MS/MS Fragmentation of VVEEVGKMK
Found in Q8R0Y6, Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh11 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Plotted from to 1000 Da
Label all possible matches ○ Label matches used for scoring @

Monoisotopic mass of neutral peptide Mr(calc): 1119.5482
Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
MS : Oxidation (M), with neutral losses 0.00000 (shown in table). 68.9953
K9 : mal_CO2 (K), with neutral loss 43.9595
Ions Score: 21 Expect: 0.023
Matches : 17/110 fragment ions using 97 most intense peaks  (help)

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MS/MS Fragmentation of **MKIGNPLDR**

**Found in Q8R016, Cytosolic 10-formyltetrahydrofolate dehydrogenase**
OG = Mus musculus
GN = Aldh111
PE = 2
SV = 1

Click mouse within plot area to zoom in by factor of two about that point

**Plot from 150 to 1050 Da**

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1128.8597**

**Fixed modifications: NMTS (C) (apply to specified residues or termini only)**

**Variable modifications:**

K2 : mal CO2 (K), with neutral loss 49.0000

**Ions Score: 28  Expect: 0.086**

**Matches: 7/78 fragment ions using 9 most intense peaks**

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MS/MS Fragmentation of MKIGNPLDR
Found in Q8R0V6, Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh111 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1144.8546
Fixed modifications: METS (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000 (shown in table), 68.9988
K2 : mal-COO (K), with neutral loss 43.9888
Ions Score: 30 Expect: 0.023
Matches : 13/110 fragment ions using 25 most intense peaks

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MS/MS Fragmentation of KLVEYCQR
Found in Q8R0Y6, Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh111 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or [Plotform] 150 to 1200 Da [Full range]

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1165.5203
Fixed modifications: MTS (C) (apply to specified residues or termini only)
Variable modifications:
K1 : mal_COO (K), with neutral loss 43.9898
Ions Score: 26 Expect: 0.022
Matches : 11/70 Fragment ions using 19 most intense peaks (help)

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Matching Ion Score: 26 Expect: 0.022
Matches: 11/70 Fragment ions using 19 most intense peaks (help)
MS/MS Fragmentation of DGKADPLGLAEAEK
Found in Q8ROYE6, Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=AldhIII PE=2 SV=1

Monoisotopic mass of neutral peptide (calc): 1447.5760
Fixed modifications: NMT5 (C) (apply to specified residues or termini only)
Variable modifications:
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**MS/MS Fragmentation of HIMKSCALSNVK**

**Found in Q8KOY6, Cytosolic 13-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Adh111 PE=2 SV=1**

Click mouse within plot area to zoom in by factor of two about that point

![Graph](image)

**Monoisotopic mass of neutral peptide Mr(calc): 1461.4778**

**Fixed modifications: HExS (C) (apply to specified residues or termini only)**

**Variable modifications:**

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MS/MS Fragmentation of HIMKSCALSNVK

Found in Q6ROV6, Cytoplasmic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1313 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
On [Plot Form] 200 to 1400 Da [Full range]
Label all possible matches [Label matches used for scoring]

Monoisotopic mass of neutral peptide Mr (calc.): 1477.6727
Fixed modifications: IGTS (C) - apply to specified residues or termini only
Variable modifications:
N
: Oxidation (M); with neutral losses 0.9880 (shown in table), 68.9883
K
: me, 0.202 (K), with neutral loss 0.9880

Raw Score: 39 Excess: 0.0022
Matches: 14/172 fragment ions using 22 most intense peaks [help]

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MS/MS Fragmentation of MLLVKNIQLEDGK
Found in Q88Y6. Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh111 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or [Plot form] 200 to 1800 Da [Full range]

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(m/z): 1691.5884
Fixed modifications: MTS (C) (apply to specified residues or termini only)
Variable modifications:
M : Oxidation (M), with neutral losses 0.0000 (shown in table), O8.9993
K : mal-CE2 (K), with neutral loss 42.0028

Ions Score: 57 Expect: 0.56e-095

Matches: 16/160 Fragment Ions using 20 most intense peaks (help)

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MS/MS Fragmentation of EAFENLGWKGINKA
Found in Q8R0V6. Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh111 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

On: Full range

Label all possible matches ☐ Label matches used for scoring ☑

Monoisotopic mass of neutral peptide Mr(calc): 1039.5111
Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
K10 : nM_2CO2 (E), with neutral loss 44.0159

Ions Score: 20 Expect: 2.01E-05

Matches : 56/129 fragment ions using 60 most intense peaks  {[help]}

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MS/MS Fragmentation of GASAINWTLIHGDKK
Found in O6R076. Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Adh111 PE=2 SV=1

Cyclize mass within plot area to zoom in by factor of two about that point
Or, select from range: 200 to 1000 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(mole) : 1468.8860
Fixed modifications: HET (C) (apply to specified residues or tandem only)
Variable modifications:
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Ions Source: 4+ Eppm: 0.00021
Matches : 11/150 fragment ions using 12 most intense peaks

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MS/MS Fragmentation of **KEGHEVVGVFTIPDK**

Found in Q8R0Y6, Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh111 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Plot from 200 to 1600 Da

Label all possible matches □ Label matches used for scoring □

---

Monoisotopic mass of neutral peptide M(calc): 1720.8720

Fixed modifications: NMET (C) (apply to specified residues or termini only)

Variable modifications:

K1: pentaOglycine (K), with neutral loss 43.91 u

Ion Score: 30 Extrap: 0.014

Matches: 42/116 fragment ions using 130 most intense peaks (Ref)

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Notes:

- **KEGHEVVGVFTIPDK** is the identified peptide from the MS/MS fragmentation of Q8R0Y6 cytosolic 10-formyltetrahydrofolate dehydrogenase.
- The peptide was found in Mus musculus (mouse) with a unique protein accession number Q8R0Y6.
- The peptide contains 15 residues with a calculated monoisotopic mass of 1720.8720 u.
- Fixed modifications include NMET (C) on specified residues.
- Variable modifications include pentaOglycine (K) with a neutral loss of 43.91 u.
- The ion score is 30, and the expected value is 0.014.
- The peptide matches 42/116 fragment ions using 130 most intense peaks.
MS/MS Fragmentation of GNDKVPGAWEACGQK
Found in Q8RYS5, Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldhd11l PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1700 Da Full range

Label all possible matches □ Label matches used for scoring □

Monoisotopic mass of neutral peptide M(Neu)=1768.7616
Fixed modifications: NMTS (C) (apply to specified residues or terminate only)
Variable modifications:
N : m/z 15 (Y), with neutral loss 41 Da

Ion Score: 38 Expect: 0.0005
Matches: 17/164 fragment ions using 28 most intense peaks (title)

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EGHEVVGVFTIPDKDGK

Found in Q8R0V6, Cytosolic 10-formyltetrahydrofolate dehydrogenase Os-Mus musculus GN-Aldh111 PE-2 SV-1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches □ □ Label matches used for scoring □

Monoisotopic mass of neutral peptide (Da) = 1511.0214
Fixed modifications: 1677.9 (C) □ apply to specified residues or termini only
Variable modifications:
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Luna Score: 83 Expect: 9.2e-09
Matches: 26/145 fragment ions using 67 most intense peaks □ □

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EGHEVVGVFTIPDKDGK
MS/MS Fragmentation of RPQPEEGATYEIGIQKK
Found in Q8R0Y6. Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh111 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches □ Label matches used for scoring □

Monoisotopic mass of neutral peptide Mr(m/z): 1842.9075
Fixed modifications: HIS9 (C) (apply to specified residues or terminal only)
Variable modifications: K15 : m+15 (N), with neutral loss 43.0056
Ion Score: 15 Random: 0.0012
Matches: 52/142 Fragment ions using 92 most intense peaks (small)

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MS/MS Fragmentation of NIQLEDGKMPASQFFK

Found in: OGR1A Y, Peptide結束

Source: Eukaryota,
OS=Homo sapiens OX=266044 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches Label matches used for scoring

Resonantion mass of neutral peptide (Details): 2784.4467
Fixed modifications: MTS (C) - Apply to specified residues or termini only
Variable modifications:
K^: m/z 16 Da, with neutral loss 43.0158
H^: Oxidation (M), with neutral losses 0.0200 shown in table: 61.9560
Score: 38 Expect: 0.0000
Matches: 18/573 fragments less using 19 most intense peaks

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Score: 38 Expect: 0.0000
Matches: 18/573 fragments less using 19 most intense peaks

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MS/MS Fragmentation of DINKALYVSDK
Found in Q8K0Y6. Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh11 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 D or Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1350.6667
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
M4 : m+1_O2 (K), with neutral loss 43.0199
Total Score: 14 Expect: 0.18
Matches: 12/114 fragment ions using 31 most intense peaks (help)

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MS/MS Fragmentation of FLFPEGIKGVMQAVR.L

Found in Q8R9Y6. Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh11 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ◆ Label matches used for scoring ◆

---

Monoisotopic mass of neutral peptide [M+H]^+: 1782.9382
Fixed modifications: MMTS (C) (apply to specified residues or term only)
Variable modifications:
  KR = [mal E20 K (R)] with neutral loss 41.005
  M0 = Oxidation (M), with neutral losses 0.0000 (shown in table), 65.0293
  Ions Score: 16 Expect: 0.21

Matches: 24/200 fragment ions using 62 most intense peaks (keep)

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### MS/MS Fragmentation of **TDVAAPFGGFKQSGFGK.D**

**Found in** Q8RO5Y, Cytoytic 10-formyltetrahydrofolate dehydrogenase OS=9.3a musculus GN=Aldh111 PE=2 SV=1

Click masses within plot area to zoom in by factor of two about that point

**Monoisotopic mass of neutral peptide Mr(calc):** 1795.3528

**Fixed modifications:** Glu->K (apply to specified residues or termini only)

**Variable modifications:**

- **K:** replacing N or K with a methyl group, with neutral loss 41.0088

**Ions Score:** 62 **Expect:** 0.0098

**Matches:** 58/106 fragment ions using 70 most intense peaks (0.1 Da)

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MS/MS Fragmentation of **KNIHPWVK**

Found in O8C106. Carboxymethyl-cysteine [ammonium], mitochondrial OS-Mus musculus GN-Cys1 PF-1 SV-?

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1950 Da  

Label all possible matches ☐  Label matches used for scoring ☐

**Monoisotopic mass of neutral peptide Mr(calc): 1106.6878**

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

H3 : c-mpl 002 (K), with neutral loss 42.0000

Ions Score: 27  Expect: 0.014

Matches: 13/56 fragment ions using 26 most intense peaks  (help)

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MS/MS Fragmentation of LFAEAVQKSR

Found in OSG196. Carboxymethyl-cysteine synthase fammonial. mitochondrial OS=Mus musculus GN=Csn1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calc): 1283.6285
Fixed modifications: MMETSS (C) (apply to specified residues or termini only)
Variable modifications:
ND : m/z -16 (N), with neutral loss 49.9996

Matches: 18/88 fragment ions using 71 most intense peaks  

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MS/MS Fragmentation of AKTAHVLEDGTK
Found in Q8C196, Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Monoisotopic mass of neutral peptide M(calc): 1467.7369
Fixed modifications: MS/MS (C) (apply to specified residues or termini only)
Variable modifications:
K  : macl 202 (K), with neutral loss 49.9928

Matches: 15/136 fragment ions using 20 most intense peaks (Pepl)
MS/MS Fragmentation of DELGLNKYMESDGIK
Found in Q8C196. Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Plot from 00 to 1700 Da
Full range

Monoisotopic mass of neutral peptide (calc) : 1786.5103
Fixed modifications: MMT3 (C) (apply to specified residues or termini only)
Variable modifications:
E7 : mal_002 (K), with neutral loss 48.9990
Tack Score : 25 Expect : 0.015
Matches : 18/192 fragment ions using 40 most intense peaks (help)

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MS/MS Fragmentation of **VVAVDCGIKNNVIR**

**Found in Q8C196, Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2**

Click mouse within plot area to zoom in by factor of two about that point.

Or, Filter from 200 to 5000 Da Full range

Label all possible matches ✅ Label matches used for scoring ✅

Monoisotopic mass of neutral peptide Mr (calc): 1630.5171

Fixed modifications: HMB (C) (apply to specified residues or termini only)

Variable modifications:

K8 : m/z Δ29 (K), with neutral loss 48.0595

Ions Score: 19 Expect: 0.10

Matches: 17/114 fragment ions using 50 most intense peaks (help)

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MS/MS Fragmentation of GTTITSVLPKPALVASR
Found in Q8C194, Carbamoyl phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from × to Da  to  Da Full range
Label all possible matches  Label matches used for scoring  

Monoisotopic mass of neutral peptide Mr[mole]: 1796.2044
Fixed modifications: HET (O) (apply to specified residues or termini only)
Variable modifications: K10 : ma,002 (O) with neutral loss 48.0150
Ion Score: 28 Expect: 0.049
Matches: 28/219 fragment ions using 44 most intense peaks

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MS/MS Fragmentation of EIGFSDKQISK
Found in Q8C196, Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da
Label all possible matches
Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1336.68110
Fixed modifications: MG(S) (C) (apply to specified residues or termini only)
Variable modifications:
M7 : ma5_C02 (K), with neutral loss 43.9590
Tons Score: 27 Expect: 0.028
Matches : 36/106 fragment ions using 93 most intense peaks

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**MS/MS Fragmentation of AMLSTGFKIPQK**

Found in **OBC190**. Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1500 Da Full range
Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1269.7275
**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)
**Variable modifications:**

**Fbra** : m/z 0.000 (X), with neutral loss 48.9698

**Tally Score:** 32 **Expect:** 0.0047

**Matches:** 22/90 fragment ions using 64 most intense peaks

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MS/MS Fragmentation of **TVDSKSLFHYR**

Found in **08-106** Catharanthus roseus leaves, homologous mitochondrial OSMs, putative CNS-CoQ1 DP=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1250 Da 
Label all possible matches  Label matches used for scoring  

---

**Monoisotopic mass of neutral peptide Mr(calc): 1457.4888**

**Fixed modifications:** M, S, K (apply to specified residues or termini only)

**Variable modifications:**

- N-terminus: #N, with neutral loss 40.0200

**Ions Score:** 36  **Expect:** 0.0016

**Matches:** 17/102 fragment ions using 39 most intense peaks  

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MS/MS Fragmentation of **TFEESFQKALR**

Found in **OEC108** (Oecolochaina cornutana, Bombyliidae) mitochondrial GS=Amo musculae GN=Coel PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from [ ] 200 to 1500 Da [ ] Full range

Label all possible matches [ ] Label matches used for scoring [ ]

Monoisotopic mass of neutral peptide Mr(calc): 1440.6888
Fixed modifications: IMS (C) (apply to specified residues or termini only)
Variable modifications:
K8 : mal-CD2 (K), with neutral loss 43.00888
Ions Score: 58 Expect: 0.0068
Matches: 26/36 Frequent ions using 44 most intense peaks (help)

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MS/MS Fragmentation of TAHIVLEDGT KMK

Found in Q8C196, Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide (Mr(calc)): 1527.7608
Fixed modifications: MGST (C) (apply to specified residues or termini only)
Variable modifications:
K11 : meI2 (I), with monoisotopic mass 44.0080
Ion Source: ESI  Detector: Q-TOF
Matches : 25/129 fragment ions using 88 most intense peaks  (help)

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MS/MS Fragmentation of QISKCLGLTEAQTR
Found in OSC196. Carboxypeptidase Y; ammonia mitochondrial OS=Mus musculus GN=Cox1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da
Label all possible matches

Monoisotopic mass of neutral peptide M(calc): 1670.0616
Fixed modifications: MMT (C) (apply to specified residues or termini only)
Variable modifications:
K8: + 15.99491 (E), with neutral loss 44.012

Ions Score: 23 Expect: 0.012
Matches : 17/150 fragment ions using 20 most intense peaks

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**MS/MS Fragmentation of VMIGESIDEKR**

Found in Q8C9B6. Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

**Monoisotopic mass of neutral peptide Mr(calc): 1341.6497**

**Fixed modifications:** NO PTMs (apply to specified residues or termini only)

**Variable modifications:**

- K10 : m/z CO2 (K), with neutral loss 43.0166

**In Silico Score:** 89.24

**Matches:** 17/50 fragment ions using 50 most intense peaks (help)

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MS/MS Fragmentation of TLKGLNSDSVTTELTR
Found in Q8C18M. Carbamoyl-phosphate synthase [mammalian], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot ions 200 to 1700 Da
Label all possible matches * Label matches used for scoring *

Neutral loss mass of neutral peptide Mr(calc): 1947.9212
Fixed modifications: MMTS (C) (apply to specified residues or remove if used as variable modifications)
Variable modifications:
K1 : mal COX (R), with neutral loss 42.0182
Ion Score: 70 Expect: 1.2e-036
Matches : 25/472 fragment ions using 62 most intense peaks (1.0)

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**MS/MS Fragmentation of QIFLGGVDK**

**QIFLGGVDK**

Found in **P51881**, ADP/ATP translocase 2

**OS** = *Mus musculus*  
**GN** = Slc25a5  
**PE** = 1  
**SV** = 3

Click mouse within plot area to zoom in by factor of two about that point

Or,  
Plot from [ ] to [ ]

Da  
Full range

Label all possible matches  
Label matches used for scoring  

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1217.6404

**Fixed modifications:**  
- 

**Variable modifications:**
- 

**K9** : m/z ΔCO2 (K), with neutral loss 43.9898

**Ions Score:** 51  
**Expect:** 0.000007

**Matches:** 20/90 fragment ions using 29 most intense peaks  

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MS/MS Fragmentation of YKQIFLGGVDK
Found in P51881, ADP/ATP translocase 2 OS=Mus musculus GN=Stc25a5 PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide M(r(calo)): 1862.6976
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications: K2 : mas-CO2 (K), with neutral loss 43.9898
Ions Score: 60  Expect: 6.6e-006
Matches: 16/90 Fragment ions using 22 most intense peaks

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**MS/MS Fragmentation of YKQIFLGGVDKR**

Found in P51881, ADP/ATP translocase 2 OS=Mus musculus GN=Sdc25a5 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da
Tick Label all possible matches Divide Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1608.7997

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

- K2 = mal CO2H (K), with neutral loss 43.01067

**Ions Score:** 46  **Expect:** 0.00019

**Matches:** 84/108 fragment ions using 61 most intense peaks  

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|---|-----|-----|-----|-----|------|-----|------|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1 | 164.0706 | 82.5389 |     |     | Y    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 2 | 334.1761 | 167.5917 | 317.1406 | 159.0784 | K    | 1302.7528 | 651.8801 | 1285.7263 | 643.3668 | 1284.7423 | 642.8748 | 11 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 3 | 462.2347 | 231.6210 | 445.2082 | 223.1077 | Q    | 1132.6473 | 566.8273 | 1115.6208 | 558.3140 | 1114.6368 | 557.8220 | 10 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 4 | 575.3188 | 288.1630 | 558.2922 | 279.6498 | T    | 1004.5887 | 502.7980 | 987.5622 | 494.2847 | 986.5782 | 493.7927 | 9 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 5 | 722.3872 | 361.6972 | 705.3606 | 353.1840 | F    | 891.5047 | 446.2560 | 874.4781 | 437.7427 | 873.4941 | 437.2507 | 8 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 6 | 835.4713 | 418.2393 | 818.4447 | 409.7260 | L    | 744.4363 | 372.7218 | 727.4097 | 364.2085 | 726.4257 | 363.7165 | 7 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 7 | 892.4927 | 446.7500 | 875.4662 | 438.2367 | G    | 631.3522 | 316.1797 | 614.3257 | 307.6665 | 613.3416 | 307.1745 | 6 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 8 | 949.5112 | 475.2607 | 932.4876 | 466.7475 | G    | 574.3307 | 287.6690 | 557.3042 | 279.1557 | 556.3202 | 278.6657 | 5 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 9 | 1048.5826 | 524.7949 | 1031.5560 | 516.2817 | V    | 517.3093 | 259.1583 | 500.2827 | 250.6450 | 499.2887 | 250.1530 | 4 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 10 | 1163.6095 | 582.3084 | 1146.5830 | 573.7051 | D    | 418.2409 | 209.6241 | 401.2143 | 201.1108 | 400.2303 | 200.6188 | 3 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 11 | 1291.7045 | 646.3559 | 1274.6780 | 637.8426 | K    | 303.2139 | 152.1106 | 286.1874 | 143.5973 | 2 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 12 | R    | 175.1190 | 88.0631 | 158.0924 | 79.5498 | 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
MS/MS Fragmentation of **DKYKQIFLGGVDK**

Found in P51881, ADP/ATP translocase 2 OS=Mus musculus GN=Sc2m5a5 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or: [Plot form: 200 to 1500 Da] [Full range]
Label all possible matches [Label matches used for scoring ]

Monoisotopic mass of neutral peptide M [calc]: 1895.8156
Fixed modifications: M(58) [apply to specified residues or termini only]
Variable modifications:
K4 : mod COO (K), with neutral loss 43.01058

Ions Score: 88, Expect: 6.0044
Matches: 44/140 fragment ions using 37 most intense peaks (help)

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MS/MS Fragmentation of DKYKQIFLGGVDKQR
Found in PS1881, ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a1 PE=1 SV=3

Monoisotopic mass of neutral peptide Mn(m/e): 1781.9206
Fixed modifications: MGEG (C) apply to specified residues or termini only
Variable modifications:
K4 : m alc2 (K), with neutral loss 42.0169
Ions Score: 55  Expect: 6.00e-17
Matches to Fragment ions using 57 most intense peaks [help]

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MS/MS Fragmentation of \textbf{VLKYAGLK}

Found in \textbf{O80ZT1}. Acetyl-CoA acetyltransferase. mitochondrial OS=\textit{Mus musculus} GN=Acat1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, plot from \textbf{100} to \textbf{950} Da

Label all possible matches \(\bigcirc\) Label matches used for scoring \(\bigcirc\)

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8 & & & & & K & \textbf{147.1128} & 74.0600 & 130.0863 & 65.5468 & 1 \\
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\end{tabular}
\end{table}

Monoisotopic mass of neutral peptide Mr(calc): 976.5593

Fixed modifications: MMT3 (C) (apply to specified residues or termini only)

Variable modifications:

KD : \textit{mal CO2 (K)}, with neutral loss 43.9899

Ions Score: 20  Expect: 0.040

Matches : 10/52 fragment ions using 40 most intense peaks  (help)
MS/MS Fragmentation of **IHMGNCAENTAK**
Found in Q6QZT1, Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Aca1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1350 Da Full range
Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(mono):** 1419.5581
**Fixed modifications:** MET5 (C) (**apply to specified residues or termini only**)
**Variable modifications:**
**K11:** mal_COOH (K), with neutral loss 48.0590
**Ions Searched:** 25, Repeat: 0.011
**Matches:** 24/106 fragment ions using 90 most intense peaks

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**Note:** The table above lists the fragment ions with their corresponding masses and sequences. The highlighted ions are those used for the analysis. The table includes information on the b, y, and b' ions, their charges, and the sequences associated with them. The mass values are rounded to the nearest decimal place for clarity.
MS/MS Fragmentation of IHMGNCENTAK
Found in Q80ZT1. Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1

Monoisotopic mass of neutral peptide Mw(calc): 1428.8620
Fixed modifications: M+H (C) (apply to specified residues or termini only)
Variable modifications:
MG : Oxidation (M), with neutral losses 0.0000 (shown in table), 61.0512
K12 : m3CO2 (K), with neutral loss 42.0000
Ions Score: 55 Expect: 0.029
Matches to 12/388 fragment ions using 10 most intense peaks (help)

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MS/MS Fragmentation of **IHMGNCAENTAK**
Found in **Q8ZT1**. Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

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Fixed modifications: **M+H** (C) (apply to specified residues or termi only)
Variable modifications: **K12** : m/z C02 (H), with neutral loss 43.0000
Ions Score: 32 Expect: 0.0079
Matches: 17/106 fragment ions using 92 most intense peaks (help)
MS/MS Fragmentation of \textbf{LEDLIKDVGLTDVYNK}

Found in Q8Z21. Acetyl-CoA acetyltransferase, mitochondrial GS-Mus musculus GN=Acat1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

Cr: Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide \textbf{Mr(calc)}: 1964.784
Fixed modifications: MET2 (C) (apply to specified residues or termini only)
Variable modifications: 
K7 - \textit{N}$_2$H$_2$CO$_2$ (H$_2$O, with neutral loss 44.003)
Ions Score: 59 Expect: 2.1e+05
Matches: 13/133 fragment ions using 18 most intense peaks (help)

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**MS/MS Fragmentation of DGLTVDYNKIHMGNCANENTA\-**

Found in Q6Q111, Acetyl-CoA acetyltransferase, mitochondrial Q8M481 mscore 20.1 L16.1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
- **PRE time:** 200 to 1800 Da
- **Full range**

Label all possible matches \[\textit{Label matches used for scoring}\]

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**Neurotrophic factors (NFToms):** 2430, 8845

Fixed modifications: NMT (O) apply to specified residues or terminal only.
**Variable modifications:**
- **E:** m/z 202, H, with neutral loss 40, 95, 98

**Ion score:** 59, **Expect:** 0.0015

**Matches:** 22/222, fragment ions using 60 most intense peaks (z=2)

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**Monoisotopic mass of neutral peptide** Ms(0) = 1742.8444
**Fixed modifications:** Cys-CO \( \text{NH} \), Acetyl-\( \text{N} \), Glu-\( \text{C} \)
**Variable modifications:** 13C

**Matches:** 17/25; frequent loss using 28 most intense peaks **Table:**
MS/MS Fragmentation of **GATPYGGVKLEDLV**K

Found in **OSOZTI.** Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or  Plot from  200  to  1700  D  Full range

Label all possible matches  ©  Label matches used for scoring  ®

---

Monoisotopic mass of neutral peptide \( \text{Mr(calc.): 1764.6247} \)

Fixed modifications: 8073 (C) (apply to specified residues or termini only)

Variable modifications:

- K  - m/z CO2 (+) , with neutral loss 44.0209

Ions Score: 21  Impact: 0.01

Matches: 27/152 fragment ions using 28 most intense peaks  (help)

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### MS/MS Fragmentation of QATLGAGLPISTPCTTVNK

**Found in Q8Q2T1. Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1**

Click mouse within plot area to zoom in by factor of two about that point.

Ch. **Start from** 200 to 1000 **Da** **Full range**

Label all possible matches **Label matches used for scoring**

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**Phenotypic mass of neutral peptide**: 370.91704

**Fixed modifications**: MG (G) (apply to specified residues or termini only)

**Variable modifications**: 

**X!** 3.m+1.30, 4.005, with neutral loss 48.0588

**Tune Score**: 18 **Expect**: 5.17

**Matches**: 14/228 fragment ions using 21 most intense peaks (100%)

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MS/MS Fragmentation of AVVKLEGDNK

Monoisotopic mass of neutral peptide Mr(calc): 1157.5928
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K4 : oxid-Cys (K), with neutral loss 48.0108
Ions Score: 44 Expect: 0.00066
Matches : 24/50 fragment ions using 54 most intense peaks (help)

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AVVKLEGDNK
MS/MS Fragmentation of GVSEIVHEGKK
Found in F32710. Fatty acid-binding protein, liver OS=Mus musculus GN=Fslp1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches Label matches used for scoring

GVSEIVHEGKK

Monocistopic mass of neutral peptide M(r)calculated: 1267.6408
Fixed modifications: M(2) (C) (apply to specified residues or termini only)
Variable modifications:
K10 : m1(O)2 (K), with neutral loss 42.0068
Ion Score: 35 Expect: 0.0000
Matches: 21/92 fragment ions using 30 most intense peaks

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**MS/MS Fragmentation of AIGLPEDLIQKGK**

Found in P12710, Fatty acid-binding protein, liver OS=Mus musculus GN=Febp1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Options:
- Plot from: 200 to 1400 Da (Full range)
- Label all possible matches
- Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1466.7880

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**
- K11 : std CO2H (K), with neutral loss 42.01068

**Ions Score:** 52  Expect: 8.0e-03

**Matches:** 26/104 fragment ions using 57 most intense peaks  

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**Total charge:** 2
MS/MS Fragmentation of \textbf{LEGDNKMVTTFK}

Found in P12710, Fatty acid-binding protein, liver OS=Mus musculus GN=Fabp1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da [Full range]

Label all possible matches [Label matches used for scoring]

Monoisotopic mass of neutral peptide Mr(calc): 1467.0915

Fixed modifications: MTMT (C) \textbf{apply to specified residues or termini only}

Variable modifications:

K6 : \textbf{MeCO2 (K), with neutral loss 48.0598}

Ions Score: 52  Expect: 9.6e-06

Matches to 10/118 fragment ions using 12 most intense peaks ([help])

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[help]
MS/MS Fragmentation of **LEGDNKMVTTFK**

Found in P12710, Fatty acid-binding protein, liver OS=Mus musculus GN=Fabp1 PE=1 SV=2

---

Monoisotopic mass of neutral peptide Mr(calc): 1685.6865

Fixed modifications: M(57) (C) (apply to specified residues or term only)

Variable modifications:

- K6 : deamidation (K), with neutral loss 0.9888
- N7 : Oxidation (M), with neutral losses 0.9800 (shown in table), 0.0080

Ions Score: 47  Expect: 0.069877

Matches toFragment ions using 22 most intense peaks

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MS/MS Fragmentation of DIGKDVSEIVHEGK

Found in P12710, Fatty acid-binding protein, liver OS=Mus musculus GN=Fetbp1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or  [Flat from]  200 to 1500 Da [Full range]

Label all possible matches  ○  Label matches used for scoring  ●

Monoisotopic mass of neutral peptide Mr(calc): 1485.7513

Fixed modifications: MMO2 (C) (apply to specified residues or termini only)
Variable modifications:
K3 : +15.99491 (K), with neutral loss 49.02698

Ion Score: 81  Expect: 0.0007

Matches : 29/136 fragment ions using 65 most intense peaks  (help)

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DIGKDVSEIVHEGK
MS/MS Fragmentation of GKDVKVSEIVREGK
Found in P12710, fatty acid-binding protein, liver OS=Mus musculus GN=FABP1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
On/Off Plot from 100 to 1700 Da
Label all possible matches
Label matches used for scoring

Monoisotopic mass of neutral peptide Mz(m/z): 1863.6332
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K
mass CO2 (M), with neutral loss 48.0595
Inc. Score: 27 Expect: 0.012
Matches: 64/188 fragment ions using 70 most intense peaks

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MS/MS Fragmentation of **MVTTFKGIK**

Found in **P12710**, Fatty acid-binding protein, liver OS=Mus musculus GN=Fabp1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1100 Da [Full range]
Label all possible matches ☐ Label matches used for scoring ☐

---

**Monoisotopic mass of neutral peptide Mr(calc): 1125.5740**

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**
- M1 : Oxidation (M), with neutral losses 0.0000 (shown in table), 61.9883
- K5 : mal_C02 (K), with neutral loss 43.9898

**Ions Score: 38  Expect: 0.0013**

**Matches : 9/106 fragment ions using 9 most intense peaks**  

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MS/MS Fragmentation of **LTITYGPKVVR**

Found in **P12710**, Fatty acid-binding protein, liver OS=**Mus musculus** GN=**Fabp1** PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Ch From: 200 to 1300 Da

Label all possible matches  Label matches used for scoring

---

Monoisotopic mass of neutral peptide Mr(calc): 1351.7445

Fixed modifications: **NMTES(C)** (apply to specified residues or termini only)

Variable modifications:

K9  : m/z C02 (K), with neutral loss 43.96898

Ions Score: 34  Expect: 0.0014

Matches: 16/50 fragment ions using 22 most intense peaks  (help)

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### MS/MS Fragmentation of YQQLIKENLK

Found in O6EQ20, Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

---

#### Monoisotopic mass of neutral peptide Mr(calc): 1361.7190

Fixed modifications: MNES (C) (apply to specified residues or termini only)

Variable modifications:

K6 : m1_C02 (K), with neutral loss 43.0098

Ions Score: 9  Expect: 0.0017

Matches to 29/98 fragment ions using 62 most intense peaks  (help)

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MS/MS Fragmentation of **KWLPHELVD**
Found in **Q0E2Q0**, Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 150 Da
Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide** Mr(calc): 1240.6452
Fixed modifications: **MNIS** (C) (apply to specified residues or termini only)
Variable modifications:
K: **mal_CO2** (K), with neutral loss 43.9898

**Ions Score:** 20  Expect: 0.078  Matches: 15/56 fragment ions using 62 most intense peaks

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MS/MS Fragmentation of ENLKEIAR
Found in O9EO20. Methylenecetone-semialdehyde dehydrogenase [full length], mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calo): 1057.5405
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:

Peaks matched using neutral loss 43.9898
Score: 29 Expect: 0.62
Matches: 7/76 fragment ions using 16 most intense peaks

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MS/MS Fragmentation of **AEMDAAVESCKR**
Found in OMP20 Methionylamino-acidichloridohydrodizosomase factorine1 mitochondrial OS=Mus musculus GN=Aldehyde PF-1 SV-1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calo) : 1440.5683
Fixed modifications: MMTS (C) [apply to specified residues or termini only]
Variable modifications:
K11 : m+1(O2) (K), with neutral loss 44.0198
Trend Score: 34 Expect: 0.0081
Matches : 10/104 fragment ions using 22 most intense peaks (help)

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MS/MS Fragmentation of CMASTAILVGEAKK

Found in Q6EQ02, Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1

Click and mouse within plot area to zoom in by factor of two about that point

Or Plot from 200 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Ne(u-amide): 1681.8086

Fixed modifications: NMTS (C) (apply to specified residues or termini only)

Variable modifications:

K2 : Oxidation (M) with neutral losses 0.0000 (shown in table), el. 4652
K4 : mal-002 (E) with neutral loss 48.9839

Ion Score: 14 Exp. Score: 0.692

Matches: 15/152 fragment ions using 05 most intense peaks

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**MS/MS Fragmentation of VQANMGAKNHGVVMPDANK**

**Found in QHEQ29**, Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial Os-Mus musculus GN=Aldh5a1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Pixel from 200 to 900

Label all possible matches **Label matches used for scoring**

---

**Non-consensus area of native peptide (Percent):** 2010.82%

**Fixed modifications:** 
- **NHSE** (C): apply to specified residues or termini only

**Variable modifications:**
- **MT** : oxidation (M), with neutral losses 5.0000 Da (found in table), 62.9528
- **KS** : mod. Cys (K), with neutral losses 0.9848

**Ion Score:** 11 **Expect:** 0.06

**Matches:** 46 (454) Fragment ions using 77 most intense peaks

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VQANMGA KNHGVVMPDANK
MS/MS Fragmentation of ITTSTLEKEASK

Found in Q9DBM12, Peroxinsomal bifunctional enzyme OS=Mus musculus GN=Ehhadh PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range

Label all possible matches ☑️ Label matches used for scoring ☑️

Monoisotopic mass of neutral peptide Mr(calc): 1604.7348
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
KM : +57.02144 Da, with neutral loss 48.06688

Matches: 22 Expect: 0.023
Matches : 19/112 fragment ions using 56 most intense peaks [help]

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### MS/MS Fragmentation of GWYQYDKPLGR

**Found in O9DRB12**

Proteasomal bifunctional enzyme OS=Mus musculus GN=Fhnd3 PF=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point

Ori. Plot from 200 to 1400 Da [Full range]

Label all possible matches [ ] Label matches used for scoring [**]

---

**Monoisotopic mass of neutral peptide Mr(calc): 1487.4783**

**Fixed modifications:** NOmods (NOmods) (apply to specified residues or termini only)

**Variable modifications:**

| K7 | ma_G3 (K) | neutral loss 43.0989 |

**Ions Score:** 57  **Expect:** 0.001

**Matches:** 17/94 fragment ions using 34 most intense peaks  ([Help])

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MS/MS Fragmentation of **KIITSTLEKEASK**
Found in Q9DBM2, Peroxiredoxin bifunctional enzyme OS=Mus musculus GN=Erhahad PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point
Or, [Full range] 200 to 1500
Label all possible matches [Label matches used for scoring]

Monoisotopic mass of neutral peptide Mr(calc): 1552.8237
Fixed modifications: NH3 (C) (apply to specified residues or terminal only)
Variable modifications:
K8 : acetyl (K), with neutral loss 48.0109
Ions Score: 55 Expect: 0.00001
Matches: 14/136 fragment ions using 25 most intense peaks (help)

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K8 : acetyl (K), with neutral loss 48.0109
MS/MS Fragmentation of **SANKWSTPSGASWK**
Found in Q9DBM2, Peroxidase bifunctional enzyme OS=Mus musculus GN=Ehbadh PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da
Label all possible matches ✓ Label matches used for scoring ✓

Monoisotopic mass of neutral peptide M(zero): 1591.7267
Fixed modifications: NMT (C) (apply to specified residues or termini only)
Variable modifications:
K4 : m/z 202 (K), with neutral loss 43.0088
Ions Score: 20 Expect: 0.0080
Matches: 20/145 fragment ions using 52 most intense peaks 

| i | b | b** | h** | k** | Seg | y | y** | y^+ | y^++ | y^+++ | 
|---|---|-----|-----|-----|-----|---|-----|-----|------|-------|     |
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| 2 | 159.0764 | 80.0418 | 141.0659 | 71.0566 | A | 1451.7121 | 731.3597 | 1444.6856 | 722.8464 | 1443.7015 | 722.3544 |
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| 8 | 914.4367 | 457.7220 | 897.4101 | 449.2087 | 896.4621 | 448.7167 | P | 732.3675 | 356.8874 | 715.3410 | 358.1741 | 714.3589 | 357.8621 |
| 9 | 1001.4873 | 501.2330 | 984.4421 | 492.7124 | 983.4951 | 492.2327 | S | 655.3148 | 318.1810 | 638.2582 | 319.6777 | 637.3042 | 319.1557 |
| 10 | 1058.4601 | 559.7487 | 1041.4566 | 521.2354 | 1040.4799 | 520.7434 | G | 548.2827 | 274.6720 | 531.2560 | 266.1317 | 530.2722 | 265.6397 |
| 11 | 1125.5274 | 605.2673 | 1112.5007 | 556.7310 | 1111.5136 | 556.2620 | A | 491.2813 | 246.1343 | 474.2347 | 237.6210 | 473.2507 | 237.1290 |
| 13 | 1402.6386 | 701.8929 | 1385.8612 | 693.3907 | 1384.8280 | 692.8177 | W | 333.1921 | 167.0997 | 316.1656 | 158.5864 | 315.6863 | 158.0684 |
| 14 | K | 147.1128 | 74.0500 | 139.0583 | 65.5468 | 1 |
MS/MS Fragmentation of KGQGLTGPSLPPGTPTR
Found in Q9DBM2, Peroxidase bifunctional enzyme OS=Mus musculus GN=Ehbad PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point
Or: Plot from 300 to 1500 Da Full range
Label all possible matches © Label matches used for scoring •

Monoisotopic mass of neutral peptide: M mono = 1743.9007
Fixed modifications: M673 (C) (apply to specified residues or termini only)
Variable modifications:
 X1 Carbamidomethyl (C), with neutral loss 48.0055
 Ion Score: 40 Exp Ions: 0.00082
Matches: 20/100 fragment ions using 0+ most intense peaks (G离子)

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**MS/MS Fragmentation of VGIPVAVESDPKQLDTAK**

Found in **Q9DBM2**, Peroxidase bifunctional enzyme OS=Mus musculus GN=Eladho PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range

Label all possible matches  
Label matches used for scoring  

---

Monoisotopic mass of neutral peptide Mr(peptide): 2051.0787

Fixed modifications: MT15 (C)  (apply to specified residues or termini only)

Variable modifications:

- K13 : +5.982 Da  with neutral loss 58.0098

Ion Score: 82  Expect: 5.4e-09

Matches: 21/172 fragment ions using 27 most intense peaks  

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MS/MS Fragmentation of KIITSTLEK
Found in OGDH
Provisional bin functional enzyme OS=Mus musculus GN=Fhbath PF=1 SV=4
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1650 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1117.6230
Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
K1 : m/z CO2 (K), with neutral loss 43.0098
Ions Score: 20 Expect: 0.16
Matches : 8/98 fragment ions using 10 most intense peaks

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MS/MS Fragmentation of KATQEA FMK
Found in O91Y07 Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aladah PF=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1144.8278
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K: mal, CO2 (K), with neutral loss 43.0000
M: Oxidation (M), with neutral losses 0.0000(shown in table), 62.9999
Ions Score: 18 Expect: 0.04
Matches: 27/128 fragment ions using 74 most intense peaks (help)

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MS/MS Fragmentation of **FPALTPEQKK**

Found in CoI1V07 Protonemus proctori acl12483 R OS=Musrumusculus GN=Ab400 PF=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da

Label all possible matches Label matches used for scoring

---

**Monsiatomic mass of neutral peptide Mr(calc): 1343.6448**

Fixed modifications: M(S) (C) (apply to specified residues or termini only)
Variable modifications:
K9 : m+1 CO2 (K), with neutral loss 43.0050

Ions Score: 32 Expect: 0.047
Matches: 9/80 fragment ions using 11 most intense peaks (help)

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- **FPALTPEQKK**
- **Monsiatomic mass of neutral peptide Mr(calc): 1343.6448**
- **Fixed modifications:** M(S) (C)
- **Variable modifications:** K9 : m+1 CO2 (K), with neutral loss 43.0050
- **Ions Score: 32 Expect: 0.047**
- **Matches: 9/80 fragment ions using 11 most intense peaks**
MS/MS Fragmentation of ALQASALAAWGGKAANK
Found in O61Y97. Fructose-bisphosphate aldolase B Os=Mas musculus GN=Aldol PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or [Plot from] 200 to 1700 Da [Full range]
Label all possible matches [Label matches used for scoring]

Monoisotopic mass of neutral peptide Mr(calc): 1712.5540
Fixed modifications:  NMT (C) (Apply to specified residues or terminal only)
Variable modifications: K3 : m/z 0.02 (K), with neutral loss 44.0549

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MS/MS Fragmentation of ALQASALAAWGGKAANKK

Found in Q81Y97, Fructose-bisphosphate aldolase B OS=Mos musculus GN=Alb2 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da
Label all possible matches □ Label matches used for scoring □

Non-identic mass of neutral peptide Mr(calc): 1640.9756
Fixed modifications: MG25 (C) (apply to specified residues or termini only)
Variable modifications:
K25 : +1.000 (K), with neutral loss 41.0107
Ion Score: 52 Expect: 6.3e-308
Matched: 22/185 fragment ions using 41 most intense peaks

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**MS/MS Fragmentation of GIVVGIKLDQGGAPLAGTNK**

Found in Q11977. Fructose-1,6-bisphosphate aldolase B 03762/001 mouse

Click mouse within plot area to zoom in by factor of two about that point

Or [Fit Full range] 100 to 1900 [Da] Full range

Label all possible matches ✔ Label matches used for scoring ☐

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**Monoisotopic mass of neutral peptide Mr(m/z): 1692.0944**

**Fixed modifications:** NMT (C) (apply to specified residues or termini only)

**Variable modifications:**

PD: ma_l02 (E), with neutral loss 53.0500

**Lys Score:** 66 **Impact:** 2.6e-06

**Matches:** 12/156 fragment ions using 15 most intense peaks

---

**GIVVGIKLDQGGAPLAGTNK**
**MS/MS Fragmentation of KYTPEQVAMATVTLHR**

Found in Q9V8Y7, Fructose-1,6-bisphosphate aldolase B OS=Mus musculus GN=AlbPh PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Or  Plot from 100 to 1500 Da  Full range

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr (calc.)**: 2000.9508

**Fixed modifications**: MET (C) (apply to specified residues or term only)

**Variable modifications**:  
E1: mal-002 (R), with neutral loss 48.9936

**Ions Source**: 2S  **Expected**: 0.0026  
**Matches**: 24/120 fragment ions using 52 most intense peaks  **(hills)**

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MS/MS Fragmentation of **KELSEIAQR**

Found in **O31Y97**. Fructose-bisphosphatase aldolase B OS=**Mus musculus** GN=Aldob PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Or. **Plot from** 100 to 1200 Da  **Full range**

Label all possible matches  Label matches used for scoring

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**Monoisotopic mass of neutral peptide Mr(calc): 1198.5880**

**Fixed modifications: MMTS (C) (apply to specified residues or termini only)**

**Variable modifications:**

**K1:** m/z CO2 (K), with neutral loss 43.01508

**Ions Score:** 34  **Expect:** 0.056

**Matches:** 14/26 fragment ions using 27 most intense peaks  

| # | m/z  | b   | b−1 | b+  | b−2 | b0  | b+1 | Seq. | y   | y−1 | y+  | y−2 | y0  | y+1 | y−2 | y0+1 | #  |
|---|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|
| 1 | 171.1128 | 86.0600 | 154.0863 | 77.5468 | K   |      |     |     |     |     |     |     |     |     |     |     |     | 9  |
| 2 | 300.1554 | 150.5811 | 283.1288 | 142.0681 | 282.1448 | 141.5761 | E   |      | 945.5000 | 473.2536 | 928.4734 | 464.7404 | 927.4894 | 464.2483 | 1  |
| 3 | 313.2395 | 207.1234 | 396.2129 | 198.6101 | 395.2289 | 198.1181 | L   | 816.4574 | 408.7323 | 799.4308 | 400.2191 | 798.4468 | 399.7271 | 7  |
| 4 | 500.2715 | 250.6364 | 483.2449 | 242.1261 | 482.2609 | 241.6341 | S   | 763.5733 | 352.1903 | 685.3468 | 343.6770 | 685.3628 | 343.1830 | 6  |
| 5 | 629.3141 | 315.1507 | 612.2875 | 306.6474 | 611.3035 | 306.1554 | E   | 616.3413 | 308.8743 | 599.3148 | 300.1610 | 598.3307 | 299.6690 | 5  |
| 6 | 742.3981 | 371.7027 | 725.3716 | 363.1894 | 724.3876 | 362.6974 | I   | 487.2987 | 244.1530 | 470.2722 | 235.6397 |          |     |     |     |     | 4  |
| 7 | 813.4353 | 407.2213 | 796.4087 | 398.7080 | 795.4247 | 398.2160 | A   | 374.2146 | 187.6110 | 357.1881 | 179.0977 |          |     |     |     |     | 3  |
| 8 | 941.4938 | 471.2506 | 924.4673 | 462.7373 | 923.4833 | 462.2453 | Q   | 303.1775 | 152.0924 | 280.1510 | 143.5791 |          |     |     |     |     | 2  |
| 9 |      |     |     |     |     |     |     |     | R   | 175.1190 | 88.0631 | 158.0924 | 79.5498 |          |     |     |     |     | 1  |
MS/MS Fragmentation of MVKGTPPPSDQEK

Found in O9EP89. Serine beta-lactamase-like protein LACTB. mitochondrial OS=Mus musculus GN=Lactb PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide M (calc): 1495.6974
Fixed modifications:  NMTS (apply to specified residues or termini only)
Variable modifications:
K3  : mzd_COOH (K), with neutral loss 43.0589

Ions Source: 26  Repeats: 0.025

Matches: 12/100 fragment ions using 20 most intense peaks  
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MS/MS Fragmentation of ASGYKLYDYMQK

Found in: COF39

Some heme-lactemoine-like protein 1. LCTR mitochondrial OS=Mus musculus GN=Lacthm PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1600 Da Full range

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide M': 1587.6864

Fixed modifications: MGPT (C) (apply to specified residues or termini only)

Variable modifications:

K5 : workflow (K), with neutral loss 48.01993

M10 : Oxidation (M), with neutral losses 0.980007 (shown in table). 63.99689

Ion Score: 65 Expect: 0.0018

Matches: 20/176 fragment ions using 30 most intense peaks

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**MS/MS Fragmentation of KNDFEQGELYLK**

Found in ODEP89, Serine beta-lectamase-like protein LACTB, mitochondrial OS=Mus musculus GN=Lactb PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1600 Da Full range

Label all possible matches Label matches used for scoring

---

Monoisotopic mass of neutral peptide Mr(calc) : 1569.7083
Fixed modifications:  N-term (C) (apply to specified residues or termini only)
Variable modifications:
K : methyl_COOH (N) , with neutral loss 40.0092

Ions Scanned: 74  Isotopic Peaks: 2.3e+06
Matches : 10/120 fragment ions using 26 most intense peaks

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MS/MS Fragmentation of **KKNDFEQGELYLKL**
Found in **Q9EP89**, Serine beta-lactamase-like protein LACTB, mitochondrial OS=Mus musculus GN=Lctb PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(m/z): 1664.8328
Fixed modifications: MMTF (C) (apply to specified residues or termini only)
Variable modifications:
E8 : m/z 202 (K), with neutral loss 10.0000

Found sequence, 26 Expect: 0.0004
Matches: 17/120 fragment ions using 25 most intense peaks (help)

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MS/MS Fragmentation of **KKNDFEQGELYLK**

Found in OERPHD Serum beta-haemolytic streptococci, Boa constrictor, Guinea pig, Periplaneta

Click mouse within plot area to zoom in by factor of two about that point

**O**r **D**a **F**ull range

Label all possible matches Label matches used for scoring

**KKNDFEQGELYLK**

**Monoisotopic mass of neutral peptide** (Mr(mass)): 1752.8312

**Fixed modifications**: MMTS (C) (apply to specified residues or termini only)

**Variable modifications**: 

**X1** : +210.00 (K), +210.00 (E), with neutral loss 48.0590

**X2** : +210.00 (K), +210.00 (E), with neutral loss 48.0590

**Ions Score**: 39 **Expect**: 0.0021

**Matches**: 12/180 fragment ions using 15 most intense peaks

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MS/MS Fragmentation of ASGYKYLDMQK

Found in Q9F889, Serine beta-lactamase-like protein LACTB, mitochondrial OS=Mus musculus GN=Lactb PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from ___ Da to ___ Da
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1651.6018
Fixed modifications: NMTSS (C) (apply to specified residues or termini only)
Variable modifications:
K3 : mal_COO2 (K), with neutral loss 43.0598
Ion score: 20 Expect: 0.097
Matches : 17/134 fragment ions using 30 most intense peaks

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MS/MS Fragmentation of **FGTKFGLDLK**

Found in Q8BWT1, 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Aaa2 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Ox Plot from 150 to 1150 Da

Label all possible matches  Label matches used for scoring

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**Monoisotopic mass of neutral peptide Mr(calc): 1210.6234**

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

K4 : mal-Co2 (K), with neutral loss 43.9898

**Ions Score:** 39  **Expected:** 0.0093

**Matches:** 9/94 fragment ions using 10 most intense peaks  (help)

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**MS/MS Fragmentation of LPMGMTAENLAAKYNISR**

**Found in QBWTL, 3-ketoacyl-CoA thiolase, mitochondrial OS=1, Mus musculus GN=Aca2 PE=1 SV=3**

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1900 Da

Label all possible matches □ Label matches used for scoring □

Nonisotopic mass of neutral peptide M+calc: 2046.6972
Fixed modifications: HK (C) (apply to specified residues or termini only)
Variable modifications:
Rid : m+202 (K), with neutral loss 43.0209
Ion Score: T2 Expect: 0.000026
Matches: 20/146 fragment ions using 21 most intense peaks

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MS/MS Fragmentation of LPGMGTAENLAAKYNISR
Found in OS:BTU1 L-betatubulin; mitochondrial OS:Mus musculus GN:Acac2 PF=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mz(m/z): 2080.9021
Fixed modifications: NEPH (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M) with neutral loss 0.0203 (shown in table), 69.9500
M3 : Malonylation (O) with neutral loss 60.0589
Ion Score: 32 Expect: 0.0044
Matches: 80/200 fragment ions using G2 most intense peaks

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MS/MS Fragmentation of KHNFTPLAR
Found in Q8BWT1, 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Aca2a PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calc): 1165.5989
Fixed modifications: MMFS (C) (apply to specified residues or termini only)
Variable modifications:
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Ions Score: 18  Expect: 0.56
Matches : 17/80 fragment ions using 42 most intense peaks  

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Fragmentation of AANEAGYFNEEMAPIEVKTK

Found in Q8BWT1, 3-hydroxyacyl-CoA thiolase, mitochondrial Orl-Mus musculus GN-Aca2 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

On/Off plots [400 to 1900 Da] [Show range]

Label all possible matches [Label matches used for scoring] [1]

Monoisotopic mass of neutral peptide (m/z): 2213.0470

Fixed modifications: K (C) [apply to specified residues or termini only]
Variable modifications:
K22: Oxidation (M), with neutral losses 0.0000 (shown in table), 63.0293
K29: m/z 0.02 (R), with neutral loss 65.0268

Score: 55 Expect: 0.0000
Matched: 16/220 fragment ions using 22 most intense peaks (m/z)

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KDGTVTAGNASGVSDGAGAVIIASEDAVK
MS/MS Fragmentation of KFFVPR
Found in Q3UEJ6, Phosphorylase OS=Mus musculus GN=Pygl PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or:  Plot from 100  to  900  Da  Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide M(r) (calc): 878.4650
Fixed modifications:  NMT5 (C) (apply to specified residues or termini only)
Variable modifications:
    K1 :  m+1 CO2 (+1), with neutral loss 43.0083
Ions Score: 30  Expect: 0.015
Matches: 7/40 fragment ions using 15 most intense peaks  (help)

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MS/MS Fragmentation of IVALFPKDISR

Found in OMMF16 Phasmidbace OS=Mus musculus GN=Pov1 PF=7 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1343.7449
Fixed modifications: NECS (C) (apply to specified residues or termini only)
Variable modifications:
K7 : me1_C02 (K), with neutral loss 43.9896
Ion Score: 81 Expect: 0.0023
Matches: 14/92 fragment ions using 22 most intense peaks (help)

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**MS/MS Fragmentation of CQEKVSQLYMNQK**

Found in Q3UEJ6. Phosphorylation O-S-Mus musculus GN-Pyr1 PE-2 SV-1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1000 Da Full range

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Hs(salo):** 5726.7672

**Fixed modifications:** M + 18 (C) (apply to specified residues or termini only)

**Variable modifications:**

- N4 : m/z Lys (K), with neutral loss 48.0895

**Identified Score:** 35  Expect: 5.9302

Matches : 26/124 fragment ions using 60 most intense peaks (salo)

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MS/MS Fragmentation of **CQEKSQLYMNQK**

Found in Q3UJ6, Phosphorylase OS=Mus musculus GN=Pygl PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from **200** to **1000** Da

Label all possible matches ○ Label matches used for scoring @

---

Monoisotopic mass of neutral peptide \( m/(m+1) \): 1745.7422

Fixed modifications: Met5 (C) (apply to specified residues or termini only)

Variable modifications:

- N4: \( \text{m loadData(N4)} \), with neutral loss 48.0590

Mono: Oxidation (M), with neutral losses 0.0000 (shown in table), 60.0000

Ions Score: 22 Expect: 0.014

Matches: 82/100 fragment ions using 07 most intense peaks (help)

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MS/MS Fragmentation of GYEAKEYYEALPELK
Found in GJUEJ6. Phosphorylation O=S=Mus musculus GN=Pvd PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 1000 Dn Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide MW(m/z): 1887.9778
Fixed modifications: M(D) (C) (apply to specified residues or termini only)
Variable modifications:
K: *mal (C) (*), with neutral loss 43.0109
Ions Searched: 25 Exponent: 0.015
Matches: 26/502 fragment ions using 76 most intense peaks

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HLEIIYEINQKHLD

Monoisotopic mass of neutral peptide Mr(calc): 2065.0221
Fixed modifications: Met(S) (C) (apply to specified residues or term ends only)
Variable modifications:
K6 : m/z 20.00 Da, with neutral loss 18.0000
Tons Score: 2, Expect: 0.012
Matches: 20/146 fragment ions using 11 most intense peaks (help)

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| 15 |     |     |     |     |     |     |     |     |     |       |       | R 175.1190  |
MS/MS Fragmentation of **EKQTIHSVFR**

Found in P05096, ATP-binding cassette sub-family D member 3 OS-Mus musculus GN-Abcd3 PE-1 SV-2

Click mouse within plot area to zoom in by factor of two about that point

![Plot](image)

Label all possible matches ✨ Label matches used for scoring ✨

---

**Monoisotopic mass of neutral peptide Mr(calc): 1329.6477**

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

K2 : mal-CO2 (K), with neutral loss 45.0050

**Ions Score:** 25  **Expect:** 0.026

**Matches:** 16/100 fragment ions using 32 most intense peaks  (help)

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**MS/MS Fragmentation of DQVIYPDGKEDQK**

Found in P55096, ATP binding cassette sub-family D member 3 OS=Mus musculus GN=Abed3 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1500 Da Full range

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mz(calc): 1416.7215**

**Fixed modifications:** NMT (C) (apply to specified residues or termini only)

**Variable modifications:**
- K: 16.0215 (N), with neutral loss 48.0690
- Z: 4.0215 (C) Expected: 9.0462

**Matches:** 52/120 fragment ions using 94 most intense peaks

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MS/MS Fragmentation of MTIMEQKYEGEYR
Found in P55096, ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1800. Do Full range.
Label all possible matches. Label matches used for scoring.

Monoisotopic mass of neutral peptide M(M+H) = 776.7542
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications: 
Ions Score: 60 Expect: 4.9e-006
Matches: 18/318 fragment ions using 26 most intense peaks.

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MTIMEQKYEGEYR
**MS/MS Fragmentation of MTIMEQKYEGEYR**

Found in PS5096, ATP-bundate cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1000 Da

Label all possible matches  Label matches used for scoring

---

### Monoisotopic mass of neutral peptide Mz(m/z): 2798.7402

**Fixed modifications:** MTG8(C) (apply to specified residues or termini only)

**Variable modifications:**

- M: Oxidation (M), with neutral losses 0.0600 (shown in table), 62.0685
- K: m/z 55 (K), with neutral loss 42.0685

Ions Score: 27  Expect: 0.011

Matched: 21/166 fragment ions using 46 most intense peaks

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**MTIMEQKYEGEYR**
MS/MS Fragmentation of LITNSEELAFYNGNKR
Found in P52096, ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Aloc3 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or Plot ions 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ♦

Monoisotopic mass of neutral peptide Pe(m/z): 1532.5412
Fixed modifications: NMTSE (C) (Apply to specified residues or termini only)
Variable modifications:
E1S  neutral loss 44.0099
Intra Scorer: G2 Extrap: 5.7e-006
Matches: 81/152 fragment ions using 76 most intense peaks [help]

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### MS/MS Fragmentation of KLVEHLHNFIFFR

**Found in P09046, ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=2**

Click mouse within plot area to zoom in by factor of two about that point

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1784.5842

**Fixed modifications:** MMDB (C) (apply to specified residues or termini only)

**Variable modifications:**

R  : sodF_2 (K), with neutral loss 43.0084

**Matches:** 16/120 fragment ions using 21 most intense peaks  

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MS/MS Fragmentation of LVADFMAKK

Found in P00329, Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2

Click and mouse within plot area to zoom in by factor of two about that point.

150 to 1500 Da

Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1107.5634
Fixed modifications: M+N3 (C) (apply to specified residues or termini only)
Variable modifications:
K8 : mod_C_O2 (K), with neutral loss 43.9698
Ions Score: 26  Expect: 0.0055
Matches : 10/66 fragment ions using 27 most intense peaks  (help)

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MS/MS Fragmentation of ICKHPESNFCSR
Found in P00329, Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mz(scale): 1557.6344
Fixed modifications: MET5 (C) (apply to specified residues or termini only)
Variable modifications:
K5 : alk_COOH (K), with neutral loss 49.9898
Ions Score: 21 Expect: 9.0039
Matches: 20/116 fragment ions using 10 most intense peaks (help)

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MS/MS Fragmentation of KFPLDPLITHVLPFEK
Found in P03529, Alcohol dehydrogenase 1 OS=Mus musculus GN=Aldh1 PE=2 SV=2

Click mouse within plot area to zoom in by factor of two about that point.

Monoisotopic mass of neutral peptide Mr(calc): 1973.0766
Fixed modifications: M+15 (+N) (apply to specified residues or termini only)
Variable modifications:
K1  mal-COOH (+105), with neutral loss 48.0956

Matches : 40/176 fragment ions using GO most intense peaks (help)

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**MS/MS Fragmentation of IKMVATGVCVR**

Found in P00329. Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2

Click mouse within plot area to zoom in by factor of two about that point

**Monoisotopic mass of neutral peptide Mz(calc): 1224.5665**

**Fixed Modifications:** M(13) (C) (apply to specified residues or terminal only)

**Variable Modifications:**

**X2** : m/z 1532 (R), with neutral loss 42.0908

**M3** : Oxidation (M), with neutral losses 0.0000 (shown in table), 60.0908

**Ions Score:** 19 **Expect:** 0.13

**Matches:** 5/126 fragment ions using 20 most intense peaks

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**MS/MS Fragmentation of IIAVDINKDK**

Found in **P00329**, Alcohol dehydrogenase 1
OS=**Mus musculus**
GN=**Adh1**
PE=2
SV=2

Click mouse within plot area to zoom in by factor of two about that point

O_r, Plot from **100** to **1300 Da**
Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1213.6554**

**Fixed modifications:**  NMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

K**0** : **mal-CO2 (K)**, with neutral loss 43.0050

**Ions Score:** 28  Expect: 0.27

**Matches:** 24/86 fragment ions using 90 most intense peaks  

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**MS/MS Fragmentation of WDIQKYAR**

Found in **O35490**, Betaine--homocysteine S-methyltransferase 1
OS=Mus musculus GN=Bhmt PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

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**MS/MS Fragmentation of LMKEGLEAAR**

Found in Q35490. Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1200 Da

Label all possible matches  Label matches used for scoring

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**Monoisotopic mass of neutral peptide Mr(calc): 1202.6965**

**Fixed modifications:** NMTS (G) (apply to specified residues or termini only)

**Variable modifications:**

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**MS/MS Fragmentation of GNYVAEKISGQK**

*Found in O55490, Betaine–homocysteine S-methyltransferase 1 OS=Mus musculus GN=Ehmt PE=2 SV=1*

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from [200] to [1000] Da  Full range

Label all possible matches ☐  Label matches used for scoring ☑

---

### Monoisotopic mass of neutral peptide Mr(calc): 1079.6729

**Fixed modifications:** METh (C) (apply to specified residues or termini only)

**Variable modifications:**

Mr  : cal. 1079.6729, with neutral loss 48.9888

**Ions Score:** 21 Expected: 0.026  
Matches : 12/114 fragment ions using 22 most intense peaks (help)

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MS/MS Fragmentation of ISGQKVNEAACDIAR
Found in O35490, Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bmmt PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1703.7702
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
KM ma e (O), with neutral loss 44.0120
Ions Score: 76 Expect: 2.2e-904
Matches : 81/554 fragment ions using 54 most intense peaks (hires)

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### Mass Spectrometric Data

**Fragmentation of LKAYLMSQPLAYHTPDCGK**

**Found in:** OAS940, Batracotoxininae Semathreptidae 1, Odorosaurus GMMBent PE=2 SV=1

**Click mouse within plot area to zoom in by factor of two about that point.**

**Or:** Plot focus 200 to 1700 Da **Full range**

**Label all possible matches**  **Label matches used for scoring**

---

**Maxent model of neutral peptide Mc(pI=3): 2233.0575**

**Fixed modifications:** M, K (apply to specified residues or termini only)

**Variable modifications:**
- **K:** m1, m2, m3, n, with neutral losses 43, 195, 196
- **M:** Oxidation (M, with neutral losses 0.0058 (invasive), 61, 195, 196

**Masses:** 26.000, 0.0002

---

**Metabolite:** 26.005 Fragment ions into using 10 most intense peaks (default)

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|----|-------|-------|-------|-------|-------|-------|-------|-------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| 1  | 114.0913 | 57.5493 |     |       |       | L     |       |       |      |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| 2  | 284.1909 | 142.6021 | 267.1708 | 134.0889 |       | K     | 2128.9708 | 1063.4898 | 2109.9442 | 1055.4758 | 2108.9602 | 1034.9834 | 18
| 3  | 385.2340 | 178.1206 | 333.2074 | 169.6074 |       | A     | 1956.8653 | 978.9363 | 1939.8387 | 970.4230 | 1938.8457 | 969.9310 | 17
| 4  | 518.2973 | 259.6525 | 501.2708 | 251.1590 |       | Y     | 1885.8281 | 943.4177 | 1868.8016 | 934.9044 | 1867.8176 | 934.4124 | 16
| 5  | 621.3914 | 316.1942 | 614.3548 | 307.8611 |       | L     | 1722.7648 | 861.3880 | 1705.7383 | 852.3728 | 1704.7442 | 852.8804 | 15
| 6  | 778.4168 | 389.7120 | 761.3902 | 381.1988 |       | M     | 1699.6807 | 805.3440 | 1592.6542 | 796.8207 | 1591.6702 | 796.3387 | 14
| 7  | 865.4488 | 433.2280 | 849.4233 | 424.7148 | 847.4321 | 424.2228 | S     | 1462.6453 | 731.8253 | 1445.6188 | 723.3130 | 1444.6548 | 722.8310 | 13
| 8  | 963.5074 | 497.2337 | 956.4808 | 488.7441 | 957.4968 | 488.2520 | Q     | 1576.6188 | 788.3103 | 1558.5588 | 779.7970 | 1557.6028 | 779.5050 | 12
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| 10 | 1203.6442 | 602.3247 | 1198.6177 | 593.8125 | 1198.5336 | 593.3205 | L     | 1190.9208 | 575.7546 | 1133.7474 | 567.2414 | 1132.4914 | 566.7492 | 10
| 11 | 1374.6811 | 677.8448 | 1357.6548 | 659.3310 | 1356.6708 | 658.8390 | A     | 1637.4179 | 519.2126 | 1600.3914 | 509.2093 | 1599.4074 | 509.2073 | 9
| 12 | 1437.7447 | 719.3760 | 1420.7181 | 710.8627 | 1419.7341 | 710.3707 | Y     | 965.3808 | 483.9640 | 949.3543 | 473.1808 | 948.3702 | 474.6888 | 8
| 13 | 1578.8034 | 787.9034 | 1557.7770 | 779.9221 | 1556.7930 | 778.9001 | H     | 803.3175 | 402.1624 | 786.2909 | 395.6491 | 783.3069 | 395.1571 | 7
| 14 | 1675.8512 | 838.4293 | 1658.8247 | 829.9160 | 1657.8407 | 829.4240 | T     | 666.2586 | 333.6329 | 649.2320 | 325.1196 | 648.2480 | 324.6276 | 6
| 15 | 1772.9040 | 886.9556 | 1755.8775 | 878.4424 | 1754.8934 | 877.9504 | P     | 565.3108 | 283.1091 | 548.1843 | 274.5958 | 547.2063 | 274.1083 | 6
| 16 | 1887.9189 | 944.4691 | 1870.9464 | 935.9538 | 1869.9204 | 935.4638 | D     | 668.1581 | 354.2382 | 651.1316 | 342.2664 | 650.1476 | 342.5774 | 7
| 18 | 2093.9493 | 1074.4737 | 2076.9228 | 1058.9610 | 2075.9358 | 1053.4730 | G     | 204.1343 | 102.5708 | 187.1077 | 94.0575 | 186.5468 | 94.0575 | 2
| 19 | 147.1128 | 74.0563 | 130.0853 | 65.5468 |       | K     | 1063.4898 | 1939.8387 | 1938.8457 | 969.9310 | 18

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**Raw Text: LKAYLMSQPLAYHTPDCGK**
MS/MS Fragmentation of GYVKAGPWTPEAAVEHPEAVR

Found in GYVKAGPWTPEAAVEHPEAVR

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Or, Plot from -500 to 1000 Da, Full range

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MS/MS Fragmentation of **KEYWQNLR**

Found in **O335490** Retaine--homocysteine S-methyltransferase

OS=Mus musculus GN=Blmt PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1650 Da Full range

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide M_r(calc):** 1221.5778

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

K1 : m/z CO2 (X), with neutral loss 43.0090

**Ion Score:** 17  **Expect:** 0.12

Matches: 6/70 fragment ions using 18 most intense peaks (**help**)

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MS/MS Fragmentation of KGILER
Found in O35490, Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1

Monoisotopic mass of neutral peptide Mr(calc): 800.4392
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K1 : mal_c02 (K), with neutral loss 43.0598
Ions Score: 70  Expect: 0.15
Matches : 7/50 fragment ions using 13 most intense peaks  (help)

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**MS/MS Fragmentation of AVEAFETAKK**

Found in Q64442, Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Or: Plot from 150 to 1060 Da

Label all possible matches ☐ Label matches used for scoring ☑

---

**Monoisotopic mass of neutral peptide**

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**Fixed modifications**: MMTS (C) (apply to specified residues or termini only)

**Variable modifications**: K9: mal-CDG (K), with neutral loss 42.0158

**Ions Score**: 24  **Expect**: 0.002

**Matches**: 29/82 fragment ions using 45 most intense peaks **(help)**

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**MS/MS Fragmentation of KPMVLGHEAAGTVTK**

- **Found in:** Q64442, Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3
- **Fixed modifications:** MMTS (C) (apply to specified residues or termini only)
- **Variable modifications:** 
  - K: alklys (K), with neutral loss 44.0268
- **Ions Score:** 28  **Expect:** 0.012
- **Matches:** 27/132 fragment ions using 81 most intense peaks

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MS/MS Fragmentation of KPMVLGHEAAGTVTK

Found in O64442. Selenated dehydro-Met
OS=Mus musculus GN=U09928 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point.
Or, Plot from 150 to 1000 Da

Label all possible matches  Label matches used for scoring

Protonic mass of neutral peptide Mz(mass): 1699.8240
Fixed modifications: HETQ (C) (apply to specified residues or termini only)
Variable modifications:
K1 : mad, C02 (K), with neutral loss 64.0958
M1 : Oxidation (M), with neutral losses 0.0280(shown in table) 64.0958
Input Score: 02 Expect: 0.0035
Matches: 41/256 fragments ions using 97 most intense peaks

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IGDFVVKKPMVLGHEAAGTVTK

The image contains a mass spectrometry analysis of a peptide sequence, IGDFVVKKPMVLGHEAAGTVTK, with a focus on fragmentation and protein sequence analysis. The table lists various fragmentation ions and their corresponding scores and masses. The analysis includes fixed modifications and variable modifications, with isotopic clusters and fragment ions shown. The data is used for identifying the peptide sequence from a mass spectrometry experiment.
IGDFVVKKPMVLGHEAAGTVTK
MS/MS Fragmentation of **KAGLLEK**
Found in O61176. Arstianet-1 OS=Mus musculus GN=Arz1 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 843.4702
**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)
**Variable modifications:**
- K: +44.01568 [K], with neutral loss 43.9898

**Ions Score:** 36  **Expect:** 0.038
**Matches:** 12/60 fragment ions using 20 most intense peaks  (b=-p)

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MS/MS Fragmentation of GGVEKGPAALR
Found in Q61776, Arginase-1 OS=Mus musculus GN=Arg1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Set from _150_ to _1650_ Da
Label all possible matches ☐ Label matches used for scoring ☐

Monoisotopic mass of neutral peptide Mr(calc): 1135.5335
Fixed modifications: NO modification (C) (apply to specified residues or termini only)
Variable modifications:
KS : ma.LCO2 (K), with neutral loss 43.01599
Ions Score: 56 Expect: 0.00010
Matches: 18/52 fragment ions using 18 most intense peaks (help)

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GGVEKGPAALR
MS/MS Fragmentation of \textit{LKETEYDVR}

Found in Q6176, Arginase-1 OS=Mus musculus GN=Arg1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from \textbf{150} to \textbf{1200} Da Full range

Label all possible matches \(\bigcirc\) Label matches used for scoring \(\bigcirc\)

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Monoisotopic mass of neutral peptide Mr(calc): 1237.5826

Fixed modifications: MNTS (C) (apply to specified residues or termini only)

Variable modifications:

K2 : ma_l(C) (K), with neutral loss 43.0095

Ions Score: 26 Expect: 0.025

Matches : 14/486 fragment ions using 30 most intense peaks (help)
ANNELAGVVAEIVQKNGR
**MS/MS Fragmentation of SVGKANEELAGVVAEVQK**

Found in Q61776, Arginine-1 OS=hsa mascot GN=Arg1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ⬇️ Label matches used for scoring ⬇️

Monoisotopic mass of neutral peptide (m/z): 1912.9749
Fixed modifications: HET (O) (apply to specified residues or term only)
Variable modifications:
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Ions Searched: 17 Expect: 2.5e-06
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**MS/MS Fragmentation of SLEIGAPFSKGQPR**

Found in Q61788, Arginase-1 OS=Mus musculus GN=Argl PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or  Plot from 200 to 1800 Da  Full range
Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide M(n, n.e.)**: 1684.8784

Fixed modifications: M + 15 (C) (apply to specified residues or termini only)

Variable modifications:

K11: m + 49 (K), with neutral loss 43.0589

Ions Score: 19  Expect: 0.984

_matches : 9/100 fragment ions using 13 most intense peaks (help)

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MS/MS Fragmentation of MVQKSLAR

Found in P54869, Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, enter plot area to zoom in by factor of two about that point

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1017.5277
Fixed modifications: HMTS (C) (apply to specified residues or termini only)
Variable modifications:
K4 : m1_O2 (K), with neutral loss 43.0050
Ions Score: 89 Expect: 0.017
Matches: 21/66 fragment ions using 40 most intense peaks (help)

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MS/MS Fragmentation of FNNVEAGKYTVGLGQTR
Found in P54869. Hydroxymethylbutyryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmcox2 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Me(calc): 1908.9426
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
E9 : ael_COO (R), with neutral loss 49.0068

Total Score: 55 Expect: 0.0000
Matches : 22/120 fragment ions using 60 most intense peaks

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### MS/MS Fragmentation of LVSSVSDLPKR

**Found in:** P54869. Hydroxymethylbilirubin-CoA synthase, mitochondrial OS=Mus musculus GN=Hmas2 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point.

Or, Plot from: 200 to 1100 Da

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide M(calc):** 1285.6978

**Fixed modifications:** M(<b>) (apply to specified residues or termini only)

**Variable modifications:**
- K10: ma1.C02 (K), with neutral loss 43.9998

**Ions Score:** 20  **Expect:** 0.038

**Matches:** 15/50 fragment ions using 18 most intense peaks  

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MS/MS Fragmentation of VSKDASPGSPLEK

Found in P54689, Hydroxymethylglycine-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Flat from ___ to ___ Da Full range

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide M(z+1): 1299.6832
Fixed modifications: MESS (C) (apply to specified matches or termini only)
Variable modifications:
NO: , male (K), with neutral loss 48.0569

Score: 38 Expect: 8.9583

Matches: 28/156 fragment ions using 40 most intense peaks (b/a)

| #  | b   | b^+  | b^++ | b^0  | b^++ | Seq| y   | y^+ | y^++ | y^0 | y^0++ |  
|----|-----|------|------|------|------|----|-----|-----|------|-----|-------|-----|
| 1  | 100.0757 | 50.5415 |      |      |      | V  |     |     |      |     |       |     |
| 2  | 187.1077 | 94.0537 |      |      |      |    | 1257.5621 | 629.3197 | 1240.6036 | 620.8084 | 1239.6216 | 620.3144 |
| 3  | 357.2132 | 179.1103 |      |      |      |    | 1170.6001 | 585.8037 | 1153.7535 | 577.2984 | 1152.5895 | 576.7984 |
| 4  | 472.2402 | 236.6237 |      |      |      |    | 1000.6816 | 500.7509 | 983.4680 | 492.2376 | 982.4840 | 491.7426 |
| 5  | 543.2763 | 272.1392 |      |      |      |    | 885.4676 | 443.2374 | 868.4111 | 434.7242 | 867.4571 | 434.2232 |
| 6  | 630.3062 | 315.6638 |      |      |      |    | 814.4365 | 407.7189 | 797.4040 | 399.2056 | 796.4199 | 398.7136 |
| 7  | 727.3321 | 364.1814 |      |      |      |    | 727.3983 | 364.2029 | 710.3119 | 355.6896 | 709.3879 | 355.1796 |
| 8  | 784.3356 | 392.6904 |      |      |      |    | 630.3457 | 315.6763 | 613.3992 | 307.1632 | 612.3352 | 306.6712 |
| 9  | 871.4156 | 436.2114 |      |      |      |    | 578.3242 | 287.1858 | 556.2977 | 278.6525 | 555.3176 | 278.1605 |
| 10 | 968.4684 | 484.7578 |      |      |      |    | 486.2922 | 243.6498 | 469.2657 | 235.1362 | 468.2817 | 234.6443 |
| 11 | 1051.5524 | 514.7298 |      |      |      |    | 389.3385 | 185.1324 | 372.2129 | 186.6101 | 371.2389 | 186.1181 |
| 12 | 1210.5950 | 603.8011 |      |      |      |    | 276.3328 | 138.3813 | 259.1289 | 130.0831 | 258.1448 | 129.5761 |
| 13 |       |       |      |      |      |    | 147.1228 | 74.0569 | 130.0833 | 65.5468 | 1 |
MS/MS Fragmentation of LEETYTNKDVDKALLK
Found in P54892, Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da
Label all possible matches ○ Label matches used for scoring ⬤

Monoisotopic mass of neutral peptide Mz(calc): 1566.5942
Fixed modifications: 5HT (C) (apply to specified residues or termini only)
Variable modifications:
K12 : m/e 49.02 [O] , with neutral loss 48.0098
Ion Score: 17 Expect: 0.005
Matches : 6/106 fragment ions using 10 most intense peaks (h为目标)

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MS/MS Fragmentation of **APNSPDVLEIEFKK**

Found in P16460, Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Ox Peptide from 200 to 1500 Da Full range Label all possible matches Label matches used for scoring

**Nonisotopic mass of neutral peptide M(calc):** 1671.3845
**Fixed modifications:** M(13) (C) (apply to specified residues or termini only)
**Variable modifications:** KE: M(14) (E, with neutral loss 48.0950)
**T ions Score:** 52  Expect: 0.00592
**Matches to Fragment ions using 20 most intense peaks**

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**MS/MS Fragmentation of TQDPAKAPNSPDVLEIEFK**

Found in P16160, Argininosuccinate synthetase OS=Mus musculus GN=Ass1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or: Plot from 300 to 2000 Da Full range
Label all possible matches □ Label matches used for scoring □

---

**Monoisotopic mass of neutral peptide (M+H): 2114.5556**

**Fixed modifications:** M(15) C (apply to specified residues or termini only)

**Variable modifications:**

- R: m/z 202 (R), with neutral loss 44.01298

**Ions Searched:** 76 Bepari; 7.1e-07

**Matches:** 46/121 fragments list using 80 most intense peaks (Child)

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GRNDLMEYAKQHGIPIPVTPK

Mass Spectrometry

Monoisotopic mass of neutral peptide M (+Na) = 2459.2421
Fixed modifications: C-47 (apply to specified residues or terminal only)
Variable modifications: 
Matched : 25/242 fragment ions using 20 most intense peaks

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MS/MS Fragmentation of YKLDCR
Found in J3OMG3. Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=4 SV=1
Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calc): 928.3782
Fixed modifications: HMTS (C) (apply to specified residues or termini only)
Variable modifications:
K2 : +1.010 Da (K), with neutral loss 43.9898
Ions Score: 27  Expect: 0.047
Matches : 5/48 fragment ions using 7 most intense peaks  (help)

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MS/MS Fragmentation of DVFNKGYGFGMVK

Found in J3OMG2. Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=4 SV=1

Align mouse within plot area to zoom in by factor of two about that point

Or [Plot from] 200 to 1500 Da [Full range]

Label all possible matches [ ] Label matches used for scoring [ ]

Monoisotopic mass of neutral peptide M_a (m/z): 1562.7076
Fixed modifications: NEQ (C) (apply to specified residues or termini only)
Variable modifications:
ES: wa/0.02 (E), with neutral loss 44.0980
MS1: Oxidation (M), with neutral losses 0.0455 (shown in table), 63.9983
Ions Score: 20 Expect: 0.0017

Matches: 37/100 fragment ions using 24 most intense peaks [help]

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MS/MS Fragmentation of LTLDTIFVPTNGKK

Found in J30MG3. Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=4 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide MW(calc): 1621.8779
Fixed modifications: MetO(S) (apply to specified residues or termini only)
Variable modifications:
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Ions Score: 28 Expect: 0.024
Matches : 11/100 fragment ions using 14 most intense peaks (link)

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LTLDTIFVPTNGKK
MS/MS Fragmentation of YKVCNYGLTFTQK
Found in JAKMA Voltage-dependent anion-selective channel protein 3 (OS=Macaurosdenum GN=Vdac3 PE=4 SV=1)

Click mouse within plot area to zoom in by factor of two about that point
Or  Plot from 200 to 800  De  Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide M0 (calc.) : 1695.7627
Fixed modifications: M0723 (C) (apply to specified residues or termini only)
Variable modifications:
K2 : maldi200 (K), with neutral loss 42 u mos
Ions Score : 83  Expect : 0.000003
Matches : 20/122 fragment ions using 50 most intense peaks  

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MS/MS Fragmentation of DVFNKGYGFGMVK
Found in J3QMG3, Voltage-dependent anion-selective channel protein 3
OS=Mus musculus GN=Vdac3 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, select from 200 to 1500 Da
Label all possible matches [ ] Label matches used for scoring [ ]

Monoisotopic mass of neutral peptide Mz(calc): 1596.7126
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K5 : mal-COO (K), with neutral loss 43.9598
Ions Score: 20 Expect: 0.10
Matches : 10/114Fragment ions using 10 most intense peaks (below)

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MS/MS Fragmentation of **AAKDVFNK**
Found in J3QMG3. Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=4 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

Or, Plot from 100 to 1000 Da
Label all possible matches
Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 977.4818
Fixed modifications: NH3 (C) (apply to specified residues or termini only)
Variable modifications:
K3 : mal_C02 (B), with neutral loss 43.9890
Ions Score: 31  Expect: 0.019
Matches : 9/66 fragment ions using 10 most intense peaks  (help)

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MS/MS Fragmentation of GPKSLIGVR

Found in Q91J35, UTP-gluco-1-phosphate uridylytransferase OS=Mus musculus GN=Ugp2 PE=2 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1011.5713
Fixed modifications: M(MS)^2 (C) (apply to specified residues or termini only)
Variable modifications:
K3 : m1_C02 (K), with neutral loss 43.0068
Ions Score: 17 Expect: 0.051
Matches : 11/76 fragment ions using 40 most intense peaks

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ADVKGGTTLTQYEGK

**MS/MS Fragmentation of ADVKGGTTLTQYEGK**

Found in **O91276**: UTP - glucose-1-phosphate uridylyltransferase OS=Mus musculus GN=Uru1 PE=2 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Or, [Plot from 200 to 1400 Da](#) [Full range](#)

Label all possible matches [Label matches used for scoring](#)

---

**Monoisotopic mass of neutral peptide Mz(m/z): 1881.7415**

**Fixed modifications**: NMT3 (C) (apply to specified residues or termini only)

**Variable modifications**:

K4 : m3s_202 (E), with neutral loss 48.0058

**Ions Score**: 48  **Expect**: 0.00007

**Matches**: 87/194 fragment ions using 43 most intense peaks (help)

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FLQEKGPSVDWGK

MS/MS Fragmentation of FLQEKGPSVDWGK
Found in O01735: UDP-glucose-1-phosphate uridyltransferase OS=Mus musculus GN=Ugt1408 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide (M(calc)): 1376.7069
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K8 : mg 329 (K), with neutral loss 49.046805
Ion Score: 2e Expert: 0.005959
Matches : 29/120 fragment ions using 65 most intense peaks (calc)

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**MS/MS Fragmentation of LGSSFTKVQDYLRL**

Found in 091715, L. deltoidea, leukocyte-derived factor.

Variable modifications: N-term (C) (apply to specified residues or termini only)

Monoisotopic mass of neutral peptide Mz(calm): 1598.7046

Fixed modifications: N-term (C) (apply to specified residues or termini only)

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MS/MS Fragmentation of IQRPPEDSIQPYEIKIK

Found in 061738 1TPMz0.1_c02.00/c03.00/peptide OMMaMus morulina GNATev2 PE=7 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ☑ Label matches used for scoring *

IQRPPEDSIQPYEIKIK

Monoisotopic mass of neutral peptide Mz(calc): 2066.0371
Fixed modifications: MMTV (C) (apply to specified residues or termini only)
Variable modifications:
K8: iTRAQ 8 (K), with neutral loss 41 Da

Matches : 24/142 fragment ions using 51 most intense peaks (help)

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Note: The table above lists fragment ions and their corresponding masses, which are used for peptide identification.
MS/MS Fragmentation of **VGDKIATR**

Found in **P40142**, Transketolase OS=Mus musculus GN=Tko PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 900 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 944.4927
Fixed modifications: HMTS (C) (apply to specified residues or termini only)
Variable modifications:
K : mal-CO2 (K), with neutral loss 43.0098

Matches : 9/72 fragment ions using 16 most intense peaks  (help)

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MS/MS Fragmentation of KAYGLALAK
Found in P40142. Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1019.5651
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K1 : m/z CO2 (K), with neutral loss 43.0098
Ions Score: 37 Expect: 0.012
Matches: 12/64 fragment ions using 26 most intense peaks  (help)

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MS/MS Fragmentation of AFGQAKHQPTAIIAK
Found in P40142. Translated as OS=Mus musculus GN=Tha PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full-range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide \( m/z \text{calc.} \): 1665.5560
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
N\&K
m/z 202.008 (F), with neutral loss 43.0070
Ions Score: 28 Impact: 0.008D
Matches: 41/126 fragment ions using 92 most intense peaks

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MS/MS Fragmentation of **EAWHGKPLPK**
Found in **P40142**, Transketolase
OS=Mus musculus  GN=Trk PE=1 SV=1

**Monoisotopic mass of neutral peptide Mr(calc): 1247.6289**
Fixed modifications: **NHE4 (C) (apply to specified residues or term only)**
Variable modifications:
K6  :  +4.002 (K), with neutral loss 43.9890

**Ions Score: 20 Expect: 0.22**

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### MS/MS Fragmentation of GITGIEDKEAWHGKPLPK

**Found in:** P40412, Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from [200] to [1500] Da

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(m/z):** 2601.0241

**Fixed modifications:** MSS (C) (apply to specified residues or terminal only)

**Variable modifications:**
- K14 : m/z 202 (K), with neutral loss 48.9588

**Ions Score:** 25  **Expect:** 6.00E-13

**Matches:** 66/100 fragments ions using 90 most intense peaks

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MS/MS Fragmentation of **FKSVDDVIK**

Found in **P24549** Retinal dehydrogenase 1

OSS=Msx mouse

GN=Aklh1al

PF=1

SV=5

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from **150** to **1150** Da Full range

Label all possible matches ○ Label matches used for scoring ○

---

**Nonisotopic mass of neutral peptide Mr(calc): 1135.5761**

**Fixed modifications:** M(18) (C) (apply to specified residues or termini only)

**Variable modifications:**

K2 : ma_l_C02 (K), with neutral loss 43.9888

**Torsion Score:** 34 Expect: 0.0013

**Matches:** 27/84 fragment ions using 45 most intense peaks [help]

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MS/MS Fragmentation of **ILDIESGKK**

Found in **P24549**, Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5

Click mouse within plot area to zoom in by factor of two about that point
Or,
Plot form 150 to 150 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1200.6601
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
K9 : mal-CO2 (K), with neutral loss 43.9598
Ions Score: 20 Expect: 0.024
Matches: 25/52 fragment ions using 46 most intense peaks

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MS/MS Fragmentation of VAFTGSTQVGKLIK
Found in P24549. Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1al PE=1 SV=5

Monoisotopic mass of neutral peptide Mr(calc): 1583.5603
Fixed modifications: MMTH (C) (apply to specified residues or termini only)
Variable modifications:
K17 : methionine oxidized
Ions Score: 40  Expect: 0.0073
Matches : 19/122 fragment ions using 86 most intense peaks  (helix)

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### MS/MS Fragmentation of IQHTKIFINNEWHNSVSGK

Found in P24549, Retinal dehydrogenase 1 O9; Mus musculus GN=Aldh1al PE=1 SV=5

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches Label matches used for scoring

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MS/MS fragmentation of KYVLGNPLTPGINQGPQIDKEQHDK
Found in E26449, Ratinal dehydrogenase 1 OS=Rattus norvegicus GN=Aldehyde dehydrogenase 1 homolog (1)
Charge monoisotopic mass plot set to zoom in by a factor of two above that point

| # | b1   | b2   | b3   | b4   | b5   | b6   | b7   | b8   | b9   | Seq | y   | y'   | y''  | y'''  | y'''' | #   |
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| 1 | 171.1125 | 154.0962 | 77.5468 |     |     |     |     |     |     |     |     |     |     |     |       | 28   |
| 2 | 334.1761 | 176.5177 | 117.1407 | 150.7074 |     |     |     |     |     |     |     |     |     |     |     |       |      |
| 3 | 433.2464 | 217.1259 | 106.2180 | 208.8126 |     |     |     |     |     |     |     |     |     |     |     |       |      |
| 4 | 546.3268 | 273.6079 | 259.3021 | 410.1547 |     |     |     |     |     |     |     |     |     |     |     |       |      |
| 5 | 603.3631 | 302.7187 | 156.2255 | 293.0554 |     |     |     |     |     |     |     |     |     |     |     |       |      |
| 6 | 617.3404 | 308.6801 | 150.3185 | 293.0554 |     |     |     |     |     |     |     |     |     |     |     |       |      |
| 7 | 614.3631 | 307.8285 | 150.3185 | 293.0554 |     |     |     |     |     |     |     |     |     |     |     |       |      |
| 8 | 612.3519 | 306.2255 | 150.3185 | 293.0554 |     |     |     |     |     |     |     |     |     |     |     |       |      |
| 9 | 607.3519 | 304.6801 | 150.3185 | 293.0554 |     |     |     |     |     |     |     |     |     |     |     |       |      |
| 10 | 602.3519 | 303.0801 | 150.3185 | 293.0554 |     |     |     |     |     |     |     |     |     |     |     |       |      |

Monoisotopic mass of neutral peptide [M+salt]+: 2074.4532
Fixed modifications: MDA2 (C) (apply to specified residues or tandem only)
Variable modifications:
   +5.94 Da (K), with neutral loss 13.0020
Zn Score: 33 Expect: 1.0e-4
Matches: 14/27 by fragment ions using 10 most intense peaks (help)
**MS/MS Fragmentation of TILNNGKTCR**

Found in P16015, Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3

Click mouse within plot area to zoom in by a factor of two about that point.

Or, Platform 150 to 12,000 Da Full range

Label all possible matches ○ Label matches used for scoring ●

![Fragmentation Graph](image)

**Monoisotopic mass of neutral peptide Mr(calc):** 1250.5747

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**
- K7 : mal-CO2 (K), with neutral loss 45.0188

**Ions Score:** 10  **Expect:** 0.013

**Matches:** 10/98 fragment ions using 10 most intense peaks  (help)

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**MB/MS Fragmentation of YAAELHLVHWNPKYNTFGEALK**

*Found in P16015, Carbonic anhydrase 3 OsMaAnasecahs GhoCaP PEn1 SVCe*

Click menu within plot area to zoom in by factor of two about that point

**Variable modification:**
- Kd : m1, m2 (C) (apply to specified residues or termini only)

**Raw score:** 50.0000
**Expect:** 6e-06

**Matches:** 51/220 fragments listed using 100 most intense peaks

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**Neuroecopic mass of neural peptide M1308(1): 1555.5179**

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**
- Kd : m1, m2 (C) (with neutral loss 43.9268)

**Ions Scored:** E0 Exempt: 6e-06

**Matches:** 50/220 fragments listed using 100 most intense peaks

---

**YAAELHLVHWNPKYNTFGEALK**
MS/MS Fragmentation of **LQSKVTAK**

Found in **J3ONG0**. MCG15755 OS=Mus musculus GN=Gm5424 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from: 100 to 850 Da

Label all possible matches ☐ Label matches used for scoring ☑

---

**Monoisotopic mass of neutral peptide Mr(calc): 958.5287**

Fixed modifications: **NMTIS (C)** (apply to specified residues or termini only)

Variable modifications:

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Matches : 19/74 fragment ions using 42 most intense peaks  (help)
MS/MS Fragmentation of **KVFIEDVSK**

Found in 3QNG0, MCG15755 OS=Mus musculus GN=Gm5424 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or,  Plot from 050 to 1200  D2  Full range

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1149.5918**

**Fixed modifications: BMFS (C) (apply to specified residues or termini only)**

**Variable modifications:**

K1 : mal-Glu (K), with neutral loss 43.9898

**Ions Score: 24  Expect: 0.046**

**Matches : 8/85 fragment ions using 19 most intense peaks** ([help](#))

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MS/MS Fragmentation of VTNIKDGTTTR
Found in J3QG0, MCG15755 OS=Mus musculus GN=Smn424 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1129.5939
Fixed modifications: MBTS (C) (apply to specified residues or termini only)
Variable modifications:
K5 : m/z CO2 (K), with neutral loss 44.012
Ions Score: 61 Expect: 0.00092
Matches : 19/100 Fragment ions using 49 most intense peaks (help)

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MS/MS Fragmentation of ALKLGAK
Found in J3QNG0, MCG15755 OS=Mus musculus GN=Gm5424 PE=3 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, plot from 100 to 800 Da
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide M_r(calc): 785.4667
fixed modifications: MNIS (C) (apply to specified residues or termini only)
Variable modifications:
KO : met.O2 (K), with neutral loss 43.0090
Ions Score: 22 Expect: 0.1
Matches : 16/44 fragment ions using 57 most intense peaks  (help)

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MSMS Fragmentation of **EGAKYVSHGATGK**

Found in **JON**

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches ☐  Label matches used for scoring ☐

---

**Monoisotopic mass of neutral peptide Mr(calc): 1939.6525**

**Fixed modifications:** **NMTS (C) (apply to specified residues or termini only)**

**Variable modifications:**

- **K4** : *mal*CO2 (K), with neutral loss 44.016

**Tune Source:** Zi, Expect: 3.22

**Matches:** 33/136 fragment ions using 16 most intense peaks

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MS/MS Fragmentation of VNVVEQEKIDK
Found in BoqZLA, Alpha-enolase (Fragment) OS=Mus musculus GN=Enol PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da
Label all possible matches □ Label matches used for scoring □

Monoisotopic mass of neutral peptide M(r/c/a): 1385.7038
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
K9  : m1_O2 (K), with neutral loss 43.9290
Tons Score: 37  Expect: 0.0054
Matches: 15/108 fragment ions using 23 most intense peaks  (help)

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MS/MS Fragmentation of **GVSQAVEHINKTIAPALVSK**

Found in **BIARR7**. Alpha-casein (Precursor) OlAaMa massdia GN=Aeol1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

**Or** Plot from 300 to 1900 Dq Full range

Label all possible matches **Label** matches used for scoring **

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Masses are in Da (ppm) with errors between 0.0006:

**Matches**: 59/210 fragment ions using 39 mass error peaks

**Note**: Monoisotopic mass of neutral peptide (m/z): 2147.1888

**Fixed modifications**: Met(S) (apply to specified residues or termini only)

**Variable modifications**: [Nla]**K** (apply only to specified residues or termini only) with neutral loss 43.9956

**Ions Score**: 56 **Expect**: 0.0006
MS/MS Fragmentation of FMKGVSQAHEINK
Found in BIARR7. Alpha-melolase (Fragment) 08=Mus musculus GN=Enol PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
- Drag plot from 200 to 1000 Da
- Label all possible matches
- Label matches used for scoring

Monoisotopic mass of neutral peptide (m/z (calc)): 1729.9647
Fixed modifications: MTS8 (C) (apply to specified residues or termini only)
Variable modifications:
M: methyl_2O (M), with neutral loss 48.0965
Ion Score: 14 Exposed: 0.12
Matches: 22/142 fragment ions using 97 most intense peaks (calc)

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MS/MS Fragmentation of **TIAPALVSKK**

Found in **BIARK7**, Alpha-enolase (Fragment) OS=Mus musculus GN=Enol PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, [plot from] 150 to 1000 Da [full range]

Label all possible matches ☐ Label matches used for scoring ☐

---

Monoisotopic mass of neutral peptide Mr(calc): 1112.6441

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:
K10 : mal-CO2 (K), with neutral loss 48.0488

Total Score: 34 Expect: 0.011

Matches: 19/30 fragment ions using 40 most intense peaks  (help)

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**MS/MS Fragmentation of LGKEAGLKPFEQVK**

Found in D2041. Long-chain fatty-acid-CoA ligase 1 OS=Mus musculus GN=Acs11 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from Ymin to Ymax  Do Full range
Label all possible matches ○ Label matches used for scoring @

---

**Monoisotopic mass of neutral peptide** M(calcd): 1628.5774
**Fixed modifications**: MM2 (C) (apply to specified residues or termini only)
**Variable modifications**:
**K** : ma1-CO2 (E), with neutral loss 44.008
**Ions Score**: 27 **Expect**: 0.0046

Matches: 11/180 fragment ions using 20 most intense peaks

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MS/MS Fragmentation of **GEGEVCVKGANVFK**

Found in **D52911**, Long-chain-fatty-acid-CoA ligase 1 OS=Mus musculus GN=Acat1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

On: Flat form 200 to 1400 Da  Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1567.7011

Fixed modifications: METh (C) (apply to specified residues or termini only)
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**MS/MS Fragmentation of AKLLELEGVENK**

Found in D3Z041, Long-chain-fatty-acid-CoA ligase 1 OS=Mus musculus GN=Acs11 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1300 Da Full range

Label all possible matches ○ Label matches used for scoring ●

---

**Monoisotopic mass of neutral peptide Mr(calc): 1298.7081**

**Fixed modifications:** NMTS (C) [apply to specified residues or termini only]

**Variable modifications:**

R2 : m/z CO2 (K), with neutral loss 43.0000

**Ions Score:** 25 **Expect:** 0.0088

**Matches:** 26/204 fragment ions using 62 most intense peaks (help)

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M. B. Fragmentation of KTITVSQDEGVRPSTTMQGLAK
Found in H. B. 3-5, 3-ketosyl-CoA thiolase A, peroxosomal OS = Mus musculus GN = Aceaapes PE = 2 SV = 1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot form: 200 to 1800 DAs
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Pe (m/z): 2481.2227
Fixed modifications: MZ2 (C) (apply to specified residues or terminal only)
Variable modifications:
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Matches: 20/226 fragment ions using 66 most intense peaks (unip)

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### Non-enriched Mass of neutral peptide N-term (kDa): 200.3239

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**Fixed modifications:** NMT (C) (apply to specified residues or termini only)

**Variable modifications:**
- K1: O-Glucosamine (K1), with neutral loss 0.0000 (shown in table), 43.6648
- K2: O-GlcNAc (K2), with neutral loss 43.6648

**Leader:** No, **Target:** 1.035

**Matches:** 4/472 fragment ions using 10 most intense peaks
MS/MS Fragmentation of SSCTIIPLMKR

Found in P19066, Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1379.6611

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

K10 : m/z CD2 (K), with neutral loss 43.9898

Ions Score: 29 Expect: 0.015

Matches : 17/28 fragment ions using 34 most intense peaks

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**MS/MS Fragmentation of SSCTIIPLMKR**

Found in P19096. Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point.
Or, Plot from <200> to <1400> Da Full range
Label all possible matches ☐ Label matches used for scoring ☐

---

Monoisotopic mass of neutral peptide Mr(calc): 1388.4560
Fixed modifications: MINS(C) (apply to specified residues or termini only)
Variable modifications:
- oxidation (M), with neutral losses 0.0000 (shown in table), 69.9883
- ma1:C02 (K), with neutral loss 43.9590
- Ions Score: 28 Expect: 0.013
Matches: 17/196 fragment ions using 50 most intense peaks (help)

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MS/MS Fragmentation of **CTVFPKAQVEDAFR**

Found in P19096, Fatty acid synthase OS:Mus musculus GN:Fasn PE:1 SV:2

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring @

Monoisotopic mass of neutral peptide M(cala): 2761.7904

Fixed modifications: HET (C) (apply to specified residues or termini only)

Variable modifications:

K6 :  m1.202 (R), with neutral loss 49.9599

Ions Scored: 10 Expect: 0.000

Matches : 16/100 fragment ions using 41 more intense peaks (b/a)

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14 matches
**Fragmentation of FDASFFGVHPKQAHTMDPQLR**

*Found in P104806, NADIR and HST.*

Click mouse within plot area to zoom by a factor of two about that point:

- **Plot from:** 200 to 1000 Da
- **Full range**

**Label all possible matches**

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**Differences from exact mass of neutral peptide (Neale): 250.1730**

**Fixed modifications:** M(<sup>CH</sup>3) (<sup>H</sup>2) apply to specified residues or termini only

**Variable modifications:**

- **K1:** +1, +42 (R), with neutral loss 62.0000
- **K2:** +3.000, with neutral losses 0.0000 (shown in table), 62.0000
- **K3:** +5.000, with neutral losses 0.0000

**Note:** K1 = 24; Expect: 8.058

**Matches:** 84/600 fragment ions using 106 most intense peaks (H2)

**FDASFFGVHPKQAHTMDPQLR**
MS/MS Fragmentation of **VKSINNPDMR**

Found in Q3N117, ATP-citrate synthase OS=Mus musculus GN=Acy PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1200 Da Full range

Label all possible matches Label matches used for scoring

---

Monoisotopic mass of neutral peptide $M_r$(calc): 1258.5976

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

K2 : met_C02 (K), with neutral loss 43.9888

Ions Score: 38  Expect: 0.002

Matches: 7/98 fragment ions using 10 most intense peaks (help)

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VKSINNPDMR
**MS/MS Fragmentation of VKSINNPDMR**

Found in Q3V117, ATP-citrate synthase OS=Mus musculus GN=Acy PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ◐ Label matches used for scoring ◐

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**Monoisotopic mass of neutral peptide Mr(calc): 1274.5925**  
Fixed modifications: MetS (C) (apply to specified residues or termini only)  
Variable modifications:  
M2 : oxidation (M), with neutral loss 15.9949  
M9 : oxidation (M), with neutral losses 0.0000 (shown in table), 15.9949  
Ions Score: 39  Expect: 0.0025  
Matches : 12/150 fragment ions using 20 most intense peaks (help)

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Found in Q8V17, ATP-citrate synthase OS=Mus musculus GN=Acly PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Oc, Plot from 150 Da to 1260 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1296.66666
Fixed modifications: M(128.0989) (apply to specified residues or termini only)
Variable modifications: KE (15.9949), with neutral loss 43.9689
Ions Score: 21 Expect: 0.11
Matches to Peptide: 36/56 fragment ions using 70 most intense peaks  (help)

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EGLKIMGIGHR
**MS/MS Fragmentation of EKLIMGIGHR**

Found in O5YV17, ATP-citrate synthase OS=Mus musculus GN=Acty PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1300 Da full range

Label all possible matches ○ Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1311.6608

**Fixed modifications:** NMT (C) (apply to specified residues or termini only)

**Variable modifications:**

- K3 : mal-CO2 (K), with neutral loss 43.9888
- M6 : Oxidation (M), with neutral losses 0.015 (shown in table), 68.9993

**Tone Score:** 10  **Expect:** 0.005

**Matches:** 28/146 fragment ions using 42 most intense peaks (help)

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MS/MS Fragmentation of AVNQGKIFK
Found in O9DSN0. Elution factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or, from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1039.5019
Fixed modifications: MetS (C) (apply to specified residues or termini only)
Variable modifications:
K6 : m/z CO2 (K), with neutral loss 43.0000
Ions Score: 32 Expect: 0.0089
Matches : 14/60 fragment ions using 37 most intense peaks (help)

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MS/MS Fragmentation of **AKDPFAHLPK**

Found in Q0DL8N0. Elongation factor 1a lambda OS=Mus musculus GN=EF1A DE-1 SV-3

Click mouse within plot area to zoom in by factor of two about that point

![Diagram](image)

**Monoisotopic mass of neutral peptide Mr(amu): 1200.6190**

**Fixed modifications:** MET (C) (apply to specified residues or termini only)

**Variable modifications:**

**K2** : mal-COO (K), with neutral loss 44.0090

**Ions Score:** 96 **Expect:** 0.016

**Matches:** 10/88 fragment ions using 10 most intense peaks

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MS/MS Fragmentation of LCEKMAQFDALK
Found in Q9D8N0, Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1414.5331
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications: K4 : mal,C02 (K), with neutral loss 43.0090
Tons Score: 54 Expect: 0.001
Matches: 21/156 fragment ions using 44 most intense peaks (help)

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MS/MS Fragmentation of ILGLLDTHLKLTR

Found in Q9DBM0, Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1400 Da Full range

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1464.88200
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K10: +162.085 (Y), with neutral loss 48.08888
Ions Score: 60  Expect: 0.00024
Matches: 20/102 fragment ions using 48 most intense peaks

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**MS/MS Fragmentation of DGSPGFSKFR**

Found in Q9QXF8, Glycine N-methyltransferase OS=Mus musculus GN=Genm PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches ✘  Label matches used for scoring ✗

---

Monoisotopic mass of neutral peptide Mr(calc): 1182.5306

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

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| 10 | 175.1190 | 88.0631 |     | 158.0924 | 79.5498 | R |     |     |     |     |     | 1    |
MS/MS Fragmentation of LALKNIASMVR
Found in Q9QXF8, Glycine N-methyltransferase OS=Mus musculus GN=Gnt PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ☐ Label matches used for scoring ☑

Monoisotopic mass of neutral peptide Mr(calc): 1316.7122
Fixed modifications: NMTB (C) (apply to specified residues or termini only)
Variable modifications:
N4 : methyl (K), with neutral loss 48.02128
M9 : Oxidation (M), with neutral losses 0.00000(shown in table), 69.9859
Tone Score: 97 Expect: 0.001
Matches: 26/182 fragment ions using 30 most intense peaks (help)

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MS/MS Fragmentation of **NIYYKSDLTK**

Found in **Q9X848**, Glycine N-methyltransferase OS=Mus musculus GN=Guinat PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

**Or**, Plot from **100** to **1200** Ds

Label all possible matches ☑ Label matches used for scoring ☑

---

**Monoisotopic mass of neutral peptide Mr(calc): 1325.6452**

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

K5 : mal-CO2H (K), with neutral loss 43.01508

**Ions Score:** 16  **Expect:** 0.67

**Matches:** 2/36 fragment ions using 22 most intense peaks  (help)

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MS/MS Fragmentation of NCIGKQFAMNELK
Found in A2A974, Protein Cyp4a12b OS=Mus musculus GN=Cyp4a12b PE=2 SV=1

Monoisotopic mass of neutral peptide Mr(m/z): 1642.7153
Fixed modifications: N/C (C) (apply to specified residues or termini only)
Variable modifications:
K8 : methionine oxidation (M), with neutral loss 15.99494
M9 : oxidation (M), with neutral losses 0.00000 (shown in table), 48.9568
Ion Score: 85 Expect: 7.4e-65
Matches : 24/188 fragment ions using 28 most intense peaks (f10m)

| u  | b   | y** | y'   | y0  | Seq. | y   | y** | y'   | y0  | y0  | y'   | y0  | y0  |
|----|-----|-----|------|-----|------|-----|-----|------|-----|-----|------|-----|-----|-----|
| 1  | 115 1226 | 38.0827 | 38.0827 | 40.5135 | N    | 1483.6599 | 743.3486 | 1668.6533 | 734.3433 | 1667.6793 | 734.3433 | 12
| 2  | 137 1127 | 247.0206 | 247.0206 | 240.0139 | C    | 1336.6829 | 668.8301 | 1319.6664 | 660.3368 | 1318.6824 | 659.8494 | 11
| 3  | 151 1133 | 360.1046 | 360.1046 | 355.5660 | I    | 1223.6099 | 612.3081 | 1206.5823 | 603.7548 | 1205.5953 | 603.3028 | 10
| 4  | 164 1138 | 417.1261 | 417.1261 | 409.0667 | G    | 1166.5874 | 583.7973 | 1149.5609 | 575.2841 | 1148.5769 | 574.7921 | 9
| 5  | 177 1382 | 587.2316 | 587.2316 | 574.1194 | K    | 995.4819 | 498.7446 | 979.4553 | 490.2213 | 978.4713 | 490.7593 | 8
| 6  | 150 1347 | 640.6620 | 640.6620 | 635.1487 | Q    | 868.4233 | 424.7153 | 851.3968 | 426.2020 | 850.4128 | 425.7100 | 7
| 7  | 183 1355 | 822.3566 | 822.3566 | 817.8629 | F    | 721.3549 | 361.1811 | 704.3284 | 352.6678 | 703.3443 | 352.1758 | 6
| 8  | 198 1314 | 993.3957 | 993.3957 | 987.2015 | A    | 582.2824 | 252.1448 | 486.2558 | 242.6316 | 485.2718 | 243.1395 | 4
| 9  | 211 1306 | 1194.4740 | 1194.4740 | 1187.7407 | M    | 389.2295 | 195.1234 | 372.2129 | 186.6101 | 371.2289 | 186.1181 | 3
| 10 | 225 1343 | 1386.6007 | 1386.6007 | 1375.7800 | E    | 1453.6873 | 727.1317 | 1435.6007 | 718.3804 | 1435.6167 | 718.3120 | 12
| 11 | 239 1353 | 1578.7483 | 1578.7483 | 1567.8043 | L    | 371.2289 | 186.6101 | 371.2289 | 186.6101 | 371.2289 | 186.6101 | 1
MS/MS Fragmentation of ILKDQDLQDLTR

Found in Protein Cyp4a12b G6-Mus musculus ON-Cyp4a12b PE-2 SV-1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1700 Da

Label all possible matches ○ Label matches used for scoring ●

Molecular mass of neutral peptide M<sub>calc</sub>: 1605.9750

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

K3: = m<sub>7</sub>CO2 (K), with neutral loss 46.0930

Intra Score: 7 Expect: 0.0010

Matches: 18/102 fragment ions using 28 most intense peaks (help)

| # | b   | y   | y<sup>+</sup> | y<sup>++</sup> | b<sup>−</sup> | b<sup>++</sup> | b<sup>+<sup>++</sup></sup> | Seq. | y<sup>−</sup> | y<sup>++</sup> | y<sup>+++</sup> | y<sup>−</sup> | y<sup>++</sup> | y<sup>+++</sup> | y<sup>−</sup> | y<sup>++</sup> | y<sup>+++</sup> | y<sup>−</sup> | y<sup>++</sup> | y<sup>+++</sup> |
|---|-----|-----|--------------|---------------|---------|-------------|----------------|----|-----------|---------------|---------------|---------|-------------|---------------|---------|-------------|---------------|---------|-------------|---------------|---------|
| 1 |     |     |              |               |         |             |                | 1 |           |               |               |         |             |               |         |             |               |         |             |               |         |
| 2 | 227 | 114 | 114.0913     | 57.5492       |         |             |               | 1 | 1499.8064 | 730.4068      | 1482.7799    | 741.8936 | 1481.7938   | 741.4016      |         |             |               |         |             |               |         |
| 3 | 397 | 199 | 199.1441     | 190.6308      |         |             |               | 1 | 1386.7223 | 693.3646      | 1369.6958    | 668.3515 | 1368.7118   | 694.3991      |         |             |               |         |             |               |         |
| 4 | 512 | 256 | 256.8576     | 248.1443      | 494.2973 | 247.8523    |               | 1 | 1110.3199 | 551.2986      | 1084.5633    | 542.7853 | 1083.5793   | 542.3933      |         |             |               |         |             |               |         |
| 5 | 640 | 320 | 320.6869     | 312.1736      | 622.3359 | 311.4816    |               | 1 | 1110.3199 | 551.2986      | 1084.5633    | 542.7853 | 1083.5793   | 542.3933      |         |             |               |         |             |               |         |
| 7 | 868 | 434 | 434.7424     | 426.2291      | 850.6689 | 425.7371    |               | 1 | 858.5043  | 429.7558      | 841.4778     | 421.2425 | 840.4938    | 420.7505      |         |             |               |         |             |               |         |
| 8 | 996 | 498 | 498.7717     | 490.2584      | 978.5253 | 489.7664    |               | 1 | 745.4263  | 373.2138      | 728.3957     | 564.7065 | 727.4097    | 364.2085      |         |             |               |         |             |               |         |
| 9 | 1111 | 556 | 556.3051     | 547.7719      | 1093.5524 | 547.2798    |               | 1 | 617.3617  | 309.1945      | 600.3352     | 300.6712 | 599.3511    | 300.1792      |         |             |               |         |             |               |         |
| 10 | 1224 | 612 | 612.8272    | 604.3139      | 1206.6615 | 603.8219    |               | 1 | 563.3848  | 251.6710      | 481.3082     | 243.1777 | 484.3242    | 242.6657      |         |             |               |         |             |               |         |
| 11 | 1337 | 669 | 669.3692    | 660.8559      | 1319.7205 | 660.3639    |               | 1 | 388.2507  | 195.1290      | 372.2241     | 166.6157 | 371.2401    | 186.1237      |         |             |               |         |             |               |         |
| 12 | 1438 | 711 | 711.9030    | 711.3788      | 1420.7682 | 710.8877    |               | 1 | 216.1666  | 138.3870      | 259.1401     | 120.0737 | 258.1561    | 120.3817      |         |             |               |         |             |               |         |
| 13 |     |     |              |               |         |             |                | 1 | 175.1190  | 88.0651       | 158.0924     | 79.5468  |             |               |         |             |               |         |             |               |         |
### MS/MS Fragmentation of NCIGKQFAMNELK

**Found in A24974. Protein Cvp4a12b OS=Mus musculus GN=Cvp4a12b PE=2 SV=1**

Click mouse within plot area to zoom in by factor of two about that point

On or off, Plot from 200 to 1600 Da

Label all possible matches or Label matches used for scoring

---

**Monoisotopic mass of neutral peptide**

- *M*<sub>calc</sub>: 1426.7204

**Fixed modifications:** MG (C) (apply to specified residues or termini only)

**Variable modifications:**
- K: am1.C02 (R), with neutral loss 41.0928

**Ions Score:** 40  **Expect:** 0.0016

**Matches:** 29/120 Fragment ions using 66 most intense peaks

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### MS/MS Fragmentation of LYSEFLGKR

**Found in A2AE89.** Glutathione S-transferase Mu 1 (Fragment) OS=Mus musculus GN=Gstmu1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plo1t from 150 to 1150 Da Full range

Label all possible matches ☐ Label matches used for scoring ☐

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1197.6030

**Fixed modifications:** MMIS (C) (apply to specified residues or termini only)

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**Ions Score:** 38  **Expect:** 0.0015

**Matches:** 25/68 fragment ions using 66 most intense peaks  (help)
MS/MS Fragmentation of MKLYSEFLGK

Found in A2AE89. Glutathione S-transferase Mu 1 (Fragment) OS=Mus musculus GN=Gstm1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1200 Da Full range

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1316.5322

Fixed modifications: MTSS (C) (apply to specified residues or termini only)
Variable modifications:
M1: Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9988
K2: met_002 (K), with neutral loss 49.9998

Ions Score: 95 Expect: 0.0026

Matches: 14/134 fragment ions using 21 most intense peaks (help)

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**MS/MS Fragmentation of MKLYSEFLGK**

Found in A2AF89, Glutathione S-transferase Mu 1 (Fragment) OS=Mus musculus GN=Gstm1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

On: Plot from 150 to 1200 Da

Label all possible matches

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MS/MS Fragmentation of **MLEYTDSSYDEKR**
Found in **A2AI89**, Glutathione S-transferase Mu 1 (Fragment) OS=Mus musculus GN=Gstmu1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Ok, Plot from 200 to 1800 Da
Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Me(sole): 1834.7391
Fixed modifications: HET3 (C) (apply to specified residues or termini only)
Variable modifications:
K15 : m/z CO2 (R), with neutral loss 44.0158
Ions Score: 45  Expect: 7.5e-065

Matches : 14/122 Fragment ions using 25 most intense peaks  (help)

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**MS/MS Fragmentation of MLMKFGDDPVTK**

Found in **A2AQN4**, Acyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ◎ Label matches used for scoring ◎

---

**Monoisotopic mass of neutral peptide Mr(calc): 1466.6785**

Fixed modifications: **MHIS (C)** (apply to specified residues or termini only)

Variable modifications:

- **K4:** m/z OOO2 (K), with neutral loss 44.9899

**Tune Score:** 46 **Expect:** 0.0012

Matches: 10/122 fragment ions using 36 most intense peaks (help)

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**m/z 1466.6785** (calc) vs. **m/z 1464.6785** (found)

**Charge:** 5

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**MLMKFGDDPVTK**
**MS/MS Fragmentation of MLMKFGDDPVTK**

Found in A2AQN4, Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acsc2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot zoom: 200 to 1400 De Full range

Label all possible matches ○ Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr(m/z): 1492.6795**

**Fixed modifications:** MAET (△) apply to specified residues or termini only.

**Variable modifications:**
- Oxidation (M)
- N-term. 0.0569 (shown in table), 69.5925
- K 49.0698

**Ion Score:** Zn: 2.82 Expect: 0.00002

**Matches:** 10/160 fragment ions using 22 most intense peaks (help)

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**MS/MS Fragmentation of MLMKFGDDPVTK**

Found in A2A0N4. Acetyl-coenzyme A synthetase, cytosolic OS=Mus musculus GN=Acss2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or (Plot from) 200 to 1400 Da (Full range)

Label all possible matches  ○  Label matches used for scoring  ○

---

**Monoisotopic mass of neutral peptide (Mono):** 1493.6684

**Fixed modifications:**  Met(O) (C) (apply to specified residues or termini only)

**Variable modifications:**
- M1: Oxidation (M, with neutral losses 0.0000 shown in table), 0.0683
- M2: Oxidation (M, with neutral losses 0.0000 shown in table), 0.0683
- M4: N-linked glycosylation (N), with neutral losses 0.0464

**Ion Source:** ESI  **Expect:** 0.02

**Matches:** 51/172 fragment ions using 22 most intense peaks

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MS/MS Fragmentation of LCENIAGHLK

Found in A2AL20, Catalase OS=Mus musculus GN=Cat PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1228.5580
Fixed modifications: MHS [C] (apply to specified residues or termini only)
Variable modifications:
K10 : m/z 442.2915 [K], with neutral loss 43.9898
Ions Score: 28 Expect: 0.009
Matches to Fragment ion spectrum: 17/94 fragment ions using 44 most intense peaks  (help)

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MS/MS Fragmentation of **KALDIAE.NEMPGLMR**

Found in **AZAL.T5**, Adenocytoxinses (Fragment) O5=Mas musculus GN=Ahcy PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, **Plot from** 500 to 1000 Da **Full range**

Label possible matches **Label matches used for scoring**

---

**KALDIAE.NEMPGLMR**

---

Monoisotopic mass of neutral peptide Mr(calc): 1772.2947

Fixed modifications: MMR (apply to specified residues or termini only)
Variable modifications:
K = S, M

last Severe: S8  K = 0.002

Matches : 50/100 fragment ions using 95 most intense peaks

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MS/MS Fragmentation of KDAVSFYVSR
Found in A2ANX6. Very long-chain acyl-CoA synthetase (Fragment) OS=Mus musculus GN=Slc27a2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Put from to Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1966.6721
Fixed modifications: YMTS (C) (apply to specified residues or termini only)
Variable modifications:
K1 : m/z 162.002 (K), with neutral loss 43.9999

Ions Score: 11 Expect: 0.25
Matches : 7/114 fragment ions using 11 most intense peaks

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MS/MS Fragmentation of ALEKISR
Found in B1AU25, Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifm1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calc): 901.4869
Fixed modifications: HYS (C) (apply to specified residues or termini only)
Variable modifications:
E4 : mal_COO2 (K), with neutral loss 43.0588

Matches : 6/60 fragment ions using 7 most intense peaks (help)

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| 5 | 597.3606 | 299.1840 | 580.3341 | 290.6707 | 579.3501 | 290.1787 | I | 375.2350 | 188.1212 | 358.2085 | 179.6079 | 357.2245 | 179.1159 | 4
| 6 | 684.3927 | 342.7000 | 667.3661 | 334.1867 | 666.3821 | 333.6947 | S | 262.1510 | 131.5791 | 245.1244 | 123.0659 | 244.1404 | 122.5738 | 3
| 7 | | | | | | | R | 175.1190 | 88.0631 | 158.0924 | 79.5498 | | | 2

Hosting: Swiss-Prot
Database: IPI_MOUSE_v3.9
MS/MS Fragmentation of VMGLGLSPEE KQR
Found in B1A125, Apoptosis-inducing factor 1, mitochondrial OS-Mus musculus GN-Aif1 PE-2 SV-1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mz(calc) : 1528.7655
Fixed modifications: NHEGS (C) (apply to specified residues or terminal only)
Variable modifications:
K11 : mal-COOH (R), with neutral loss 43.9500
Ions Score: 20 Expect: 0.088
Matches : 4/106 fragment ions using 11 most intense peaks (help)

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**MS/MS Fragmentation of GNMVKLNDGSQITFEK**

Found in **BLAU25**, Apoptosis-inducing factor 1, mitochondrial OS=**Mus musculus** GN=Aimf1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

**Or:** Plot from **200** to **6000** Da

Label all possible matches ☐ Label matches used for scoring ☐

---

**Heteroatomic mass of neutral peptide Hm(m/e):** 888.8624

**Fixed modifications:** M(r2) (C) (Apply to specified residues or terminal only)

**Variable modifications:**
- **K** (n=1) **CO2H** (E), with neutral loss 0.9890

**Tons Score:** 25  **Expect:** 0.51

**Matches:** 25/162 fragment ions using 40 most intense peaks  

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MS/MS Fragmentation of GNMVKLNDGSQITFEK
Found in B1A25, Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aif1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches Label matches used for scoring

Nonisotopic mass of neutral peptide M+H+ (Da): 1541.3772
Fixed modifications: M+H+ (C) (apply to specified residues or termini only)
Variable modifications:
K : Oxidation (M) with neutral losses 0.001000 shown in table. 63.9983
ES : m/z, Da (R) with neutral losses 0.001000
Ion Score: 44 Feature: 9.9958
M: Matches: 24/242 fragment ions using 54 most intense peaks

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MS/MS Fragmentation of **IIKDGQHEDLNEVAK**

Found in **BIAU25**. Apoptosis-inducing factor 1, mitochondrial OS-MyoD1 mouse GN-Arin1 PE-2 SV-1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

---

Monoisotopic mass of neutral peptide Mr (calc): 1922.9221

Fixed modifications: **M** (C) (apply to specified residues or termini only)

Variable modifications:

K ≤ + m1 CCQ (K), with neutral loss 43.01068

Ions Score: 27 Expect: 0.002

Matches: 24/166 fragment ions using 60 most intense peaks (help)

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MS/MS Fragmentation of KIJKDGEQHEDLNEVAK

Found in BLAU15, Apoptosis-inducing factor 1, mitochondrial Os=Muscus musculus GN=Adm1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mz(calc): 2051.0771
Fixed modifications: M+C, (C) (apply to specified residues or term only)
Variable modifications:
E4 + m1-CO2 (R), with neutral loss 44.01236

Matches: 46/176 fragment ions using 97 most intense peaks (help)

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M/C/M Fragmentation of KVETDHIVTAVGLEPNVELAK

Found in BLAC25, Apoptosis-inducing factor 1, mitochondrial OS-Musculus NO-Alf1 PE-2 S1-1

Click mouse within plot area to zoom in by factor of two about that point

O  1  Plot range  200 to 1500 Da

Nonisotopic mass of neutral peptide [M+H](calc): 2247.2271

Fused modifications: M</sub>15</sup> (G) (apply to specified residues or term only)

Variable modifications:

K = [m+239](K), with neutral loss 43.0285

Table 1: 18/22 fragment ions using 28 most intense peaks

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**MS/MS Fragmentation of VVAGVAAALAHKYH**

Found in ADRKX4. Remnant: OS=Mouse; entrezGene: CN=5718; h) P|E=57 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot area. 200 to 1400. Dz. Full range.
Label all possible matches. Label matches used for scoring.

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**Monoisotopic mass of neutral peptide Mr(mono):** 1461.7526

Fixed modifications: **NMT2 (C)** (apply to specified residues or termini only)

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Found in A2ARH3, Phosphotransferase-related protein (Fragment) O6-Musculus GN-Prot PE-2 SV-1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

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Variable modifications:
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Matches: 12/172 fragment ions using 62 most intense peaks [help]
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Variable modifications:
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Ions Score: 34  Expect: 0.015
Matches : 25/78 fragment ions using 42 most intense peaks  

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MS/MS Fragmentation of **IFKSGQTALEK**

Found in **B1ATQ3**, Malate dehydrogenase, cytoplasmic (Fragment) O8=Mus musculus GN=Mdh1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from **150** to **1200** Da

Label all possible matches ○  Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr(calc): 1306.4765**

Fixed modifications: **NMTS [C]** (apply to specified residues or termini only)

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MS/MS Fragmentation of **ANVKIFK**

Found in **B1ATQ3. Malate dehydrogenase, cytoplasmic (Fragment)** OS=Mus musculus GN=Mdh1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 900 Da

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): **904.5018

**Fixed modifications: **M+H (C) (apply to specified residues or termini only)

**Variable modifications: **

- K: mal+CO2 (K), with neutral loss 93.9898

**Ions Score: **28  Expect: 0.064

**Matches:** 9/46 fragment ions using 16 most intense peaks  **(help)**

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### MS/MS Fragmentation of **AAIKHALSAGYR**

**Found in BIANW3, Alcohol dehydrogenase [NADP(+)](Fragment) OS=Mus musculus GN=Akr1a1 PE=2 SV=1**

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1400 Da

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1342.6939

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

| K4  | =nal C02 (K), with neutral loss 43.0088 |

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**MS/MS Fragmentation of GDNPFPKNADGTVR**

Found in **BLAXW3**. Alcohol dehydrogenase [NADP(+)] (Fragment) OS=Mus musculus GN=Akri1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two around that point

- For full range

Label all possible matches ○ Label matches used for scoring ◇

---

**Monoisotopic mass of neutral peptide Mr(m/z): 1572.7166**

**Fixed modifications:** MetO (+) (apply to specified residues or termini only)

**Variable modifications:**

- K7: mal-COOH (K), with neutral loss 43.0565

**Input:**

- Exp: 1.1e-05

**Match:** 1/16 Fragment ions using 24 most intense peaks (help)

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ATAVMPDGQF KDISLSEYK
MS/MS Fragmentation of VVKQASEGPLK

Found in DvV108 Citrobacter rodhodferox dehydrogenase CN=Mus musculus CN=Gim6316 PF=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 150 to 1200 Da
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1240.6663
Fixed modifications: Mono (C) (apply to specified residues or termini only)
Variable modifications:
KX : malate (K), with neutral loss 43.05598
Ions Score: 92 Expect: 0.012
Matches : 50/98 fragment ions using 78 most intense peaks (help)

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MS/MS Fragmentation of TVDGPSGKLWR
Found in D3YU05, Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gmd6316 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 10 to 1400 Da
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mz(c大胆): 1200.6412
Fixed modifications: MSGD (C) (apply to specified residues or termini only)
Variable modifications:
MSK: [mal-COO] (K), with neutral loss 42.0608
Ions Score: 97 Expect: 0.00027
Matches : 17/96 fragment ions using 92 most intense peaks

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TVDGPSGKLWR
LVINGKPITIFQER

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Ions Score: 46  Expect: 9.00616
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MS/MS Fragmentation of AVGKVIPELNGK
Found in D3YU05, Glyceroldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gmd316 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1200 Da [Full range]
Label all possible matches ○ Label matches used for scoring ♦

Monoisotopic mass of neutral peptide M(calc): 1509.7242
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K4 = met 552 (K), with neutral loss 43.0549
Ions Score: 60 Expect: 0.00568
Matches : 27/104 fragment ions using 60 most intense peaks (help)

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MS/MS Fragmentation of **GAAQNIIPASTGAAKAVGK**

*Found in DSYUM. Glyoxylate 3-phosphate dehydrogenase* 
*OS=Mus musculus* 
*GN=Gmds16* 
*PE=3* 
*SV=1*

Click mouse within plot area to zoom in by factor of two about that point.

Or, Plot from 200 to 1700 Da. Full range.

Label all possible matches. Label matches used for scoring.

**Monoisotopic mass of neutral peptide (MISDa):** 1091.5006

**Fixed modifications:** MMTS (C) (apply to specified residues or terminal only)

**Variable modifications:**

K15 : no MOD (X), with neutral loss 43.9458

**Ion score:** 82, Repeat: 24-66

**Matches:** 62/176 fragment ions using 100 most intense peaks (main)

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MS/MS Fragmentation of VFANPEDCAGFGKGENAK
Found in DJyU00. Microsomal glutathione S-transferase 1 OS=Mus musculus GN=Mgst1 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches Label matches used for scoring

Methionine is neutral, peptide Met(cys): 1564.5105
Fixed modifications: MM3 (C) (apply to specified residues or termini only)
Variable modifications: KE : Nε-Lys (R), with neutral loss 48.0861
Ions Score: 104 Expect: 1e-100
Matches : 81/152 fragment ions using 46 most intense peaks

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ITNKVFANPDECAGFGK

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Variable modifications:
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Fasta Source: Rl. Expect: 0.00017
Matches: 17/174 fragments ionized using 69 most intense peaks (in a)

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**MS/MS Fragmentation of VAFTQVNSEDKGALAK**

Found in O3YU93. Uncharacterized protein OB-Mus musculus Q1=R017a.93 PE=4 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, [Fit form] 300 to 2000 Da [Full range]

Label all possible matches [Label matches used for scoring]

---

**Monoisotopic mass of neutral peptide Mr(m/z):** 2115.0317

**Fixed modifications:** MM2 (C) apply to specified residues or terminal only

**Variable modifications:**

- Ox : m/z 202.98, with neutral loss 41.0828

- Nε : 62 Repet: 1 m/z-0.66

**Matches:** 22/200 fragment ions using 10 most intense peaks. [help]

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*Note: The above table contains precursor ion mass-to-charge (m/z) values for the fragment ions generated from the protein sequence VAFTQVNSEDKGALAK. The table provides details such as the masses of the b- and y-series ions, their respective charge states (e.g., b2, b3, b4), and the corresponding y-series ions.*
MS/MS Fragmentation of **GKNCVAIAADR**

Found in **D3YUM8**, Proteasome subunit beta type

OS=Mus musculus  GN=Gm4950  PE=3  SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or,  Plot from  750 to  1100 Da  [Full range]

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1248.6891**

Fixed modifications: **NMT5 (C)** (apply to specified residues or termini only)
Variable modifications:
K2 : mal-COO2 (K), with neutral loss 43.0000

Ions Score: 16  Expect: 0.040

Matches: 9/30 frequent ions using 27 most intense peaks  (help)

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MS/MS Fragmentation of **FVTNTTKESK**

Found in **D3VUN7** Histacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment) OS=Mus musculus GN=Hdhp1 PF=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

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Label all possible matches ☐  Label matches used for scoring ☑

### Monoisotopic mass of neutral peptide Mr(calc): 1299.6982
Fixed modifications: **M+57** (G)  (apply to specified residues or termini only)
Variable modifications:
K7 : **mal-CO2** (K), with neutral loss 43.9399

Ion Source: ESI  Exp Int: 0.631
Matches: 21/96 fragment ions using 62 most intense peaks (help)

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MS/MS Fragmentation of CATITPDEKR
Found in D3VYV3, Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment) OS=Mus musculus GN=Idh1 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calcd): 1264.5428
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K9 : me₇GSO₂ (K), with neutral loss 49.9980
Ions Score: 25 Expect: 0.015
Matches: 12/84 fragment ions using 19 most intense peaks (help)

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MS/MS Fragmentation of YKLLGGLAVR
Found in D3YV43.40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 750 to 1150 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1174.6710
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
R2 : male_002 (R), with neutral loss 43.0050
Score: 40 Expect: 0.0011
Matches: 20/70 fragment ions using 57 most intense peaks

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MS/MS Fragmentation of DATNDQVTKDAEAEIK
Found in DJ3V31. Isocitrate dehydrogenase (NADP) cytosolic (Fragment) OS=Mus musculus GN=Idh1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1776.5221
Fixed modifications: NMT S (C) (apply to specified residues or termini only)
Variable modifications: H2N : can2 (R), with neutral loss 0.0938
Loss Score: 20 Expect: 0.002
Matches : 56/169 fragments ions using 55 most intense peaks (hla)

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MS/MS Fragmentation of SKSLFK
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Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 794.4174
Fixed modifications: MMIS (C) (apply to specified residues or termini only)
Variable modifications:
K2 : mal CO2 (K), with neutral loss 63.9898
Ions Score: 34 Expect: 0.016
Matches : 8/52 fragment ions using 6 most intense peaks (help)

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MS/MS Fragmentation of **AADLKYIEACAR**

Found in **D3YX99**, UDP-glucose 6-dehydrogenase (Fragment) OS=Mus musculus GN=Ugdh PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Set range: 200 to 1400 Da

Label all possible matches ○ Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1454.6583

**Fixed modifications:** MMTS (C) [apply to specified residues or termini only]

**Variable modifications:**

K5 = m(+15)Da, with neutral loss 43.9590

Ions Score: 33, Expscore: 0.084

Matches: 8/112 fragment ions using 12 most intense peaks (help)

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MS/MS Fragmentation of LEKPAKYDDIKK

Found in D3Y15, Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm7293 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ○

LEKPAKYDDIKK

Monoisotopic mass of neutral peptide Mr(calc): 1832.8086
Fixed modifications: M(8) S(7) C(1) (apply to specified residues or terminal only)
Variable modifications:
K : ma1.CO2 (K), with neutral loss 43.0088
Ions Score: 29 Expect: 0.0004
Matches : 21/120 fragment ions using 38 most intense peaks (help)

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MS/MS Fragmentation of RYEEIVKEVSTYIK
Found in D3Y768. Elongation factor 1-alpha 1 (Fragment) OS=Mus musculus GN=Elf1al PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or Plot from 200 to 1700 Da Full range Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide [M+H] + (calc) : 1641.6411
Fixed modifications: NMTD (C) (apply to specified residues or terminus only)
Variable modifications:
K1 : allyl CO2 (K), with neutral loss 42.0202
Ions Score: 52 Expect: 0.0028
Matches : 69/516 fragment ions using 97 most intense peaks (kda)

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MS/MS Fragmentation of SLNPELGTDADKEQWK
Found in D3YQ9, L-lactate dehydrogenase (Fragment) OS=Mus musculus GN=Ldhb PE=2 SV=1

Crop mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calc): 1515.6789
Fixed modifications: M + 16(C) (apply to specified residues or termini only)
Variable modifications:
KES : +150.9496 (K, with neutral loss 49.0949)
Ion Score: 32 Expect: 0.0001
Matches: 56/157 (fragment ions using 67 most intense peaks)
SLNPELGTDADKEQWKEVHK

MS/MS Fragmentation of SLNPELGTDADKEQWKEVHK
Found in D0Y7C9 T-Lactate dehydrogenase (Fragment) OfaMis marina GNaf2_0_1

Click mouse within plot area to zoom in by factor of two about that point
Or: [Pan Tool] 200 to 1900 [X] [Pan Tool] Full range
Label all possible matches □ Label matches used for scoring □

Neutron and mass of neutral peptide M(sole) : 2490.1468
Fixed modifications: IMS (C) (apply to specified residues or termini only)
Variable modifications:
K12  sulph02 (C) , with neutral loss 44.0596
Ion Score: 26.0  Expect: 0.13
Matches : 26/213 fragment ions using 11 most intense peaks  

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MS/MS Fragmentation of $IVSSKDYC\text{CVTANSK}$
Found in D3YZQ9, L-lactate dehydrogenase (Fragment) OS=Mus musculus GN=Ldhpe2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide $m/z$ (mDa) : 1468.7827
Fixed modifications: NMTMR (2) (apply to specified residue or termini only)
Variable modifications:
K5 : male CO2 (K), with neutral loss 48.0356
Total Score: 87 Expect: 0.00005

Matches : 22/142 Fragment ions using 27 most intense peaks (half)

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MS/MS Fragmentation of LTTDVQEFKSSFK
Found in D3LQ02, ATP-binding cassette sub-family B member 8, mitochondrial Os=Mus musculus GN=Abo8 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da
Full range
Label all possible matches
Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1026.7777
Fixed modifications: METS (C) (apply to specified residues or termini only)
Variable modifications:
K9 : mal [CGG] (K), with neutral loss 43.00883
Ions Source: DEEI Ejection: 0.0001
Matches : 12/120 fragment ions using 14 most intense peaks

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MS/MS Fragmentation of **DQFTTLPEVKDR**  
Found in D524U1. Uricase OS=Mus musculus GN-Uox PE=3 SV=1 
Click mouse within plot area to zoom in by factor of two about that point  
Or, Plot from **200** to **1500** Da **Full range**  
Label all possible matches ○  Label matches used for scoring ○

**Monoisotopic mass of neutral peptide Mr(calc): 1583.7831**  
**Fixed modifications:  **MS/MS (C) (apply to specified residues or termini only)  
**Variable modifications:**  
K10 : mal_C02 (E); with neutral loss 43.0590  
**Ions Score: 26  Expect: 0.01**  
**Matches: 32/128 fragment ions using 107 most intense peaks**  

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MS/MS Fragmentation of PGLLDLKGK

Found in D3Z563. Acyl-CoA binding protein OS=Mus musculus GN=Dbi PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calc): 1025.5757
Fixed modifications: MMA (C) (apply to specified residues or termini only)
Variable modifications:
K7 : mas_002 (K), with neutral loss 43.9598

Ions Score: 51  Expect: 4.3e-009
Matches: 16/68 fragment ions using 24 most intense peaks

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MS/MS Fragmentation of **AKWDSWNK**
Found in **D32563**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point

**Monoisotopic mass of neutral peptide Mr(calc): 1119.4985**
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
K : mal002 (K), with neutral loss 43.0090
Ions Score: 26  Expect: 0.011
Matches : 9/70 fragment ions using 20 most intense peaks  (help)

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MS-MS Fragmentation of **LTFDTTFSPNTGKK**

Found in **D3YZZ**. Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Mus musculus GN=Vdac2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or [Full range]

Label all possible matches  Label matches used for scoring  

---

Monoisotopic mass of neutral peptide Mr(calcd): 1641.7056
Fixed modifications: Met(5) [C] (apply to specified residues or termini only)
Variable modifications: 
K14 : m+2CO2 (H), with neutral loss 48.0358
Ions Score: 21  Expect: 0.04

Matches : 12/130 fragment ions using 26 most intense peaks  

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LTFDTTFSPNTGKK
MS/MS Fragmentation of VLKSHGQDYLVGNR

Found in BYAVX (Omphalospermum monspessulanum CN=Flata7 PF=7 SV=1)

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 206 to 1500 Da

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mz(calc): 1670.8076
Fixed modifications: MTH (C) (apply to specified residues or termini only)
Variable modifications:
K3 = +16.052 (C), with neutral loss 45.0288

Ion Score: 30 Expect: 0.0007
Matches: 26/184 fragment ions using 52 most intense peaks (help)

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MS/MS Fragmentation of EPWVEQD KFGK

Found in D521U3, 4-hydroxypyruvate dioxygenase (Fragment) OS=Mus musculus GN=Hpd PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1497.6620
Fixed modifications: AMT (C) (apply to specified residues or termini only)
Variable modifications:
K : m1_C02 (K), with neutral loss 48.0264
Ions Score: 20 Expect: 0.081

Matches : 19/102 Fragment ions using 15 most intense peaks  (help)

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Note: The table shows the fragmentation ions and their corresponding mass values for the peptide EPWVEQD KFGK.
**VLLGGDETPEGQKAVR**

MS/MS Fragmentation of **VLLGGDETPEGQKAVR**

Found in D123F, UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugfd PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from [200] to [1700] Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1773.8940

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

K13  =  m1_O2O (K), with neutral loss 95.9999

T913  =  m1_O2O (K), with neutral loss 95.9999

Tons Score: 43 Expect: 0.00005

Matches: 48/126 fragment ions using 128 most intense peaks (help)

| Precursor | b1 | b1+ | b1++ | b1+++ | y1 | y1+ | y1++ | y1+++ | y2 | y2+ | y2++ | y3 | y3+ | y3++ | y4 | y4+ | y4++ | y5 | y5+ | y5++ | y6 | y6+ | y6++ | y7 | y7+ | y7++ | y8 | y8+ | y8++ |
|-----------|----|-----|------|-------|----|-----|------|-------|----|-----|------|----|-----|------|----|-----|------|----|-----|------|----|-----|------|----|-----|------|----|-----|------|----|-----|------|----|-----|------|
| Peptide   |    |     |      |       |    |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
|           |    |     |      |       |    |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 1         | 100.0727 | 50.5412 |        |        |    |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 2         | 213.1598 | 107.0835 |        |        | L  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 3         | 326.2438 | 163.6255 |        |        | I  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 4         | 383.2535 | 192.1363 |        |        | G  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 5         | 480.2667 | 240.6704 |        |        | G  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 6         | 555.3137 | 278.1601 |        |        | D  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 7         | 681.3583 | 341.6816 |        |        | E  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 8         | 785.4049 | 393.2058 |        |        | T  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 9         | 832.4567 | 416.2330 |        |        | P  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 10        | 1011.4993 | 506.2533 |        |        | E  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 11        | 1088.5208 | 544.7640 |        |        | G  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 12        | 1196.5794 | 598.7933 |        |        | Q  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 13        | 1366.6549 | 683.3261 |        |        | K  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 14        | 1437.7220 | 719.3646 |        |        | A  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 15        | 1536.7964 | 768.8988 |        |        | V  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
| 16        | 175.1190 | 88.0631 |        |        | R  |     |      |       |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |    |     |      |
MS/MS Fragmentation of VEA AVG KDL FR

Found in D3Z3XS, Glutathione S-transferase theta 1 OS=Mus musculus GN=Gstt1 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range

Label all possible matches ☑ Label matches used for scoring ☐

Monoisotopic mass of neutral peptide M+ (calc): 1205.6618
Fixed modifications: MSTR (C) (apply to specified residues or termini only)
Variable modifications:
K7 : mal_CO2 (K), with neutral loss 43.0958
Ions Score: 58 Expect: 0.002
Matches : 27/100 fragment ions using 60 most intense peaks

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### MS/MS Fragmentation of IVAPISDSPKPPPQR

**Found in D3Z4X1, 6-phosphogluconolactonase OS=Mus musculus GN=Phg1 PE=4 SV=1**

Click mouse within plot area to zoom in by factor of two about that point

**Plot from 200 to 1600 Da**

Label all possible matches

**Monoisotopic mass of neutral peptide Ne(male): 1866.9441**

**Fixed modifications:** MGFS (C) (apply to specified residues or termini only)

**Variable modifications:**

**K(In) 5: ma(H)(K), with neutral loss 43.0055**

**Ions Score:** 77 **Expect:** 0.00002

**Matches:** 22/126 fragment ions using 50 most intense peaks

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QATVDGVNVTDRPGLLDDLKKGK
MS/MS Fragmentation of **ISEQSDAKLK**

Found in **D3Z6FS**. ATP synthase subunit alpha OS=Mus musculus GN=Ato5a1 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

Plot from 150 to 1100 Da

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1203.5930**

Fixed modifications: **MHTS (C)** (apply to specified residues or termini only)

Variable modifications:

N0 : ma_l002 (K), with neutral loss 43.0090

Ions Score: 24 Expect: 0.037

Matches: 19/32 fragment ions using 46 most intense peaks

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MS/MS Fragmentation of **KLLDAAGANLR**

Found in **DREG4**, Glyoxylate reductase/hydroxypruvinate reductase OS=Mus musculus GN=Gnhpr PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1100 Da Full range

Label all possible matches Label matches used for scoring

---

Monoisotopic mass of neutral peptide Mr(calc): 1226.6615
Fixed modifications: Met(5) (C) (apply to specified residues or termini only)
Variable modifications:
K1 : ma_G02 (K), with neutral loss 43.0090
Ions Score: 21 Expect: 0.046
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MS/MS Fragmentation of RLKELIGEAAGK
Found in E0CX12, Argininosuccinate lyase OS=Mus musculus GN=Asl PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from ___ Da to ___ Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1365.7585
Fixed modifications: TRYP (C) (apply to specified residues or term only)
Variable modifications:
K : mas_C02 (K), with neutral loss 43.01068
Ions Score: 41  Expect: 0.0016
Matches : 14/118 fragment ions using 32 most intense peaks  (help)

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MS/MS Fragmentation of **GLEKAGLLTK**

Found in **E6CX82**, Argininosuccinate lyase OS=Mus musculus GN=Asg PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1050 Da

Label all possible matches ○ Label matches used for scoring ○

---

Monoisotopic mass of neutral peptide Mr(calc): 1114.6234

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

K4 : Met1_COOH (K), with neutral loss 45.0500

Ions Score: 33  Expect: 0.0056

Matches: 9/96 fragment ions using 9 most intense peaks  (∞ help)

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**MS/MS Fragmentation of KVAEAFAR**

Found in *E. coli*, Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Mus musculus GN=Gpd1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, plot from [ ] Da to [ ] Da Full range
Label all possible matches ○ Label matches used for scoring ○

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**Monoisotopic mass of neutral peptide Mr(calc):** 976.4978  
Fixed modifications: MetO (C) (apply to specified residues or termini only)  
Variable modifications:  
K1 : mal_CO2 (K), with neutral loss 42.9898  
Ions Score: 26 Expect: 0.002  
Matches : 12/70 fragment ions using 36 most intense peaks (help)

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MS/MS Fragmentation of LFGLDIKGR

Found in E0CZH6, MOSC domain-containing protein 2, mitochondrial (Fragment) OS=Mus musculus GN=Marc2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calc): 1103.5975
Fixed modifications: NMTS (C)  (apply to specified residues or termini only)
Variable modifications:
K7  ms_l_COO (K), with neutral loss 43.9898

Ions Score: 20  Expect: 0.014
Matches : 27/69 fragment ions using 53 most intense peaks  (help)

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**MS/MS Fragmentation of VVKEDGHMVTAR**

Found in **EBZ10**, MOSC domain-containing protein 2, mitochondrial (Fragment) OS=Mus musculus GN=Mar2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, [Full range] 200 to 1300 Da  [Full range]

Label all possible matches ☐  Label matches used for scoring ☑

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1426.68875

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

**Ions Score:** 29  **Expect:** 0.027

**Matches:** 14/118 fragment ions using 31 most intense peaks  ([help])

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### MS/MS Fragmentation of NVKYVDLGGSYVGPTQNR

Found in E9PVT9, Aminopeptidase [Mammalian]; Bo=Mus musculus; GN=Mash PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1900 Da

Label all possible matches □ Label matches used for scoring □

---

**Neuroepitope mass of central peptide Hb (calc):** 2021.5122

**Fixed modifications:** M+2 (C) (apply to specified residues or terminal only)

**Variable modifications:**
- K: i-cis, 202 (R), with neutral loss 40.0000

**Ions Score:** 80 **Expect:** 1.5e-07

**Matches:** 90/100 fragment ions using 73 most intense peaks (Calc)

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M8/MS Fragmentation of WVWNKSSQFLAPK

Found in E9PV99: PCTP-like protein Os-Mus musculus GN=Stnd10 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches  ○  Label matches used for scoring  ○

Monoisotopic mass of neutral peptide Mr(mol): 1889.8246

Fixed modifications: MET(5-C) (apply to specified residues or termini only)
Variable modifications:
RS  : ac (R), with neutral loss 48.0693

Ion Score: 28  Expect: 0.0022

Matches: 16/114 fragment ions using 25 most intense peaks  (help)

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MS/MS Fragmentation of SSQFLAPKAMK
Found in D9VP0, PCTP-like protein OS=Mus musculus GN=Stard10 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ☐ Label matches used for scoring ☐

Monoisotopic mass of neutral peptide Mr(Calc): 1252.6434
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications: Nε1C2 (K), with neutral loss 45.0500
Ions Score: 34 Expect: 0.018
Matches : 9/98 fragment ions using 11 most intense peaks (help)

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MS/MS Fragmentation of **LKDAVIQNTR**

Found in **FDPXVA** Rdh1c and Cda synthase OS=Mus musculus GN=St77a5 PF=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from **200** to **1080** Da Full range

Label all possible matches ○ Label matches used for scoring ●

---

Monoisotopic mass of neutral peptide \( \text{M}_r(\text{calc}) \): **1242.6888**

Fixed modifications: **MTS (C)** (apply to specified residues or termini only)

Variable modifications:

**K2**: **rm.CD2 (K)**, with neutral loss 43.9888

Ions Score: **23** Expect: **0.042**

Matches: **6/100** fragment ions using 9 most intense peaks (help)

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MS/MS Fragmentation of VMLGETNPADSKPGTIR
Found in E9PZFO, Nucleotide diphosphate kinase OS=Mouse GN=Gm20396 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point.
Or, Plot from 100 to 1700 Da Full range
Label all possible matches Label matches used for scoring

Peptide mass of neutral peptide (Da): 1868.0066
Fixed modifications: HET (apply to specified residues or termini only)
Variable modifications:
DA : Cadaverine (N), with neutral losses 0.9995 (shown in table), 0.9995
ES2 : mal-202 (B), with neutral loss 58.0000
Ions Score: 13 Expect: 0.006
Matches: 16/246 fragment ions using 14 most intense peaks (help)

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MS/MS Fragmentation of ELTGDMQLSKSEILR

Found in E9PJ78. Activating signal regulator 1 complex subunit 3 O8=Mus musculus QN=Asc23 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Ms (m/z): 1004.3976
Fixed modifications: M67S (C) (apply to specified residues or terminal only)
Variable modifications:
K6O : m+2 (K), with neutral loss 46.0053
Ions Score: 49 Expect: 0.00063
Matches : 52/145 fragment ions using 106 most intense peaks

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| 4  | 401.2031 | 201.1012 | 383.1923 | 192.0699 | G   | 1418.7308 | 709.8960 | 1401.7042 | 701.3538 | 1400.7302 | 700.8838 | 12
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MS/MS Fragmentation of QASLKDYEETIGK
Found in E9Q1HS, Alpha-aminoacid semialdehyde dehydrogenase (Fragment) OS=Mus musculus GN=Aldh7a1 PE=4 SV=2
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot area 200 to 1500 De
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mz(calc.) = 1566.7413
Fixed modifications: DEEF (C) (apply to specified residues or termini only)
Variable modifications:
K5: m1 [202 (K), with neutral loss 43.9896]
Z Ind Score: 23 Expect: 0.027
Matches: 10/124 fragment ions using 85 most intense peaks (based)

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MS/MS Fragmentation of EMLQQSKILK

Monoisotopic mass of neutral peptide Mr(calc): 1902.6863
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
K7 : phi(OG2) (K), with neutral loss 49.9898

Matches: 92/94 fragment ions using 41 most intense peaks  

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MS/MS Fragmentation of GASKEILSEVER

Found in EQ133, T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 2402.6340
Fixed modifications: MITES (C) (apply to specified residues or termini only)
Variable modifications:
RT : methionine oxidation (M), with neutral loss 10.0000
Monoisotopic mass of neutral peptide Mr(calc): 2402.6280
Matches to peptide GASKEILSEVER

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MS/MS Fragmentation of GVMINKDVTTHPR

Found in EQ333, T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 260 to 1260 Da Full range

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide \( M_n \) (calc): 1451.7191
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K6: oxidation (M), with neutral loss 41.0080
Input Search: 12 K Report: 0.064
Matches: 20/100 fragment ions using 54 most intense peaks (help)

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Monoisotopic mass of neutral peptide Mr(calc): 1590.0041
Fixed modifications: M(+23) (C) - apply to specified residues or termini only
Variable modifications:
K11 : ma022 (A), with neutral loss 42.0058

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MS/MS Fragmentation of **TVEGALKER**

Found in **E9O800**. Mitochondrial inner membrane protein OS=Musculus GN=Inmt PE=2 SV=1

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Fixed modifications: M+H (C) (apply to specified residues or termini only)
Variable modifications:
K7 : mal CO2 (K), with neutral loss 43.9898
Ions Score: 27  Expect: 0.12
Matches: 10/62 Fragment ions using 18 most intense peaks (help)
MS/MS Fragmentation of TFDSAVA KALEHHR

Found in E9Q800, Mitochondrial inner membrane protein OS=Mus musculus GN=Imnt PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide M(mono) = 1666.8062

Fixed modifications: M+H (C) (apply to specified residues or termini only)
Variable modifications:
K = methyl 0.02 (K), with neutral loss 42.0698

Monoisotopic mass of neutral peptide m/z (calc) = 1666.8062

Matched: 12/326 fragment ions using 10 most intense peaks

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MS/MS Fragmentation of FPAGGKMSQYLENMK
Found in F223V0, NADH-cytochrome b5 reductase 3 (Fragment) OS=Mus musculus GN=Cybbr3 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da
Label all possible matches
Label matches used for scoring

Monoisotopic mass of neutral peptide M(odal): 1798.85066
Fixed modifications: MMTS (C) (apply to specified residues or terminal only)
Variable modifications:
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Score: 14 Expect: 0.10
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Found in F223V0, NADH-cytochrome b5 reductase 3 (Fragment) OS=Mus musculus ON=Cyb5r3 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or  Plot from: 200 to 2000 Da  Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(m/z): 2013.0418
Fixed modifications: MNTS (C)  apply to specified residues or termini only
Variable modifications: K13: m+2 (K), with neutral loss 44.0560

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**MS/MS Fragmentation of EAQDKVAVLSQNR**

Found in F27459, Protein Acet3 OS=Mus musculus GN=Acet3 PE=2 SV=1

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Monoisotopic mass of neutral peptide (Otttalic): 1562.7638

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Variable modifications:

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Inva Score: 52 Expect: 0.00047

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**MM/MS Fragmentation of AEHAQKAGHFDFKEIVPVLVSSR**

Found in P22469, Protein Ace3 Oryzias latipes moribund G5=Ace3 PE=2 SV=1

**Fixed modifications:** Met (C) (apply to specified residues or terminal only)

**Variable modifications:**

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**Ions Searched:** 77.69-77.699 with neutral loss 43.2946

**Matches:** 45/240 fragment ions using 86 most intense peaks

**Table:**

- **Seq.** column lists the sequence of the fragment.
- **y** and **y++** columns represent the fragment's charge states.
- The table includes a selection of fragment ions with their respective charges and sequence.

**Legend:**

- **AEHAQKAGHFDFKEIVPVLVSSR** is the sequence of the protein.
- **Ions Searched** specifies the range of ions searched.
- **Matches** indicates the number of matches found.

**Additional notes:**

- The search parameters include fixed modifications Met (C) and variable modifications.
- The table provides a detailed view of the fragment ions, including their charges and sequence.
MS/MS Fragmentation of DVFTKGYGFGLIK
Found in F2Z71, Voltage-dependent anion selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide (m/z): 1289.7766
Fixed modifications: LYS (K) (apply to specified residues or termini only)
Variable modifications:
K5 (Cys) oxidized (K), with neutral loss 41.9948
Ions Score: 50 Expect: 0.592
Matches: 31/195 fragment ions using 50 most intense peaks (help)

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MS/MS Fragmentation of LTFDSSFSPNTGKK
Found in F2Z471, Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(m/z): 1610.7870
Fixed modifications: Lys8 (C) (apply to specified residues or terminal only)
Variable modifications:
K3 : m/z 0.02 (E), with neutral loss 42.0186
Ion Score: 45 Expect: 0.00361
Matches: 21/100 fragment ions using 26 most intense peaks (hla)

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ELQAAGKSPEDLEK

MS/MS Fragmentation of ELQAAGKSPEDLEK
Found in F68AC3, Glucose-6-phosphate isomerase O8=Mus musculus GN=Gm1846 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1500 Da  Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1592.7628
Fixed modifications: MG73 (C) apply to specified residues or terminal only
Variable modifications:
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Ions Saved: 45  Exponent: 0.0000
Matches : 26/150 fragment ions using 87 most intense peaks (help)

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KFLQPGSQR

Monoisotopic mass of neutral peptide Mr(calc): 1145.5829
Fixed modifications: MMIS (C) (apply to specified residues or termini only)
Variable modifications:
K  :  miss_COO (K), with neutral loss 43.0088
Ions Score: 28  Expect: 0.16
Matches : 15/60 fragment ions using 25 most intense peaks  (help)

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### MS/MS Fragmentation of LYKASPDLVPMGEWTAR

**Found in:** FvSP9, AP-2 complex subunit alpha-1 (Fragment)  OS=Mus musculus  GN=Ap2a1  PE=4  SV=1

Close mouse within plot area to zoom in by factor of two about that point.

Or, Plot from 200 to 1900 Da  Full range.

Label all possible matches  Label matches used for scoring

---

**Noncovalent mass of neutral peptide Mr(mDa):** 2018.971

**Fixed modifications:** M(8) S(5) (apply to specified residues or terminals only)

**Variable modifications:**
- K(6) CO2 (with mutual loss 44.013)

**Image Score:** 17  **Expect:** 0.0012  **Rank:** 47

#### Table: 40-176 fragment (core using 105 most intense peaks)[link]

| # | b1   | b** | b*** | b#   | b##  | Seq. | y  | y** | y*** | y## | y#   | y## | y#   | y## | y#   | y## | y#   | y## | y#   | y## | y#   | y## | y#   | y## | y#   | y## | y#   | y## | y#   | y## | y#   | y## | y#   |
|---|------|-----|------|------|------|------|----|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|
| 1 | 114.091 | 57.5493 | L | Y | 1862.9105 | 0391.8589 | 1885.8840 | 923.4155 | 1844.9000 | 229.9536 |
| 2 | 277.1547 | 139.0810 | K | 1999.8472 | 850.4272 | 1682.8207 | 841.9149 | 1681.8367 | 844.4260 |
| 3 | 147.2402 | 72.1337 | 430.2336 | 215.6205 | A | 1529.7417 | 765.3741 | 1512.7153 | 756.6612 | 1511.7311 | 756.3892 |
| 4 | 518.2973 | 259.6523 | 501.2708 | 251.1300 | S | 1418.7646 | 729.8559 | 1441.6780 | 721.3427 | 1440.6940 | 720.8506 |
| 6 | 702.3821 | 351.6947 | 685.3556 | 343.1814 | 684.3713 | 342.6994 | D | 1274.6198 | 657.8135 | 1257.5952 | 629.3003 | 1256.6092 | 628.8002 |
| 7 | 817.4098 | 409.2082 | 808.3285 | 490.6949 | 799.3989 | 409.2029 | L | 1359.5928 | 760.3001 | 1412.5665 | 757.7868 | 1414.5823 | 757.2948 |
| 8 | 936.4931 | 465.7022 | 913.4666 | 457.2359 | 912.4823 | 456.7449 | V | 1466.5688 | 823.7580 | 1509.4802 | 815.2448 | 1508.4982 | 814.7257 |
| 9 | 1025.5961 | 515.2844 | 1012.5350 | 506.7111 | 1011.5310 | 506.2791 | Y | 1584.6088 | 853.7580 | 1629.4802 | 815.2448 | 1628.4982 | 814.7257 |
| 10 | 1126.6143 | 563.8108 | 1109.5877 | 555.2973 | 1108.6079 | 554.8035 | F | 1647.6494 | 747.2425 | 1690.4138 | 645.7105 | 1692.4298 | 645.2185 |
| 11 | 1257.6548 | 629.3119 | 1240.6282 | 620.8178 | 1239.6442 | 620.3257 | M | 1798.6876 | 825.6974 | 1833.6361 | 417.1842 | 1832.7707 | 416.0922 |
| 12 | 1314.7022 | 657.8418 | 1297.6947 | 640.2832 | 1296.6657 | 648.8385 | G | 1819.7041 | 860.1770 | 1872.6320 | 851.6659 | 1871.6659 | 851.1719 |
| 14 | 1629.7981 | 815.4027 | 1612.7716 | 806.8984 | 1611.7876 | 806.3974 | W | 2058.8283 | 967.1452 | 2115.6256 | 958.6319 | 2116.6256 | 958.1452 |
| 15 | 1730.8458 | 865.9265 | 1713.8193 | 857.4133 | 1712.8353 | 856.9213 | T | 2147.8267 | 174.1055 | 2100.7772 | 165.9222 | 2101.7772 | 165.9222 |
| 16 | 1801.8829 | 901.4451 | 1784.8564 | 892.9318 | 1783.8724 | 892.4398 | A | 248.1561 | 123.9817 | 229.1295 | 115.0984 | 2 |
| 17 | 175.1190 | 88.0683 | 155.0924 | 79.5468 | 1 |
MS/MS Fragmentation of **LYKASPDLVPMPGEWTAR**

*Found in FUSP9, AP-2 complex subunit alpha-1 (Fragment) OS=Mus musculus GN=Ap2a1 PE=4 SV=1*

Click mouse within plot area to zoom in by factor of two about that point:

Or, Plot from 450 to 1900 Da Full range

Label all possible matches □ Label matches used for scoring □

**Proteolytic enzyme of selected peptide Nt(cleak):** Trypsin

**Fixed modifications:** MOWSEO □ (apply to specified residues or termini only)

**Variable modifications:**

K: □, □ □, □ □ with neutral loss 91.93225
Q1: □ Glutamine (Q) with neutral losses 0.0000 (shown in table), 0.0000

**Int Score:** 22 □ Expect: 0.70

**Matches:** 22/272 Fragment ions using 45 most intense peaks [help]

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### MS/MS Fragmentation of ISAYMKSSR

Found in F6WHQ7, Glutathione S-transferase Mu 1 (Fragment) OS=Mus musculus GN=Gstmu PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1100 Da Full range

Label all possible matches ⭕ Label matches used for scoring ⭕

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1127.5281

**Fixed modifications:** MMTC (C) (apply to specified residues or termini only)

**Variable modifications:**

- K6 : m/z CO2 (H) with neutral loss 43.0090

Ions Score: 35 Expected: 0.0043

Matches to 10/82 fragment ions using 19 most intense peaks  

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The table above represents the fragmentation pattern of ISAYMKSSR, showing the fragment ions produced from the peptide. Each row indicates a different fragment ion with its corresponding mass and sequence. The ions are identified based on their masses and are compared to the expected masses. The sequence I, S, A, Y, M, K, S, and R are highlighted to show the matches with the fragment ions.
**MS/MS Fragmentation of ISAYMKSSR**

Found in FoWHDQ7. Glutathione S-transferase Mu 1 (Fragment) OS=Mus musculus GN=Gstml PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da
Label all possible matches ○ Label matches used for scoring ○

![Graph showing MS/MS fragmentation of ISAYMKSSR](image)

**Monoisotopic mass of neutral peptide Mr(calc): 1143.5220**
**Fixed modifications: NMT5 (C) (apply to specified residues or termini only)**
**Variable modifications:**
- N5 : Oxidation (M), with neutral losses 0.00000 (shown in table), 61.9883
- K6 : m/s-CO2 (K), with neutral loss 45.0896
**Ions Score:** 50  **Expect:** 0.00022
**Matches:** 17/128 fragment ions using 27 most intense peaks

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STDEPSEKDALQPGR

MS/MS Fragmentation of **STDEPSEKDALQPGR**

Found in E6Y565, Fructose-1,6-bisphosphatase 1 (Fragment) OS=Mus musculus GN=Fbp1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or: [Full range]

Label all possible matches [Label matches used for scoring]

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Monoisotopic mass of neutral peptide Mn(calc): 1714.7666

Fixed modifications: **M** : C (apply to specified residues or termini only)

Variable modifications:

MS : **K** : **O** : [all] with neutral loss 43.0107

Intra Source: 80 Expect: 0.0010

Matches: 26/142 Fragment ion using 51 most intense peaks  (calc: 158.0010)
AGGLATTGDKDILDIVPTEIHQK
MS/MS Fragmentation of IYESHVGISSHEGKIASYK

Found in F62HD8, 1,4-alpha-3-fucan-debranching enzyme O5-Mas musculus O6-Ob1 PE-4 SV-2

Click mouse within plot area to zoom in by factor of two about that point

Oc. (Plot from 200 to 1500 Da Full range)

Label all possible matches □ Label matches used for scoring □

Monoisotopic mass of neutral peptide Mz(calc): 2106.9893
Fixed modifications: M(=O) (apply to specified residues or termini only)
Variable modifications:
K14: m/z 162 (+1), with neutral loss 48.0658

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Note: The table shows the fragment ions and their corresponding m/z values. The intensity values indicate the relative abundance of each fragment.
MS/MS Fragmentation of AMVASGSELGKK

Found in F7BP55, Adenylate kinase 2, mitochondrial (Fragment) OS=Mus musculus GN=Ak2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da  Full range

Label all possible matches  Label matches used for scoring

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Fixed modifications: MHTS (C) (apply to specified residues or termini only)
Variable modifications:
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Matches: 17/96 fragment ions using 30 most intense peaks  (help)

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**MS/MS Fragmentation of AVLLGPPGAGKGTQAPK**

Found in **F7BP55**, Adenylate kinase 2, mitochondrial (Fragment) OS=Mus musculus GN=Ak2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or **Plot from** 200 to 1600 Da **Full range**
Label all possible matches § Label matches used for scoring ¶

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MS/MS Fragmentation of **ALSTGEKGFGYK**

Found in **FBVNP3**, Peptidyl-prolyl cis-trans isomerase OS=Mus musculus GN=Gm5160 PE=3 SV=2

*Click mouse within plot area to zoom in by factor of two about that point*

*Or, Plot from 200 to 1400 Da Scale Full range*

*Label all possible matches ○ Label matches used for scoring ○*

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1242.6406

**Fixed modifications:** **NMTS (C)** (*apply to specified residues or termini only*)

**Variable modifications:**

- **K7:** **m7-CO2** (K), with neutral loss 43.9898

*Tone Score: 21 Expect: 0.045*

*Matches: 9/204 fragment ions using 21 most intense peaks (help)*

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**MS/MS Fragmentation of TEWLDGKHVVFGK**

Found in F8VPN3, Peptidyl-prolyl cis-trans isomerase OS=Mus musculus GN=0m5160 PE=3 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, Platform from 200 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

---

**Monoisotopic mass of neutral peptide M(calc): 1466.7666**

**Fixed modifications: **NMT (C) (apply to specified residues or termini only)

**Variable modifications:**

- NW: mal-COOH (K), with neutral loss 41.01098

**Ions Score:** 96 Expect: 0.0016

**Matches:** 18/116 fragment ions using 34 most intense peaks

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MS/MS Fragmentation of KYTEITATHFQGVR
Found in F8VPN4, Protein Agl OS=Mus musculus GN=Agl PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or Plot from 200 to 1000 Da
Label all possible matches □ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mz(cals) = 1798.8820
Fixed modifications: NMT (C) (apply to specified residues or termini only)
Variable modifications:
R1 = Me, CO2 (K), with neutral loss 44.0109
Ions Search: 30 Expect: 0.0006
Matches: 8/140 fragment ions using 12 most intense peaks (heka)
**MS/MS Fragmentation of EHLKIIQDPEYR**

Found in F8VP4. Protein Agl OS=Mus musculus GN=Ag1 PE=4 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr(calc): 1625.8049**

**Fixed modifications: NMTS (C) [apply to specified residues or termini only]**

**Variable modifications:**

K4: m+1, S102 [161], with neutral loss 43.9699

**Tons Score: 1.8** Expect: 0.045

**Matches: 11/122 fragment ions using 20 most intense peaks (help)**

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MS/MS Fragmentation of HGKVVAVSYDEWNR
Found in F6XX6. Protein Agl (Fragment) OS=Mus musculus GN=Agl PE=4 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mz(calc): 1872.5118
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
K : m + 2 (H), with neutral loss 44.0120
(score: 18  Expect: 0.14)
Matches : 26/145 fragment ions using 48 most intense peaks

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MS/MS Fragmentation of AVQNACQILMKR
Found in G3X982, Aldehyde oxidase 3, isoform CRA_a OS=Mus musculus GN=Aox3 PE=4 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1505.7152
Fixed modifications: NH2 (C) (apply to specified residues or termini only)
Variable modifications:
K75 : ma_C82 (K), with neutral loss 68.01098
Ions Score: 28 Expect: 0.004
Matches : 21/84 fragment ions using 66 most intense peaks

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MS/MS Fragmentation of AQFLVEKAK

Found in F6QPR1. Prohibitin-2 (Fragment) OS=Mus musculus GN=Phb2 PE=4 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 100 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1118.5972
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K7 : mll_002 (K), with neutral loss 43.9890
Ions Score: 29  Expect: 0.0068
Matches : 12/78 fragment ions using 18 most intense peaks  (help)

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MS/MS Fragmentation of SYLKEFR
Found in G3UWF1, MCG11048, isoform CRA_c OS=Mus musculus GN=Teer PE=4 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or [Plot from] [150] to [950] Da [Full range]
Label all possible matches [ ] Label matches used for scoring [ ]

Monoisotopic mass of neutral peptide Mr(calc): 1027.4974
Fixed modifications: MMTS (+) (apply to specified residues or termini only)
Variable modifications:
K4 : i.e. CO2 (K), with neutral loss 43.9898
Ions Score: 20  Expect: 0.49
Matches: 4/62 Fragment ions using 8 most intense peaks  (help)

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**MS/MS Fragmentation of MIFAGIKK**

Found in G3UWG1, MCG115977 OS=Mus musculus GN=Gm10108 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da  Full range
Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 892.5365**

Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:

F7 : mal-CO2 (O), with neutral loss 41.9888

Ions Score: 18  Expect: 0.74

Matches : 19/44 fragment ions using 69 most intense peaks  (help)

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MS/MS Fragmentation of **KIFVQK**

Found in **G3UWG1**. MCG115977 OS=Mus musculus GN=Gm10108 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Orient from [100] to [750] Da  [Full range]

Label all possible matches  Label matches used for scoring

---

Monoisotopic mass of neutral peptide Mr(calc): 847.4803

Fixed modifications: **M(57) (C)** (apply to specified residues or termini only)

Variable modifications:

K : **Glu -> Q**, with neutral loss 43.9598

Ions Score: 26  Expect: 0.13

Matches : 11/40 fragment ions using 20 most intense peaks  (help)

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**MS/MS Fragmentation of HKTGPNLHGLFGR**

**Found in G3UWG1, MCG11.977 OS=Mus musculus GN=Gm10108 PE=3 SV=1**

Click mouse within plot area to zoom in by factor of two about that point

**Label all possible matches**  
**Label matches used for scoring**

---

**Monoisotopic mass of neutral peptide (Mr(calc))**: 1333.7692  
**Fixed modifications**: MMTS (C)  
**Variable modifications**:  
**K**: macl 02G (K), with neutral loss 42.0698  
**Ion Score**: 20  
**Peptidematcher Score**: 0.0000  
**Matches**: 34/118 fragment ions using 82 most intense peaks  
**Help**

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### MS/MS Fragmentation of KTGQAAGFSYTDANK

**Found in**: G3WUG1. MCG115977 O9=Mus musculus GN=Gm10108 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point

- [Full range](#)
- [Center](#)

Label all possible matches * Label matches used for scoring *

---

**Monoisotopic mass of neutral peptide Mr(mole):** 1462.7427

**Fixed modifications:**  ME(D) (apply to specified residues or termini only)

**Variable modifications:**

- K

**Ion Source:** ESI; **Expect:** 1e-005

**Matched:** 21/1680 fragment ions using 50 most intense peaks

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MS MS Fragmentation of QLKEELGAAQPDLK
Found in G3UX3X. Scrosotinae reductae GS-MA Mus musculus GN=6 Ser PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from to Da] [Full range]
Label all possible matches 🌈 Label matches used for scoring 🌈

Monoisotopic mass of neutral peptide M(z)e(m) : 1681.8822
Fixed modifications: HMTS (C) (apply to specified residues or terminal only)
Variable modifications:
K - m/z 40.0262 (R), with neutral loss 68.0690
Ions Score: 28 Expect: 0.031
Matches : 21/146 fragment ions using 46 most intense peaks (help)

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QLKEELGAAQPDLK
MS/MS Fragmentation of **DYEEIGKAK**

Found in **E991G1**, Alpha-aminoacidic semialdehyde dehydrogenase (Fragment) OS=Mus musculus GN=Aldh7a1 PE=2 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from: 150 to 1150 Da

Label all possible matches □ Label matches used for scoring □

---

**Monoisotopic mass of neutral peptide Mr(calc): 1238.8686**

Fixed modifications: HETs (C) (apply to specified residues or termini only)

Variable modifications:

**K** : ala_COOH (K), with neutral loss 43.0107

Ions Score: 15  Expect: 0.27

Matches: 16/34 fragment ions using 47 most intense peaks  (help)

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MS/MS Fragmentation of LAGDEKIQSAVATLR
Found in GMYVL, Serine hydroxymethyltransferase (Fragment) O=S-Musculus ON-Shunt1 PE=3 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches □ Label matches used for scoring □

Non-isotopic mass of neutral peptide (M+H): 1666.6662
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
R6 = mal_002 (X), with neutral loss 90.0096
Total Score: 65 Expect: 4.6e-05
Matched: 24/148 fragment ions using 31 most intense peaks (Help)

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MS/MS Fragmentation of **GIVVLAQSYKENEIK**
Found in G5X9Y6, Aldo-keto reductase family 1, member C19 OS=Mus musculus GN=Akr1c19 PE=4 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or: Plot from 200 to 1700Da Full range

Label all possible matches ☐ Label matches used for scoring ☑

---

Monoisotopic mass of neutral peptide Mr(mol): 1796.9065
Fixed modifications: MT3 (C) (apply to specified residues or terminal only)
Variable modifications:
K5O : m/z 154.0986 (K), with neutral loss 48.0986

Ions Score: 26 Expect: 0.0019

Matches: 26/128 fragment ions using 52 most intense peaks [help]

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GIVVLAQSYKENEIK
MS/MS Fragmentation of QVVTLLNELKR

Found in H3BJ29, 3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acsa1a PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from ___ to ___ Da
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1597.7878
Fixed modifications: Met(S) (C) (apply to specified residues or termini only)
Variable modifications:
K1.0 : melan_2O (K), with neutral loss 43.0050
Ions Score: 82 Expect: 0.0092
Matches: 26/108 fragment ions using 46 most intense peaks

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MS/MS Fragmentation of **VIADNVKDWSK**

Found in H7BXC3, Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches  Label matches used for scoring

![Fragmentation spectrum](image)

Monoisotopic mass of neutral peptide Mr(calc): 1359.6675

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications: K7 : m+2 (K), with neutral loss 49.9890

Tons Score: 35  Expected: 0.0017

Matches : 29/134 fragment ions using 86 most intense peaks  

| # | b | b'' | b* | b''' | b0 | b0'' | Seq. | y | y'' | y' | y''' | y0 | y0'' | # |
|---|---|-----|----|------|----|------|------|---|-----|----|------|----|------|--|---|
| 1 | 100.0757 | 20.5415 | V | | | | | | | | | | | 11 |
| 2 | 213.1598 | 107.0835 | I | **1217.6161** | 609.3117 | 1200.5895 | 600.7984 | 1199.6055 | 600.3064 | 10 |
| 3 | 284.1959 | 42.6021 | A | **1104.5320** | 552.7656 | 1087.5055 | 544.2564 | 1086.5214 | 543.7644 | 9 |
| 4 | **399.2238** | 200.1155 | 381.2132 | 191.1103 | D | **1632.4940** | 517.2511 | 1016.4684 | 508.7378 | 1015.4843 | 508.2458 | 8 |
| 5 | 513.2607 | 257.1530 | 496.2402 | 248.6237 | 495.2502 | 248.1317 | N | **918.4660** | 459.7376 | 901.4414 | 451.2243 | 900.4574 | 450.7323 | 7 |
| 6 | **612.3352** | 306.6712 | 595.3086 | 298.1579 | 594.3246 | 297.6659 | V | **804.4250** | 402.7162 | 787.3985 | 394.0209 | 786.4143 | 393.7109 | 6 |
| 7 | **782.4407** | 391.7240 | 765.4141 | 383.2107 | 764.4301 | 382.7187 | K | **705.5366** | 353.1819 | 688.3301 | 344.6687 | 687.3461 | 344.1767 | 5 |
| 8 | 897.4676 | 449.2374 | 880.4411 | 440.7242 | 879.4571 | 440.2322 | D | **535.2511** | 268.1292 | 518.2245 | 259.6159 | 517.2465 | 259.1239 | 4 |
| 9 | **1083.5469** | 542.2771 | 1066.5204 | 533.7638 | 1065.5364 | 533.2718 | W | **420.2241** | 210.6157 | 403.1976 | 202.1024 | 402.2136 | 201.6104 | 3 |
| 10 | 1170.5790 | 585.7931 | **1153.5524** | 577.2798 | **1152.5684** | 576.7878 | S | 234.1448 | 117.5761 | 217.1183 | 109.0628 | 216.1343 | 108.5708 | 2 |
| 11 | **147.1128** | 74.0600 | 130.0863 | 65.5468 | 1 |
VVLAYEPVWAIGTGKTATPQQAQEVHEK
TGKAVSYLGPK

MS/MS Fragmentation of TGKAVSYLGPK

Found in **O08997**, Copper transport protein ATOX1 OS=Mus musculus GN=Atox1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1200 Da Full range

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1205.6252
**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

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With neutral loss 43.01068

**Ions Score:** 48  **Expect:** 0.00012

**Matches:** 25/106 fragment ions using 57 most intense peaks (help)

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**TGKAVSYLGPK**
MS/MS Fragmentation of WKPFEIPK

Found in O09173, Homogentisate 1,2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Oxidation (M+H) (+15) to (+150) Da

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1129.5808
Fixed modifications: HTIS (C) (apply to specified residues or termini only)
Variable modifications:
K2 : mal-CO2 (K), with neutral loss 43.9898
Tons Score: 28  Expect: 0.15
Matches: 23/68 fragment ions using 46 most intense peaks  (help)

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AAQNISKTIATSQNR

MS/MS Fragmentation of AAQNISKTIATSQNR
Found in F6QPRI, Prohibitin-2 (Fragment) OS=Mus musculus GN=Phb2 PE=4 SV=1

Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
KM: m1,Lys (K), with neutral loss 43.0548

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MS/MS Fragmentation of VLSQMEKIVR

Found in P05201. Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Get1 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1287.6887
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K7 : male CO2 (K), with neutral loss 43.0088
Ions Score: 28 Expect: 0.0084
Matches : 6/90 fragment ions using 10 most intense peaks (help)

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MS/MS Fragmentation of VLSQMEKIVR
Found in P05201, Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Got1 PE=1 SV=3

Monoisotopic mass of neutral peptide M(r)=1303.6006
Fixed modifications: HET5 (C) (apply to specified residues or termini only)
Variable modifications:
MS : Oxidation (M), with neutral loss 0.0000 (shown in table), 61.9945
X7 : N-trial (K), with neutral loss 40.0000
Ions Score: 20 Expected: 0.066
Matches: 20/144 fragment ions using 94 most intense peaks (help)

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MS/MS Fragmentation of EFSYMKTGDR
Found in P05202, Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da
Label all possible matches ☐ Label matches used for scoring ☑

Monoisotopic mass of neutral peptide Mr(calc): 1417.6124
Fixed modifications: M+N(C) (apply to specified residues or termini only)
Variable modifications:
K6 : ma_1CO2 (K), with neutral loss 48.02959
Tone Score: 21 Expect: 0.016
Matches : 7/102 Fragment ions using 11 most intense peaks (use3p)

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AADKDTCFSTEGBPNLVTR

Mass spectrometric mass of neutral peptide \( \text{M} \) (calc) : 2005.0073
Fixed modifications: MMT (C) (apply to specified residues or terminal only)
Variable modifications:
Hb : a/a, s/a (R) (with neutral loss 18.0000)
Ions Score : 61 Expect : 0.00146
Matches : 52/102 fragment ions using 42 more intense peaks

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MS/MS Fragmentation of **ELISKFLLNR**

Found in **P07758**, Alpha-1-antitrypsin 1-1. OS=Mus musculus GN=Serpina1a PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Flat from 100 to 1300 Da

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1417.7592**

**Fixed modifications: M(S) (C) (apply to specified residues or termini only)**

**Variable modifications:**

K5  =  mal,CO2 (K), with neutral loss 42.01568

**Ions Score: 31, Expect: 0.00000**

**Matches:** 22/88 fragment ions using 62 most intense peaks

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MS/MS Fragmentation of LCAATATILDKPEDR

Found in O35215, Dopamine decarboxylase OS=Mus musculus GN=Ddc PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point.
Or, [Plot zoom] 200 to -600 Dn [Full range]
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(mol) : 1747.8129
Fixed modifications: M + H (C) Supply to specified residue or termini only
Variable modifications:
K15 = mzzarella C, with neutral loss 48.05993
Ions Score: 27 Da Expect: 0.016
Matches : 20/100 fragment ions using 40 most intense peaks (halo)

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HYGGLTGLNKAETAAK
MS/MS Fragmentation of LSHSIEKLWDQTSSEVK
Found in O88451, Retinal dehydrogenase 7 O8=Mus musculus ON=RaR? PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot form: 100 to 1500 Dn Full range
Label all possible matches © Label matches used for scoring ♦

Nonisotopic mass of neutral peptide Mz(calc): 2072.0062
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K = m1 CO2 (+), with neutral loss 42.0148

TIC Score: 16. Expect: 0.691
Matches: 47/174 fragment ions using 101 most intense peaks. (help)

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**MS/MS Fragmentation of VLAACLTEKGAEQLR**

*Found in O88451, Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=2 SV=1*

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Monoisotopic mass of neutral peptide (kDa): 1782.4650

**Fixed modifications:** MetO (C) *(apply to specified residues or termini only)*

**Variable modifications:**
- Nél 0.02 (B)
- with neutral loss 49.0000

**Ions Score:** 21  **Expect:** 0.0002

**Matches:** 8/154 fragment ions using 14 most intense peaks  *(help)*
MS/MS Fragmentation of FLTNNNSAIDKTQSEK

Found in P01860, Cytochrome P450 1A2 OS=Mus musculus GN=Cyp1a2 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1800 Da Full range

Label all possible matches © Label matches used for scoring ©

Monoisotopic mass of neutral peptide Mr (calc.): 1954.8096

Fixed modifications: MMT (C) (apply to specified residues or termini only)
Variable modifications:
K11  = M:126.020 (R), with neutral loss 48.0265

Topscore: 24 Expert: 0.011

Matches: 17/168 fragment ions using 20 most intense peaks

|   | b3  | b4  | b5  | b6  | g3  | g4  | g5  | g6  | y3  | y4  | y5  | y6  | y7  | y8  | y9  | y10 | y11 | y12 | y13 | y14 | y15 | y16 |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 148.0757 | 74.3415 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | 261.1598 | 131.0383 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | 362.2074 | 181.6074 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | 476.2564 | 238.6288 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | 590.2934 | 295.6014 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | 704.3364 | 345.6727 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | 791.3562 | 396.1871 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 8 | 862.4054 | 431.7063 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 9 | 975.4894 | 485.2483 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 10 | 1099.5164 | 544.7568 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 11 | 1260.6219 | 630.8146 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 12 | 1361.6966 | 681.3384 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 13 | 1449.7281 | 743.3067 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 14 | 1576.7602 | 788.8837 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 15 | 1705.8028 | 853.4020 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 16 | 1920.8454 | 977.4419 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

[Graph showing peptide fragmentation peptides]
**MS/MS Fragmentation of VLSGEDKSNIK**

Found in P01942, Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1150 Da

Label all possible matches □ Label matches used for scoring □

---

**Monoisotopic mass of neutral peptide Mr(calc): 1274.6354**

**Fixed modifications:** MG/MS (C) (apply to specified residues or termini only)

**Variable modifications:**

K7: n-maleimide (K), with neutral loss 45.0030

**Ions Score:** 32  Expect: 0.514

**Matches:** 22/98 fragment ions using 49 most intense peaks  (help)

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**MS/MS Fragmentation of SQDLSKIMADIR**

Found in P05784, Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from ___ to ___ Da Full range
Label all possible matches ○ Label matches used for scoring ○

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**Monoisotopic mass of neutral peptide Mr(calc): 1461.7133**

**Fixed modifications:** M(ethyl) (C) (apply to specified residues or termini only)

**Variable modifications:**

K8 : m/z CO2 (K), with neutral loss 44.0128

**Tide Score: 28  Expect: 0.011**

**Matches : 9/126 fragment ions using 11 most intense peaks**

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MS/MS Fragmentation of IWLVDSKGLIVK

Found in P06801. NADP-dependent malic enzyme OS=Mus musculus GN=Mal PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1461.7133

Fixed modifications: M(+H) (C) (apply to specified residues or termini only)
Variable modifications: K8 = mal-COOH (K), with neutral loss 48.01528

Tic Score: 28 Expect: 0.011
Matches : 9/128 fragment ions using 11 most intense peaks

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### VFLTTAEVISQQVSDLKHLQEGR

**MMB Fragmentation of VFLTTAEVISQQVSDLKHLQEGR**

Found in: P00801, NADP-dependent malic enzyme Os-Ma musculus Q5=Ma(m) PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

[Extracted Main Output]

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**Match Score:** 28/222 fragment ions using 67 most intense ions

**Ions Score:** 3.60E-06

**Expected:** 3.60E-06

**Match:** 28/222 fragment ions using 67 most intense ions
MS/MS Fragmentation of GKYVTIYTNYENGK

Found in P19157, Glutathione S-transferase P1 OS=Mus musculus GN=Gstp1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Flat from 200 to 1800 Da Full range

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide M r(m/e): 1047.9961
Fixed modifications: MMTS (C) apply to specified residues or termini only
Variable modifications:
K2 : Met_1056 (B), with neutral loss 42.0106
Ions Scored: 66 ExactMass: 1.7e+006
Matches : 12/152 fragment ions using 15 most intense peaks (help)

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**Fragmentation of IKAFLSSPEHVNRPINGNGK**

Found in P19157, Gutathione S-transferase P | OrthoDB accession OGRGtp1 | Peptidase S182

Click mouse within plot area to zoom in by factor of two about that point.

Label all possible matches ✉️ Label matches used for scoring ✉️

### Monoisotopic mass of neutral peptide Metabolife 2023.5700
Fixed modifications: **MSS** (C) (apply to specified residues or terminal only)
Variable modifications:
**GS** = m/z 0.059 (K), with neutral loss 49.964

### Matches: 17/194 fragment ions using 25 most intense peaks (Help)

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MS/MS Fragmentation of EMLQQSILK
Found in E9Q3D6, Heat shock protein HSP 90-beta (Fragment) OS=Mus musculus GN=Hsp90ab1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Pxl from 160 to 1580 Da
Label all possible matches  Label matches used for scoring

Nonisotopic mass of neutral peptide Mr(calc): 1302.6853
Fixed modifications: M(C) (apply to specified residues or termini only)
Variable modifications:
K7: m+1_COO (K), with neutral loss 45.0990

Ions Score: 20  Expect: 0.047
Matches: 20/54 fragment ions using 32 most intense peaks  (help)

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### MS/MS Fragmentation of ILKVIR

**Found in** P07901, **Heat shock protein HSP 90-alpha OS=** Mus musculus **GN=** Hsp90aa1 **PE=1 SV=4**

Click mouse within plot area to zoom in by factor of two about that point.

**Monoisotopic mass of neutral peptide Mr(calc): 826.5276**

**Fixed modifications:** 
- **MS/MS (C)** (apply to specified residues or termini only)

**Variable modifications:**
- **K**
  - **mal_C02 (K), with neutral loss 48.9898**

**Ions Score:** 37  **Expect:** 0.0054

**Matches:** 10/36 fragment ions using 14 most intense peaks  (help)

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MS/MS Fragmentation of TMVVHEKQDDLGK

Found in P08228, Superoxide dismutase (Cu-Zn) OS=Mus musculus GN=Sod1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from blank 200 to blank 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mz (calc): 1554.7454
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K7: oxidation (K), with neutral loss 43.0086
Incor Score: 28.0 Repeat: 6.02
Matches: 12/120 fragment ions using 20 most intense peaks (help)

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### MS/MS Fragmentation of FHVEEEGKGK

Found in P00401. Phosphoglycerate kinase 2. OS=Mus musculus. GN=Pgk2. PE=1. SV=1.

Click mouse within plot area to zoom in by factor of two about that point.

Or, Plot from 150 to 1150 Da

Label all possible matches □  Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr(calc): 1244.5673**

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

XN : male_C02 (K), with neutral loss 43.00508

Ions Score: 36  Expect: 0.0084

Matches : 17/80 fragment ions using 38 most intense peaks  (help)

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Hypothetical mass of neutral peptide M (calcd): 2110.9560
Fixed modifications: ME/2 (C) apply to specified residues or termini only
Variable modifications: XI 0: |val_CDE| (D), with neutral loss 0.0808
Ion Score: 94 Expect: 9.60E23
Matches: 14/176 fragment ions using 15 most intense peaks (20%)
MS/MS Fragmentation of VDFNVPMKNNQITNNQR
Found in Peptide, Phosphorylase kinase 2 OS=Mus musculus GN=Phk2 PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1000 Da Full range
Label all possible matches □ Label matches used for scoring *

Monoisotopic mass of neutral peptide (Prtcalc): 2132.9099
Fixed modifications: M + H (apply to specified residues or terminal only)
Variable modifications:
N : Oxidation (M), with neutral losses 0.0000 (shown in table), 62.0153
K : ma002 (K), with neutral loss 44.0096
Loss Source: □ Expect: 0.00000
Matches: 22/271 fragment ions using 60 most intense peaks

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MS/MS Fragmentation of **KYAEAVGR**

Found in **P09411**, Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from: 150 to 900 Da  Full range

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): **978.4770

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

K1 : met_COO$^-$ (K), with neutral loss 49.0000

**Ions Score:** 42  **Expect:** 0.0028

**Matches:** 9/70 fragment ions using 15 most intense peaks  **(help)**

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(help)
SVVLMSHLGRPDGVPMPDKYSLEPVAAELK
MS/MS Fragmentation of QTVAVGVIKAVDK
Found in P101256, Elongation factor 1-alpha 1 OS=Mus musculus GN=Esf1a1 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1200 Da [Full range]
Label all possible matches [Label matches used for scoring]

QTVAVGVIKAVDK

Monoisotopic mass of neutral peptide Mr(calc): 1412.7876
Fixed modifications: Met(O) (C) (apply to specified residues or termini only)
Variable modifications:
K9 : ala2-COO (K), with neutral loss 43.00955
Ions Score: 20 Expect: 0.289
Matches : 25/110 Fragment ions using 41 most intense peaks (hkl)

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MBD Fragmentation of LPLQDVYKIGGIGTVPVGR
Found in P10126, Elongation factor 1 alpha 1 OS=Mus musculus GN=EF1al PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point:
Or, Plot from 100 to 1700 Da Full range
Label all possible matches Label matches used for scoring

LPLQDVYKIGGIGTVPVGR

Monoisotopic mass of neutral peptide (m) (calc): 2467.1168
Fixed modifications: HMTS (C) apply to specified residues or termini only
Variable modifications:
K: m1_22G (K) with neutral loss 41 Da
Ion Score: 52 Expect: 0.0048
Matches: 18/122 fragment ions using 14 most intense peaks [help]

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LPLQDVYKIGGIGTVPVGR
MS/MS Fragmentation of **VGEFSGANKEK**

Found in P10639, Thioredoxin OS=Mus musculus GN=Txm PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1200 Da Full range

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1260.6779**

Fixed modifications: HMTS (C) (apply to specified residues or termini only)

Variable modifications: K9 : ma_C=O (K), with neutral loss 43.9898

Ions Score: 42 Expect: 0.00069

Matches : 18/100 fragment ions using 40 most intense peaks  

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**VGEFSGANKEK**
LLLPGELAKHAVSEGTK

MS/MS Fragmentation of LLLPGELAKHAVSEGTK
Found in P10853, Histone H2B type 1-F, J. Ob. Mus musculus GN=Hist1h2bf PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from to Da Full range
Label all possible matches Label matches used for scoring

Macroscopic mass of neutral peptide Mr(m/z): 1047.3998
Fixed modifications: M (C) apply to specified residues or termini only
Variable modification: K : m1_c
with neutral loss 48.0595
$iu$ score: 88 Expect: 0.0005
Matches : 45/156 fragments using 55 most intense peaks

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MS/MS Fragmentation of SLHDALCVVKR

Found in P11983, T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide M(m/z): 1071.6659
Fixed modifications: HexS (C) (apply to specified residues or termini only)
Variable modifications:
K10: mal_CDG (E), with neutral loss 41.9908
Ions Score: 80 Expect: 0.0013
Matches: 17/35 fragment ions using 43 most intense peaks  (help)

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**MS/MS Fragmentation of DLYLENPEIKIR**

Found in P21981, Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus GN=Tgm2 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or Range [200] to [1500] Da Full range
Label all possible matches Label matches used for scoring

---

### Monoisotopic mass of neutral peptide Mr(m/z): 1597.8144

- Fixed modifications: M25 (O) (apply to specified residues or termini only)
- Variable modifications: K10: mal-COO (K), with neutral loss 63.01503

**Zone Score: 21** Expect: 0.1

Matches: 16/114 fragment ions using 30 most intense peaks

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**DLYLENPEIKIR**
SVEVSDPVPGDLVKAR
**MS/MS Fragmentation of FHYKTDQGIK**

Found in P24270, Catalase O8-Mus musculus GN=Cat PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da
Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1331.6303

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**
- K4 : mas_G2O (K), with neutral loss 43.0598

**Score:** 72, **Expect:** 0.17

**Matches:** 7/80 fragment ions using 10 most intense peaks

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**FHYKTDQGIK**
MS/MS Fragmentation of **TFYTKVLNEEER**

Found in P24270. Catalase OS=Mus musculus GN=Cat PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point

O1, Platform from 200 to 1500 Da [Full range]
Label all possible matches ☑ Label matches used for scoring ☑

**Monoisotopic mass of neutral peptide Mr(mole): 1613.7972**

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**
- K6: w, m(+), o(+)
- K: w, m(+), o(+)
- N: w, m(+), o(+)

**Ions Score:** 24  **Expect:** 0.0009

**Matches:** 76/122 fragment ions using 70 most intense peaks  

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MS/MS Fragmentation of GASIVEDKLVEDLK
Found in P26443, Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1000 Da

Label all possible matches ☐ Label matches used for scoring ☐

Monoisotopic mass of neutral peptide Mr(calc): 1600.9196
Fixed modifications: M(T) (C) (apply to specified residues or terminal only)
Variable modifications:
K8 = mal, CO2 (K), with neutral loss 42.0058

Ions Score: 27 Mascot Prob: 0.0007
Matches : 52/124 fragment ions using 80 most intense peaks

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MS/MS Fragmentation of YNLYGKDMK
Found in P30116, Glutathione S-transferase A3 OS=Mus musculus GN=Gsta3 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, plot from 150 to 1150 Da
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1222.59933
Fixed modifications: M(D) (C) (apply to specified residues or termini only)
Variable modifications:
K6 : niV (V), with neutral loss 41.0080
M8 : Oxidation (M), with neutral losses 0.0000 (shown in table), 60.9880
Ions Score: 27 Expect: 0.0080
Matches : 18/124 fragment ions using 10 most intense peaks (help)

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MS/MS Fragmentation of YFPAFEKVLK
Found in P30115, Glutathione S-transferase A3 OS=Mus musculus GN=Gsta3 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1326.6250
Fixed modifications: C(5) (C) (apply to specified residues or termini only)
Variable modifications:
K7  : m/z CO2 (K), with neutral loss 43.0150
Ions Score: 16  Expect: 0.22
Matches: 28/75 fragment ions using 74 most intense peaks (help)

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YFPAFEKVLK
MS/MS Fragmentation of KLEEGEQFVK
Found in P32020, Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1420.6722
Fixed modifications: HETR (C) (apply to specified residues or termini only)
Variable modifications:
K: Fla_002 (M), with neutral loss 44.0590
Ions Score: 34 Expect: 0.0037
Matches : 21/108 fragment ions using 22 more intense peaks (help)

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MS/MS Fragmentation of IETVNKSWNALAAPSEK
Found in P23717, Cytoplasmic aconitate hydratase OG=Mus musculus ON=Aco1 PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Me(calc): 1442.5464
Fixed modifications: NMTS (C)  Apply to specified residues or terminal only
Variable modifications:
NA<br> : m/z, 282 (R), with nominal mass 68.0000
Ion Score: 99, Expect: 9.00E-11
Method: 24/180 fragment Ion using 61 most intense peaks (calc)

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| 17 |          |          |          |          |          |          | K  | 147.1125 | 74.0600 | 130.0863 | 65.3468 | 147.1125 | 74.0600 | 1
**MS/MS Fragmentation of DFESECLGAKQGFK**

**Found in P28271, Cytoplasmic acetyl-CoA hydrolase OS=Mus musculus GN=Aco1 PE=1 SV=3**

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide M(��olo): 1560.6889**

**Fixed modifications: **MSS3 (C) (apply to specified residues or termini only)

**Variable modifications: **

**R9** : m/z 0.022 (K), with neutral loss 42.0568

**Ions Score:** 17 **Expect:** 0.043

**Matches:** 20/110 fragment ions using 58 most intense peaks **(best)**

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**DFESCLGAKQGFK**
MS/MS Fragmentation of MKNPFAHLAEPLDAQQPGKR

Found in P28271, Cytosolic acyl-CoA hydrolase Os-1

Fixed modifications: Carbonyl S (C), Oxidation (M)

Variable modifications:
K: M100 (50), with neutral loss 43 Da

Exact Mass: 2276.1371
Monoisotopic mass of neutral peptide Precursor: 2276.1371

Matched: 20/364 fragment ions using 15 most intense pairs
MS/MS Fragmentation of **KPFDDAKCVESAK**

Found in **FJ0115**, Glutathione S-transferase A3 OS=Mus musculus GN=GstA3 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, **Platform** 200 to 1000 Da **Full range**

Label all possible matches ✂ Label matches used for scoring ✡

---

**Monoisotopic mass of neutral peptide Mz (calc):** 1260.0021

**Fixed modifications:** NMTS (C) **(apply to specified residues or terminal only)**

**Variable modifications:** K7: **mal_CYS (K)**, with neutral loss 44.9598

**Ion Score:** 27 **Expect:** 5.0005

**Matches:** 24/184 fragment ions using 30 most intense peaks (help)

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|---|---|---|---|---|-----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 126.1022 | 65.0548 | 112.0757 | 56.5415 | K | 1397.6076 | 690.3074 | 1280.5810 | 690.7941 | 1279.5970 | 690.3021 | 13 |
| 2 | 226.1550 | 113.5811 | 209.1285 | 105.0570 | P | 1397.6076 | 690.3074 | 1280.5810 | 690.7941 | 1279.5970 | 690.3021 | 12 |
| 4 | 488.3584 | 244.6288 | 471.2238 | 236.1155 | D | 1153.4864 | 577.2468 | 1136.4598 | 568.7335 | 1135.4758 | 568.2415 | 10 |
| 5 | 603.2773 | 302.1423 | 595.2598 | 292.6290 | D | 1058.4594 | 519.7334 | 1021.4229 | 511.2201 | 1020.4484 | 510.7281 | 9 |
| 6 | 674.3144 | 337.6608 | 657.2879 | 326.1476 | A | 923.4235 | 462.2199 | 906.0406 | 453.7065 | 905.4219 | 453.2146 | 8 |
| 7 | 844.4199 | 422.7136 | 827.3934 | 414.2003 | K | 852.3954 | 426.7013 | 835.3683 | 418.1881 | 834.3848 | 417.6950 | 7 |
| 8 | 902.4160 | 497.2121 | 876.3903 | 488.9088 | C | 682.2899 | 341.6866 | 665.2633 | 333.1353 | 664.2793 | 332.6433 | 6 |
| 9 | 1092.4833 | 566.7463 | 1075.4337 | 558.2390 | Y | 593.2900 | 261.1501 | 516.2664 | 258.6668 | 512.2824 | 258.3102 | 5 |
| 10 | 1221.5279 | 611.2676 | 1204.5013 | 602.7543 | E | 434.2245 | 217.6159 | 417.1900 | 209.1026 | 416.2140 | 208.6106 | 4 |
| 11 | 1380.5399 | 654.7836 | 1291.5333 | 646.2703 | S | 305.1819 | 153.0946 | 288.1543 | 144.5813 | 287.1714 | 144.0893 | 3 |
| 12 | 1379.5970 | 660.3012 | 1362.5705 | 651.7880 | A | 218.1490 | 109.5786 | 201.1234 | 101.6063 | 2 |
| 13 | 1471.1128 | 74.0600 | 130.0683 | 65.5463 | K | 147.1128 | 74.0600 | 130.0683 | 65.5463 | 1 |
MS/MS Fragmentation of LQNLQLQPGKAK
Found in P32020, Non-specific lipid-transfer protein OS=Mus musculus GN=Sep2 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide M(H2O): 1422.7821
Fixed modifications: HET3 (C) (apply to specified residues or termini only)
Variable modifications:
K16 : =N COO (-), with neutral loss 42.0106
Ions Score: 35 Expect: 0.01
Matches: 24/36 Fragment ions using 50 most intense peaks

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**MS/MS Fragmentation of SYENQKPPFDAO**

Found in P37040, NADPH-cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da

Label all possible matches ☑️ Label matches used for scoring ☐

---

**Monoisotopic mass of neutral peptide** Mr(calc): 1508.6780

Fixed modifications: MCF8 (C) (apply to specified residues or termini only)

Variable modifications:

K5 : m/z 50.988 (K) with neutral loss 48.9090

Ions Score: 23 Expect: 0.0048

Matches: 12/127 fragment ions using 23 most intense peaks

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MS/MS Fragmentation of ILGYIKSGQQEGAK
Found in P47738, Aldolase A, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1576.0287
Fixed modifications: M(15) N(12) (apply to specified residues or termini only)
Variable modifications:
K : mal(9) (K), with neutral loss 41.992
Ions Score: 27 Expect: 0.0072
Matches : 15/220 Segments ions using 22 most intense peaks

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ILGYIKSGQQEGAK
VPAINVNDHSVTKSK

Monoisotopic mass of neutral peptide M(prot) = 1555.8646
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K10: m/z CO2 (K), with neutral loss 43.0058
Ions Score: 25 Expect: 9.0695
Matches: 49/132 fragment ions using 91 most intense peaks (help)

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**MEMBI Fragmentation of HGEVCPAGWKPGSDTIKPDVNK**

**Found in:** R9E9Q0, Pseudocotyle sp. 1, Cnidarians; R8E9Q0, Pseudocotyle sp. 1, Cnidarians

Click near the plot area to zoom in by a factor of two around that point.

O: [Full range] 200 to 1900 Da

**Label all possible matches &** [Label matches used for scoring]

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**Neuroendocrine mass of neutral peptide** (Picograms): 246.1005

**Fixed modifications:** M(m/z) C(H) [apply to specified residues or termini only]

**Variable modifications:**

**KET:** m/z 202.0081 with neutral loss 46.0264

**Score:** 52

**Matches:** 61/124 fragment ions using 109 most intense peaks.
MS/MS Fragmentation of DGLQNEKSVPTPVK
Found in P38069, Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Mus musculus GN=Hmgcl PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or [ Plot from 200 to 1000 Da ] [ Full range ]
Label all possible matches ◐ Label matches used for scoring ◐

Monotopic mass of neutral peptide Mr(m+e) : 1702.8856
Fixed modifications: M(128) (C) (apply to specified residues or termini only)
Variable modifications:
W7   n1:C02 (F), with neutral loss 43.9580
Ions Score: 81 Expect: 0.0039
Matches : 26/156 fragment ions using 11 most intense peaks (m/z)

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**MS/MS Fragmentation of KFSGVYLEKEVVEK**

**Found in P40566, Indolealkylamine N-methyltransferase**

**OS=Mus musculus, GN=Indmt, PE=1, SV=1**

Click mouse within plot area to zoom in by factor of two about that point

Or: Plot from 200 to 1000 Da

Label all possible matches © Label matches used for scoring *

---

**Monoisotopic mass of neutral peptide Mr(calc): 1729.8981**

**Fixed modifications: 4HET (C) (apply to specified residues or terminal only)**

**Variable modifications:**

KO: m/z CO2 (K), with neutral loss 45.99540

**Ions Score: 66 Exponent: 0.00020**

**Matched / Fragment ions using 105 most intense peaks**

---

| z | b       | b''      | b|b'' | y       | y''      | y|y'' | y|y'' | y|y'' | y|y'' | y|y'' | m/e |
|---|---------|----------|-----|-----|---------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 129.0222| 65.0348  | 112.0757 | 56.5415 | K | 1568.8297 | 784.9140 | 1251.7941 | 778.4007 | 1520.8101 | 775.9087 |
| 2 | 276.1707 | 138.3890 | 259.1441 | 130.0737 | F | 1421.7212 | 711.3798 | 1404.7257 | 702.8665 | 1403.7417 | 702.3745 |
| 5 | 519.2526 | 260.1499 | 502.2600 | 251.6366 | 501.2820 | 251.1446 | V | --- | --- | --- | --- | --- |
| 6 | 682.3559 | 341.6816 | 665.3293 | 333.1683 | 664.3453 | 332.6763 | Y | --- | --- | --- | --- | --- |
| 7 | 792.4400 | 396.2236 | 777.4154 | 388.7103 | 777.4284 | 388.2133 | L | --- | --- | --- | --- | --- |
| 8 | 924.4825 | 462.7440 | 907.4560 | 454.2316 | 906.4720 | 453.7396 | E | --- | --- | --- | --- | --- |
| 9 | 1094.5881 | 547.7977 | 1077.5815 | 538.2844 | 1076.5773 | 538.7524 | K | --- | --- | --- | --- | --- |
| 10 | 1253.6307 | 612.3190 | 1236.6041 | 603.8057 | 1235.6201 | 603.3137 | F | --- | --- | --- | --- | --- |
| 11 | 1322.6991 | 661.8332 | 1305.6721 | 653.3599 | 1304.6813 | 652.8479 | V | --- | --- | --- | --- | --- |
| 12 | 1421.7675 | 711.2874 | 1404.7409 | 702.8741 | 1403.7569 | 702.8382 | V | --- | --- | --- | --- | --- |
| 13 | 1550.8101 | 772.9087 | 1533.7825 | 765.3934 | 1532.7992 | 766.9034 | E | --- | --- | --- | --- | --- |
| 14 | K | 147.1128 | 74.0600 | 130.0863 | 65.5468 | 1 |
**MS/MS Fragmentation of FSGVYLEKEVVEK**

Found in P40936. Indole/tryptamine N-methyltransferase OS=Mus musculus GN=mmt PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

**Monoisotopic mass of neutral peptide Mr(calc): 1011.0032**

Fixed modifications: NMES (C) (apply to specified residues or termini only)

Variable modifications: 

KM: m/z CO2 (K), with neutral loss 44.0159

Ions Score: 51 Expect: 2e-05

Matches: 27/120 fragment ions using 60 most intense peaks (help)

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MS/MS Fragmentation of \textbf{VYIGGDEYKEFTPK}

Found in \textbf{P40936}. Isolated tryptic peptide of \textit{N}-methyltransferase OS=Mus musculus ON-Innt PE=1 SV=1

Click: mouse within plot area to zoom in by factor of two about that point

Or: Plot from \textbf{300} to \textbf{1900} Da

Label all possible matches \checkmark Label matches used for scoring \checkmark

Monoisotopic mass of neutral peptide Mr(m/z): 1889.8465

Fixed modifications: Met(OAc) (C) (apply to specified residues or termini only)

Variable modifications:

K10: \textit{N}\textsuperscript{-}methyl (K), with neutral loss 42 u

Ions Score: 25 Expect: 0.01

Matches: 20/186 fragment ions using 50 most intense peaks

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3 & 506.2660 & 245.6366 & & & G & 1441.6782 & 721.3277 & 714.6216 & 712.8144 & 712.3224 & 12 \\
4 & 406.2660 & 204.6366 & & & G & 1384.6267 & 692.8170 & 684.6002 & 684.3037 & 683.8117 & 11 \\
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MS/MS Fragmentation of VSEVKPTYR
Found in P42689, Transcriptional activator protein Pur-alpha
OS=Mus musculus GN=Pur PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or: Plot from 150 to 1100 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1163.8522
Fixed modifications: Met5 (C) (apply to specified residues or termini only)
Variable modifications: 
Ions Score: 25 Expect: 0.042
Matches : 15/32 fragment ions using 28 most intense peaks

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DFLAGGIAAAAVSKTAVAPIER

**MM/MS Fragmentation of DFLAGGIAAAAVSKTAVAPIER**
Found in PS1831, ADP/ATP translocase 2 Olemus marinus Q1m4c2.5a P6a1 SV=3

Click mouse within plot area to zoom by a factor of two about that point
Or [ Zoom in to 200 ] [ Full range ]
Label all possible matches & [ Label matches used for scoring ]

![Fragmentation Graph](image)

**Neurospora Crassa mass of neutral peptide Mz(m/z): 2142.1021**

**Fixed modifications:** MetO (5) (apply to specified residues or termini only)

**Variable modifications:** EL3 = m/z 203 (N), with neutral loss 48.0555

**Ion Score**: 28 **Expect**: 0.83

**Matches**: 42/214 fragment ions using 100 most intense peaks

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**MS/MS Fragmentation of YFPTQALNFAFKDK**

Found in **P43801**, ADP-ATP translocase 1 (OS=Mus musculus GN=5l21s4 PE=1 SV=4)

Click mouse within plot area to zoom in by factor of two about that point:
Or, Flat from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr (amu): 1774.9566**

**Fixed modifications:** MSHS (C) (apply to specified residues or termini only)

**Variable modifications:**

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**Intra-Repeat: 72 Expect: 4e-006**

**Matches:** 94/140 fragment ions using 59 most intense peaks (help)

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MS/MS Fragmentation of ALVSTKWLAESIR

Found in P52196, Thiosulfate sulfurtransferase Os=Mus musculus GN=Tst PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

Label all possible matches ✓ Label matches used for scoring ✓

Monoisotopic mass of neutral peptide Mr(calc): 1536.8355

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

K8 : +1.000 (N-term), with neutral loss 48.0152

Matches : 7/124 fragment ions using 24 most intense peaks (help)

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|---|-----|-----|----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 72  |     |    |      | A   |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 2 | 185 | 93  | 67 |      | L   | 1444.| 722.| 1427.| 714.| 838.| 713.| 606.| 713.| 563.| 713.| 542.| 713.|
| 8 | 941.| 543.| 34.|      | L   | 688.| 344.| 671.| 336.| 189.| 671.| 336.| 189.| 671.| 336.| 189.| 671.|
| 9 | 1012.| 582.| 20.|      | A   | 575.| 283.| 558.| 279.| 647.| 279.| 555.| 279.| 555.| 279.| 555.| 279.|
| 11 | 1228.| 657.| 57.|      | S   | 375.| 188.| 358.| 179.| 607.| 179.| 595.| 179.| 595.| 179.| 595.| 179.|
| 13 |     |     |    |      | R   | 175.| 88.6.| 158.| 79.5.| 498.| 79.5.| 498.| 79.5.| 498.| 79.5.| 498.| 79.5.|

Help
MS/MS Fragmentation of QALKNLGEILK
Found in P52760, Ribonuclease UK114 OS=Mus musculus ON=Hrsp12 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mz(calc): 1211.7398
Fixed modifications: M+N3 (C) apply to specified residues or termini only
Variable modifications:
K4 : mal-COO (K), with neutral loss 43.0096
Ions Score: 51 Expect: 0.0076
Matches : 14/100 fragment ions using 24 most intense peaks (help)

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VISTTKAPAAIGPYSQAVQVDR
KVISTTKAPAAIGPYSQAVVQVDR

MS/MS Fragmentation of KVISTTKAPAAIGPYSQAVVQVDR
Found in P07709, Ribosomal protein S11
OS=Homo sapiens GN=RP12 DE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or: (Full range) 200 to 3500 Da (Standard)
Label all possible matches © Label matches used for scoring ©

Monoisotopic mass of neutral peptide m/z (calc): 1385.6746
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K* : N-term (X), with neutral loss 43.0107
Ion score: 43 EXACT: 0.000264
Matches: 51/136 fragment ions line using 115 most intense peaks (calc)

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MS/MS Fragmentation of **ELFDELVKK**

Found in **P55264**, Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1200 Da [Full range]

Monoisotopic mass of neutral peptide Mr(calc): 1205.6180
Fixed modifications: MMSS (C) (apply to specified residues or termini only)
Variable modifications:
**K** = ma_lCO2 (K), with neutral loss 43.9998

Ions Score: 30 Expect: 0.011
Matches: 14/74 fragment ions using 19 most intense peaks  (help)

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MS/MS Fragmentation of GQKVLDSGAPIK
Found in P56480, ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1200 Da
Label all possible matches ○ Label matches used for scoring  ●

Monoisotopic mass of neutral peptide Mr(scaled): 1297.6878
Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
K5: mal_COO (K), with neutral loss 49.9596
Ions Scored: 0, Expect: 0.018
Matches: 27/110 fragment ions using 16 most intense peaks (help)

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MBMS Fragmentation of GQKVLDGAPIKVPGPETLG

Found in P64390, ATP synthase subunit beta, mitochondrial, G5-Mus musculus GN=Atp8b PE=1 SV=2

Click cross within plot area to zoom in or factor of two above that point
Or, Plus from 200 to 1400 Delta Full range
Label all possible matches or matches used for scoring

GQKVLDGAPIKVPGPETLG
MS/MS Fragmentation of **DFIDYYLIKQK**

Found in **P86650**,Cytochrome P450 2C39 OS=**Mus musculus** GN=Cyp2c39 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from __200__ to __1500__ Da Full range

Label all possible matches ✔ Label matches used for scoring ✔

Monoisotopic mass of neutral peptide Mr(mono): 1530.7606
Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
K9: + ma1,002 (K), with neutral loss 42.0668

Ions Searched: 21  Expect: 0.01
Matches: 10/30 fragment ions using 40 most intense peaks  [help]

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MS/MS Fragmentation of FKQHVQDWAIPR

Found in P88710, L-gulonolactone oxidase OS=Mus musculus GN=Gulo PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide M<sub>z</sub> (calc): 1809.90011
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K2: sul, C02 (K), with neutral loss 48.0089

Matches: 14/101 frequent ions using 50 most intense peaks (help)

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**MS/MS Fragmentation of IKIIAPPER**

Found in B1ATY1, Actin, cytoplasmic 2
OS=Mus musculus GN=Act21 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, the plot from 150 to 1050 Da full range

Label all possible matches ○ Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1121.6444

Fixed modifications: M(C) (apply to specified residues or termini only)
Variable modifications:
- N2: ms1.CO2 (K), with neutral loss 49.0090

Lons Score: 22 Expect: 0.2

Matches: 15/28 fragment ions using 44 most intense peaks (help)

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**MS/MS Fragmentation of IKIIAPPERK**

**Found in BLATV1, Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=2 SV=1**

Click mouse within plot area to zoom in by factor of two about that point

![Graph with peaks and masses](image)

Monoisotopic mass of neutral peptide Mr(calo): 1249.7394

Fixed modifications: H3N (C) (apply to specified residues or termini only)

Variable modifications:

- K2: mal-CO2 (K), with neutral loss 49.9898

Ions Score: 19 Expect: 0.13

Matches: 19/88 fragment ions using 52 most intense peaks  

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MVGM
GQKD
SYVG
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K

Monoisotopic mass of neutral peptide N(t calc): 2446.0984
Fixed modifications: C=NH (apply to specified residues or to whole sequence)
Variable modifications:
HC: Oxidation (M), with neutral losses 0.00000 (shown in table), 0.00000
HS: Deamidation (N), with neutral losses 0.00000 (shown in table), 0.00000
K13: M+COOH (K), with neutral losses 43.0086
Ions Score: 96 Expect: 0.0016
Matches: 20/206 fragment ions using 26 most intense peaks

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MS/MS Fragmentation of VAVEAKNPADLPK

Found in P58252, Elongation factor 2 OS=Mus musculus GN=Elf2 PE=1 SV=2

Monoisotopic mass of neutral peptide Mz(calc): 1496.7011
Fixed modifications: M+H (+) (apply to specified residues or term only)
Variable modifications:
K8  : miss202 (K), with neutral loss 43.01058

Matches : 11/122 fragment ions using 12 most intense peaks

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MS/MS Fragmentation of EITALAPSTMKIK

Found in B1ATY1, Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Flat from 200 to 1500 Da

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mz(scale): 1467.7805
Fixed modifications: HET0 (C) (apply to specified residues or termini only)
Variable modifications:
K11: std COO (R), with neutral loss 42.0500

Sequence: EITALAPSTMKIK

Matches: 14/516 Fragment ions using 115 most intense peaks (help)
**MS/MS Fragmentation of EITALAPSTMKIK**

Found in **B1ATY1**, Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1200 Da

Label all possible matches □ Label matches used for scoring

---

Monoisotopic mass of neutral peptide M (+calc): 1208.7504

Fixed modifications: MTM (C) (apply to specified residues or termini only)

Variable modifications:

- **M**40 : Oxidation (M, with neutral losses 0.0000(shown in table), 0.9500

Ions Scored: 21  Expect: 6.28

Matches: 28/164 fragment ions using 59 most intense peaks

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MS/MS Fragmentation of YSVDIPLDKTVVNK

Found in A2A4Q6, 60S ribosomal protein L27 (Fragment) OS=Mus musculus GN=Rpl27 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot zoomed 200 to 1700 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mz(calc): 1579.8866
Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
K9 : nalc_204 (E), with neutral loss 48.9595
Ion Score: 50 Expect: 0.00018
Matches: 19/130 fragment ions using 29 most intense peaks (help)

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**MS/MS Fragmentation of KAVIVKNIDDGTSRDPYPYSHALVAGIDR**

**Found in**: Peptide L27, 892 Da, mass matches GN:Rig127 DB:2 SV:2

Click mouse within view area to zoom in to better view this image.

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MS/MS Fragmentation of SFQKIQVR

Found in F6SVV1. Protein Gm9493 OS=Mus musculus GN=Gm9493 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range

Monoisotopic mass of neutral peptide Mr(calc): 1090.5771
Fixed modifications: MMIS (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Male CO2 (K), with neutral loss 43.0150

Ions Score: 49 Expect: 0.0011
Matches : 13/66 fragment ions using 19 most intense peaks  (help)

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MS/MS Fragmentation of FSGKHVVVFIAQR

Found in F6SVV1. Protein Cm0493 OS=Nasus musculus GN=Cm0493 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ▼

Monoisotopic mass of neutral peptide Mr(calc): 1470.7720
Fixed modifications: wt/C (C) (apply to specified residues or termini only)
Variable modifications: X4 : m1_Cys (K), with neutral loss 42.0050
Ions Score: 28 Expect: 0.73
Matches: 10/105 fragment ions using 10 most intense peaks (half)

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MS/MS Fragmentation of GLIKLVSK

Found in E9Q7lH0, Protein Gm16490 OS=Mus musculus GN=Gm16490 PE=4 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calo): 942.5750
Fixed modifications: MBIS (C) (apply to specified residues or termini only)
Variable modifications:
K4 : mal.CO2 (K), with neutral loss 43.9898

Ions Score: 25, Expect: 0.037
Matches: 16/64 fragment ions using 57 most intense peaks (help)

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MS/MS Fragmentation of **GGKPEPPAMPQPVPTA**
Found in **P52908**, 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1400 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1674.7520
Fixed modifications: MET3 (C) (apply to specified residues or termini only)
Variable modifications:
K3 : methionine S, with neutral loss 69.0096
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 69.0096
Tons Score: 11 Expect: 0.38
Matched : 6/246 fragment ions using 11 most intense peaks  [help]

| # | b | b'' | b' | b''' | b'''' | Seq | y | y'' | y' | y''' | y'''' | y'''' | y'''' | y'''' | y'''' | y'''' |
|---|---|-----|---|-----|------|-----|---|-----|---|-----|------|------|------|------|------|------|------|
| 1 | 8 | 16 | 8 | 16 | 8 | G | 1574.7883 | 788.8978 | 1557.7618 | 779.3845 | 1556.777 | 778.8925 | 1556.777 | 778.8925 |
| 2 | 285.1597 | 143.0815 | 285.1292 | 134.5682 | K | 1517.7666 | 759.3871 | 1500.7403 | 759.3738 | 1499.7563 | 750.3818 | 1499.7563 | 750.3818 |
| 3 | 382.206 | 191.6079 | 385.1819 | 183.0946 | P | 1547.6613 | 764.3343 | 1530.6348 | 665.8210 | 1529.6508 | 556.329 | 1529.6508 | 556.329 |
| 4 | 511.2537 | 255.1292 | 494.2145 | 247.6159 | 493.2405 | 247.6129 | E | 1250.6086 | 625.8079 | 1233.5820 | 617.2646 | 1232.5980 | 616.8026 | 1232.5980 | 616.8026 |
| 5 | 608.3039 | 304.6556 | 591.2773 | 296.1423 | 590.2933 | 295.6503 | P | 1121.5666 | 561.2866 | 1104.5394 | 552.7333 | 1103.5554 | 552.2813 | 1103.5554 | 552.2813 |
| 6 | 705.3566 | 353.1819 | 688.3301 | 344.6877 | 678.3461 | 344.1767 | P | 1094.5133 | 512.7502 | 1077.4856 | 504.2470 | 1066.5026 | 503.750 | 1066.5026 | 503.750 |
| 7 | 816.3937 | 388.7005 | 799.5672 | 380.1872 | 788.3332 | 379.6952 | A | 927.4604 | 464.2339 | 910.4339 | 455.7206 | 909.4499 | 455.2286 | 909.4499 | 455.2286 |
| 8 | 923.4291 | 462.2182 | 906.4026 | 453.7049 | 905.4186 | 453.2129 | M | 856.4237 | 428.7153 | 839.3988 | 420.2020 | 838.4128 | 419.7100 | 838.4128 | 419.7100 |
| 10 | 1148.5405 | 574.7739 | 1131.5199 | 566.2506 | 1130.5229 | 565.7666 | Q | 612.3352 | 306.6712 | 593.3068 | 298.1579 | 594.3246 | 297.6569 | 594.3246 | 297.6569 |
| 11 | 1245.5932 | 624.3003 | 1228.5677 | 614.7870 | 1227.5257 | 614.2090 | P | 484.2764 | 242.6410 | 466.2690 | 233.6366 | 466.2690 | 233.6366 | 466.2690 | 233.6366 |
| 12 | 1344.6617 | 672.8345 | 1327.6351 | 664.3212 | 1326.6511 | 663.8292 | V | 387.2286 | 194.1153 | 369.2132 | 185.1103 | 369.2132 | 185.1103 | 369.2132 | 185.1103 |
| 13 | 1441.7144 | 721.3608 | 1424.6879 | 712.8475 | 1423.7038 | 712.3556 | P | 288.1554 | 144.5813 | 270.1448 | 135.5761 | 270.1448 | 135.5761 | 270.1448 | 135.5761 |
| 14 | 1542.7621 | 771.8478 | 1525.7353 | 763.3714 | 1524.7515 | 762.8794 | T | 191.1026 | 96.0350 | 173.0821 | 87.0487 | 173.0821 | 87.0487 | 173.0821 | 87.0487 |
| 15 | A | 90.0550 | 45.5311 | 1 |
### MS/MS Fragmentation of LIFAGKQLEDGR

Found in I9Q4P0, KxDL motif-containing protein 1 (Fragment) OS=Mus musculus GN=Kxd1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches □ Label matches used for scoring □

---

**Monoisotopic mass of neutral peptide M (Da):** 1431.7339

**Fixed modifications:** M+H (C) (apply to specified residues or terminal only)

**Variable modifications:**

| M6 | m/z, C12 (K) with neutral loss 44.9900 |

**Ions Score:** 38  **Expect:** 0.15

**Matches:** 9/102 fragment ions using 12 mass intense peaks (help)

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**LIFAGKQLEDGR**

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**Monoisotopic mass of neutral peptide M (Da):** 1431.7339

**Fixed modifications:** M+H (C) (apply to specified residues or terminal only)

**Variable modifications:**

| M6 | m/z, C12 (K) with neutral loss 44.9900 |

**Ions Score:** 38  **Expect:** 0.15

**Matches:** 9/102 fragment ions using 12 mass intense peaks (help)
MS/MS Fragmentation of EAFSLFDKGDGDGTITTK
Found in P6204. Calmodulin OS=Mus musculus GN=Caln1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or,  Plot from 200 to 1800 Da
Label all possible matches or Label matches used for scoring

Nanospray mass of revised peptide Mz(calcd): 1920.3044
Fixed modifications: Methyl (C) (apply to specified residues or terminal only)
Variable modifications:
K8  : m1CO2 (K), with neutral loss 44.0264
Ions Score: 58 Expect: 8.0017
Matches: 88/154 fragment ions using 70 most intense peaks (help)

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MS/MS Fragmentation of SVPTWLKLTSDDVK
Found in P62301, 40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2

Monoisotopic mass of neutral peptide Mr(mass): 1672.8812
Fixed modifications: HETQ (C) (apply to specified residues or termini only)
Variable modifications:
KV : nalc_COOH (K), with neutral loss 43.01067
Yons Score: 29 Expect: 0.015

Matches : 29/149 fragment ions using 75 most intense peaks (help)
MS/MS Fragmentation of GNKPWISLPR

Found in P62702, 40S ribosomal protein S1, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from ___ to ___ Da  Full range
Label all possible matches © Label matches used for scoring ©

Monoisotopic mass of neutral peptide Mr(calc): 1252.6564
Fixed modifications: MET(C) (apply to specified residues or termini only)
Variable modifications:
X:  mal-COOH (R), with neutral loss 42.0088
Ions Score: 51 Expect: 0.018
Matches : 11/60 fragment ions using 22 most intense peaks  (help)

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MS/MS Fragmentation of NKEAAEYAKLLAK
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Click mouse within plot area to zoom in by factor of two about that point.
Or, Plot from 200 to 1600 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide M (calc): 1562.9064
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K10 : m+2 Da, with neutral loss 43.0590
Ion Score: 27 Expect: 0.0017
Matches : 22/158 fragment ions using 50 most intense peaks (m/z)

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**MS/MS Fragmentation of EVPNYKLITPAVVSER**

Found in P61852, 4OS ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Fill zoom to 200 to 1700 Da Full range

Label all possible matches Label matches used for scoring

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**Monoisotopic mass of peptide (M+H)+ of [655.9282]**

**Fixed modifications:** M(18) (apply to specified residues or termini only)

**Variable modifications:**

**Ions Score:** 15 **Expect:** 0.00079

**Matched:** 21/172 fragment ions using 47 most intense peaks (help)

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**GGKPEPPAMPQPVP**

**MS/MS Fragmentation of GGKPEPPAMPQPVP**

*Found in P62908, 40S ribosomal protein S3 Os-Mus musculus ON-Rps3 PE-1 SV-1*

Click menu within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da
Label all possible matches

**Monoisotopic mass of neutral peptide (calc):** 1655.7974
**Fixed modifications:** M: C (apply to specified residues or termini only)
**Variable modifications:**

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MS/MS Fragmentation of MVNHFIAEFKR

Found in P63017, Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1476.7164
Fixed modifications: MET(S) (apply to specified residues or termini only)
Variable modifications:
K10 : mal_C02 (K), with neutral loss 43.0050
Ions Score: 54  Expect: 0.0017
Matches: 14/99 fragment ions using 28 most intense peaks  (help)

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MS/MS Fragmentation of *MVNHFIAEFKR*

Found in *P38017*, Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hsp70 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two above that point

Or, Plot from 200 to 1500 Da Full range

Label all possible matches □ Label matches used for scoring □

---

**MS/MS Fragmentation of MVNHFIAEFKR**

**M**

---

**Monoisotopic mass of neutral peptide Mx(calc):** 1492.7110

**Fixed modifications:** MMET (C) (apply to specified residues or termini only)

**Variable modifications:**

- Oxidation (M), with neutral losses 9.01098 (shown in table), 64.9953
- Nε\(^{-}\)acetyl, with neutral loss 49.0652

**Matches:** 25/128 fragment ions using 65 most intense peaks

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MS/MS Fragmentation of ELEKVCNPIITK

Found in P63017, Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mz(m/z): 1537.7466

Fixed modifications: MTM (C) (apply to specified residues or termini only)

Variable modifications:
K8 : mal-COOH (R), with neutral loss 43.0156

Matches: 22/124 fragment ions using 90 most intense peaks (help)

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|-----|------|-----|-----|------|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
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| 2   | 243.1339 | 122.0706 | 225.1234 | 113.0653 | L    | 13  |
| 3   | 372.1765 | 186.3919 | 334.1680 | 177.3886 | E    | 12  |
| 4   | 542.2821 | 271.6447 | 325.2555 | 263.1314 | K    | 11  |
| 5   | 641.3505 | 321.1789 | 624.2329 | 312.6656 | V    | 10  |
| 6   | 790.3474 | 395.6774 | 773.2208 | 387.1641 | C    | 9   |
| 7   | 904.3903 | 452.6988 | 887.3638 | 444.1855 | N    | 8   |
| 8   | 1001.4431 | 501.2252 | 984.4165 | 492.7119 | P    | 7   |
| 9   | 1114.5277 | 557.7672 | 1097.5005 | 549.2359 | I    | 6   |
| 10  | 1227.6112 | 614.3092 | 1210.3846 | 605.7900 | I    | 5   |
| 11  | 1328.6589 | 648.3831 | 1311.6323 | 656.2198 | T    | 4   |
| 12  | K    | 147.1128 | 74.0600 | 120.0865 | 65.4568 | 1   |
**MS/MS Fragmentation of KAAIISAEGDSK**

Found in P67778, Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

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Fixed modifications: Methionine_C (C) (apply to specified residues or termini only)
Variable modifications: K1 - mal_002 (K), with neutral loss 43.0089
Ions Score: 22 Expect: 0.019
Matches: 12/120 fragment ions using 21 most intense peaks (help)
MS/MS Fragmentation of **FVVEKAEQQK**

Found in P07778, Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from [ ] to [ ] Da  Full range

Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1290.6466

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

Met : m+1 (K), with neutral loss 49.9698

Ions Score: 30  Expect: 0.0067

Matches: 20/50 fragment ions using 50 most intense peaks  (help)

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### MS/MS Fragmentation of HLTSQSVLDSKV MK

Found in P70245, 3 beta hydroxysteroid Delta(8),Delta(7)-isomerase OS=Mus musculus GN=Ebp PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point. 
Or, Plot from 200 to 1600 Da [Full range]

Label all possible matches [Label matches used for scoring]

---

**Monoisotopic mass of neutral peptide (M+H) + : 1770.9716**

**Fixed modifications:** MMTSF (C) (apply to specified residues or termini only)

**Variable modifications:**

K12 : +15.99498 (K), with neutral loss 42.0159

**Ion Score:** 26 **Exponent:** 0.0088

**Matches:** 32/146 fragment ions using 115 most intense peaks

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MS/MS Fragmentation of **VLDDLKNIR**

Found in **P70694**, Estradiol 17 beta dehydrogenase 5 OS=Mus musculus GN=Akr1c6 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ⊗ Label matches used for scoring ⊗

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**Monoisotopic mass of neutral peptide Mr(calc):** 1284.8676

**Fixed modifications:** MMTS (C) (apply to specified residues or termini only)

**Variable modifications:**

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**Tide Score:** 72  **Expect:** 0.0006

**Matches:** 12/82 Fragment ions using 30 most intense peaks  (help)

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**VLDDLKNIR**
MS/MS Fragmentation of ILKKPGLK
Found in D323P8, Estradiol 17 beta-dehydrogenase 5 (Fragment) OS=Mus musculus GN=Akr1c6 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Fullrange
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 981.6222
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
K3 : m+1CO2 (K), with neutral loss 43.0589
Ions Score: 25 Expect: 0.028
Matches : 0/52 fragment ions using 16 most intense peaks  (help)

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**MS/MS Fragmentation of DAGLAKSIGVSNFNR**

Found in D2Z3PS, Estradiol 17 beta dehydrogenase 3 (Fragment) OS=Mus musculus GN=Akr1c6 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or Plot from 200 to 1800 Dn Full range
Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mz(calc): 1663.5560**

**Fixed modifications:  HET (C) (apply to specified residues or termini only)**

**Variable modifications:**

ES - m/z 0.002 (E), with neutral loss 18.0036

**Tops Score: 293 Expect: 0.007**

**Matches : 22/150 fragment ions using 72 most intense peaks**

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MS/MS Fragmentation of **AVKEVLLNHK**

Found in **Q95421**, Cytochrome P450 2E1 OS=Mus musculus GN=Cyp2e1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, **Platform** from 150 to 1050 Da **Full range**

Label all possible matches ○ **Label matches used for scoring** ↳

---

**Monoisotopic mass of neutral peptide**: 1235.0074

**Fixed modifications**: MTMT (C) (apply to specified residues or termini only)

**Variable modifications**: **K** : \( \text{mei} \_ \text{CO2} \) (with neutral loss 43.0050)

**Ions Score**: 20 **Expected**: 0.096

**Matches**: 7/86 fragment ions using 5 most intense peaks

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MS/MS Fragmentation of **KYLIPK**

Found in Q3UT49, Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 750 Da Full range

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 846.4851**

**Fixed modifications: MMTH (C) (apply to specified residues or termini only)**

Variable modifications:

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**Ions Score: 70**  Expect: 0.032

**Matches**: 12/40 fragment ions using 37 most intense peaks  (help)

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MS/MS Fragmentation of KSDYFMPFSTGK
Found in Q3T19, Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29 PE=2 SV=1

Monoisotopic mass of neutral peptide M(r)calc. = 1462.6444
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K1 : mal-COO\(^{-}\) (K) with neutral loss 43.0259
Ions Score: 36 Expected: 0.00009
Matches : 14/126 fragment ions using 47 most intense peaks  (help)

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SDYFMPFSTGKR

MS/MS Fragmentation of SDYFMPFSTGKR
Found in Q3UT49, Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Nonisotopic mass of neutral peptide Mz(calc): 1520.6056
Fixed modifications: MMT8 (C) (apply to specified residues or termini only)
Variable modifications:
 Kil: mal CCG (R), with neutral loss 43.0608
Ions Score: 27  Expect: 0.01
Matches: 21/106 fragment ions using 66 most intense peaks  (help)

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**MS/MS Fragmentation of LIGELAKEVR**

Found in P97352, Protein S100-A13 OS=Mus musculus GN=S100a13 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or: Plot from 100 to 1150 Da  Full range

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1212.6714

**Fixed modifications:** Methionine (C) (apply to specified residues or termini only)

**Variable modifications:**

- K7: *mal* CO2 (R), with neutral loss 42.0080

**Ions Score:** 80  Expect: 0.00007

**Matches:** 52/66 fragment ions using 20 most intense peaks  ([help](#))

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**MS/MS Fragmentation of DICKGGNAVVDGCSK**

Found in P97494, Glutamate-decarboxylase like catalytic subunit OS=Mus musculus GN=Gkek PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

Or, Plot from 200 to 1500 Da Full range

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide M(z+1):** 1662.6650

**Fixed modifications:** M(+57) (apply to specified residues or termini only)

**Variable modifications:**

K(+49) m/z 15.00 (B), with neutral loss 42 u

**Ions Score:** 27 **Expect:** 0.04

**Matches :** 12/100 fragment ions using 26 most intense peaks

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MS/MS Fragmentation of **VPTDKYYGAQTVR**

Found in P07807, Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1800 Da

Label all possible matches Label matches used for scoring

**Monoisotopic mass of neutral peptide Mr(calc): 1582.7627**

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

ES : [mal-ODG (E), with neutral loss 42.0308]

Ions Score: 51 Expect: 0.00051

Matches : 21/128 fragment ions using 24 most intense peaks  

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VPTDKYYGAQTVR
**MS/MS Fragmentation of KTILTTEEDR**

Found in P97872, Dimethylaniline monoxygenase [N-oxide-forming] 3 OS= Mus musculus GN=Fmo3 PE=2 SV=4

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from: 150 to 1150 Da Full range

Label all possible matches ☐ Label matches used for scoring ☐

---

**Monoisotopic mass of neutral peptide Me(calc): 1161.60577**

**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)

**Variable modifications:**

K1 : methyl CO2 (K), with neutral loss 48.0155

Ions Score: 35 Expect: 0.0012

Matches: 16/92 fragment ions using 38 most intense peaks (hla)

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MS/MS Fragmentation of KLPSQSEMMAEINK
Found in P97872, Dimethylamine N-monooxygenase [N-oxide-forming] 3 OS=Mus musculus GN=Fn201 PE=2 SV=4

Click mouse within plot area to zoom in by factor of two about that point:
Or, [Plot form] 200 to 1400 [Dx] [Full range]
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1690.7906
Fixed modifications: MTMS (C) (apply to specified residues or termini only)
Variable modifications:
KL : [mal_202 (F)], with neutral loss 43.9590
Ions Scored: 20  Expect: 0.052
Matches : 50/144 fragment ions using 12 most intense peaks  (help)

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MS/MS Fragmentation of KILDSVGIEADDDR
Found in P99207, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point.
Or, Plot from 200 to 1500 Da Full range.
Label all possible matches ✗ Label matches used for scoring ☑

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**Monoisotopic mass of neutral peptide (Mr(calc))**: 1680.7066
**Fixed modifications**: M(15) C (apply to specified residues or terminal only)
**Variable modifications**: K: m/z Δ20 (K), with neutral loss 41.0107

**Scan range**: 54 - 148

**Matches**: 15/148 fragment ions using 26 most intense peaks (help)

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MS/MS Fragmentation of KILDSVGIEADDDRLNK
Found in P99027, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplb2 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point:
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Me(calcd): 1993.9926
Fixed modifications: NMT (C) (apply to specified residues or termini only)
Variable modifications:
K: m+1 CO2 (E), with neutral loss 44.012
Ion Score: 23 Expect: 0.008
Matches: 21/278 fragment ions using 61 most intense peaks (kcal/mol)

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**MS:MS Fragmentation of DHCVAHKLFK**

*Found in P99028, Cytochrome b-c1 complex subunit 6, mitochondrial OS=Mus musculus GN=Uqcrh PE=1 SV=2*

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1300 Da [Full range]

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1925.6000**

**Fixed modifications: MetO (C) (apply to specified residues or termini only)**

**Variable modifications:**

- K7  :  mal-COO\(^{-}\) (R), with neutral loss 44.0090

**Ions Score: 27  Expect: 0.019**

**Matches: 40/78 fragment ions using 21 most intense peaks  (help)**

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MS/MS Fragmentation of EIADKFINEVVVK

Found in Q3U367, 4-trimethylamobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, plot from ___ Da to ___ Da  Full range
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1459.7664
Fixed modifications: NMTS (C) (apply to specified residues or termnini only)
Variable modifications:
KS : N-term, O-acetyl, with neutral loss 43.0599
MSn Source: 300  Emitter: 0.015
Matches: 7/110 frequent ions using 13 most intense peaks  

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MS/MS fragmentation of AQGKPVSQGEKSQSPYER
Found in QUPF0.0. Protein transport protein Sec31a OS=Mus musculus GN=Sec31a PE=1 SV=2
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1900 Dn Full range
Label all possible matches Label matches used for scoring

AQGKPVSQGEKSQSPYER
IKEHKESLDVTNPR

MS/MS Fragmentation of IKEHKESLDVTNPR
Found in Q3UT49, Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
OxPlot from 100 to 1500 Da Full range
Label all possible matches Label matches used for scoring

Molecular mass of neutral peptide Mz (amu): 2019.0124
Fixed modifications: M(12) C (apply to specified residues or termini only)
Variable modifications:
EN: H, C(12), (R), (S), with neutral loss 60.0500
Ions Score: 57 Expect: 0.0010
Matches: 21/120 Fragment ions using 65 most intense peaks

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MS/MS Fragmentation of VKQLPLVKPYLR

Found in Q5XR6, Clatrin heavy chain 1 OS=Mus musculus GN=Clte PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1380.9154
Fixed modifications: M=15 (+) (apply to specified residues or termini only)
Variable modifications:
K: methionine oxidation (+15.9946 Da), with neutral loss 43.959 Da

Ions Score: 26 Expect: 0.0005
Matches : 10/86 fragment ions using 18 most intense peaks  (help)

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MS/MS Fragmentation of AVNYFSKVK

Found in Q5SRX6. Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Label all possible matches Label matches used for scoring

### Monoisotopic mass of neutral peptide M(m/e): 1140.5015

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:
K9 : ma1_C02 (K), with neutral loss 48.0390

Score: 20  Impact: 0.085

Matches: 10/76 fragment ions using 18 most intense peaks

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MS/MS Fragmentation of **KYDAFLASESLIK**

Found in **D3VXT2**, Ribosomal protein O5=Nas musculus G0=Rpl10a-ps2 PE=3 SV=1

Click mouse within plot area to zoom in by factor of two about that point

**[Plot from]** 206 to 1500 **[Da Full range]**

Label all possible matches ○ Label matches used for scoring ☑

---

**Monoisotopic mass of neutral peptide Mr(ma/c):** 1509.7226

**Fixed modifications:** MMRE (C) (apply to specified residues or termini only)

**Variable modifications:**

- K1: mal-COOH (K), with neutral loss 46.0150

**Ions Searched:** D0 Target:

**Matches:** 16/104 fragment ions using 60 most intense peaks (help)

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MS/MS Fragmentation of VGVGKVIR

Found in Q62446, Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Mus musculus GN=Fkbp3 PE=1 SV=2

Monoisotopic mass of neutral peptide Mr(calc): 912.5383
Fixed modifications: NH3 (C) (apply to specified residues or termini only)
Variable modifications:
K5 : ma_G (R), with neutral loss 43.9888

Ions Score: 37  Expect: 0.0076
Matches : 5/48 fragment ions using 7 most intense peaks  (help)

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LPVDKTTSCCFGGK

Monoisotopic mass of neutral peptide Mz(x16) : 1812.6658
Fixed modifications: M+H (apply to specified residues or terminal only)
Variable modifications: K : methyl (K), with neutral loss 16.0050
Ions Score: 1.52 Expect: 0.14
Matches: 10/109 fragment ions using 24 most intense peaks (help)

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MS/MS Fragmentation of HQGSLYSLFPFDHSVKK
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Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from to Da
Label all possible matches ✔ Label matches used for scoring ✔

Monoisotopic mass of neutral peptide M(n,calc): 1327.9120
Fixed modifications: MET (C) (apply to specified residues or termini only)
Variable modifications:
K85 : alk,0.000 (B), with neutral loss 58.038
Ions Score: 22  Expect: 0.040
Matches : 44/100 fragment ions using 72 most intense peaks  (help)

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HQGSLYSLFPFDHSVKK
MS/MS Fragmentation of LQTVKLPVDK

Found in O64374. Racuclain OS=Mus musculus GN=Ren PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1200 Da
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1225.6318
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
KM: ma1_COO (K), with neutral loss 43.0089
Ions Score: 30 Expect: 0.0098
Matches: 6/100 fragment ions using 11 most intense peaks (help)

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MS/MS Fragmentation of SQGKVLQATVVAVGSGGK

SQGKVLQATVVAVGSGGK

MONOISOTOPE MASS OF NEUTRAL PEPTIDE ( Da) : 1779.9476

Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications: X:
: X : M + 15 (K), with neutral loss 42.01064

Inte score: 70  Expect: 9.6e-06

Matches : 25/106 fragment ions using 60 most intense peaks

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MS/MS Fragmentation of KIGCGNFGELR
Found in Q6P2B2, Casein kinase II isoenzyme gamma-1 OS=Mus musculus GN=Csnk1g1 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(mono) : 1224.5404
Fixed modifications: HETR2 ( ubiquitous ) (apply to specified residues or termini only)
Variable modifications:
K1 : mal-CO2 (K), with neutral loss 42.0068
Ions Saved: 51 Expect: 0.001
Matches : 12/100 fragment ions using 21 most intense peaks  (help)

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KIGCGNFGELR
**MS/MS Fragmentation of LADKVNSSWQK**

Found in Q80ZV3, Proline synthase co-transcribed bacterial homolog protein OS=Mus musculus GN=Prosc PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

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**Monoisotopic mass of neutral peptide Mz (calc): 1060.6620**

Fixed modifications: NH2 (C) (apply to specified residues or termini only)

Variable modifications:

K: m/z 15.995 (E), with neutral loss 44.0039

Ions Score: 58 Expect: 8.0e-005

Matches: 18/104 fragment ions using 22 most intense peaks (help)
LVAVSKTPADMIEAYGHGQR
MS/MS Fragmentation of SYVLK AQTEGAR

Found in Q0BH00. Aldehyde dehydrogenase family 8 member A1 OS=Mus musculus GN=Aldh8a1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or [Plot from] 250 to 1250 Da [Full range]
Label all possible matches ○ Label matches used for scoring *

Monoisotopic mass of neutral peptide Mr(calc): 1407.6994
Fixed modifications: NH3 (C) (apply to specified residues or termini only)
Variable modifications:
K5 : ma1_Cys (K), with neutral loss 48.0101
Ions Score: 31  Expect: 0.02
Matches : 19/118 fragment ions using 34 most intense peaks  (help)

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MS/MS Fragmentation of AIKLTNVNDFVR

Found in Q8BH59. Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus musculus GN=Slc25a12 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1200 Da Full range
Label all possible matches Label matches used for scoring

Homoxiostopic mass of neutral peptide [M+calc]: 1380.7361
Fixed modifications: N-tr( C) (apply to specified residues or termini only)
Variable modifications: K58: m+1 CO2 (K), with neutral loss 48.0107
Ions Score: 20 Expect: 0.040
Matches : 9/102 fragment ions using 10 most intense peaks [help]

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MS/MS Fragmentation of TGKVSAAIDFR

Found in Q9QQX4, Calcium-binding mitochondrial carrier protein Aralar2
OS=Mus musculus GN=Sla25a13 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, plot from 100 to 1200 Da
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1178.5933
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K3 : m+1 CO2 (K), with neutral loss 49.9999
Ions Score: 62 Expect: 4.5e-006
Matches : 13/100 fragment ions using 20 most intense peaks (help)

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MS/MS Fragmentation of KIYSTLAGNR

Found in Q90XX4. Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1300 Da Full range

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(cala): 1207.6197
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
KL : mal-CO2 (K), with neutral loss 40.0000

Ions Score: 16 Expect: 0.062
Matches: 4/92 fragment ions using 11 most intense peaks (help)

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MS/MS Fragmentation of GQQQVFKGLNDK
Found in Q8BMS1. Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide M(calc): 1446.7103
Fixed modifications: Met(C) (apply to specified residues or termini only)
Variable modifications:
K7 : m+1, CO2 (K) with neutral loss 44.0205
Ions Scored: 26 Expect: 0.00
Matches : 12/100 fragment ions using 21 most intense peaks (help)

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**MS/MS Fragmentation of GFYIYQEGSKNK**

Found in O8BMS1. Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1

Chick mouse within plot area to zoom in by factor of two about that point

Or, Plot from __________ to __________ Da  [Full range]

Label all possible matches ○  Label matches used for scoring ○

---

**Monoisotopic mass of neutral peptide Mr(mole):** 1518.6091

**Fixed modifications:** MMTS (C) (apply to specified residues or terminal only)

**Variable modifications:**

K: 57.020528 (K), with neutral loss 48.0648

**Ions Score:** 20  **Expect:** 0.049

**Matches:** 18/104 fragment ions using 41 most intense peaks  **(kcal)**

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MS/MS Fragmentation of FVDLYGAQKVVDR

Found in Q8BMS1, Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide (Mr(calc): 1594.7921)
Fixed modifications: MMTS (C) (apply to specified residues or terminal only)
Variable modifications:
KM : mél_002 (R), with neutral loss 40.009
Total Score: 27 Expect: 0.0078
Matches: 23/124 fragment ions using 112 most intense peaks

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MS/MS Fragmentation of TVDPTTAPSKTR
Found in Q8BP40, Lysophosphatidic acid phosphatase type 6 OS=Mus musculus GN=Acp6 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot form 100 to 1300 Da Full range

Monoisotopic mass of neutral peptide Mr(cale): 558.6478
Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
K10 : mal_SO2 (K), with neutral loss 46.0590
Ions Score: 44 Expect: 0.0011
Matches: 11/112 fragment ions using 11 most intense peaks (help)

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MS/MS Fragmentation of KLCELYAK

Found in Q8BW75. Amine oxidase [flavin-containing] B OS=Mus musculus GN=Maob PE=1 SV=4

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MS/MS Fragmentation of NVKYVDLGGSYVGPTQNR

Found in E9PVLQ. Amino oxidase [flavin-containing] B Os Mussculosmusculus GN=Masb PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1900 Da Full range

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr (calc): 2941.9912
Fixed modifications: MRZS (C) (apply to specified residues or termini only)
Variable modifications:
K1 : m+20 Da (K) with neutral loss 42.015
Inst Score: 80 Expect: 1.5e-67
Match: 49/1285 fragment ions using 71 most intense peaks

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MS/MS Fragmentation of AYVDTPAEQMKAE
Found in QSGC7, bifunctional glutamate-proline-RNA ligase Os=Mus musculus GN=Eprn PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1700 Da
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide (Mr(calc.): 1506.7557
Fixed modifications: 8H73 (C) (apply to specified residues or termini only)
Variable modifications:
K12 : N/C-poly(2K) (X), with neutral loss 43.9805
Ion Source: 40 Expt: 0.000625
Matches: 19/162 fragment ions using 20 most intense peaks (help)

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MS/MS Fragmentation of KPNQPYKWISYK
Found in Q8JRZ0. Long chain fatty-acid--CoA ligase 5 OS=Mus musculus GN=Acsl5 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Enter from 300 to 1500 Da to Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide M+ (calc): 1636.9249
Fixed modifications: MMTF (C) (apply to specified residues or termini only)
Variable modifications:
K7: Met_002 (K), with neutral loss 10.0000
Ions Score: 27 Expect: 0.0098
Matches: 19/110 fragment ions using 51 most intense peaks (calc)

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MS/MS Fragmentation of ALQSIEKER

Found in Q91X88, Transmembrane protein 205 OS=Mus musculus GN=Tmem205 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 50 to 1200 Da
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1138.5880
Fixed modifications: METS (C) (apply to specified residues or termini only)
Variable modifications:
K7 : m/z CO2 (K), with neutral loss 49.9899

Ions Score: 21  Expect: 0.044
Matches to 12/34 fragment ions using 16 most intense peaks (help)

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### MS/MS Fragmentation of FCYADKALLNR

**Found in Q8CH10.** Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh1al PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from \( 200 \) to \( 1400 \) Da Full range

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc): 1444.6476**

**Fixed modifications:** M(S) (C) (apply to specified residues or terminal only)

**Variable modifications:**

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**Tune Score:** 48  **Expt.** 0.0041

**Matches:** 19/90 fragment ions using 23 most intense peaks (help)

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### MS/MS Fragmentation of ALKPTVFPTVPR

*Found in Q8JZ00, Long-chain-fatty-acid-CoA ligase 5 OS=Mus musculus GN=Acs5 PE=3 SV=1*

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1250 Da Full range

Label all possible matches ☐ Label matches used for scoring ☐

![Fragmentation Diagram](image)

---

**Monoisotopic mass of neutral peptide Mr(male):** 3410.7871

**Fixed modifications:** NMT (C) (apply to specified residues or termini only)

**Variable modifications:**

- K: + 15.99491 (O), with neutral loss 48.0695

**Ions Scored:** 16  **Expect:** 0.062

**Matches:** 15/714 fragment ions using 30 most intense peaks  

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GLSLLLYGSIPKAAVR

MS/MS Fragmentation of GLSLLLYGSIPKAAVR
Found in Q8Z1L2. Protein Slk25sa1 OS=Mus musculus GN=Slk25sa1 PE=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot type] [Cartesian] [Bar] [Pie] [Full range]
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide (M+H): 1526.8440
Fixed modifications: TMT (C) [apply to specified residues or terminal only]
Variable modifications: Oxidation (M), with neutral loss 43.0108
Ion Score: 55 Expect: 0.00011
Matches: 20/140 fragment ions using 87 most intense peaks [help]

| 1 | 58.0287 | 29.5180 | G | 16 |
| 2 | 171.1128 | 86.0600 | L | 1616.9170 | 808.9721 | 1599.9105 | 800.4891 | 1598.9265 | 799.9869 | 15 |
| 3 | 229.1448 | 129.5761 | S | 1503.8530 | 752.4281 | 1486.8264 | 743.9168 | 1485.8424 | 743.4248 | 14 |
| 4 | 345.1769 | 173.0921 | S | 1516.8209 | 708.9141 | 1509.7944 | 700.4006 | 1508.8104 | 699.9083 | 13 |
| 5 | 412.2009 | 229.6341 | L | 1339.7989 | 665.3981 | 1322.7764 | 656.8819 | 1319.7898 | 656.3928 | 12 |
| 6 | 571.3459 | 286.1761 | L | 1216.7548 | 658.8561 | 1199.8783 | 650.3428 | 1198.8943 | 599.8208 | 11 |
| 7 | 734.4083 | 367.7078 | V | 1192.6398 | 552.3140 | 1186.5943 | 543.8007 | 1185.6102 | 543.3087 | 10 |
| 8 | 781.4298 | 366.2185 | G | 946.5574 | 470.7824 | 929.5809 | 462.2691 | 922.5469 | 461.7771 | 9 |
| 9 | 878.4618 | 439.7345 | S | 883.5360 | 442.2716 | 866.5969 | 433.7534 | 855.5224 | 433.2063 | 8 |
| 10 | 991.5429 | 486.2766 | I | 796.5839 | 399.7256 | 779.4774 | 390.2423 | 7 |
| 11 | 1088.5986 | 544.8030 | P | 683.4199 | 342.2136 | 666.3933 | 333.7003 | 6 |
| 12 | 1258.7042 | 629.8357 | K | 583.3671 | 293.6872 | 569.3406 | 285.1759 | 5 |
| 13 | 1329.7413 | 665.3743 | A | 416.2616 | 208.8344 | 399.2350 | 200.1212 | 4 |
| 14 | 1400.7784 | 700.8928 | 1383.7518 | 692.3706 | 1382.7678 | 691.8876 | 1382.6978 | 3 |
| 15 | 1499.8468 | 750.4270 | V | 274.1874 | 137.5973 | 257.1608 | 129.0640 | 2 |
| 16 | R | 173.1190 | 88.0651 | 158.0824 | 79.5488 | 1 |
MS/MS Fragmentation of RPNKPLFTGLVTQCQK
Found in Q8K128. NAD(P)H-depolymerase OS=Mus musculus GN=Apoa1bp PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, set from 200 to 1400 Da
Label all possible matches Label matches used for scoring

Phenotypic mass of neutral peptide [M]+ (calc): 1596.8658
Fixed modifications: MMT (C) (apply to specified residues or terminal only)
Variable modifications:
X = m/z 0.992 (N), with neutral loss 44.0580
Ion Source: ESI Impact: 1.3
Matches: 28/135 fragment ions using 16 most intense peaks (Q31.1a)

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RPNKPLFTGLVTQCQK
MS/MS Fragmentation of AVKSAEEAAAETK

Found in Q8VC30, Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Mus musculus GN=Dak PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da

Label all possible matches ☑ Label matches used for scoring ☑

Nonisotopic mass of parental peptide M (calc): 1081.6003
Fixed modifications: M7 (C) (apply to specified residues or termini only)
Variable modifications:
K : max 35% (X) with neutral loss 102.0506

Matches : 26/112 fragment ions using 82 most intense peaks  [help]

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**MS/MS Fragmentation of QKQDAFALASQQK**

Found in Q8VCH0, 3-koesterol-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acan1b PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1500 Da Full range
Label all possible matches Label matches used for scoring

---

Nonisotopic mass of neutral peptide M: (calc): 1647.7100
Fixed modifications: MMT (C) (apply to specified residues or termini only)
Variable modifications:
K: mad_C02 (K), with neutral loss 48.0100
Ions Source: 23 Expect: 6.021
Matches: 21/112 fragment ions using 56 most intense peaks

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MS/MS Fragmentation of QDAFALASQKAAASAQSR
Found in QFYCH0, 3-ketoacyl-CoA thiolase B, pancreatic OS=Mus musculus GN=Acasa1 PS=2 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Options: Plot from: 0 to 1200 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of central peptide (M+H)+ 1562.5355
Fixed modifications: M+H+ (apply to specified residues or terminal only)
Variable modifications:
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Ions Score: 44 Expect: 0.00004
Matches : 24/200 fragment ions using 41 most intense peaks

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### Mass Spectrometry Data

**MIMS Fragmentation of QKQDALASQQKAASQSR**

- **Found in:** QSYCHO, 3-hydroxy-CoA thiolase B, paracoccidioides brasiliensis GS
- **MS/MS:** PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

**Q** - Plot from 200 to 1000 Da

Label all possible matches - Label matches used for scoring

---

**Protein Identification**

**Species:** H. sapiens (human)

**Peptide:** QKQDALASQQKAASQSR

**Protein:** [Protein name]

**Confidence:** High

**Score:** 97

**Expect:** 0.0014

---

**Monoisotopic mass of neutral peptide Mr(cals):** 2210.0026

**Fixed modifications:** Met(C) (apply to specified residues or termini only)

**Variable modifications:**

- **K8** : m/z 0.02 (K), with neutral loss 43.0148

**Ion Score:** 97

**Expect:** 0.0014

**Matches:** 35/3529 fragment ions using 33 most intense peaks

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MS/MS Fragmentation of GALQHAKAFLK
Found in Q8VCN5, Cystathionine gamma-lyase OS=Mus musculus GN=Cth PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(m/z): 1288.6897
Fixed modifications: MGST (C) (apply to specified residues or termini only)
Variable modifications:

Ion Score: 96 Expect: 0.0026
Matches: 14/74 fragment ions using 19 most intense peaks

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MS/MS Fragmentation of TKLLEAAITPQTK

Found in Q8VNC5, Cystathionine gamma-lyase OS=Mus musculus GN=Cth PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point.
Or, Plot from 200 to 1400 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide M (calc.): 1669.3214
Fixed modifications: Met (C) (apply to specified residues or termini only)
Variable modifications:
K2 : m/z 1621.5909 (P), with neutral loss 43.0068
Ion Score: 47 Expect: 0.00028
Matches : 8/140 fragment ions using 11 most intense peaks (help)

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**MS/MS Fragmentation of LVLWDINKR**

Found in **Q8YCR2**, 17-beta-hydroxysteroid dehydrogenase 13 OS=Mus musculus GN=Hsd17b13 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1200 Da  [Full range]

Label all possible matches  Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1241.6788

**Fixed modifications:** MMIS (C) (apply to specified residues or termini only)

**Variable modifications:**

- R: mat_C02 (R), with neutral loss 43.0088

**Ions Score:** 27  **Expect:** 0.011

**Matches:** 6/68 fragment ions using 11 most intense peaks  (help)

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MS/MS Fragmentation of QFKTQQYYDILK
Found in Q8WCX8, Acyl-CoA synthetase family member 2, mitochondrial OS=Mus musculus GN=Acsf2 PE=2 SV=1

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Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ○

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Fixed modifications: MET( Hex ) (apply to specified residues or terminus only)
Variable modifications: K3 : Me CO2 (K), with neutral loss 42.0106
Ions Score: 85 Expect: 0.0011
Matches : 9/130 Fragment ions using 12 most intense peaks (help)
VVLITSGGTKVPLEAR

MS/MS Fragmentation of VVLITSGGTKVPLEAR
Found in QV6DG5. Phosphopantothenate--cysteine ligase Os--Mus musculus GN=Ppcos PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from to 1000 Da Full range

Label all possible matches 5 Label matches used for scoring 4

Monoisotopic mass of neutral peptide M(m/z): 1724.6473
Fixed modifications: HEM (C) apply to specified residues or terminal only
Variable modifications:
K66: m/z 0,023 (K), with neutral loss 43.0168
Ions Searched: 50 Expect: 0.0019
Matches: 48/166 fragment ions using 118 most intense peaks

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MS/MS Fragmentation of EIQNLIKASAPESGLLSK

Found in Q91V64. Isocitrate lyase domain-containing protein 1 Os=Mus musculus ON=iso1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or: Plot from 300 to 1800 Da
Label all possible matches ○ Label matches used for scoring ■

Phenolcotropic mass of neutral peptide Mr(m/z): 1692.5298
Fixed modifications: METS (C) (apply to specified residues or term only)
Variable modifications:
K : m1, m2, m3 (K), with neutral loss 43.0269
Ions Score: 17 Export: 0.627
Matches: 10/126 fragment ions using 15 most intense peaks (da)

| # | b | b' | b'' | b''' | w0 | w0'' | Seq | y | y'' | y''' | y* | y''* | y'''* | y0 | y0'' | y0''' | y0* | y0''* | y0'''* | # |
| 1 | 1 | 130.4399 | 62.5286 | 112.0393 | 56.5233 | E | 1811.0273 | 906.0173 | 1794.0007 | 897.5040 | 1793.0167 | 897.0192 | 18 |
| 2 | 243.1339 | 122.0706 | 225.1224 | 113.0653 | I | 353.3192 | 175.1596 | 353.3192 | 175.1596 | 353.3192 | 175.1596 | 18 |
| 3 | 371.1925 | 186.0998 | 354.1600 | 177.5685 | Q | 1679.9432 | 849.4775 | 1680.9167 | 849.9620 | 1679.9237 | 840.4700 | 18 |
| 4 | 485.2354 | 243.1214 | 468.2089 | 234.6081 | G | 676.9237 | 343.4618 | 676.9237 | 343.4618 | 676.9237 | 343.4618 | 18 |
| 5 | 596.3195 | 299.0664 | 581.2950 | 291.1501 | L | 1435.8417 | 728.4295 | 1438.8122 | 729.1912 | 1437.3112 | 719.1022 | 14 |
| 6 | 711.4036 | 356.2024 | 694.3770 | 347.6221 | I | 1342.7277 | 671.3683 | 1353.7311 | 665.3692 | 1324.7741 | 662.8772 | 13 |
| 7 | 881.5010 | 441.2582 | 844.4825 | 432.7449 | A | 1039.5681 | 530.2877 | 1042.5413 | 521.7744 | 1041.3577 | 521.2824 | 12 |
| 8 | 952.5462 | 476.7767 | 933.5197 | 468.2633 | A | 988.3130 | 494.7691 | 971.3044 | 485.2558 | 970.5204 | 485.6763 | 10 |
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| 10 | 1093.6388 | 553.8118 | 1093.6388 | 547.2980 | 1092.6068 | 546.8060 | A | 901.0899 | 451.2331 | 884.7472 | 442.7998 | 838.4884 | 442.2478 | 8 |
| 12 | 1336.7167 | 668.8590 | 1319.6842 | 660.3457 | 1318.7001 | 659.8537 | E | 733.4090 | 367.2062 | 716.3825 | 358.6494 | 715.3985 | 358.2029 | 7 |
| 13 | 1423.7472 | 712.3750 | 1406.7162 | 709.8167 | G | 804.3685 | 392.6869 | 787.3994 | 392.1736 | 786.3599 | 393.6816 | 6 |
| 14 | 1480.7640 | 740.8857 | 1463.7377 | 732.3725 | G | 517.3344 | 259.1708 | 500.3079 | 250.6576 | 499.3290 | 250.1656 | 5 |
| 15 | 1593.8485 | 797.4278 | 1576.8217 | 788.9145 | L | 480.3140 | 230.6061 | 443.2884 | 222.1468 | 442.3024 | 221.6548 | 4 |
| 17 | 1799.9644 | 897.4838 | 1786.9276 | 888.9725 | S | 234.1448 | 117.5761 | 217.1183 | 109.6628 | 216.1345 | 108.3702 | 2 |
| 18 | K | 147.1128 | 74.0600 | 140.0083 | 65.5468 | 1 |
**MS/MS Fragmentation of VKAHIMPAEFSSCPLNSDEAVNK**

Found in Q8Y7Y6, Rasm. homolog GenBank accession P9m21 TVal

Click mouse within plot area to zoom in by factor of two about that point

**Variable modifications:**
- K: oxidation (15.204 Da), with neutral loss 32.013

### Tandem Mass Spectrometry Data

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**Monoisotopic mass of neutral peptide Mr(calc):** 2614.8185
**Exact mass:** 2614.8185
**Charge:** 1

**Matches:** 29/572 fragment ions using 55 most intense peaks

**Tolerance:** 5.0000 ppm
DNPKVVHAFDMEDLGDK
DNPKVVHAFDMEDLGDK

MS/MS Fragmentation of DNPKVVHAFDMEDLGDK
Found in Q91W80, CDGSH iron-sulfur domain-containing protein 1 (O. sativa, Mus musculus, GN=Cld1, PE=1, SV=1)
Click mouse within plot area to zoom in or by factor of two about that point.
Or, Plot from 300 to 1500 Da Full range
Label all possible matches * Label matches used for scoring *

Monoisotopic mass of neutral peptide Mr(calc): 2014.59446
Fixed modifications: MMTS (C) (apply to specified residues or terminal only)
Variable modifications:
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Ion type: b + y
Matches: 8/155 fragment ions using 51 most intense peaks (100.0M)

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Found in Q91X83, S-adenosylmethionine synthase isoform type-1, OS=Mus musculus, GN=Mat1a, PE=2, SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide MW(calc): 1347.7264
Fixed modifications: 555S (C) (apply to specified residues or termini only)
Variable modifications:
K4 : methionine oxidation (M), with neutral loss 41.0107
Ions Score: 51 Expect: 0.0005
Matches : 56/156 fragment ions using 97 most intense peaks  (help)

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**MS/MS Fragmentation of KPIYQKTACYGHFGR**

Found in Q91X33, S-adenosylmethionine synthase isoform type-1 OS=Mus musculus GN=Mad1a PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

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MS/MS Fragmentation of **EVLEYNALGGGKYNR**

Found in Q98F5, Farnesyl pyrophosphate synthase Os=Mus musculus GN=Fedps PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point

![Plot of EVLEYNALGGGKYNR fragmentation](image)

**Morol toxicopeptide**

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MS/MS Fragmentation of NKLQQLPADFGR
Found in Q92Q8, Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=2 SV=1

Monoisotopic mass of neutral peptide M[calc]: 1471.7419
Fixed modifications: HET8 (C) (apply to specified residues or termini only)
Variable modifications:
K2 : [mal CO2 (K), with neutral loss 43.0408]
Scores:
Match Score: 49 Expect: 0.0014

NKLQQLPADFGR

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MS/MS Fragmentation of VAGDCLDEKQCK
Found in Q921Q6, Leucine-rich repeat-containing protein 19 OS=Mus musculus GN=Lrrc39 PE=6 SV=1

Click mouse within plot area to zoom in by factor of two about that point.
Or, Enter start to 1400 Dq Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1485.98089
Fixed modifications: M+H (C) (apply to specified residue or termini only)
Variable modifications:
K9 : ma1:C02 (E), with neutral loss 48.0086
Ions Score: 58 Expect: 4e-005
Matches : 12/120 fragment ions using 12 most intense peaks

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MS/MS Fragmentation of AAQTSDESEKIHLDKEK
Found in Q60992, Transaldolase O5-Mus musculus ON-Taldo1 PE-1 SV-2

Click mouse within plot area to zoom in by factor of two about that point:

Or, [ Zoom in ] 200 to 1600 Da [ Zoom out ]
Label all possible matches [ ] Label matches used for scoring [ ]

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MS/MS Fragmentation of VGDLSKPQEEALAK
Found in Q90708, SEC14-like protein 2 OS=Mus musculus GN=Sec14L2 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or. (Plot from) 200 to 1400 Da (Full range)
Label all possible matches ○ Label matches used for scoring ○

VGDLSPKQEEALAK

Monoisotopic mass of neutral peptide Mr(mole): 1566.7888
Fixed modifications: MetO (C) (apply to specified residues or termini only)
Variable modifications:
K' : +15.9949, with neutral loss 41.0558
Ions Score: 31 Expect: 0.013
Matches: 20/102 fragment ions using 36 most intense peaks (hnspx)

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MS/MS Fragmentation of WIKQYTGVNAISK
Found in Q9HJS9, Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ☐ Label matches used for scoring ☐

Monoisotopic mass of neutral peptide M(n,m) = 1862.8128
Fixed modifications: MTEF (C) (apply to specified residues or termini only)
Variable modifications:
K : m/z CO2 (M), with neutral loss 48.0890
Ion Score: 24 Expect: 0.017
Matches: 25/129 fragment ions using 97 most intense peaks (help)

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WIKQYTGVNAISK
MS/MS Fragmentation of **IFYTTTPVKK**

**Found in Q9KR3.** Beta-lactamase-like protein 2 OS=Mus musculus GN=Lactb2 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

Label all possible matches Label matches used for scoring

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Monoisotopic mass of neutral peptide Mr(calc): 1292.6809

Fixed modifications: MMTS (C) (apply to specified residues or termini only)

Variable modifications:

KLQ : mez_CO2 (K), with neutral loss 49.9090

Ions Score: 27 Expect: 0.012

Matches : 6/78 fragment ions using 11 most intense peaks (help)
VAPMKGQVCVVTGASR

MS/MS Fragmentation of VAPMKGQVCVVTGASR
Found in Q9L04. Dehydrogenase-reductase SDR family member 1
OS=Mus musculus GN=Dhrs1 PE=2 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da

VAPMKGQVCVVTGASR

Monoisotopic mass of neutral peptide Mr(calc): 1765.3203
Fixed modifications:  NMTS (C) (apply to specified residues or termini only)
Variable modifications:
K6 : m1_D2O (K), with neutral loss 42.0686
 Ion Score: 31 Expect: 0.00018
Matches: 21/148 fragment ions using 40 most intense peaks  

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VAPMKGQVCVVTGASR
MS/MS Fragmentation of RFEELGVKFVK
Found in Q8CPU0, Lectolyzathiokina lyase OS=Mus musculus GN=Glom PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da  [Full range]
Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide M (amu): 1636.7664
Fixed modifications: MGST3 (C) (apply to specified residues or termini only)
Variable modifications:
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Ions Score: 21  Expect: 0.001
Matches: 28/100 fragment ions using 92 most intense peaks

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**MG/MS Fragmentation of GFGHIGIAVPDVYSACKR**

*Found in 09CP100, Lactobacillus strains OseMin and Gm1 PE=1 SV=5*

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da Full range

Label all possible matches ✓ Label matches used for scoring □

**Monoisotopic mass of neutral peptide (Mr):** 3930.9499

**Fixed modifications:** MTG (C) (apply to specified residues or terminal only)

**Variable modifications:**
- M7 : m/z 0.02 (C), with neutral loss 41.0388

**Ions Score:** 15 **Expect:** 0.15

**Matches:** 27/144 fragment ions using 44 most intense peaks

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MS/MS Fragmentation of **FEELGVKFVK**

Found in **Q9CPU0**, Lactoylglutathione lyase OS=Mus musculus GN=Gl01 PE=1 SV=3

Click mouse within plot area to zoom in by factor of two about that point

Plot from 100 to 1300 Da

Label all possible matches □ Label matches used for scoring □

**Monoisotopic mass of neutral peptide Mr(calc): 1290.6669**

**Fixed modifications: MMTS (C) (apply to specified residues or termini only)**

**Variable modifications:**

K7 : mal-COO (K), with neutral loss 43.0090

**Ions Score: 25 Expect: 0.002**

**Matches : 21/20 fragment ions using 72 most intense peaks (hinge)**

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MS/MS Fragmentation of FAEIIEKNLK

Found in QCPY7, Cytosol aminopeptidase. OS=Mus musculus. GN=Lap3. PE=1. SV=3.

Click mouse within plot area to zoom in by factor of two about that point.

Or, Ret from: 0 to 1200 Da. Full range.

Label all possible matches. Label matches used for scoring.

Monoisotopic mass of neutral peptide Mr(calc): 1289.6887
Fixed modifications: NMTS (C) (apply to specified residues or termini only)
Variable modifications:
K7: m+1 CO2 (K), with neutral loss 43.0107
Charge state: 3+
Ion Score: 83. Expected: 0.0027
Matches: 16/84 fragment ions using 32 most intense peaks.

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MS/MS Fragmentation of IAGQVAAANKK
Found in Q9CYX8, 4OS ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=3
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1166.6249
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K10 : mal-CO2 (K), with neutral loss 62.01528
Ions Score: 52 Expect: 0.00011
Matches : 19/74 fragment ions using 20 most intense peaks  

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MS/MS Fragmentation of TQAYPDQKPGTSGLR
Found in Q9D0F9, Phosphoglucomutases-1
OS=Mus musculus GN=Pgm1 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from: 200 to 1700 Da Full range
Label all possible matches Label matches used for scoring

Mannitol enriched mass of neutral peptide Mv(valine): 1702.8115
Fixed modifications: MOW (C) (apply to specified residues or termini only)
Variable modifications: K8 = ma_con (X), with neutral loss 42.0093
Ions Score: 64 Expect: 4e-008
Matches: 46/160 fragment ions using 14 most intense peaks (help)

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MS/MS Fragmentation of **STHDYW KALVTK**

Found in Q9DR819, Inorganic pyrophosphatase OS=Mus musculus GN=Pppl PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

Or, Plot from ___ to ___ Da Full range

Label all possible matches ☐ Label matches used for scoring ☑

---

**Monoisotopic mass of neutral peptide Mr(calc): 1529.7464**

**Fixed modifications: **MTB (C) (apply to specified residues or termini only)

**Variable modifications: **

R7 : +57.0215 Da, with neutral loss 43.0269

**Ions Score: 21 Expect: 0.041**

Matches : 21/110 fragment ions using 60 most intense peaks (base)

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MS/MS Fragmentation of VPDGKPENEFAFNAEFK
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Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(m/z) : 2222.9142
Fixed modifications: MAS (C) (apply to specified residues or termini only)
Variable modifications:
K8 : m/z 145.099 (N), with neutral loss 44.0505
Ion Score: 26 ExpMass: 0.0001
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MS/MS Fragmentation of YKVPDGKPENEFAFNAEFK
Found in Q98619. Inorganic pyrophosphatase OS=Mus musculus GN=Ppal PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches Label matches used for scoring

Neoclistropic mass of neutral peptide M(m/e): 2116.0716
Fixed modifications: MET2 (C) (apply to specified residues or termini only)
Variable modifications:
PT Term(D96) (N), with neutral loss 46.015
Ion Source: ES Mass Spec: Q-TOF 1.0.2013
Matches : 28/292 fragment ions using 54 most intense peaks (HPLC)

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PLISVYSEKGESSGK
MS/MS Fragmentation of KNPDSQYGELIEK

Found in Q9DBP5, UMP-CMP kinase OS=Mus musculus GN=Cmpk1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot zoom: 200 to 1500 Da

Monoisotopic mass of neutral peptide Mr(calc): 1665.7822
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
K: csi-Cys (K), with neutral loss 42.0189

Matches: 44/136 fragment ions using 105 most intense peaks (Help)
MS/MS Fragmentation of VVGAQSLKDMVSK
Found in Q9DC00, 6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=2 SV=3

Click mouse within plot area to zoom in by factor of two about that point
Or, Flat from 200 to 1400 Da
Label all possible matches ○ Label matches used for scoring @

Monoisotopic mass of neutral peptide M(calc): 1666.7248
Fixed modifications: MTW8 (C) (apply to specified residues or termini only)
Variable modifications:
K8 : mal-COOH (K), with neutral loss 48.0898

Tons Score: 41 Expect: 0.0006
Matches : 12/124 fragment ions using 22 most intense peaks (99.9999)

| # | b   | b'' | b^a | b''^a | b^b | b''^b | Seq | y   | y'' | y^a | y''^a | y^b | y''^b | y^c | y''^c | y^d | y''^d | y^e | y''^e | y^f | y''^f | y^g | y''^g |
|---|-----|-----|-----|-------|-----|-------|-----|-----|-----|-----|-------|-----|-------|-----|-------|-----|-------|-----|-------|-----|-------|-----|-------|-----|-------|
| 1 | 100.0737 |     |     |       | V   |       |     | V   |     |     |       |     |       |     |       |     |       |     |       |     |       |     |       |
| 2 | 199.1441 | 100.0757 |     |       | V   | 1304.6879 | 652.8476 | 1287.6613 | 644.3243 | 1286.6773 | 642.8422 | 12 |
| 3 | 256.1656 | 128.5846 |     |       | G   | 1205.6195 | 603.3134 | 1188.3929 | 594.8001 | 1187.6089 | 594.3081 | 11 |
| 4 | 327.2027 | 164.1050 |     |       | A   | 1148.5980 | 574.8026 | 1131.5714 | 566.2894 | 1130.5874 | 565.7973 | 10 |
| 5 | 452.2613 | 228.1346 | 438.2347 | 219.6210 | Q   | 1077.5609 | 539.2841 | 1069.5343 | 530.7708 | 1059.5303 | 530.2788 | 9 |
| 6 | 542.2933 | 271.6303 | 525.2667 | 263.1370 | 524.2827 | 262.6430 | S   | 949.5023 | 475.2548 | 932.4757 | 466.7415 | 931.4817 | 466.2495 | 8 |
| 7 | 655.3774 | 328.1923 | 638.3508 | 319.6790 | 637.3688 | 319.1870 | L   | 862.4703 | 431.7388 | 845.4437 | 423.2225 | 844.4597 | 422.7335 | 7 |
| 8 | 825.4203 | 413.2421 | 808.4563 | 404.7318 | 807.4723 | 404.2398 | K   | 749.3862 | 375.1967 | 732.3597 | 366.8833 | 731.3756 | 366.1915 | 6 |
| 10 | 1071.5385 | 536.2788 | 1054.5238 | 527.7055 | 1053.5397 | 527.2372 | M   | 464.2537 | 236.6203 | 447.2272 | 224.1172 | 446.2432 | 223.6232 | 4 |
| 12 | 1257.6508 | 629.5290 | 1240.6242 | 620.8157 | 1239.6402 | 620.3357 | S   | 234.4148 | 117.7561 | 217.1183 | 109.0628 | 216.1343 | 108.5708 | 2 |
| 13 | 147.1128 | 74.0600 | 139.0863 | 65.5468 | K   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
MS/MS Fragmentation of KVLQEVQR
Found in Q9DD20. Methyltransferase-like protein 7B OS=Mus musculus GN=Mett7b PE=2 SV=2

Click mouse within plot area to zoom in by factor of two about that point

Monoisotopic mass of neutral peptide Mr(calc): 1084.5377
Fixed modifications: MetC(57) (apply to specified residues or termini only)
Variable modifications:
K1: mal-CO2 (K), with neutral loss 43.0098

Matches: 20/70 fragment ions using 52 most intense peaks

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MS/MS Fragmentation of **TQQHYYDKCPK**

Found in Q9ET01, Glycogen phosphorylase, liver form OS=Mus musculus GN=Pygl PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range.
Label all possible matches ✅ Label matches used for scoring ✅

Monoisotopic mass of neutral peptide Mr(calc): 1241.6479
Fixed modifications: Met(S) (C) (apply to specified residues or termini only)
Variable modifications:
X0: nitrilotriacetic acid (K), with neutral loss 92.0106
Ion Score: 20 Expected: 0.004
Matches : 18/110 fragment ions using 82 most intense peaks (help)

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| 2 | 230.1135 | 115.5504 | 213.0870 | 107.0471 | 212.1030 | 106.5531 | Q | 1397.5977 | 699.3023 | 1380.5711 | 690.7892 | 1379.5871 | 690.2972 | 10
| 3 | 358.1721 | 179.5397 | 341.1456 | 171.0764 | 340.1615 | 170.5844 | Q | 1269.5291 | 635.2732 | 1232.5125 | 626.7359 | 1231.5285 | 626.2679 | 9
| 4 | 495.2310 | 248.1151 | 478.2045 | 239.6059 | 477.2205 | 239.1139 | H | 1141.4865 | 571.2459 | 1124.4540 | 562.7206 | 1123.4699 | 562.2386 | 8
| 6 | 821.3577 | 411.1825 | 804.3311 | 402.6692 | 803.3471 | 402.1772 | Y | 841.5853 | 421.1828 | 824.3317 | 412.6693 | 823.3477 | 412.1773 | 6
| 7 | 956.3846 | 468.6960 | 939.3581 | 460.1827 | 918.3741 | 459.6907 | D | 678.2949 | 339.6511 | 661.2684 | 331.1378 | 660.2844 | 330.6458 | 5
| 8 | 1106.4902 | 553.7487 | 1089.4636 | 545.2354 | 1088.4796 | 544.7424 | K | 563.2689 | 282.1376 | 546.2415 | 273.6244 | 4
| 9 | 1225.4871 | 628.2472 | 1208.4602 | 619.7339 | 1207.4762 | 619.2419 | C | 393.1625 | 197.0349 | 376.1239 | 188.2716 | 3
| 10 | 1352.5388 | 676.7735 | 1335.5133 | 668.2603 | 1334.5293 | 667.7683 | P | 244.1656 | 122.5864 | 227.1390 | 114.0731 | 2
| 11 | 1471.1128 | 74.0600 | 1390.0863 | 65.5468 | 1 |
MS/MS Fragmentation of GIVGVENVAELKK
Found in QET01, Glycogen phosphorylase, liver form OS=Mus musculus GN=Pygl PE=1 SV=4

Click mouse within plot area to zoom in by factor of two about that point
On/Plot from 200 to 1400 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mz (Dal): 1440.7024
Fixed modifications: MBD5 (C) (apply to specified residues or termini only)
Variable modifications:
K12 : N-ace_COOH (E), with neutral loss 44.0005
Ions Search: 29 Peptid: 0.0525
Matches : 28/116 fragment ions using 46 most intense peaks (best)

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GIVGVENVAELKK
MS/MS Fragmentation of AVEKAAAHGSKPNVYATR

Found in Q9JLF6. Protein-glutamine gamma-glutamyltransferase K OS=Mus musculus GN=Tgm1 PE=1 SV=2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da. Full range
Label all possible matches. Label matches used for scoring.

Fixed modifications: C (C) (apply to specified residues or termini only)
Variable modifications: K: [mal] C (H) with neutral loss 43.0109

Matches: 17/178 [Sequence ions using 26 most intense peaks]

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MS/MS Fragmentation of KTQEILSQLPFK
Found in O9OUH0. Ch: Torpedo O:18 Mus musculus GN: Glu PE:1 SV:3
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(mole): 5518.8127
Fixed modifications: MMTS (C) (apply to specified residues or termini only)
Variable modifications:
KL : m1_f12 (R), with neutral loss 48.0195
Matches : 12/120 fragment ions using 40 most intense peaks (help)

| # | b   | b'' | b' | b++ | b++ | Seq. | y   | y'' | y' | y'++ | y'' | #
|---|-----|-----|----|-----|-----|------|-----|-----|----|------|-----|---
| 1 | 171.1128 | 86.0600 | 154.0863 | 77.5468 | K | 1302.7256 | 652.3665 | 1286.6991 | 643.8332 | 1285.7151 | 643.8362 |
| 2 | 272.1605 | 136.3839 | 255.1339 | 128.0706 | 254.1469 | 127.3786 | T | 1302.7256 | 652.3665 | 1286.6991 | 643.8332 | 1285.7151 | 643.8362 |
| 3 | 400.2191 | 200.6132 | 383.1925 | 192.0999 | 382.2083 | 191.4079 | Q | 1302.6780 | 601.8426 | 1183.6514 | 503.3293 | 1184.6674 | 502.8373 |
| 4 | 529.2617 | 265.1345 | 512.2351 | 256.6212 | 511.2511 | 255.1282 | E | 1047.6194 | 537.8133 | 1057.5928 | 529.3001 | 1056.6085 | 528.8083 |
| 5 | 642.3457 | 321.0676 | 625.3192 | 313.1632 | 624.3332 | 312.6712 | I | 945.5768 | 473.2920 | 928.2390 | 464.7788 | 927.5662 | 464.2867 |
| 6 | 755.4298 | 378.2183 | 738.4032 | 369.7053 | 737.4192 | 369.2132 | L | 832.4927 | 416.7300 | 815.4662 | 408.2367 | 814.4282 | 407.7447 |
| 7 | 842.4618 | 421.7343 | 825.4353 | 413.2212 | 824.4512 | 412.7203 | S | 719.4087 | 360.2080 | 702.3281 | 351.6947 | 701.3981 | 351.2027 |
| 8 | 970.5204 | 485.7618 | 953.4938 | 477.2506 | 952.5098 | 476.7582 | Q | 612.3786 | 316.6920 | 613.3501 | 308.1787 | 613.3501 | 308.1787 |
| 9 | 1083.6048 | 542.3059 | 1066.5779 | 533.7926 | 1055.5939 | 533.3006 | L | 504.3150 | 252.6627 | 487.2915 | 244.1494 | 252.6627 | 487.2915 |
| 10 | 1180.6572 | 590.8222 | 1163.6307 | 582.3190 | 1162.6467 | 581.8270 | P | 391.2240 | 196.1206 | 374.2074 | 187.6074 | 196.1206 | 374.2074 |
| 11 | 1327.7256 | 664.3663 | 1310.6991 | 655.8522 | 1309.7151 | 655.3612 | F | 294.1812 | 147.5942 | 277.1547 | 139.0810 | 147.5942 | 277.1547 |
| 12 | 147.1128 | 74.0600 | 130.0868 | 65.5468 | F | 294.1812 | 147.5942 | 277.1547 | 139.0810 | 147.5942 | 277.1547 | 139.0810 | 147.5942 | 277.1547 |
MS/MS Fragmentation of TGKVSAIDFR
Found in Q9QXX4, Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ☐ Label matches used for scoring ☐

Monoisotopic mass of neutral peptide Mw(mono): 1178.6002
Fixed modifications: NMTG (C) [apply to specified residues or termini only]
Variable modifications:
K3: m+1_C02 (R), with neutral loss 43.0030
Ions Score: 62 Expect: 4.5e-008
Matches: 18/100 fragment ions using 20 most intense peaks (help)

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MS/MS Fragmentation of LNLYELKEGR
Found in Q8R1P1. Proteasome subunit beta-type-3 OS=Mus musculus GN=Psb3 PE=1 SV=1
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da
Label all possible matches ○ Label matches used for scoring ○

Monoisotopic mass of neutral peptide Mr(calc): 1329.6721
Fixed modifications: iodoacetamide (C) (apply to specified residues or termini only)
Variable modifications:
K7 : mal-CO2 (K), with neutral loss 43.0595
Lons Score: 98 Expect: 0.00072
Matches: 10/94 fragment ions using 31 most intense peaks (help)

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### MS/MS Fragmentation of **SLQKVTTAAK**

Found in **Q9W688**, Peroxinsomal 2,4-dienoyl-CoA reductase OS=Mus musculus GN=Dec2 PE=1 SV=1

Clic mouse within plot area to zoom in by factor of two about that point

Or, Plot from [ ] to [900] Da [ ] Full range

Label all possible matches [ ] Label matches used for scoring [ ]

---

**Monoisotopic mass of neutral peptide Mr(calc): 1131.6135**

**Fixed modifications:** Met8 (C) (apply to specified residues or termini only)

**Variable modifications:**

- K4: mal-COOH (K), with neutral loss 42.0000

**Ions Score:** 22  Exponent: 0.068

**Matches:** 7/98 fragment ions using 0 most intense peaks [help]

| # | b   | b++ | b+ | b+++ | b0  | b00 | Seq. | y   | y++ | y+  | y+++ | y0  | y00 |
|---|-----|-----|----|------|-----|-----|------|-----|-----|-----|------|-----|-----|------|
| 1 | 88.0393 | 44.5233 | 70.0287 | 35.5180 | S   | 1001.5990 | 501.3031 | 984.5724 | 492.7899 | 982.5384 | 492.2978 |
| 2 | 201.1234 | 101.0653 | 183.1128 | 92.0600 | L   | 329.1819 | 165.0946 | 312.1354 | 156.5813 | 311.1714 | 156.0893 |
| 3 | 495.2875 | 250.1474 | 482.2609 | 241.6341 | Q   | 760.4563 | 380.7318 | 743.4298 | 372.2185 | 742.4458 | 371.7285 |
| 4 | 598.3559 | 299.6816 | 581.3293 | 291.1683 | V   | 596.3508 | 295.6790 | 573.3243 | 287.1658 | 572.3402 | 286.6738 |
| 5 | 699.4036 | 350.2054 | 682.3770 | 341.6921 | T   | 491.3282 | 246.1448 | 474.2558 | 237.6316 | 473.2718 | 237.1396 |
| 6 | 780.4512 | 400.7299 | 763.4247 | 392.2160 | T   | 390.3347 | 195.6210 | 373.2082 | 187.1077 | 372.2241 | 186.6157 |
| 7 | 871.4884 | 436.2478 | 854.4181 | 427.7345 | A   | 289.1870 | 145.0972 | 272.1603 | 156.3839 | 288.2197 |
| 8 | 942.5255 | 471.7664 | 925.4989 | 463.2531 | A   | 218.1199 | 109.5786 | 201.1234 | 101.0653 | 218.1199 |
| 9 | 147.1128 | 74.0600 | 120.0863 | 65.5468 | K   | 147.1128 | 74.0600 | 120.0863 | 65.5468 | 147.1128 |

---

**Note:** The table above shows the fragment ions for the peptide **SLQKVTTAAK**, including b-, b++, b+, b+++ ions, and y-, y++, y+, y+++ ions. The ions are scored based on their mass-to-charge ratio (m/z) and the sequence coverage. The modifications include a fixed modification at Met8 (C) and a variable modification at K4: mal-COOH (K), with a neutral loss of 42.0000 Da.
**MS/MS Fragmentation of FKVDLSYPYTISHINK**

Found in Q9VW10. Maleylacetoacetate isomerase OS=Mus musculus GN=Gstz1 PE=1 SV=1

Click mouse within plot area to zoom in by factor of two about that point.

Label all possible matches Label matches used for scoring

---

**Monoisotopic mass of neutral peptide Mr(m/z):** 1982.0003

**Fixed modifications:** M(15) C (apply to specified residues or termini only)

**Variable modifications:**

E2  n-hex-2-ene (E), with neutral loss 44.0095

**Ions Scored:** 68 **Expect:** 4.8e-005

**Matches:** 42/164 fragment ions using 92 most intense peaks

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