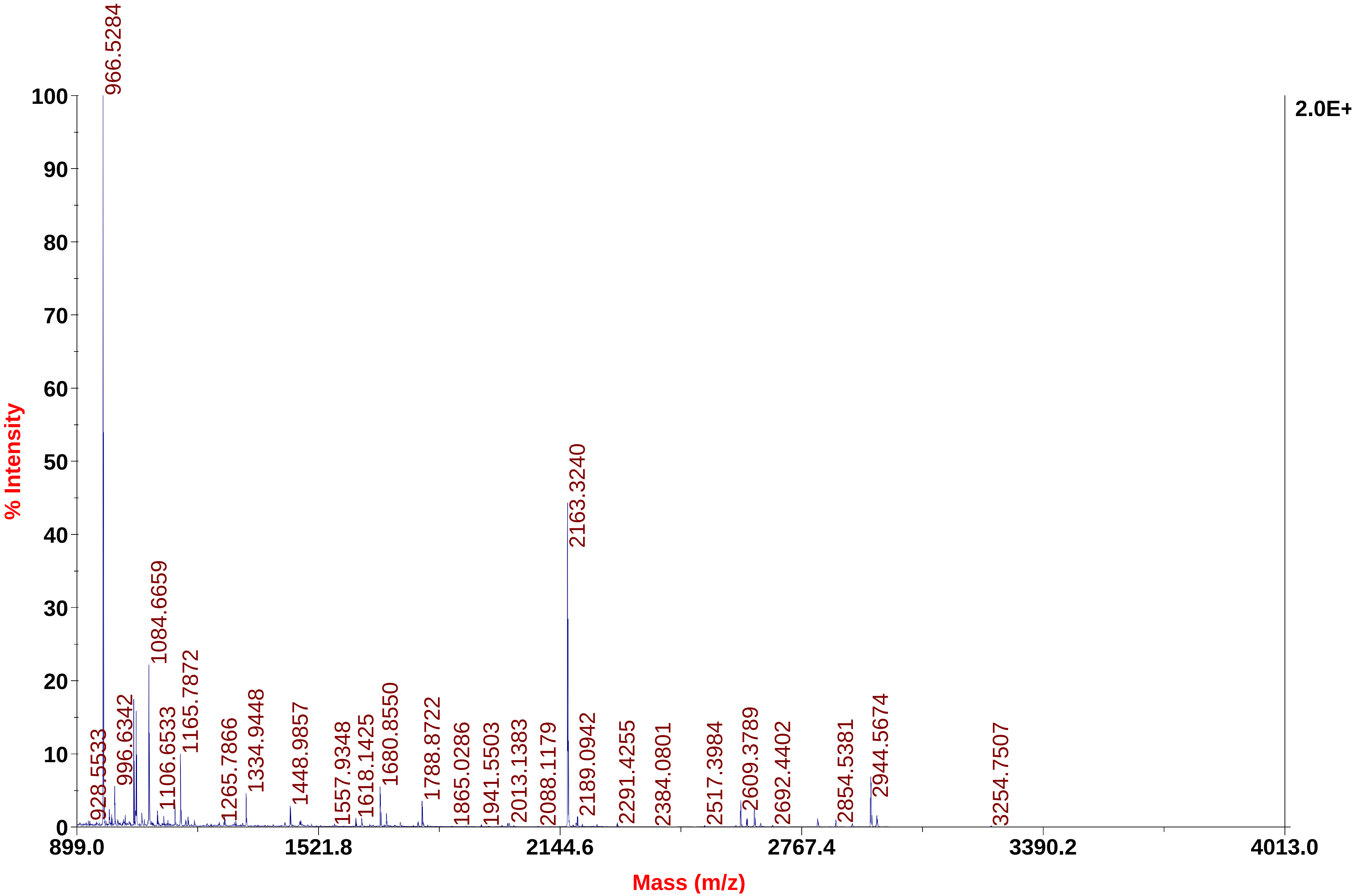
Matched peptides shown in Bold Red

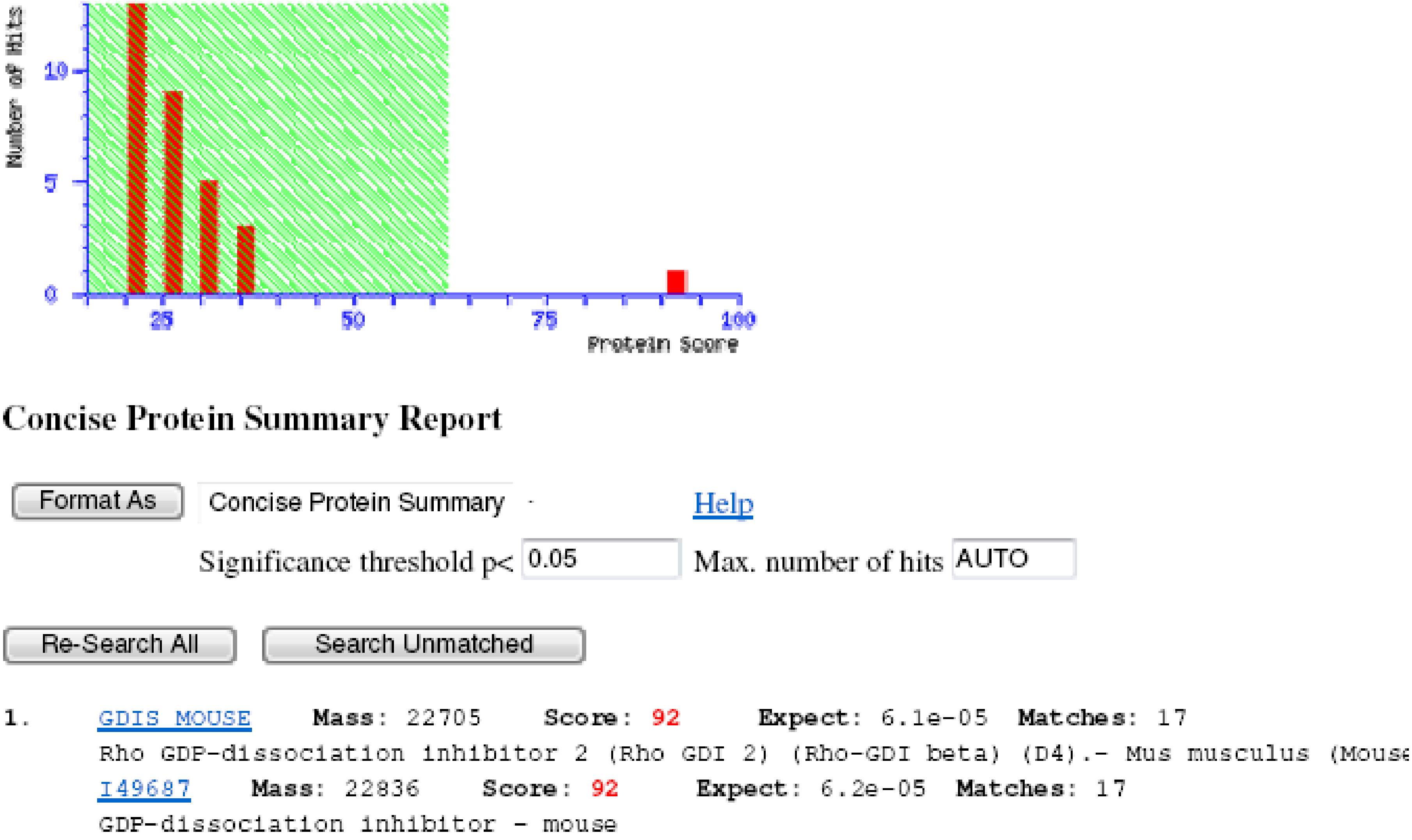
     1 MTERRVPFSL LRSPSWEPFR DWYPAHSRLF DQAFGVPRLP DEWSQWFSAA
    51 GWPGYVRPLP AATAEGPAAV TLAAPAFSRA LNRQLSSGVS EIRQTADRWR
   101 VSLDVNHFAP EELTVKTKEG VVEITGKHEE RQDEHGYISR CFTRKYTLPP
   151 GVDPTLVSSS LSPEGTLTVE APLPKAVTQS AEITIPVTFE ARAQIGGPEA
   201 GKSEQSGAK
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss  Sequence
    5 - 12       987.6417   986.6344   986.6025       32      1  R.RVPFSLLR.S  (Ions score 18)
   13 - 28      2018.0139  2017.0066  2016.9231       41      1  R.SPSWEPFRDWYPAHSR.L  (Ions score 14)
   21 - 28      1031.5046  1030.4973  1030.4621       34      0  R.DWYPAHSR.L  (Ions score 22)
   29 - 38      1149.6465  1148.6392  1148.5979       36      0  R.LFDQAFGVPR.L  (Ions score 62)
   84 - 93      1075.6113  1074.6040  1074.5669       35      0  R.QLSSGVSEIR.Q  (Ions score 46)
  101 - 116     1798.0094  1797.0021  1796.9309       40      0  R.VSLDVNHFAPEELTVK.T  (Ions score 68)
  145 - 175     3193.8574  3192.8501  3192.7170       42      1  R.KYTLPPGVDPTLVSSSLSPEGTLTVEAPLPK.A  (
  176 - 192     1833.0530  1832.0457  1831.9680       42      0  K.AVTQSAEITIPVTFEAR.A  (Ions score 69)
  193 - 202      927.5178   926.5105   926.4821       31      0  R.AQIGGPEAGK.S  (Ions score 36)
```

Sample M22

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 966.5, 20298]

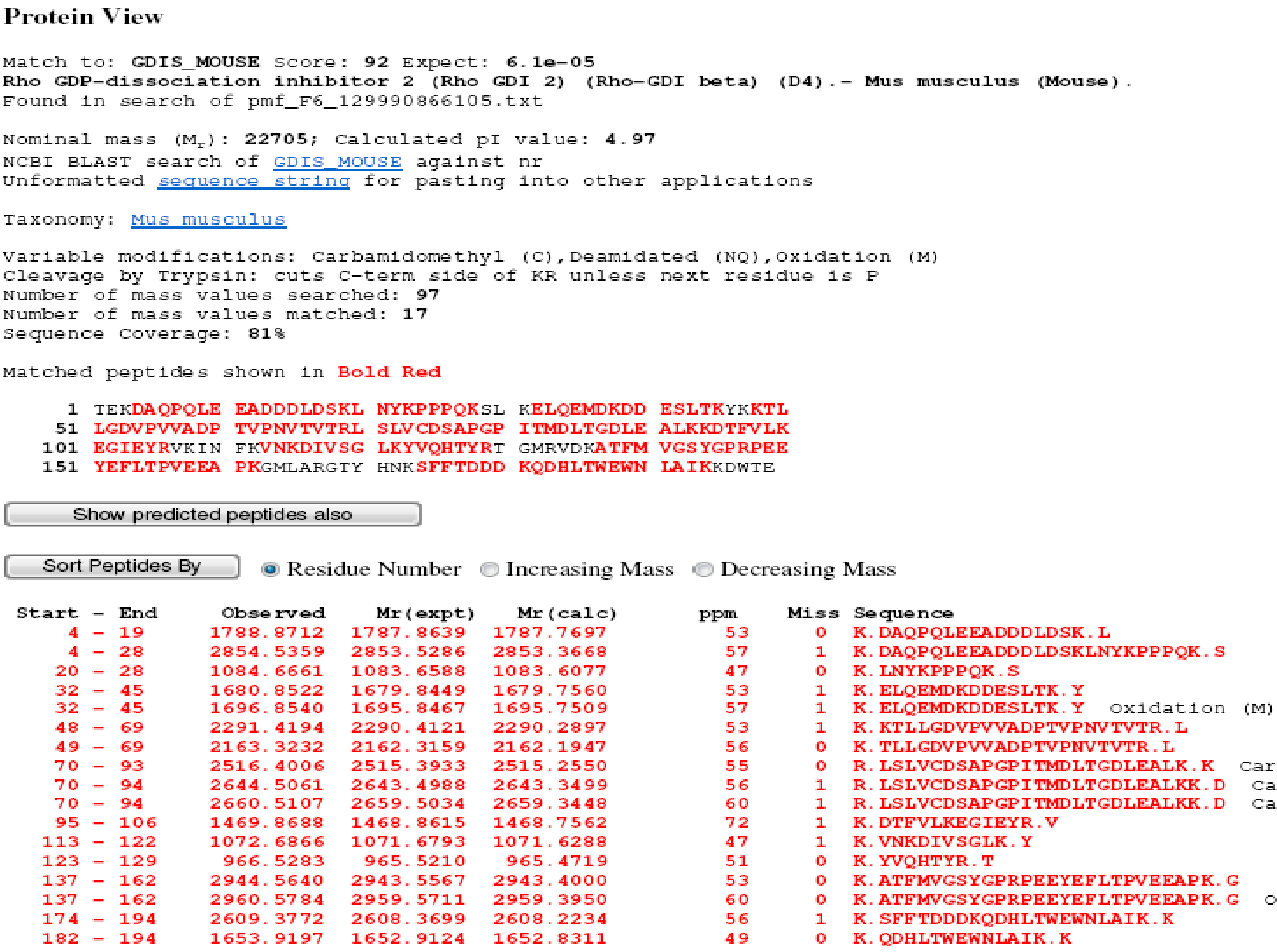




Concise Protein Summary Report

Significance threshold p< 0.05 Max. number of hits AUTO

1. GDIS_MOUSE **Mass:** 22705 **Score:** 92 **Expect:** 6.1e-05 **Matches:** 17
Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (D4).- Mus musculus (Mous
I49687 **Mass:** 22836 **Score:** 92 **Expect:** 6.2e-05 **Matches:** 17
GDP-dissociation inhibitor - mouse



Protein View

Match to: **GDIS_MOUSE** Score: **92** Expect: **6.1e-05**
Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (D4).- Mus musculus (Mouse).
Found in search of pmf_F6_12990866105.txt

Nominal mass (M_r): **22705**; Calculated pI value: **4.97**
NCBI BLAST search of GDIS_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

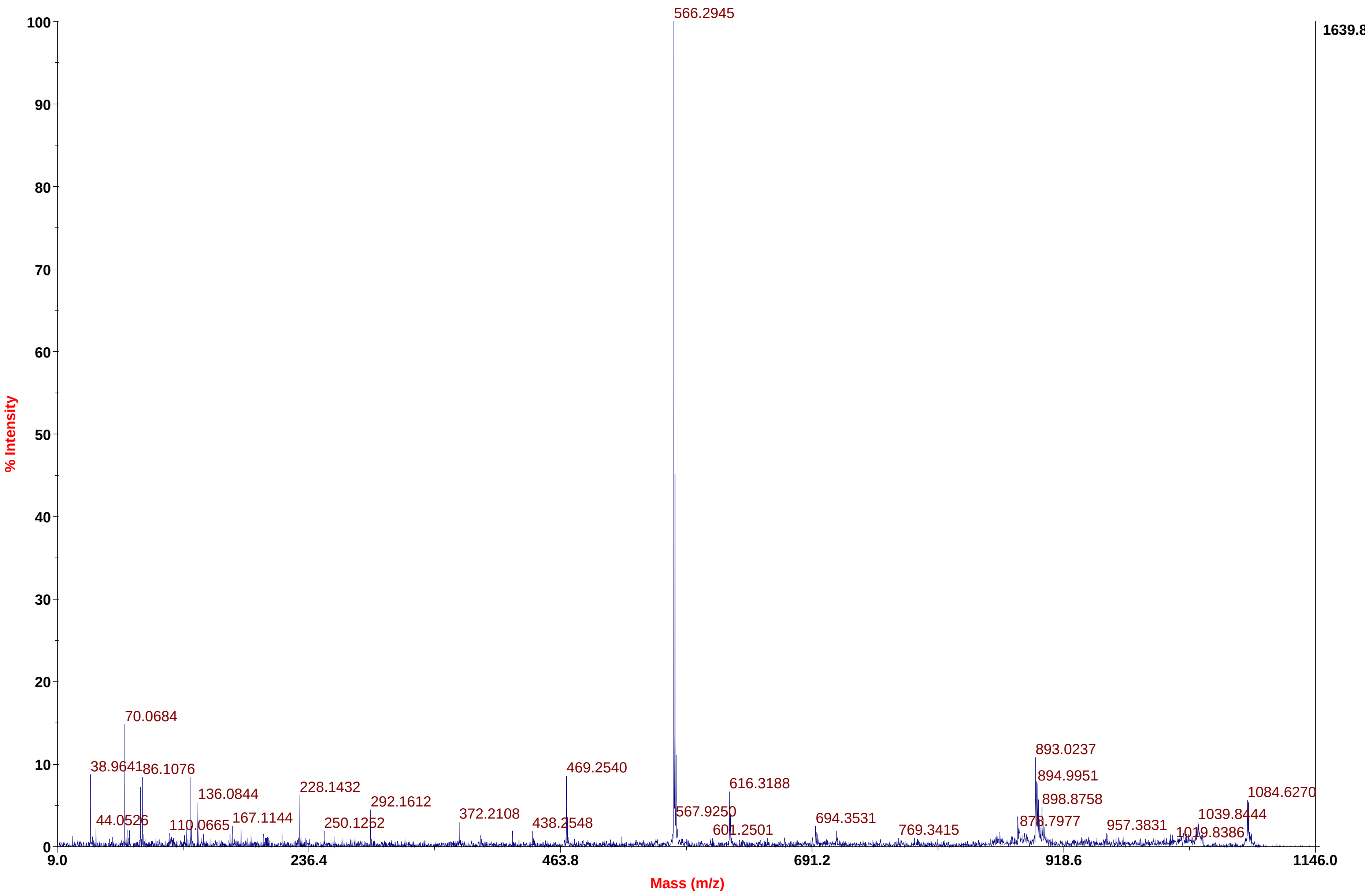
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **97**
Number of mass values matched: **17**
Sequence Coverage: **81%**

Matched peptides shown in **Bold Red**

1 TEK**DAQPQLE EADDDLDSKL NYKPPPQK**SL K**ELQEMDKDD ESLTK**YK**KTL**
51 **LGDVPVVADP TVPNVTVTRL SLVCDSAPGP ITMDLTGDLE ALKKDTFVLK**
101 **EGIEYR**VKIN FK**VNKDIVSG LKYVQHTYR**T GMRVDK**ATFM VGSYGPRPEE**
151 **YEFLTPVEEA PK**GMLARGTY HNK**SFFTDDD KQDHLTWEWN LAIK**KDWTE

Start – End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
4 – 19	1788.8712	1787.8639	1787.7697	53	0	K.DAQPQLEEADDDLDSK.L	
4 – 28	2854.5359	2853.5286	2853.3668	57	1	K.DAQPQLEEADDDLDSKLNYKPPPQK.S	
20 – 28	1084.6661	1083.6588	1083.6077	47	0	K.LNYKPPPQK.S	
32 – 45	1680.8522	1679.8449	1679.7560	53	1	K.ELQEMDKDDESLTK.Y	
32 – 45	1696.8540	1695.8467	1695.7509	57	1	K.ELQEMDKDDESLTK.Y	Oxidation (M)
48 – 69	2291.4194	2290.4121	2290.2897	53	1	K.KTLLGDVPVVADPTVPNVTVTR.L	
49 – 69	2163.3232	2162.3159	2162.1947	56	0	K.TLLGDVPVVADPTVPNVTVTR.L	
70 – 93	2516.4006	2515.3933	2515.2550	55	0	R.LSLVCDSAPGPITMDLTGDLEALK.K	Car
70 – 94	2644.5061	2643.4988	2643.3499	56	1	R.LSLVCDSAPGPITMDLTGDLEALKK.D	Ca
70 – 94	2660.5107	2659.5034	2659.3448	60	1	R.LSLVCDSAPGPITMDLTGDLEALKK.D	Ca
95 – 106	1469.8688	1468.8615	1468.7562	72	1	K.DTFVLKEGIEYR.V	
113 – 122	1072.6866	1071.6793	1071.6288	47	1	K.VNKDIVSGLK.Y	
123 – 129	966.5283	965.5210	965.4719	51	0	K.YVQHTYR.T	
137 – 162	2944.5640	2943.5567	2943.4000	53	0	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	
137 – 162	2960.5784	2959.5711	2959.3950	60	0	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	O
174 – 194	2609.3772	2608.3699	2608.2234	56	1	K.SFFTDDDKQDHLTWEWNLAIK.K	
182 – 194	1653.9197	1652.9124	1652.8311	49	0	K.QDHLTWEWNLAIK.K	

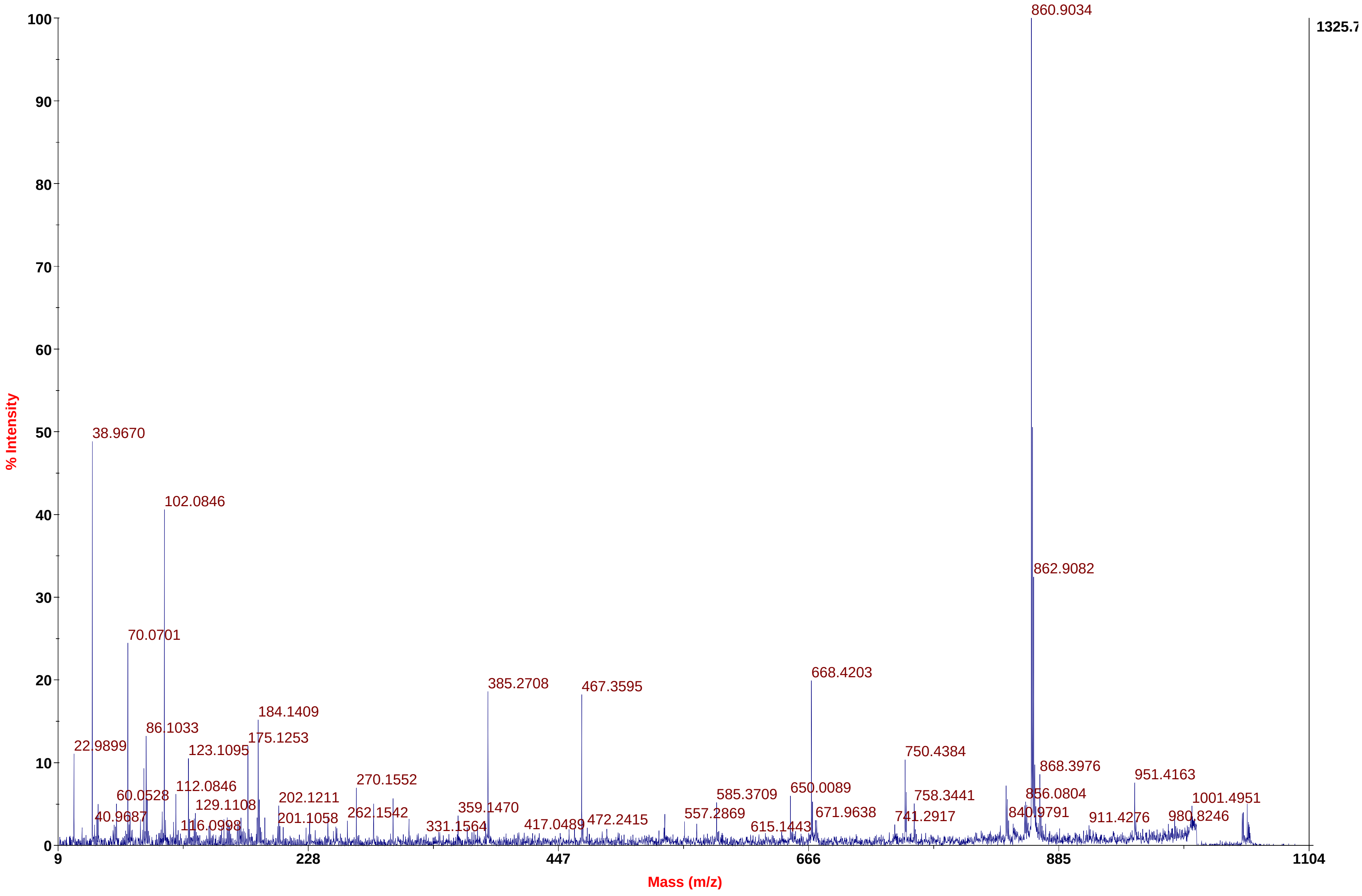
M22

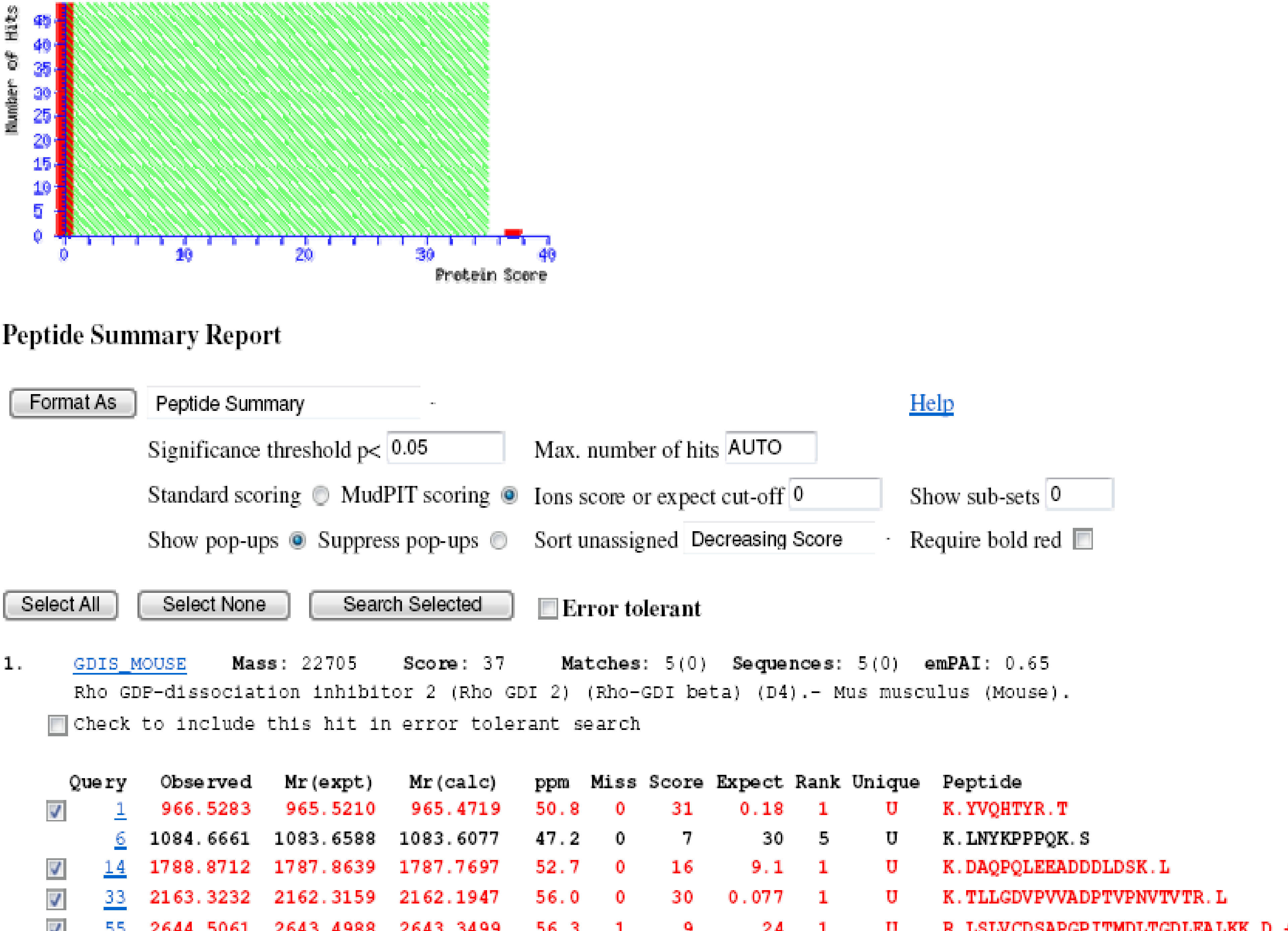


4700 MS/MS Precursor 1084.67 Spec #1 MC[BP = 566.3, 1640]

M22

4700 MS/MS Precursor 1045.62 Spec #1 MC[BP = 860.9, 1326]





Peptide Summary Report

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

Require bold red ☐

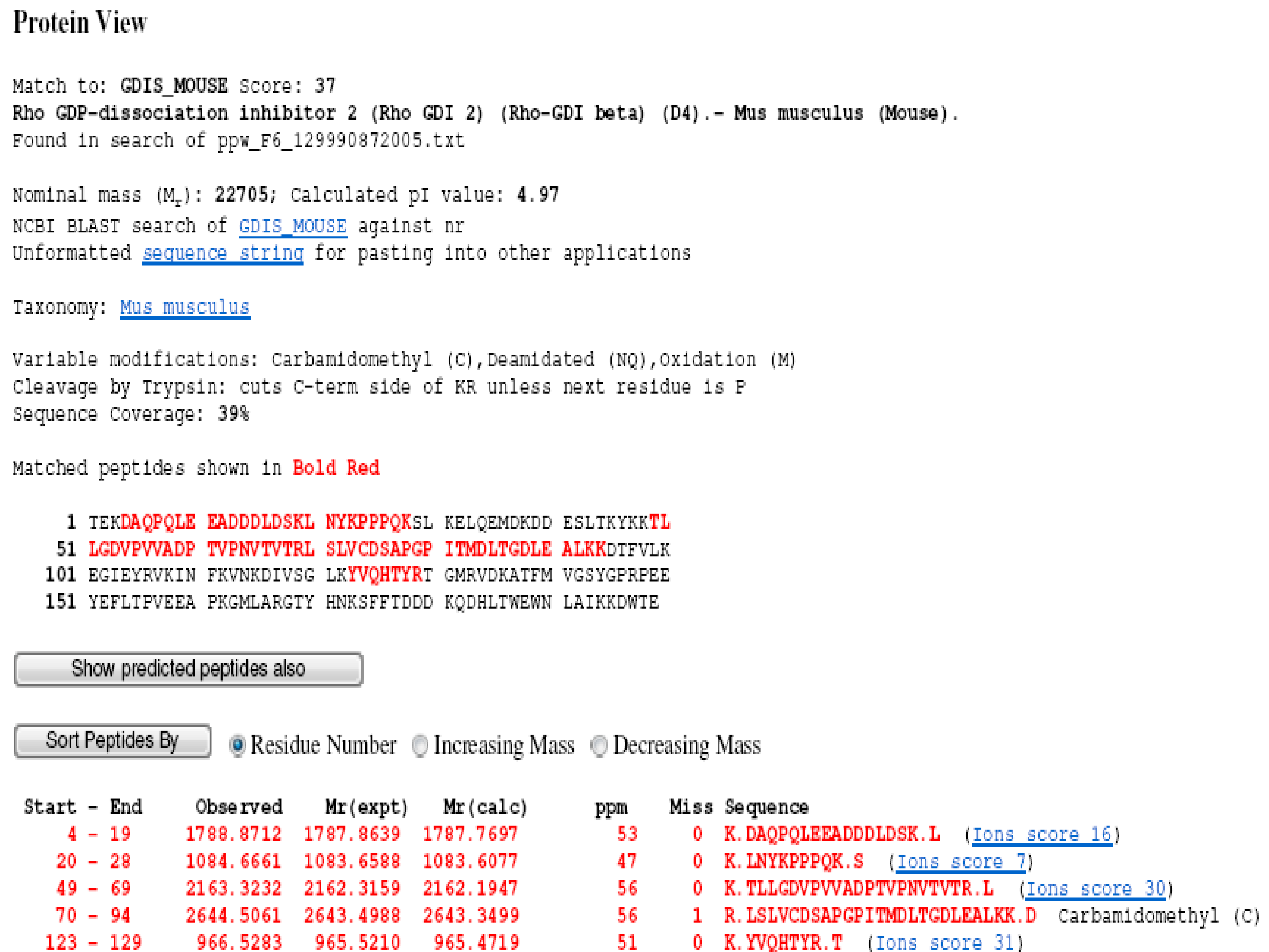
☐ Error tolerant

1. **GDIS_MOUSE** **Mass:** 22705 **Score:** 37 **Matches:** 5(0) **Sequences:** 5(0) **emPAI:** 0.65

Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (D4).- Mus musculus (Mouse).

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	966.5283	965.5210	965.4719	50.8	0	31	0.18	1	U	K.YVQHTYR.T
	6	1084.6661	1083.6588	1083.6077	47.2	0	7	30	5	U	K.LNYKPPPQK.S
☑	14	1788.8712	1787.8639	1787.7697	52.7	0	16	9.1	1	U	K.DAQPQLEEADDDLDSK.L
☑	33	2163.3232	2162.3159	2162.1947	56.0	0	30	0.077	1	U	K.TLLGDVPVVADPTVPNVTVTR.L
☑	55	2644.5061	2643.4988	2643.3499	56.3	1	9	24	1	U	R.LSLVCDSAPGPITMDLTGDLEALKK.D



Protein View

Match to: **GDIS_MOUSE** Score: 37
Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (D4).- Mus musculus (Mouse).
Found in search of ppw_F6_129990872005.txt

Nominal mass (M_r): **22705**; Calculated pI value: **4.97**
NCBI BLAST search of GDIS_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **39%**

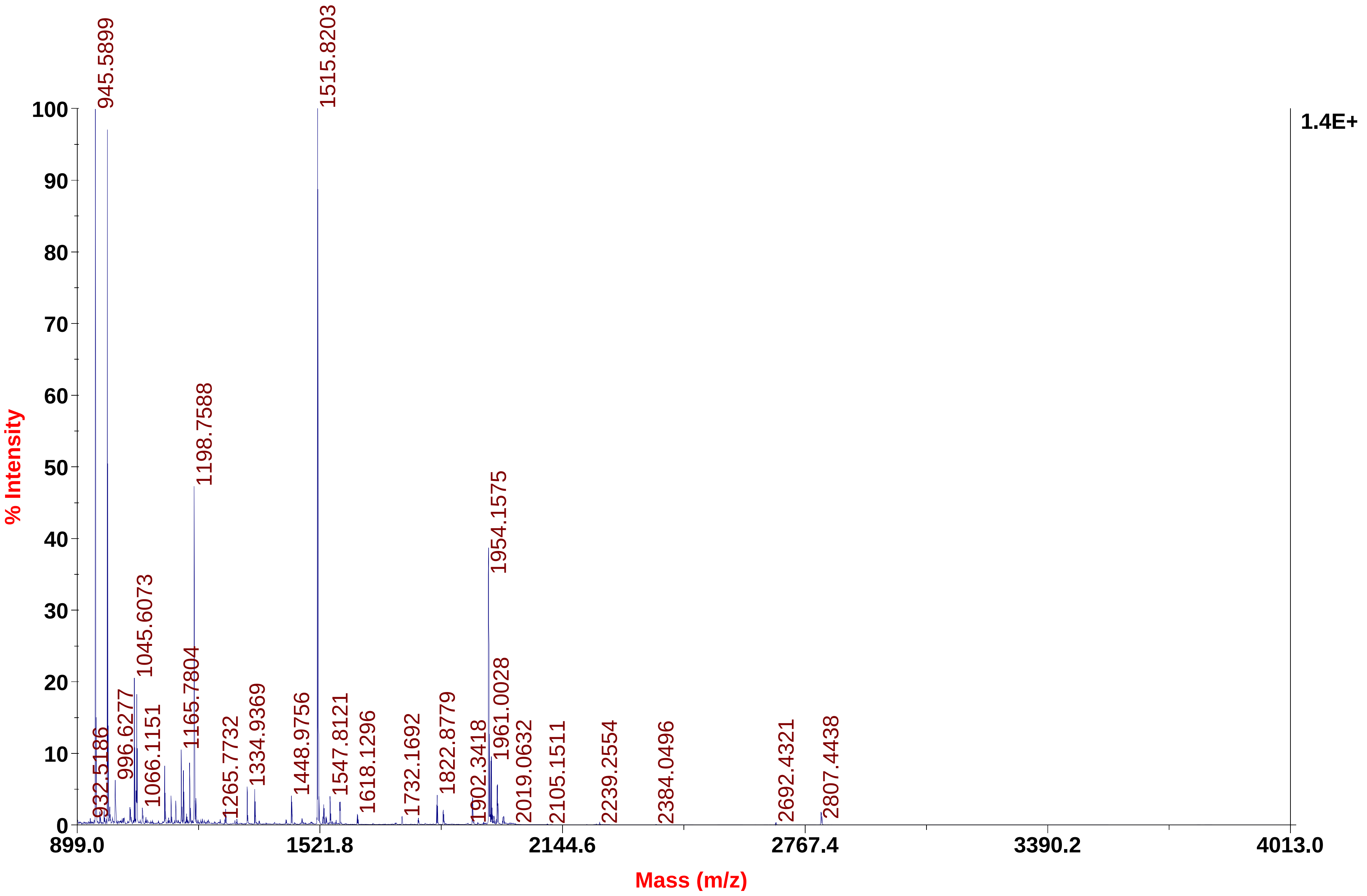
Matched peptides shown in **Bold Red**

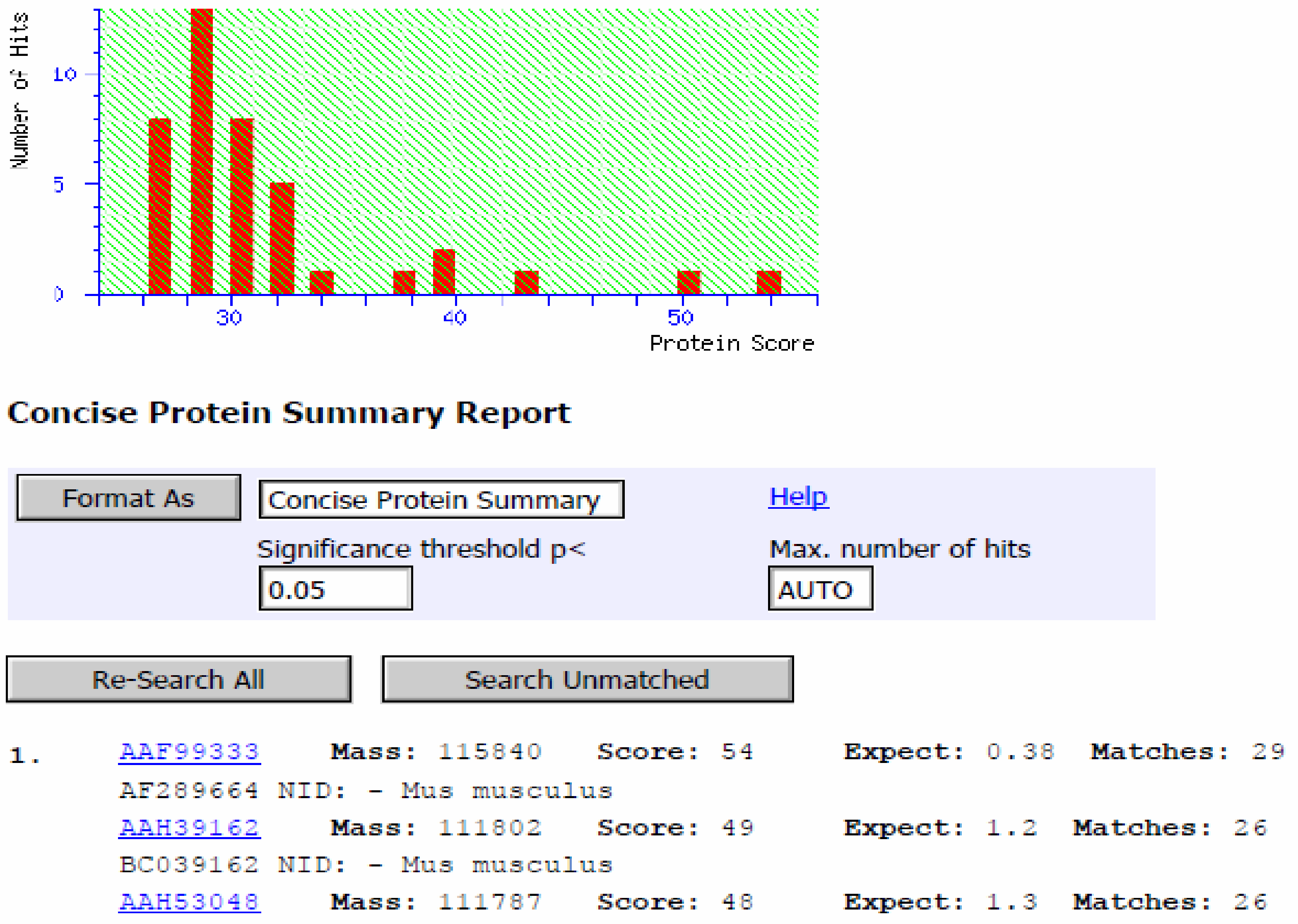
```
  1 TEKDAQPQLE EADDDLDSKL NYKPPPQKSL KELQEMDKDD ESLTKYKKTL
 51 LGDVPVVADP TVPNVTVTRL SLVCDSAPGP ITMDLTGDLE ALKKDTFVLK
101 EGIEYRVKIN FKVNKDIVSG LKYVQHTYRT GMRVDKATFM VGSYGPRPEE
151 YEFLTPVEEA PKGMLARGTY HNKSFFTDDD KQDHLTWEWN LAIKKDWTE
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
    4 - 19     1788.8712  1787.8639  1787.7697       53      0  K.DAQPQLEEADDDLDSK.L  (Ions score 16)
   20 - 28     1084.6661  1083.6588  1083.6077       47      0  K.LNYKPPPQK.S  (Ions score 7)
   49 - 69     2163.3232  2162.3159  2162.1947       56      0  K.TLLGDVPVVADPTVPNVTVTR.L  (Ions score 30)
   70 - 94     2644.5061  2643.4988  2643.3499       56      1  R.LSLVCDSAPGPITMDLTGDLEALKK.D  Carbamidomethyl (C)
  123 - 129     966.5283   965.5210   965.4719       51      0  K.YVQHTYR.T  (Ions score 31)
```

Sample M23

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1515.8, 14221]





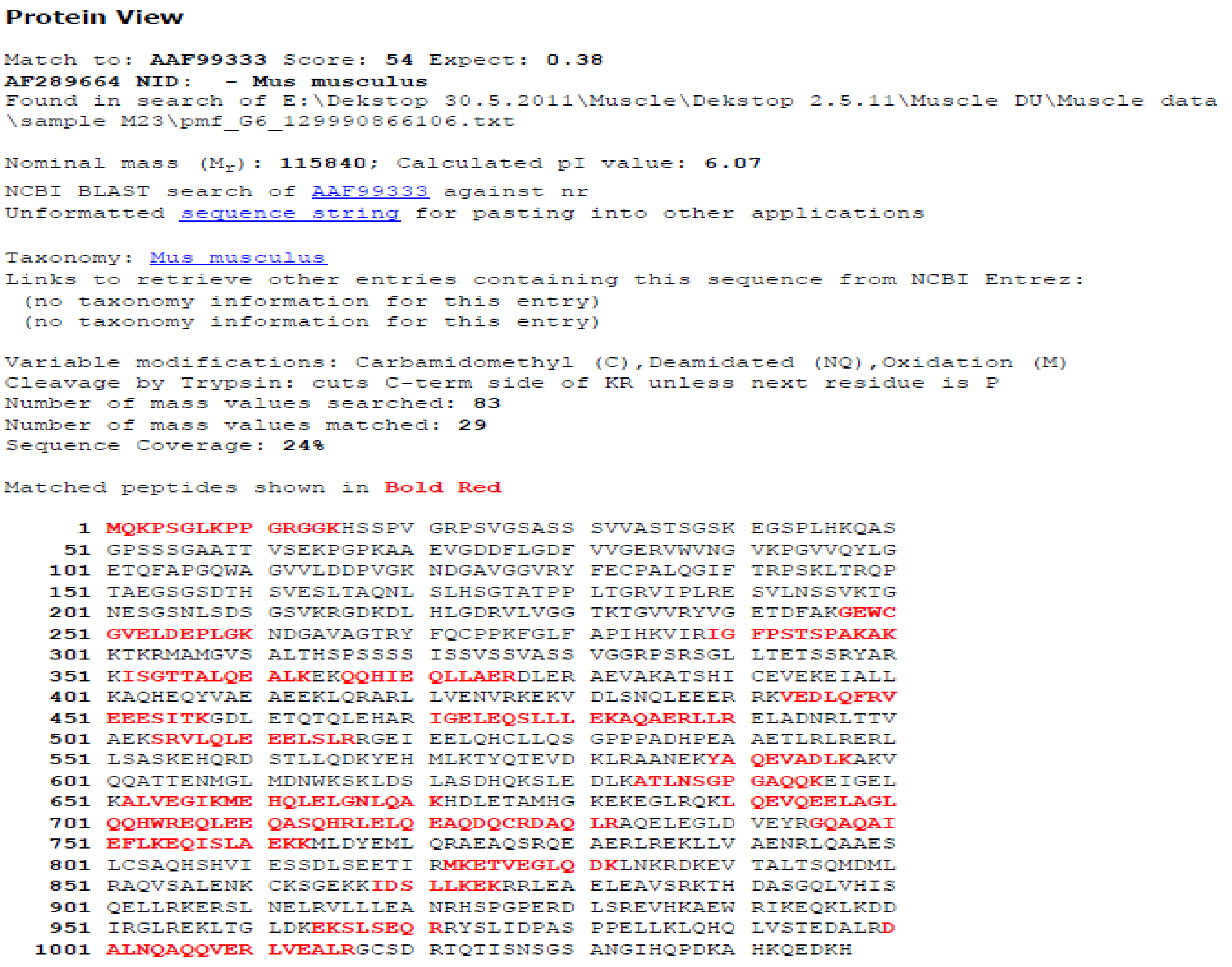
Concise Protein Summary Report

Format As: Concise Protein Summary

Significance threshold p< 0.05

Max. number of hits AUTO

```
1.     AAF99333     Mass: 115840    Score: 54      Expect: 0.38   Matches: 29
       AF289664 NID: - Mus musculus
       AAH39162     Mass: 111802    Score: 49      Expect: 1.2   Matches: 26
       BC039162 NID: - Mus musculus
       AAH53048     Mass: 111787    Score: 48      Expect: 1.3   Matches: 26
```



Protein View

Match to: **AAF99333** Score: **54** Expect: **0.38**
AF289664 NID: - Mus musculus
Found in search of E:\Dekstop 30.5.2011\Muscle\Dekstop 2.5.11\Muscle DU\Muscle data \sample M23\pmf_G6_12990866106.txt

Nominal mass (M_r): **115840**; Calculated pI value: **6.07**

NCBI BLAST search of AAF99333 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)
(no taxonomy information for this entry)

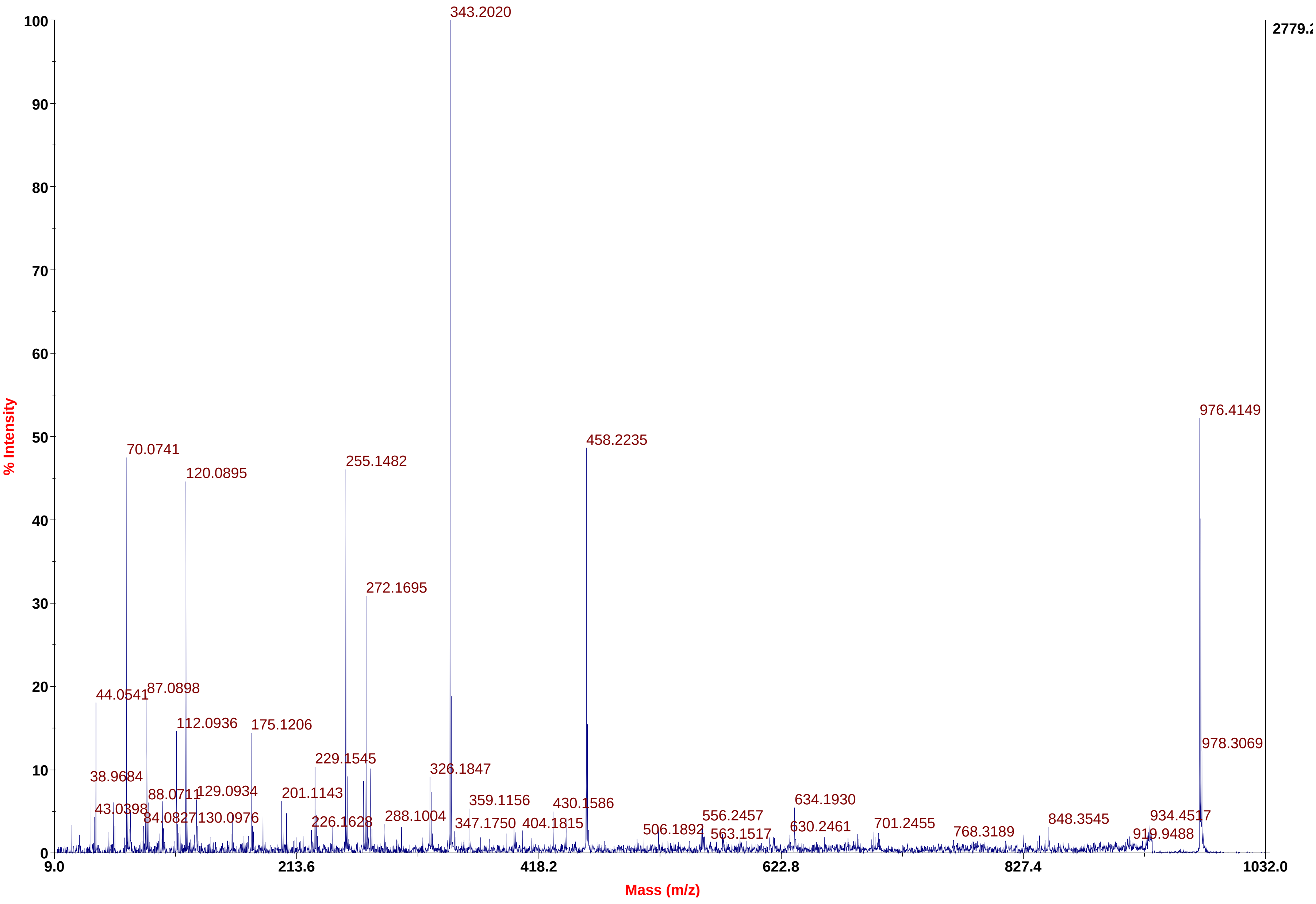
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **83**
Number of mass values matched: **29**
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

1 **MQKPSGLKPP GRGGK**HSSPV GRPSVGSASS SVVASTSGSK EGSPLHKQAS
51 GPSSSGAATT VSEKPGPKAA EVGDDFLGDF VVGERVWVNG VKPGVVQYLG
101 ETQFAPGQWA GVVLDDPVGK NDGAVGGVRY FECPALQGIF TRPSKLTRQP
151 TAEGSGSDTH SVESLTAQNL SLHSGTATPP LTGRVIPLRE SVLNSSVKTG
201 NESGSNLSDS GSVKRGDKDL HLGDRVLVGG TKTGVVRYVG ETDFAK**GEWC**
251 **GVELDEPLGK** NDGAVAGTRY FQCPPKFGLF APIHKVIR**IG FPSTSPAKAK**
301 KTKRMAMGVS ALTHSPSSSS ISSVSSVASS VGGRPSRSGL LTETSSRYAR
351 K**ISGTTALQE ALKEKQQHIE QLLAER**DLER AEVAKATSHI CEVEKEIALL
401 KAQHEQYVAE AEEKLQRARL LVENVRKEKV DLSNQLEEER RK**VEDLQFRV**
451 **EEESITK**GDL ETQTQLEHAR **IGELEQSLLL EKAQAERLLR** ELADNRLTTV
501 AEK**SRVLQLE EELSLR**RGEI EELQHCLLQS GPPPADHPEA AETLRLRERL
551 LSASKEHQRD STLLQDKYEH MLKTYQTEVD KLRAANEK**YA QEVADLK**AKV
601 QQATTENMGL MDNWKSKLDS LASDHQKSLE DLK**ATLNSGP GAQQK**EIGEL
651 **KALVEGIKME HQLELGNLQA K**HDLETAMHG KEKEGLRQK**L QEVQEELAGL**
701 **QQHWREQLEE QASQHRLELQ EAQDQCRDAQ LR**AQELEGLD VEYR**GQAQAI**
751 **EFLKEQISLA EKK**MLDYEML QRAEAQSRQE AERLREKLLV AENRLQAAES
801 LCSAQHSHVI ESSDLSEETI R**MKETVEGLQ DK**LNKRDKEV TALTSQMDML
851 RAQVSALENK CKSGEKK**IDS LLKEK**RRLEA ELEAVSRKTH DASGQLVHIS
901 QELLRKERSL NELRVLLLEA NRHSPGPERD LSREVHKAEW RIKEQKLKDD
951 IRGLREKLTG LDK**EKSLSEQ R**RYSLIDPAS PPELLKLQHQ LVSTEDALR**D**
1001 **ALNQAQQVER LVEALR**GCSD RTQTISNSGS ANGIHQPDKA HKQEDKH

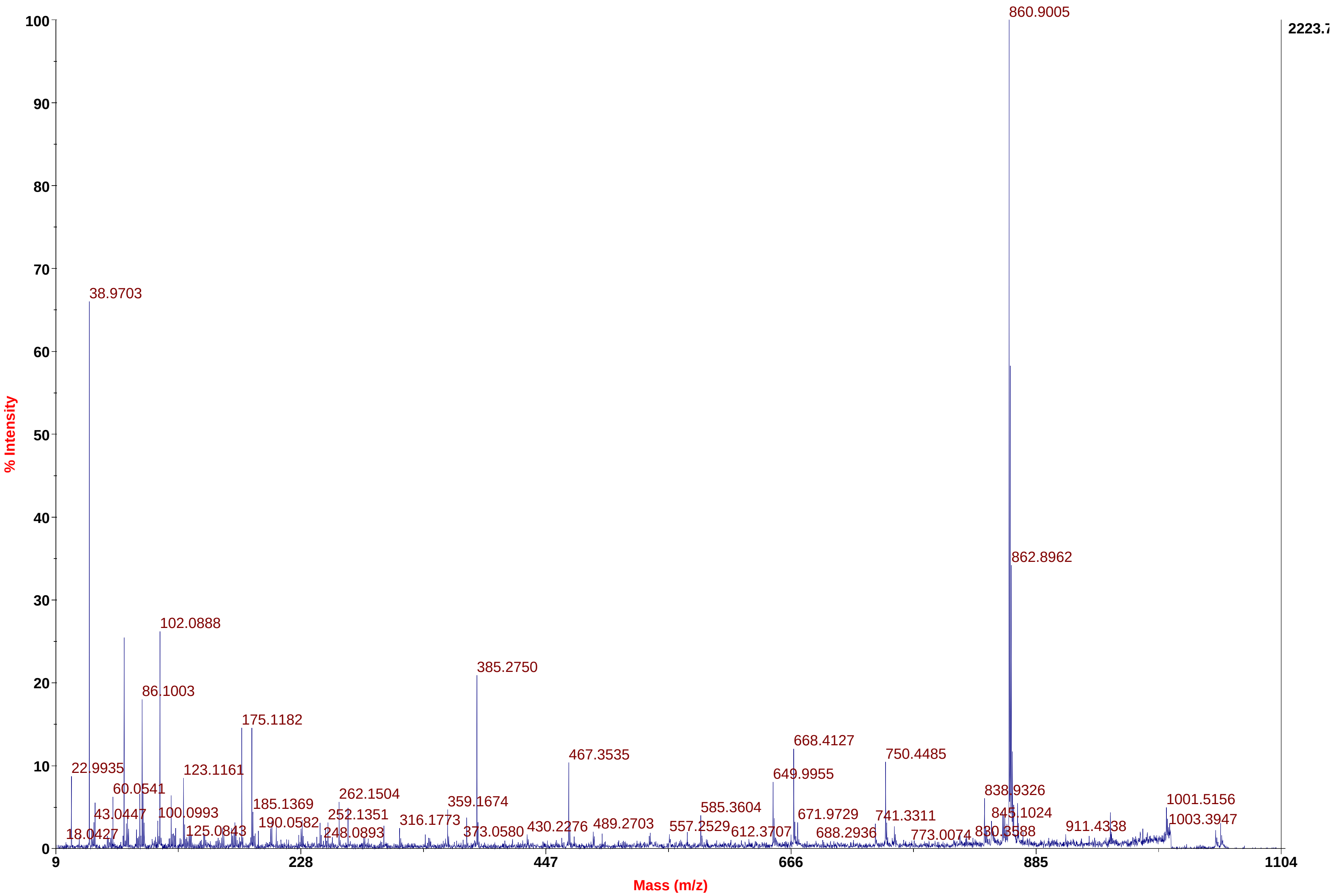
M23

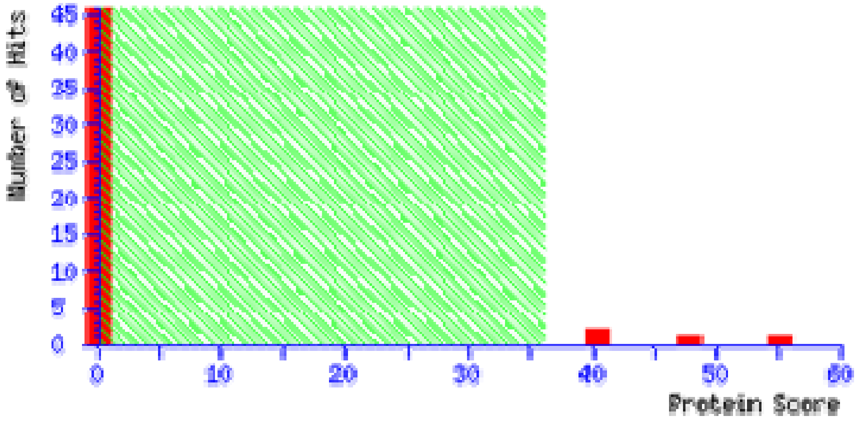
4700 MS/MS Precursor 976.488 Spec #1 MC[BP = 343.2, 2779]

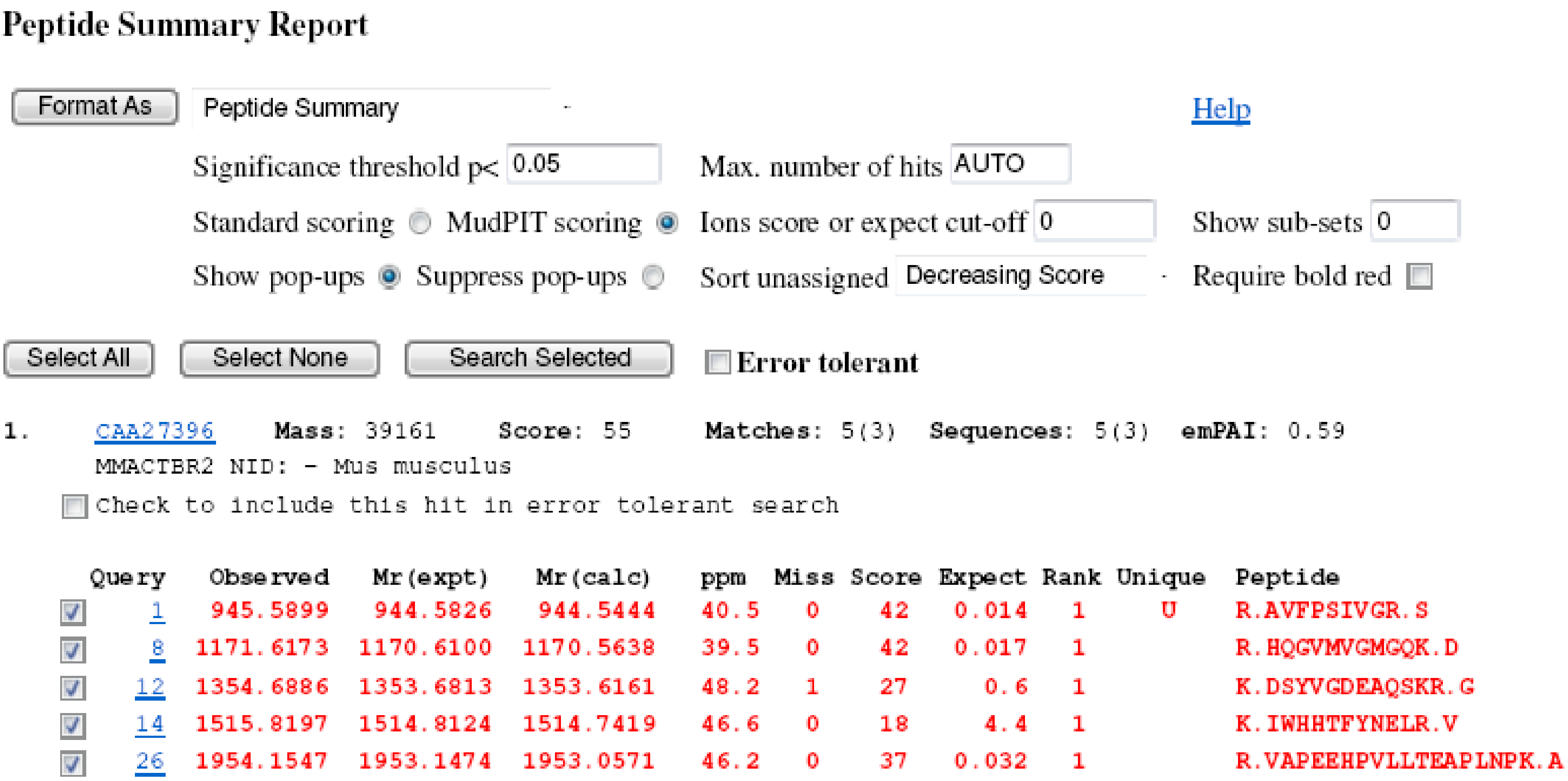


M23

4700 MS/MS Precursor 1045.61 Spec #1 MC[BP = 860.9, 2224]







Peptide Summary Report

Peptide Summary

Significance threshold p< 0.05

Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ●

Ions score or expect cut-off 0

Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○

Sort unassigned Decreasing Score

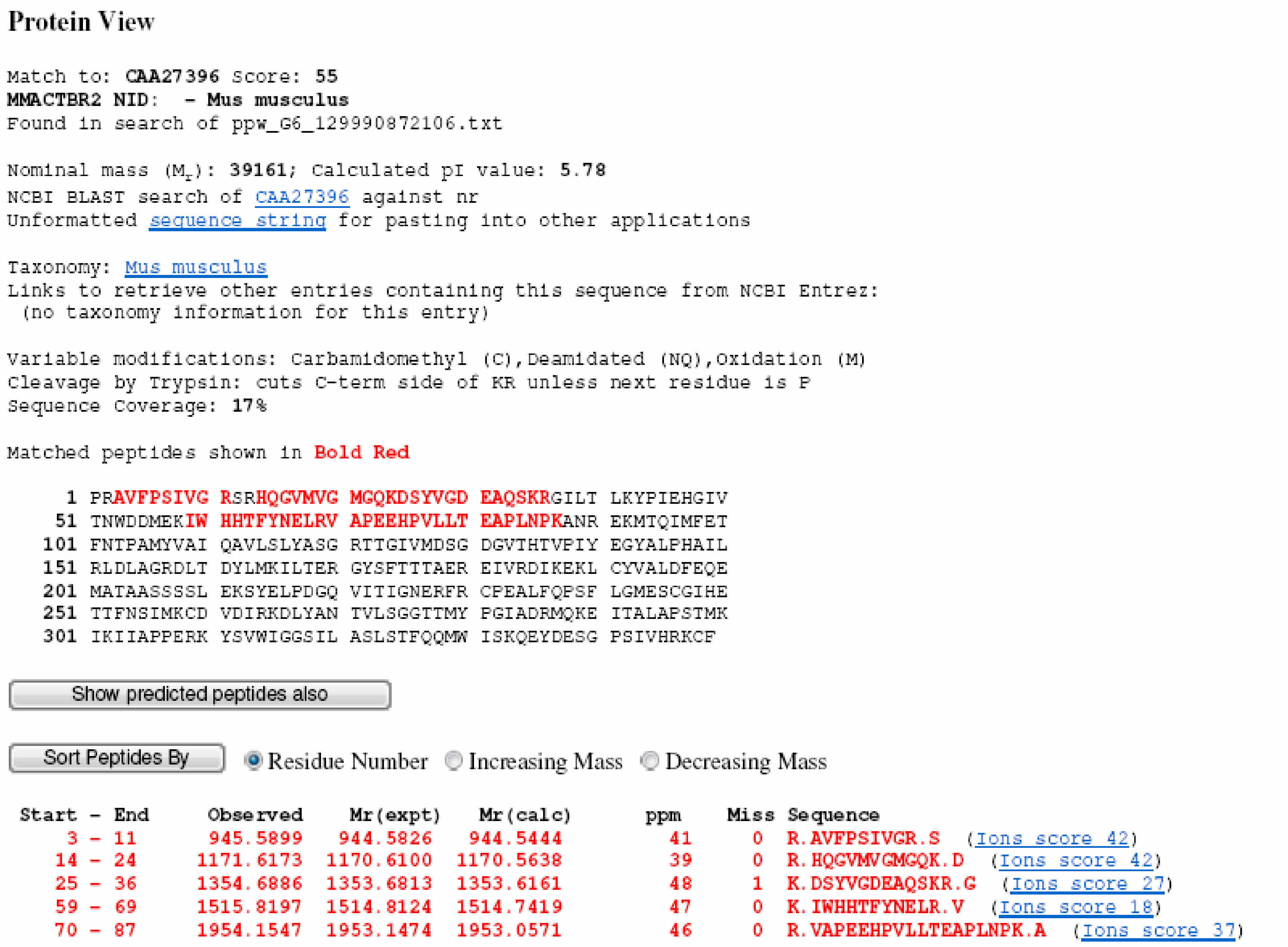
Require bold red ☐

☐ **Error tolerant**

1. CAA27396 **Mass:** 39161 **Score:** 55 **Matches:** 5(3) **Sequences:** 5(3) **emPAI:** 0.59
MMACTBR2 NID: - Mus musculus

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	945.5899	944.5826	944.5444	40.5	0	42	0.014	1	U	R.AVFPSIVGR.S
☑	8	1171.6173	1170.6100	1170.5638	39.5	0	42	0.017	1		R.HQGVMVGMGQK.D
☑	12	1354.6886	1353.6813	1353.6161	48.2	1	27	0.6	1		K.DSYVGDEAQSKR.G
☑	14	1515.8197	1514.8124	1514.7419	46.6	0	18	4.4	1		K.IWHHTFYNELR.V
☑	26	1954.1547	1953.1474	1953.0571	46.2	0	37	0.032	1		R.VAPEEHPVLLTEAPLNPK.A



Protein View

Match to: **CAA27396** Score: **55**
MMACTBR2 NID: - Mus musculus
Found in search of ppw_G6_129990872106.txt

Nominal mass (M_r): **39161**; Calculated pI value: **5.78**
NCBI BLAST search of CAA27396 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

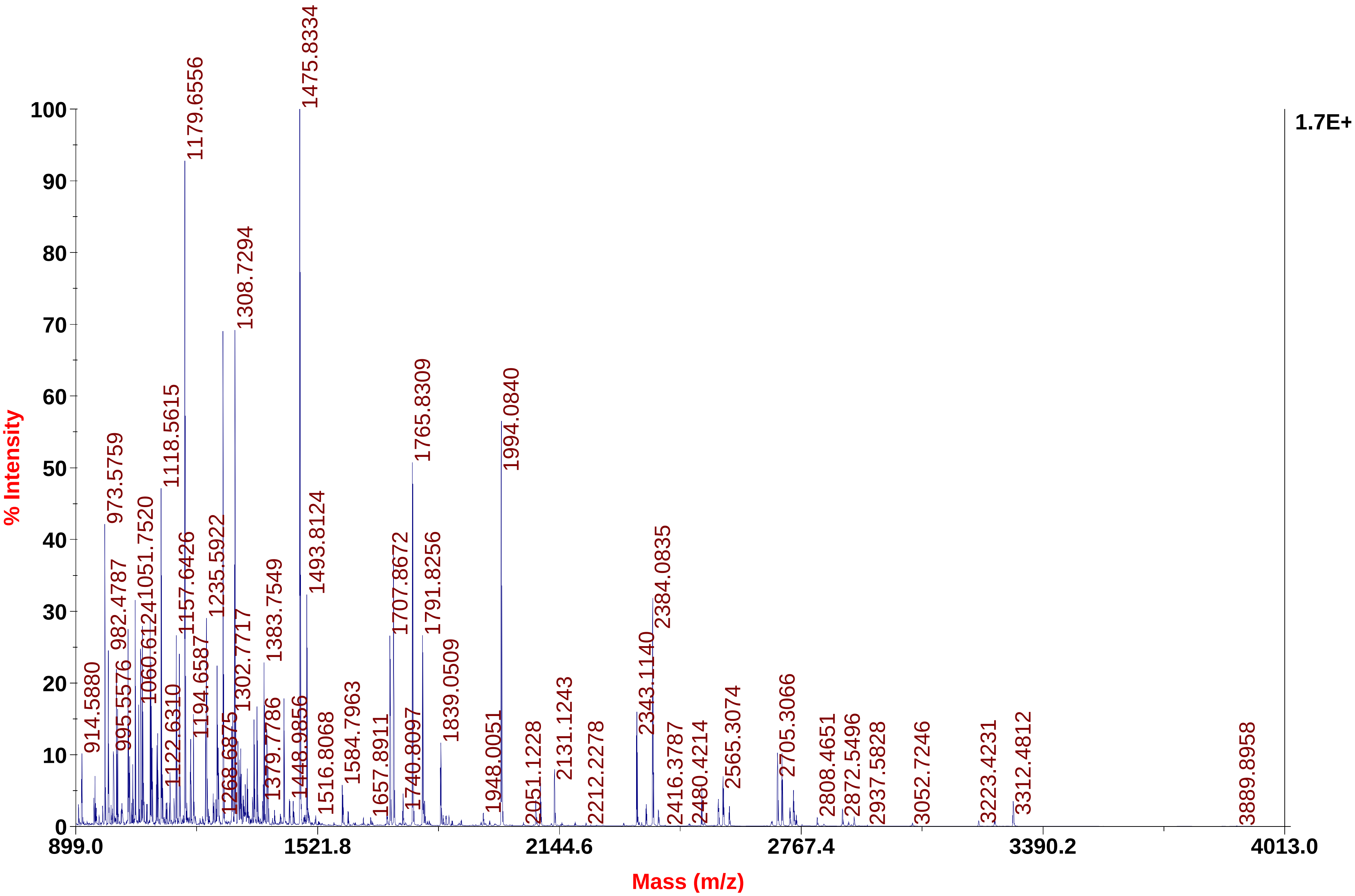
Matched peptides shown in **Bold Red**

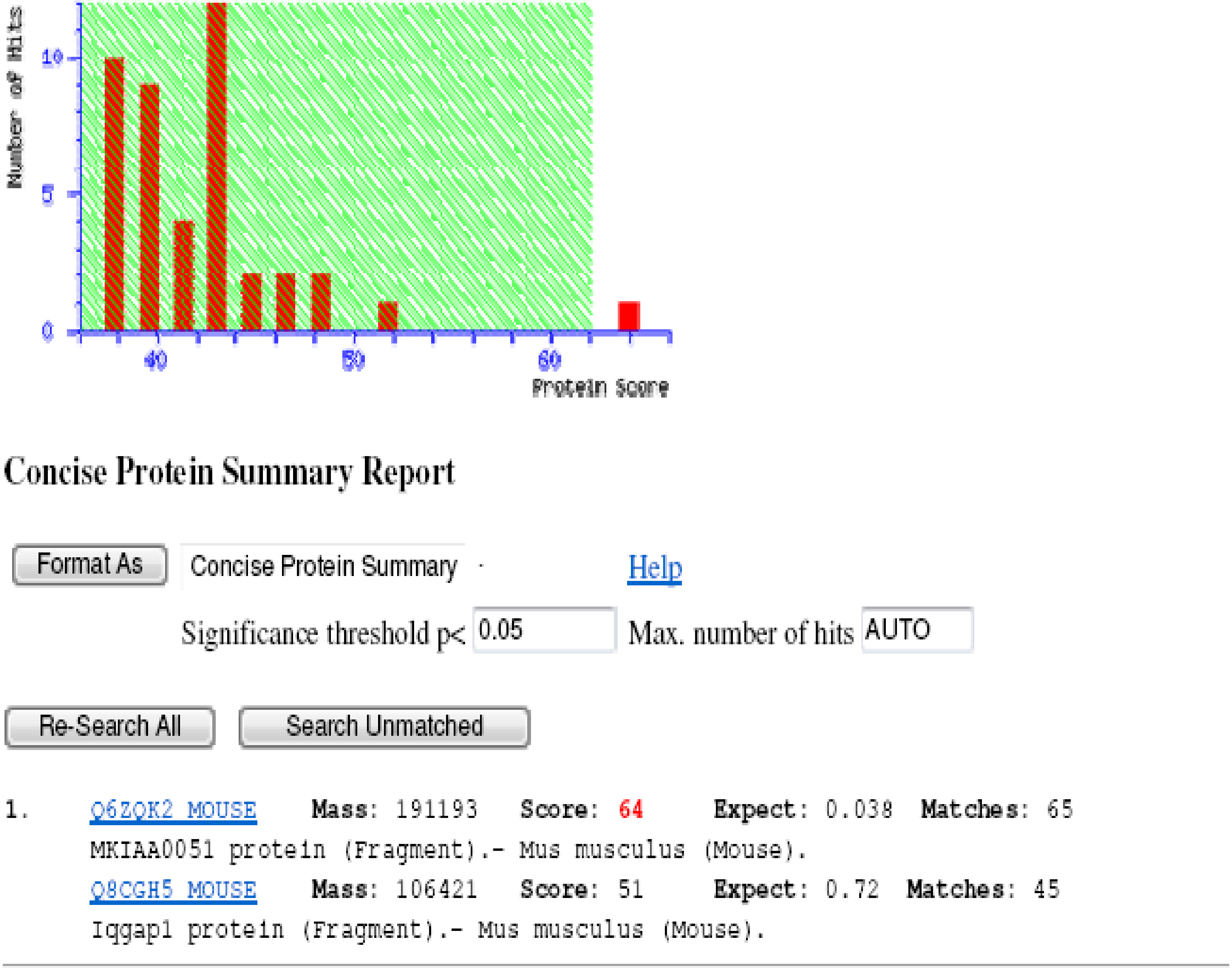
1 PR**AVFPSIVG** **R**SR**HQGVMVG** **MGQKDSYVGD** **EAQSKR**GILT LKYPIEHGIV
51 TNWDDMEK**IW** **HHTFYNELRV** **APEEHPVLLT** **EAPLNPK**ANR EKMTQIMFET
101 FNTPAMYVAI QAVLSLYASG RTTGIVMDSG DGVTHTVPIY EGYALPHAIL
151 RLDLAGRDLT DYLMKILTER GYSFTTTAER EIVRDIKEKL CYVALDFEQE
201 MATAASSSSL EKSYELPDGQ VITIGNERFR CPEALFQPSF LGMESCGIHE
251 TTFNSIMKCD VDIRKDLYAN TVLSGGTTMY PGIADRMQKE ITALAPSTMK
301 IKIIAPPERK YSVWIGGSIL ASLSTFQQMW ISKQEYDESG PSIVHRKCF

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
3 - 11	945.5899	944.5826	944.5444	41	0	R.AVFPSIVGR.S (Ions score 42)
14 - 24	1171.6173	1170.6100	1170.5638	39	0	R.HQGVMVGMGQK.D (Ions score 42)
25 - 36	1354.6886	1353.6813	1353.6161	48	1	K.DSYVGDEAQSKR.G (Ions score 27)
59 - 69	1515.8197	1514.8124	1514.7419	47	0	K.IWHHTFYNELR.V (Ions score 18)
70 - 87	1954.1547	1953.1474	1953.0571	46	0	R.VAPEEHPVLLTEAPLNPK.A (Ions score 37)

Sample M24

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1475.8, 16515]





Concise Protein Summary Report

Concise Protein Summary

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.    Q6ZQK2_MOUSE   Mass: 191193   Score: 64    Expect: 0.038  Matches: 65
      MKIAA0051 protein (Fragment).- Mus musculus (Mouse).
      Q8CGH5_MOUSE   Mass: 106421   Score: 51    Expect: 0.72  Matches: 45
      Iqgap1 protein (Fragment).- Mus musculus (Mouse).
```

Protein View

Match to: **Q6ZQK2_MOUSE** Score: **64** Expect: **0.038**
MKIAA0051 protein (Fragment).- Mus musculus (Mouse).
Found in search of pmf_H6_12990866107.txt

Nominal mass (M_r): **191193**; Calculated pI value: **6.15**
NCBI BLAST search of Q6ZQK2_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **180**
Number of mass values matched: **65**
Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

1	LLLLRSPASS	RSLRFLTGDL	DSAAMSAAEE	VDGLGVVRPH	YGSVLDNER**L**
51	**TAEEMDERR**R	**QNVAYEYLCH**	**LEEAK**RWMEA	CLGEDLPPTT	ELEEGLRNGV
101	YLAKLGNFFS	PKVVSLKK**IY**	**DREQTRYKAT**	**GLHFR**HTDNV	IQWLNAMDEI
151	GLPKIFYPET	TDIYDRK**NMP**	**RCIYCIHALS**	**LYLFK**LGLAP	QIQDLYGK**VD**
201	**FTEEEINNMK**	**IELEKYGIQM**	**PAFSK**IGGIL	ANELSVDEAA	LHAAVIAINE
251	AIDRR**VAADT**	**FTALKNPNAM**	**LVNLEEGLAP**	**TYQDVLYQAK**	QDKMTNAKNR
301	**TENSDRER**DV	YEELLTQAEI	QGNVNKVNTS	SALANISLAL	EQGCAVTLLK
351	**ALQSLALGLR**	**GLQTQNSDWY**	**MKQLQSDLQQ**	**K**RQSGQTDPL	QKEEVQAGVD
401	AANSAAQQYQ	R**RLAAVAAIN**	**AAIQK**GIAEK	**TVLELMNPEA**	**QLPQVYPFAA**
451	**DLYQK**ELATL	QQQSPEHSLT	HPELTVAVEM	LSSVALINR**A**	**LESGDMTTVW**
501	**K**QLSSSVTGL	TNIEEENCQR	YLDELMKLKA	QAHAENNAFI	TWNDIQACVD
551	HVNLVVHEEH	ERILAIGLIN	EALDEGDAQK	TLQALQIPAA	K**LEGVLAEVA**
601	**QHYQDTLIRA**	**K**REKAQETQD	ESAVLWLDEI	QGGIWQSNKD	TQEAQR**FALG**
651	**ISAINEAVDS**	**GDVGRTLSAL**	**R**SPDVGLYGV	IPECGETYRS	DLAEAKKK**RL**
701	**AAGDNNSKWV**	**KHWVK**GGYHY	YHNLETQAGG	WAEPPDFVQN	SVQLSR**EEIQ**
751	**SSISGVTAAY**	**NREQLWLANE**	**GLITKLQACC**	**RGYLVR**QEFR	SRMNFLKKQI
801	PAITCIQSQW	RGYKQKKAYQ	DRLAYLHSHK	DEVVKIQSLA	RMHQARKRYR
851	DRLQYFR**DHI**	**NDIIKIQAFI**	**RANK**ARDDYK	**TLINAEDPPM**	**IVVRKFVHLL**
901	**DQSDQDFQEE**	**LDLMKMREEV**	**ITLIRSNQQL**	**ENDLNLMDIK**	**IGLLVK**NKIT
951	LQDVVSHSKK	LTKKNK**EQLS**	**DMMMINK**QKG	GLKALSKEKR	EKLEAYQHLF
1001	YLLQTNPTYL	AK**LIFQMPQN**	**KSTK**FMDSVI	FTLYNYASNQ	REEYLLLRLF
1051	QTALQEEIKS	KVDQIQEIVT	GNPTVIKMVV	SFNRGARGQN	ALR**QILAPVV**
1101	**KEIMDDKSLN**	**IK**TDPVDIYK	SWVNQMESQT	GEASK**LPYDV**	**TPEQALSHEE**
1151	**VKTRLDNSIR**	**NMRAVTDKFL**	**SAIVSSVDK**I	PYGMRFIAKV	LKDSLHEKFP
1201	DAGEDELLKI	IGNLLYYRYM	NPAIVAPDAF	DIIDLSAGGQ	LTTDQRR**NLG**
1251	**SIAKMLQHAA**	**SNK**MFLGDNA	HLSIINEYLS	QSYQKFR**RFF**	**QVACDVPELQ**
1301	**DK**FNVDEYSD	LVTLTKPVIY	ISIGEIINTH	TLLLDHQDAI	APEHNDPIHE
1351	LLDDLGEVPT	IESLIGESCG	NSNDPNKEAL	AK**TEVSLTLT**	**NKFDVPGDEN**
1401	**AEMDARTILL**	**NTK**RLIVDVI	R**FQPGETLTE**	**ILETPATNEQ**	**EAEHQR**AMQR
1451	RAIRDAKTPD	KMKK**SKPMKE**	**DNNLSLQEKK**	EKIQTGLKKL	TELGTVDPKN
1501	R**YQELINDIA**	**K**DIRNQRRYR	QRRKAELVK**L**	**QQTYSALNSK**	**ATFYGEQVDY**
1551	**YK**SYIKTCLD	NLASKGKVSK	KPREMKGKKS	KKISLKYTAA	R**LHEKGVLLE**
1601	**IEDLQANQFK**	NVIFEIGPTE	EVGDFEVKAK	FMGVQMETFM	LHYQDLLQLQ
1651	YEGVAVMKLF	DRAKVNVNLL	IFLLNKKFYG	K	

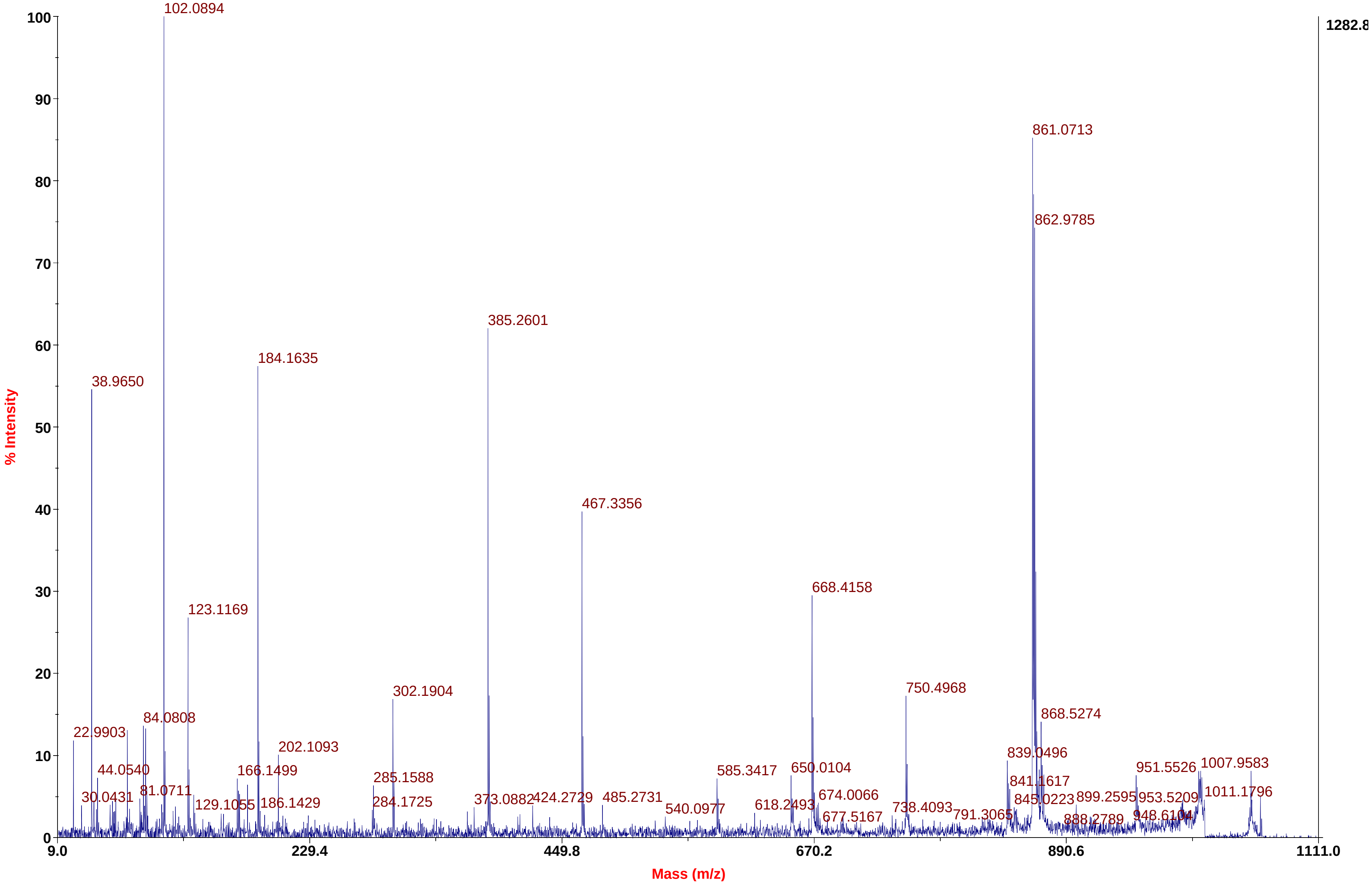
Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

Start – End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
50 – 58	1109.5443	1108.5370	1108.4706	60	0	R.LTAEEMDER.R	Oxidation (M)
50 – 59	1265.7042	1264.6969	1264.5717	99	1	R.LTAEEMDERR.R	Oxidation (M)
61 – 75	1868.0181	1867.0108	1866.8458	88	0	R.QNVAYEYLCHLEEAK.R	Carbamido
119 – 126	1081.5437	1080.5364	1080.5200	15	1	K.IYDREQTR.Y	Deamidated (NQ)
127 – 135	1092.5634	1091.5561	1091.5876	-29	1	R.YKATGLHFR.H	
168 – 185	2315.2419	2314.2346	2314.1424	40	1	K.NMPRCIYCIHALSLYLFK.L	2 Carb

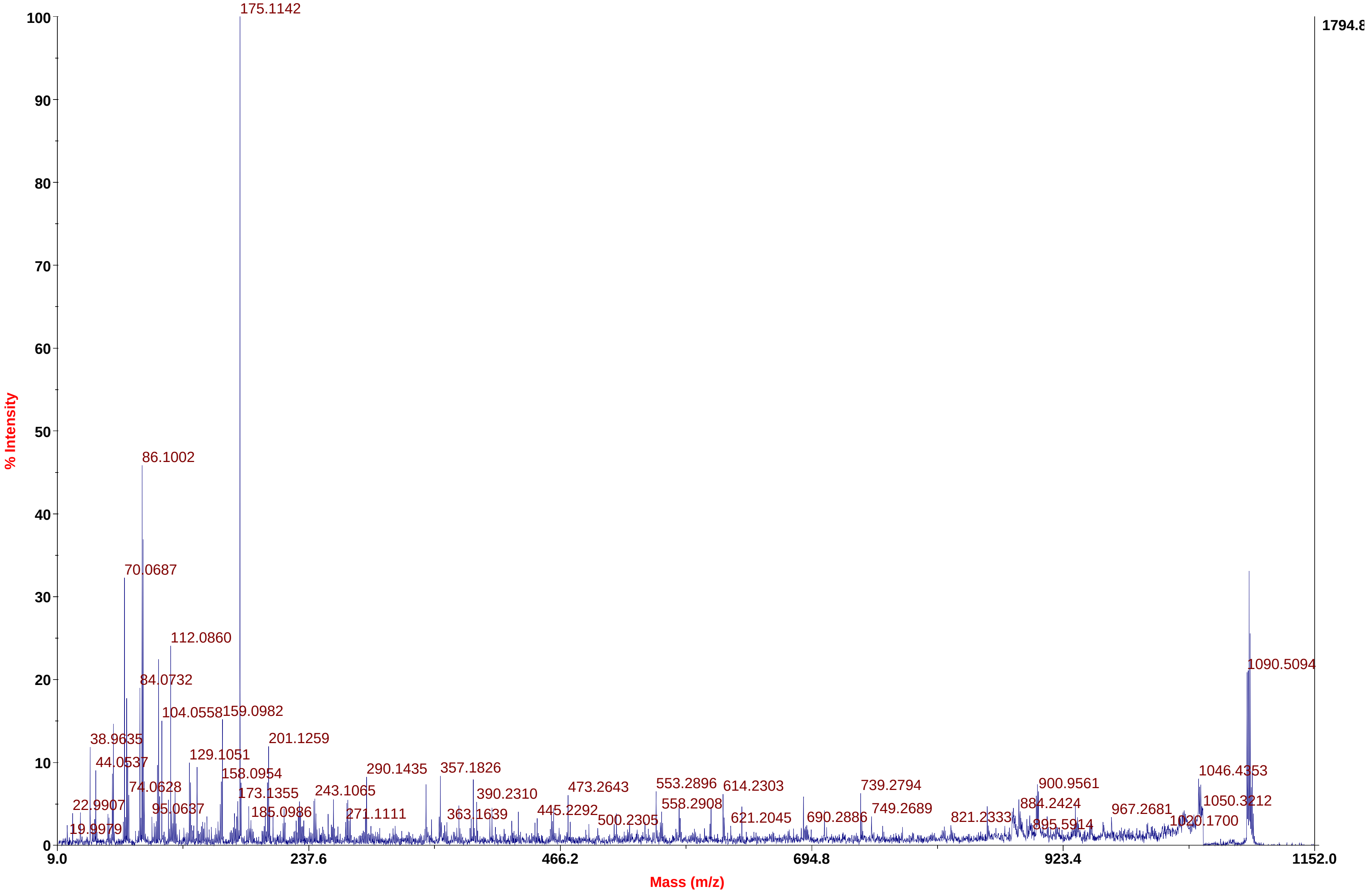
M24

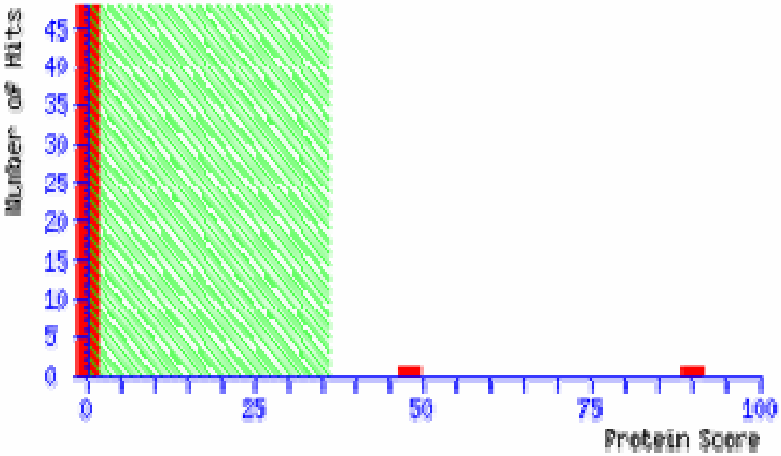
4700 MS/MS Precursor 1051.75 Spec #1 MC[BP = 102.1, 1283]

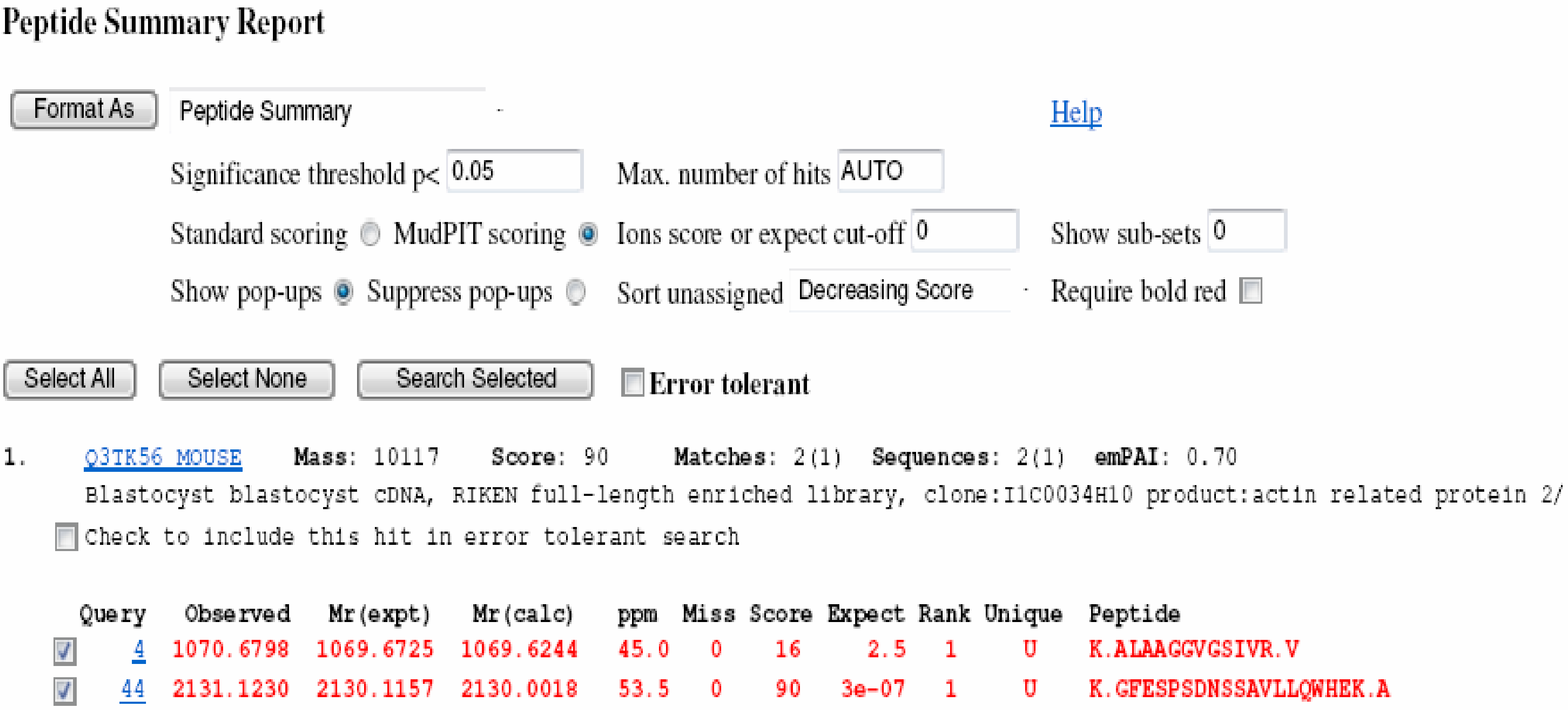


M24

4700 MS/MS Precursor 1090.58 Spec #1 MC[BP = 175.1, 1795]







Peptide Summary Report

Peptide Summary

Significance threshold p< 0.05 Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 Show sub-sets 0

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

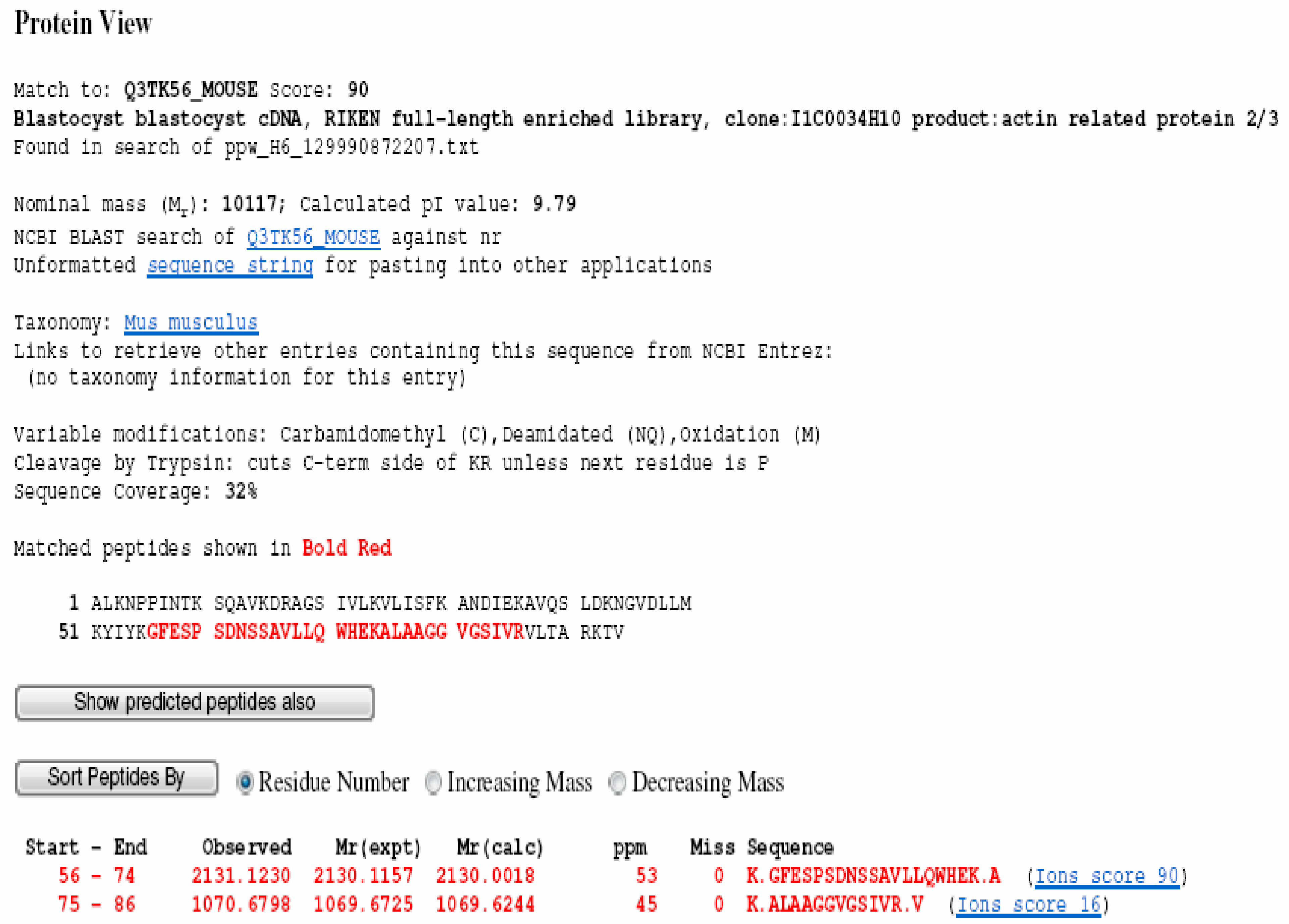
☐ **Error tolerant**

1. Q3TK56_MOUSE **Mass:** 10117 **Score:** 90 **Matches:** 2(1) **Sequences:** 2(1) **emPAI:** 0.70

Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0034H10 product:actin related protein 2/

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	4	1070.6798	1069.6725	1069.6244	45.0	0	16	2.5	1	U	K.ALAAGGVGSIVR.V
☑	44	2131.1230	2130.1157	2130.0018	53.5	0	90	3e-07	1	U	K.GFESPSDNSSAVLLQWHEK.A



Protein View

Match to: **Q3TK56_MOUSE** Score: **90**
Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0034H10 product:actin related protein 2/3
Found in search of ppw_H6_129990872207.txt

Nominal mass (M_r): **10117**; Calculated pI value: **9.79**
NCBI BLAST search of Q3TK56_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 32%

Matched peptides shown in **Bold Red**

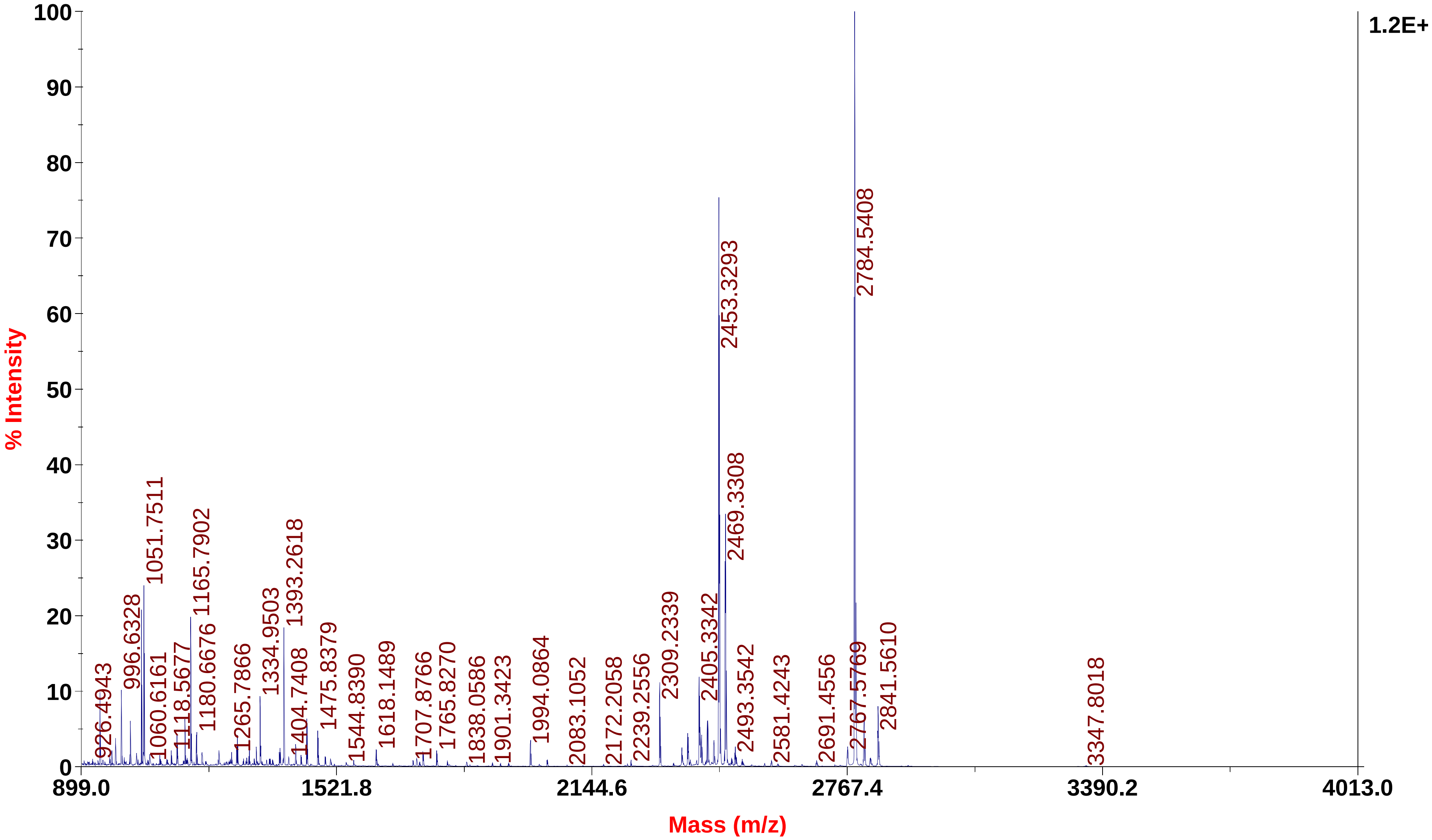
1 ALKNPPINTK SQAVKDRAGS IVLKVLISFK ANDIEKAVQS LDKNGVDLLM
51 KYIYK**GFESP SDNSSAVLLQ WHEKALAAGG VGSIVR**VLTA RKTV

● Residue Number ○ Increasing Mass ○ Decreasing Mass

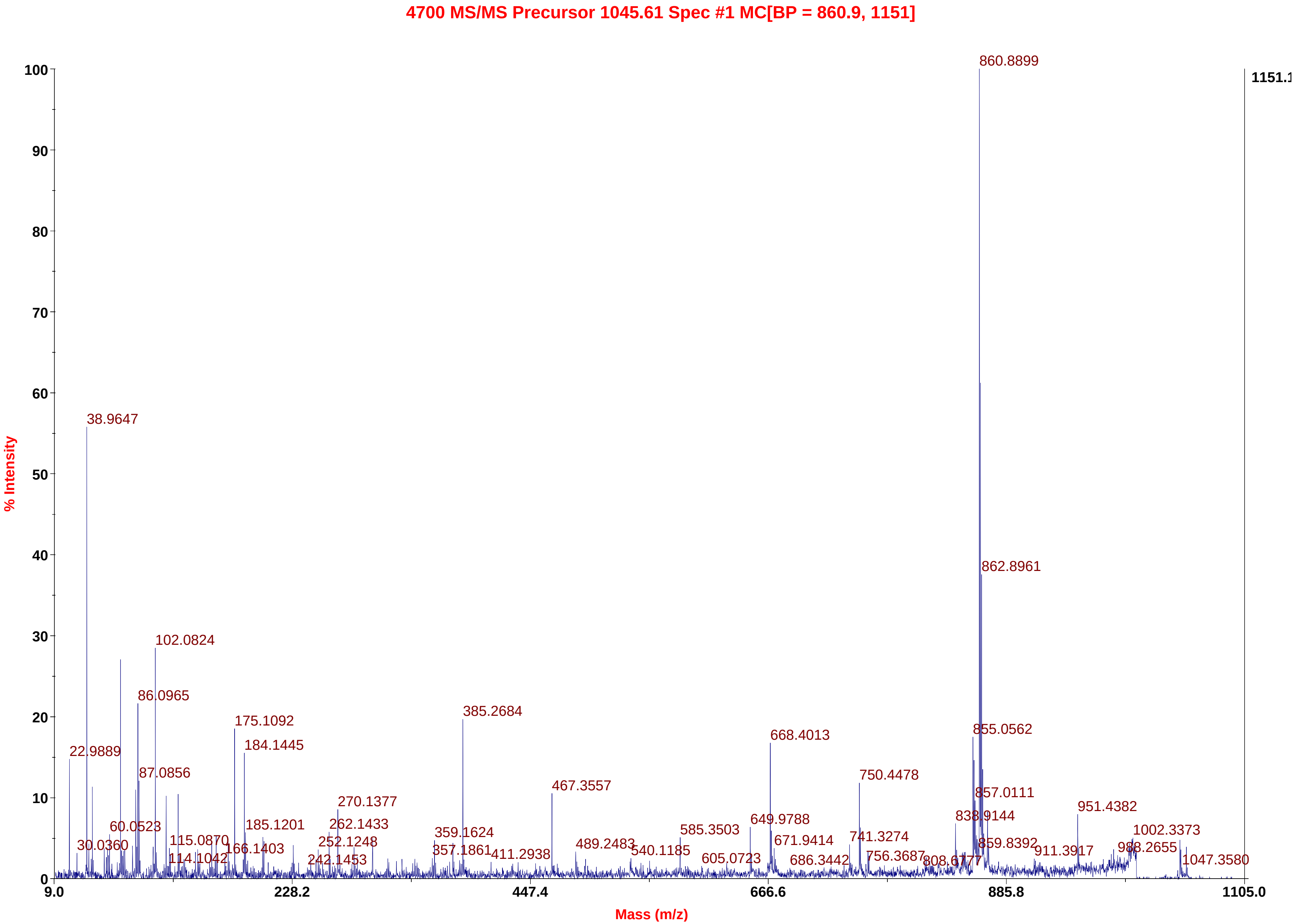
```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   56 - 74      2131.1230  2130.1157  2130.0018       53      0  K.GFESPSDNSSAVLLQWHEK.A   (Ions score 90)
   75 - 86      1070.6798  1069.6725  1069.6244       45      0  K.ALAAGGVGSIVR.V  (Ions score 16)
```

Sample M25

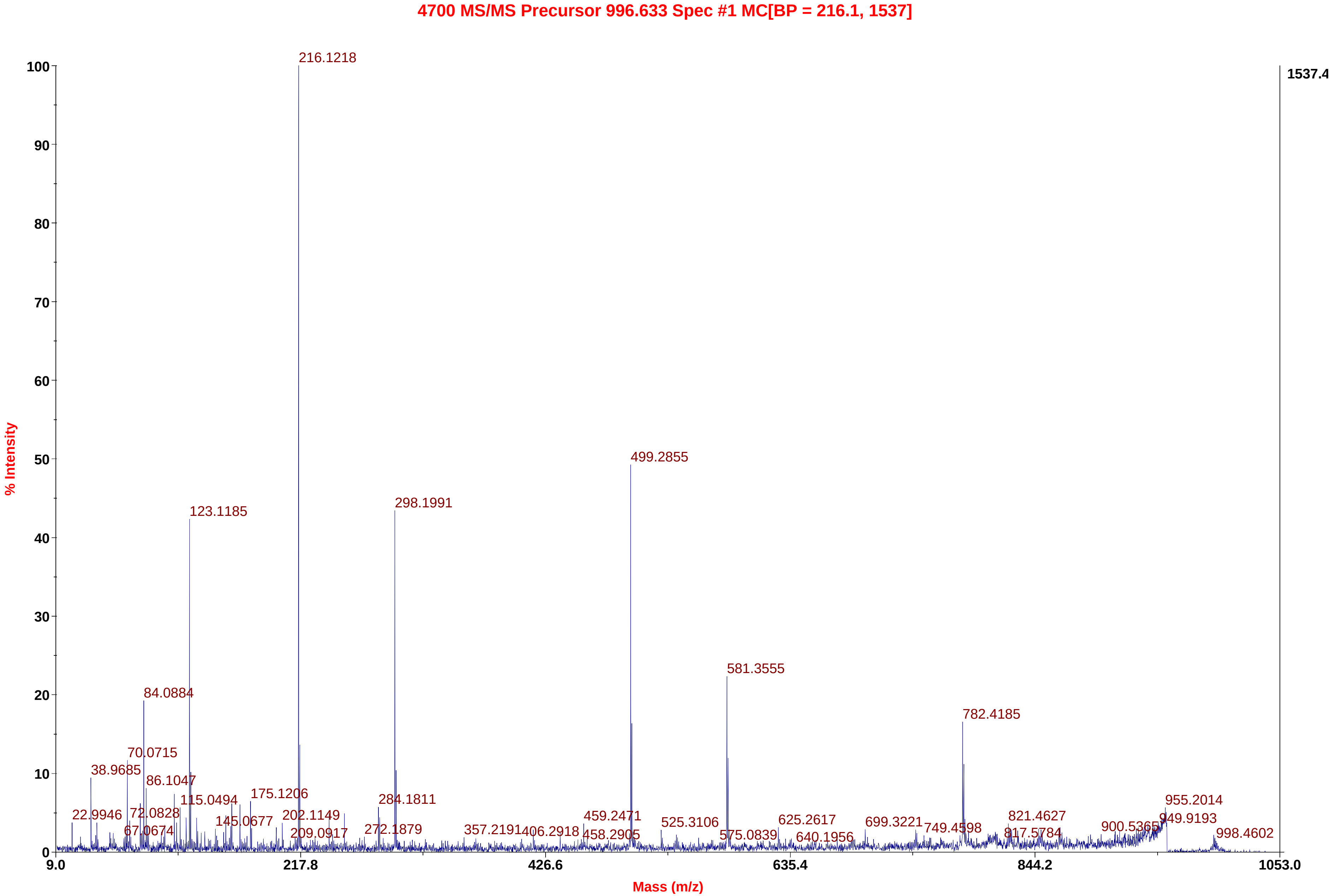
4700 Reflector Spec #1 MC=>NR(2.00)[BP = 2785.5, 12229]



M25

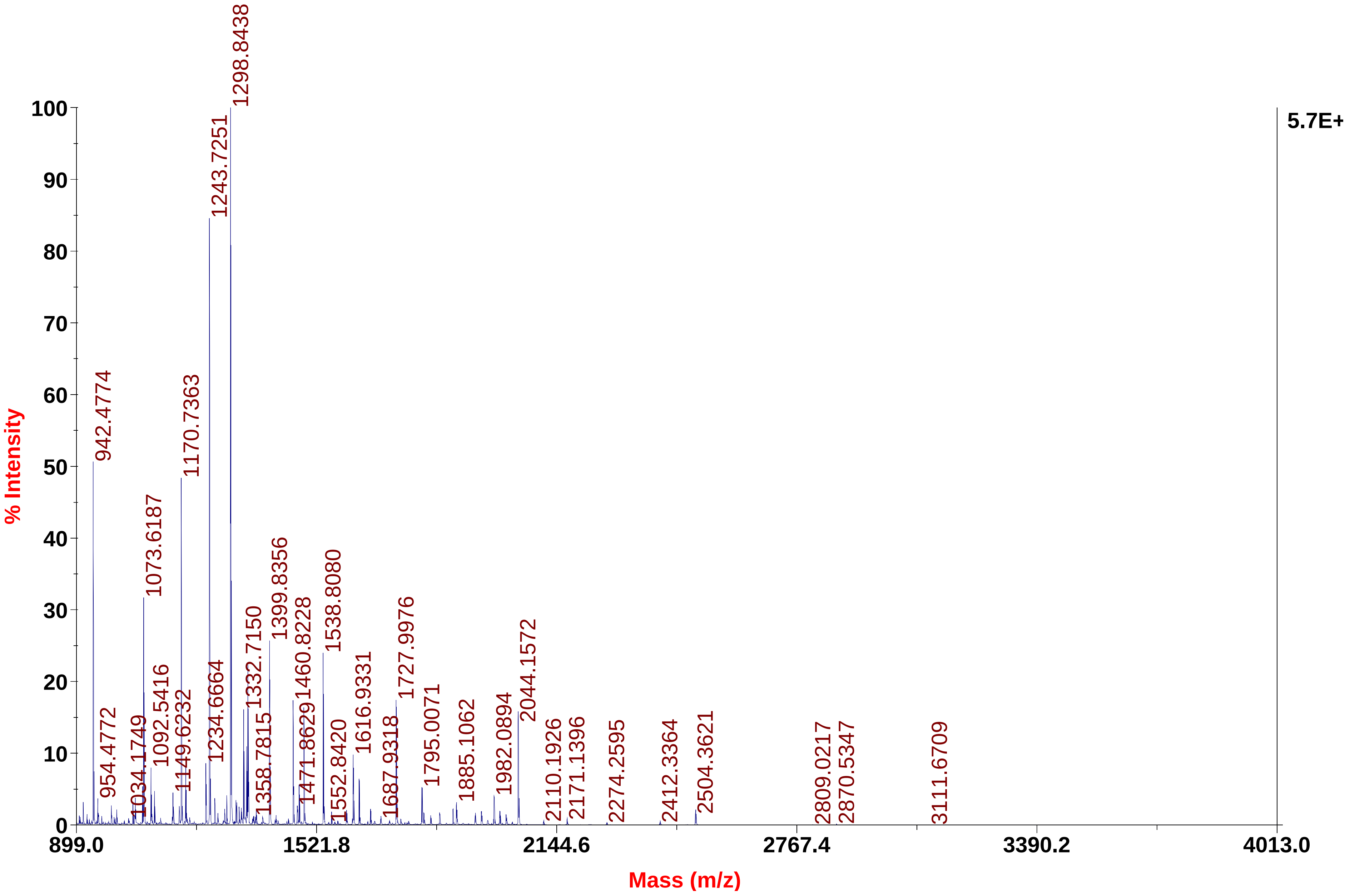

4700 MS/MS Precursor 1045.61 Spec #1 MC[BP = 860.9, 1151]
% Intensity
Mass (m/z)
0
10
20
30
40
50
60
70
80
90
100
9.0
228.2
447.4
666.6
885.8
1105.0
860.8899
1151.1
38.9647
862.8961
102.0824
86.0965
385.2684
175.1092
855.0562
668.4013
184.1445
22.9889
87.0856
750.4478
467.3557
857.0011
270.1377
951.4382
649.9788
838.9144
60.0523
185.1201
262.1433
585.3503
1002.3373
359.1624
741.3274
115.0870
252.1248
671.9414
30.0360
166.1403
489.2483
859.8392
988.2655
357.1861
540.1185
911.3917
411.2938
756.3687
114.1042
605.0723
242.1453
686.3442
808.6777
1047.3580

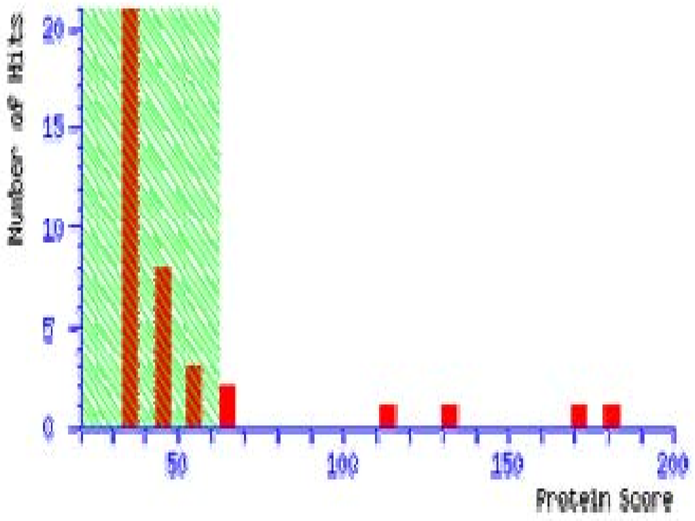
M25


4700 MS/MS Precursor 996.633 Spec #1 MC[BP = 216.1, 1537]
% Intensity
Mass (m/z)
1537.4
100
90
80
70
60
50
40
30
20
10
0
9.0
217.8
426.6
635.4
844.2
1053.0
216.1218
499.2855
123.1185
298.1991
581.3555
84.0884
782.4185
70.0715
38.9685
86.1047
175.1206
115.0494
284.1811
955.2014
22.9946
72.0828
202.1149
459.2471
821.4627
145.0677
525.3106
625.2617
949.9193
699.3221
749.4598
900.5365
67.0674
272.1879
357.2191
406.2918
209.0917
458.2905
575.0839
640.1956
817.5784
998.4602

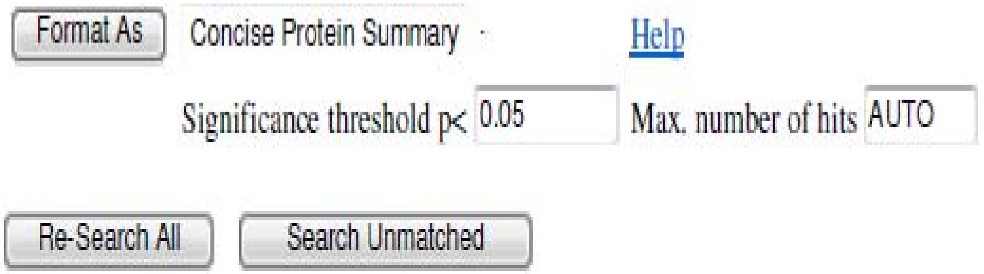
Sample M26

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1298.8, 57153]



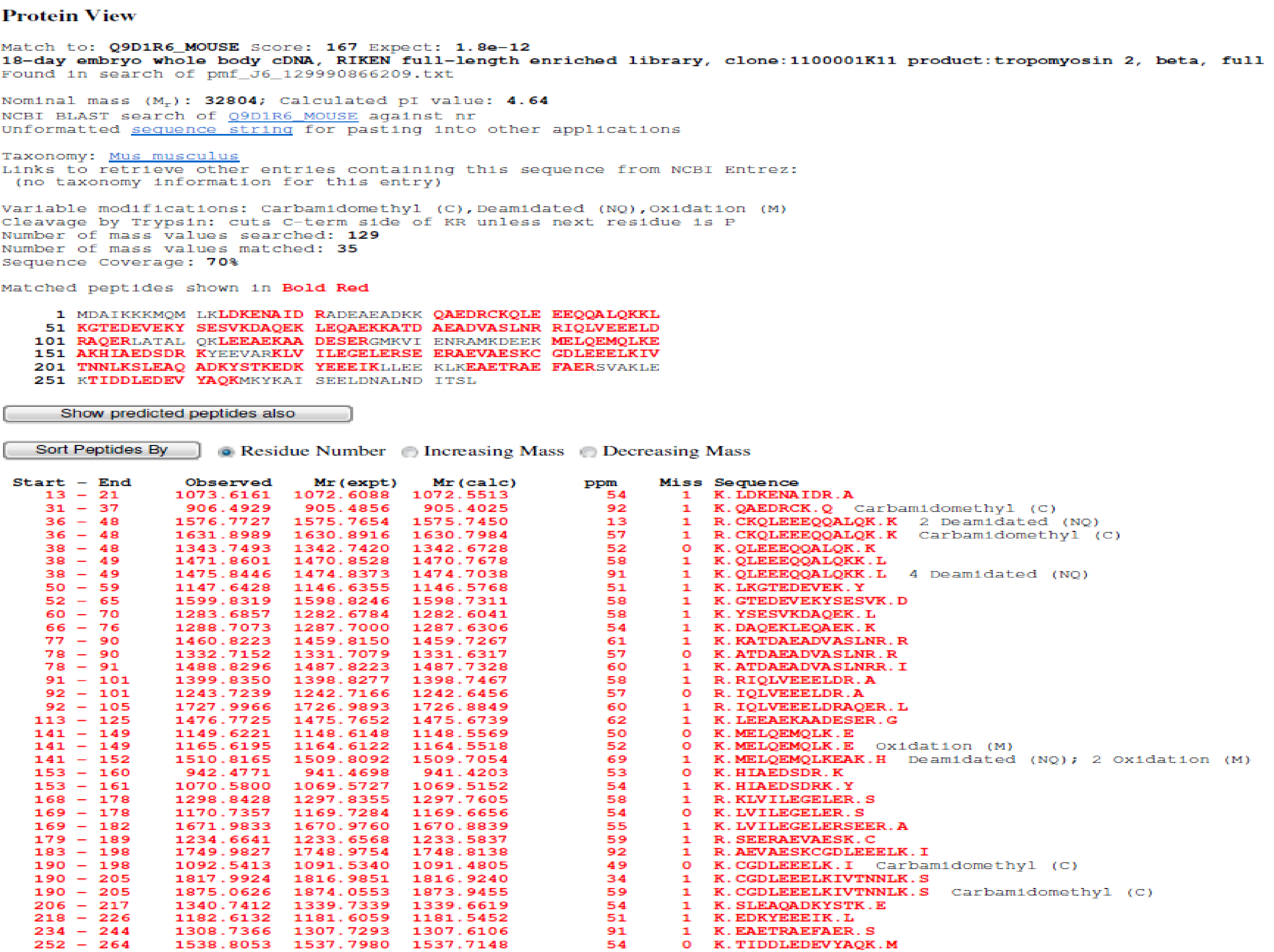


Concise Protein Summary Report



Significance threshold p< 0.05 Max. number of hits AUTO

```
1.    Mixture 1    Total score: 181    Expect: 7.3e-14  Matches: 45
      Components (only one family member shown for each component):
      Q9D1R6_MOUSE    Mass: 32804    Score: 167    Expect: 1.8e-12  Matches: 35
      18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1100001K11 product:tropomyosin 2, beta, full insert sequ
      Q9CY74_MOUSE    Mass: 17645    Score: 53    Expect: 0.43  Matches: 11
      8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730592G18 product:RIKEN cDNA 5730592G18.- Mus musculus
```



Protein View

```
Match to: Q9D1R6_MOUSE Score: 167 Expect: 1.8e-12
18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1100001K11 product:tropomyosin 2, beta, full
Found in search of pmf_J6_129990866209.txt

Nominal mass (Mr): 32804; Calculated pI value: 4.64
NCBI BLAST search of Q9D1R6_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)

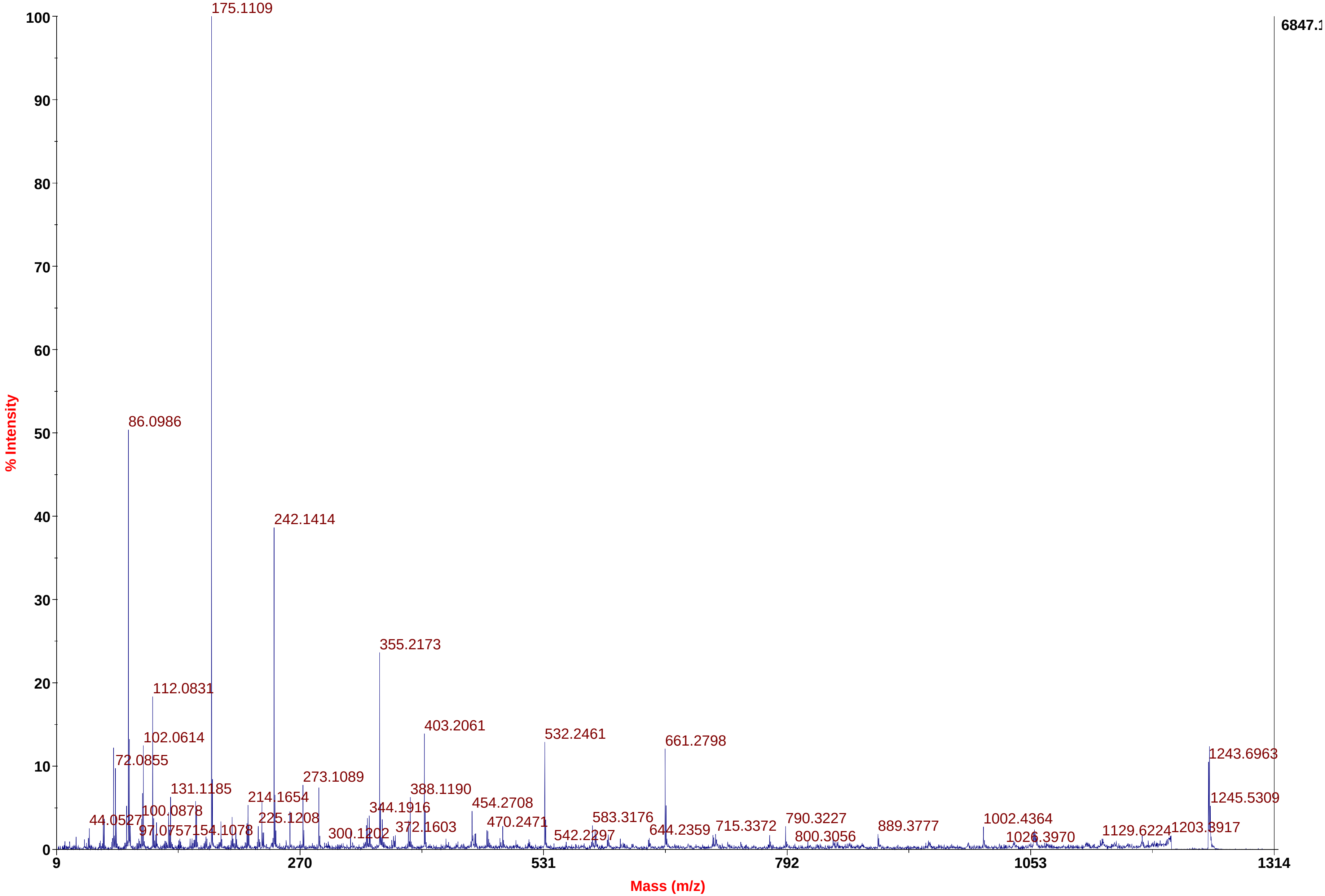
Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 129
Number of mass values matched: 35
Sequence Coverage: 70%

Matched peptides shown in Bold Red

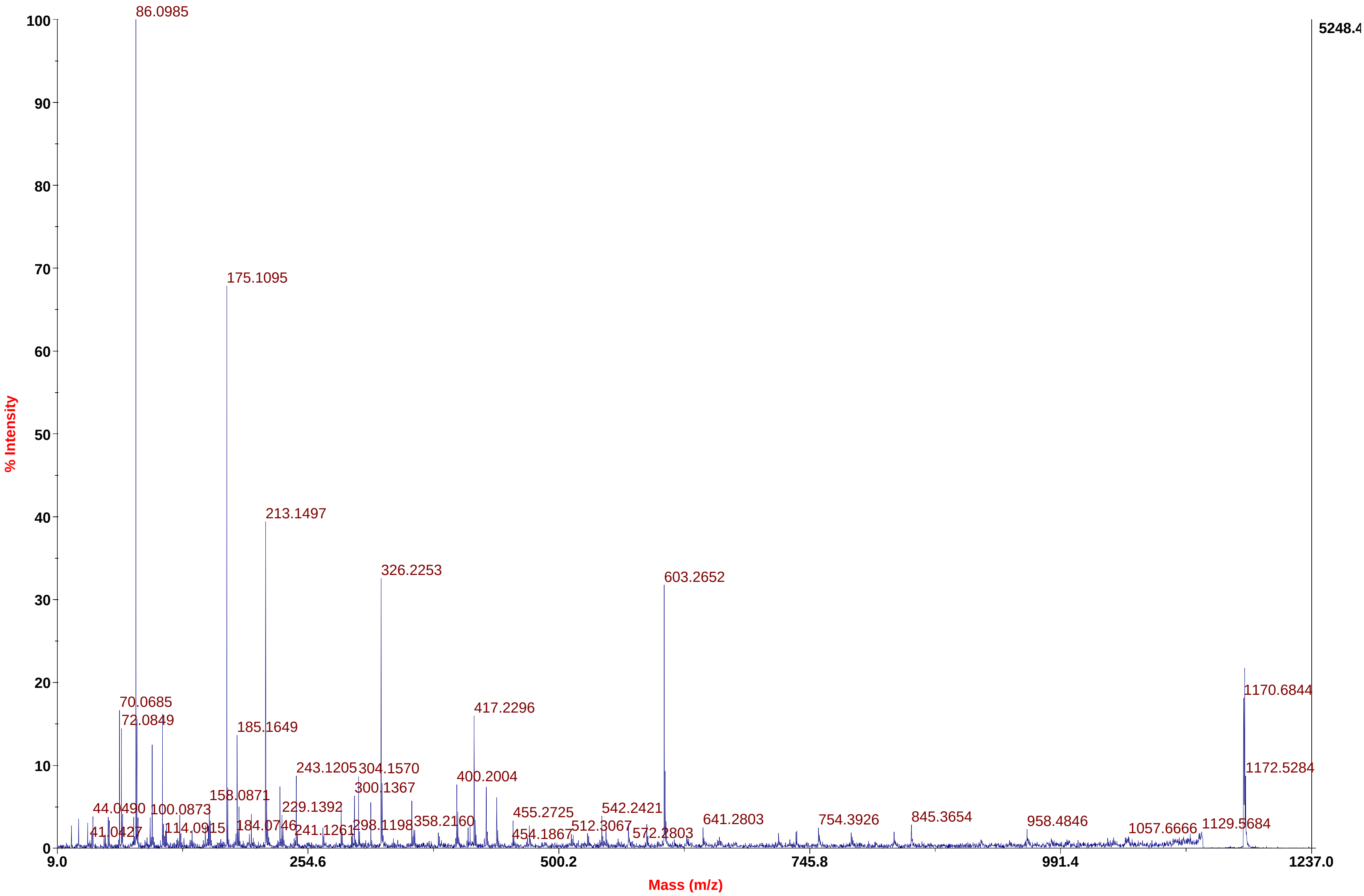
     1 MDAIKKKMQM LKLDKENAID RADEAEADKK QAEDRCKQLE EEQQALQKKL
    51 KGTEDEVEKY SESVKDAQEK LEQAEKKATD AEADVASLNR RIQLVEEELD
   101 RAQERLATAL QKLEEAEKAA DESERGMKVI ENRAMKDEEK MELQEMQLKE
   151 AKHIAEDSDR KYEEVARKLV ILEGELERSE ERAEVAESKC GDLEEELKIV
   201 TNNLKSLEAQ ADKYSTKEDK YEEEIKLLEE KLKEAETRAE FAERSVAKLE
   251 KTIDDLEDEV YAQKMKYKAI SEELDNALND ITSL
```

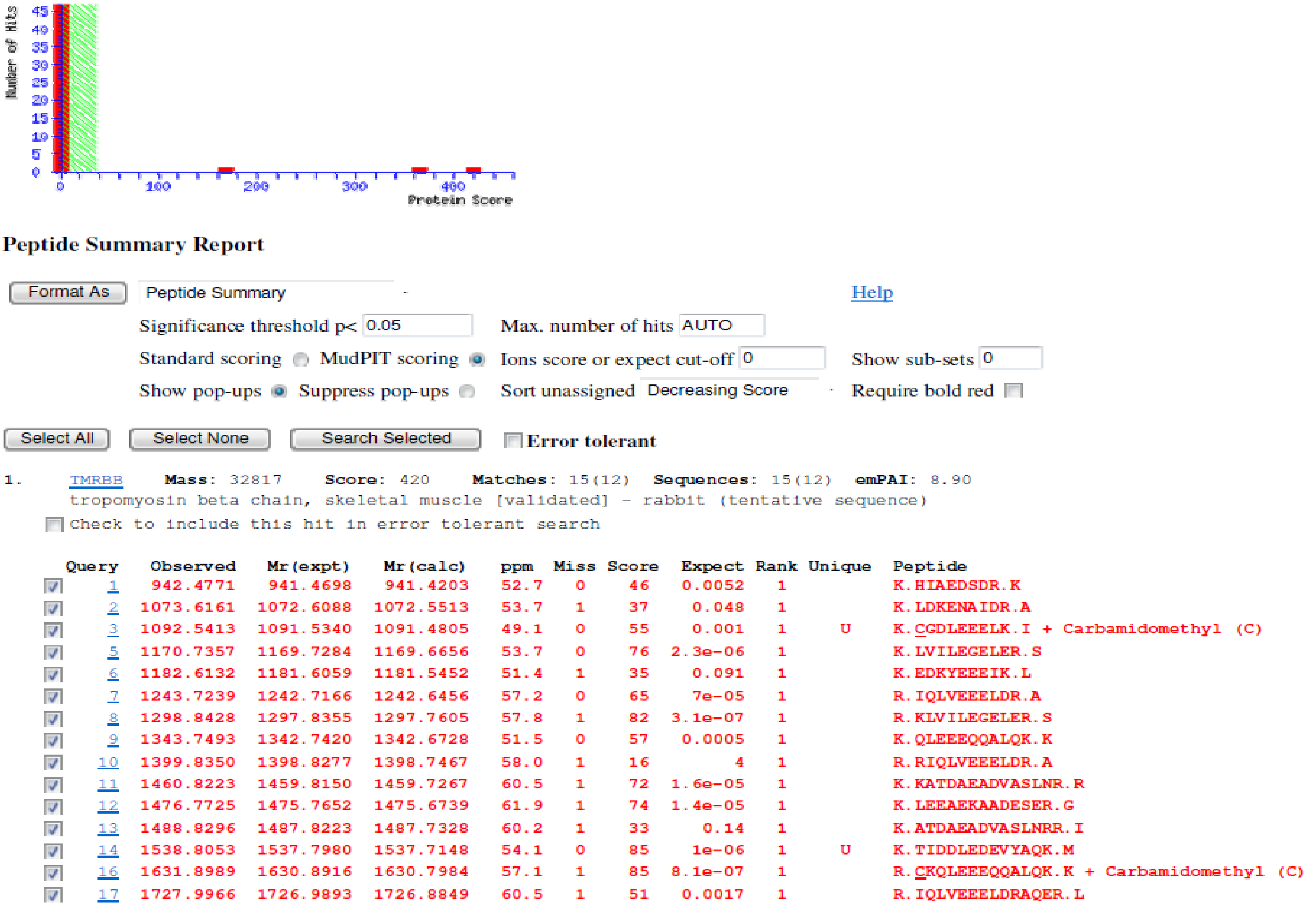
```
Start - End    Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
   13 - 21    1073.6161  1072.6088  1072.5513      54    1  K.LDKENAIDR.A
   31 - 37     906.4929   905.4856   905.4025      92    1  K.QAEDRCK.Q  Carbamidomethyl (C)
   36 - 48    1576.7727  1575.7654  1575.7450      13    1  R.CKQLEEEQQALQK.K  2 Deamidated (NQ)
   36 - 48    1631.8989  1630.8916  1630.7984      57    1  R.CKQLEEEQQALQK.K  Carbamidomethyl (C)
   38 - 48    1343.7493  1342.7420  1342.6728      52    0  K.QLEEEQQALQK.K
   38 - 49    1471.8601  1470.8528  1470.7678      58    1  K.QLEEEQQALQKK.L
   38 - 49    1475.8446  1474.8373  1474.7038      91    1  K.QLEEEQQALQKK.L  4 Deamidated (NQ)
   50 - 59    1147.6428  1146.6355  1146.5768      51    1  K.LKGTEDEVEK.Y
   52 - 65    1599.8319  1598.8246  1598.7311      58    1  K.GTEDEVEKYSESVK.D
   60 - 70    1283.6857  1282.6784  1282.6041      58    1  K.YSESVKDAQEK.L
   66 - 76    1288.7073  1287.7000  1287.6306      54    1  K.DAQEKLEQAEK.K
   77 - 90    1460.8223  1459.8150  1459.7267      61    1  K.KATDAEADVASLNR.R
   78 - 90    1332.7152  1331.7079  1331.6317      57    0  K.ATDAEADVASLNR.R
   78 - 91    1488.8296  1487.8223  1487.7328      60    1  K.ATDAEADVASLNRR.I
   91 - 101   1399.8350  1398.8277  1398.7467      58    1  R.RIQLVEEELDR.A
   92 - 101   1243.7239  1242.7166  1242.6456      57    0  R.IQLVEEELDR.A
   92 - 105   1727.9966  1726.9893  1726.8849      60    1  R.IQLVEEELDRAQER.L
  113 - 125   1476.7725  1475.7652  1475.6739      62    1  K.LEEAEKAADESER.G
  141 - 149   1149.6221  1148.6148  1148.5569      50    0  K.MELQEMQLK.E
  141 - 149   1165.6195  1164.6122  1164.5518      52    0  K.MELQEMQLK.E  Oxidation (M)
  141 - 152   1510.8165  1509.8092  1509.7054      69    1  K.MELQEMQLKEAK.H  Deamidated (NQ); 2 Oxidation (M)
  153 - 160    942.4771   941.4698   941.4203      53    0  K.HIAEDSDR.K
  153 - 161   1070.5800  1069.5727  1069.5152      54    1  K.HIAEDSDRK.Y
  168 - 178   1298.8428  1297.8355  1297.7605      58    1  R.KLVILEGELER.S
  169 - 178   1170.7357  1169.7284  1169.6656      54    0  K.LVILEGELER.S
  169 - 182   1671.9833  1670.9760  1670.8839      55    1  K.LVILEGELERSEER.A
  179 - 189   1234.6641  1233.6568  1233.5837      59    1  R.SEERAEVAESK.C
  183 - 198   1749.9827  1748.9754  1748.8138      92    1  R.AEVAESKCGDLEEELK.I
  190 - 198   1092.5413  1091.5340  1091.4805      49    0  K.CGDLEEELK.I  Carbamidomethyl (C)
  190 - 205   1817.9924  1816.9851  1816.9240      34    1  K.CGDLEEELKIVTNNLK.S
  190 - 205   1875.0626  1874.0553  1873.9455      59    1  K.CGDLEEELKIVTNNLK.S  Carbamidomethyl (C)
  206 - 217   1340.7412  1339.7339  1339.6619      54    1  K.SLEAQADKYSTK.E
  218 - 226   1182.6132  1181.6059  1181.5452      51    1  K.EDKYEEEIK.L
  234 - 244   1308.7366  1307.7293  1307.6106      91    1  K.EAETRAEFAER.S
  252 - 264   1538.8053  1537.7980  1537.7148      54    0  K.TIDDLEDEVYAQK.M
```

4700 MS/MS Precursor 1243.72 Spec #1 MC[BP = 175.1, 6847]



4700 MS/MS Precursor 1170.74 Spec #1 MC[BP = 86.1, 5248]





Peptide Summary Report

Format As: Peptide Summary

Significance threshold p< 0.05 Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 Show sub-sets 0

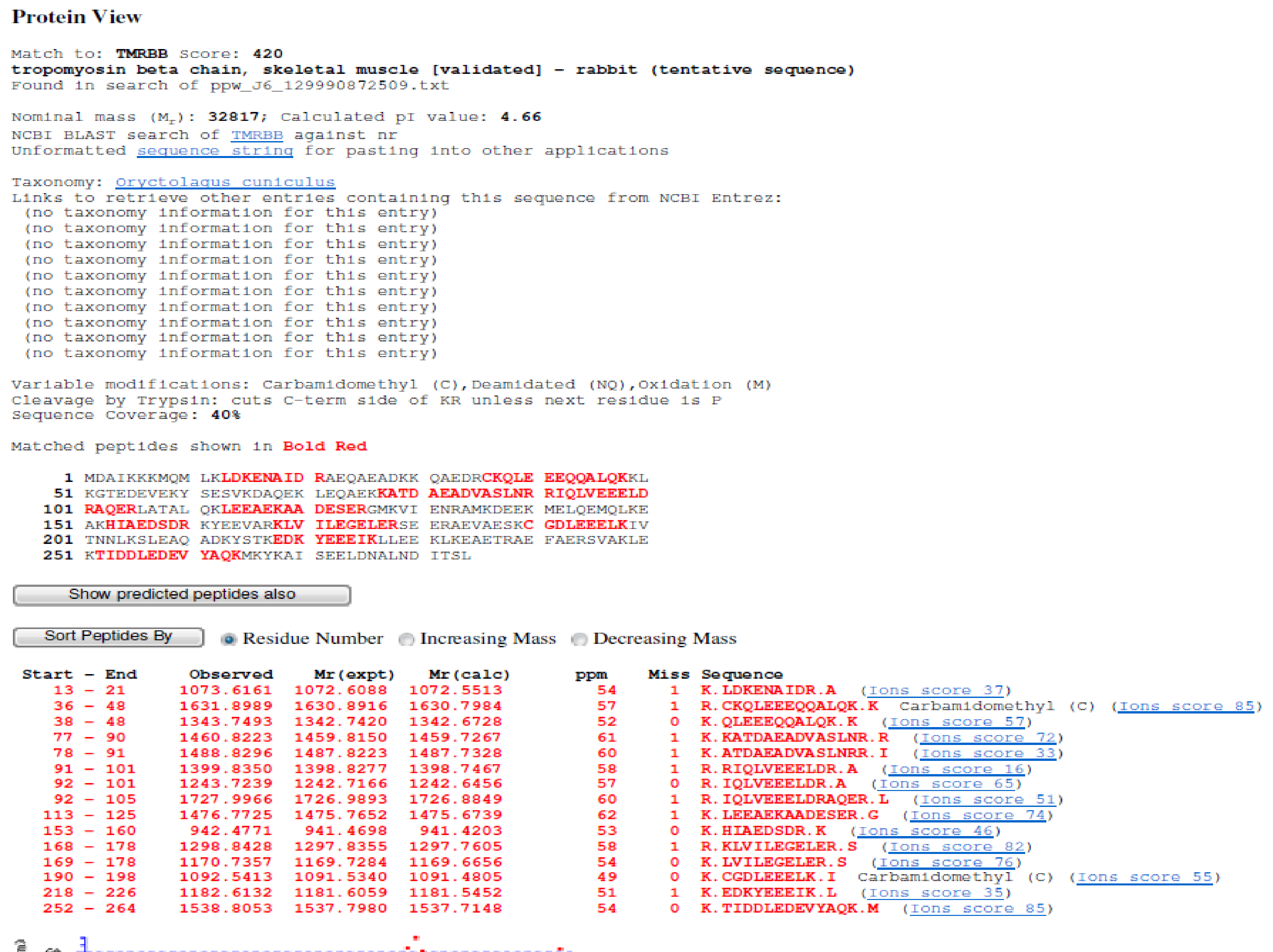
Show pop-ups ● Suppress pop-ups ○ Sort unassigned Decreasing Score Require bold red ☐

☐ **Error tolerant**

1. TMRBB **Mass:** 32817 **Score:** 420 **Matches:** 15(12) **Sequences:** 15(12) **emPAI:** 8.90
tropomyosin beta chain, skeletal muscle [validated] - rabbit (tentative sequence)

☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	942.4771	941.4698	941.4203	52.7	0	46	0.0052	1		K.HIAEDSDR.K
☑	2	1073.6161	1072.6088	1072.5513	53.7	1	37	0.048	1		K.LDKENAIDR.A
☑	3	1092.5413	1091.5340	1091.4805	49.1	0	55	0.001	1	U	K.CGDLEEELK.I + Carbamidomethyl (C)
☑	5	1170.7357	1169.7284	1169.6656	53.7	0	76	2.3e-06	1		K.LVILEGELER.S
☑	6	1182.6132	1181.6059	1181.5452	51.4	1	35	0.091	1		K.EDKYEEEIK.L
☑	7	1243.7239	1242.7166	1242.6456	57.2	0	65	7e-05	1		R.IQLVEEELDR.A
☑	8	1298.8428	1297.8355	1297.7605	57.8	1	82	3.1e-07	1		R.KLVILEGELER.S
☑	9	1343.7493	1342.7420	1342.6728	51.5	0	57	0.0005	1		K.QLEEEQQALQK.K
☑	10	1399.8350	1398.8277	1398.7467	58.0	1	16	4	1		R.RIQLVEEELDR.A
☑	11	1460.8223	1459.8150	1459.7267	60.5	1	72	1.6e-05	1		K.KATDAEADVASLNR.R
☑	12	1476.7725	1475.7652	1475.6739	61.9	1	74	1.4e-05	1		K.LEEAEKAADESER.G
☑	13	1488.8296	1487.8223	1487.7328	60.2	1	33	0.14	1		K.ATDAEADVASLNRR.I
☑	14	1538.8053	1537.7980	1537.7148	54.1	0	85	1e-06	1	U	K.TIDDLEDEVYAQK.M
☑	16	1631.8989	1630.8916	1630.7984	57.1	1	85	8.1e-07	1		R.CKQLEEEQQALQK.K + Carbamidomethyl (C)
☑	17	1727.9966	1726.9893	1726.8849	60.5	1	51	0.0017	1		R.IQLVEEELDRAQER.L



Protein View

Match to: **TMRBB** Score: **420**
tropomyosin beta chain, skeletal muscle [validated] - rabbit (tentative sequence)
Found in search of ppw_J6_129990872509.txt

Nominal mass (M_r): **32817**; Calculated pI value: **4.66**
NCBI BLAST search of TMRBB against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryctolagus cuniculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)
(no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **40%**

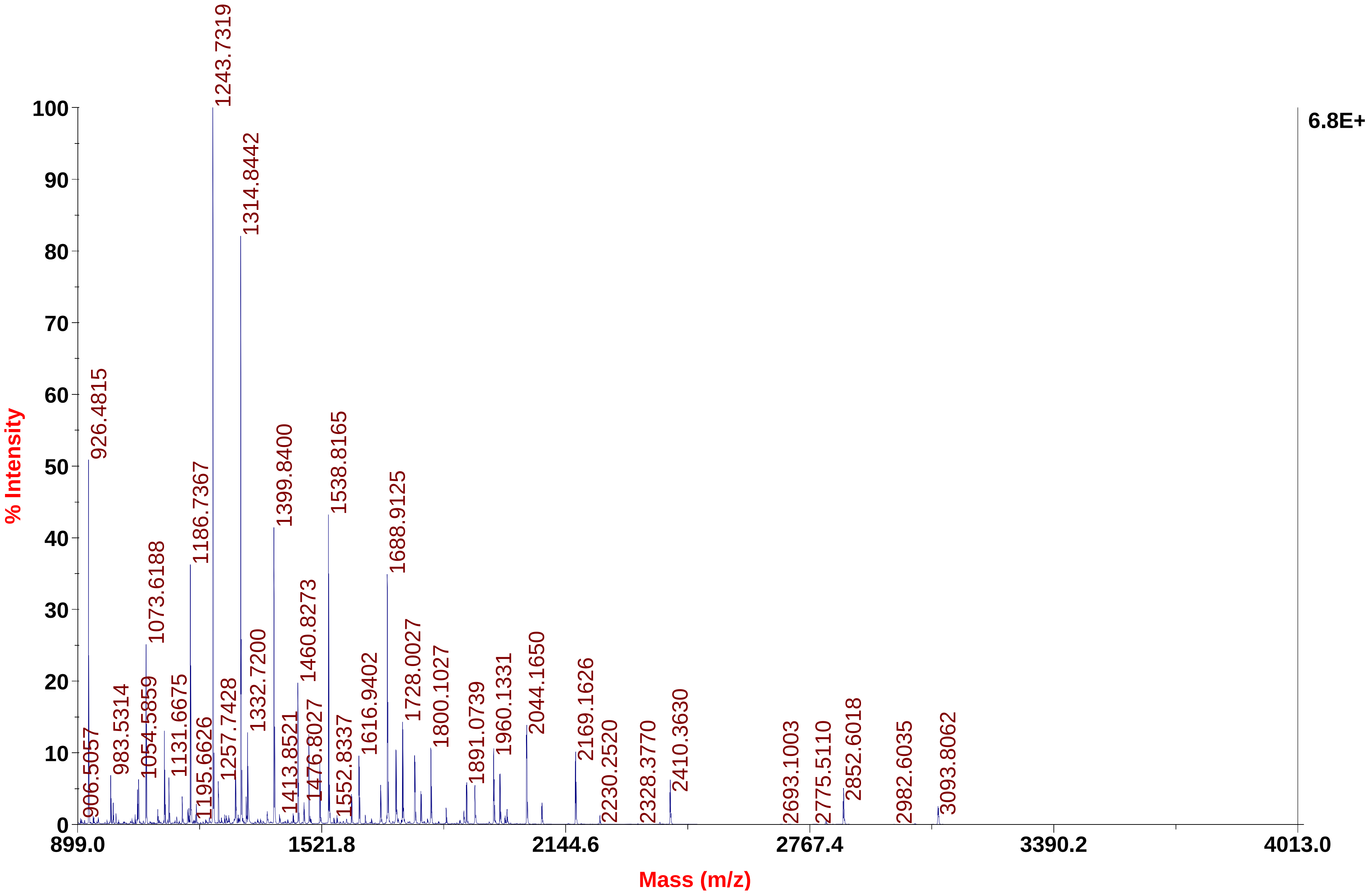
Matched peptides shown in **Bold Red**

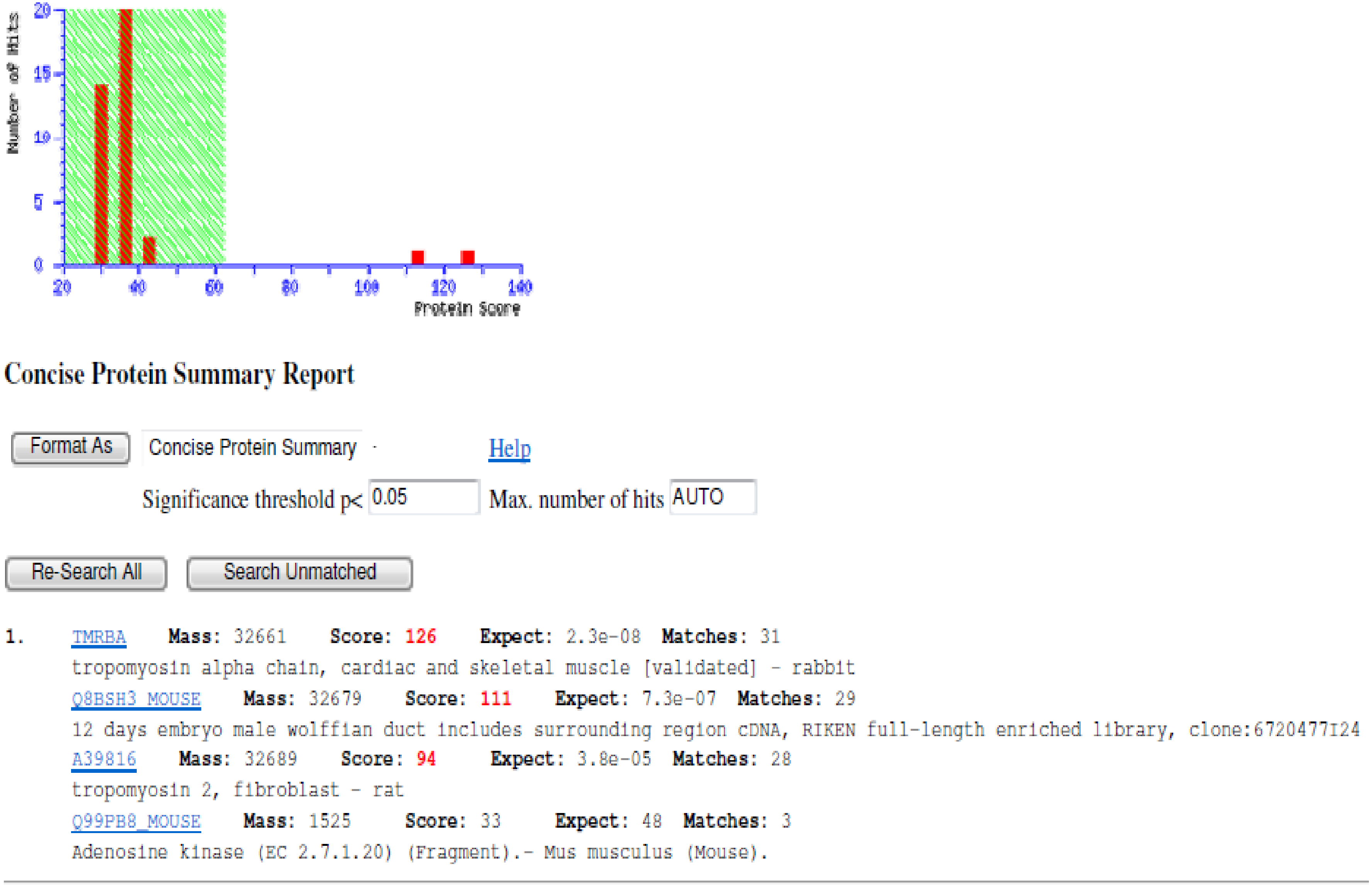
```
  1 MDAIKKKMQM LKLDKENAID RAEQAEADKK QAEDRCKQLE EEQQALQKKL
 51 KGTEDEVEKY SESVKDAQEK LEQAEKKATD AEADVASLNR RIQLVEEELD
101 RAQERLATAL QKLEEAEKAA DESERGMKVI ENRAMKDEEK MELQEMQLKE
151 AKHIAEDSDR KYEEVARKLV ILEGELERSE ERAEVAESKC GDLEEELKIV
201 TNNLKSLEAQ ADKYSTKEDK YEEEIKLLEE KLKEAETRAE FAERSVAKLE
251 KTIDDLEDEV YAQKMKYKAI SEELDNALND ITSL
```

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   13 - 21     1073.6161  1072.6088  1072.5513       54      1  K.LDKENAIDR.A  (Ions score 37)
   36 - 48     1631.8989  1630.8916  1630.7984       57      1  R.CKQLEEEQQALQK.K  Carbamidomethyl (C)  (Ions score 85)
   38 - 48     1343.7493  1342.7420  1342.6728       52      0  K.QLEEEQQALQK.K  (Ions score 57)
   77 - 90     1460.8223  1459.8150  1459.7267       61      1  K.KATDAEADVASLNR.R  (Ions score 72)
   78 - 91     1488.8296  1487.8223  1487.7328       60      1  K.ATDAEADVASLNRR.I  (Ions score 33)
   91 - 101    1399.8350  1398.8277  1398.7467       58      1  R.RIQLVEEELDR.A  (Ions score 16)
   92 - 101    1243.7239  1242.7166  1242.6456       57      0  R.IQLVEEELDR.A  (Ions score 65)
   92 - 105    1727.9966  1726.9893  1726.8849       60      1  R.IQLVEEELDRAQER.L  (Ions score 51)
  113 - 125    1476.7725  1475.7652  1475.6739       62      1  K.LEEAEKAADESER.G  (Ions score 74)
  153 - 160     942.4771   941.4698   941.4203       53      0  K.HIAEDSDR.K  (Ions score 46)
  168 - 178    1298.8428  1297.8355  1297.7605       58      1  R.KLVILEGELER.S  (Ions score 82)
  169 - 178    1170.7357  1169.7284  1169.6656       54      0  K.LVILEGELER.S  (Ions score 76)
  190 - 198    1092.5413  1091.5340  1091.4805       49      0  K.CGDLEEELK.I  Carbamidomethyl (C)  (Ions score 55)
  218 - 226    1182.6132  1181.6059  1181.5452       51      1  K.EDKYEEEIK.L  (Ions score 35)
  252 - 264    1538.8053  1537.7980  1537.7148       54      0  K.TIDDLEDEVYAQK.M  (Ions score 85)
```

Sample M27

4700 Reflector Spec #1 MC=>NR(2.00)[BP = 1243.7, 68319]

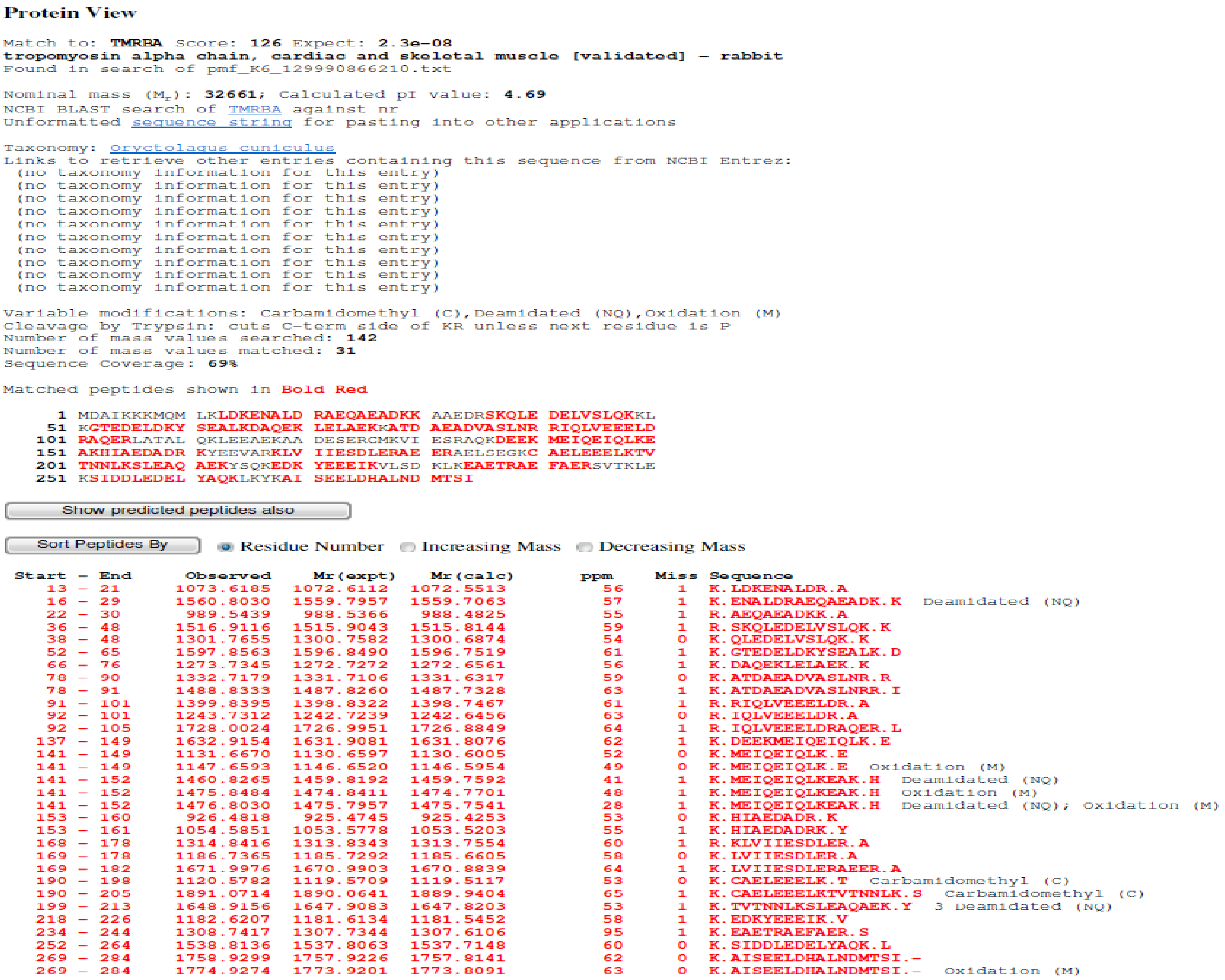




Concise Protein Summary Report

Significance threshold p< 0.05 Max. number of hits AUTO

```
1.   TMRBA       Mass: 32661     Score: 126     Expect: 2.3e-08  Matches: 31
     tropomyosin alpha chain, cardiac and skeletal muscle [validated] - rabbit
     Q8BSH3_MOUSE      Mass: 32679     Score: 111     Expect: 7.3e-07  Matches: 29
     12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720477I24
     A39816      Mass: 32689     Score: 94      Expect: 3.8e-05  Matches: 28
     tropomyosin 2, fibroblast - rat
     Q99PB8_MOUSE      Mass: 1525      Score: 33      Expect: 48   Matches: 3
     Adenosine kinase (EC 2.7.1.20) (Fragment).- Mus musculus (Mouse).
```



Protein View

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Match to: TMRBA Score: 126 Expect: 2.3e-08
tropomyosin alpha chain, cardiac and skeletal muscle [validated] - rabbit
Found in search of pmf_K6_129990866210.txt

Nominal mass (Mr): 32661; Calculated pI value: 4.69
NCBI BLAST search of TMRBA against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryctolagus cuniculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
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 (no taxonomy information for this entry)
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Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 142
Number of mass values matched: 31
Sequence Coverage: 69%

Matched peptides shown in Bold Red

     1 MDAIKKKMQM LKLDKENALD RAEQAEADKK AAEDRSKQLE DELVSLQKKL
    51 KGTEDELDKY SEALKDAQEK LELAEKKATD AEADVASLNR RIQLVEEELD
   101 RAQERLATAL QKLEEAEKAA DESERGMKVI ESRAQKDEEK MEIQEIQLKE
   151 AKHIAEDADR KYEEVARKLV IIESDLERAE ERAELSEGKC AELEEELKTV
   201 TNNLKSLEAQ AEKYSQKEDK YEEEIKVLSD KLKEAETRAE FAERSVTKLE
   251 KSIDDLEDEL YAQKLKYKAI SEELDHALND MTSI
```

```
 Start - End     Observed     Mr(expt)     Mr(calc)       ppm     Miss  Sequence
   13 - 21     1073.6185    1072.6112    1072.5513        56      1   K.LDKENALDR.A
   16 - 29     1560.8030    1559.7957    1559.7063        57      1   K.ENALDRAEQAEADK.K  Deamidated (NQ)
   22 - 30      989.5439     988.5366     988.4825        55      1   R.AEQAEADKK.A
   36 - 48     1516.9116    1515.9043    1515.8144        59      1   R.SKQLEDELVSLQK.K
   38 - 48     1301.7655    1300.7582    1300.6874        54      0   K.QLEDELVSLQK.K
   52 - 65     1597.8563    1596.8490    1596.7519        61      1   K.GTEDELDKYSEALK.D
   66 - 76     1273.7345    1272.7272    1272.6561        56      1   K.DAQEKLELAEK.K
   78 - 90     1332.7179    1331.7106    1331.6317        59      0   K.ATDAEADVASLNR.R
   78 - 91     1488.8333    1487.8260    1487.7328        63      1   K.ATDAEADVASLNRR.I
   91 - 101    1399.8395    1398.8322    1398.7467        61      1   R.RIQLVEEELDR.A
   92 - 101    1243.7312    1242.7239    1242.6456        63      0   R.IQLVEEELDR.A
   92 - 105    1728.0024    1726.9951    1726.8849        64      1   R.IQLVEEELDRAQER.L
  137 - 149    1632.9154    1631.9081    1631.8076        62      1   K.DEEKMEIQEIQLK.E
  141 - 149    1131.6670    1130.6597    1130.6005        52      0   K.MEIQEIQLK.E
  141 - 149    1147.6593    1146.6520    1146.5954        49      0   K.MEIQEIQLK.E  Oxidation (M)
  141 - 152    1460.8265    1459.8192    1459.7592        41      1   K.MEIQEIQLKEAK.H  Deamidated (NQ)
  141 - 152    1475.8484    1474.8411    1474.7701        48      1   K.MEIQEIQLKEAK.H  Oxidation (M)
  141 - 152    1476.8030    1475.7957    1475.7541        28      1   K.MEIQEIQLKEAK.H  Deamidated (NQ); Oxidation (M)
  153 - 160     926.4818     925.4745     925.4253        53      0   K.HIAEDADR.K
  153 - 161    1054.5851    1053.5778    1053.5203        55      1   K.HIAEDADRK.Y
  168 - 178    1314.8416    1313.8343    1313.7554        60      1   R.KLVIIESDLER.A
  169 - 178    1186.7365    1185.7292    1185.6605        58      0   K.LVIIESDLER.A
  169 - 182    1671.9976    1670.9903    1670.8839        64      1   K.LVIIESDLERAEER.A
  190 - 198    1120.5782    1119.5709    1119.5117        53      0   K.CAELEEELK.T  Carbamidomethyl (C)
  190 - 205    1891.0714    1890.0641    1889.9404        65      1   K.CAELEEELKTVTNNLK.S  Carbamidomethyl (C)
  199 - 213    1648.9156    1647.9083    1647.8203        53      1   K.TVTNNLKSLEAQAEK.Y  3 Deamidated (NQ)
  218 - 226    1182.6207    1181.6134    1181.5452        58      1   K.EDKYEEEIK.V
  234 - 244    1308.7417    1307.7344    1307.6106        95      1   K.EAETRAEFAER.S
  252 - 264    1538.8136    1537.8063    1537.7148        60      0   K.SIDDLEDELYAQK.L
  269 - 284    1758.9299    1757.9226    1757.8141        62      0   K.AISEELDHALNDMTSI.-
  269 - 284    1774.9274    1773.9201    1773.8091        63      0   K.AISEELDHALNDMTSI.-  Oxidation (M)
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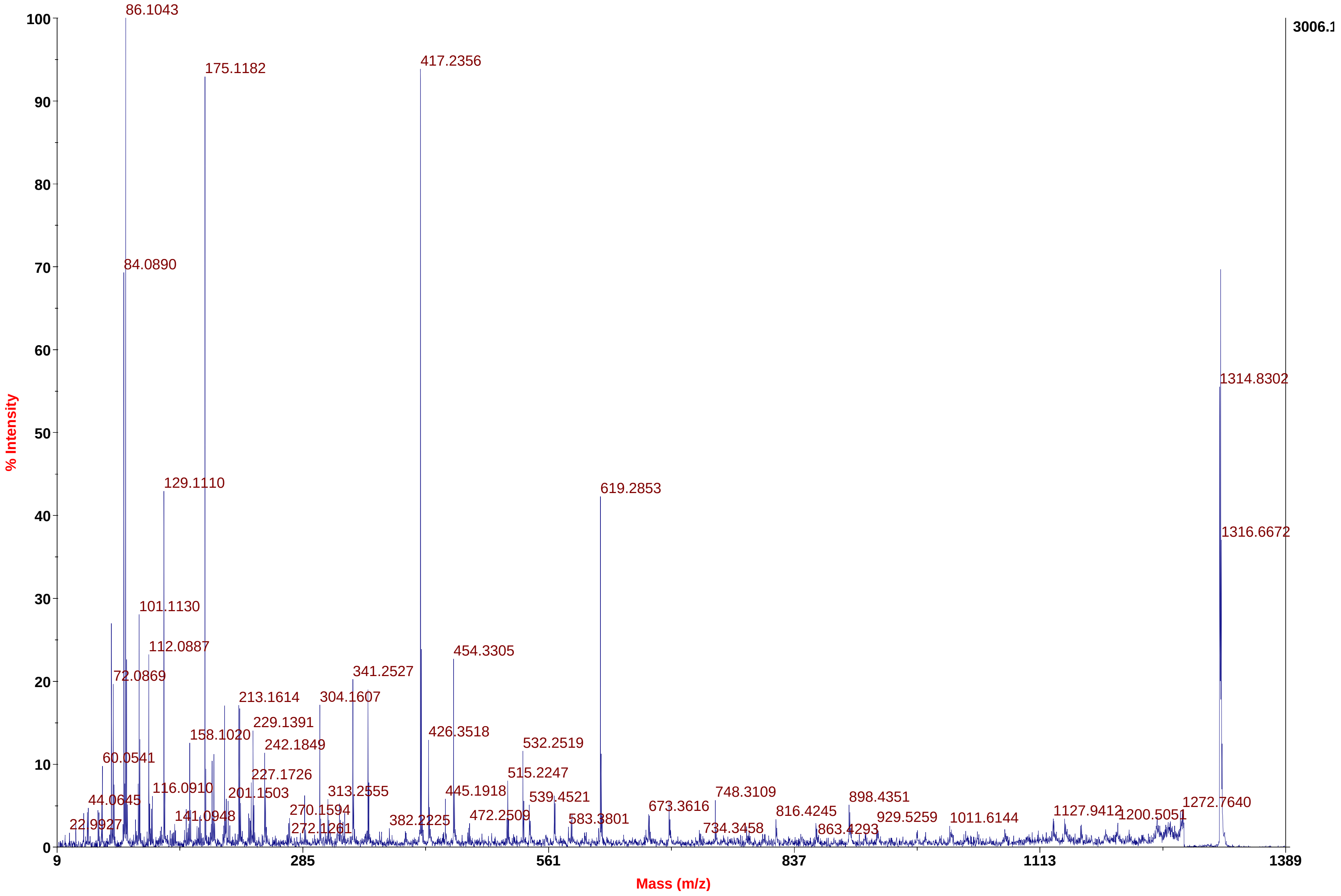
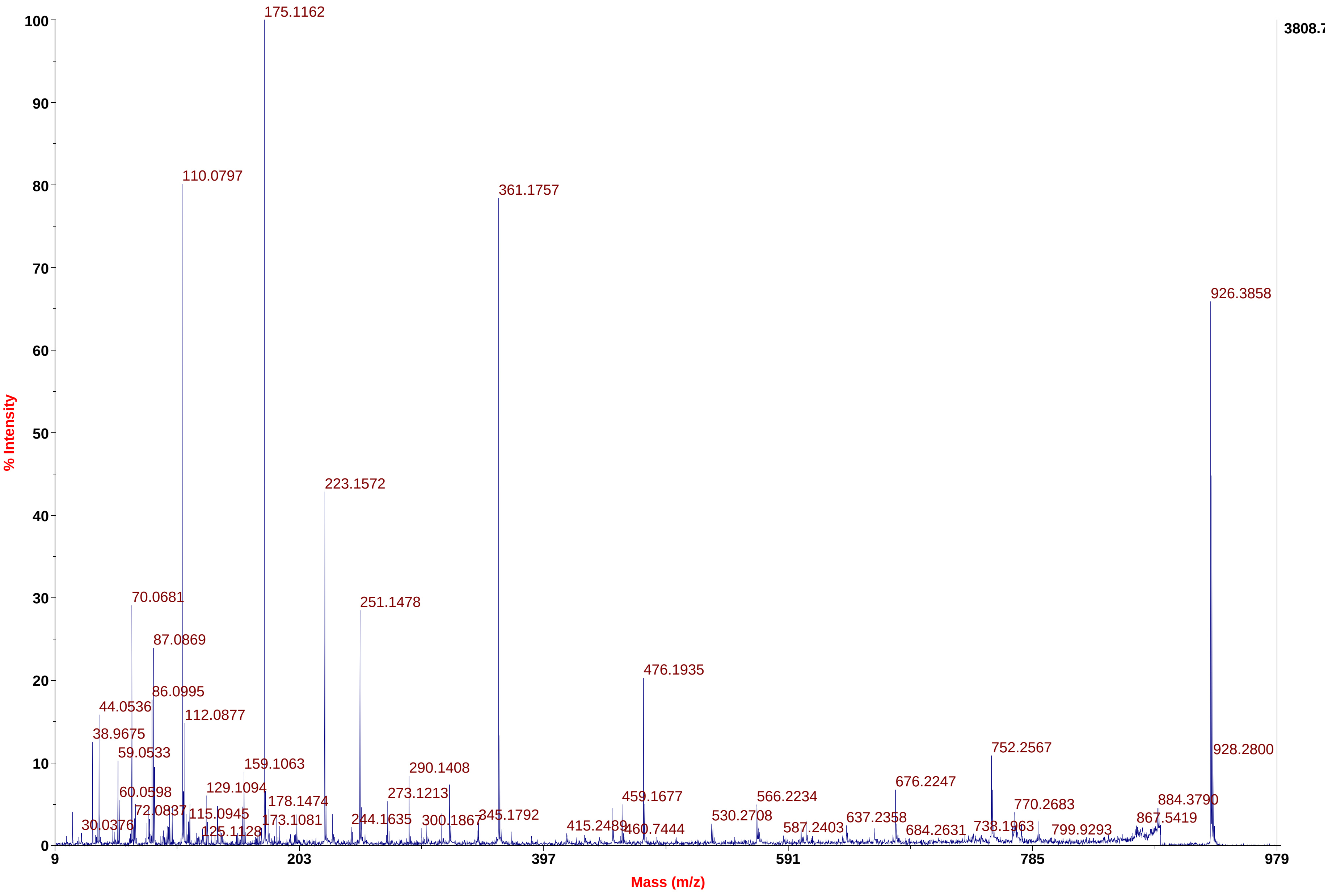
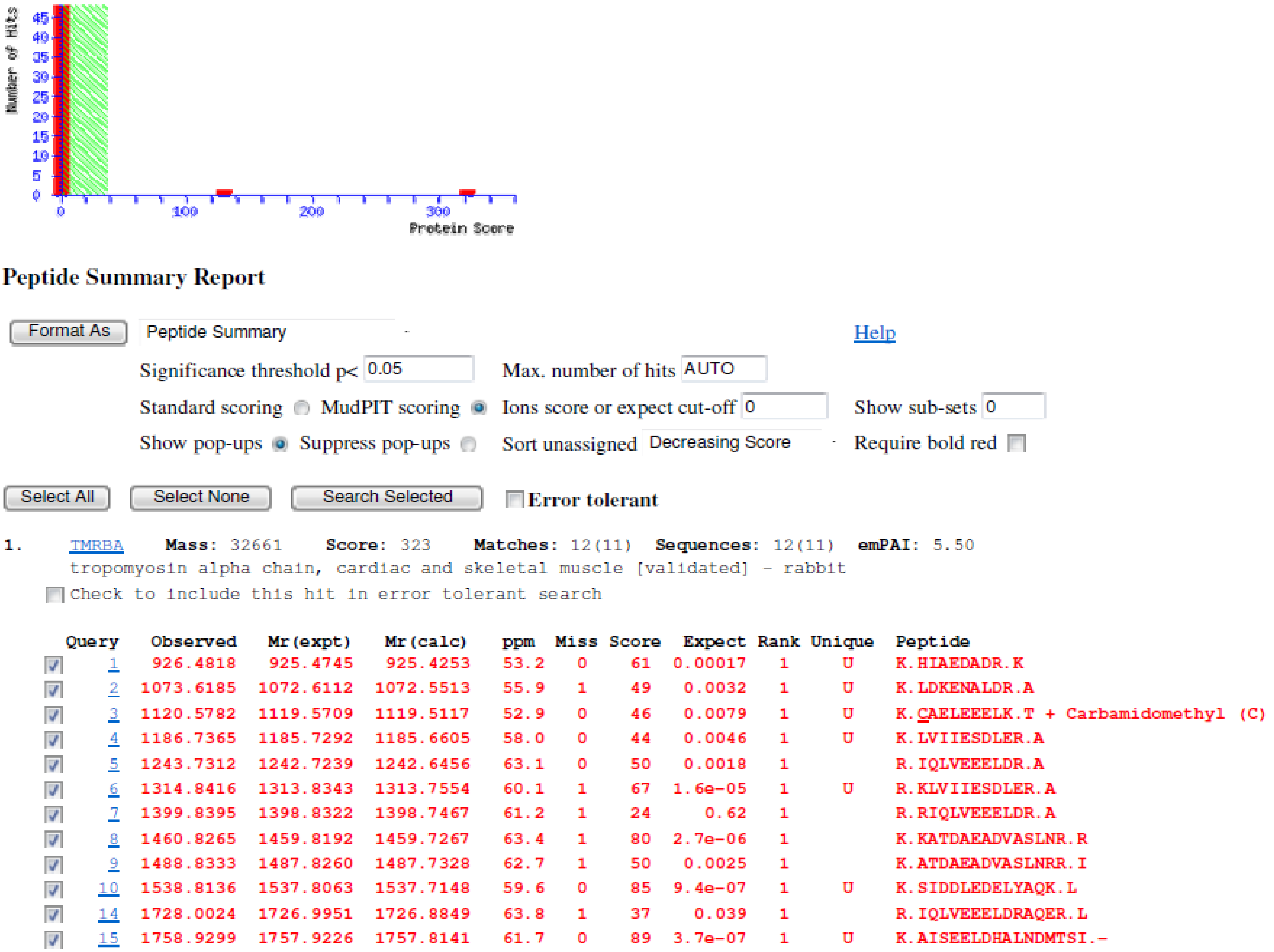
4700 MS/MS Precursor 1314.84 Spec #1 MC[BP = 86.1, 3006]





4700 MS/MS Precursor 926.482 Spec #1 MC[BP = 175.1, 3809]



Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05 Max. number of hits AUTO

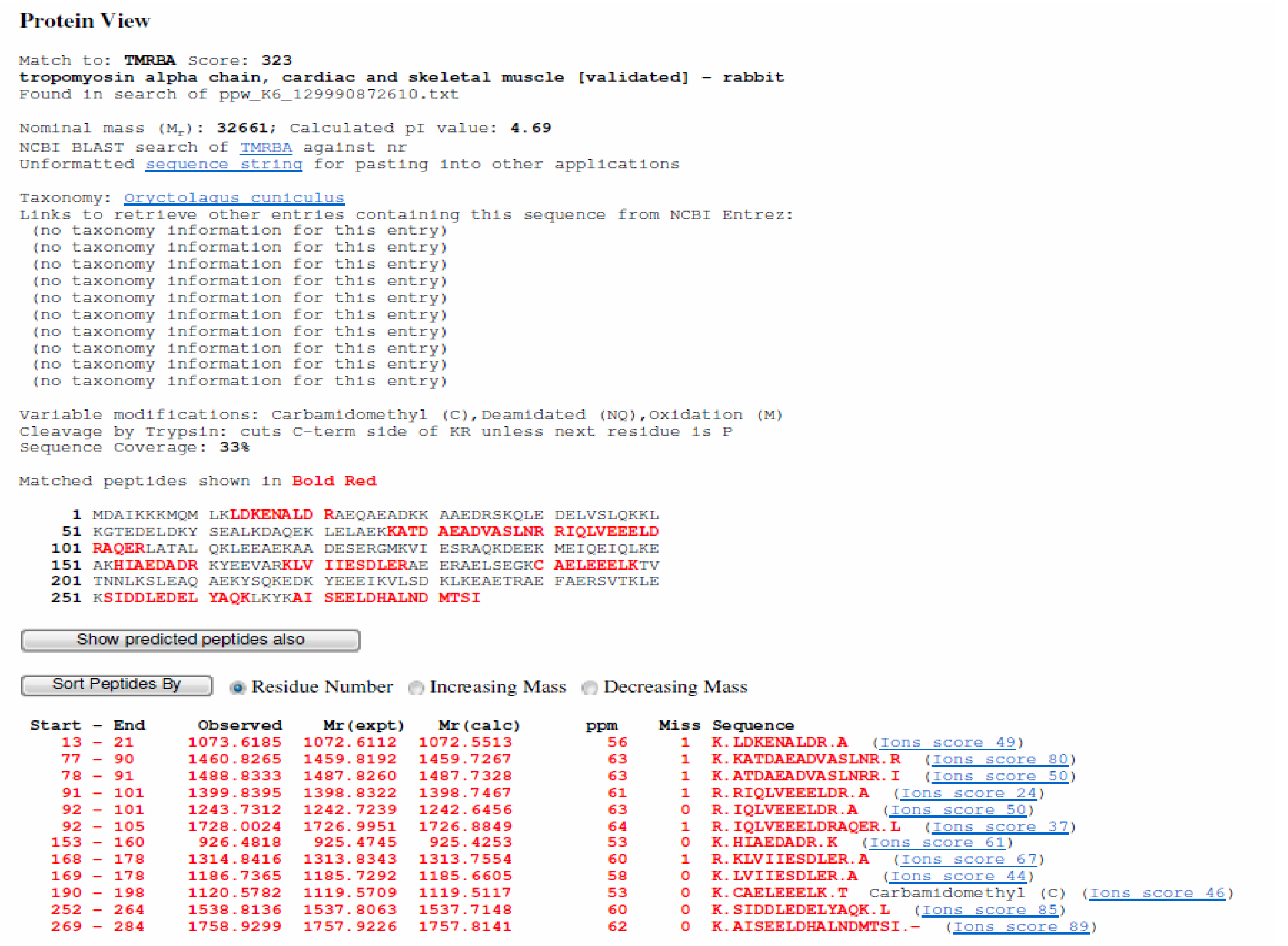
Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 Show sub-sets 0

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

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

1. TMRBA **Mass:** 32661 **Score:** 323 **Matches:** 12(11) **Sequences:** 12(11) **emPAI:** 5.50
tropomyosin alpha chain, cardiac and skeletal muscle [validated] - rabbit
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☑	1	926.4818	925.4745	925.4253	53.2	0	61	0.00017	1	U	K.HIAEDADR.K
☑	2	1073.6185	1072.6112	1072.5513	55.9	1	49	0.0032	1	U	K.LDKENALDR.A
☑	3	1120.5782	1119.5709	1119.5117	52.9	0	46	0.0079	1	U	K.CAELEEELK.T + Carbamidomethyl (C)
☑	4	1186.7365	1185.7292	1185.6605	58.0	0	44	0.0046	1	U	K.LVIIESDLER.A
☑	5	1243.7312	1242.7239	1242.6456	63.1	0	50	0.0018	1		R.IQLVEEELDR.A
☑	6	1314.8416	1313.8343	1313.7554	60.1	1	67	1.6e-05	1	U	R.KLVIIESDLER.A
☑	7	1399.8395	1398.8322	1398.7467	61.2	1	24	0.62	1		R.RIQLVEEELDR.A
☑	8	1460.8265	1459.8192	1459.7267	63.4	1	80	2.7e-06	1		K.KATDAEADVASLNR.R
☑	9	1488.8333	1487.8260	1487.7328	62.7	1	50	0.0025	1		K.ATDAEADVASLNRR.I
☑	10	1538.8136	1537.8063	1537.7148	59.6	0	85	9.4e-07	1	U	K.SIDDLEDELYAQK.L
☑	14	1728.0024	1726.9951	1726.8849	63.8	1	37	0.039	1		R.IQLVEEELDRAQER.L
☑	15	1758.9299	1757.9226	1757.8141	61.7	0	89	3.7e-07	1	U	K.AISEELDHALNDMTSI.-



Protein View

```
Match to: TMRBA Score: 323
tropomyosin alpha chain, cardiac and skeletal muscle [validated] - rabbit
Found in search of ppw_K6_129990872610.txt

Nominal mass (Mr): 32661; Calculated pI value: 4.69
NCBI BLAST search of TMRBA against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryctolagus cuniculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
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 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)
 (no taxonomy information for this entry)

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 33%

Matched peptides shown in Bold Red

     1 MDAIKKKMQM LKLDKENALD RAEQAEADKK AAEDRSKQLE DELVSLQKKL
    51 KGTEDELDKY SEALKDAQEK LELAEKKATD AEADVASLNR RIQLVEEELD
   101 RAQERLATAL QKLEEAEKAA DESERGMKVI ESRAQKDEEK MEIQEIQLKE
   151 AKHIAEDADR KYEEVARKLV IIESDLERAE ERAELSEGKC AELEEELKTV
   201 TNNLKSLEAQ AEKYSQKEDK YEEEIKVLSD KLKEAETRAE FAERSVTKLE
   251 KSIDDLEDEL YAQKLKYKAI SEELDHALND MTSI
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
    13 - 21     1073.6185  1072.6112  1072.5513       56      1  K.LDKENALDR.A  (Ions score 49)
    77 - 90     1460.8265  1459.8192  1459.7267       63      1  K.KATDAEADVASLNR.R  (Ions score 80)
    78 - 91     1488.8333  1487.8260  1487.7328       63      1  K.ATDAEADVASLNRR.I  (Ions score 50)
    91 - 101    1399.8395  1398.8322  1398.7467       61      1  R.RIQLVEEELDR.A  (Ions score 24)
    92 - 101    1243.7312  1242.7239  1242.6456       63      0  R.IQLVEEELDR.A  (Ions score 50)
    92 - 105    1728.0024  1726.9951  1726.8849       64      1  R.IQLVEEELDRAQER.L  (Ions score 37)
   153 - 160     926.4818   925.4745   925.4253       53      0  K.HIAEDADR.K  (Ions score 61)
   168 - 178    1314.8416  1313.8343  1313.7554       60      1  R.KLVIIESDLER.A  (Ions score 67)
   169 - 178    1186.7365  1185.7292  1185.6605       58      0  K.LVIIESDLER.A  (Ions score 44)
   190 - 198    1120.5782  1119.5709  1119.5117       53      0  K.CAELEEELK.T  Carbamidomethyl (C)  (Ions score 46)
   252 - 264    1538.8136  1537.8063  1537.7148       60      0  K.SIDDLEDELYAQK.L  (Ions score 85)
   269 - 284    1758.9299  1757.9226  1757.8141       62      0  K.AISEELDHALNDMTSI.-  (Ions score 89)
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