



**EU FT-ICR MS**

Sample preparation  
FT-ICR MS sample analysis  
Top down of proteins  
**Data interpretation**

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# mMass – freely available

<http://mmass.org/>

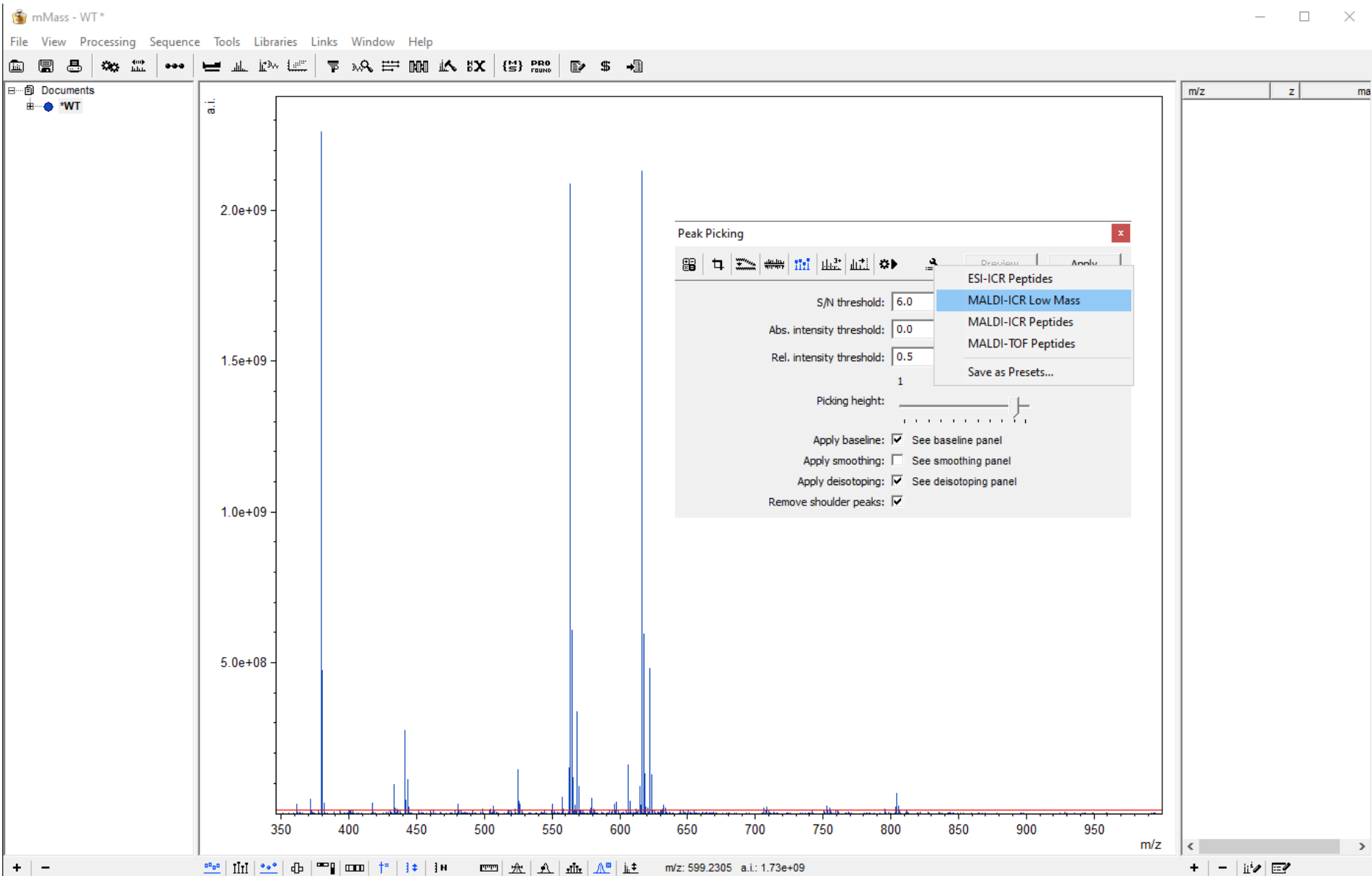
- Works with open format data
- Direct import of Bruker data (if the CompassXport is installed)
- Platform independent + no installation required
- Manual + YouTube videos (<https://www.youtube.com/user/martinstrohaln/videos>)
- Configuration in easily editable \*.xml files

```
<?xml version="1.0" encoding="utf-8" ?>
<mspyModifications version="1.0">
  <modification name="-NH3">
    <description>NH3 loss</description>
    <formula gain="" loss="N1H3" />
    <specify amino="QN" terminus="N" />
  </modification>
  <modification name="-Nterm Met">
    <description>loss of Nterm Methionine</description>
    <formula gain="" loss="C5H9N101S1" />
    <specify amino="" terminus="N" />
  </modification>
  ...
</mspyModifications>
```

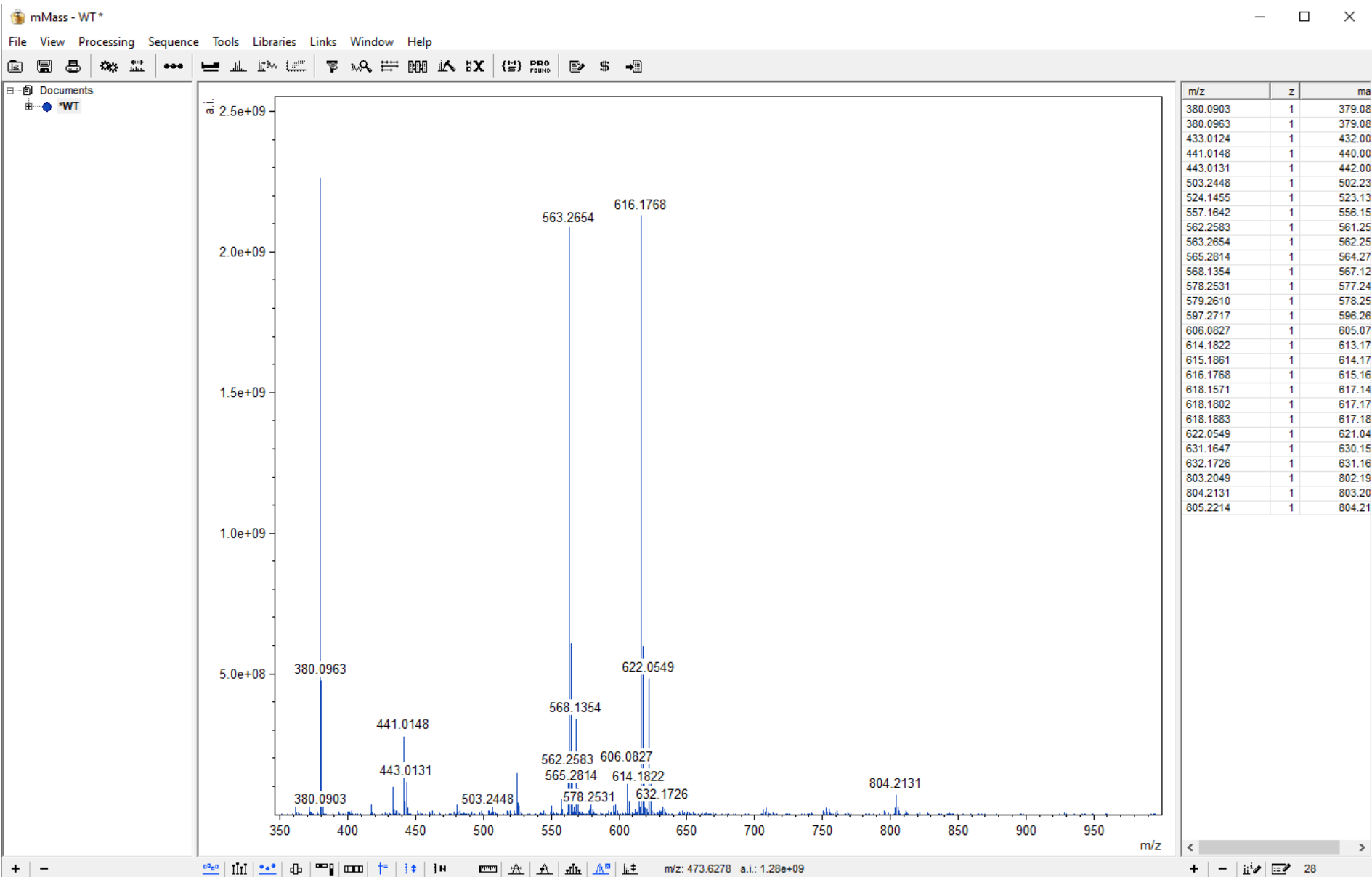
aminoacids	xml
compounds	xml
config	xml
elements	xml
enzymes	xml
fragments	xml
mascot	xml
modifications	xml
monomers	xml
presets	xml
references	xml

Strohaln M et al. *Anal Chem* 82 (11), 4648-4651 (2010).

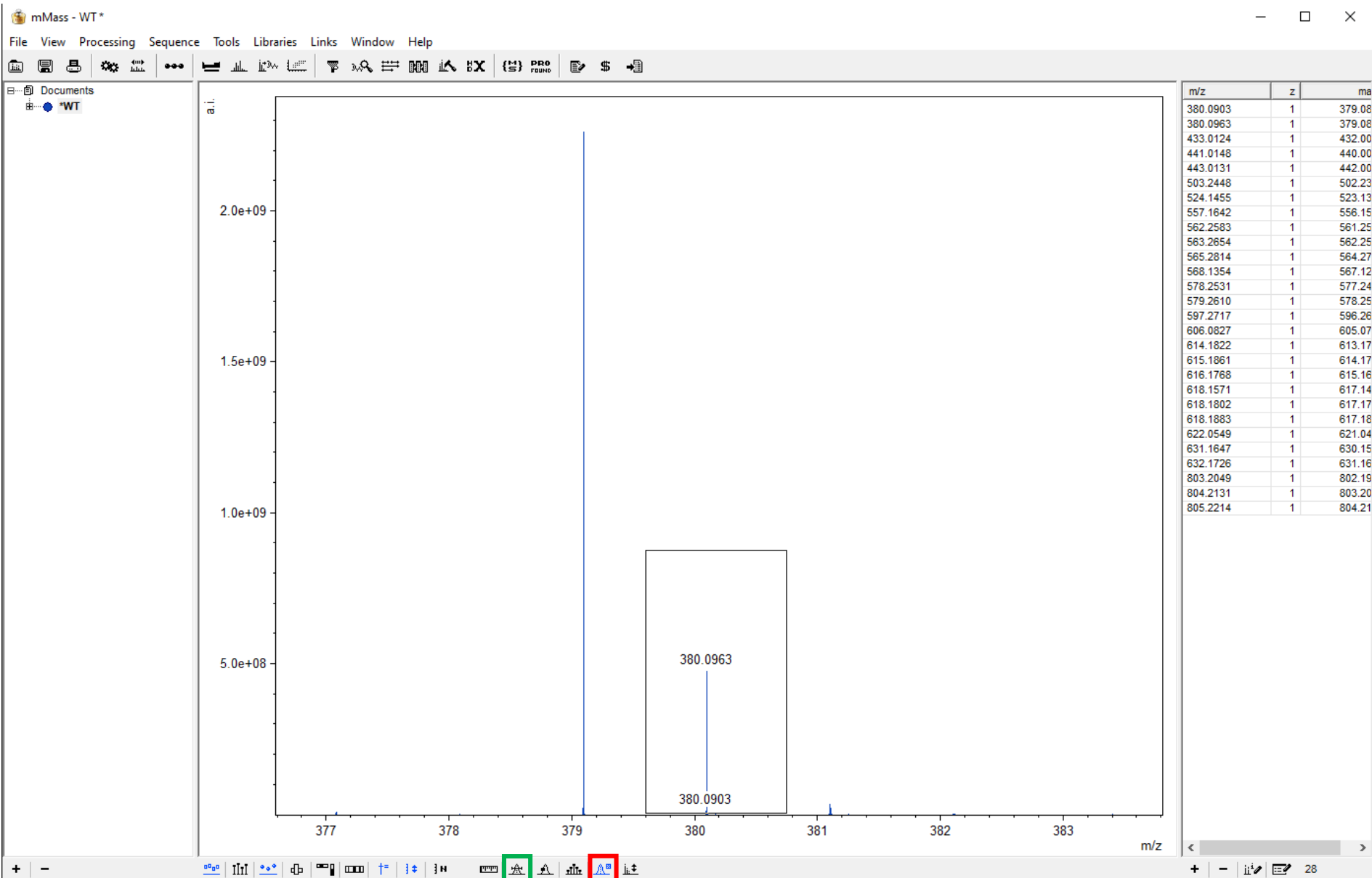
# mMass – import, peak picking (ctrl+F)



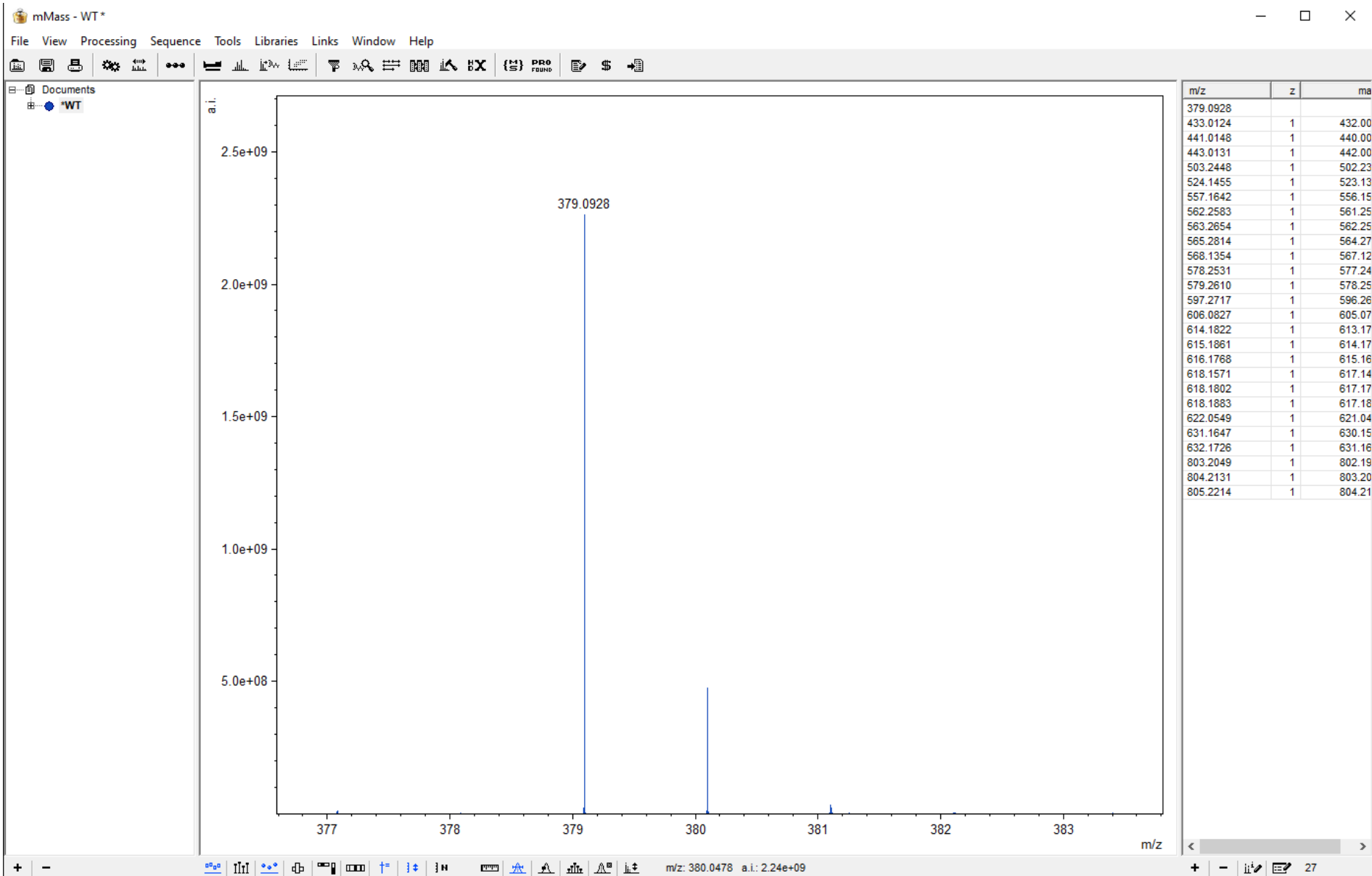
# mMass – import, peak picking (ctrl+F)



# mMass – import, peak picking (manual editing)



# mMass – import, peak picking (manual editing)



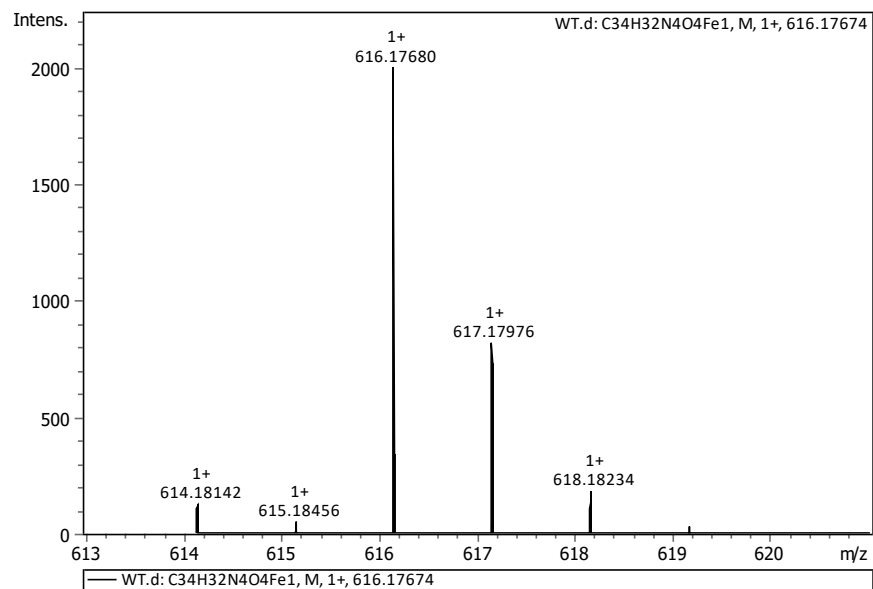
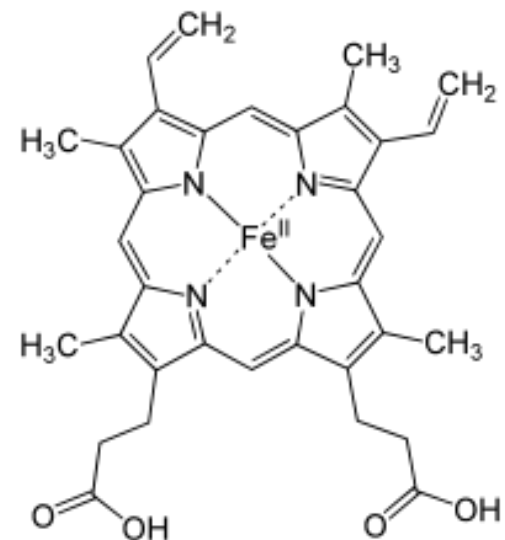
# mMass – heme compounds

## Heme



- isotopes of iron: <sup>54</sup>Fe 5.85%
- <sup>56</sup>Fe 91.75%
- <sup>57</sup>Fe 2.12%
- <sup>58</sup>Fe 0.28%

- Fe<sup>3+</sup> / 2 x COO<sup>-</sup> (M+)
- Fe<sup>2+</sup> / 2 x COO<sup>-</sup> (M+H+)



# mMass – editing compounds or references

## Compounds vs references

```
<group name="HCCA Clusters - MALDI Pos Mo">  
  <reference name="HCCA [M+H-H2O]+" mass="172.039304" />  
  <reference name="HCCA [M+H]+" mass="190.049869" />  
  <reference name="HCCA [M+Na-H2O]+" mass="194.021249" />  
  <reference name="HCCA [M+Na]+" mass="212.031814" />  
  <reference name="HCCA [M+K-H2O]+" mass="209.995186" />  
  <reference name="HCCA [M+K]+" mass="228.005751" />  
  <reference name="HCCA [2M+H-H2O]+" mass="361.081897" />  
  <reference name="HCCA [2M+H]+" mass="379.092462" />  
  <reference name="HCCA [2M+Na-H2O]+" mass="383.063842" />  
  <reference name="HCCA [2M+Na]+" mass="401.074407" />  
  <reference name="HCCA [2M+K-H2O]+" mass="399.037779" />  
  <reference name="HCCA [2M+K]+" mass="417.048344" />  
  <reference name="HCCA [2M+K+Na-H2O]+" mass="422.027000" />
```

Definition by:

mass vs by elemental composition

- Has to enter Na<sup>+</sup> or K<sup>+</sup> etc. or can be calculated by mMass (see later)
- Formula can be directly submitted to peak modelling

```
<mMassCompounds version="1.0">
```

```
<group name="LIPID MAPS Fatty Acyls [FA]">  
  <compound name="LMFA00000001" formula="C40H66O5">Fatty Acyls [FA] with formula: C40H66O5</compound>  
  <compound name="LMFA00000002 (Serratamic acid)" formula="C13H25NO5">Fatty Acyls [FA] with formula: C13H25NO5</compound>  
  <compound name="LMFA00000003" formula="C38H74N2O5">Fatty Acyls [FA] with formula: C38H74N2O5</compound>  
  <compound name="LMFA00000004 (N-linolenoyl-glutamine)" formula="C23H38N2O4">Fatty Acyls [FA] with formula: C23H38N2O4</compound>  
  <compound name="LMFA00000005" formula="C37H71NO6">Fatty Acyls [FA] with formula: C37H71NO6</compound>
```



# mMass – editing compounds or references

## Prepare template in Excel

```
<group name="Heme-like">
```

```
  <reference name="Heme(M+)" mass="616.177300" />
```

...

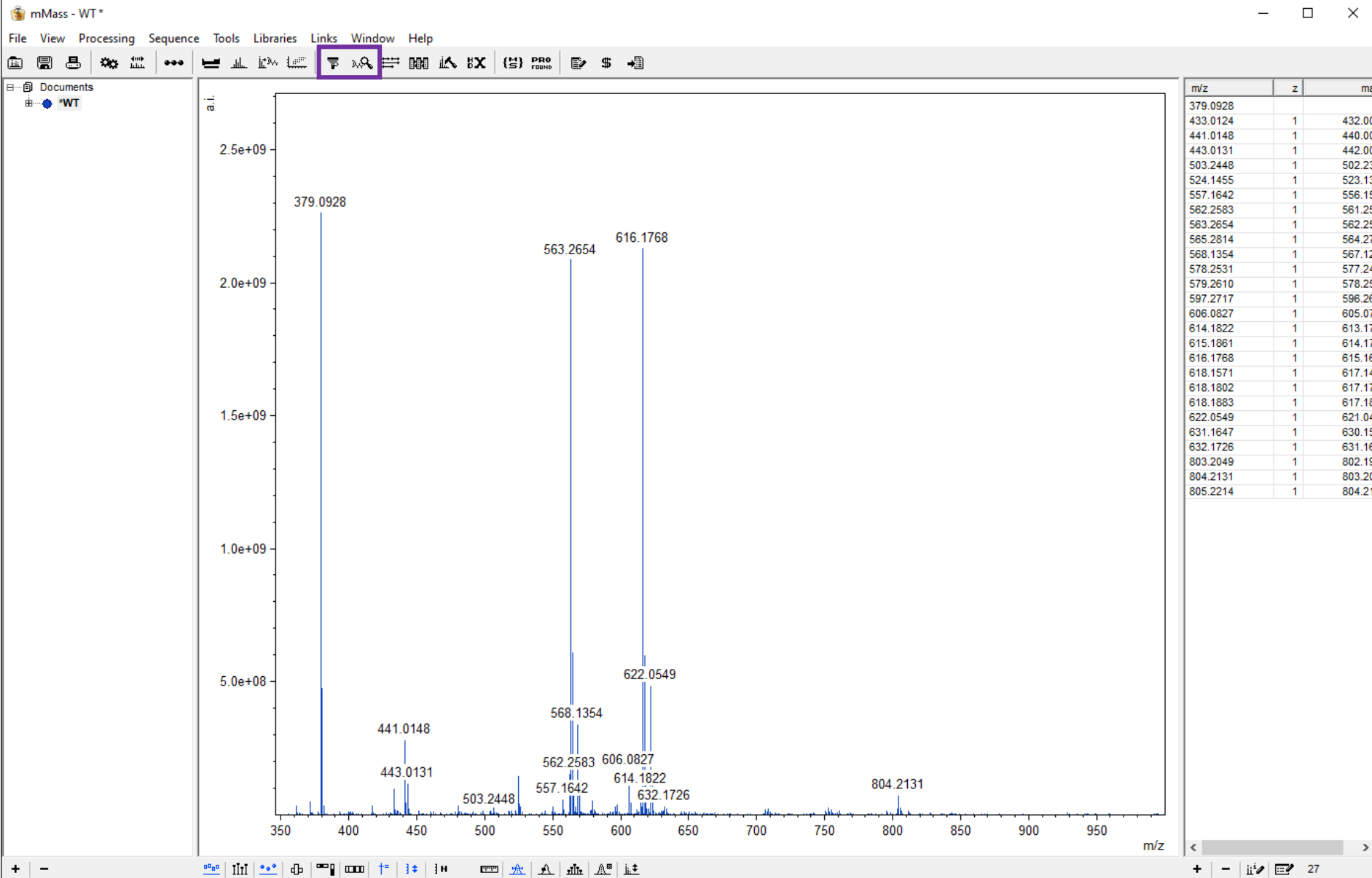
...

```
</group>
```

	A	B	C	D	E	F	G	H
1								
2		<reference name="		" mass="		" />		=CONCATENATE(B2,C2,D2,E2,F2)
3								
4								

	A	B	C	D	E	F	G	H
1								
2		<reference name="	PPIX(M+H+)	" mass="	563.26530	" />		=CONCATENATE(B2,C2,D2,E2,F2)
3		<reference name="	vPPIX(M+H+)	" mass="	566.25240	" />		<reference name="vPPIX(M+H+)" mass="566.2524" />
4		<reference name="	Biliverdin(M+H+)	" mass="	583.25510	" />		<reference name="Biliverdin(M+H+)" mass="583.2551" />
5		<reference name="	Bilirubin(M+H+)	" mass="	585.27080	" />		<reference name="Bilirubin(M+H+)" mass="585.2708" />
6		<reference name="	Heme(M+)	" mass="	616.17730	" />		<reference name="Heme(M+)" mass="616.1773" />
7		<reference name="	Verdoheme(M+)	" mass="	619.16440	" />		<reference name="Verdoheme(M+)" mass="619.1644" />

# mMass – assigning references / compounds



# mMass – assigning references / compounds

mMass - WT\*

File View Processing Sequence Tools Libraries Links Window Help

Documents  
\*WT

Mass Filter

References: Heme-like **Match** Annotate Remove

reference	m/z	error
Bilirubin(M+H+)	585.2708	
Bilirubin(M+K+)	623.2267	
Bilirubin(M+Na+)	607.2527	
Biliverdin(M+H+)	583.2551	
Biliverdin(M+K+)	621.2110	
Biliverdin(M+Na+)	605.2370	
Heme(M+)	616.1773	
Heme(M+K)	655.1405	
Heme(M+Na)	639.1665	
Heme+H1O4(M+)	681.1648	
Heme+H1O4(M+K)	720.1280	
Heme+H1O4(M+Na)	704.1540	
Heme+O1(M+)	632.1722	
Heme+O1(M+K)	671.1354	
Heme+O1(M+Na)	655.1614	

622.0549	1	621.04
631.1647	1	630.15
803.2049	1	802.19
804.2131	1	803.20
805.2214	1	804.21

m/z: 853.3401 a.i.: 1.53e+09

# mMass – assigning references / compounds

mMass - WT\*

File View Processing Sequence Tools Libraries Links Window Help

Documents  
\*WT

Mass Filter

References: Heme-like Match Annotate Remove

reference	m/z	error
Bilirubin(M+H+)	585.2708	
Bilirubin(M+K+)	623.2267	
Bilirubin(M+Na+)	607.2527	
Biliverdin(M+H+)	583.2551	
Biliverdin(M+K+)	621.2110	

Match References

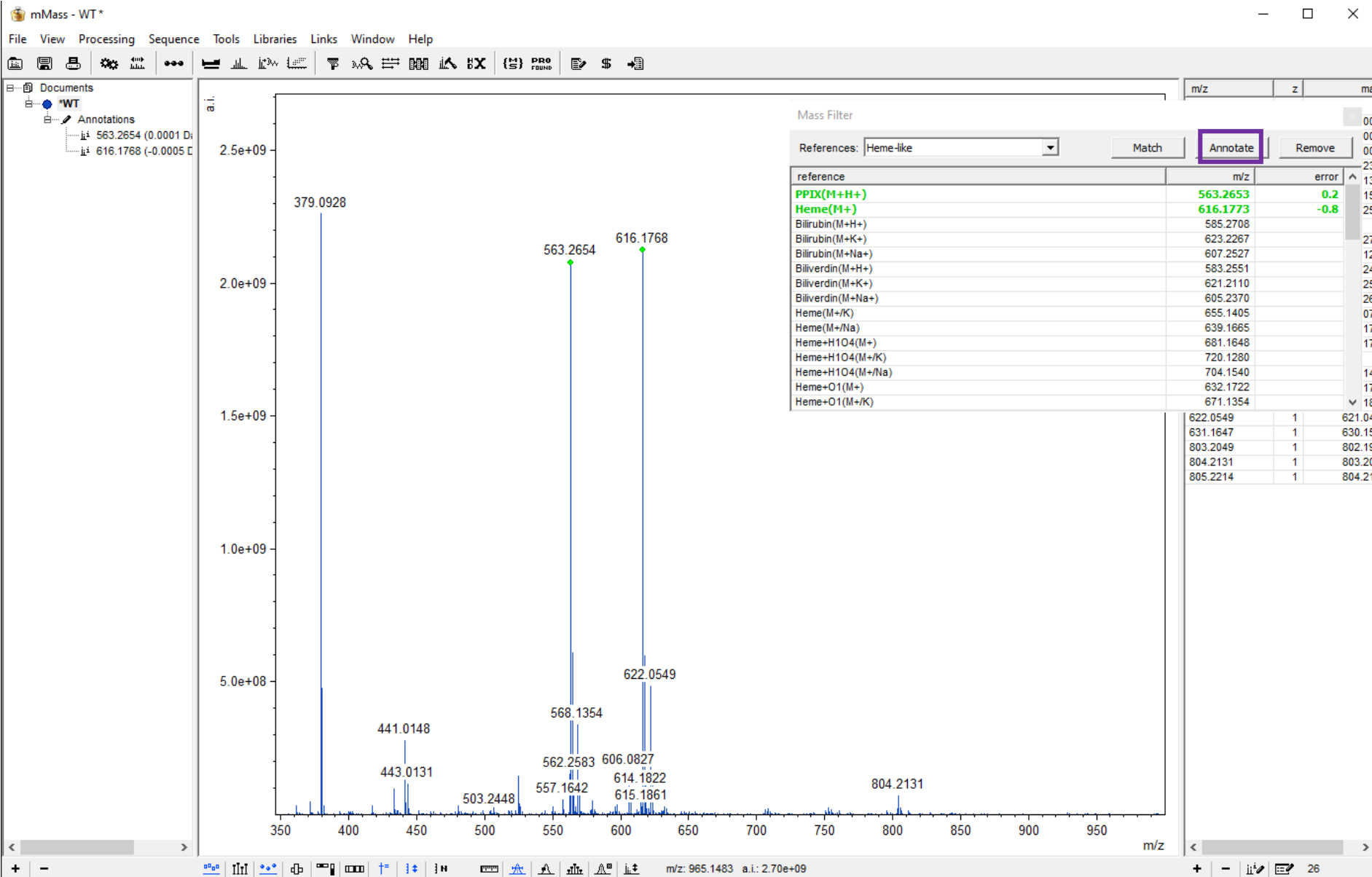
Tolerance: 5.0 Da ppm Ignore charge Match Calibrate

Remove:  Annotated  Matched  Unselected  Isotopes  Unknown

error (ppm)

m/z

# mMass – assigning references / compounds



# mMass – assigning references / compounds

mMass - WT\*

File View Processing Sequence Tools Libraries Links Window Help

Documents

- WT
  - Annotations
    - 562.2583 (0.0009 Da)
    - 563.2654 (0.0001 Da)
    - 616.1768 (0.0 Da) H

Compounds Search

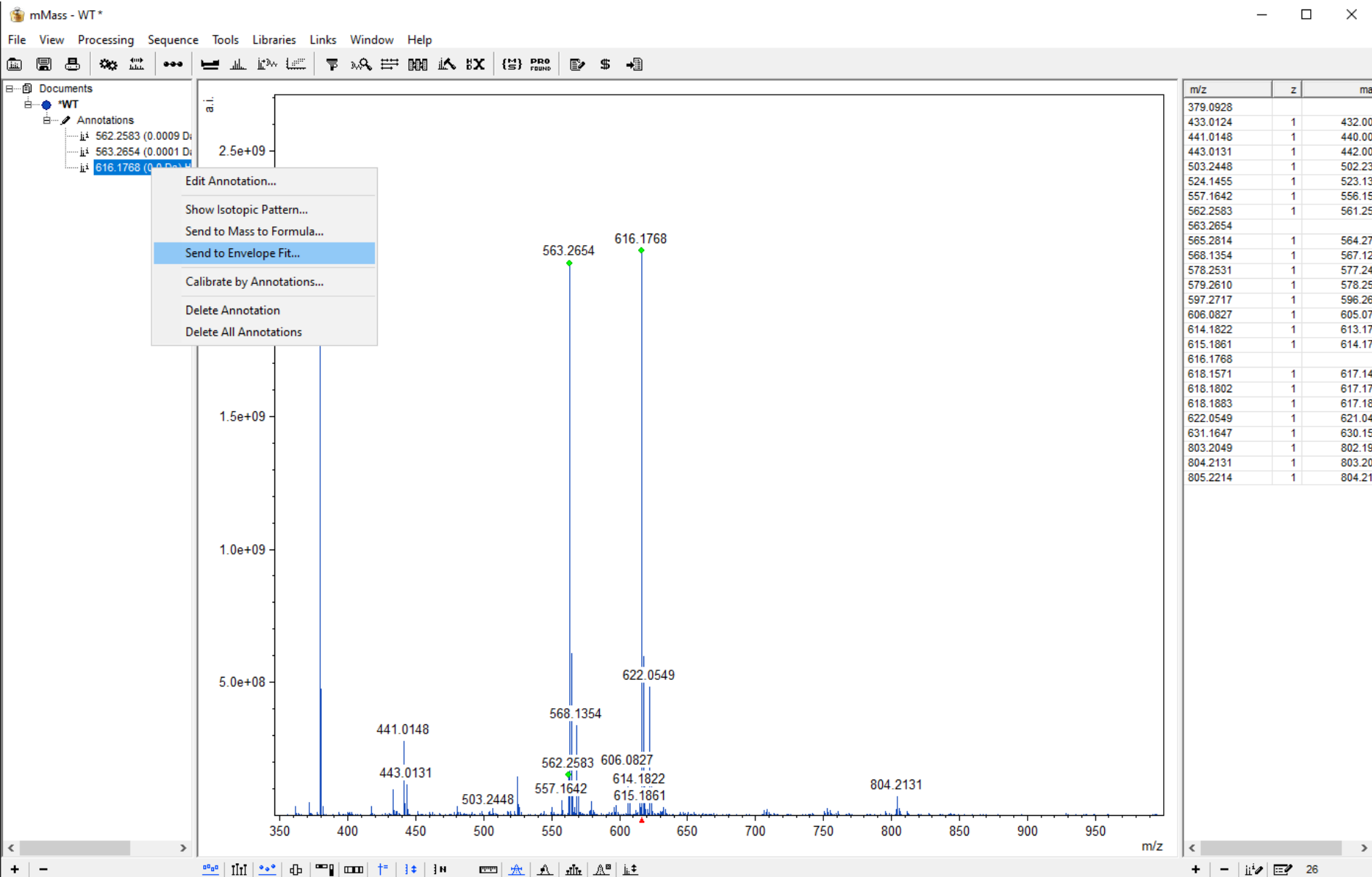
Compounds: Heme related compounds

Mass:  Mo  Av  Max charge: 1  M\* Adducts:  Na  K  Li  NH4  -H2O  ACN  MeOH

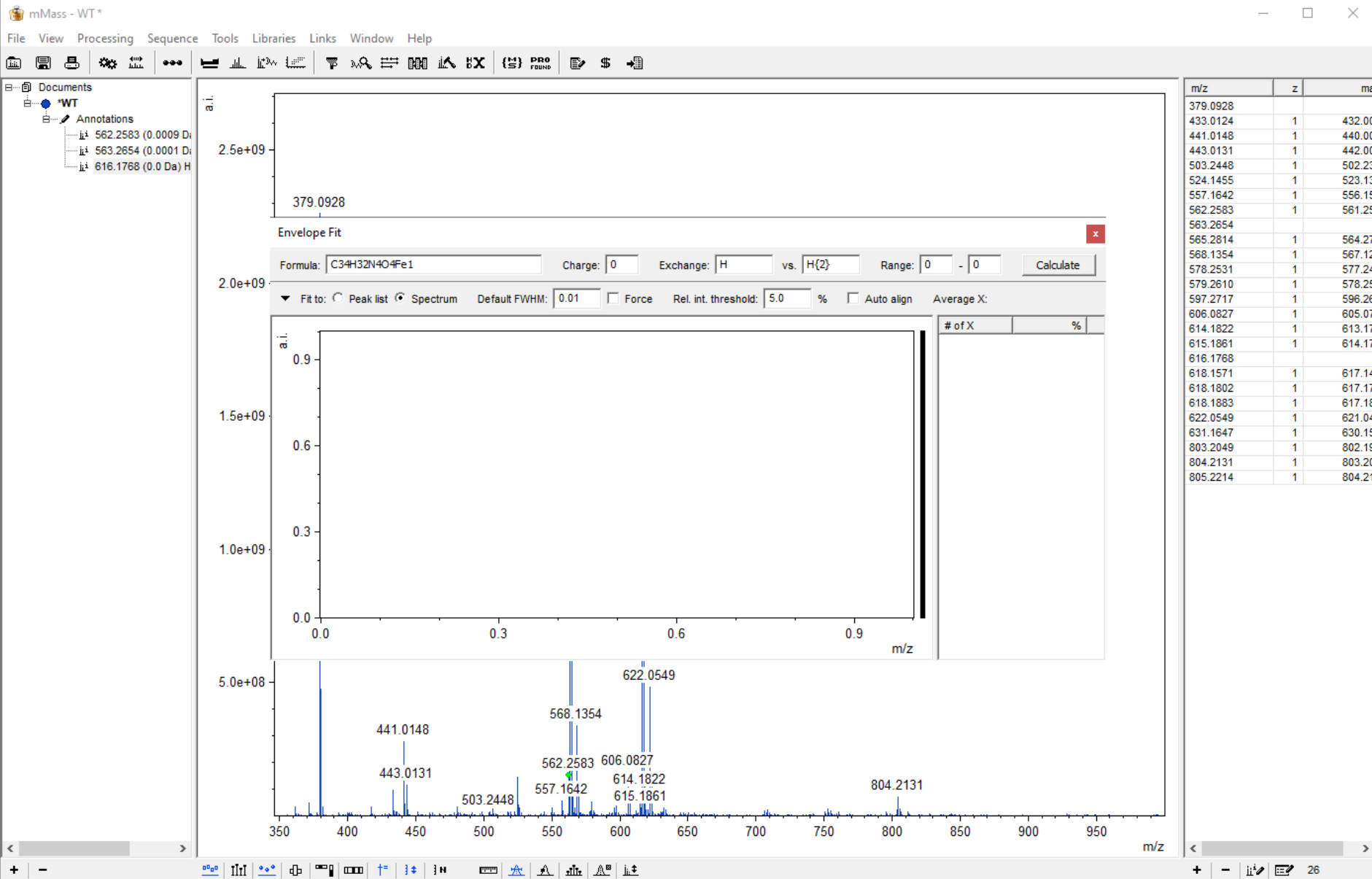
compound	m/z	z	adduct	formula	error
Bilirubin	584.2629	1	radical	C33H36N4O6	
Bilirubin	585.2708	1		C33H36N4O6	
Bilirubin	607.2527	1	Na	C33H36N4O6(Na)(H-1)	
Bilirubin	623.2266	1	K	C33H36N4O6(K)(H-1)	
Biliverdin	582.2473	1	radical	C33H34N4O6	
Biliverdin	583.2551	1		C33H34N4O6	
Biliverdin	605.2371	1	Na	C33H34N4O6(Na)(H-1)	
Biliverdin	621.2110	1	K	C33H34N4O6(K)(H-1)	
Heme	616.1767	1	radical	C34H32N4O4Fe1	0.1
Heme	617.1846	1		C34H32N4O4Fe1	
Heme	639.1665	1	Na	C34H32N4O4Fe1(Na)(H-1)	
Heme	655.1405	1	K	C34H32N4O4Fe1(K)(H-1)	
Heme+H1O4	681.1642	1	radical	C34H33N4O8Fe1	
Heme+H1O4	682.1721	1		C34H33N4O8Fe1	
Heme+H1O4	704.1540	1	Na	C34H33N4O8Fe1(Na)(H-1)	
Heme+H1O4	720.1279	1	K	C34H33N4O8Fe1(K)(H-1)	
Heme+O1	632.1717	1	radical	C34H32N4O5Fe1	
Heme+O1	633.1795	1		C34H32N4O5Fe1	

m/z: 707.4086 a.i.: 2.16e+09

# mMass – envelope fit

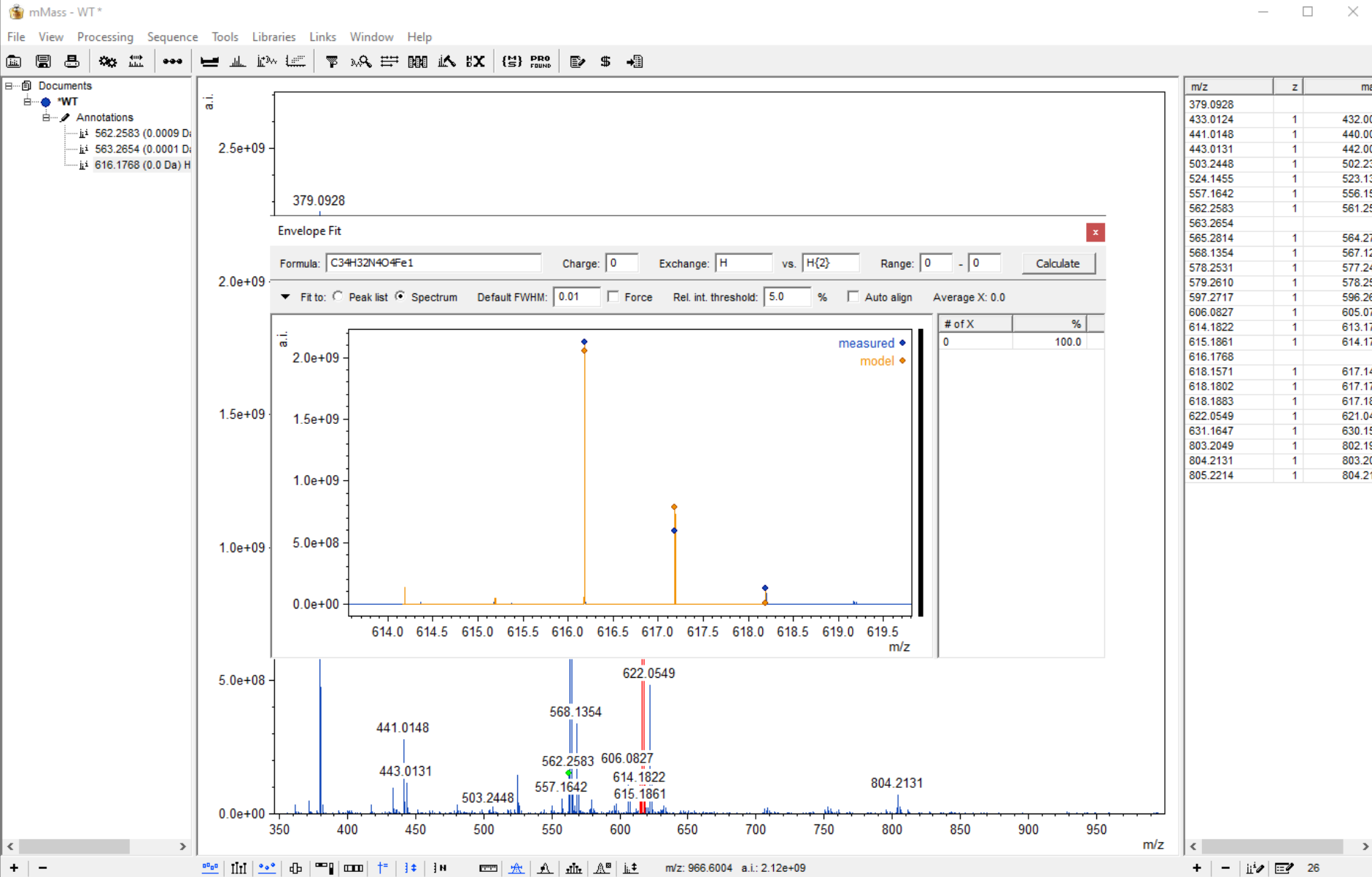


# mMass – envelope fit

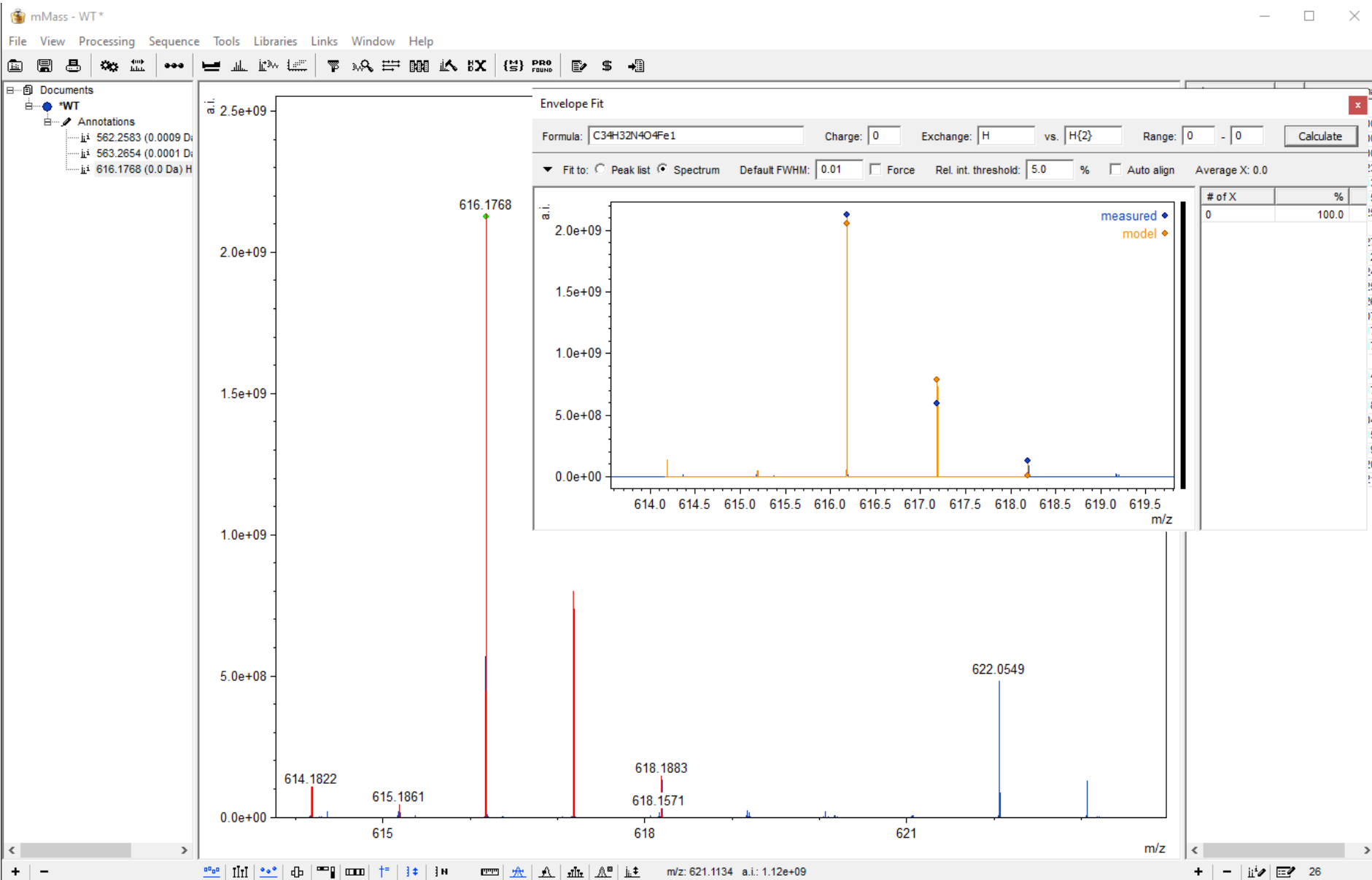




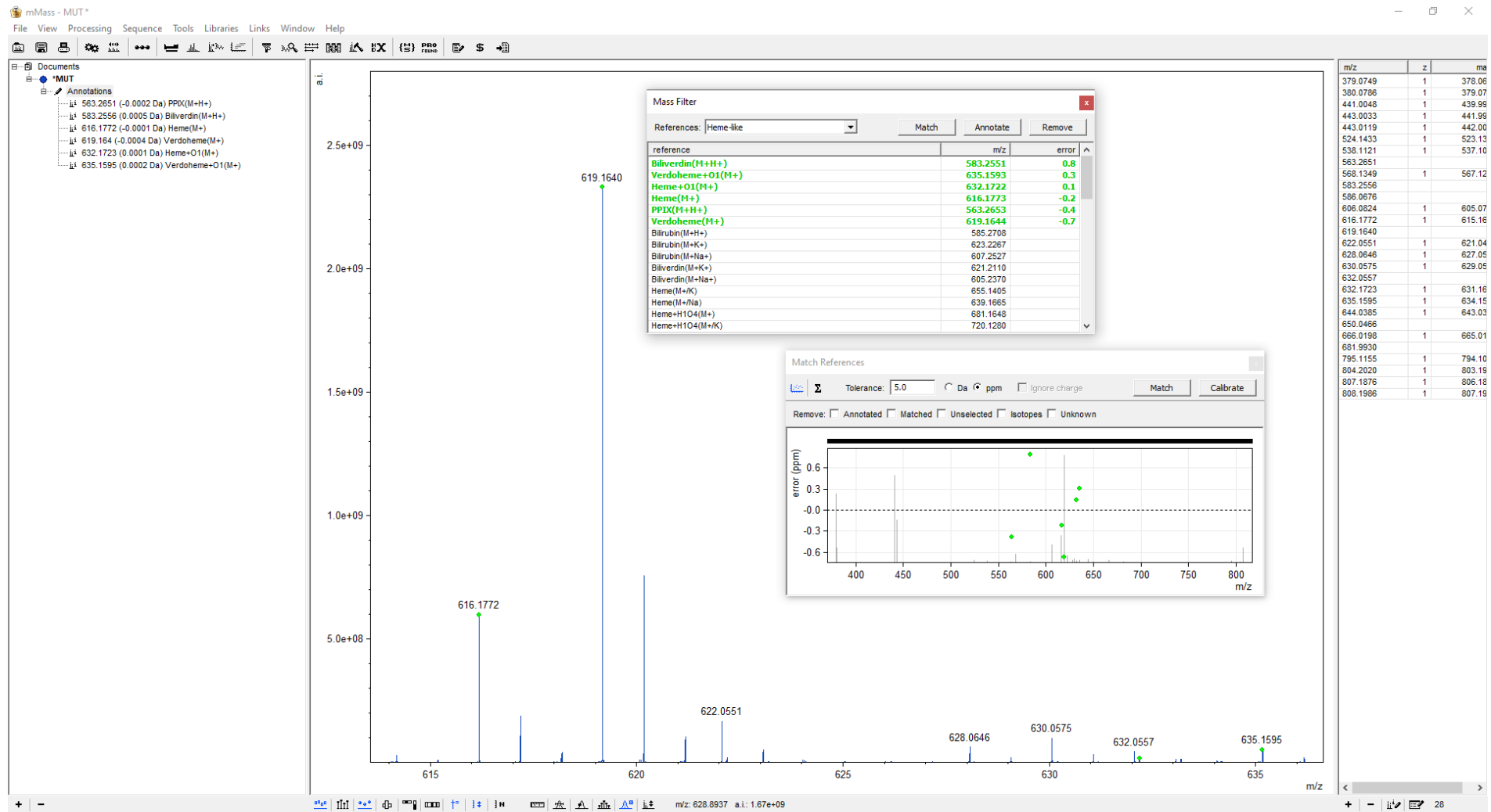
# mMass – envelope fit



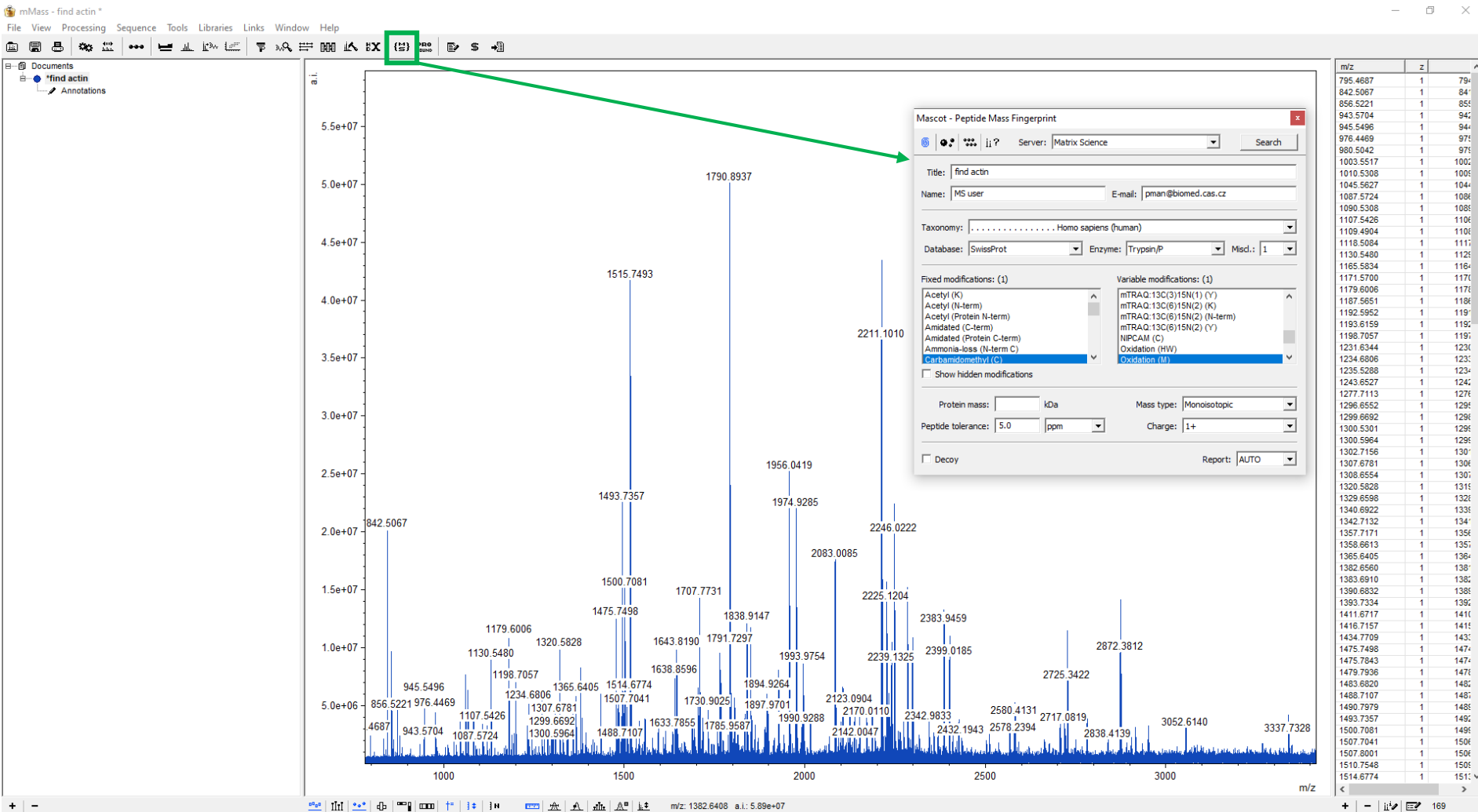
# mMass – envelope fit



# mMass – heme oxidation/degradation



# mMass – contaminated peptide mixture (find actin)



# mMass – contaminated peptide mixture (find actin)

## not very optimistic search result

Concise Summary Report (find) x +

www.matrixscience.com/cgi/master\_results.pl?file=.%2Fdata%2F20210924%2FFTmSrumL.dat

### MATRIX SCIENCE Mascot Search Results

User : MS user  
Email : pman@biomed.cas.cz  
Search title : find actin  
Database : SwissProt 2021\_03 (565254 sequences: 203850821 residues)  
Taxonomy : Homo sapiens (human) (20387 sequences)  
Timestamp : 23 Sep 2021 at 23:11:19 GMT  
Top Score : 72 for **K1C10\_HUMAN**, Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6

#### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
Protein scores greater than 56 are significant ( $p < 0.05$ ).

Protein Score	Number of Hits
0	2
5	30
10	5
15	2
20	1
25	1
30	1
35	1
40	1
45	1
50	1
55	1
60	1
65	1
70	1
72	18
75	1

#### Concise Protein Summary Report

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

Significance threshold  $p < 0.05$  Max. number of hits: AUTO

Preferred taxonomy: All entries

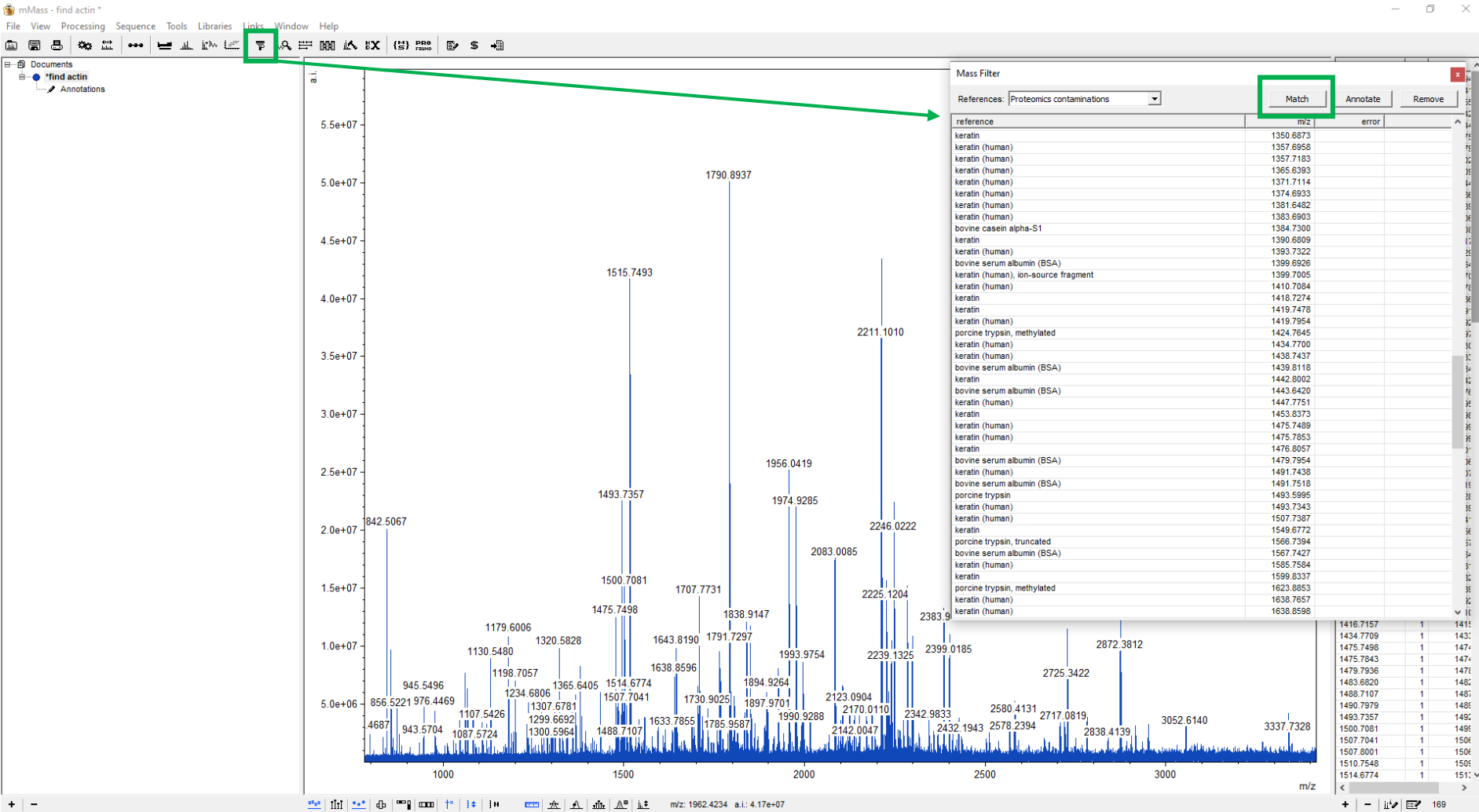
Re-Search All Search Unmatched

- [K1C10\\_HUMAN](#) Mass: 59020 Score: 72 Expect: 0.0013 Matches: 18  
Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
- [K2C1\\_HUMAN](#) Mass: 66170 Score: 49 Expect: 0.25 Matches: 15  
Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6

#### Search Parameters

Type of search : Peptide Mass Fingerprint  
Enzyme : Trypsin/P  
Fixed modifications : Carbamidomethyl (C)  
Variable modifications : Oxidation (M)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 5$  ppm

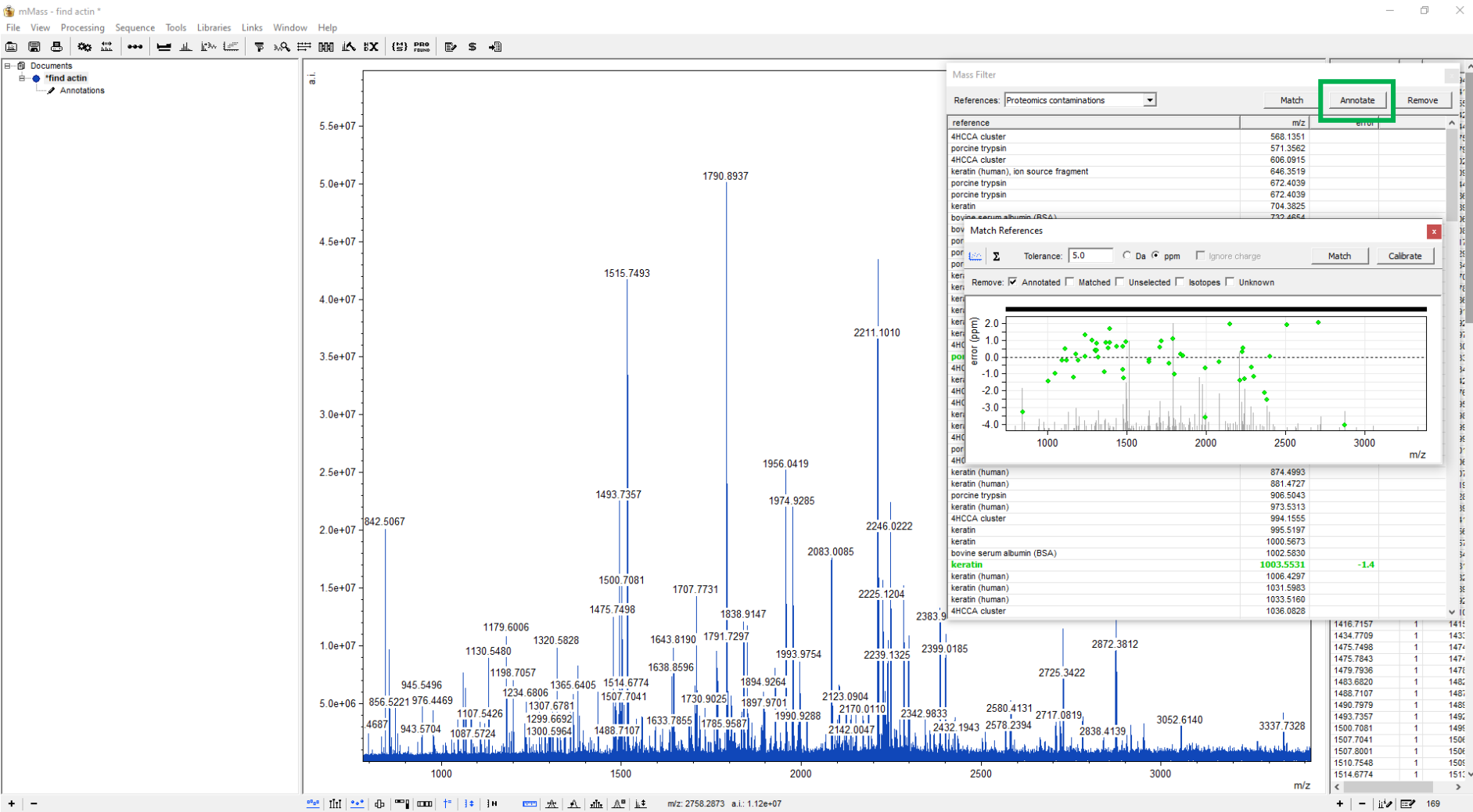
# mMass – contaminated peptide mixture (find actin) *filter out contaminations*



**Interferences and contaminants encountered in modern mass spectrometry.**  
Keller BO et al. Anal Chim Acta 627(1):71-81 (2008).

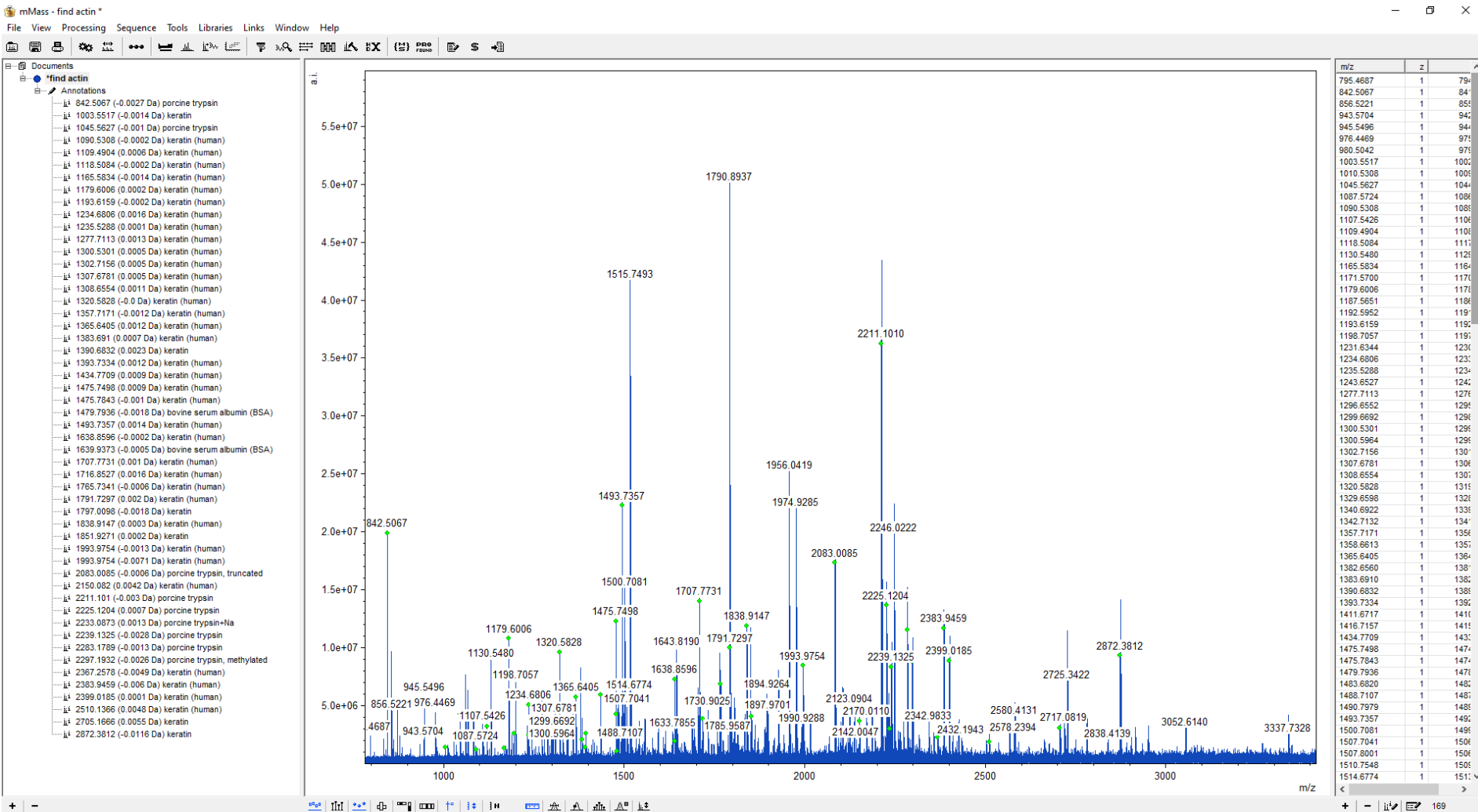
# mMass – contaminated peptide mixture (find actin)

## match and annotate



# mMass – contaminated peptide mixture (find actin)

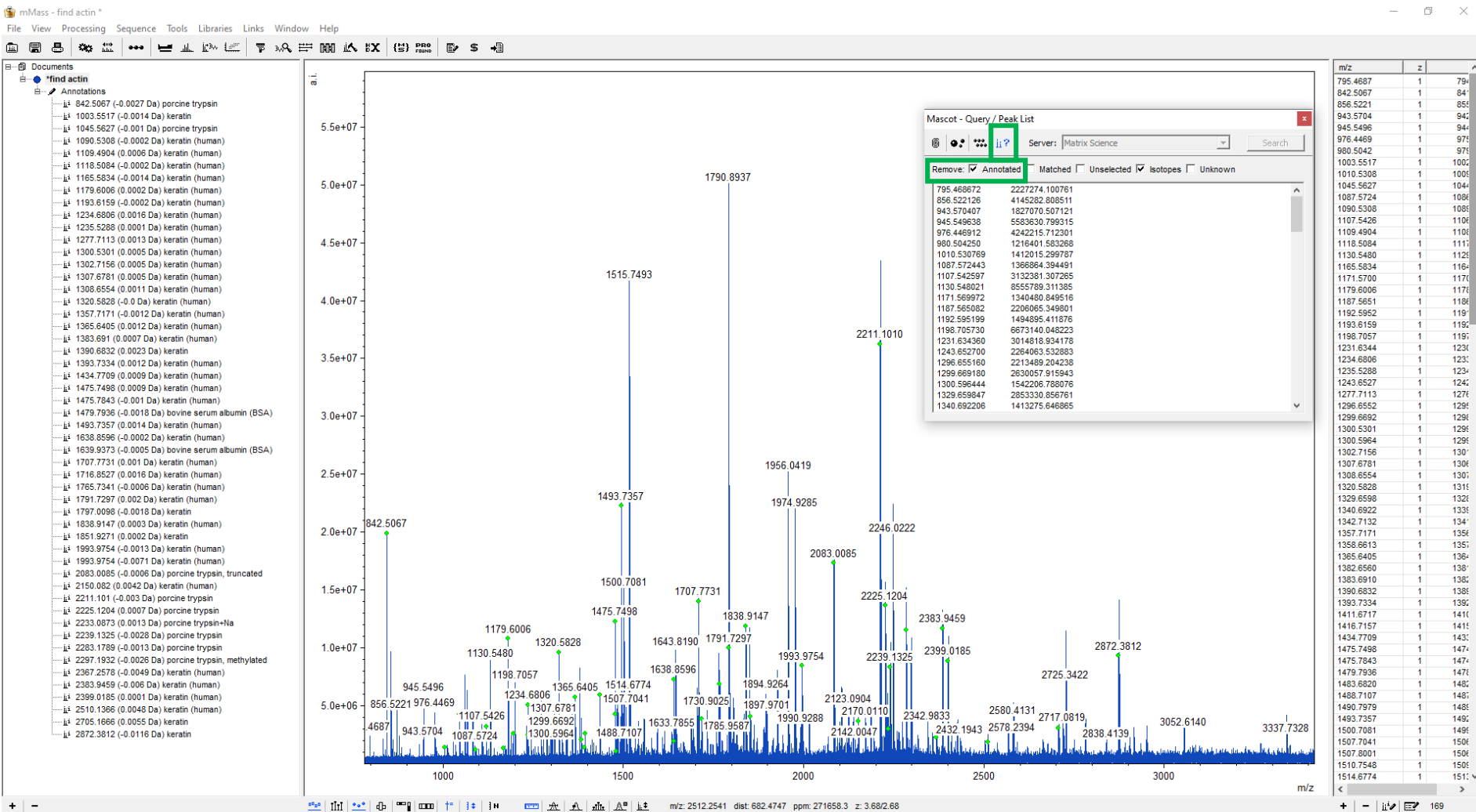
*green dots mark the contaminations*





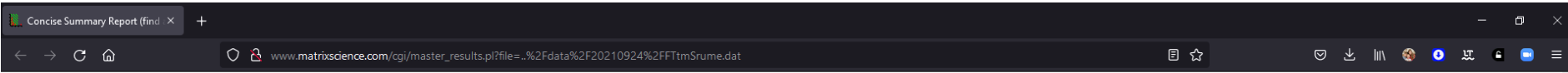
# mMass – contaminated peptide mixture (find actin)

## running the search again, now filtering out the contaminants



# mMass – contaminated peptide mixture (find actin)

## now actin is identified

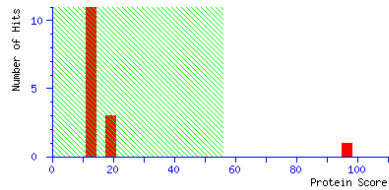


## Mascot Search Results

User : MS user  
Email : pman@biomed.cas.cz  
Search title : find actin  
Database : SwissProt 2021\_03 (565254 sequences; 203850821 residues)  
Taxonomy : Homo sapiens (human) (20387 sequences)  
Timestamp : 23 Sep 2021 at 23:16:46 GMT  
Top Score : 96 for ACTS\_HUMAN, Actin, alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
Protein scores greater than 56 are significant ( $p < 0.05$ ).



### Concise Protein Summary Report

Format As  [Help](#)  
Significance threshold  $p <$   Max. number of hits   
Preferred taxonomy

- [ACTS\\_HUMAN](#) Mass: 42366 Score: 96 Expect: 4.6e-06 Matches: 12  
Actin, alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1  
[ACTC\\_HUMAN](#) Mass: 42334 Score: 78 Expect: 0.00036 Matches: 11  
Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1  
[ACTA\\_HUMAN](#) Mass: 42381 Score: 61 Expect: 0.016 Matches: 10  
Actin, aortic smooth muscle OS=Homo sapiens OX=9606 GN=ACTA2 PE=1 SV=1  
[ACTH\\_HUMAN](#) Mass: 42249 Score: 46 Expect: 0.57 Matches: 9  
Actin, gamma-enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2 PE=1 SV=1  
[ACTB\\_HUMAN](#) Mass: 42052 Score: 30 Expect: 22 Matches: 8  
Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1  
[ACTS\\_HUMAN](#) Mass: 42108 Score: 30 Expect: 22 Matches: 8  
Actin, cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1  
[TRIM65\\_HUMAN](#) Mass: 58742 Score: 15 Expect: 6.6e+02 Matches: 2  
Tripartite motif-containing protein 65 OS=Homo sapiens OX=9606 GN=TRIM65 PE=1 SV=3  
[GPMV\\_HUMAN](#) Mass: 12606 Score: 13 Expect: 1.5e+02 Matches: 1

# mMass – contaminated peptide mixture (find actin)

## details of the identification + copy-paste the sequence for mMass

Mascot Search Results: ACTS\_H X +

www.matrixscience.com/cgi/protein\_view.pl?file=.%2Fdata%2F20210924%2FFFTmSrume.dat&hit=1&db\_idx=1

### Protein View: ACTS\_HUMAN

Actin, alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1

Database: SwissProt  
Score: 96  
Expect: 4.6e-06  
Monoisotopic mass (M<sub>r</sub>): 42366  
Calculated pI: 5.23  
Taxonomy: [Homo sapiens](#)

Sequence similarity is available as [an NCBI BLAST search of ACTS\\_HUMAN against nr](#).

#### Search parameters

Enzyme: Trypsin/P: cuts C-term side of KR.  
Fixed modifications: [Carbamidomethyl \(C\)](#)  
Variable modifications: [Oxidation \(M\)](#)  
Mass values searched: 118  
Mass values matched: 12

Protein sequence coverage: 33%

Matched peptides shown in **bold red**.

```
1 MCDDEDTTAL VCDNGSGLVK AGFAGDDAPR AVFPPSIVGRP RHQGMVMGMG
51 QKDSYVGVDEA QSKRGILITLK YPIEHGIITN WDDMEKIMWH TFYNELRVAP
101 EHHPTLLTEA PLNPKANREK MTQIMFETFN VPAMYVAIQ A VLSLYASGR
151 TGIIVLDSGDG VTHNVPIYEG YALPHAIMRL DLAGRDLDY LMKILTERGY
201 SFVTTAEREI VRDIKEKLCY VALDFENEMA TRASSSSLEK SYRLPDGQVI
251 TIGNERFRCP ETLFQPSFIG MESAGIHETT YNSIMKCID ID IRKDLYANNV
301 MSGGTTMYPG IADRMQKEIT ALAPSTMKIK IIAPPERKYS VMIGGSILAS
351 LSTFQQMWIT KQEYDEAGPS IVHRKCF
```

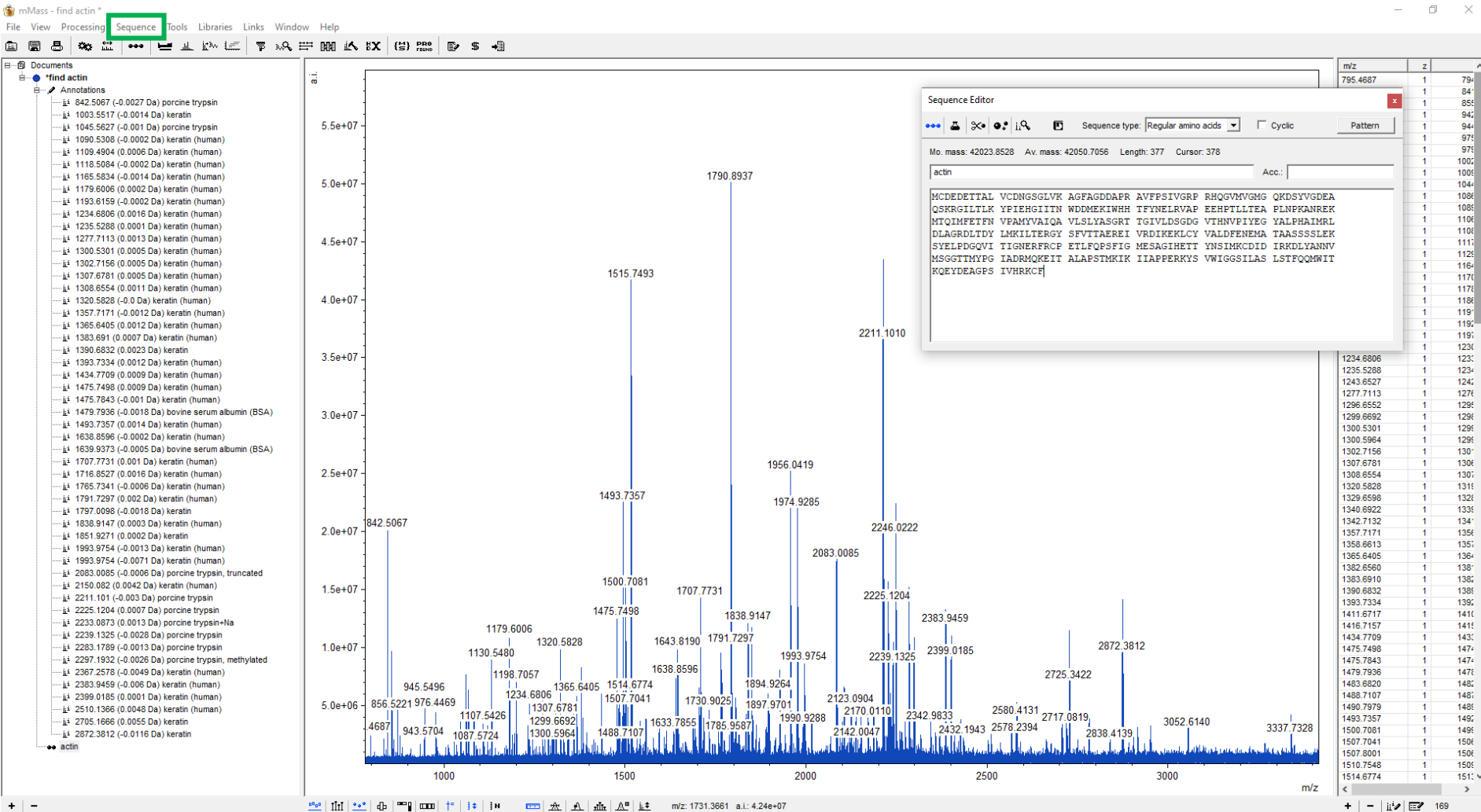
Unformatted sequence string: [377 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
Show  matched peptides only  predicted peptides also

Start – End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
21 – 30	976.4469	975.4396	975.4410	-1.41	0	K.AGFAGDDAPR.A
31 – 39	945.5496	944.5424	944.5444	-2.11	0	R.AVFPPSIVGR.P
31 – 41	1198.7057	1197.6985	1197.6982	0.19	1	R.AVFPPSIVGRP.R
42 – 52	1171.5700	1170.5627	1170.5638	-0.94	0	R.HQGMVMGMGQK.D
42 – 52	1187.5651	1186.5578	1186.5587	-0.77	0	R.HQGMVMGMGQK.D + Oxidation (M)
87 – 97	1515.7493	1514.7421	1514.7419	0.14	0	K.IWHHTFYNELR.V
98 – 115	1956.0419	1955.0346	1955.0364	-0.88	0	R.VAPEEHPTLLTEAPLNPK.A
199 – 208	1130.5480	1129.5407	1129.5404	0.31	0	R.GYSFVTTAER.E
241 – 256	1790.8937	1789.8864	1789.8846	0.98	0	K.SYELPDGQVITIGNER.F
294 – 314	2246.0222	2245.0150	2245.0143	0.27	0	K.DLYANVMMSGGTTMYPGIADR.M
331 – 337	795.4687	794.4614	794.4650	-4.55	0	K.IIAPPER.K
362 – 374	1500.7081	1499.7008	1499.7005	0.22	0	K.QEYDEAGPSIVHR.K

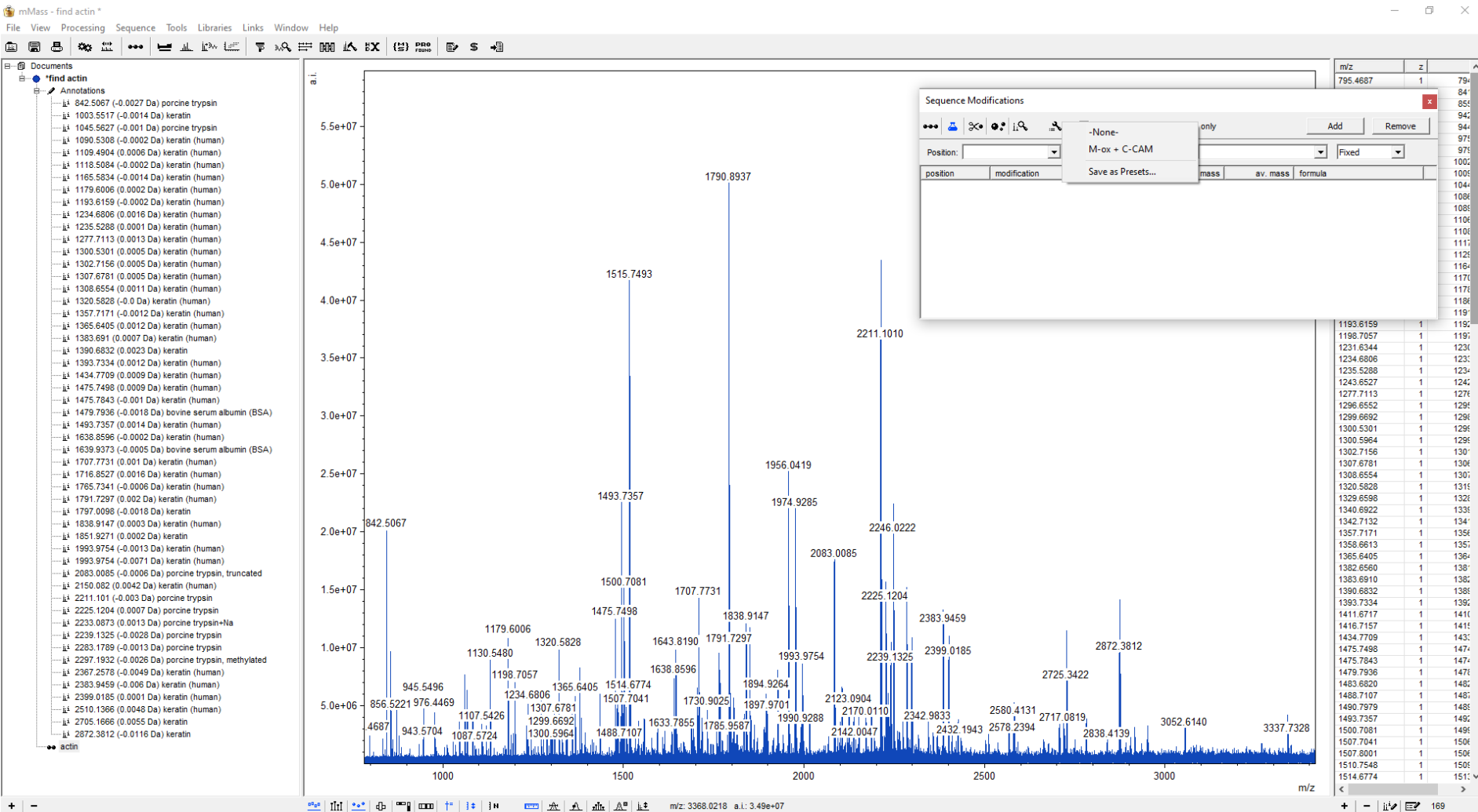
No match to: 856.5221, 943.5704, 980.5042, 1010.5308, 1087.5724, 1107.5426, 1192.5952, 1231.6344, 1243.6527, 1296.6552, 1299.6692, 1300.5964, 1329.6598, 1340.6922, 1342.7132, 1358.6613, 1382.6560, 1411.6717, 1416.7157, 1483.6820.

# mMass – contaminated peptide mixture (find actin)

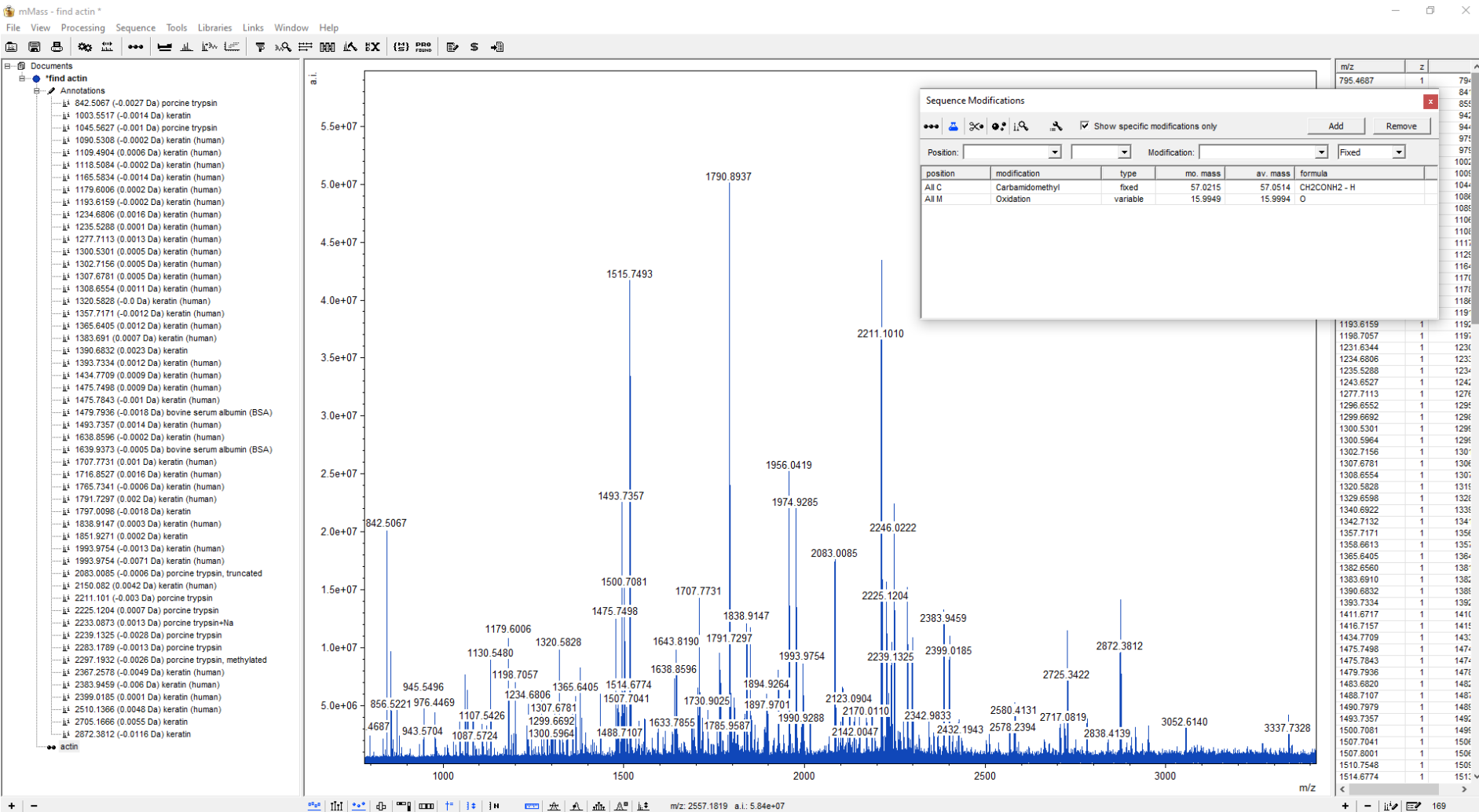


# mMass – contaminated peptide mixture (find actin)

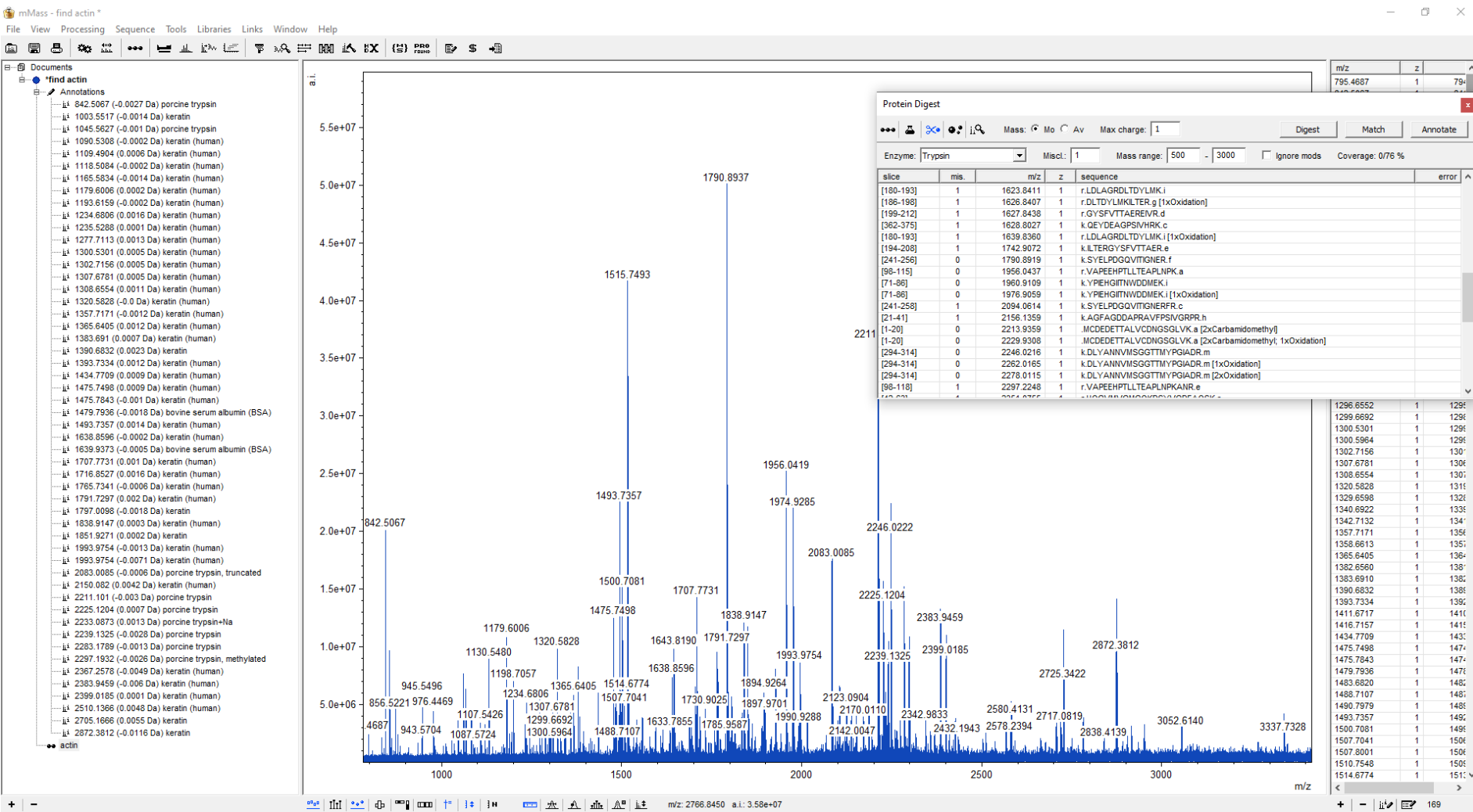
## add modifications (can use pre-sets)



# mMass – contaminated peptide mixture (find actin)

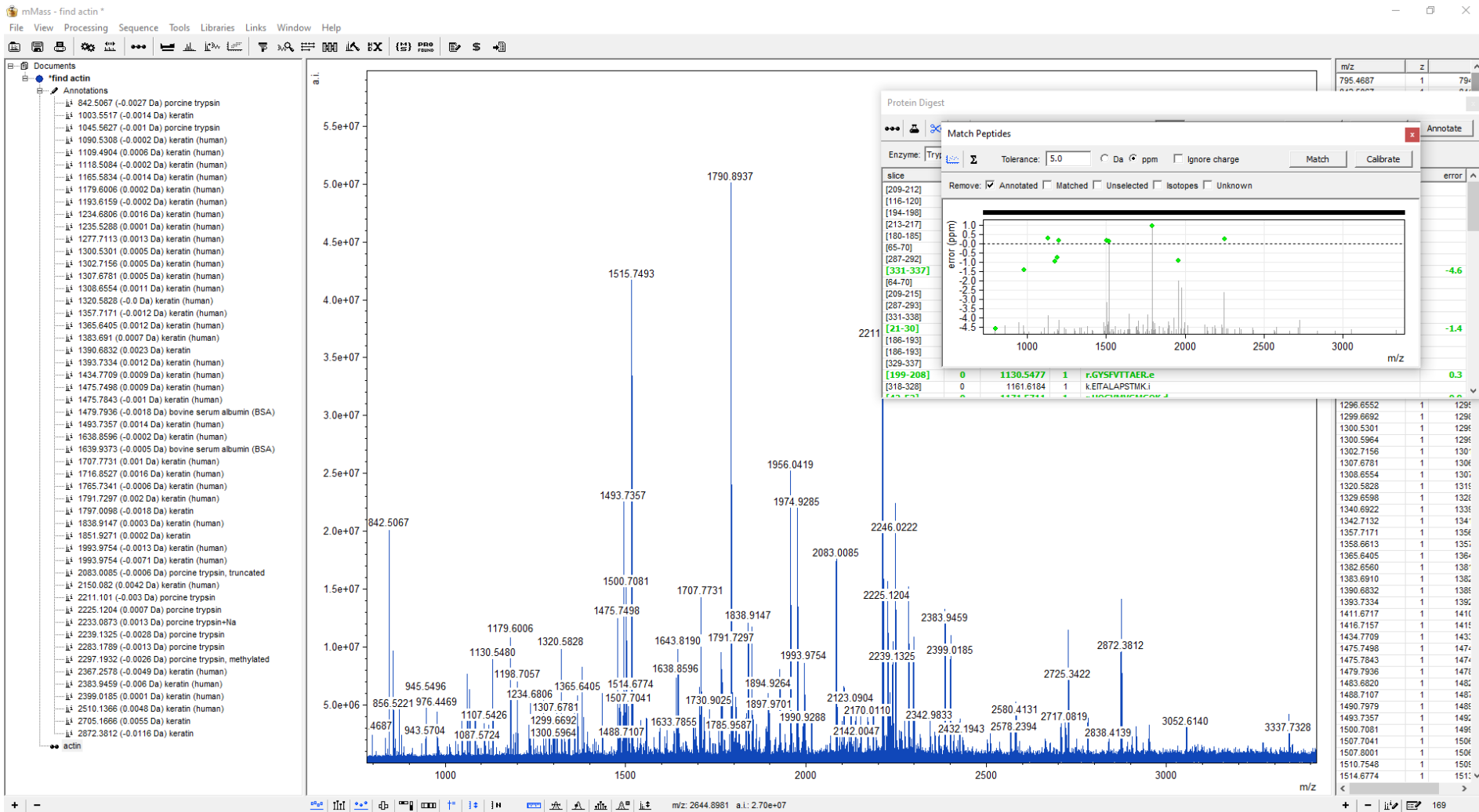


# mMass – contaminated peptide mixture (find actin) in silico digestion...



# mMass – contaminated peptide mixture (find actin)

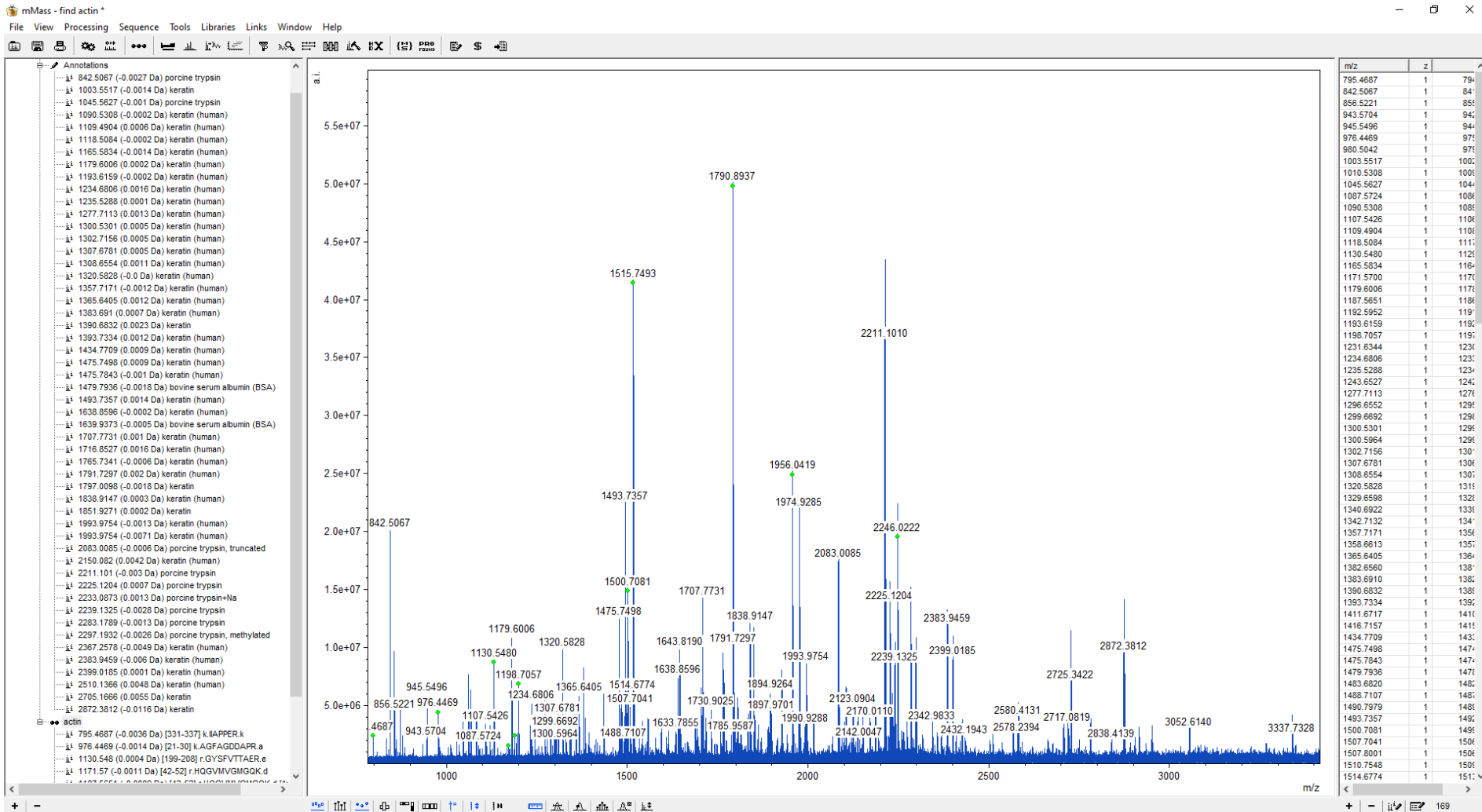
## ...and its assignment





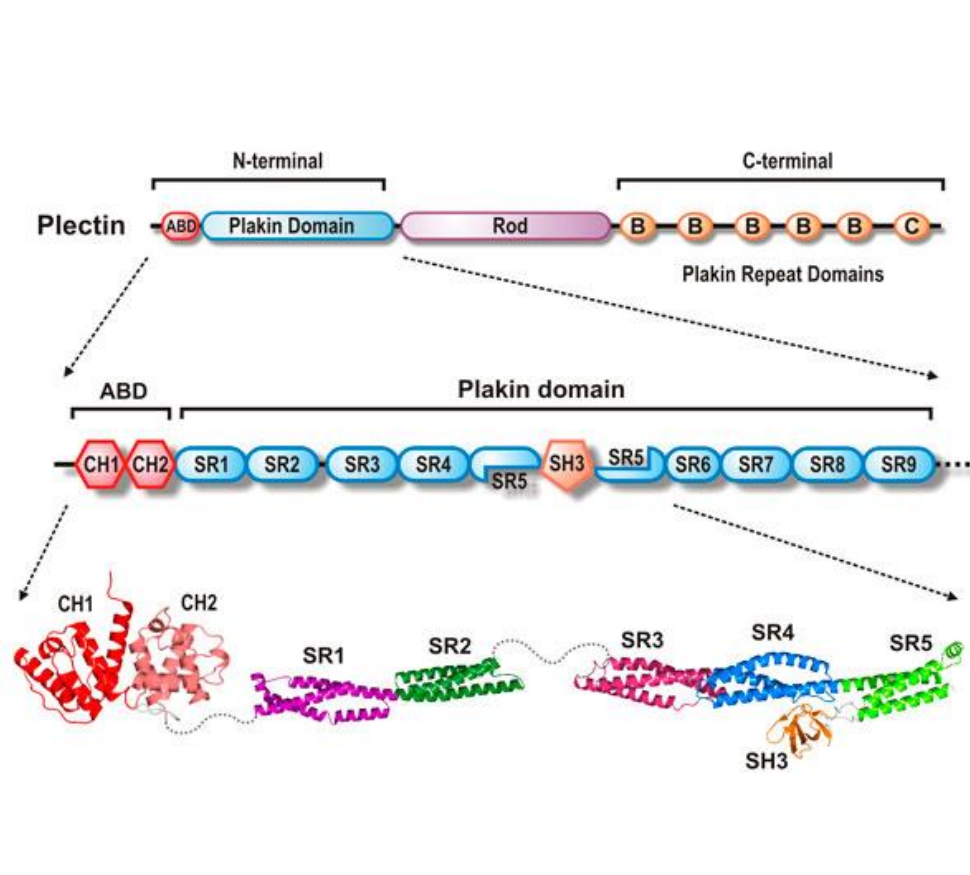
# mMass – contaminated peptide mixture (find actin)

## fully annotated spectrum



# mMass – the power of high resolution peptide mass fingerprinting - plectin

*Plectin* – huge cytoskeletal protein (530kDa, 4900 AAs, various splice variants)



MVAGMLMPRDLRAIYEVLFREGVMVAKKDRRPRSLPHVPGVTNLQVMMRAMASLRAGLVRETFWACHFYWYLTNEGIAHLRQYI  
 HLPPEIVPASLQRVRRPVAMVMPARRTPHVQAVQGGLGSPPKRGPLTEEQRVYRRKLEEVSPETVPVATTORTLARPGEPEP  
 ATDERDRVQKTKFTFKVWVKHLKIQKRHSIDLIEDLQDGNLISLLEVLSSGDSLPREKGRMRFHKLQNVQIALDYLRRHQVRLNIRND  
 DIADGNPKLTGLIWTIILHFQISDQVSGOSEDMTAKEKLLWSQRMVEGYQGLRCDNFNTSSWRROEGLFNAIHHRKPLLDIMNKVYRQ  
 TNLENLDOAFSAERDLGVTRLDPEDVDVPOPEKSIITYVSSLYDAMPVPRVDVODGVNARELQLRWQVEYRELVLLQLLWMRHHTA  
 AFEERRFSSFEIEILWSQFLKFKEMELPAKEADKNRSKGIYOSLEGAQVQGLKVPVGGYHPLDVEKEWGLHVAILEREKQLRSEF  
 ERLECLQRVITKLQMEAGLCEEQNLQADALLOSDVRRLLAAGKVPORAGEVERDLKADSMIRLLFNDVOTLTKDGRHPQGEQMYRVR  
 YRLHERLVAIRTEYNRLKAGVAAPATQVAQVTLQSVQRRPELEDSTLRYLQDLLAWVENQHRVDGAEWGDLPVSEAOQLGSHRG  
 LHQSIEEFKRAKIERARSDEGQLSPATRGAYRDCGLRDLQYAKLLNSKARLRLSLESHFSVAAATKELMWLNKEHEEVGFQWDSOR  
 NTNMTAKKESYSALMRELEKKEKKELQNGADRLREDHPARPTVESFOAALQTQWSWMQLCCICIEHLKENAAAYFOFFSDVREA  
 EGOLQKLEALRRKYSCDRSATVTRLEDLQDAQDEKEQNLNEYKGLSHLAKRAKAVVQLKPRHPHMRGRLLP LAVCDYQVQEV  
 TVHKGDECQLVGPAPSHWKVLLSSGSEAAVPSVCFVPPNPQEAQAVTRLEAQHOALVTLWHQLHVDMKSLLAWQSLRSDVQL  
 IRSWSLATFRTLKPEEQROALHSILEHYQAFLRDSDODAGGFPEDRLMAEREYSGCSHHYQQLLSQLEOGAQEESRCRQISELKDI  
 RLQLEACETRTVHRLRPLDKPEARECAQRIEQQKAAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELETLGKLEQVRSL  
 SAIYLEKLKLTISLVRGTQGAEEVLRAHEEQLKEAQAQVATLPELEATKASLKLRAQEAQAQPTFDALRDELGAQOEVGERLQORHG  
 ERDVEWRWRERVAIHLQFQSDIQVSGOSEDMTAKEKLLWSQRMVEGYQGLRCDNFNTSSWRROEGLFNAIHHRKPLLDIMNKVYRQ  
 ALLEEIERHGKEVVECFQAKFYINAQIDYELQVLYKQAEPLVSPAKPKVQSGSEVIOEVYDLRTHYSELTTLSQYKFISETLRR  
 MEEERLAEQQRAEERLAEVEAELEKQRLAEAAQAKAQAEREAKELOQRMOQEEVYRREEAAVDAQOQKRISQIELLEQLORLS  
 SEAEIQAKARQAEAEERSRLRIEIEIRVRLQLEATERQGAEGEQLARARAEAEAAQKRAQEAERLRRVQDQESQORKROAE  
 VELASRVKAEAAAREKORALQAEELRLQAEAEARLRQAEVERARQVQVALETAORSAAEALQSKRASFAEKTAQLESHEEH  
 VAVAQLEAEARRAQQAEEAREAREERELERWQLKANEALRLQLEAVEAQKSLAQAEAEKQKEAEERARRRQKAEQEAQV  
 QRELAEOELEKORLAEGTAQORLAEOELRLRAETEEOEQORLLEELARLQREAAATQRKQRELEAEALKVRAMEVLLASKA  
 RAEEESRSTSEKSKORLEAEAGRRELAEAAARLALAEAKRQRLAEEDAARQRAEAERVLAELAAIGEAERLTKTEAIALKEKE  
 AENRRLRLAEDEAFORRRLEEQAAHQKADIEERLAQLRKSADSELEROKGLVEDTLRORROVEEELIALKASFKAAGKAELEEL  
 GRIRSNADTLRSKEQAELEEARQRLAAEERRRRAEERVQKSLAAEAAARQKAALEEVERLKAQVVEARRLRERAEQESAR  
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 SAEQOQAARQAQAQAQAEKLRKAEQEAARRAAQEAALRQKAQAADAEKHKKFAEQTLRQKAQVQELTTLRLQLEETDHOXKLL  
 DEELORLKAEAEARQRSQVEEELFSVRVQMEELSKLKARIEAENRALLRDKDNTORFLQEAEEKMQVAEEAARLSVAAQEAAR  
 RLQLEAEEDLAQORALAEKMLKEMKQAVQEAERLKAEAELLQQQKELAEQOARRLOEDKEQMAQQLAETGORTLEAERQRLE  
 MSAAERLRLVAEMSRQAQRAEDAQRFRKQAEIEGKHLRTELATQEVTLVOTLEIQRQSDHDAERLREIAELEREKEKLOQ  
 EAKLLQLKSEEMQTVQOQLEQLQOQSLSEKDSLLQRRERFIEQEKAKLEQLQFQDEVAQAQQLREEQORQQQOQMEQERQLVA  
 SMEAARRRQHEAEEGVRRKQOEELQLEQORROQEELLAENORLREQLLLEEQHRAALAHSEVTAASQVAATKTLPNGRDALDG  
 PAEAEPHFSFDGLRRKVSQAORLQEAAGLISAEELQRLAQGHITVDLARREDRVRHLQGRSIAAGLLKATNEKLSVYALQRLQSLP  
 GTAILLEAQAAAGFLDVPVNRRLTVNEAVKEGVGPELHKLHLLSAERAVTYKDPYTGQOISFOAMQKGLVREHGRILLEAQIAT  
 GGVIDPVHSHRVPVDVAVYRGGFDEEMNRVLADPDDTKGFFDPNTHENTLTYLQLLERCVEDPGLCLPLTKAAKAGGELVYDTS  
 EARDVFEKATVSAPPKGFQKTVIWEINSEYFTEAQRDRLLRQFRTRGRITVEKIIKTIIVVEEQEKRLVLSVPAEELLESV  
 IDRELQYQQRGERSVDAEVDTVRRALRANVIAQVWLEEGQKLSYNAKLLKLLPSMDMAVALLAEQAQGTGHIDPATRSARLTV  
 EAVRAGLVGPEHKEALLSAEKAVTGYRDPYTVGGVSLFQALKGLLPRFOGLRLLDAQLSTGVIDPYSKSHRVPDLACARGCLDEET  
 SRLASPRADAKAYSDPSTGEPATYELGQKCRPDQLTGLSLPLSEKAARQEELEYSLOEAERTFEKTPVEVPVGGFKGRVTYV  
 WELISSEYFTEAQRQELLROFRTKGTVEKIVTEVEVETLRQERLSFSGLRAPVSEALLASGLVLSRAQFELKDKGKTTVKDLSL  
 GSVRTLQSGSGLAGILEDTKEKVSIEAMRRGLRATTAALLAEQAATGFLVDPVNRQRLVYHEAVKAVGVGPELHEQLLSAEKA  
 VTGYRDPYSGSTISLFOAMQKGLVLRHQGIRLLEAQIATGQIDPVHSHRVPVDVAVYRGGFDEEMNRVLADPDDTKGFFDPNTHEN  
 LTYRQLLERCVEDPGLRLLPLKGAKEAVVETTVQVYTEETRRFAFEITQIDPFGGSHGSGTMSLWVEMQDLPEEQARQLMAD  
 FGAGRVTKERMIHIIIIEKTEIIRQOGLASVYVRRRLTAEDLFEARISLETYLLRREGSRRLREALEEAESAVCYLGTGSAVGYLPGS  
 ROTLSYQALKGLLSAEVAARLLEAAQAATGFLDVPVKGERLTVDEAVRKGVLGPELHDLRLLSAERAVTYGYPYQETGTLGQAMKKE  
 LIPTAEALLLDAQLTAQVDPRLGFHPLLEVAVRQYLVNKTQHDQLEPSEVRSYVDPSTDERLSYTLQRCRRDDKGTGVLPLS  
 DAKLTFRGLRKQITMEEVRSQVMDAATLQLREGLTSIEEVTNKLQKLFEGTSGIAGVFVADATKREYSYQAMKGIIRGPATFELLE  
 AQATGYVIDPIKGLKLTVEAVRMGIVGPEFKDKLLSAERAVTYGYPYSGKLSLFOAMQKGLVLRHQGIRLLEAQIATGQIDPEESH  
 RLPVEVAYKRGFLDEEMNILLTDPDDTKGFFDPNTEENLTYLQLMERCITDPOTGLCLPLKKEKRRKTSKSSVRRKRVYMDPST  
 GKEMSVYEAARKGLIDHQTLYLESECEVEEITSSSDGVVKSMDIRRSRQYDIDDIAKNLDRSALDQYRAGLSTIEFADMLVSG  
 NAGGFRSSSSVSGSSYPIPAVSRTQLASVDPTEETGPVAGILDTETLEKVSITEAMHNRNLVDNITGQRLLLEAQACTGQIDPSTG  
 ERFPVTDVANKGLVDKIMVDRINLAQKAFCEGFEDPRRTKMSAAQALKKGLWLYYEAQRGLVDEVOYLTGLLEPDTPGAAGLDELQR  
 GTVDARTAQKLRDVGAYSXYLTKPKTKLSYKDALDRMSVVEETGLRLLLEAAQAQTKGYSPYSVSGSGSTAGSRGTSRGSRA  
 SRRGSDATGSGFSMTFSSSYSSSYGRRYASGSSASLGGPESA

# mMass – the power of high resolution

## Analytical challenge

trypsin digestion (500-3000, Met-ox, Cys-CAM, 1 missed cleavage)  
yields 1171 theoretical peptides, 102 are isobaric

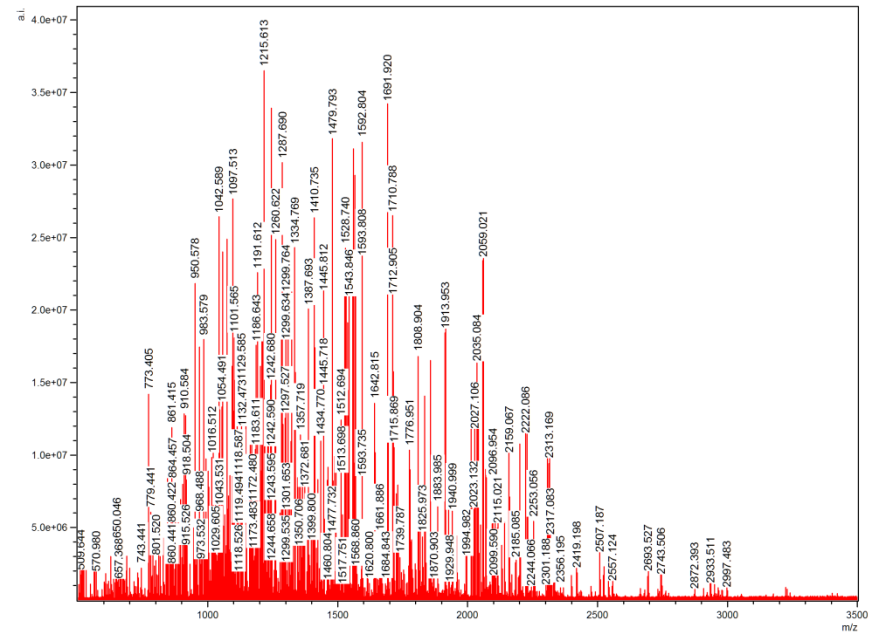
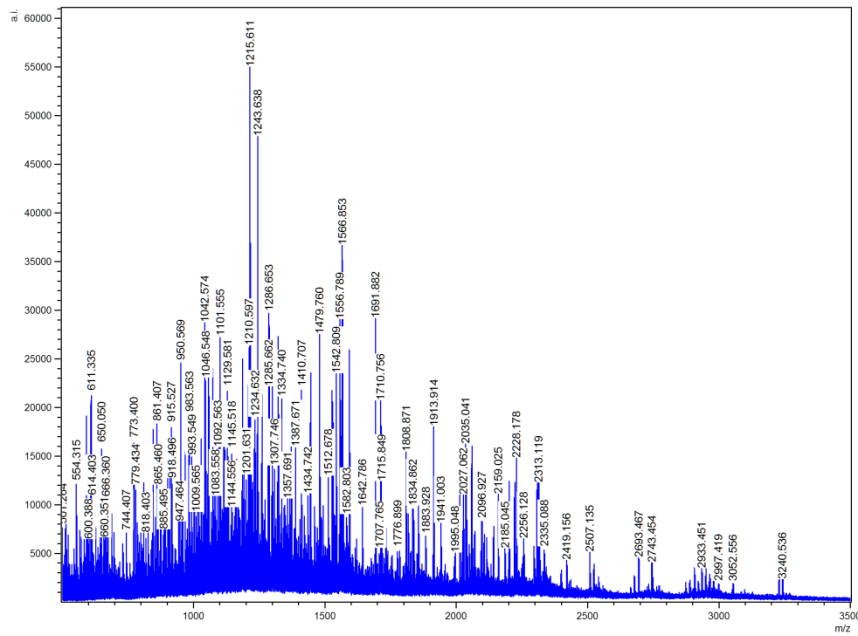
significant number of repetitive sequences

[1745-1749]	0	633.28385	EEAER
[1762-1766]	0	633.28385	EEAER
[1804-1808]	0	633.28385	EEAER
[2122-2126]	0	633.28385	EAEER

[1493-1498]	1	789.38496	AEEER
[1745-1750]	1	789.38496	EEAER
[2121-2126]	1	789.38496	REAER

PAAEAEPEHSFDGLRRKVSQAQLQEAGILSAEELQRLAQGHTTVDELARREDVRHYLQGRSSIAGLLLKATNEKLSV  
YAALQRQLLSPGTALILLEAQAASGFLLDPVRNRRLTVNEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTQQQISLF  
QAMQKGLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYRRGYFDEEMNRVLADPSDDTKGFFDPNTHENLTYLQ  
LLERCVEDPETGLCLLPLTDKAAKGELVYTDSEARDVFEKATVSAPFGKFQKTVTIWEIINSEYFTAQRDLLR  
QFRTGRITVEKIIKIIITVVEEQEQKGRLCFEGLRSLVPAELLESRVIDRELYQQLQRGERSVRDVAEVDTVRRAL  
RGANVIAGVWLEEAGQKLSIYNALKKDLLPSDMAVALLEAQAAGTGHIDPAT SARLTVDEAVRAGLVGPEFHEKLLS  
AEKAVTGYRDPYTQGSVSLFQALKKGLIPREQGLRLLDAQLSTGGIVDPSKSHRVPLDVA CARGCLDEETS RALSAP  
RADAKAYSDPSTGEPATYGELQQRCPDQLTGLSLLPLSEKAARARQEELYSELQARETFEKT PVEVPVGGFKGRTV  
TVWELISSEYFTAQRQELLRQFRTGKVTVEKVIKILITIVVEVETLRQERLSFSGLRAPVPASELLASGVLSRAQF  
EQLKDGKTTVKDLSELGSRVTLQSGGCLAGIYLEDTKEKVSIEAMRRGLLRATTAALLLEAQAATGFLVDPVRNQ  
RLYVHEAVKAGVVGPPELHEQLLSAEKAVTGYRDPYSGSTISLFQAMQKGLVLRQHGI RLLLEAQIATGGIIDPVHSHR  
VPVDVAYQRGYFSEEMNRVLADPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGAEKAEEVETTQVYT  
EEETRRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEKTEIIRQQG  
LASDYVRRRLTAEDLFEARIISLETYNLLREGTRSLREALEAESAWCYLYGTGSVAGVYLPGSRQTL SIYQALKKG  
LLSAEVARLLLEAQAATGFLLDPVKGERLTVDEAVRKGVLVGPPELHDLRLLSAERAVTGYRDPYTEQTI SFLQAMKKE  
IPTEEALRLLDAQLATGGIVDPRLG FHLPLEVAYQRGYLNKTDHDLQLEPSEVRSYVDPSTDERLSY TQLLRRCRRD  
DGTGQLLLPLSDARKLTFRGLRKQITMEELVRSQVMD EATALQLEGLTSIEEVTKNLQKFLGTS CIAGVFVDATK  
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LISLFQAMKKGILKDHGIRLLEAQIATGGIIDPEESHRLPVEVAYKRGLFDEEMNEILTDPSDDTKGFFDPNTEEN  
LTYLQLMERCITDPQTGLCLLPLKEKKRERKTSKSSVRKRRVVIDVPETGKEMSVYEAYRKGLIDHQTYLELSEQE

## MALDI-TOF vs MALDI-FT-ICR



# mMass – the power of high resolution

## Only FT-ICR data are reliable

TOF

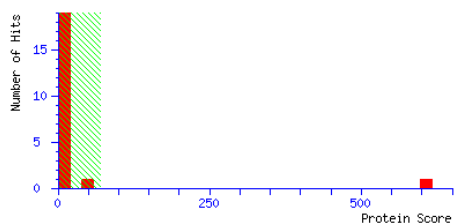
ICR

### MATRIX SCIENCE Mascot Search Results

User : petr  
 Email : pman@biomed.cas.cz  
 Search title : PM1  
 Database : SwissProt 2015\_08 (549008 sequences; 195692017 residues)  
 Timestamp : 19 Aug 2015 at 08:45:54 GMT  
 Top Score : 608 for PLEC\_HUMAN, Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3

### 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 70 are significant ( $p < 0.05$ ).



### Concise Protein Summary Report

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

Significance threshold  $p < 0.05$  Max. number of hits: AUTO

Preferred taxonomy: All entries

[Re-Search All](#) [Search Unmatched](#)

1. [PLEC\\_HUMAN](#) Mass: 533462 Score: 608 Expect: 8.7e-56 Matches: 384  
 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3

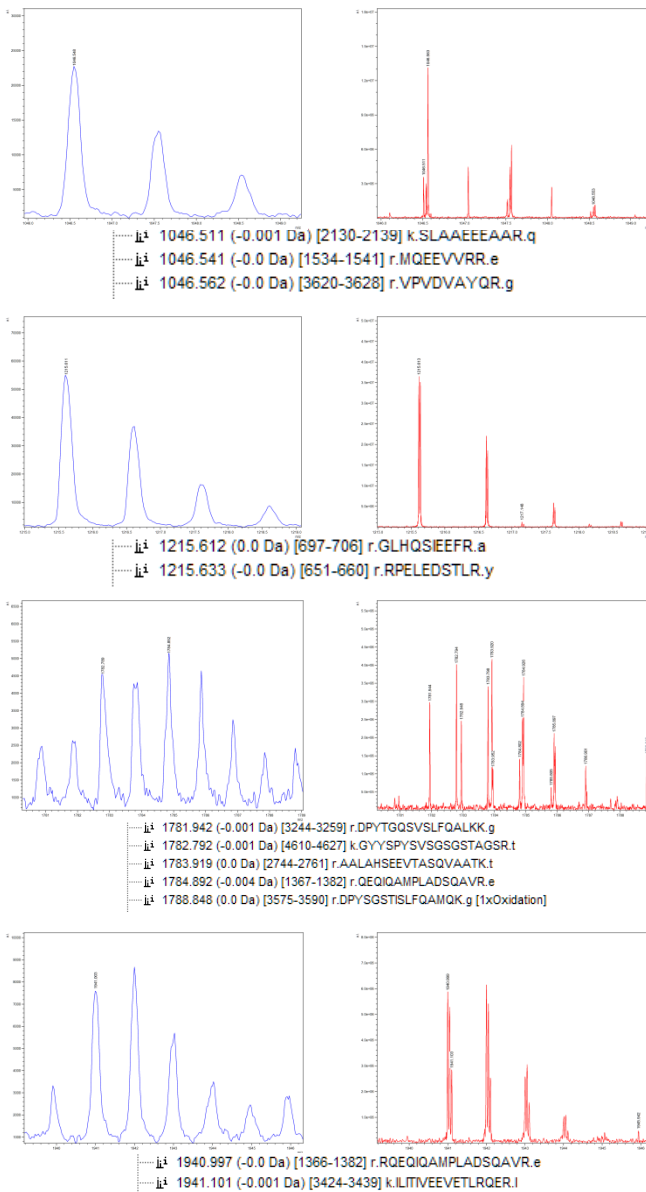
nearly 400 peptides  
 assigned and seq. cov ~70%

Protein sequence coverage: 67%

Matched peptides shown in **bold red**.

```

1 MVAQMLNRQD QLAALVEILP RSTFQVARD RRRSLRSLVY FSTYLQNRG
51 ANGLAARGL VRETFANCR YVLTITRDA RLKFLKLPF EIVFAELQYF
101 RRFQSNMFA RFFTPYQVQ DLSDFYFRH RLKFKRQYF SGEELTFYR
151 EIPYVFAITG RILARPOPFR APATRDESRV QDQTFIQVR RKLIDQGRH
201 SDLVYLRDQ INLLALLLVL SGLSLFRSD RRRFRKIQRY QIALYLRSE
251 QYQVTRSD DIGNDFPST LQDNTIILV FFLDQVPSD QDGTAKAVK
301 LALAQDQRE QVGLRQVLR TNRGCGPFL MRRFRKPLV LIRNRYVTR
351 TMLERLQAF SVARCELVG RLLVDREDAV PQRKESLIT YVSLVLDAMP
401 RYVYDQVLR ANLIDQLDQ YVSLVLLIQ MRRHTAAGE ERDFPSPFEE
451 RELLANGLV RQELRDLRQ ADRNSGGLV QDLRANQAG QLVFQPFQR
501 LQVREWRRL KALLERERQ ISEFERLRG LQRVTLQDM EAGGLERDQL
551 QNALLQSDV RLLAGWTFP RAGEVERLD RASMERLLF RQVTLQDRG
601 RYDQDQVLR YVLESLRDA IFTYRDLRQ AVAARPAQV ADYVQVQVR
651 RPELEDSTLR KILLAWARV RQKRVGQGR MVDVLSVLR QDGLRGLQD
701 IIEFRPACIE RANRORQQA PATRGAVPCD LQGLLQYAR LIRNSGAEK
751 ILESLRQVA AYVLELRQK RSEKQYRVR VWRSTGTEK RSEVYLRMR
801 ELEIKERKIC ELQAGKRLR RRRFRPFTY ESTGALQTC RNSGLDCCO
851 IEARLRQMA YVDFRQVH AEQLQVQGR ALRKYVCCR SATYVLRDL
901 LQVQKQSDR LNRGLRQVL LADQDVAQV LKRFRRPVR RQELVLYLV
951 DLYVQVTVR RQECQLQVQ AGRFRQVLS RQSEAAVPS YVDFYFRQD
1001 LKAEAVTLE AQCVALTIR KLVYDQSLR LAMHLRSDV QLRNSLQAT
1051 RPTLRFQDR QALLRLLRQ QVLRQNSLA GQFRQRRAR RERQVQNRH
1101 RYQQLQRLS QDQSRERQD RCIKRLDTR LQLEKQETH YRHLRSLQR
1151 RPARCQARI AEQQQAAEV EQLRQVQAR SAZEAVVAL PPSRPAQPL
1201 RHEVLYLNR LQVQRLSLR VLERITRVL VYRQVQARE VAAHRRKQK
1251 RQAVYVLRK ELRATQVSR LQKQKQDQ PTERLRALR RQAVRQRV
1301 QDGRQZTE VERARRVQD LIRNQVALA QTVRQRLR QLRQVAYR
1351 RIRYGLRML QNRQGRQD QMP LKQVQ VYRQLQDR LKESIRQSE
1401 RYECRQKIE QVNLVETIR LQVYVQVQE ESTVALQSD PQDQVRRVH
1451 DEYVLRTRY SELTITLQV IYVIRYLAR RQDEERLQD QRAEERELA
1501 RYVALEQRQ QVLRARQGR AGRFQEARQ QDQKQYRVR RERVAVQDQ
1551 QYRQLQVDR QVLRQVSRV QVRRQKQAR RSHVLRLEK QVLRQVQDR
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1651 RYVLRQVGR RARARERQR ALQALTEEL QAELERELR QVRRVQVQY
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1751 AQQQAAEVA RERARERELR RQLVSRLEL RQVLRQVQD QVLRQVQAR
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1851 RYLRLQVTE QDQKQVQDR LKQVLRQVQ RERVQVQAR RQVLRARQD
1901 RYVLRARER RERARERTE RSHQVLRAR QVLRQVQAR ALRQVLRAR
1951 RYVLRARER RARQVQVQR VLAELAAIQ EATRLYRTE TALRRERAR
2001 RYVLRARER RYVLRARER RYVLRARER RYVLRARER RYVLRARER
2051 RYVLRARER RYVLRARER RYVLRARER RYVLRARER RYVLRARER
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2151 RYVLRARER RYVLRARER RQVLRQVQD QVLRQVQDR RYVLRARER
2201 RYVLRARER RYVLRARER RYVLRARER RYVLRARER RYVLRARER
2251 RYVLRARER RYVLRARER RYVLRARER RYVLRARER RYVLRARER
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4601 RYVLRARER RYVLRARER RYVLRARER RYVLRARER RYVLRARER
4651 RYVLRARER RYVLRARER RYVLRARER RYVLRARER RYVLRARER
    
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# mMass – the power of high resolution

Only FT-ICR data are reliable

TOF

ICR

MS  
SC

User  
Email  
Search  
Database  
Time  
Top Sc

Mass

Protein  
Protein

Number of Hits

Conc

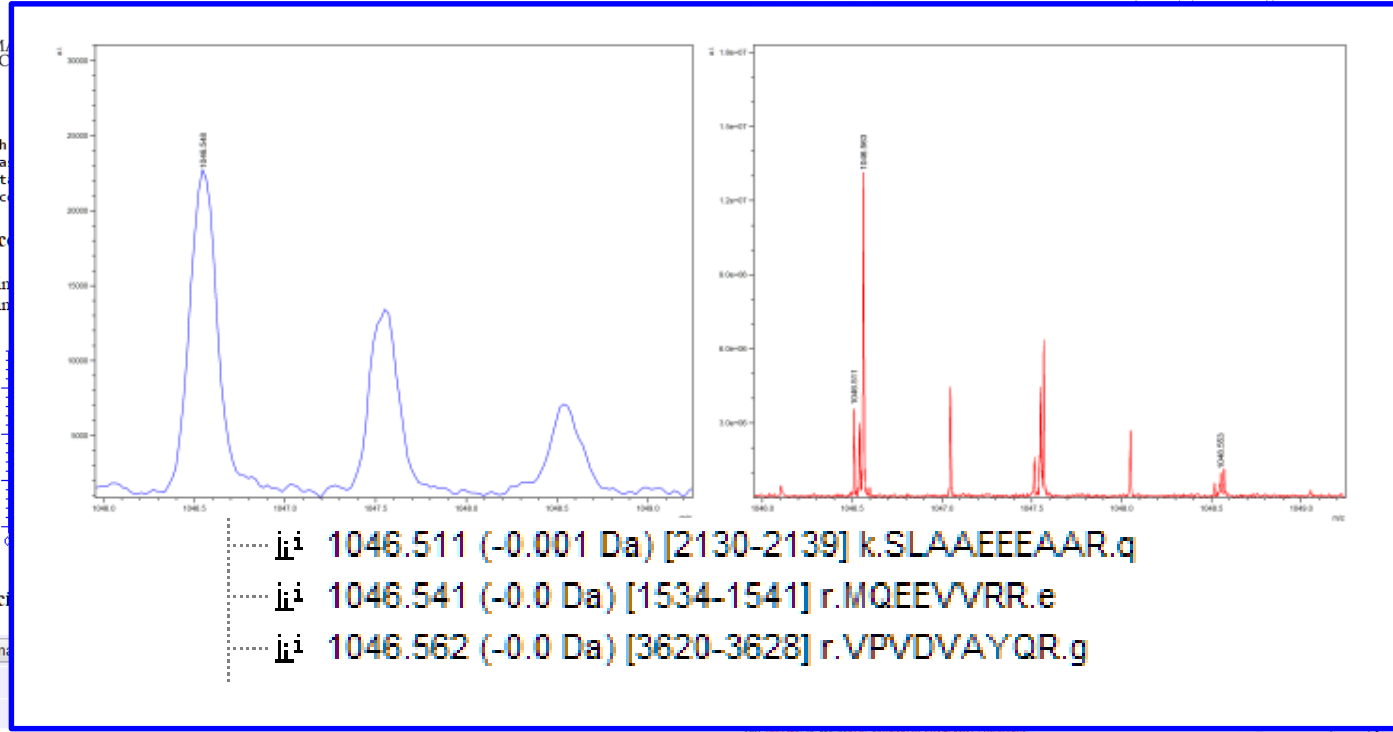
Form

Re-Search All Search Unmatched

1. [PLEC\\_HUMAN](#) Mass: 533462 Score: 608 Expect: 8.7e-56 Matches: 384  
Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3

nearly 400 peptides  
assigned and seq. cov ~70%

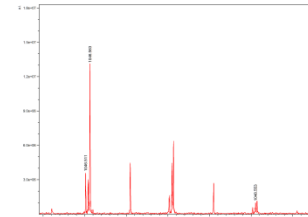
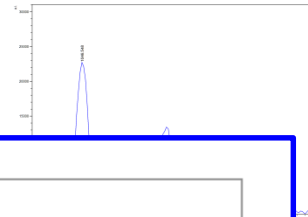
Protein sequence coverage: 67%  
Matched peptides shown in **bold red**.



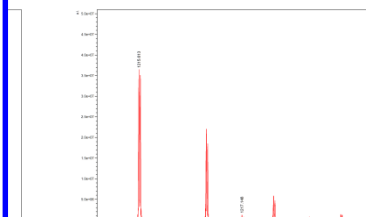
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3351 EQGARGRE LYRQAMET FETPTVEY GFFRIVTV WELISSEVPT
3401 ARQQLLQK PRIGYVTEK VKEILITVE PVTYLERL SFQGRAPVP
3451 AELALADVL SDQRFQGR GPTVWVLSL LQVWELLDL SGLDCTVLE
3501 STREKIVSIE AMHGLIAT TAALLKGA ATGVLDVPR IQLVYVRAV
3551 SDVAVFRLR KQLLAKGV TQDRPFSR TSLPQAKR QVLRQKQIR
3601 LKGLDQIG IIPVNRNR PAVHAGNR FERRRMTLA DEELCTQFF
3651 DYNTRNLYL KQLLERQSD PFTGLRLL KQSEGVNVE TTYVTEET
3701 BRPFEEIQL IPGQSHQSD TSLRNVGS DLIFEEKRAQ LMAQKQRY
3751 TRENIIIII EILDETELR QQLAVDNY RMLTADLF EAKLILFTY
3801 NLRKTEEL RSLKESAM CVTQVDFP QVCESEDF LSTQDAKRY
3851 LLSAEVALL LEQAATVFL LEPVRESLV VEGAVKVLV GPELRELLS
3901 LEMVDFDR PFTQVLSL QMRELLPT EEARLLDQ LATGVDFPR
3951 LKFLPLDQ VQKILSDY IQGAKRPM RAVYKPTTE RLVTELES
4001 CRDDDTQL LFLSDARL TFRLEKDT MELVRSQM DEATGLSE
4051 GLIIEPTV HGFLEDFP CIAQVQAT KRLVQAN RQGLRQPLA
4101 RLLKADAT QVDFVQL VLRVAVNM GQVFRVEM LLSARATL
4151 YQVYKSLI SLQAWQGL ILKQDPLL EAKIATGII DPEERSLPT
4201 KVALRGLD RENNLIQF SDQTRFPP NTRNLYAQ LMRKIQTPQ
4251 TUGLLPLSE RQSEKLSR SFQSRVAT VQVTRVNM VEGVRSLL
4301 DQVTELEL QECREIITL SSSQVYVM IIRRSQGV DIDLAKQL
4351 IIRALADIR AGTLSTRA DMSKAGR RSESSVGS SVFESVAVS
4401 YGLASDFP TELIPVAV IICETLEVP TRVNRVNV DNTQGLLE
4451 AQACTGIID PSTRDFPT DAVSSLVCE DVCEDLQK RPFQRFDR
4501 YTRNSAQA LKQWLYEA QGFLVQVL TQGLREPTP GRVLEDAQ
4551 RQVYDARQ RLVGAVNR YVDFPQCE LTRRDLRQ RYDZQDLC
4601 LKAACTGK VYFVNGA QVAGKQES RQSRAGRA SFKATQSF
4651 DNTFSSSV SSVQRVAS QSASLQSE SAVA
    
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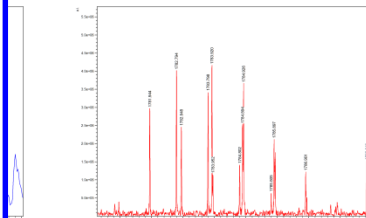
**li**<sup>i</sup> 1784.892 (-0.004 Da) [1367-1382] r.QEQIAMPLADSQAVR.e  
**li**<sup>i</sup> 1788.848 (0.0 Da) [3575-3590] r.DPYSGSTSLFQAMQK.g [1xOxidation]



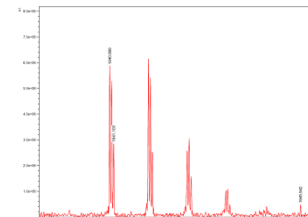
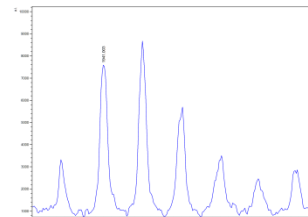
**li**<sup>i</sup> [2130-2139] k.SLAEEEEAAAR.q  
**li**<sup>i</sup> [1534-1541] r.MQEEVVRR.e  
**li**<sup>i</sup> [3620-3628] r.VPVDVAYQR.g



**li**<sup>i</sup> [697-706] r.GLHQSIEEFR.a  
**li**<sup>i</sup> [651-660] r.RPELEDSTLR.y



**li**<sup>i</sup> [3244-3259] r.DPYTQGSVSLFQALKK.g  
**li**<sup>i</sup> [4610-4627] k.GYYSPYSVSGSGTAGSR.t  
**li**<sup>i</sup> [4-2761] r.AALAHSEEVTSQVAATK.t



**li**<sup>i</sup> 1940.997 (-0.0 Da) [1366-1382] r.QEQIAMPLADSQAVR.e  
**li**<sup>i</sup> 1941.101 (-0.001 Da) [3424-3439] k.LITVVEETLRQER.I

# mMass – the power of high resolution

Only FT-ICR data are reliable

TOF

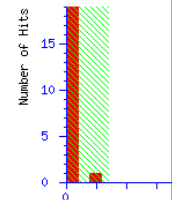
ICR

## MATRIX SCIENCE Mascot Search Results

User : p  
 Email : p  
 Search title : P  
 Database : S  
 Timestamp : 1  
 Top Score : 6

### Mascot Score Histogram

Protein score is  $10^4 \times$   
 Protein scores greater



### Concise Protein Summary

Format As Concise  
 Significant  
 Preferred  
 Re-Search All

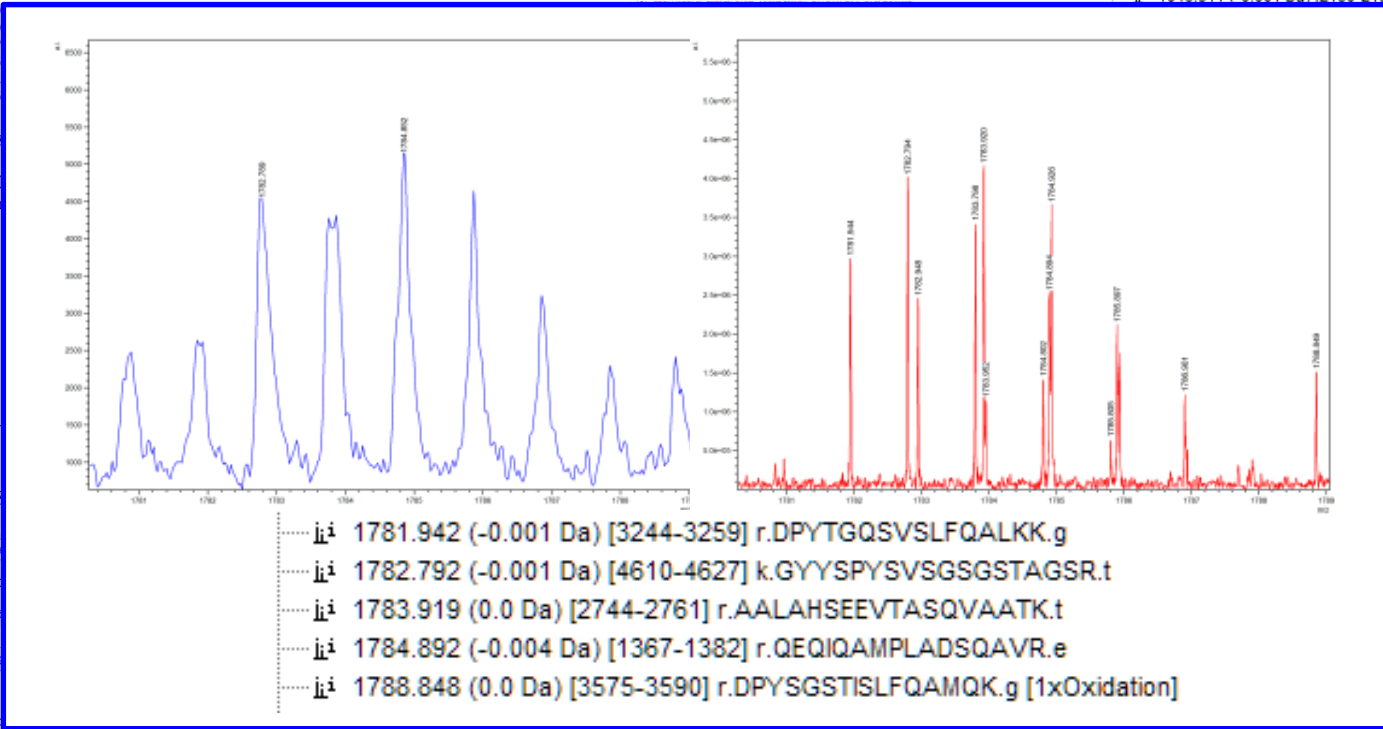
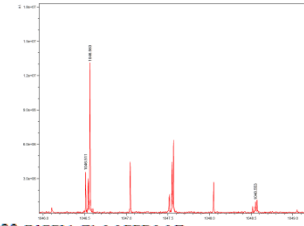
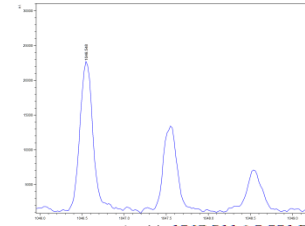
1. [PLEC\\_HUMAN](#)  
 Plectin OS=H

Protein sequence coverage: 67%

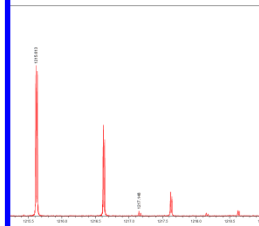
Matched peptides shown in **bold red**.

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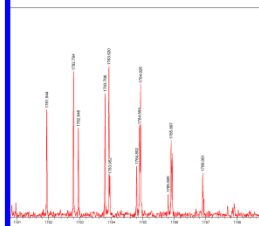
1 MVAQMLNRQD QLAIVLEVF RSTFQVARD RRFSLSEVY FVTILQNR
51 AAGSLAARGL VRETFANCF YVLTREDAE RLKCYRLPP EIVFALQPY
101 RQFAMHMA RHTFQVAVY QVDSFFVDS PLFMRKQTY SGELETFY
151 EIPVFAITG RILASPOEF APATERSDY QDQTFIQVY RKLIDQRIE
201 SDLVLELSDG INLLILLEVY SGEFLRFSD RMRFRKIQVY QIALVLRSE
251 QVQVTRISD DIADDFPST LQINTIILA FQISFVQSD QRCNTAKRY
301 LALMQDREH QVGLQKQDF TRNSGDFEL MLRFRKQPL LIRNRYTRQ
351 TMLERLQAF SVARSLCQV RLLDREDAV PQRERSKIT YVSLVLDAMP
401 RVPVQVQRV ARDLQVQRF TRFDVLLIQ MRHRTAGE RRFPRFEE
    
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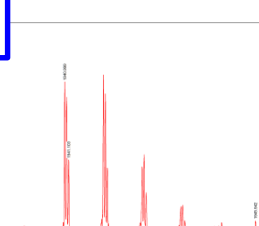
i.i 1046.511 (-0.001 Da) [2130-2139] k.SLAEEEEAAAR.q  
 .MQEEVRR.e  
 .VPVDVAYQR.g



.HQSEEFR.a  
 PELEDSTLR.y

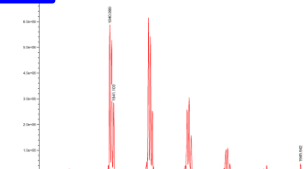
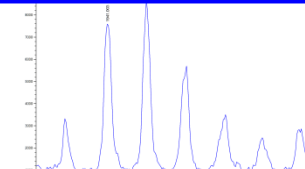


QSVSLFQALKK.g  
 PYSVSGSGTAGSR.t  
 EVTASQVAATK.t  
 AMPLADSQAVR.e  
 ISLFQAMQK.g [1xOxidation]



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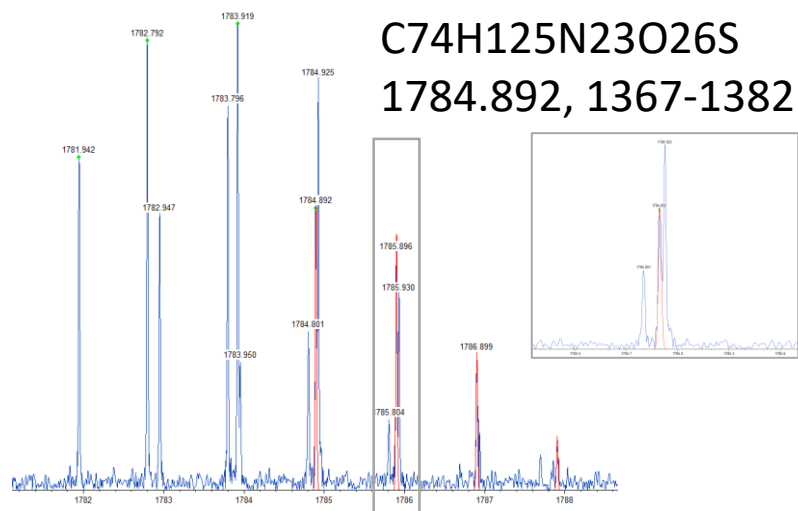
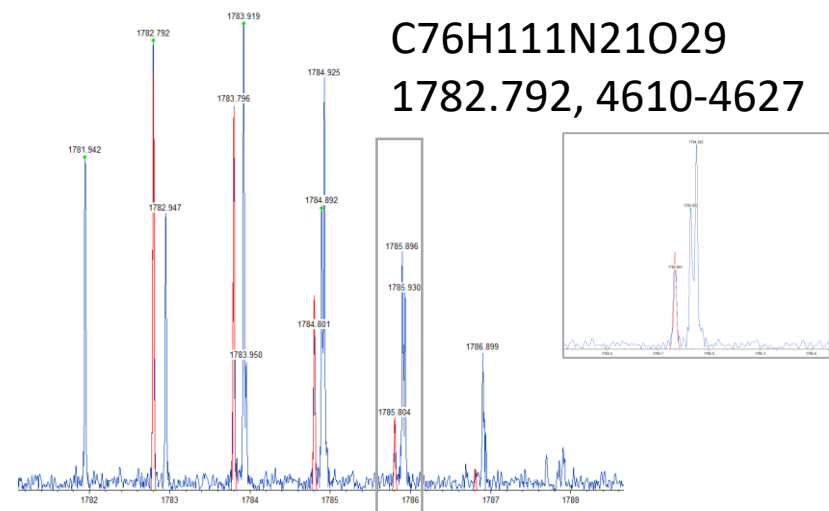
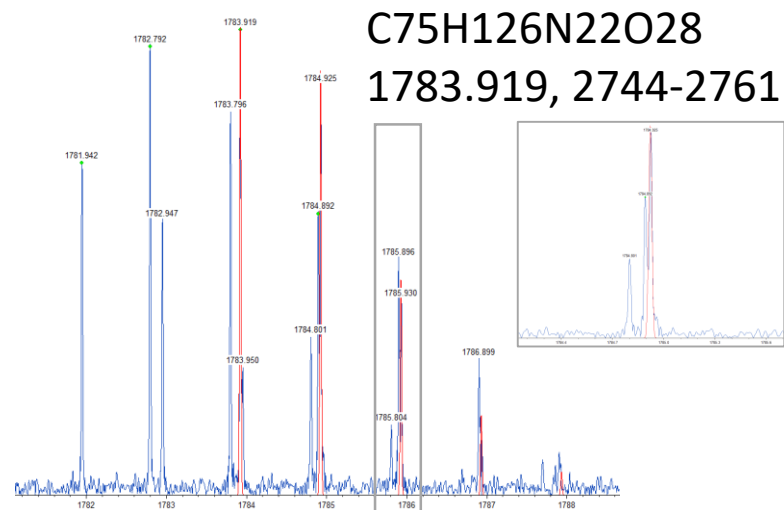
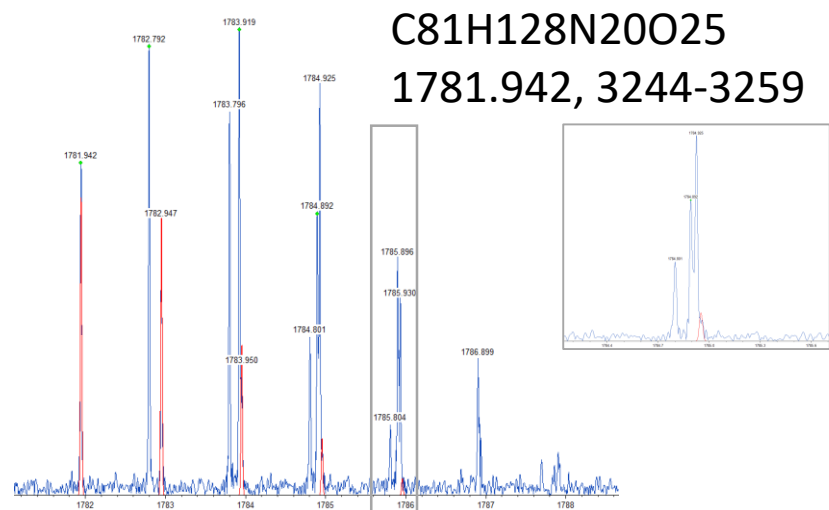
3901 MLRSETRH REALEAERW CYYTQVFA QYLRPEQD LSTQAKRR
3951 LLSARVALL LEAQATQFL LEPVRSRLL VDEAVKGLV QPELEKLLS
3961 LERAVTQDR FVTQVTSLE QMRRELPT REALLLIDQ LATQGVQPR
3981 LKRLPLDAG VQKLEISFL IDGALRQDF RAYVQPTTE RLKTLVLRSE
4001 CRDDDTQQL LFLSDARSL TRQLEKQIT MEELVRSQM DEATGALRE
4051 GLIIEPTIK HQTQLEQY CIAGVQVAT RKLQVQAN RQGLRQVPL
4101 RELLQADAT QVDTQVQEL VLVEAVQW GQVRFYEW LSAASRTIS
4151 YQFYSQKLI SLQAWQDGL ILKQDPLAL EKIATGQII DPEERSLPT
4201 KVALRGLAD RENNELTDP SEQTRFQFP ITRNLYTQD LMRCTITQD
4251 TUGLLPLRE RQREKLVSD SPQSRQVAT VQVRFQRM VDEAVKGLS
4301 DQVITLSE QECREKETT SSSQVYQW IIRBRSQVQ DIDLARQIL
4351 IIRALAZIR AGTLSTERA DMLSKRQV RERSVQSS SVYFESRVS
4401 LKLLASQDF VEELFQVLA LQCTLELVY TRMHRVRY DNTQGLLE
4451 AQACTGQID PSTGRFPYD DQSSQVLYE LQVLDLIDQ RARFQDRFR
4501 YTRNSAAGA LQKQVLYEA QDFLEQVIL TQGLIEPTP QVPLRQALQ
4551 RQVTCARQD RLRQVQVSN YLQVPTQEL IYRRLDARL QVETQELIC
4601 LERACTQV YVYFQVQW GQVQKQCTH RQSRBAGRA RQFATQVDF
4651 DHTFSSSV SSVQFQVAV QSASLQSEF SAVA
    
```



i.i 1940.997 (-0.0 Da) [1366-1382] r.RQEQIQAMPLADSQAVR.e  
 i.i 1941.101 (-0.001 Da) [3424-3439] k.LITVEEVETLRQER.I

nearly 400 peptides assigned and seq. cov ~70%

# mMass – the power of high resolution *using envelope fit to validate the assignments*







**EU FT-ICR MS**

*H2020*

*EUROPEAN NETWORK OF FOURIER-TRANSFORM ION-  
CYCLOTRON-RESONANCE MASS SPECTROMETRY CENTERS*

*PROJECT AGREEMENT NO.731077*

